University of Pennsylvania, CIS502

Analysis of Algorithms

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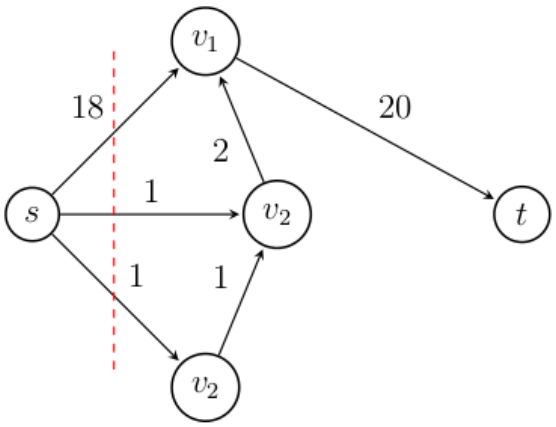

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1 Lecture

1.1 Introduction

Algorithms are used to solve computational problems. But what is really a computational problem?

Definition 1. *A computational problem is a problem that takes any set of inputs and for each input it has a well defined output.*

An example of a computational problem that we're all familiar with is sorting. The input is a list of numbers and the output is a permutation of this list with the numbers in sorted orders.

More generally, we can take as input a string of bits and deliver as an output a string of bits, so we can think of a computational problem as a function $f : \{0,1\}^* \to \{0,1\}^*$. Note that each computational problem has a specification of what a correct output looks like, and while we can write this specification using formal methods, we won't get caught up in formalities. f specifies what you want to compute, and an algorithm describes **how** you compute the function.

1.2 Running Times

Running times or number of steps for an algorithm will be a big theme in this course. For an algorithm that describes a computational problem π, we measure the running time as a function of the input's length. Running time will be a function $f(n)$. Note that this system allows us to cheat, as we can take an input of length n, add junk to it so that it's much larger in length, and then solve the problem in reasonable time, making it look like our algorithm was very fast. To solve this, we will only allow reasonable input encodings.

For instance, consider the problem of factoring n. A simple algorithm will go through the number 1 to n to test if each number is a factor of n. This algorithm takes $O(n)$, right? Did we just solve cryptography? Not really, we cheated. We didn't specify how long n is. In fact, the input string is around $\log(n)$, and the problem runs in exponential time. The takeaway is that we should be careful when we specify the input size.

Another problem is that many inputs of size n might take a different time. For instance, in sorting, the input size is fixed but different inputs might make the sorting algorithm take longer. What we will consider in this course is worst-case input (see Definition 2).

Definition 2. *An algorithm runs in time $f(n)$ in inputs of length n if it runs in time $f(n)$ for **all** inputs of length n.*

We will also talk about upper and lower bounds in this course, which we will also consider on the worst-case input.

Definition 3. *A problem π has an upper bound of $O(f(n))$ if there **exists** an algorithm that solves all inputs of length n in time $f(n)$.*

Definition 4. *A problem π has a lower bound of $\Omega(g(n))$ if for all algorithms there exists an input for which the algorithm takes at least $g(n)$ time.*

You can see that proving a lower bound is much more difficult than proving an upper bound, as we have to reason about all possible algorithms.

We will also consider the number of steps that an algorithm takes, but to do so we need to introduce a model of computation.

Definition 5. *A model of computation is a list of primitive operations or steps and the cost of each.*

1.2.1 Comparison Tree Model

One example of a model of computation is the comparison tree model, in which the only primitive operation is a comparison, and it takes 1 step. Suppose we want to find the maximum of x_1, x_2 and x_3 and we are working in the comparison tree model. In Figure 1.1 we can see the number of comparisons we would need to find the maximum.

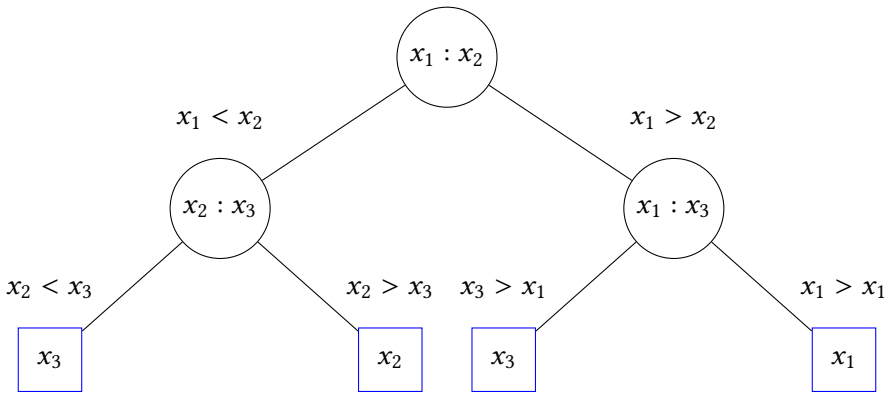

Figure 1.1: Finding the maximum under the tree comparison model, where each x_i is distinct.

In this scenario, the running time is equal to the height of the comparison tree, and answers correspond to leaves. If you have a comparison tree algorithm that takes h steps, how many answers can you have? Since it's a binary tree with height h, we have at most 2^h distinct answers.

Consider now the task of proving a lower bound for sorting under the comparison tree model. The input are numbers $x_1, x_2, \ldots, x_n$, and the number of possible answers (brush up on combinatorics) is $n!$. This implies that the comparison tree must have $n!$ leaves. Using our reasoning above, the number of comparisons to sort is at least

$$\log_2(n!) = \Omega(n \log(n)) \tag{1.1}$$

How did we conclude Equation 1.1? We use Sterling's approximation. We know $n! = n \cdot (n-1) \cdot \ldots \cdot 1$, and we also know $\log(n!) = \log(n \cdot (n-1) \cdot \ldots \cdot 1) = \sum_i^n \log(i)$ using logarithm properties. Now observe that for $i = \frac{n}{2}$, we have that $\log(\frac{n}{2}) = \log(n) - 1$, so for all numbers above i we get at least $\log(n) - 1$. Therefore $\sum_i^n \log(i) \geq \frac{n}{2}(\log(n) - 1) = \Omega(n \log(n))$. We have just proved that any sorting algorithm under the comparison tree model must perform at least $n \log(n)$ steps. This technique is called the information theoretic lower bound.

Consider another example under the comparison tree model, which is finding the median of $x_1, x_2, \ldots, x_n$. The number of possible answers is n because any solution must be some x_i, so with the above reasoning is the lower bound $\log(n)$? Indeed, *a* lower bound is $\log(n)$, but it's simply not that interesting. Can we do better? The key question to ask ourselves is when an algorithm knows that it has found the median. We know that half of the inputs must be smaller than the median, so the number of possible answers is the number of ways of choosing a median times the number of ways of choosing the half of inputs that are less than the median. There are n possibilities for the median and $\binom{n-1}{\frac{n-1}{2}}$ possibilities for the set of elements which are smaller than the median. So the information theoretic lower bound is $\log(n\binom{n-1}{\frac{n-1}{2}}) = \Omega(n)$.

1.2.2 Pancake Flipping Model

Consider a stack of pancakes, each having a burnt face and a regular face. In this model, there is only one operation which is to flip the stack of pancakes at position i with a cost of 1 step. For instance, if we denote 0 for a regular facing pancake and 1 for a burnt facing pancake, a possible stack would be 1011001, and if we flip it on top of the fourth pancake, the new configuration will be 1011011.

With this model, we ask ourselves: what is the lower bound and the upper bound to take a stack of pancakes and have them all facing regularly? A simple algorithm goes from right to left, flipping the stack whenever there is a disagreement (prove it using induction). This takes at most n steps, so we have an upper bound of n. As for the lower bound, we can also show that it is n. What we must do is find one input for which any algorithm, no matter how clever it is, must take n steps to beautify the stack. To do this we introduce potential functions.

Definition 6. *A potential function f is a function that needs to be changed from some initial value to some final value by an algorithm. If one can show that each step of the algorithm does not change the potential too much, we can get a lower bound on the number of steps.*

For this problem, we choose the potential function f = number of pairs of pancakes that are in disagreement. Any solution must have a potential of 0, and if we choose the input 01010…10101 of alternating pancakes, then the potential in the beginning is $n-1$. Any algorithm can decrease the potential at most 1 by inserting the spatula between two pancakes in disagreement, so therefore a lower bound if n steps.

2 Lecture

2.1 Potentials For Upper Bounds

Recall the pancake flipping problem. To show the lower bound, we constructed a potential function f and an input for which the potential was n. We also showed the potential at the solution is 0. We can also use potentials to prove upper bounds. To do this we need to show that every configuration has a potential bounded by Δ, and when we reach the solution we have a configuration with potential δ. We also need to show that every step of the algorithm reduces the potential **at least** x. If we can show this, we have shown that the algorithm has an upper bound of

$$\frac{\Delta - \delta}{x}$$

Consider once more the problem of finding the maximum of n elements in the comparison tree model, and consider the potential function f = number of elements that haven't been beaten yet in a comparison. In other words, f indicates the number of candidates for the maximum. Initially, $f = n$. When the algorithm concludes, $f = 1$. Furthermore, any good algorithm that compares only unbeaten elements will ensure that the potential decreases at least by 1. Using all of this, we have just shown an upper bound of n.

2.2 Adversary Method

One problem that we have with proving lower bounds is that different algorithms have different worst-cases. Thus we cannot set up one input and analyze all algorithms on this input and get a good lower bound. The two techniques we have discussed so far do not create bad inputs tailored to each algorithm to prove lower bounds. The adversary technique does. How can we demonstrate a worst-case input for each of a potentially infinite collection of algorithms?

The trick is to design a strategy for the adversary that fields questions made by any algorithm and answers these questions in such a way that the progress of the algorithm to the solution is slowed down as much as possible. A strategy for an adversary defines an answer for each possible question in each possible "state", where a state is the set of questions that have been asked and answers that have been given to these questions. Thus it can be seen that the adversary is adaptively creating a worst-case input for the algorithm. One constraint is that the adversary should give a consistent set of answers, i.e., it should be possible to create an input for which all of the adversary's answers are correct.

2.2.1 Edge Probe Model

Consider a graph $G = (V, E)$, and suppose we ask a question about the graph. In the edge probe model our primitive operation is to probe a pair of vertices (i, j) to learn if there is an edge connecting i and j or not. Each probe costs 1 step. Using the edge probe model, the adversary will answer the algorithm's probes, making sure to slow down the algorithm as much as possible. We can deduce that an immediate upper bound is $\binom{n}{2}$ on the number of probes required (probing every vertex against every vertex).

Is The Graph Connected?

In this problem, the adversary maintains the connected components of the graph created so far. For a query (i, j), the adversary answers yes if and only if the connection between i and j is the last possible connection between the component of i and the component of j.

2.2.2 Evasiveness

Definition 7. *A graph property that requires any algorithm to query all pairs in the edge probe model is called evasive.*

Definition 8. *(Informal) A property of a graph is monotone if the addition of more edges makes the property more true.*

This leads to the following conjecture.

Conjecture 1. *Every monotone graph property is evasive.*

We will now show informally that knowing if the graph is connected is an evasive property. We will need the following lemma.

Lemma 2.1. *Fix the above adversary strategy. For any algorithm A, at any stage, let C be a connected component that has been revealed by the probes that A has made. Then A must have probed every pair of distinct vertices in C.*

Theorem 2.1

Under the adversary strategy, any correct algorithm must perform $\binom{n}{2}$ queries to determine if a graph is connected.

Proof 2.1

(Informal) By induction. Suppose by induction we know C_1 and C_2 are connected components by probing every pair of vertices in C_1 and C_2 (using Lemma 2.1). When we connect C_1 and C_2 to form $C = C_1 \cup C_2$, since we are using the adversary method, all vertices between C_1 and C_2 have been probed, maintaining the inductive invariant. □

2.3 Divide and Conquer

This is a technique to solve problems. It consists of three steps.

- Divide: divides the problem into roughly equal-sized pieces.
- Conquer: solves each piece.
- Combine: combines the solutions to the pieces.

The classic problem to solve using divide and conquer is mergesort.

2.3.1 Mergesort

- Divide: trivial, split the array into two subarrays.
- Conquer: recurse.
- Combine: this is the merge algorithm. Given sorted arrays A and B, this algorithm merges A and B to give a sorted array C (see here for more info). The number of comparisons is $2n - 1$. What is the lower bound for this algorithm? Using the adversary strategy, the adversary will initially assume that $a_1 < b_1 < a_2 < b_2 \ldots$. The algorithm will proceed to compare adjacent elements, satisfying the adversary's plan. If at any point the algorithm tries to shortcut by comparing non-adjacent elements, the adversary can swap to slow down the algorithm. Therefore, the lower bound for this algorithm is again the number of adjacent comparisons which is $2n - 1$.

Let $T(n)$ be the number of comparisons performed by mergesort on an array of n elements. We know $T(1) = 0$. Then for a general n we have that

$$T(n) \leq 2T(\frac{n}{2}) + 2n$$

3 Lecture

3.1 Master Theorem

We now introduce the master theorem to solve recurrence relations.

Theorem 3.1: Master Theorem

Suppose $T(n) \leq aT(\frac{n}{b}) + n^c$, where a is the number of subproblems, each of size n/b.

- If $\frac{a}{b^c} < 1$, then $T(n) = O(n^c)$
- If $\frac{a}{b^c} = 1$, then $T(n) = O(\log_b(n) \cdot n^c)$
- If $\frac{a}{b^c} > 1$, then $T(n) = O(n^{\log_b(a)})$

We can picture the Master Theorem using a recursion tree as in Figure 3.1. The key intuition is that the number of leaves is $n^{\log_b(a)}$.

Going back to mergesort, we have that

$$T(n) \leq 2T(\frac{n}{2}) + kn$$

In this case we have that $a = 2$, $b = 2$, and $c = 1$. Using the Master Theorem (Theorem 3.1), we learn $T(n) = O(n \log(n))$.

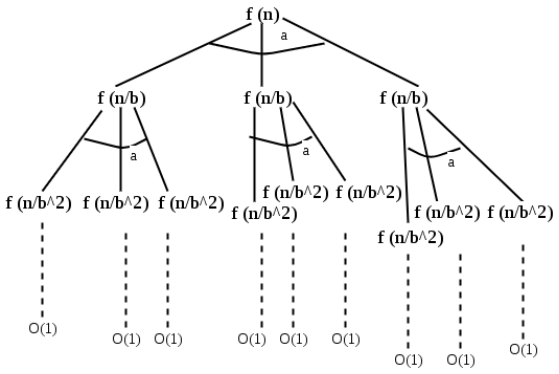

Figure 3.1: Recursion tree to visualize the master theorem

3.2 Quicksort

Another classic divide and conquer algorithm is quicksort. We have as input an array of n integers, and as output we have the integers in sorted order. The idea is to pick an element in the array to act as the pivot element x. By comparing each other element with the pivot, we create a partition with $S = \{y : y < x\}$ and $L = \{y : y > x\}$ and recursively quicksort S and L.

A minor problem with quicksort is that it has worst-case running time of $O(n^2)$ (consider when the input is already sorted). That is why we sometimes consider the average-case complexity. We won't consider average case complexity in this course, as we are pessimistic people.

There is a component of quicksort that is random (choosing the pivot). Therefore in general we need to talk about expected worst case behavior. In the algorithm, we pick the pivot uniformly at random from the elements to be sorted.

Let X be the total number of comparisons performed by quicksort. Since we have randomized the algorithm, X is a random variable. Let X_{ij} be the random variable that is 1 if the i-th smallest element and j-th smallest element are compared and 0 otherwise. How do we relate X to X_{ij}? Well, we have that

$$X = \sum_{i<j} X_{ij}$$

Since we are studying the expected worst case behavior, we need to analyze the expectation of X. By linearity of expectation, we have that

$$\begin{aligned}
E[X] &= E[\sum_{i<j} X_{ij}] && (3.1)\\
&= \sum_{i<j} E[X_{ij}] && (3.2)\\
&= \sum_{i<j} P(X_{ij} = 1) && (3.3)\\
&= \sum_{i<j} \frac{2}{j-i+1} && (3.4)\\
&= 2\sum_{d=1}^{n-1} \frac{n-d}{d+1}, \quad \text{where } d = j-i && (3.5)\\
&= 2n\sum_{d=1}^{n-1} \frac{1}{d+1} - 2\sum_{d=1}^{n-1} \frac{d}{d+1} && (3.6)\\
&\leq 2n\sum_{d=1}^{n-1} \frac{1}{d+1} && (3.7)\\
&\implies O(n\log(n)) && (3.8)
\end{aligned}$$

where (2.4) follows because there are $j - i + 1$ possibilities that will determine the values of X_{ij}, and only 2 compare i with j and (2.8) follows because (2.7) follows a harmonic series of order $\log(n)$.

3.3 Order Statistics

In order statistics we look at finding the r-th smallest element in an array. We immediately see a solution that takes $O(n \log(n))$ by first sorting the array and then choosing the r-th index. But can we do better?

Definition 9. *An element x in an array A has rank k if x is the k-th smallest element in A.*

3.3.1 Quick Select

As with quicksort, choose a random pivot and split the remaining elements into S and L. If $|S| \geq r$, then we simply recurse on S. If $|S| = r - 1$, then the pivot is the output. Finally, if $|S| = k < r - 1$, then we recurse in L but now we want to find the $k + 1$-th smallest element in L.

We will not do the expected worst case analysis, but one can show that it is $O(n)$.

3.3.2 Deterministic Linear Time Selection

Consider n elements.

1. Create $n/5$ groups of 5 elements each.
2. Find the median of each group (this can be done in 6 comparisons). We now have performed $6n/5$ comparisons or equivalently $1.2n$.
3. Recursively find the median $m*$ of the medians, which takes $T(5/n)$. We claim $m*$ has rank somewhere in the middle. More precisely, $3n/10$ are smaller than $m*$ and $3n/10$ are bigger, i.e., $0.3n \leq \text{rank}(m*) \leq 0.7n$.
4. Pivot using $m*$
5. Recurse with no more than $T(7n/10)$. The recurrence relation for this algorithm is

$$T(n) \leq T(\frac{n}{5}) + T(\frac{7n}{10}) + 2.2n$$

   which has solution $T(n) \leq n$ for $n \geq 22$.

Remark. *Honestly, I recommend looking at this resource for a better explanation.*

4 Lecture

4.1 More Divide and Conquer

4.1.1 Polynomial Multiplication

The problem we will solve will be to multiply two polynomials. Let $A = a_d x^d + a_{d-1}x^{d-1} + \ldots + a_1 x + a_0$, and let $B = b_d x^d + b_{d-1}x^{d-1} + \ldots + b_1 x + b_0$. In high school we would multiply A and B as $C = A \cdot B$ with

$$C = \underbrace{a_d b_d x^{2d} + a_d b_{d-1} x^{2d-1} + \ldots + a_d b_0 x^d}_{\text{first term in the product}} + \ldots$$

This technique has an upper bound of $O(n^2)$ however. We want to beat this algorithm using divide and conquer.

Remark. *One can use this technique to multiply integers. Just set $x = 10$ and let a_i be the i-th digit of the integer.*

First Attempt

Let's assume that the number of coefficients of the polynomials are a power of 2 (for simplicity). That means $d = 2^k - 1$. We split each polynomial in half so that each half has $\frac{d+1}{2}$ elements. For instance for A we have that $A'_h = a_d x^d + \ldots + a_{\frac{d+1}{2}} x^{\frac{d+1}{2}}$ and $A_l = a_{\frac{d-1}{2}} x^{\frac{d-1}{2}} + \ldots + a_1 x + a_0$. Now we have that $A = x^{\frac{d+1}{2}} A_h + A_l$ and similarly $B = x^{\frac{d+1}{2}} B_h + B_l$. We are now in a position to multiply

$$A \cdot B = (x^{\frac{d+1}{2}} A_h + A_l)(x^{\frac{d+1}{2}} B_h + B_l) \tag{4.1}$$

$$= A_h B_h + x^{\frac{d+1}{2}} (A_h B_l + A_l B_h) + A_l B_l \tag{4.2}$$

Let $T(n)$ be the time taken to multiply two polynomials with n coefficients. Then

$$T(n) \leq 4T(\frac{n}{2}) + cn \implies T(n) = O(n^2)$$

Unfortunately, this technique didn't save us time. But we can refine it in the following manner with a little trick. Notice that on (4.2) we want to multiply three products.

- A_hB_h: we have to multiply this no matter what.
- A_lB_l: same as above.
- $A_hB_l + A_lB_h$: this consists of two products which is what is making the above technique have a $O(n^2)$ upper bound. Can we somehow multiply only one product? Yes! Notice that

$$(A_h + A_l)(B_h + B_l) = \underbrace{A_hB_h}_{\text{what we have}} + \underbrace{A_hB_l + A_lB_h}_{\text{what we want}} + \underbrace{A_lB_l}_{\text{what we have}}$$

  So then

$$A_hB_l + A_lB_h = (A_h + A_l)(B_h + B_l) - A_hB_h - A_lB_l$$

  We've reduced the steps necessary as now we only need one multiplication instead of two to find $A_hB_l + A_lB_h$.

Using the above, we have that

$$T(n) \leq 3T(\frac{n}{2}) + kn$$

and using the Master Theorem with $a = 3$, $b = 2$ and $c = 1$ we learn that the upper bound is $O(n^{\log_2(3)}) \approx O(n^{1.6})$.

4.1.2 Convex Hulls on the Plane

Definition 10. *A set $S \subset \mathbb{R}^n$ is said to be convex if for all $x, y \in S$ the line segment joining x and y is contained in S.*

(a) Non convex set

(b) Convex set

Figure 4.1: Examples of convex sets

Definition 11. *Given two points $x = (x_1, x_2)$ and $y = (y_1, y_2)$, the convex combination of x and y is defined by*

$$\lambda x + (1 - \lambda)y$$

for some $\lambda \in [0, 1]$.

The convex combination is a way of finding all the points that are in the line segment of x and y.

Definition 12. *The convex hull of a finite set of points S is the set of all points that can be expressed as convex combinations of points in S.*

A more pictoral way of defining the convex hull is, given $S = \{x_1, ..., x_n\}$, to think of each x_i as a nail, and we take a rubber band that is originally stretched to infinity, and we let go of the rubber band. The final position of the rubber band is the convex hull.

Definition 13. *(Another definition of convex hull) The convex hull of a set of points is the smallest convex set that contains the points.*

Lemma 4.1. *A convex hull is a convex polygon (i.e. no interior angle is larger than π).*

4.1.3 Algorithms to Find the Convex Hull

Let $(x_1, y_1), ..., (x_n, y_n)$ be the inputs. The output for the algorithm will be the sequence of points in the boundary in counter clockwise order.

Naive Way

We first produce a simple test: Given a line by two points and a third point, determine which side of the line the third point lies on. We claim this is sufficient to find the convex hull.

To implement this test, suppose we have the line joining (x_1, y_1) and (x_2, y_2) and we consider a point (x_3, y_3). Which side is this point on? First, we determine the equation of the line, which is

$$y - y_1 = \frac{y_2 - y_1}{x_2 - x_1}(x - x_1)$$

Then we plug in (x_3, y_3) and determine whether $y_3 < mx_3 + b$ or $y_3 > mx_3 + b$ to determine which side of the line the point lies.

Going back to our naive algorithm:

- Take the point p_k with the highest x-coordinate. We know this point must be on the convex hull.
- Consider p_k with all other points in S.
- For each pair (p_k, p_i) check if all the other points lie on the same side of the line segment joining the pair (use the simple test above).
- When you find one such pair (p_k, p_j), stop looking for more, and repeat this process without considering p_k and comparing every other point with p_j.

This naive algorithm takes $O(n^2)$.

Divide and Conquer Approach

Definition 14. *A point in one convex hull can* see *a point in another convex hull if the segment joining the two points does not intersect either hull.*

Definition 15. *The upper tangent is the highest line segment joining two points on each hull that see each other.*

Definition 16. *The lower tangent is the lowest line segment joining two points on each hull that see each other.*

Definition 17. *We say the line joining point p in hull C_1 and point q in hull C_2 stabs C_2 if the continuation of the line goes through the interior of C_2.*

Remark. *Recall the simple test above. We can find out when a line stabs C_2 if the successor of point q in C_2 is one side of the line and the predecessor of q is on the other side of the line.*

The approach for the algorithm is the following:

- Divide: Order all points p_i by their x-coordinate and take the median. Call this point p_m. This separates the points into two sets, L and H.
- Conquer: Find the convex hull of L and H. The base case is when you have three points, which is simply a triangle.
- Combine: (Not rigorous at all, mostly shown by picture in class) Start by choosing p to be the right-most point in the left hull, and q the left-most point in the right hull. Then p and q see each other. While the line segment joining these two points stabs either C_1 or C_2, keep "swiveling" these until the line segment doesn't stab either hull. You've found the upper tangent and lower tangent. This operation takes at most n for each tangent. Once you've found the upper and lower tangent, combine the two hulls as in Figure 4.2.

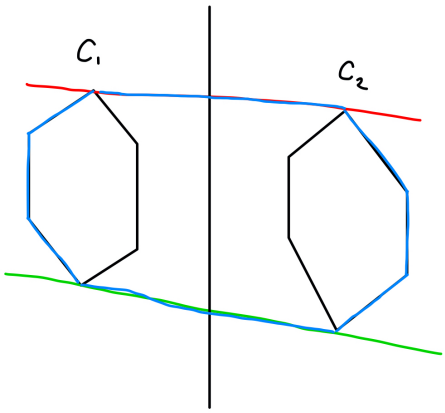

Figure 4.2: Convex hull combine: In red the upper tangent, in green the lower tangent, and in blue the new, merged hull.

5 Lecture

5.1 More Convex Hull

Convex hulls have many domains. One such examples is in collision detection.

5.1.1 Quickhull

(Spent 5 minutes in class, not very important). The idea is to get the point with the minimum x-coordinate and the point with the maximum x-coordinate. Draw a line between these two points, and hopefully we have divided the points into two sets. Repeat this for subproblems and merge.

5.2 Graphs

Let $G = (V, E)$ where V is a finite set of vertices and E is a set of unordered pairs of vertices. There are two representations of graphs: adjacency lists and adjacency matrices.

Definition 18. *An adjacency list is an array of size $|V|$ where entry i is a linked list consisting of the neighbors of vertex i.*

Definition 19. *An adjacency matrix is a $|V| \times |V|$ matrix M where $M_{ij} = 1$ if $(i, j) \in E$ and 0 otherwise. Note the adjacency matrix is symmetric for undirected graphs.*

The default representation of graphs is adjacency lists. Note we will not need to say every time that G is undirected, this is implied.

Definition 20. *An edge (u, v) has endpoints u and v or equivalently, is incident on vertices u and v. We also say u and v are adjacent if $(u, v) \in E$.*

Definition 21. *The degree of a vertex v is the number of edges incident on v, denoted as $d(v) \in \mathbb{N}$.*

Definition 22. *A path in a graph G is a sequence of vertices $v_1, v_2, \ldots, v_k$ such that $(v_i, v_{i+1}) \in E$ for all $i = 1 \to k - 1$.*

Definition 23. *A path is simple if it does not repeat vertices.*

Definition 24. *A (simple) cycle is a sequence of vertices $v_1, v_2, \ldots, v_k$ such that $(v_i, v_{i+1}) \in E$ for all $i = 1 \to k - 1$ and $(v_k, v_1) \in E$ with the v_i distinct except v_1.*

Definition 25. *A graph is acyclic if there are no cycles.*

Definition 26. *We say u and v are connected if there is a path between them. G is connected if for all $u, v \in V$ there is a path connecting u and v.*

Definition 27. *The connected components of G are the maximal subsets of G that are pairwise connected.*

Remark. *Connectedness is an equivalence relation.*

5.2.1 Trees

Definition 28. *A tree is a connected, acyclic graph.*

Definition 29. *(Inductive definition) A rooted tree is either*

- *A graph consisting of a single vertex v with v as the root.*
- *If $(T_1, r_1), (T_2, r_2), \ldots, (T_k, r_k)$ are rooted trees, then the tree (T, r) consisting of a new node r as the root and edges $(r, r_1), \ldots, (r, r_k)$ is a rooted tree.*

Typically problems in this domain can be solved with structural induction. An example of structural induction is the following:

Lemma 5.1. *Any tree of n nodes has $n - 1$ edges.*

Proof. We prove that any rooted tree on n nodes has $n - 1$ edges which implies our lemma. To prove this we first prove the base case. Indeed, the statement holds for any single node rooted tree with no edges. For the inductive step, we want to prove this for a rooted tree built up from $(T_1, r_1), (T_2, r_2), \ldots, (T_k, r_k)$. Assume the statement is true for all the trees T_i. Tree T_i has n_i nodes. So then T has $1 + \sum_i^k n_i$ nodes. By the inductive assumption, there are $n_i - 1$ edges in T_i, so the total number of edges in T is $k + \sum_i^k (n_i - 1) = \sum_i^k n_i$ which is one less than the number of nodes, proving our lemma. □

5.2.2 Traversals

How can we traverse a rooted tree? In other words, how can we visit all the nodes of a tree? We introduce post order traversal.

Algorithm 1 Post order traversal

Require: T is a tree with root r
  for child c of r **do**
    Post order traversal of sub tree with root c
  end for
  Visit r

6 Lecture

6.1 More Graph Traversals

We continue talking about graph traversals.

6.1.1 Breadth First Search (BFS)

Let $G = (V, E)$ be a graph and let $s \in V$ be the source. The goal of this algorithm is to visit all the vertices in the graph. A way to visualize BFS is picturing a ripple in the water. At time t the algorithm will visit nodes a distance t from s.

There will three possible states for each vertex.

- Undiscovered: A vertex has not yet been visited.
- Discovered: Just visited a vertex but not its neighbors.
- Finished: Visited vertex and neighbors.

Algorithm 2 Breadth first search

```
Require: G a graph, s a source vertex
  Q = queue({s})
  seen = {s}
  while Q is not empty do
    v = Q.dequeue()
    visit v
    if v not in seen then
      seen = seen ∪ {v}
      for neighbor n in v do
        Q = Q ∪ {n}
      end for
    end if
  end while
```

We can associate levels with the vertices in BFS. The level of s is 0, the neighbors of s have level 1, and so on. Vertex v is discovered when we dequeue some vertex u, and we will set the level $l(v) = l(u) + 1$.

Theorem 6.1. *The level of a vertex v is the smallest number of hops to get from the source s to v.*

Proof. Let $\delta(s, v)$ be the smallest number of hops to get from s to v.

- Claim 1: $\delta(s, v) \leq l(v)$. If v has level l, then there is a sequence of vertices $s, v_1, ..., v_{l-1}, v$ with $l(v_1) = 1$, $l(v_2) = 2$, and so on. Each vertex was discovered from the previous in the sequence. This constitutes a path from s to v. The smallest path, $\delta(s, v)$, must be therefore smaller or equal to this path.
- Claim 2: $\delta(s, v) \geq l(v)$. Suppose for a contradiction this claim does not hold. For all the v such that $\delta(s, v) < l(v)$ find the one with smallest $\delta(s, v)$. By definition of δ, there is a path from s to v with $\delta(s, v)$ hops. Let $s, ..., u, v$ be the path with the fewest hops from s to v. What does u look like? We know $\delta(s, u) = \delta(s, v) - 1$. By the way we constructed v as being the smallest that contradicts Claim 2, then u satisfies Claim 2, so therefore $l(u) \leq \delta(s, u) = \delta(s, v) - 1$. We also know that $l(v) \leq l(u) + 1$. Putting it all together, we have that
$$l(v) \leq l(u) + 1 \leq \delta(s, v)$$
which is a contradiction.

□

Remark. *Look at the edges for which new vertices are discovered. These edges form a tree (think of the tree as directed away from s).*

6.1.2 Depth First Search (DFS)

The idea is that you explore one path as far as it will go, then backtrack minimally and repeat. More formally, look at Algorithm 3.

Algorithm 3 Depth first search

Require: G a graph, s a source vertex, *seen* a set
  visit s
  $seen = seen \cup \{s\}$
  for each neighbor n of s **do**
    if n not in *seen* **then**
      recursively call DFS with source n
    end if
  end for

As in BFS, there will three possible states for each vertex. In BFS the order of exploration of vertices is the same as the order of discovery (first in, first out). In DFS, however, we use a stack (or the recursion stack), so we do last in first out. In other words, the last discovered vertex is the one first fully explored.

The DFS tree is formed by the set of edges on which new vertices are discovered.

Lemma 6.2. *If (u, v) is an edge in the graph that is not in the DFS tree, then either u is an ancestor of v or v is an ancestor of u in the DFS tree.*

Proof. Proof by picture. Do it as an exercise (hint: assume contradiction). □

Definition 30. *The start time $s(u)$ for vertex u is the time for which DFS of u is invoked, and the finish time $f(u)$ is the time for which DFS of u finishes. The duration is the interval from start time to finish time.*

Note that for all u, v we can't have that $s(u) < s(v) < f(u) < f(v)$ by the properties of stacks.

Another claim that is useful for DFS is the following. Let's begin with a wrong, too strong claim.

Lemma 6.3. *(False lemma!). Suppose u is discovered before v and there is a path between u and v. Then during DFS, v will become a descendant of u.*

Why is this wrong? Let's find a counterexample. Consider Figure 6.1.

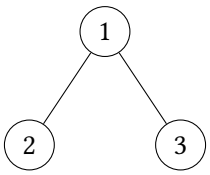

Figure 6.1: Counterexample to the wrong lemma

Suppose DFS visits 2 before 3. There is clearly a path from 2 to 3, but 3 is not going to be a descendant of 2. The problem is that the path between 2 and 3 has vertices that have already been visited. Let's fix the lemma.

Lemma 6.4. *Suppose u is discovered before v and there is a path of undiscovered vertices between u and v. Then during DFS, v will become a descendant of u.*

If you want to prove this, use contradiction.

6.2 Connectivity

Definition 31. *A graph is called biconnected if the removal of any vertex leaves the graph connected. A graph is called k-connected if the removal of any $k-1$ vertices leaves the graph connected.*

A tree is a good example of a connected graph that is not biconnected (e.g. Figure 6.1).

Definition 32. *A vertex whose removal disconnects the graph is called an articulation point.*

7 Lecture

7.1 More Graphs

Definition 33. *(Informal) Biconnected components are "maximal" pieces of the graph that are biconnected.*

Let's define an equivalence relation R on $E \times E$ where $(e_1, e_2) \in R$ if and only if there exists a simple cycle that contains e_1 and e_2 (Exercise: show it's an equivalence relation). R partitions the edges into equivalence classes $E_1, \ldots, E_k$. Note that if R only has one equivalence class then the graph is biconnected. Let component G_i be the graph containing edges in E_i together with the vertices in V_i consisting of the endpoints of E_i.

Let's go back to DFS. Assume G is connected and start DFS at node s. When is s an articulation point?

- Case 1: s has only one child in the DFS tree. In this case s is not an articulation point.
- Case 2: s has more than one child. Then s is an articulation point because non-tree edges go between ancestors and descendants. In other words, any vertex in the subtree generated by one child of s must go through s to reach any vertex in the subtree of another child of s.

What conditions make any vertex v in the DFS tree of s an articulation point? Suppose v has children $u_1, u_2, \ldots, u_k$. An internal node v is an articulation point if and only if it has a child u_i such that there is no back edge from the subtree rooted at u_i to a proper ancestor of v. See Figure 7.1 for a diagram.

7.1.1 Finding Biconnected Components

We first must do a DFS starting on a source s and we must do a post order traversal of the DFS tree as it is produced. As it finds biconnected components, it outputs them.

Recall that if u is an ancestor of v in the DFS tree, then the start times $s(u) < s(v)$. Define $\text{low}(x)$ as the smallest number (start time) vertex reachable by a back edge from the subtree rooted at x. Suppose for simplicity v has only two children u_1, u_2. Then

$$\text{low}(v) = \min(\text{low}(u_1),\ \text{low}(u_2),\ \underbrace{s(u) : (v,u) \text{ is a back edge}}_{\text{we must consider the back edges of } v})$$

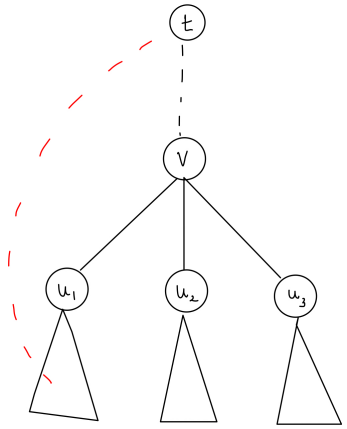

Figure 7.1: Condition that makes v an articulation point. In this case, it is because the subtree generated by a child of v has a back edge to an ancestor of v.

Lemma 7.1. *An internal node v is articulation point if and only if there is a child u_i of v such that $low(u_i) \geq s(v)$.*

7.2 Directed Graphs

In directed graphs, edges are ordered pairs, so that $(u, v) \in E$ means u is directed to v. Naturally, algorithms that we talked about for undirected graphs might change for directed graphs. Consider DFS for a directed graph. What type of edges do you encounter? You can have forward edges, back edges or cross edges. An example of a cross edge can be seen in Figure 7.2.

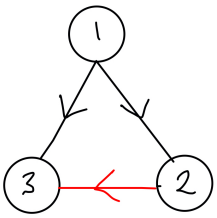

Figure 7.2: Example of a cross edge in red.

If (u, v) is a cross edge, then $s(u) > s(v)$.

7.2.1 Directed Acylic Graphs (DAGs)

An example of a DAG is your university course dependency graph, where some nodes have precedence over others. In general, our goal is to find an ordering of the vertices such that for each edge (u, v) we have that u precedes v in the ordering. This problem is called **topological sorting**.

Lemma 7.2. *Any DAG has a topological ordering.*

Proof. Exercise. Use induction. Or contradiction. □

Definition 34. *The in degree of a vertex is the number of incoming edges.*

Theorem 7.3. *If G is a DAG and (u, v) is an edge then for any DFS, $f(u) > f(v)$.*

Proof. We show $f(u) > f(v)$.

- Case 1: $s(u) < s(v)$. Then v will become a descendant of u (not necessarily a child), so then $f(u) > f(v)$.
- Case 2: $s(u) > s(v)$. If we discovered u in the course of DFS of v, then there must be a path from v to u, which means G has a cycle, and this is a contradiction. Therefore, $s(v) < f(v) < s(u) < f(u)$

In both cases, $f(u) > f(v)$. □

Remark. *Once you prove this theorem, finding a topological sort of a DAG is very easy. Find the finish time of all the vertices and output them in reverse finish time order.*

8 Lecture

8.1 Strongly Connected Components

Suppose $G = (V, E)$ is a directed graph. What is the correct connectivity relation in a directed graph? Define a relation $R = \{(u, v) : \text{there is a path from } u \text{ to } v \text{ and from } v \text{ to } u\}$. Note we bake into the definition symmetry. For instance, for the graph $1 \longrightarrow 2$, we have that $R = \{(1, 1), (2, 2)\}$. This relation is in fact an equivalence relation (exercise: show it). We know then that R partitions V into equivalence classes $V_1, V_2, ..., V_k$.

Definition 35. *For any $i = 1 \longrightarrow k$, we have that $G_i = (V_i, E \cap V_i \times V_i)$ is a strongly connected component of G.*

Note that you could have an edge connecting G_i and G_j. Let each G_i denote a vertex in a new graph G_{SCC}. This is the strongly connected component graph of G. More formally, we have that $G_{SCC} = (V_{SCC}, E_{SCC})$ where $V_{SCC} = \{ C_i : C_i \text{is a strongly connected component}\}$ and $E_{SCC} = \{(c_i, c_j) : \text{there exists } v_i \in C_i \text{ and } v_j \in C_j \text{ such that } (v_i, v_j) \in E \}$. For an example, take a look at Figure 8.1.

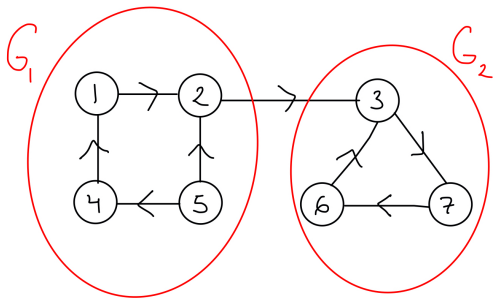

Figure 8.1: Example of a graph with strongly connected components. The equivalence classes are $\{\{1, 2, 4, 5\}, \{3, 6, 7\}\}$. The G_{SCC} is simply $C_1 \longrightarrow C_2$.

Lemma 8.1. *G_{SCC} is acyclic.*

DFS will decompose a directed graph G into its SCC. Let G be an arbitrary directed graph. We know G_{SCC} is a DAG by the above lemma.

Lemma 8.2. *(False lemma!) If C_1 and C_2 are SCC and $(C_1, C_2) \in E_{SCC}$ then in a DFS of G, every vertex in G_1 finishes after every vertex in G_2.*

Why is this wrong? Look at Figure 8.1 and figure it out.

Lemma 8.3. *(Correct lemma) If C_1 and C_2 are SCC and $(C_1, C_2) \in E_{SCC}$ then in a DFS of G, there exists a vertex in G_1 that finishes after every vertex in G_2.*

Proof. Look at the book. □

Let's recapitulate.

- We know G_{SCC} is a DAG.
- G_{SCC} has one or more vertices with no incoming edges. These vertices are called sources. Therefore, if v has the largest finishing time $f(v)$ in a DFS of G, then v must lie in a source component.

Kosaraju's Algorithm

(Very informal, for more info visit here). Perform one DFS to record the order of finishing times. Let $f_1(v)$ be the finish time of v in this DFS. Now reverse all the edges in G to create the graph G^R and perform a second DFS of G^R with one constraint: In the outer procedure always choose the undiscovered vertex v with greatest $f_1(v)$ (note that the vertex v with greatest $f_1(v)$ lies in a sink component in G^R). We know G and G^R have the same strongly connected components. We also know that, since v is in a sink component, the DFS of G^R started at v will only discover the SCC containing v. When the inner call to DFS(G^R, v) finishes, output all the discovered vertices as one SCC of G. When we return to the outer loop and pick the undiscovered vertex with greatest finish time, we know inductively that we will find all SCCs. The running time of the algorithm is the time it takes to performs two DFS, which is $O(n)$.

8.2 Optimization

In this type of problems, we would like to minimize/maximize some function subject to some constraints. A special class of optimizations problems is the following: Given a set of elements, pick a subset, where the constraints tell you which subsets are allowed (we call them **feasible** solutions). We will have an objective function that assigns a value to every feasible solution.

8.2.1 Minimum Spanning Tree

The input to this problem is an undirected, connected graph $G = (V, E)$ together with weights on the edges, where $w : E \to \mathbb{R}^+$. A feasible solution will be a set of edges that form an acyclic, connected graph on all vertices. The cost of a solution is the sum of the weights of the edges in the solution.

8.3 Greedy Algorithms

There are problems for which the optimum solution can be chosen by choosing one element at a time. We can solve this problems with greedy algorithms.

Definition 36. *A greedy algorithm builds up a solution S by taking at each turn the next element with optimal cost that can be added feasibly.*

8.3.1 Activity Selection Problem

This is a classic problem that can be solved using a greedy algorithm. The input is n activities, where $a_i = (s_i, f_i)$ starts at time s_i and finishes at time f_i. A feasible solution will be any subset of these activities such that no two activities overlap. The optimization problem will be to maximize the number of activities scheduled.

Let's propose some criteria to be greedy on.

- Pick the activity with shortest duration. This won't work, because if you have long activities $n_1 = (1, 10)$ and $n_2 = (11, 20)$ and a short activity $n_3 = (9, 12)$, this approach will only pick n_3 with a value of 1 while an optimal solution will have a value of 2 (by choosing n_1 and n_2).
- Pick the activity that finishes first. Sort the activities by finish time and reorder them as $a_1, a_2, ..., a_n$ so that $f_1 \leq f_2, ... \leq f_n$. Now pick a_1 and remove all activities that have a conflict with a_1, and repeat this process.

The second approach is correct, but can we prove this?

Definition 37. *The greedy choice property states that the first choice made by a greedy algorithm is not wrong.*

In this case, the greedy choice property means that if we choose a_1 first, then there is an optimal feasible solution that contains a_1. Suppose for a contradiction that no optimal solution uses a_1. Let O be the subset of activities in some optimal solution. We can order the activities in O by finish time. Let $a_{i_1}, ..., a_{i_k}$ be this ordering. We claim that we can throw away a_{i_1} and replace it with a_1. This is called the **exchange** argument. We now have $O' = O - \{a_{i_1}\} \cup \{a_1\}$. But by our greedy assumption the finish time of a_1 is less than the finish time of a_{i_1}, so a_1 doesn't overlap with a_{i_2} and O' is an optimal solution, which is a contradiction.

We've just shown there is an optimal solution that starts with a_1. This optimal solution should certainly exclude activities that have a conflict with a_1. Recursively, we need to solve a smaller problem consisting of activities that don't conflict with a_1. In this set of activities, we need to pick an optimal, feasible subset.

Let A be the original set of activities, and let A' be the remaining set of activities after throwing out a_1 and its conflicting activities. Any solution to A' that gives a value of k can be extended to A with value $k + 1$. This shows that we need the optimal solution to A'.

Remark. *This may seem obvious to you, but there are some problems where you need to find a suboptimal solution in A' to get the optimal solution for A. It just happens to be that for activity selection the optimal solution in A' gives the optimal solution in A.*

Definition 38. *A problem is said to have optimal substructure if an optimal solution can be constructed from optimal solutions of its subproblems.*

Inductively assume that the greedy approach solves problems with fewer than n activities optimally. Then the optimal substructure and the fact that the greedy approach solves the n activity problem optimally finishes the proof.

Complexity

The complexity of this problem is $O(n \log(n))$, as we need to sort the activities by finish time.

9 Lecture

9.1 Vector Spaces Review

Definition 39. *V is vector space over $\mathbb{R}^n$ if*

- *For any $v_1, v_2 \in V \implies v_1 + v_2 \in V$.*
- *For any $\alpha \in \mathbb{R}$ and $v \in V$ then $\alpha v \in V$.*

Definition 40. *Given a finite set of vectors $v_1, ..., v_k$, the span $S(v_1, ..., v_k)$ is the set of all linearly combinations, i.e.*

$$S(v_1, ..., v_k) = \{\alpha_1 v_1 + ... + \alpha_k v_k : \alpha_i \in \mathbb{R}\}$$

Definition 41. *A set of vectors $v_1, ..., v_k$ is linearly dependent if there exist some non-trivial $\alpha_1, ..., \alpha_k$ with*

$$\alpha_1 v_1 + ... + \alpha_k v_k = 0$$

Lemma 9.1. *The span is a vector space.*

Definition 42. *A set of vectors is said to be linearly independent if they are not linearly dependent.*

Definition 43. *Let $v_1, ..., v_k$ be linearly independent and suppose their span is V, then $v_1, ..., v_k$ form a basis for V.*

Lemma 9.2. *If $v_1, ..., v_k$ is a basis for V and $u_1, ..., u_k$ is another basis for V, then $m = k$.*

Proof. (Sketch). Suppose for a contradiction that $m > k$. Then we have

$$\begin{aligned} u_1 &= \alpha_{11} v_1 + ... + \alpha_{1k} v_k \\ u_2 &= \alpha_{21} v_1 + ... + \alpha_{2k} v_k \\ &\vdots \\ u_m &= \alpha_{m1} v_1 + ... + \alpha_{mk} v_k \end{aligned}$$

We need to show that $u_1, ..., u_m$ is linearly dependent. To show this, we need to find some non-trivial $x_1, ..., x_m$ such that $\sum_i x_i u_i = 0$. So suppose $\sum_i x_i u_i = 0$. Substitute each u_i with the equations above. Collect terms, and you'll get a system of equations with k equations and m unknowns, which leads to infinitely many solutions since $m > k$ by assumption. This leads to a contradiction. □

9.2 More Greedy Algorithms

9.2.1 Basis of Maximal Weight

Problem: Suppose you are Google and you assign a vector to each possible document. When a user searches for a term, you want to collect some vectors that are indicative of that search term. You also want to be diverse, e.g., if a user searches for "jaguar" you want to return some documents with cars and others with the animal. We could model this by returning vectors that are linearly independent.

More abstractly, given vectors $v_1, ..., v_n$ with weights $w_1, ..., w_n$, we need to return a basis (note there can be many!) for the space spanned by these vectors of maximum total weight.

Greedy Approach

Sort the vectors by decreasing order of weights $v_1, ..., v_n$. Let S be a set of vectors. For each vector v_i in this order, if $S \cup \{v_i\}$ is linearly independent, then assign $S = S \cup \{v_i\}$.

Correctness

By contradiction. Suppose the greedy approach returns vectors $G = \{v_{i_1}, ..., v_{i_k}\}$, and suppose there is an optimal solution with better total weight that returns vectors $O = \{v_{j_1}, ..., v_{j_k}\}$.

Note: the next part is the start of lecture 10, but I'll put it here for continuity.

Remark. *Suppose A and B are finite subsets of linearly independent vectors in $\mathbb{R}^d$ and suppose $|A| < |B|$. Then, using the exchange property, there exist some vector $b \in B$ such that $A \cup \{b\}$ is linearly independent. Indeed, there must be a vector in B that lies outside the space spanned by A because of the dimensions of $\langle B \rangle$ and $\langle A \rangle$.*

Let v_{i_l} be the first vector chosen by the greedy algorithm that is not in O. Using our remark, we have that $A = \{v_{i_1}, ..., v_{i_l}\}$, and $B = O$.

- Case 1: $l = k$. But then G is at least as good as O, which is a contradiction.
- Case 2: $l < k$, i.e., $|A| < |B|$. Apply our remark. By the exchange property repeatedly, we can keep adding vectors from B to A, preserving linear independence of A until $|A| = |B|$. At the end, A has v_{i_l} instead of some vector in O that has weight less than v_{i_l}. Therefore, $w(A) \geq w(O)$. Note that even if $w(A) = w(O)$, A agrres more with our greedy solution than O, so by induction greedy must be as good as O.

Definition 44. *(Hereditary property). If $R \subset S$ and S is a linearly independent set of vectors, then R is also linearly independent.*

The greedy algorithm for finding a maximum weight basis works because vectors have the exchange and hereditary properties.

10 Lecture

Note: Some of Lecture 10 is at the end of Lecture 9's notes for continuation.

10.1 Matroids

Definition 45. *A matroid is a pair (S, I) where S is a finite set and I is some set of subsets of S, designated "independent sets", such that*

- *I satisfies the hereditary property. More formally, if $A \subset B$ and $B \in I$, then $A \in I$.*
- *I satisfies the exchange property. More formally, if $A, B \in I$ and $|A| < |B|$, then there exists some $x \in B - A$ such that $A \cup \{x\} \in I$.*

All maximal independent sets in a matroid have the same size. A greedy algorithm is optimal for finding a maximum weight maximum independent set in a matroid.

10.1.1 Graphic Matroid

Let $M = (S, I)$ be a matroid. Given a weighted, connected, undirected graph $G = (V, E)$ where $S = E$

- $A \subset S$ is called independent if and only if A is acyclic.
- If $B \in I$ and $A \subset B$, then $A \in I$, and M is hereditary.

Lemma 10.1. *If $A, B \in I$ and $|A| < |B|$, then there exist $e \in B - A$ such that $A \cup \{e\} \in I$.*

Proof. The graph on B has $n - |B|$ components, and the graph on A has $n - |A|$ components. Therefore, $n - |A| > n - |B|$. B must contain at least one edge (u, v), where u and v lie in different connected components of the graph formed by A. This edge (u, v) can be added to A to get a larger independent set. □

10.1.2 Maximum Weight Minimum Spanning Tree

Our input is a connected, weighted, undirected graph $G = (V, E)$ with some weight function $w : E \to \mathbb{R}$. Our goal is to find a maximum weight spanning tree in G.

Because this is the problem of finding a maximum weight maximum independent set in a graphic matroid, the greedy algorithm (Kruskal's) is optimal.

Definition 46. *A cut in a graph is defined by a non-trivial partition $V_1 \cup V_2$ of V. The cut (V_1, V_2) is the set of edges that have exactly one endpoint in V_1.*

11 Lecture

11.1 Kruskal's Algorithm

Kruskal's algorithm finds a minimum weight spanning tree in a connected, weighted, undirected graph.

- Step 1: Sort and renumber the edges in increasing order of weight as $e_1, \ldots, e_n$.
- Step 2: Create a graph G with the same vertices as the original graph.
- Step 3: For each edge $e_i = (u, v)$, add the edge to the graph if and only if u and v lie in different components. To do this, we need two routines.
  - Find: return the component for a vertex u.
  - Union: merge two components together.

  We are going to define a union-find data structure to solve this, which we will initialize to n singleton components.

Union-Find

Let's look at various attempts to implement this data structure.

1. First attempt. Keep an array where the index i tells you what component v_i is in. Initially, each vertex belongs to its component, so the array is $A = [1, 2, 3, \ldots, n]$. We immediately notice that we can perform the find operation in $O(1)$ (just index into the array). What about union of u and v? This takes $O(n)$ (you might need to reassign $n - 1$ components). Using this approach, in the course of Kruskal's algorithm we will perform $n - 1$ unions (we start from n components and get to 1 component). Each takes order n, so we'll get overall $O(n^2)$. We want to do better.
2. Second attempt. Notice that when we perform union(u, v), u's set contains n_1 elements and v's set contains n_2 elements. To do less operations, we ideally want to change the components of the set that is smaller. This operation still takes in the worst case $O(n)$. In this attempt, in addition to the array, we maintain a linked list for each set containing the elements in that set (think of it as a reverse indexing from the component to the elements). An individual union operation could still take $\Theta(n)$ steps. However, any k union operations performed by Kruskal take only $O(k \log(n))$ steps. We've moved from analyzing one operation to analyzing a sequence of operations (amortized analysis, we'll

talk about this in a minute). Indeed, suppose you take the union of A and B, where $|A| > |B|$. The cost of the operation is equal to the size of B. Set up a counter for each element in the data structure, and charge 1 to each element in B for a union operation. How many times does an element get charged? Every time an element is charged, it joins a set that is as twice as large. Therefore, we can charge at most $\log(n)$ times, so the total cost of all $n-1$ unions is $n\log(n)$. More careful analysis will show you that k unions cost at most $k\log(k)$. This is an example of amortized analysis.

3. Third attempt. The idea is to maintain each connected component as a tree (see Figure 11.1). How long does the find operation take? Say the name of the component is the element at the root of the tree. For each node in the tree, keep a pointer to its parent. Finally, traverse up the tree until you find the root and you will have found the component. The cost is proportional to the height of each tree (note that all tree heights at all times are $O(\log(n))$, so this is what it costs to do a find). To do a union operation, have one root point to the other root. We can do the same amortized trick we performed above, and we can make the root of the tree with fewer elements point up to the root of the other tree. Unions of arbitrary pairs of elements is also $O(\log(n))$. We've established that Kruskal performs $n-1$ unions, but how many finds does it perform? It does $O(m)$ finds. Therefore, performing all the union-finds takes $O(m\log(n))$.

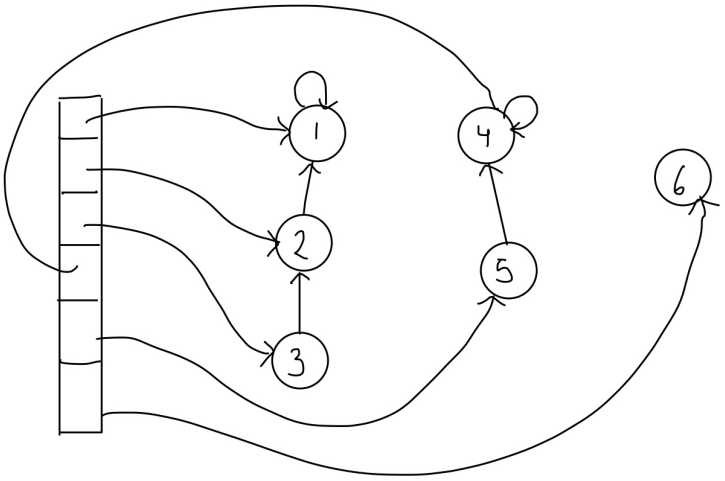

Figure 11.1: Data structure used for the third attempt

The time complexity for Kruskal is $O(m\log(n))$. Indeed, we have to first sort the edges by weights, so the union-finds are not in fact the bottleneck. One optimization in the third attempt is called path compression. The idea is that when you perform find(u), for each vertex encountered from the path from u to the root, make it a child of the root.

Any sequence of m operations starting from the initial union find data structure on n elements takes at most $O(m\log^*(n))$ time, where $\log^*(x)$ is the number of times you need to take the log of x to make the value less than or equal to 1. For instance, $\log^*(16) = 3$, since you need to do $16 \to 4 \to 2 \to 1$. The fact is $\log^*(n)$ is a **really** slow growing function, so we can take

interpret it as a constant. For example, $\log^*(2^{16} = 65,536) = 4$, and $\log^*(2^{65,536}) = 5$. This is more than the number of particles in the universe, so there's no way that you will get a problem with an input bigger than this. Therefore, we can treat it as almost constant.

11.2 Prim's Algorithm

In Prim's algorithm, we keep a set S, which we call the source side, and we consider $V - S$, the remaining vertices that are not in S. At every step we take the cheapest edge joining S and $V - S$. For each $v \in V - S$, maintain $d(v)$, which is the weight of the cheapest edge from v to some vertex in S.

Initially, $S = \{s\}$, and for every $v \in V - S$, we have that $d(v) = w(s, v)$ if (s, v) is an edge and ∞ otherwise. At each iteration (see Figure 11.2), when we move the vertex y that has the cheapest edge to a vertex in S, we need to update every neighbor v of y so that $d(v) = \min(d(v), w(v, y))$.

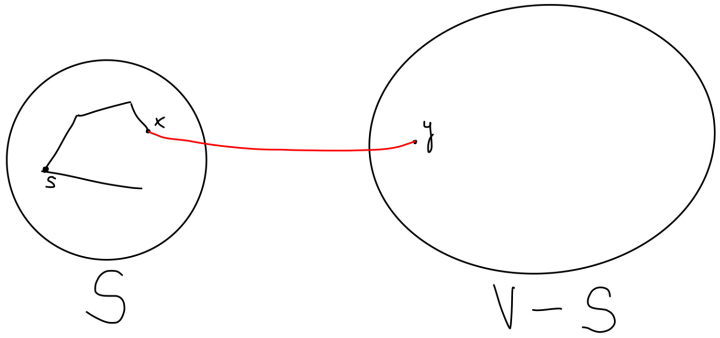

Figure 11.2: Prim's algorithm visualization

Time Complexity

If we maintain the $d(v)$s in an array A, the complexity is $O(n^2)$ because we need to first find the minimum in A, and once we've found the minimum we need to update all the neighbors of the minimum.

If we maintain the $d(v)$s in a min-heap, the complexity is $O(m \log(n))$.

11.3 Shortest Paths

Let $G = (V, E)$ be a directed, weighted graph with a weight function $w : E \to \mathbb{R}$. We assume G is directed because we can easily convert undirected shortest paths to directed shortest paths.

One common variation for this problem is the single source shortest path. The problem is to find the shortest path from a given vertex s to all the other vertices. Another variant is all-paths shortest path, in which we need to find the shortest path from any u to any v.

11.3.1 Single Source Shortest Path

We will assume all edge weights are non negative, and we will solve this using Dijkstra's Algorithm. The idea is to maintain a quantity $d(v)$ for each vertex v which is an upper bound on the length of the shortest path from s to v.

12 Lecture

12.1 More Shortest Paths

12.1.1 Dijkstra's Algorithm

High Level Overview

Recall we are trying to find the single source shortest path in a directed, weighted graph $G = (V, E)$ from the source s to all vertices. For this problem we will assume all weights are non-negative.

Definition 47. *We say the length of a path is the sum of the weights of all the edges going through that path.*

Consider the single source $s \in V$. The shortest path from s to itself is 0. Think of this as the base case for the inductive procedure. For the inductive step, partition V into S, which we call the source side, as the set of vertices for which we know the shortest path from s, and $V - S$, as the rest of vertices for which we don't know the shortest path from s. The idea is to grow S until $S = V$. Initially, $S = \{s\}$, $d(s) = 0$, and $d(v) = \infty$ for all other vertices.

Definition 48. *A path from s that stays entirely within S will be called a source-side path.*

At each stage find the vertex $v \in V - S$ for which there is a vertex $u \in S$ such that the $d(s, u) + w(u, v)$ is minimum over all $x \in V - S$. Then add v to S and update appropiately. As you may have noticed, this is a greedy algorithm.

Details

For each vertex v, maintain a quantity called $d(v)$. For vertices in $V - S$, $d(v)$ is the length of the shortest path from s to v consisting of a source side path to some vertex $u \in S$ followed by the edge (u, v) (see Figure 12.1).

At each iteration, we bring the vertex $v \in V - S$ with minimum $d(v)$ to S. Then, for each neighbor x of v, we update $d(x)$ to be

$$d(x) = \min(d(x), d(v) + w(v, x))$$

Proof of Correctness

The correctness of this algorithm relies on Theorem 12.1.

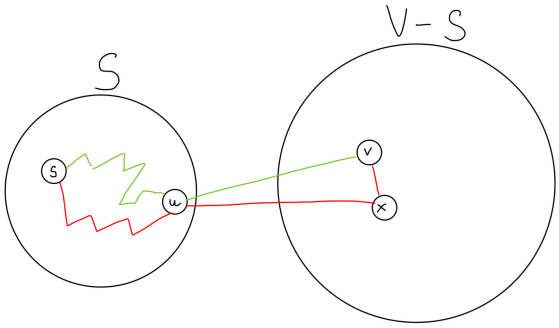

Figure 12.1: The green path is a form we allow $d(v)$ to be in, while the red path is a form we don't allow, as we had an intermediate $x \in V - S$ before our final v.

Theorem 12.1. *For each vertex $v \in S$, $d(v)$ is equal to the shortest path from s to v.*

Proof. By induction. In the base case, after the first iteration, $S = \{s\}$ and $d(s) = 0$, which is correct. Assume for the inductive hypothesis that the statement is true for $|S| = k$, and suppose v is the $k + 1$th vertex brought into S. Recall v is brought into S because $d(v)$ is minimum. Let P be the path with length $d(v)$. For a contradiction, suppose there is a shorter path P' to v. We know P' must include one edge from S to $V - S$, so let $(x, y) \in E$ be such edge, where $x \in S$ and $y \in V - S$. Then (s, y) portion of P' is at least as long as P by the way our algorithm works, and therefore P' is at least as long as P. This proves that at the point the algorithm brings v into S, $d(v)$ is the length of the shortest path to v. □

12.2 Huffman Coding

Suppose you have a text over a large alphabet (say an English text). When you transmit this text over a network, you need to encode the text in binary for storage and communication. Therefore, it would be nice to encode this with the fewest bits possible.

We're only interested in the following restricted problem. The code has to be a mapping from the symbols in the original alphabet Σ to binary strings, and the decoding has to be unambiguous. For instance, if our alphabet is A, B, C, D with mapping $A \to 01$, $B \to 011$, $C \to 100$, and $D \to 00$, then the binary string 01100 can either be BD or AC. We don't want that!

Furthermore, if one word is a prefix of another, this could lead to ambiguity, so our code has to be prefix free.

Definition 49. *Codes that are prefix free are called prefix codes.*

An example of a code is ASCII. This is not very efficient, as every letter in the alphabet has a mapping to a bitstring that is the same size as the rest. Naturally, we would like frequent letters in a text to have a shorter bitstring and letters that occur unfrequently to have a longer bitstring.

Let $\Sigma = \{\sigma_i, \sigma_2, ..., \sigma_n\}$, and let f_i be the frequency of σ_i. You can think of these frequencies as probabilities so that $\sum_i f_i = 1$. The goal is to find a prefix code that maps σ_i to $c(\sigma_i)$ that minimizes $\sum_i f_i |c(\sigma_i)|$, which is the average code length.

A binary code can be thought of as a binary tree. For instance, for $A \to 00$, $B \to 010$, $C \to 011$, and $D \to 1$, we have that the binary tree is Figure 12.2.

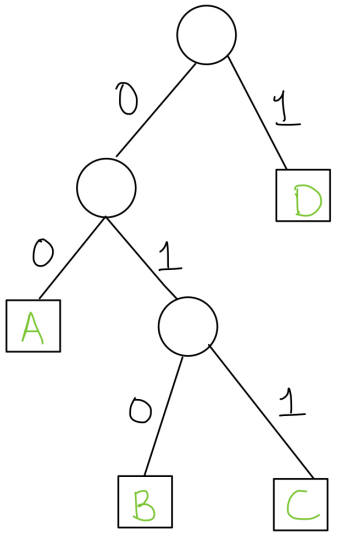

Figure 12.2: Example Huffman Coding

Definition 50. *A full binary tree is a tree where every internal node has two children.*

Notice symbols are at the leaves for a prefix code. Also, the tree corresponding to an optimal code must be a full binary tree. For if the tree is not a full binary tree, there must be an internal node v with only one child. But then v is redundant and you can remove v.

Suppose we know the shape of the optimal tree (which is a full binary tree).

Lemma 12.2. *Any full binary tree has a pair of sibling leaves at the deepest level.*

Proof. Look at a leaf at the deepest level. Look at its parent. By definition of a full binary tree, the parent must have two children. So the leaf has a sibling. □

Lemma 12.3. *In the optimal tree, the two symbols of least frequency are at the deepest level of the tree.*

Proof. By exchange argument. Suppose x and y are the two symbols with least frequency, and suppose that the two leaves at the deepest level have symbols a and b, where $\{a, b\} \neq \{x, y\}$. By exchanging positions of a with x and b with y we can bring x and y to the deepest level. One can show using simple algebra that this is an improvement (exercise: show it). □

Suppose you have two symbols x and y at depth $d+1$ which are siblings in the binary tree. Construct a new symbol xy in place of x and y that is going to be the parent of x and y with depth d. We know $f(xy) = f(x) + f(y)$, and if you look at the contribution of x and y to the average code length, we have that they contribute $(f(x) + f(y))(d+1) = f(xy)(d+1)$, where $d+1$ is the depth of x and y. However, the contribution that xy makes to the average code length is $f(xy)d$. Therefore, the same tree with this new symbol has cost $f(xy)$ lower.

Huffman's Algorithm

(Sketch) Combine the two least frequent symbols x and y into one symbol xy with frequency $f(xy) = f(x) + f(y)$. Recursively solve the problem on $n-1$ symbols, since Huffman's coding has optimal substructure.

13 Lecture

13.1 Dynammic Programming

13.1.1 Station Placement Problem

Image there is a bunch of towns $t_1, \ldots, t_n$ in a train line, where $t_i \in \mathbb{N}$. Now you want to put k stations to minimize the maximum distance that a resident of any town has to commute to the nearest station.

How many towns should be served by the last station? In the DP approach, we try all possible answers. For example, we could set the last station to serve the last town, or we could set the last station to serve the last two towns, etc. More generally, suppose the last station serves towns $t_i, t_{i+1}, \ldots, t_n$. Then we should put the station at the mean of the two extreme towns it is serving, i.e., at $\frac{t_i+t_n}{2}$. Note that then the cost of any person in the extreme towns going to station at $\frac{t_i+t_n}{2}$ is $\frac{t_n-t_i}{2}$ (see Figure 13.1).

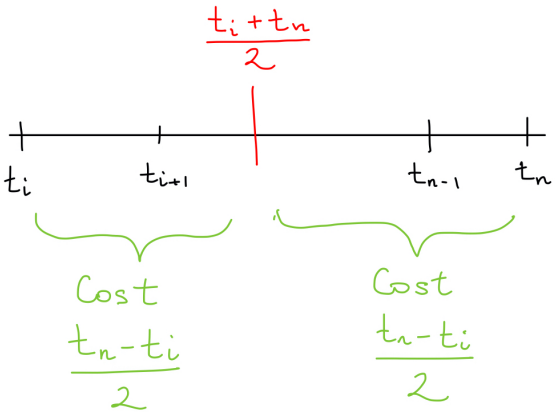

Figure 13.1: Where to put the station when considering the last $n - i + 1$ towns.

Let's introduce some notation. The cost $C(n, k)$ is the cost of serving towns $t_1, \ldots, t_n$ with k stations. More generally, the cost $C(i, j)$ is the cost of serving towns $t_1, \ldots, t_i$ through j stations.

If we decide to make the last station serve towns t_i through t_n, then

$$C(n, k) = \max\left(\frac{t_n - t_i}{2},\ C(i-1, k-1)\right)$$

Since we don't know the best i, we can write

$$C(n,k) = \min_{i=1 \to n} \max\left(\frac{t_n - t_i}{2},\ C(i-1,k-1)\right)$$

This defines a recurrence relation or a tree (see Figure 13.2).

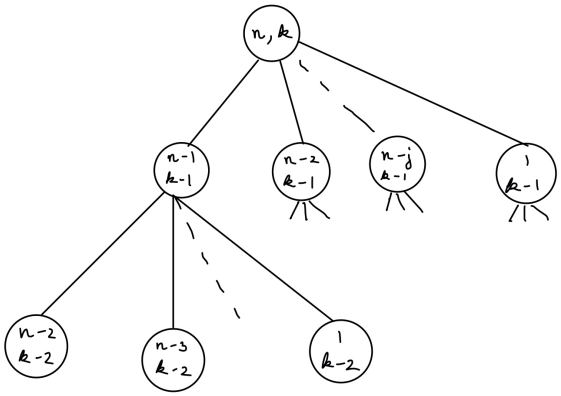

Figure 13.2: Subproblems in the stations problem.

Naive Algorithm

Compute $C(n,k)$ exactly as in the recurrence above.

Algorithm 4 Algorithm to calculate $C(n,k)$

```
if n is 0 then
    return 0
end if
if k is 1 then
    return (t_i − t_1)/2
end if
currmin = ∞
for i = 1 to n do
    C = max((t_n − t_i)/2, C(i − 1, k − 1))
    if currmin < C then
        currmin = C
    end if
end for
return currmin
```

This recursive algorithm runs in exponential time. What will save us is that in fact there are not too many distinct subproblems. The problem in this algorithm is that we are solving the same subproblem repeatedly.

Memoization (Top Down) Algorithm

The idea is to maintain solutions to subproblems in an array instead of computing them repeatedly, so every subproblem is solved only once.

Algorithm 5 Algorithm to calculate $C(n, k)$

Require: A is a 2d array shared between all recursive calls
  if $A[n][k]$ is not null **then**
    return $A[n][k]$
  end if
  if n is 0 **then**
    update $A[n][k]$
    return 0
  end if
  if k is 1 **then**
    update $A[n][k]$
    return $\frac{t_i - t_1}{2}$
  end if
  $currmin = \infty$
  for $i = 1$ to n **do**
    $C = \max\left(\frac{t_n - t_i}{2},\ C(i-1, k-1)\right)$
    if $currmin < C$ **then**
      $currmin = C$
    end if
  end for
  update $A[n][k]$ to be $currmin$
  return $currmin$

We have nk subproblems, each taking $O(n)$ time, which leads to a $O(n^2k)$ algorithm.

13.1.2 Binary Strings in Unary Representation

For this problem, given a number n in unary, count the number of binary strings of length n that do not contain the pattern 11. For instance, 3 is represented as 111 in unary. The bitstrings 000, 001, 010, 100, 101 do not contain the pattern, so the answer is 5.

Remark. *The reason we give n in unary is because if we give it in binary the algorithm will take exponential time.*

Say a string is valid if it does not contain the pattern 11. Then the top level question is to count the number of valid strings of length n ending in 0 and similarly count the number of valid strings of length n ending in 1. What can we say about a valid bitstring of length n? We have two cases

- Case 1: The bitstring ends in 0. Then the first $n - 1$ bits can be any valid bitstring of

length $n-1$.

- Case 2: The bitstring ends in 1. Then the first $n-1$ bits can be any valid bitstring of length $n-1$ ending with a 0.

Let $S_1(n)$ be the number of valid strings of length n ending in 1, and let $S_0(n)$ be the number of valid strings of length n ending in 0, so that $S(n) = S_0(n) + S_1(n)$. The recurrence then becomes

$$\begin{aligned} S_1(n) &= S_0(n-1) \\ S_0(n) &= S(n-1) = S_0(n-1) + S_1(n-1) \\ S(n) &= 2S_0(n-1) + S_1(n-1) \end{aligned}$$

This follows a Fibonacci sequence, and can be solved with dynamic programming.

13.1.3 Subsequences

Definition 51. *Given a sequence of positive integers $a_1, \ldots, a_n$, a subsequence is a sequence $a_{i_1}, \ldots, a_{i_k}$, where $i_1 < \ldots < i_k$.*

Definition 52. *We say a subsequence is increasing if $a_{i_1} < \ldots < a_{i_k}$.*

Suppose you are given a sequence 9, 5, 27, 2, 6, 1, 8, 3, 11. An increasing subsequence is 5, 6, 8, 11.

Remark. *(Aside). Given any sequence of length $n^2 + 1$, it either has an increasing subsequence of length $n+1$ or a decreasing subsequence of length $n+1$. This is a generalization of the pigeonhole principle.*

Let $a_1, \ldots, a_n$. We will now try to find the longest increasing subsequence. A wrong top level question you could ask is: is a_n in the longest increasing subsequence?

Let $\text{Best}(i, l) = x$ if the increasing sequence of length l in the prefix of $a_1, \ldots, a_i$ with the smallest ending number ends in x. Take the sequence 100, 1, 2, 3, 4, 8. Then $\text{Best}(1, 1) = 100$, $\text{Best}(2, 1) = 1$, $\text{Best}(2, 2) = \infty$.

14 Lecture

(Some time spent on discussing the midterm).

14.1 Longest Increasing Subsequence Problem

For this problem, the input is a sequence of integers. The output for this problem is the longest increasing subsequence.

Recall that Best$(i, l) = x$ if the increasing sequence of length l in the prefix of $a_1, ..., a_i$ with the smallest ending number ends in x. Inductively, assume that for some i we have computed Best(i, l) for all l. When we see a_{i+1}, what should we do? Consider the sequence

$$5, 10, 7, 3, 8, 4, 9, 6$$

Then Best$(1, 1) = 5$, and Best$(1, l) = \infty$ for any l that is greater than 1. We also have for instance that Best$(4, 1) = 3$, Best$(4, 2) = 7$, and Best$(4, l) = \infty$ for any l that is greater than 2. We also have that Best$(5, 1) = 3$, Best$(5, 2) = 7$, Best$(5, 3) = 8$.

There's an $O(n \log(n))$ algorithm relying on binary search to solve this problem. For more info, see here.

14.2 All Pairs Shortest Paths

The input to this problem is a weighted, directed graph $G = (V, E)$. The goal is to compute a matrix D of shortest paths distances between every pair of vertices. More formally, D_{ij} denotes the shortest path from vertex i to vertex j.

14.2.1 Adjacency Matrix Approach

Suppose we have the adjacency matrix A of G where $A[i, j] = w(i, j)$ if $(i, j) \in E$ and ∞ otherwise. What does A^2 mean? In the traditional matrix multiplication sense, we would have that $A^2[i, j] = \sum_k A[i, k] \cdot A[k, j]$. But replace the multiplication with addition and we will let $A^2[i, j] = \min_k A[i, k] + A[k, j]$. Note that $(+, \min)$ form a semiring. Notice that then A^2 in the $(+, \min)$ semiring gives the length of the shortest path consisting of at most two hops between every pair of vertices.

You can prove by induction that A^n contains the lengths of shortest paths consisting of at most n hops between every pair of vertices.

First of all notice that any shortest path doesn't contain cycles, for if it did, you could remove the cycle (all weights are non-negative), and it will still be the shortest path (so all shortest paths are simple). The longest simple path on n vertices is $n-1$, and therefore A^{n-1} gives the length of the shortest paths between every pair of vertices.

The best algorithm that computes standard matrix multiplication runs in approximately $n^{2.3}$. For our semiring, it's still roughly n^3.

What if instead of computing A^{n-1} we compute A^l for some $l \geq n-1$? Since $n-1$ is the longest possible path, computing A^l will still equal A^{n-1}, so we can choose to compute any A^l for any $l \geq n-1$. For ease of computation, choose A^{2^k} where $2^k \geq n-1$. The computation will now be $A \to A^2 \to A^{2^2} \to \ldots \to A^{2^k}$, which means we only perform $k \approx \log(n)$ multiplications. Each one takes n^3, so the algorithm runs in $O(n^3 \log(n))$.

This algorithms assumes there are no negative weight cycles. If there are negative weight cycles, and i is a vertex in such a cycle, then $A^l[i,i]$ will be negative instead of 0, so this algorithms also gives us a way of finding negative weight cycles in a graph.

14.2.2 DP Approach: Floyd-Warshall Algorithm

Fix a numbering of the vertices as $1, 2, \ldots, n$. Let $C^k(i,j)$ be the length of the shortest path from i to j where every intermediate vertex is numbered less than or equal to k. Note $C^n(i,j)$ is just the shortest path from i to j with no constraints, and

$$C^0(i,j) = \begin{cases} 0 & i = j \\ w(i,j) & (i,j) \in E \\ \infty & \text{otherwise} \end{cases}$$

and this is just the adjacency matrix of G! The approach for the Floyd-Warshall Algorithm is to incrementally compute $C^k(i,j)$ until $k = n$. The key question is then: given we know $C^k(i,j)$ for all i, j, how do we compute $C^{k+1}(i,j)$? There are two possibilities.

- The path from i to j restricted to vertices numbered $k+1$ or less does not go through vertex $k+1$. In which case $C^{k+1}(i,j) = C^k(i,j)$.
- The path from i to j restricted to vertices numbered $k+1$ or less does indeed go through vertex $k+1$. Then it only goes through it exactly once (otherwise we would have a cycle). Therefore
$$C^{k+1}(i,j) = \min\left(C^k(i,j),\ C^k(i,k+1) + C^k(k+1,j)\right)$$