CMSC451 - 0301

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Contents

Stable Marriage Problem

Find a stable arrangement from 2 equal-sized lists of preferences.

Example

Let's say we have 3 pairs of people.

Number	Men's women preferences	Women's men preferences
1	1,2,3	1,2,3
2	1,2,3	2,3,1
3	1,2,3	3,1,2

Man 3 starts.

He proposes to women 1, and women 1 accepts him.

Number	Men	Women
1		3
2		
3	1	

Man 2 then goes and proposes to 1. Women 1 accepts, and rejects man 3.

Number	Men	Women
1		2
2	1	
3		

Man 3 then tries again, and goes to women 2, and she accepts.

Number	Men	Women
1		2
2	1	3
3	2	

Man 1 then proposes to women 1, and she accepts, rejecting man 2.

Number	Men	Women
1	1	1
2		3
3	2	

Man 2 then proposes to women 2, and she accepts, rejecting man 3.

Number	Men	Women
1	1	1
2	2	2
3		

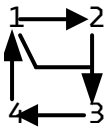
Man 3 then proposes to women 3, and she accepts.

Number	Men	Women
1	1	1
2	2	2
3	3	3

Graph Algorithms

Representing a Graph

Take this graph:



This is usually done in one of two ways:

Adjacency (bit) Matrix

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

Left to top.

So, for example, if we have a path from the 6th node to the 3rd node, also denoted $(6, 3)$.

If the graph is undirected, the matrix is symmetric.

The size of the matrix is $\Theta(n^2)$. Specifically, you can store it in n^2 **bits** (bits are small).

Adjacency list

$$[[2, 3], [3], [4], [1, 4]]$$

You may have a hell of pointers as well to connect stuff together to easily delete edges.

It takes $\Theta(m + n)$ space.

If you'd like to be silly, it takes $\Theta((m + n) \lg n)$ space because of the number of bits.

List all edges

Adjacency list

$\Theta(m + n)$ time.

Adjacency matrix
$\Theta(n^2)$ time.

You have to go to every place.

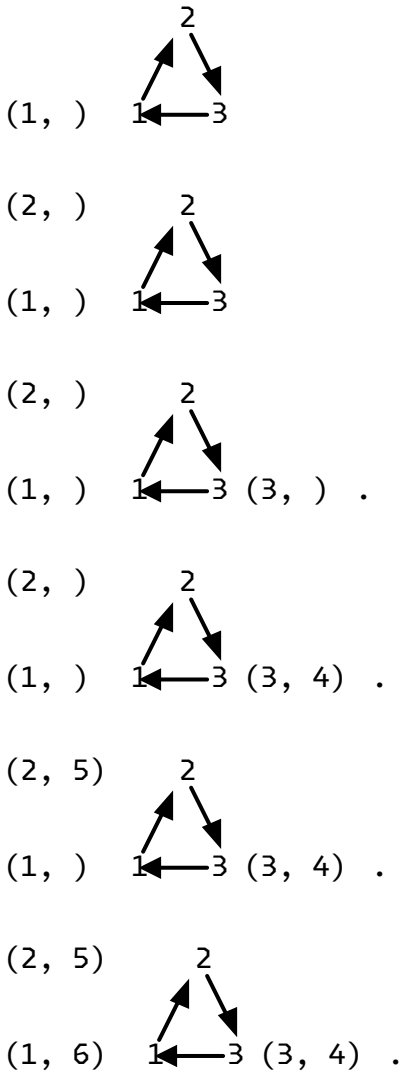
Something to note is that both of these algorithms run in linear time because they are linear with respect to the input size.

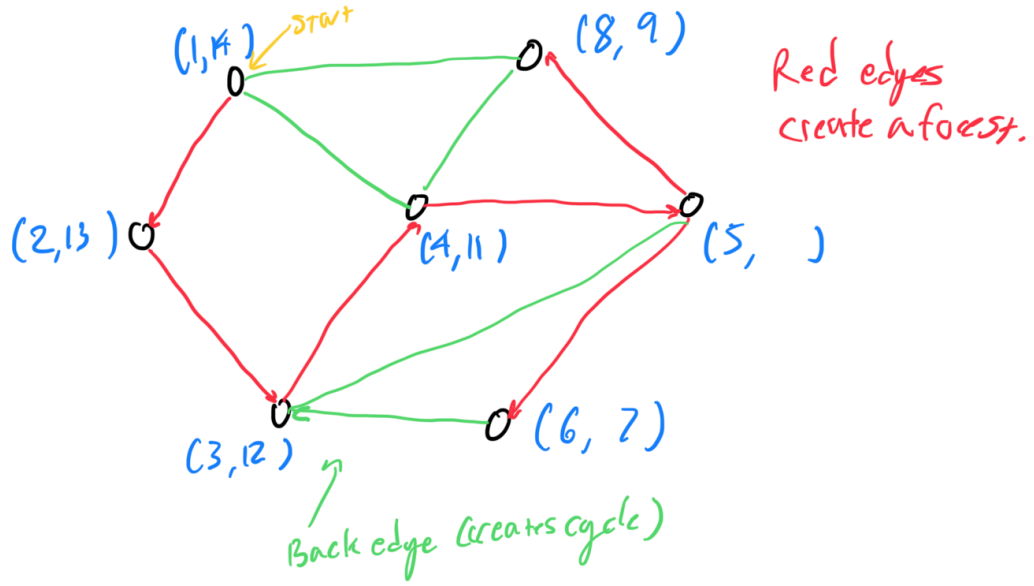
This also means that if you have a matrix multiplication algorithm that takes $\Theta(n^3)$ time, it takes $\Theta\left(N^{\frac{3}{2}}\right)$ time because the size is $N = n^2$.

Depth-First Search

You start at some point and select an arbitrary edge to walk to, dropping breadcrumbs as you go. When you get stuck, return to where you were when you weren't stuck and choose another path until you get to your destination.

You can also add discovery and finish times. Have one counter, and when you number a vertex, you increment the counter. You start at a vertex labeled with discovery 1 and then go to another vertex. Number the vertex's discovery time, and then walk on to another edge. If you explore every edge from a vertex, number the vertex's finish time and back up. For example:





Code of depth-first search

```
for x in vertices(graph):
    x.color = White

t = 0
for x in vertices(graph):
    if x.color == White:
        depth_first_search(x)

def depth_first_search(x: Node):
    x.color = Gray
    t += 1
    x.discovery_number = t
    for y in adjacent(x):
        if y.color == White:
            depth_first_search(y)
    x.color = Black
    t += 1
    x.finish_time = t
```

This is the generic code for DFS and abstracts finding the vertices and the adjacent nodes.

Adjacency matrix vs adjacency lists

```
for x in vertices(vertices):
```

For an adjacency list or matrix, this part is the same:

```
for x in range(0, n):
```

But this:

```
for y in adjacent(x):
```

Becomes this for the adjacency matrix `A`:

```
for y in range(0, n):
    if A[x, y] != 0:
```

This then leads to $\Theta(n^2)$ complexity because, for every node, you're looping through every other vertex.

For the adjacency list, this becomes:

```
for y in adjacency_list[x]:
```

Which then takes a more complicated amount of time to process.

For this, each node will take the number of edges time. In sum, this will go over each edge twice, leading to $\Theta(n+m)$ time, where n is the number of nodes, and m is the number of edges.

Both of these take linear time with respect to the size of the input.

Connected components

A graph is connected if there is a path between every pair of vertices.

A connected subgraph of a graph is a subgraph of a graph if it is connected.

A connected component is a maximally connected subgraph. You cannot add any more vertices or edges to increase the size while still remaining connected.

Maximum connected subgraph: is as "large" as possible.

Find connected components

```
for x in vertices(graph):
    x.visited = False

num = 0

for x in vertices(graph):
    if not x.visited:
        num += 1
        depth_first_search(x)

def depth_first_search(x: Node):
    x.visited = True
    x.component = num

    for y in adjacent(x):
        if not y.visited:
            depth_first_search(x)
```

Note that the dot accesses on the nodes could be replaced with external arrays of size n.

This algorithm takes the same time as the generic depth-first search.

Biconnected

A graph is biconnected if the removal of any one vertex (and its edges) leaves the graph connected.

Articulation point

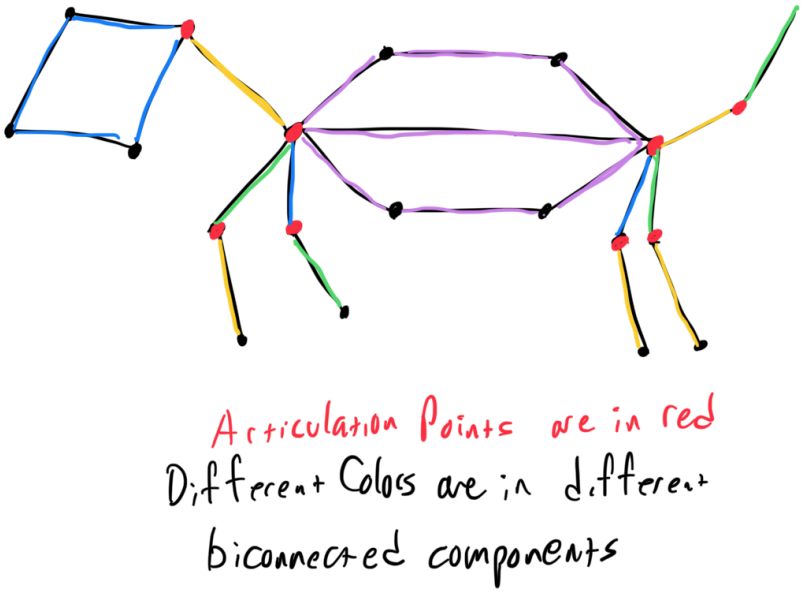
An articulation point is a vertex whose removal disconnects the graph.

This may be good to avoid if you want redundancy.

The articulation points separate the biconnected components.

Biconnected components

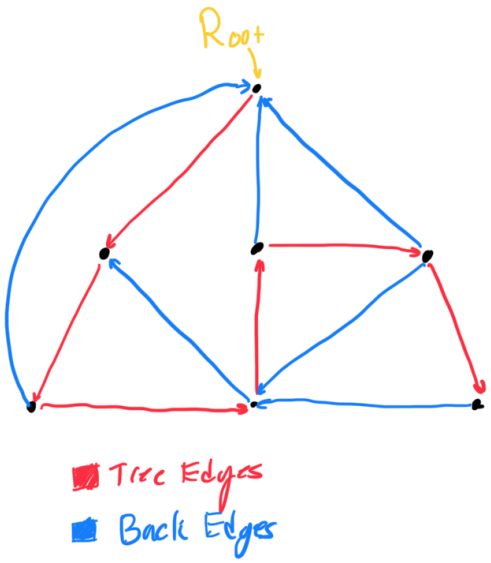
Biconnected components are maximal biconnected subgraphs



Find the tree edges and back edges

```
for x in vertices(graph):
    x.color = White

back_edges = []
tree_edges = []

for x in vertices(graph):
    if not x.visited:
        depth_first_search(x)

def depth_first_search(x: Node, parent: Node | None = None):
    x.color = Gray

    for y in adjacent(x):
        if y.color == White:
            tree_edges.append((x, y))
            depth_first_search(y, x)
        elif y.color == Gray and y != parent:
            back_edges.append((x, y))

    x.color = Black
```

Example Outcome



Find the biconnected components

1. Find the back edges and tree edges. If there is no back edge pointing to before a point (by the depth of the tree edges) for all child edges, then that point is an articulation point.
2. You only care if your subgraph goes above you, so you can just return the minimum discovery number you discover through back-edges.

Pseudocode

My code:

```
for x in vertices(graph):
    x.discovery_number = None
    x.color = White

articulation_points = []
num = 0

for x in vertices(graph):
    if x.color == White:
        dfs(x)

def dfs(x: Node, parent: Node | None = None) -> int:
    x.color = Gray
    num += 1
    x.discovery_number = num
    minimum = x.discovery_number

    for y in adjacent(x):
        if y.color == White:
            # tree edge
            minimum = min(minimum, dfs(y, x))
        elif y.color == Gray and y != parent:
            # back edge
```

```
            minimum = min(minimum, y.discovery_number)

    if minimum < x.discovery_number:
        articulation_points.append(x)

    x.color = Black
    return minimum
```

Kruskal's Code:

```
t = 0
stack = []
connected_components = []

for x in vertices(graph):
    x.discovery_number = 0

for x in vertices(graph):
    if x.discovery_number == 0:
        bicon(x, None)

def bicon(x: Node, parent: Node | None):
    t += 1
    x.discovery_number = t
    x.low_point = t
    for y in adjacent(x):
        if y.discovery_number == 0: # tree edge
            index = len(stack)
            stack.append((x, y))
            bicon(y, x)
            x.low_point = min(x.low_point, y.low_point)
            if y.low_point >= x.discovery_number:
                # x is either an articulation point relative to y
                # or x is the root of the tree.
                # Form a new connected component of all edges on
                # the `stack` up to and including (x, y). Remove these
                # edges from the stack.

                # this can be done in O(1) time with a linked list, but I'm lazy
                connected_components.append(stack[index:])
                while len(stack) != index:
                    stack.pop()
        elif y.discovery_number < x.discovery_number and y != parent: # back edge
            stack.append((x, y))
            x.low_point = min(x.low_point, y.discovery_number)
```

To form the connected components, the idea is that you find the articluation point, and when you return to it again, you found everything it's connected to and so what you found was all of what is in the connected component.

Alternate Algorithm

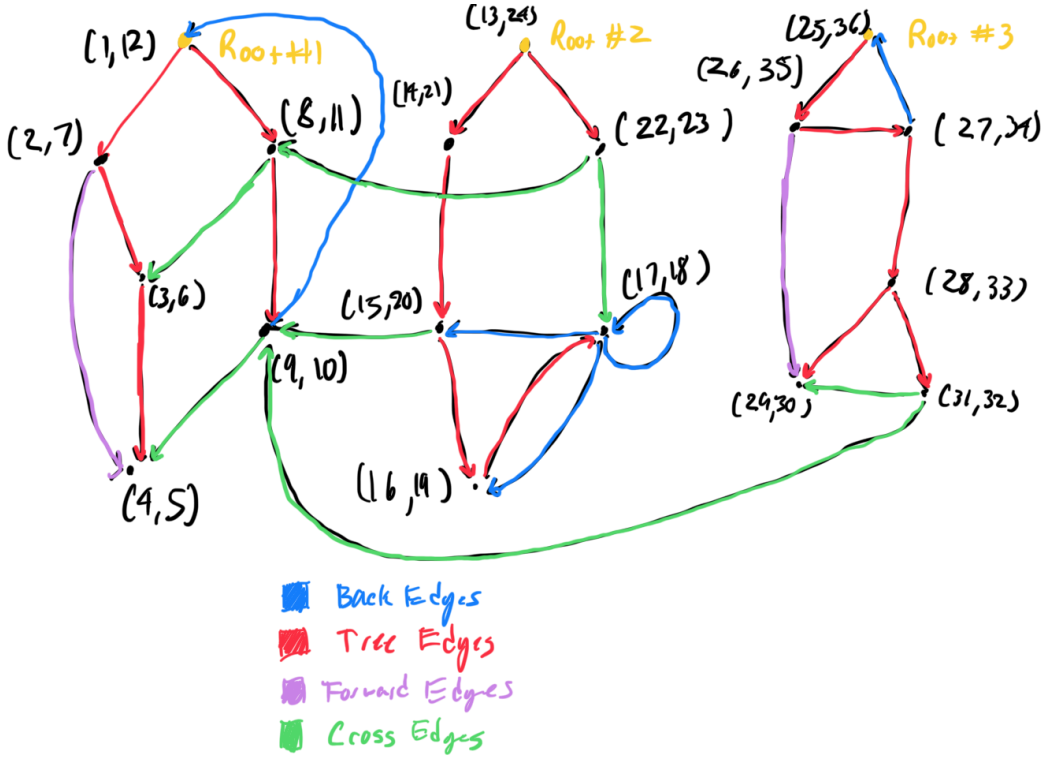
This uses depth.

```
t = 0
stack = []
connected_components = []
```

```
for x in vertices(graph):
    x.depth = 0

for x in vertices(graph):
    if x.depth == 0:
        bicon(x, 0)

def bicon(x: Node, depth: int):
    x.depth = depth + 1
    x.low_point = depth + 1
    for y in adjacent(x):
        if y.depth == 0:
            stack.append((x, y))
            bicon(x, d + 1),
            x.low_point = min(x.low_point, y.low_point)
            if y.low_point >= x.depth:
                # this can be done in O(1) time with a linked list, but I'm lazy
                connected_components.append(stack[index:])
                while len(stack) != index:
                    stack.pop()
        elif y.depth < x.depth:
            stack.append((x,y))
            x.low_point = min(x.low_point, y.low_point)
```

Directed Graphs

DFS



After running DFS, you can divide the remaining edges into forward or cross edges by the discovery and finish numbers.

Let d_1, f_1, d_2, f_2 be the discovery and finish numbers of two nodes that are connected by a remaining edge.

If $(d_1, f_1) \subset (d_2, f_2)$, then the edge from $1 \to 2$ is a forward edge.

Directed Acyclic Graph
A graph that has no cycles and is directed.

Getting Ready in the Morning Example

Iterate through all the edges, and add one to the node that they point to.

Take all the nodes with 0 edges. This is the set of nodes that you can immediately go to.

Then pull off an arbitrary node in the zero set and add that to a list of tasks.

For each of that node's edges, subtract one from the count on the node. If this causes something to become a zero, add it to the zero set.

When the zero set is empty, you're done, and you've constructed a valid topological sorting in the list of tasks.

The zero set can be implemented as an array or anything with $O(1)$ removal and $O(1)$ addition. Additionally, you know the maximum possible size (n) ahead of time.

The zero set could alternatively be constructed in sorted order (with a BTree, perhaps?), allowing one to retrieve a topological sorting additionally sorted by another comparator.

Alternative
You could do this with a depth-first search instead.

Whenever you leave a node, add it to the start of the list. All this requires is a visited array.

The list requires $O(1)$ prepending or $O(1)$ appending and $O(n)$ reversal.

Note that you know the full size ahead of time.

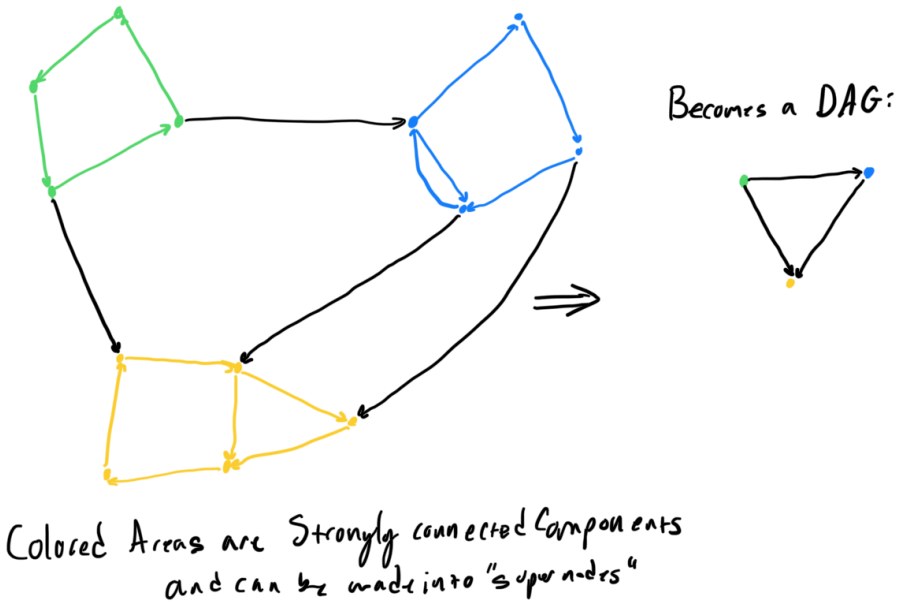
Alternatively, just reverse the edges first, and the order works out. With an adjacency matrix, this is just switching the meaning of the indices. (Kruskal doesn't think there's something nice with an adjacency list to reverse the edges).

Strongly Connected Graph

If every vertex is reachable from every other vertex, then a graph is strongly connected.

Strongly Connected Component

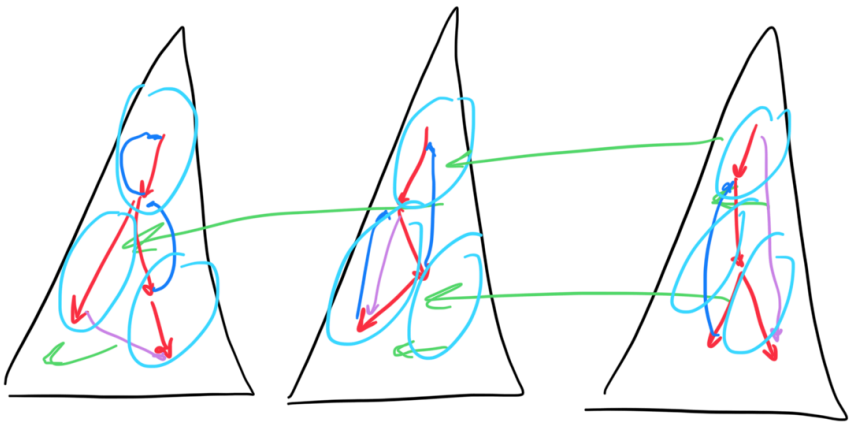
A maximal subgraph of a graph that is strongly connected.



Finding them

Note that if you do a depth-first search, strongly connected components are only within each subtree.

Reverse the edges of the graph, then do a depth-first search in reverse order of finish numbers. When you return from a depth-first search, remove all the nodes you found. They form a strongly connected component.



Breath-First Search

Create a queue. Add a node to the queue.

Repeatedly take a node off the queue and add all nodes attached to that node to the queue. When the queue is empty, you're done.

Order Notation

Proofs are:

1. Boring
2. Unhelpful

Justifying is not generally helpful, particularly if you already have a function.

How relations relate to order notation:

Relations	Order Notation	Vibes	Latex
$=$	Θ	Grows at the same rate	`\Theta`
$\leq$	O	Grows at most as fast	`O`
$\geq$	Ω	Grows at least as fast	`\Omega`
$<$	o	Grow faster than	`o`
$>$	ω	Grow slower than	`\omega`

To remember things, Θ has an equal sign in it and Ω points up.

Examples

- $2n^2 + 7 = \Theta(n^2)$

  If you wrote something like $\Theta(2n^2 + 7)$, that is unhelpful (albeit true), so you will get points off for it.

- $2n^2 + n \lg n = O(n^3)$
- $$\begin{aligned} 2n^2 + 4n + 3 &= 2n^2 + O(n) \\ &= 2n^2 + o(n^2) \\ &\sim 2n^2 \end{aligned}$$

$\sim$ is used for approximately equal to.

Limit Definitions

$$f(n) = o(g(n)) \leftrightarrow \lim_{h \to \infty} \frac{f(n)}{g(n)} = 0$$

$$f(n) = \omega(g(n)) \leftrightarrow \lim_{h \to \infty} \frac{f(n)}{g(n)} = \infty$$

Note that there should probably be some $\sup$'s thrown around here, but that's almost never a real issue.

Greedy Algorithms

Minimum Spanning Tree

You're given an undirected graph with weights on the edges, and you aim to minimize the total weight of the tree.

Theorem: Adding Minimum Edges Keeps minimum spanning tree

Assume we have a partial minimum spanning tree with subtrees separated by a boundary. Then the cheapest edge crossing the boundary is in a partial minimum spanning tree compatible with the previous one.

Proof

The general idea is that there is a certifier that can tell if an edge is in the minimum spanning tree.

Then, at some time, it says a minimal edge can't be part of the algorithm and constructs the rest of the tree to prove it.

Given the rest of the tree, since it's a spanning tree, it must have constructed edges crossing the boundary to reach all vertices.

Add the minimal edge the certifier didn't approve onto the tree. Since this tree was already spanning, adding this edge creates a cycle. You can then remove any edge across the boundary that the certifier chose in its optimal construction to form a spanning tree again. But because that edge was, at worst, the same cost, it was totally fine to add our minimal edge instead, and the certifier was wrong.

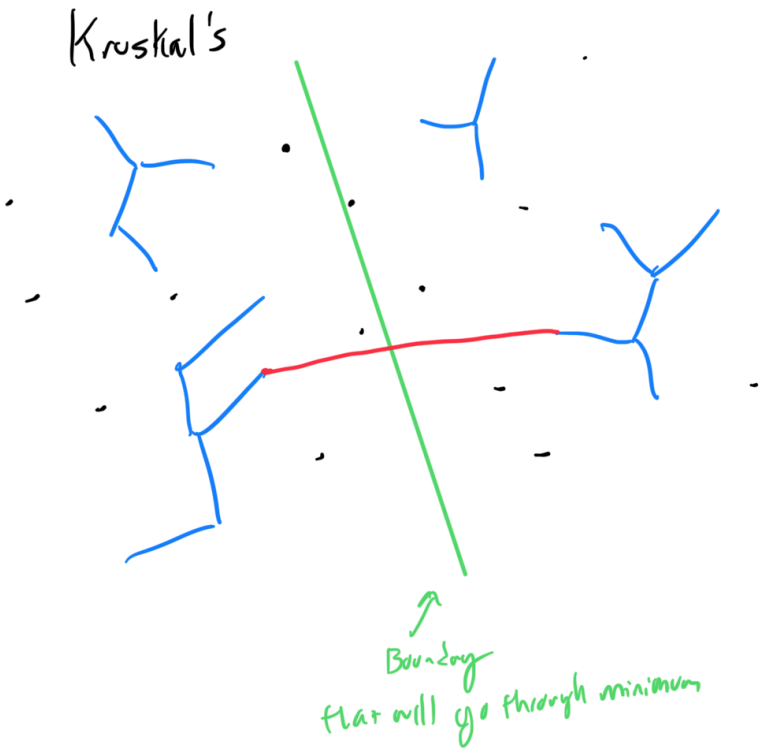
Kruskal's Algorithm

First, sort the edges by weight. Let this be in the list A. Go through the edges. If adding the edge to the tree wouldn't create a cycle, add it.

1. Sort edges:

Proof

Construct the boundary such that the minimum edge would be through the boundary.



Algorithm

Sort edges such that $e_1 \leq e_2 \leq e_3 \leq \cdots \leq e_m$.

Sorting will take $\Theta(m \log m) = \Theta(m \log n)$ time (since $n \leq m \leq n^2$).

For i from 1 to m, put edge e_i onto the tree if it does not create a cycle.

But how do you find these cycles?

By using the union-find problem.

If you're adding another edge, that edge should connect two different trees together. If it connected to the same tree, that would be a cycle.

(Something to note is that these trees can start from any vertex, and they will still be a tree)

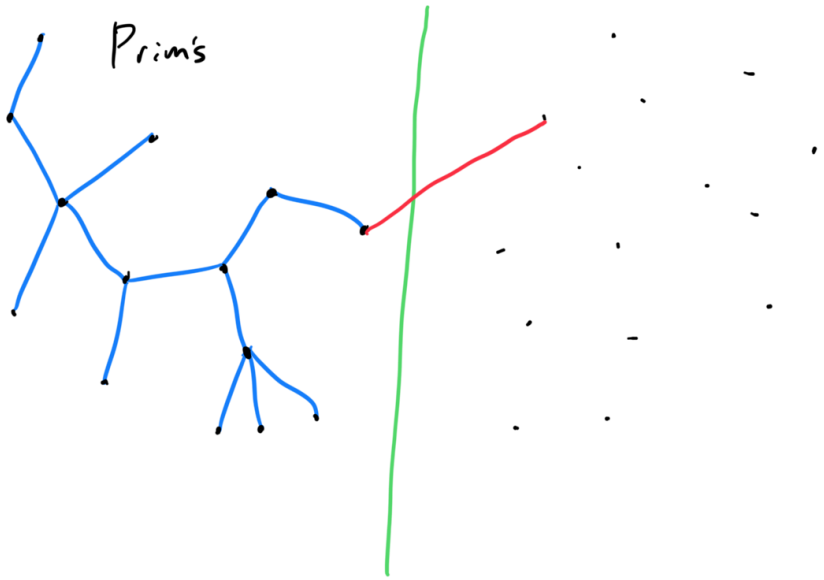
Trees of size s will have height at most $\log s$, when you balance the trees. (try to prove this with induction)

Prim's Algorithm

Start with any vertex. Put in the closest (least weight) vertex in the tree.

Proof

Construct the boundary such that the MST built so far is within the boundary, with no other nodes.



Interval Scheduling

Given some intervals, $I_i = [a_i, b_i]$, find the intervals that are nonoverlapping that maximizes= the number of tasks you can do.

Theorem

Scheduling by the earliest finish time gives the optimal solution.

Proof

Minimize Lateness

Minimize your maximal lateness.

Given tasks that are required to be done by d_i and take t_i time, find the arrangments such that $\max(\{f_i - t_i\})$ is as small as possible.

Algorithm

Sort by deadline.

$$d_1 \leq d_2 \leq \cdots \leq d_n$$

Then, work on each task, one at a time, 1 to n.

Basically, do the thing that's due next.

Theorem

Sorting by deadline finds the optimal solution.

Proof

Let a certifier reject some choice k, $d_1 \leq d_2 \leq d_k$, which would then result in $d_1 \leq d_2 \leq \cdots \leq d_k \leq \cdots \leq d_n$.

They instead choose something of the form $d_1 \leq d_2 \leq \cdots \leq d_{k-1} \leq \cdots \leq d_k \leq \cdots \leq d_b$.

In doing so, the increased the lateness of d_k by $t_a + t_{a+1} + \cdots + t_{k-1}$. This was not an improvement since the time must have increased because the deadlines are further in the future.

Caching

Keep stuff you access often in a cache, and then you can do things faster.

The optimal solution for this is to discard information that is needed farthest in the future. This is called Bélády's algorithm.

It relies on temporal locality, where you use things in the future "soon."

Spatial locality would rely on data that is close together being used together.

Least Recently Used (LRU) cache

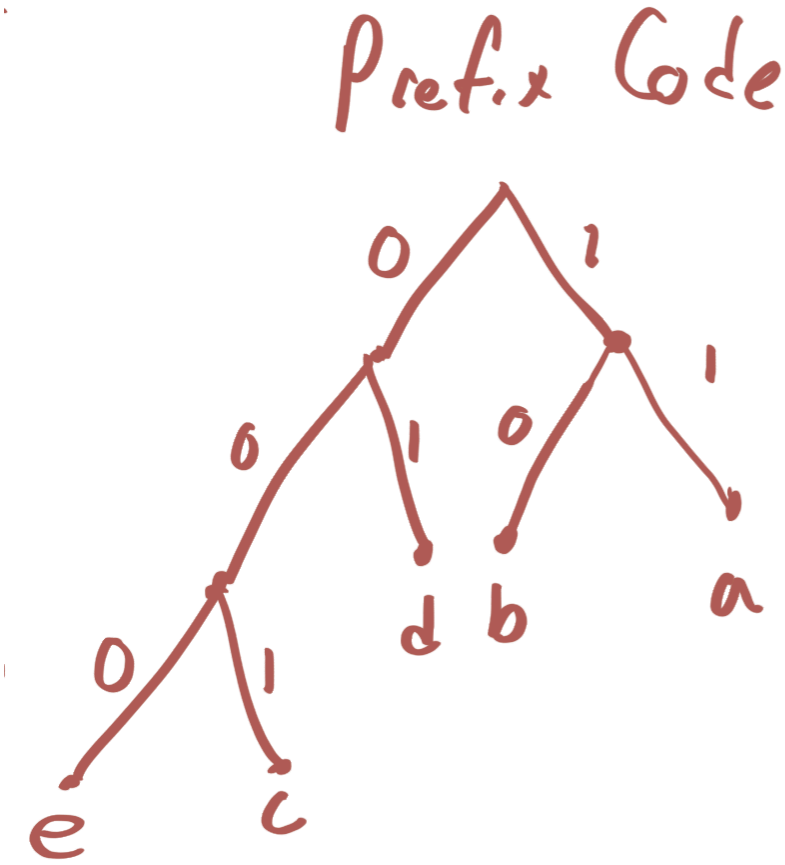
Evict what was the least recently used. Generally a good heuristic. It is what is usually used, or an approximation of it.

Huffman Encoding

Prefix Code

Guarantee that every character has a unique path on a binary tree, and you have a prefix code.

Letter	Frequency	Basic Encoding	Prefix Code	Huffman
a	0.32	`000`	`11`	`00`
b	0.25	`001`	`10`	`01`
c	0.20	`010`	`001`	`10`
d	0.18	`011`	`01`	`110`
e	0.05	`100`	`000`	`111`



Furthermore, the expected length of a letter is

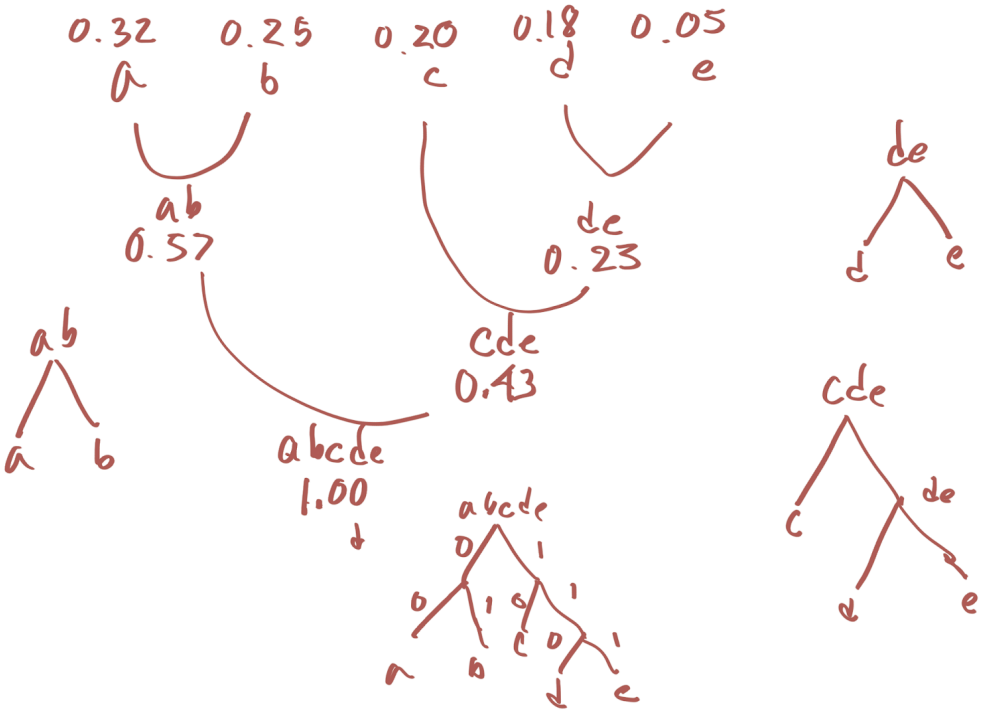
$$E[X] = \sum_{c \in \text{ chars}} p(c)\ \text{len}(c)$$

where p is the probability of getting the letter.

For our prefix code, this results in $0.32 \times 2 + 0.25 \times 2 + 0.20 \times 3 + 0.18 \times 2 + 0.05 \times 3 = 2.25$.

The real thing

The idea of Huffman encoding is to build up a binary tree.



For the Huffman code, this turns out to be $0.32 \times 2 + 0.25 \times 2 + 0.20 \times 2 + 0.18 \times 3 + 0.05 \times 3 = 2.23$, which is barely better.

Divide and Conquer

Merge Sort

In lecture online.

Other Examples

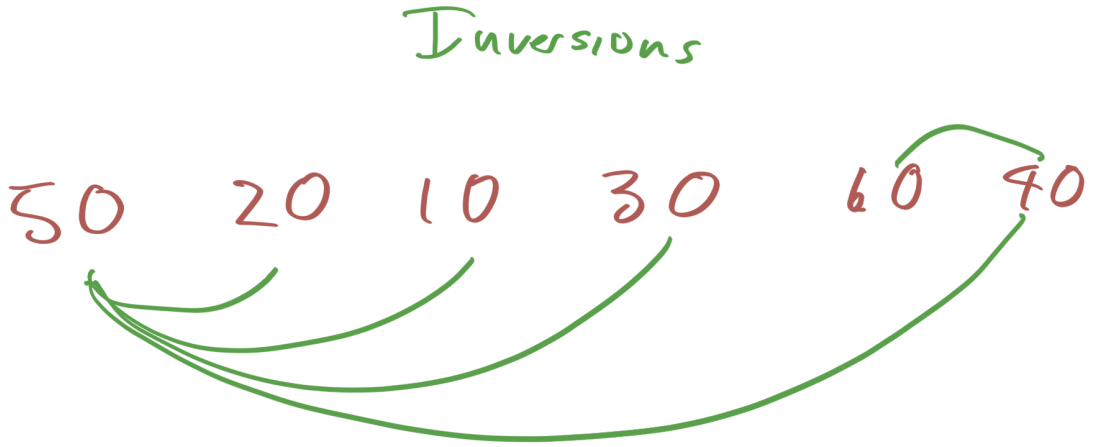
- Merge sort
- Maximum contiguous sum (bad solution)
- Quick sort
- Karatsuba

In general, you do something to create subproblems, then solve the subproblems, and then do something to the data you get.

Counting Inversions

$$A = [50, 20, 10, 30, 60, 40]$$

The inversions are numbers that are out of place relative to other numbers.



There are 6 inversions in this list.

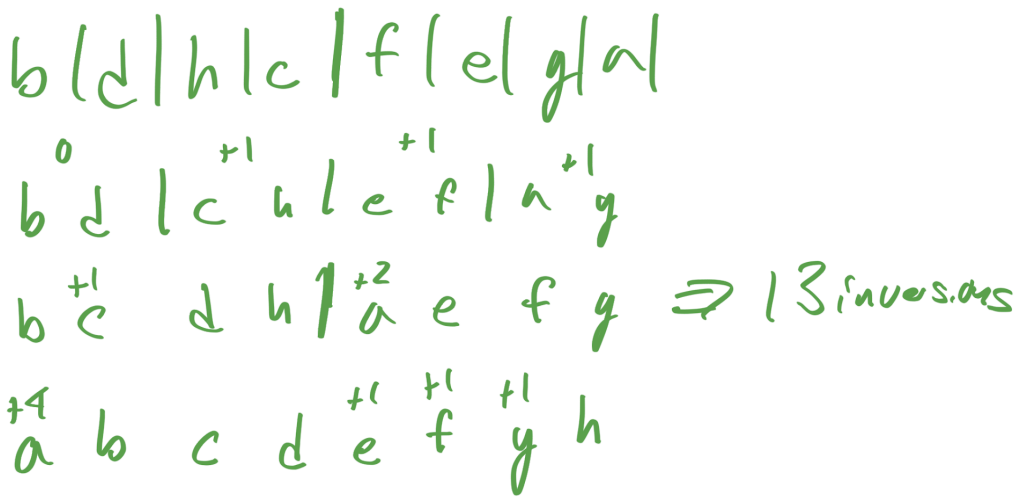
The number of inversions is the same as the number of exchanges that bubble sort would do.

The worst case occurs when the list is reversed, resulting in $\binom{n}{2}$ inversions.

Then the average case is $\frac{1}{2}\binom{n}{2}$ inversions.

To count inversions efficiently, perform merge sort. While merging, compare how far you invert.

For example, if you were merging bd and ch, when you moved the c down, it was inverted with the d.



Closest Pair

You are given n points with distances between them. Find the closest distance.

Bruteforce algorithm:

```
m = 0
for i in range(n):
    for j in range(i + 1, n):
        m = min(m, dist(i, j))
```

What about on a line?

1. Sort points.
2. Find the closest pair next to each other.

This is then a $n \log n$ algorithm, bounded by sorting.

```
m = 0
# sort points
for i in range(n-1):
  m = min(m, dist(i, i + 1))
```

Divide and Conquer a Line

High-level:

1. partition on the median such that half is on the left and half is on the right
2. Find the closest pair on the left and on the right side (recursive)
3. check the rightmost left point and the leftmost right point, and check their distance

Then $T(n) = \Theta(n) + 2T(\frac{n}{2}) + \Theta(1) = 2T(\frac{n}{2}) + \Theta(n)$, which implies $\Theta(n \log n)$.

Alternatively:

1. Sort points
2. Recurse on the left and right. And then find the endpoints, and compare them.

On a plane!

Similarly to the divide and conquer solution, cut the solution space in half.

We will decide to split on a line $x = x_0$.

First, sort by x values and by y values (separately).

Choose the middle value, and split it such that half is to the left and half is to the right. You can split by the x_0, and this will then give you two sorted sublists (you may want to pass these down).

You can split the y into sublists by splitting them in two by comparing the x value of a point to x_0.

Solve the problem on the left, resulting in δ_1 and solve the problem on the right, resulting in δ_2.

Let $\delta = \min(\delta_1, \delta_2)$.

Going down the y values on one half within the delta, compare to the next and previous 2 y-values on the other side.

Then, this is:

Before recursing, you do $\Theta(n \lg n)$ work to sort.

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

And therefore, the total time is $\Theta(n \lg n)$

Strassen's algorithm

For multiplying matrices more quickly than $\Theta(n^3)$.

Let there be two 2×2 matrices A and B.

$$A = \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} \qquad B = \begin{pmatrix} b_{11} & b_{12} \\ b_{21} & b_{22} \end{pmatrix}$$
$$\begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} \times \begin{pmatrix} b_{11} & b_{12} \\ b_{21} & b_{22} \end{pmatrix} = \begin{pmatrix} c_{11} & c_{12} \\ c_{21} & c_{22} \end{pmatrix}$$

Traditionally this is:

$$\begin{aligned} c_{11} &= a_{11}b_{11} + a_{12}b_{21} \\ c_{12} &= a_{11}b_{12} + a_{12}b_{22} \\ c_{21} &= a_{21}b_{11} + a_{22}b_{21} \\ c_{22} &= a_{21}b_{12} + a_{22}b_{22} \end{aligned}$$

For a general matrix, this can be $c_{ij} = \sum_{k=1}^{n} a_{ik}b_{kj}$, where n is the dimension of the matrix.

In general, if A and B are $n \times n$ matrices, where $n = 2^k$, $k \in \mathbb{Z}^+$, we can multiply A and B by partitioning A and B into 4 submatrices each of size $(\frac{n}{2}) \times (\frac{n}{2})$. Interestingly, the above rule for multiplying 2×2 matrices still works where $A_{ij}B_{jk}$ means doing matrix multiplication on two $(\frac{n}{2}) \times (\frac{n}{2})$ matrices. This is called block matrix multiplication.

This can be converted into a recursive (divide and conquer) algorithm for matrix multiplication. Since the algorithm performs 8 recursive multiplications and 4 matrix additions on matrices of size $(\frac{n}{2}) \times (\frac{n}{2})$, the running time is derived from the recurrence:

$$T(n) = 8T\Big(\frac{n}{2}\Big) + 4\Big(\frac{n}{2}\Big)^2\alpha$$

Assuming $T(1) = \mu, T(n) = n^2(n-1)\alpha + n^3\mu = \Theta(n^3)$.

This is the same as just doing it normally, so it doesn't really help.

But there is a clever way to it instead with 7 multiplies and 18 adds.

This results in

$$T(n) = 7T\Big(\frac{n}{2}\Big) + 18\Big(\frac{n}{2}\Big)^2\alpha, T(1) = \mu$$

$$T(n) = \mu n^{\lg 7} + 6\alpha\big(n^{\lg(7)} - n^2\alpha\big)$$

For multplications this becomes $T(n) = n^{\lg 7} \approx n^{2.80735}$

Carry look ahead addition

If you have two 0s added, you know there will not be a carry. If you know that there are two 1s added, you know there will be a carry.

You can use this to do work ahead of time.

Log Transform

If you have a lot of multiplies, you can take the logarithm since it converts multiples to additions.

Fast Fourier Transform

$$\begin{aligned} A(x) &= a_0 + a_1 x + a_2 x^2 + \cdots + a_{n-1} x^{n-1} \\ B(x) &= b_0 + b_1 x + b_2 x^2 + \cdots + b_{n-1} x^{n-1} \\ C(x) &= A(x)B(x) \\ &= c_0 + c_1 x + c_2 x^2 + \cdots + c_{2n-2} x^{2n-2} \end{aligned}$$

Then, evaluate A, B at $2n$ values.

$$\begin{aligned} & x_1, x_2, ..., x_{2n} \\ \Rightarrow\ & A(x_1), A(x_2), ..., A(x_{2n}) \\ \Rightarrow\ & B(x_1), B(x_2), ..., B(x_{2n}) \end{aligned}$$

Using those values, compute C at $2n$ values:

$$\begin{aligned} C(x_1) &= A(x_1)B(x_1) \\ C(x_2) &= A(x_2)B(x_2) \\ &\vdots \\ C(x_{2n}) &= A(x_{2n})B(x_{2n}) \end{aligned}$$

You can then reconstruct $C(x)$ using those values.

$$\begin{aligned} A_{\text{even}}(x) &= a_0 + a_2 x + a_4 x^2 + ... + a_{n-2} x^{\frac{n-2}{2}} \\ A_{\text{odd}}(x) &= a_1 + a_3 x + a_5 x^2 + ... + a_{n-1} x^{\frac{n-2}{2}} \end{aligned}$$

Then notice:

$$A(x) = A_{\text{even}}(x^2) + x A_{\text{odd}}(x^2)$$

Using this, we can evaluate polynomials via divide and conquer:

```
def evaluate(A, x):
    if A.degree == 0:
        return A[0]
    x_squared = x**2
    a_even = evaluate(A.even, x_squared)
    a_odd = evaluate(A.odd, x_squared)
    return a_even + x * a_even
```

On its own, this takes $T(n) = 2T(\frac{n}{2}) + 2$ time, and $T(1) = 0$, counting multiplies.

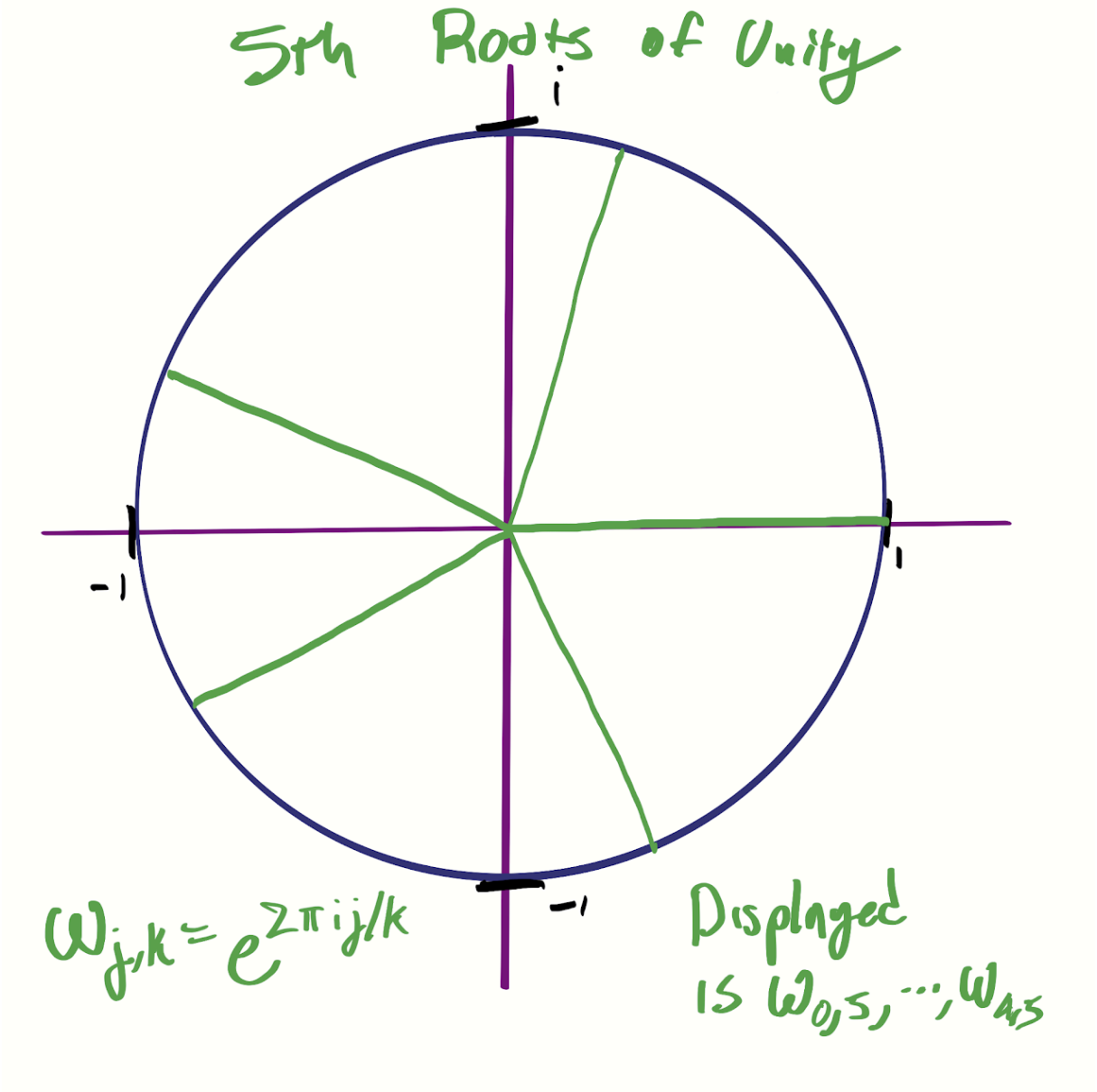
Then, $T(n) = 2(n-1) = \Theta(n)$, which is the same complexity as the normal way to evaluate polynomials.

This then makes the $2n$ evaluations take $\Theta(n^2)$ time.

Finding the $c_0, ..., c_{2n}$ values takes $\Theta(n)$ time.

But we can select our roots better!

$$\omega_{j,k} = e^{\tau i j / k}$$



Evaluate $A(x)$ at the $2n$ roots of unity.

Assume n is a power of two.

$$\begin{aligned} A(\omega_{j,2n}) &= A_{\text{even}}(\omega_{j,2n}^2) + \omega_{j,2n} A_{\text{odd}}(\omega_{j,2n}^2) \\ &= A_{\text{even}}(\omega_{j,n}) + \omega_{j,2n} A_{\text{odd}}(\omega_{j,n}) \end{aligned}$$

Done with the example $A(x) = 1 + 4x - 3x^2 + 2x^3$, and do one split:

x	$A(x)$	x^2	$A_{\text{even}}(x^2)$	$A_{\text{odd}}(x^2)$	$xA_{\text{odd}}(x^2)$	$A_{\text{even}}(x^2) + xA_{\text{odd}}(x^2)$
1	4	1	-2	6	6	4
-1	-8	1	-2	6	-6	-8
i	$4+2i$	-1	4	2	$2i$	$4+2i$
$-i$	$4-2i$	-1	4	2	$-2i$	$4-2i$

See that there is only 1 and –1. This is very convenient; we have reduced the solution space.

To produce the values for all the roots of unity, this will take:

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

Which is a very nice improvement on the previous $\Theta(n^2)$.

We want

$$C(x) = \sum_{s=0}^{2n-1} c_s x^s$$

But define

$$D(x) = \sum_{s=0}^{2n-1} d_s x^s$$

Where $d_s = C(\omega_{s,2n})$, which we know from evaluating before.

Then:

$$\begin{aligned}
D(\omega_{j,2n}) &= \sum_{s=0}^{2n-1} d_s (\omega_{j,2n})^s \\
&= \sum_{s=0}^{2n-1} C(\omega_{s,2n})(\omega_{j,2n})^s \\
&= \sum_{s=0}^{2n-1} \left[\sum_{t=0}^{2n-1} \left(c_t \cdot (\omega_{s,2n})^t \right) \right] (\omega_{j,2n})^s \\
&= \sum_{t=0}^{2n-1} \sum_{s=0}^{2n-1} c_t \cdot (\omega_{s,2n})^t (\omega_{j,2n})^s \\
&= \sum_{t=0}^{2n-1} c_t \sum_{s=0}^{2n-1} \left(e^{\tau is/(2n)}\right)^t \left(e^{\tau ij/(2n)}\right)^s \\
&= \sum_{t=0}^{2n-1} c_t \sum_{s=0}^{2n-1} e^{\tau its/(2n)} e^{\tau isj/(2n)} \\
&= \sum_{t=0}^{2n-1} c_t \sum_{s=0}^{2n-1} e^{\tau its/(2n) + \tau isj/(2n)} \\
&= \sum_{t=0}^{2n-1} c_t \sum_{s=0}^{2n-1} e^{\tau is(t+j)/(2n)} \\
&= \sum_{t=0}^{2n-1} c_t \sum_{s=0}^{2n-1} (\omega_{t+j,2n})^s
\end{aligned}$$

Let $\omega_{k,2n} \neq 1$, and $k = t + j$:

$$\sum_{s=0}^{2n-1} (\omega_{k,2n})^s = \frac{1 - (\omega_{k,2n})^{2n-1+1}}{1 - \omega_{k,2n}} = \frac{1 - (\omega_{k,2n})^{2n}}{1 - \omega_{k,2n}} = \frac{1 - \left(e^{\tau ik/(2n)}\right)^{2n}}{1 - \omega_{k,2n}} = \frac{1-1}{1 - \omega_{k,2n}} = \frac{0}{1 - \omega_{k,2n}} = 0$$

However, when $\omega_{k,2n} = 1$,

$$\sum_{s=0}^{2n-1} 1 = 2n$$

Let $t + j = 2n$ since everything else becomes zero. Then $t = 2n - j$:

$$\begin{aligned} D(\omega_{j,2n}) &= c_{2n-j} \sum_{s=0}^{2n-1} (\omega_{2n,2n})^s \\ &= c_{2n-j} 2n \\ &= 2n c_{2n-j} \end{aligned}$$

And therefore, $D(\omega_{k,2n}) = 2nc_{2n-j}$, and finally

$$c_{2n-j} = \frac{D(\omega_{j,2n})}{2n}$$

Using this property, you can find c_m by varying j.

You can evaluate $D(\omega_j, 2n)$ for all j in $\Theta(n \lg n)$ time. Dividing takes $\Theta(1)$ time for each, and so takes $\Theta(n)$ for all values of j. In sum, this takes $\Theta(n \lg n)$ time.

Adding this on to the other program to evaluate the $C(\omega)$'s, this takes in total $\Theta(n \lg n)$ time to generate the polynomial $C(x)$.

Dynamic Programming

Fibonacci

Fibonacci, to find the nth number, using variables:

```
F_n_minus_1 = 1
F_n = 1

for i in range(3, n + 1):
    F_n_minus_2 = F_n_minus_1
    F_n_minus_1 = F_n
    F_n = F_n_minus_1 + F_n_minus_2
print(F_n)
```

You can also just use arrays:

```
F = [None] * n
F[0] = 1
F[1] = 1
for i in range(2, n + 1):
    F[i] = F[i-1] + F[i - 2]
print(F[n])
```

Or do it recursively:

```
def f(n):
    if n == 1 or n == 2:
        return 1

    return f(n - 1) + f(n - 2)
```

Comically terrible complexity, but oh well. It takes $\Theta(\varphi^n)$ time, where φ is the golden ratio (due to the asymptotic complexity of the Fibonacci sequence)

If you memoize the results, it works fine.

Richard Bellman called this dynamic programming because “it’s impossible to use the word dynamic in a pejorative sense” and he wanted to shield his work from Charles Wilson, who he knew didn’t like math.

```
fib = [None] * (n + 1)

def f(n):
    nonlocal fib
    if fib[n] != None:
        return fib[n]

    if n == 1 or n == 2:
        return 1

    fib[n] = f(n - 1) + f(n - 2)
    return fib[n]
```

Alternatively, in python:

```
from functools import cache

@cache
def f(n):
    if n == 1 or n == 2:
        return 1
    return f(n - 1) + f(n - 2)
```

But to optimize this, you can do it in a for loop instead:

```
fib = [None] * (n+1)

fib[1] = 1
fib[2] = 1

for i in range(3, n + 1):
    fib[i] = fib[i - 1] + fib[i - 2]
```

Notice that we went back to the array method! In truth, the best method was just the first one we did since it only requires $\Theta(1)$ memory. But, by doing this through dynamic programming, this idea of remembering can be generalized to different problems!

Subset Sum

Given a list of integers

$$w_1, w_2, ..., w_n$$

and a target w, and we want to find a subset of the w_i whose sum is as large as possible but does not exceed w.

For example

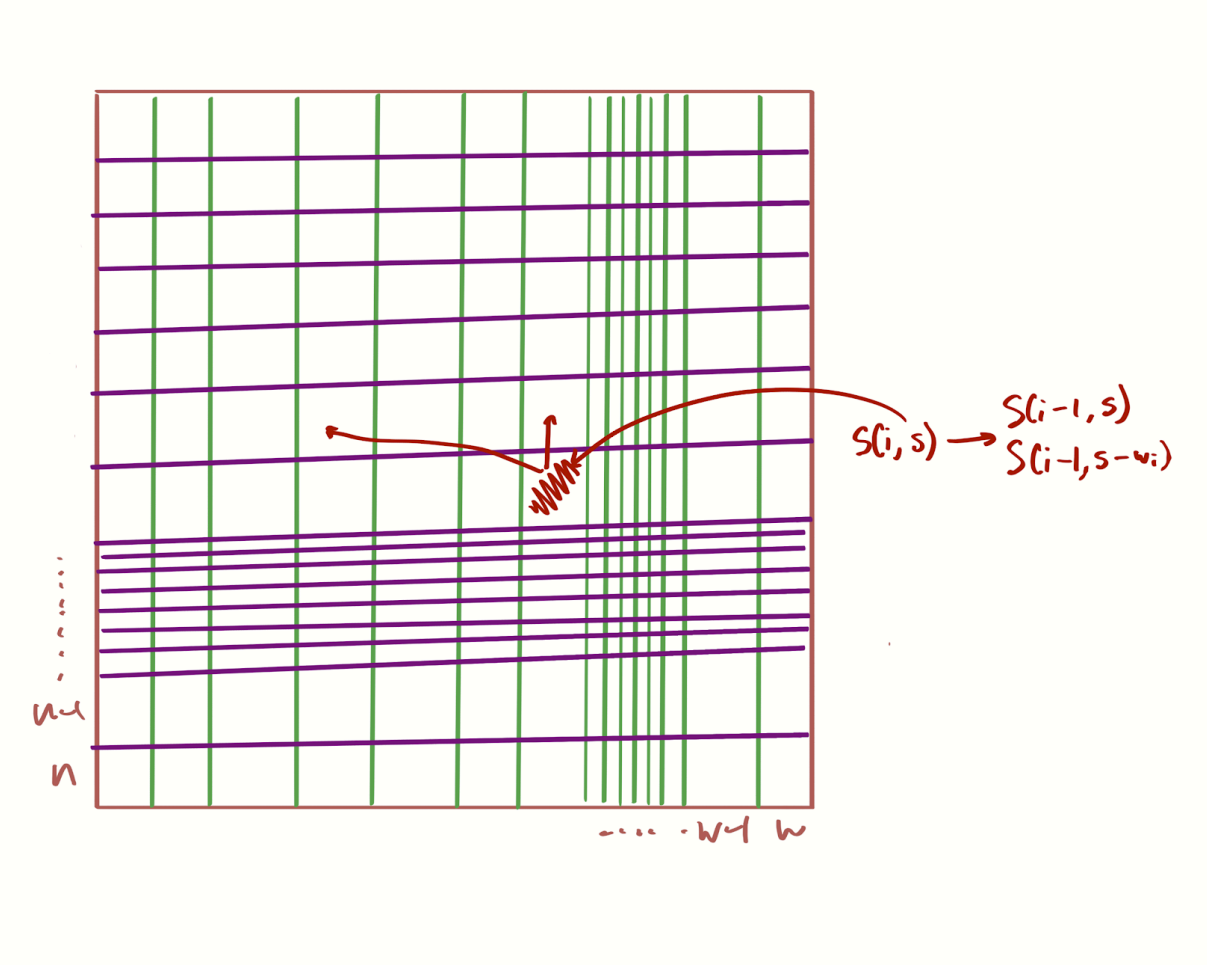
$$[3, 5, 8, 11]$$
$$w = 20$$

$$8 + 11 = 19$$
$$3 + 5 + 11 = 19$$

How can we make a recurrence? Splitting up the problem is usually a good idea. Let $S(i)$ be the maximum sum not exceeding s that only uses elements $1, ..., i$ of the list.

$$
\begin{aligned}
S(i, s) = \max(& \\
& S(i-1), \\
& S(i-1, s-w_i) + w_i \\
&)
\end{aligned}
$$

In this problem, we have a 2-dimensional table, with the values on one side and the things to sum to on the other axis.




```
for s in range(0, w + 1):
    S[0, s] = 0


for i in range(0, n + 1):
    S[i, 0] = 0


for i in range(1, n + 1):
    for s in range(1, w + 1):
        if s - w[i] < 0:
            S[i, s] = S[i - 1, s]
        else:
```

```
S[i, s] = max(
  S[i - 1, s],
  S[i - 1, s - w[i]] + w[i],
)
```

You can save memory by going backward with s, which eliminates the nw memory complexity and takes w memory instead.

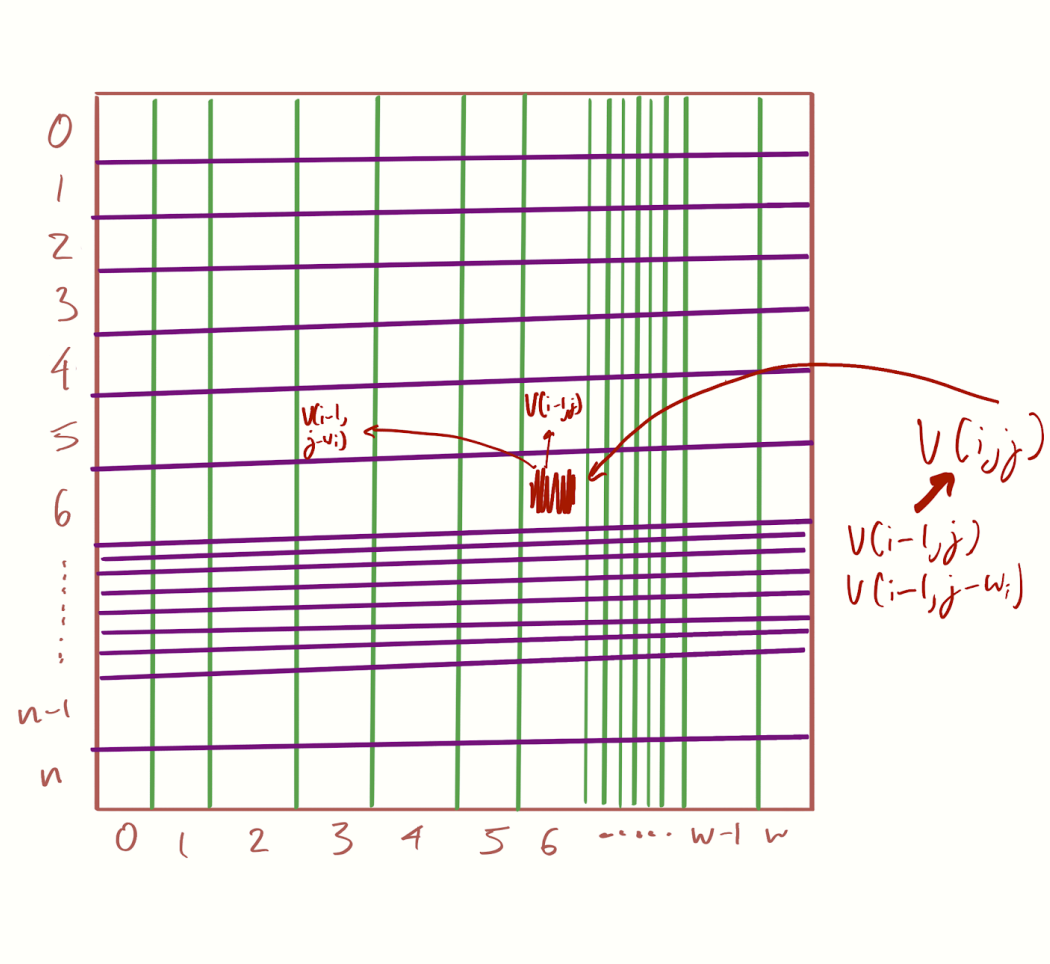
This takes $\Theta(nw)$ time. Note that this is *not* polynomial time since w is in bits, which makes $\Theta(nw) = \Theta\left(n2^{\lg w}\right)$ and therefore, it's exponential.

Knapsack Problem

Have weights $w_1, w_2, ..., w_n$ with a max weight w and values $v_1, v_2, ..., v_n$. Maximize total value.

Let $V(i, j)$ be the maximum sum of values that can be packed only using items $1, ..., i$ with total weight less than or equal to j.

$$
\begin{aligned}
V(i,j) = \max(& \\
& V(i-1,j), \\
& V(i-1,j-w_i) + v_i \\
&) \\
V(i,0) &= 0 \\
V(0,j) &= 0
\end{aligned}
$$



```
for i in range(0, n + 1):
    value[i, 0] = 0

for j in range(1, w + 1):
    value[0, j] = 0

for i in range(1, n + 1):
    for j in range(1, weight[i]):
        value[i, j] = value[i - 1, j]
    for j in range(weights[i] + 1, w + 1):
        value[i, j] = max(
            value[i - 1, j]
            value[i - 1, j - weights[i]] + values[i]
        )
```

Chained Matrix Multiplication

Given matrices $A_1, A_2, ..., A_n$, form the product $A_1A_2A_3 \cdots A_n$.

For a matrix multiplication

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

If you multiply two matrixes

$$A \in M(\mathbb{R})_{p \times q}, B \in M(\mathbb{R})_{q \times r}, AB \in M(\mathbb{R})_{p \times r}$$

Then, to do the multiplication the traditional way, it takes $p \times q \times r$ atomic multiplies.

Then, notice if you take

$$(AB)C = A(BC)$$

they have different numbers of multiplications.

The real question here is given $p_0, p_1, p_2, ..., p_n$, representing $p_0 \times p_1, p_1 \times p_2, ..., p_{n-1} \times p_n$ size matrices, find the best place to put parentheses.

Take matrices: $A_1A_2 \cdots A_n$

Split them: $(A_1A_2 \cdots A_k)(A_{k+1}A_{k+2} \cdots A_n)$

You have two subproblems!

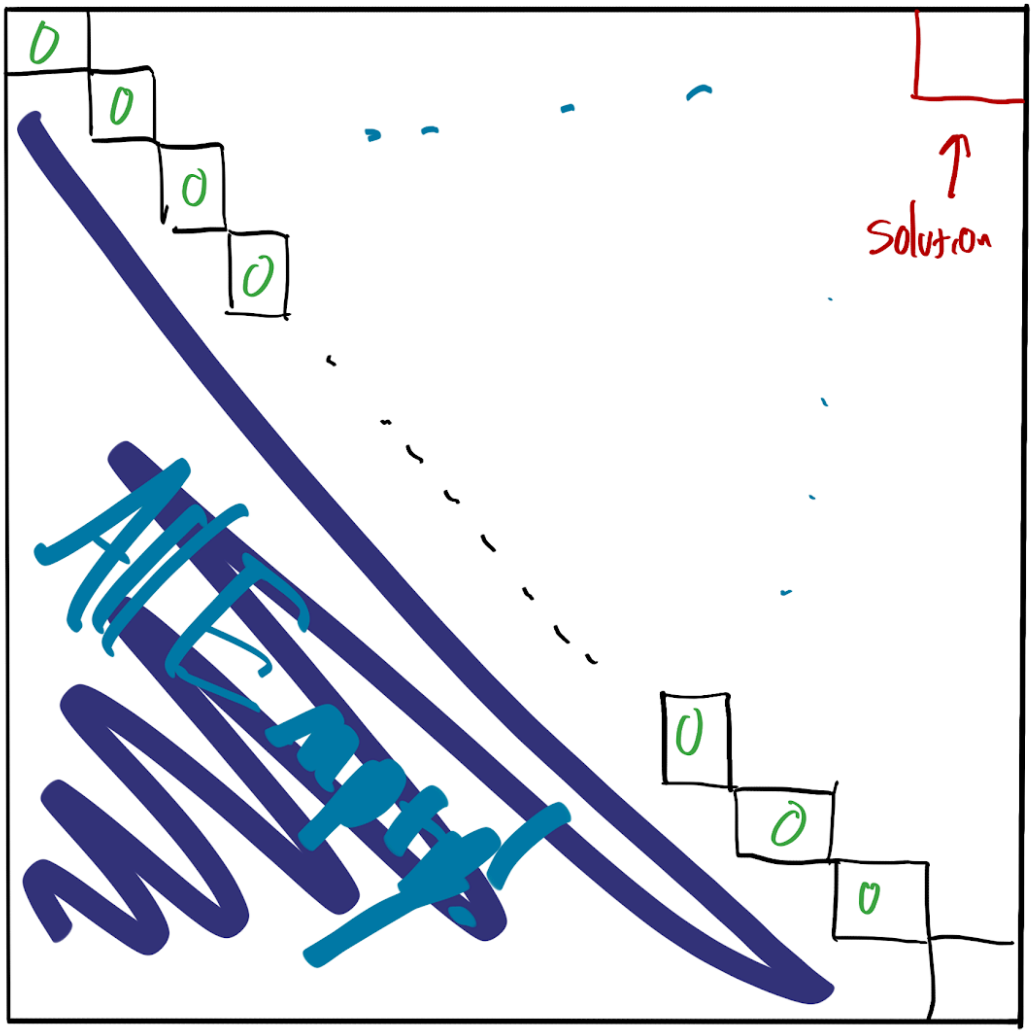
Let $M(i, j)$ be the minimum cost to multiply matrices $A_i, A_{i+1}, ..., A_j$.

$$m(i, j) = \min\{m(i, k) + m(k + 1, j) + p_{i-1}p_kp_j \mid k \in \{i, ..., j - 1\}\}$$

$$m(i, i) = 0$$

Notice that to evaluate a $m(i, j)$, you need the values at all $m(k, m)$ where $k < i$ or $j < i$ and $k \leq i$ and $j \leq i$.

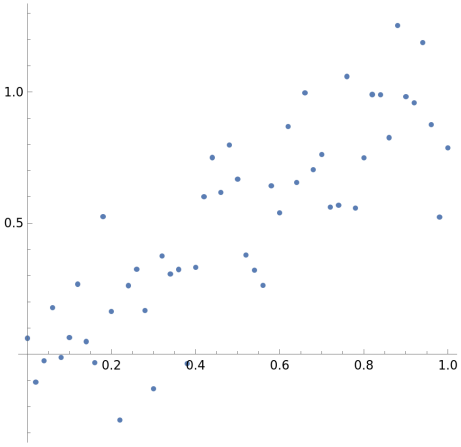
To evaluate this, we can evaluate diagonally.



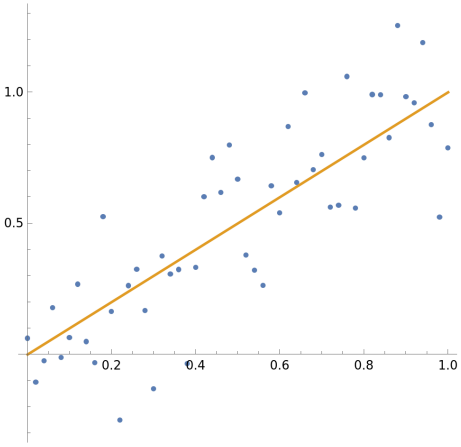

```
for i in range(1, n + 1):
    m[i, i] = 0

for l in range(2, n + 1):
    for i in range(1, n - l + 1 + 1):
        j = i + l - 1
        M = float("inf")
        for k in range(i, j):
            M = min(M,
              m[i, k] + m[k + 1, j] + p[i - 1] * p[k] * p[j]
            )

        m[i, j] = M
```

Segmented Least Squares

Given a plot, with random data:

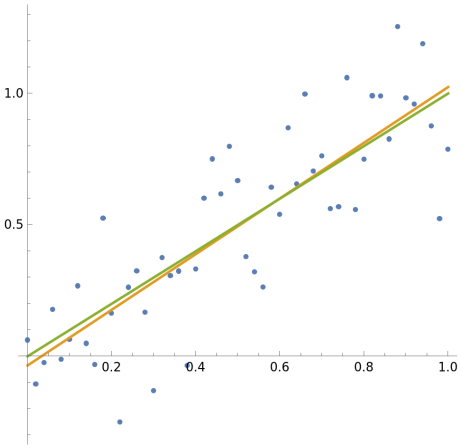


Find a line that fits well through it:



But how can we know that this is the best line? We can't, but we can make the goal to have the sum of the squares as minimal as possible.

This results in this line, the one in orange:



The line in green is the previous plot.

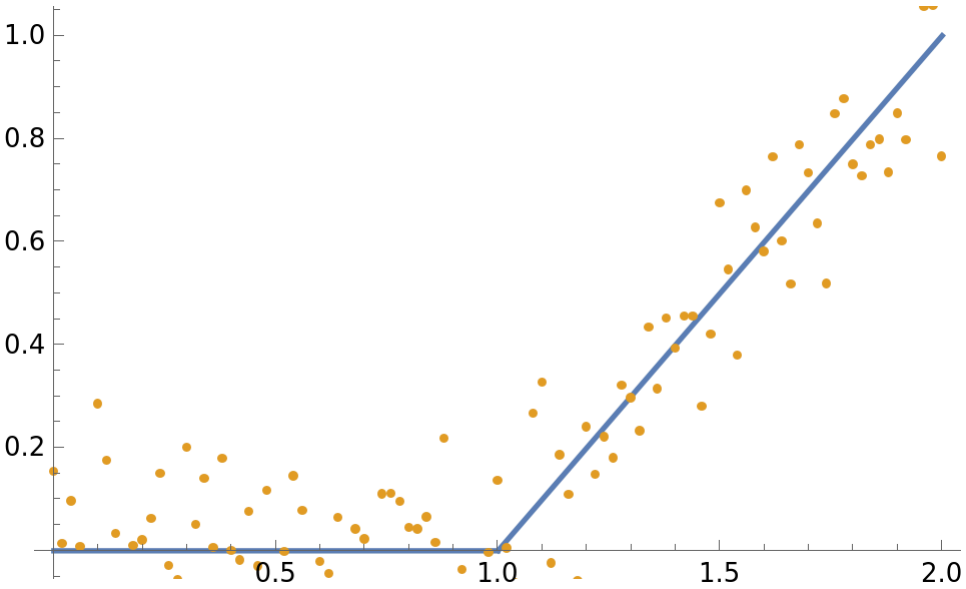
The error that we seek to minimize is given by this formula

$$\text{Error}(L,p) = \sum_{i=1}^{n} (i_i - ax_i - b)^2$$

$$a = \frac{n(\sum x_i y_i) - (\sum x_i)(\sum y_i)}{n(\sum x_i^2) - (\sum x_i)^2}$$

$$b = \frac{\sum y_i - a \sum x_i}{n}$$

But, for segmented least squares, you can also make lines like this:



The cost is the same as the normal least squares fit, and an additional cost for each additional line.

Let

$$e(i, j) = \sum_{k=i}^{j} (i_k - a x_k - b)^2$$

$\mathrm{OPT}(j)$ is the minimal cost of a segmented least squares fit for points $1, \ldots, j$.

$$\mathrm{OPT}(j) = \min_{1 \le i \le j} (c + \mathrm{OPT}(i-1) + e(i, j))$$

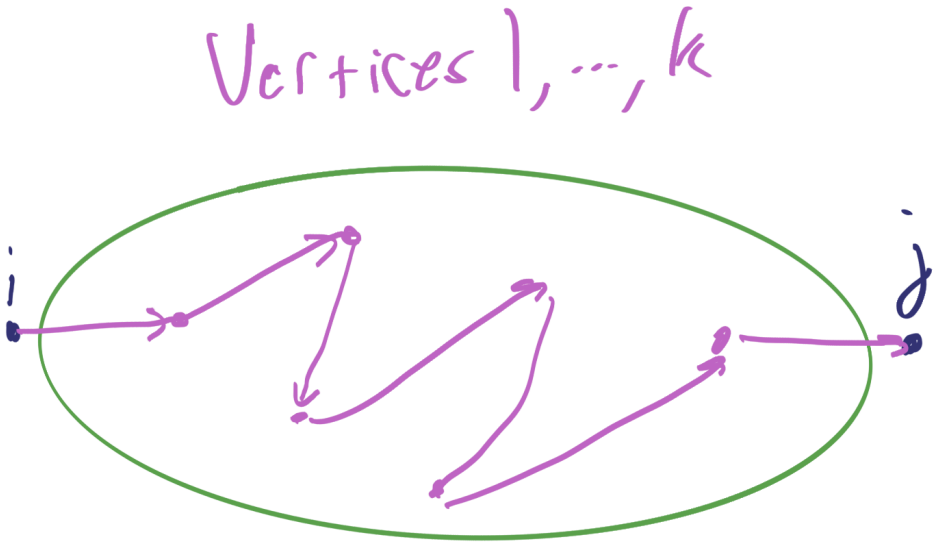
$$\mathrm{OPT}(1) = 0$$

```
for i in range(1, n + 1):
    for j in range(1, n + 1):
        # compute least squares fit for points i to j.
        e[i, j] = magic()

for j in range(1, n + 1):
    m = float("inf")
    for i in range(1, j + 1):
        m = min(
            m,
            e[i, j] + c + M[i - 1]
        )
    M[j] = m
```

Shortest path

Weight matrix: $W[i, j]$. Assume $W[i, i] = 0$.

$D^k[i, j]$ is the length of the shortest path from i to j that only uses internal vertices from the set $\{1, k\}$.



You either use the kth vertex or you don't:

$$D^k[i, j] = \min\big(D^{k-1}[i, j], \\ D^{k-1}[i, k] + D^{k-1}[k, j]\big)$$

For the base case, if you have no in-between nodes, you have no choice but to use the weight between the nodes.

$$D^0[i, j] = W[i, j]$$

```
for i in range(1, n + 1):
    for j in range(1, n + 1):
        D[0, i, j] = W[i, j]


for k in range(1, n + 1):
    for i in range(1, n + 1):
        for j in range(1, n + 1):
            D[k, i, j] = min(
                D[k - 1, i, j],
                D[k - 1, i, k] + D[k - 1, k, j]
            )
```

This takes $\Theta(n^3)$ time by the second loop.

This currently takes $\Theta(n^3)$ space, but you can reduce it to $\Theta(n^2)$ by only keeping the $k-1$ matrix while producing the k matrix.

Even better, you can just do:

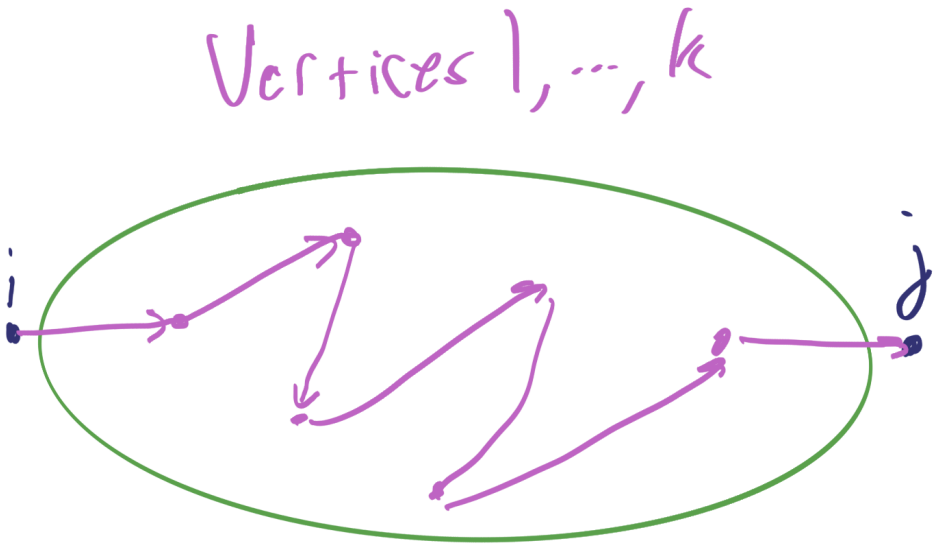
```
for i in range(1, n + 1):
    for j in range(1, n + 1):
        D[i, j] = W[i, j]
```

```
for k in range(1, n + 1):
    for i in range(1, n + 1):
        for j in range(1, n + 1):
            D[i, j] = min(
                D[i, j],
                D[i, k] + D[k, j]
            )
```

Transitive Closure

Given an adjacency matrix $A[i, j]$, form the transitive closure matrix $T[i, j]$, which tells you if there are paths from i to j.

$T^k[i, j]$ is 1 if there is a path from i to j that only uses internal vertices from the set $\{1, ..., k\}$.



$$T^k[i, j] = T^{k-1}[i, j] \vee \left(T^{k-1}[i, k] \wedge T^{k-1}[k, j]\right)$$

$$T^0[i, j] = A[i, j]$$

Which then becomes:

```
for i in range(1, n + 1):
    for j in range(1, n + 1):
        T[0, i, j] = A[i, j]
```

```
for k in range(1, n + 1):
    for i in range(1, n + 1):
        for j in range(1, n + 1):
            T[k, i, j] =
                T[k - 1, i, j] or (T[k - 1, i, k] and T[k - 1, k, j])
```

But notice if `T[k - 1, i, k] == 1`, `T[k, i, j] = T[k - 1, i, j] or T[k - 1, j]`. Alternatively, if `T[k - 1, i, k] == 0`, `T[k, i, j] = T[k - 1, i, j]`.

And then:

```
for i in range(1, n + 1):
    for j in range(1, n + 1):
        T[0, i, j] = A[i, j]


for k in range(1, n + 1):
    for i in range(1, n + 1):
        if T[i, k]:
            for j in range(1, n + 1):
                T[i, j] = T[i, j] or T[k, j]
```

Random Note

You can use the fourier transform to multiply integers to do it much faster: $O(n \lg n \lg \lg n)$.

This has since been improved to $O(n \lg n)$.

Segmented Alignment

```
ocurrance
occurrence
```

These strings differ. But how?

Define a gap penalty δ and a mismatch penalty $\alpha(p, q)$. Note that $\alpha(p, p)$ is 0.

Define $\text{opt}(i, j)$ as the cost of matching the first i letters of the first word with the first j letters of the second word.

Then:

$$\begin{aligned}\text{opt}(i, j) = \min\big(&\\ &\text{opt}(i-1, j-1) + \alpha\big(x_i, y_j\big),\\ &\text{opt}(i-1, j) + \delta,\\ &\text{opt}(i, j-1) + \delta\\ &\big)\\ \text{opt}(0, i) = \text{opt}(i, 0) &= i\delta\end{aligned}$$

To create greater indexed values, we need every value that is indexed one lower.

```
# A[0...m, 0...n]

for i in range(0, m + 1):
    A[i, 0] = delta * i
for j in range(1, n + 1):
    A[0, j] = delta * j

for i in range(1, m + 1):
    for j in range(1, n + 1):
        A[i, j] = min(
          A[i - 1, j - 1] + alpha(x[i], y[i]),
          A[i - 1, j] + delta,
          A[i, j - 1] + delta
        )
```

NP-completeness

Problems in P can be solved in polynomial time. Problems in NP can be verified in polynomial time.

3-SAT, SAT, and circuit SAT are in NP-complete.

The meaning of NP-complete means that if one of them can be solved in polynomial time, everything in NP can be. If one of them cannot be solved in polynomial time, then $P \neq \mathrm{NP}$.

Hamiltonian Cycle

A simple cycle that hits every vertex exactly once.

Theorem

Finding a Hamiltonian cycle is NP-complete.

Proof

1. Show it is in NP
2. Show it hard for NP

To do so, we will show $3\text{-SAT} \underset{P}{\leq} \text{Hamiltonian Cycle}$

Where $a \underset{P}{\leq} b$ means that a is polynomially reducible to b. (it will only take a polynomial amount of time, assuming that you have b as an oracle).

This is in NP because the verifier just checks if a produced Hamiltonian cycle is a Hamiltonian cycle, which it can do by making sure each node is visited, and that you make no illegal moves (attempting to go on nonexistent routes).

This takes $O(n^2)$ time, which is polynomial.

To prove this is hard for NP, we will see if we can solve 3-SAT with it.

3-SAT has a bunch of clauses, $c_1, c_2, c_3, ..., c_k$ and a bunch of variables, $x_1, x_2, ..., x_n$. Each clause has 3 variables ored together, and each variable may or may not be negated.

Karp reduction can only produce one instance, and must have the same output. We will always do Karp reductions in this class.

Let us take the example of a 3-SAT problem $(x_1 \vee \neg x_2 \vee x_3) \wedge (\neg x_1 \vee \neg x_2 \vee x_3) \wedge (\neg x_1 \vee x_2 \vee \neg x_3)$

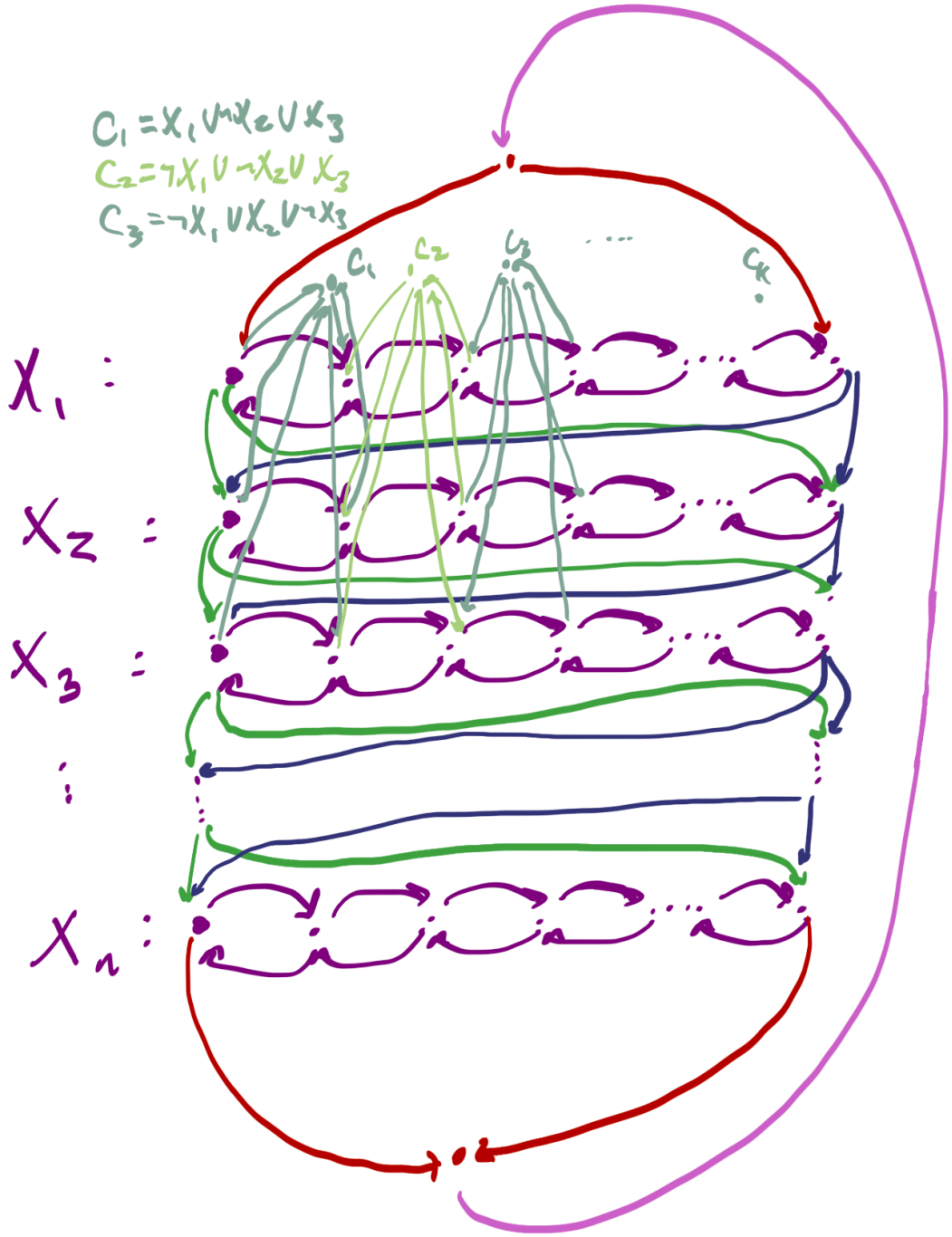
Going left to right on a path across indicates true and going right to left on a path indicates false.

By adding clause nodes, since they are required to be passed through, you can require that at least one direction required by a clause is chosen, since a Hamiltonian cycle must pass through all vertices.

For example, if a clause is $x_1 \vee \neg x_2 \vee x_3$, this will require that x_1 goes right, x_2 goes left or x_3 goes right. To enforce this, connect the first node of x_1 to the clause node and then the clause node to the second node of x_1. Further, connect the second node of x_2 to the clause node and then the clause node to the first node of x_2. Finally, connect the first node of x_3 to the clause node and then the clause node to the second node of x_3.

This construction has $2 + k + (k + 1)n$ vertices and $1 + 6k + 2nk + 4n$ edges. These are both polynomials, and therefore this is a Karp reduction.

For a Hamiltonian path, simply remove the pink edge on the right.



Traveling Salesman Problem

Find the optimal path for a salesman to go through a series of cities in a graph, visiting all of them.

The decision problem version of this is to say whether or not there is a path that is at most some length.

Proof

We will show $\text{Hamiltonian Cycle} \underset{P}{\leq} \text{Traveling Salesman}$

Given a Hamiltonian Cycle with $G = (V, E)$, where V is the vertices and E is the edges in the graph G.

(x, y) has weight 1 if $(x, y) \in E$. Otherwise, (x, y) has weight 2. Then, set your target to the number of vertices in the graph G. Then the correct result will be output by the traveling salesman decision problem.

This works because to go through all the vertices, it must take at least n edges.

Perfect Marriage Problem

The 2 dimensional problem:
Every man and every women has a set of the opposite gender they are willing to marry. Is there an arrangement such that everyone's sets are satisfied?

The 3 dimensional problem:
There are n men, women, and pets. There is a list of all the triples such that everyone is happy. Is there an arrangement such that everyone is happy?

Proof

Prove that 3-dimensional matching is NP-complete.

It is in NP because if you have a correct arrangement, you can check it by going through the list of triples and making sure that each is satisfied. Furthermore, make sure that the arrangement given is actually an arrangement.

We will show that $\text{3-SAT} \underset{P}{\leq} \text{3DM}$.

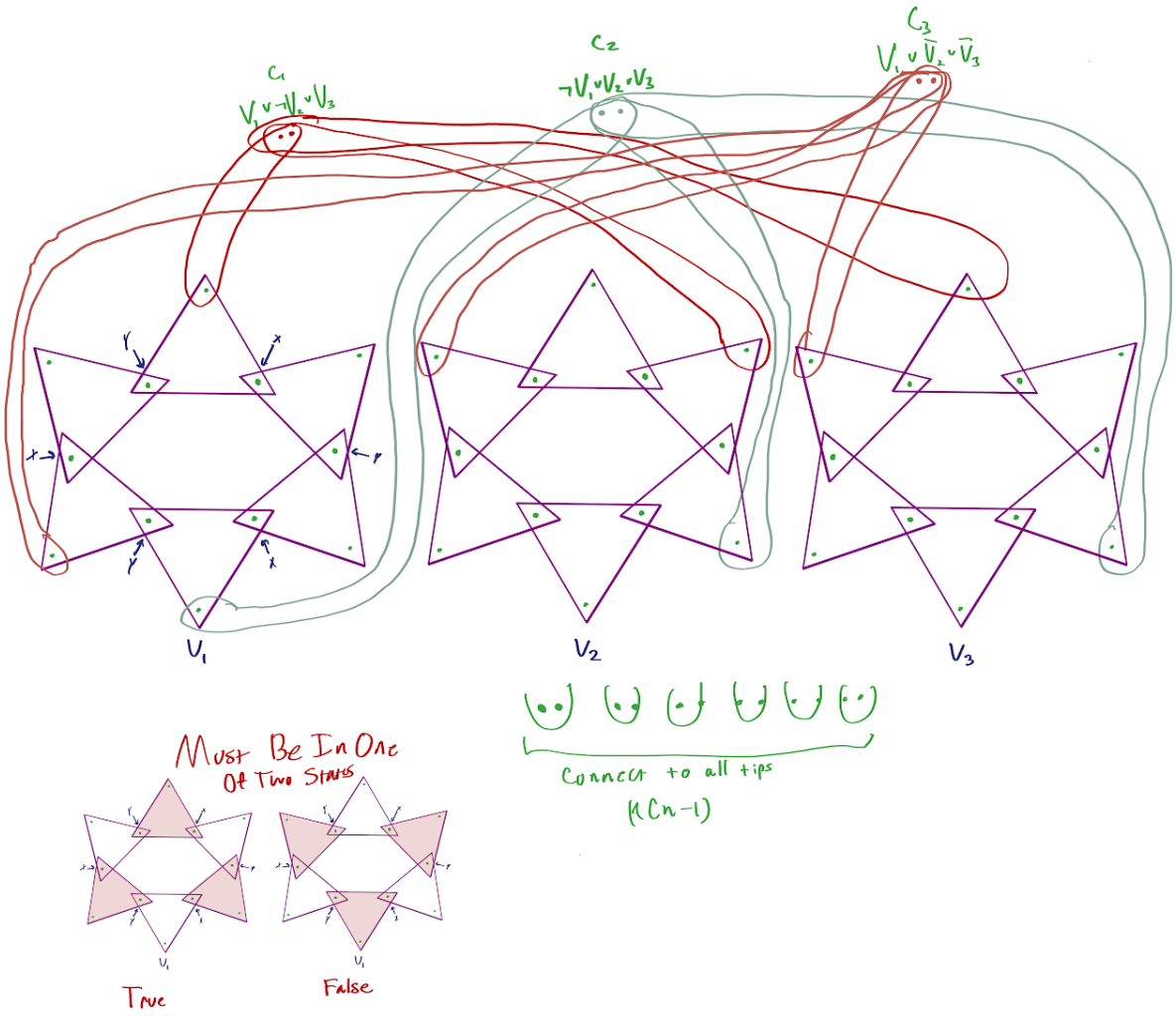
For 3-SAT we have variables $v_1, v_2, ..., v_n$ and clauses $c_1, c_2, ..., c_k$.

For 3-d matching we have sets X, Y, Z, and $T \subset X \times Y \times Z$, where T is the set of triples.

You create $2k$ tips in total, for $2kn$ in total. These tips are in the set Z.

For a clause gadget i, create two people in the X and Y sets. For a clause $v_1 \vee \neg v_2 \vee v_3$, connect to the $2i$th tip for v_1, the $2i + 1$th tip for v_2 and the $2i$th tip for v_3.

After adding clause gadgets, we have $k(n - 1)$ uncovered tips. These still need to have families, so we will add $k(n - 1)$ additional gadgets, but this time we will connect to everything.



This construction will have $2kn$ tips and therefore sets of size $2kn$. Furthermore, it will have $k(n-1) \times 2kn$ connections for the garbage gadgets, $3k$ for the clause gadgets, and $2kn$ for the tips for the variables.

This is in sum $3k + 2kn - 2k^2n + 2k^2n^2 = \Theta(k^2n^2)$, which is polynomial size.

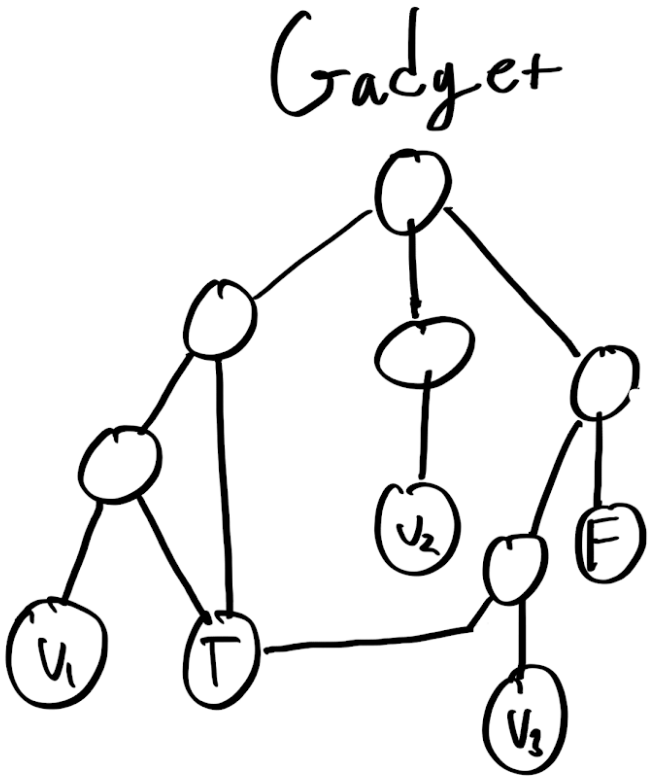
3-Coloring

Given a graph, see if it can be colored using only three colors.

Proof

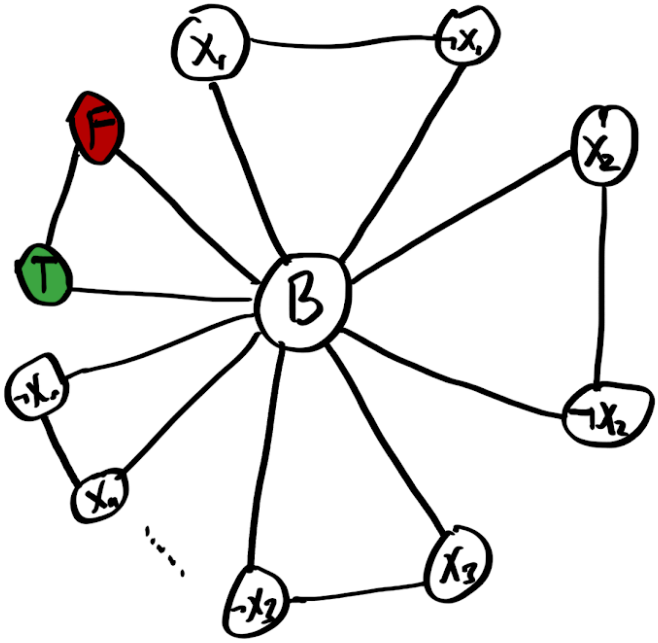
It is in NP.

We will show $3\text{-SAT} \underset{P}{\leq} 3\text{-coloring}$.



This gadget is satisifed with coloring iff at least one of v_1, v_2 and v_3 is the same color as true.

The main component is:



Then you just add a gadget for each clause in the 3-SAT problem.

Subvector Sum

Given a list of vectors $v_1, v_2, ..., v_n$ and a target vector v, is there some subset of the vectors that sum to v?

$$V = \left\{ \begin{pmatrix} 3 \\ 2 \\ 7 \end{pmatrix}, \begin{pmatrix} 4 \\ 5 \\ 2 \end{pmatrix}, \begin{pmatrix} 1 \\ 2 \\ 3 \end{pmatrix} \right\}$$

$$v = \begin{pmatrix} 4 \\ 8 \\ 10 \end{pmatrix}$$

$$v_1 + v_3 = v$$

Note that this is *not* linear alegbra. You cannot add multiples.

Theorem

Subvector sum is NP-complete.

We will show $3\text{d matching} \underset{P}{\leq} \text{subvector sum}$.

$$v_i = \left(\underbrace{0,0,0,0,1,0,0,0}_{n}, \underbrace{0,0,0,0,0,0,1,0,0}_{n}, \underbrace{0,1,0,0,0,0,0,0,0}_{n} \right)$$

This represents the triple $t_i = (5, 6, 2)$

We target the vector $(1, .., 1)$. This means that every individual must be represented once.

Subset Sum

Given a list of numbers $a_1, a_2, ..., a_n$, and a target vector k, is there a subset of the numbers that sum to k?

Theorem

This is NP complete if you use the same reduction as subvector-sum, but you interpret the vectors as trinary numbers, subset sum can also solve that problem.

This is almost the same size problem.

k-Coloring

Given a graph, can you give it k colors such that no colors touch via edges?

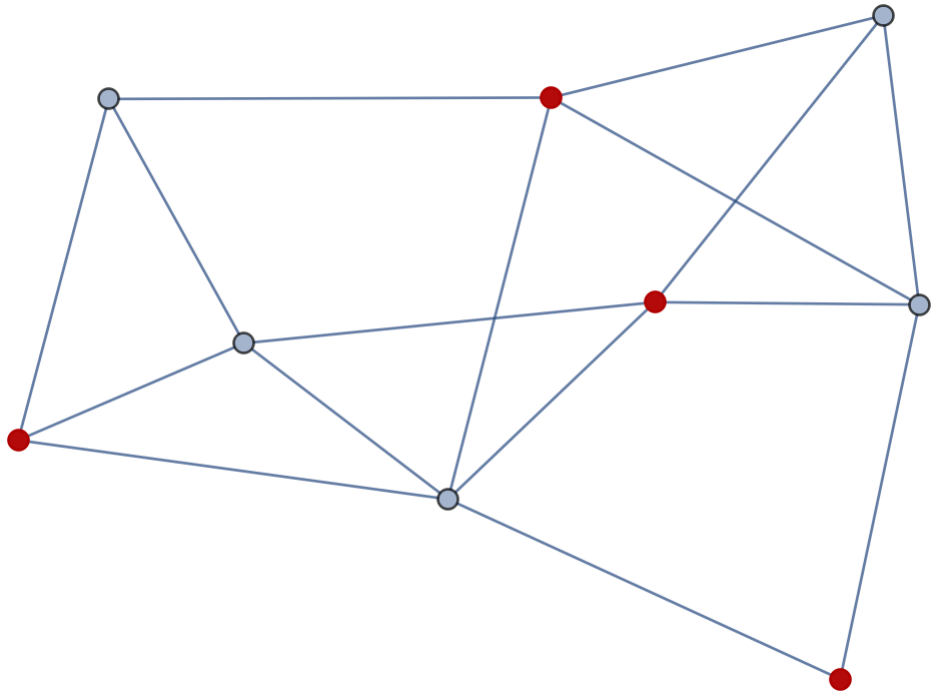
Theorem

For $k \geq 3$, show that $3\text{-Coloring} \underset{P}{\leq} \text{k-Coloring}$. Given a 3-coloring, add $k - 3$ vertices that each connect to all other vertices (including each other).

Independent Set

In a graph, an independent set is a set of vertices with no edges between any pair in the set.

For example:



The optimization problem is to find the largest independent set.

The decision problem is given a graph, and a target k, does G have an independent set of size k?

Theorem

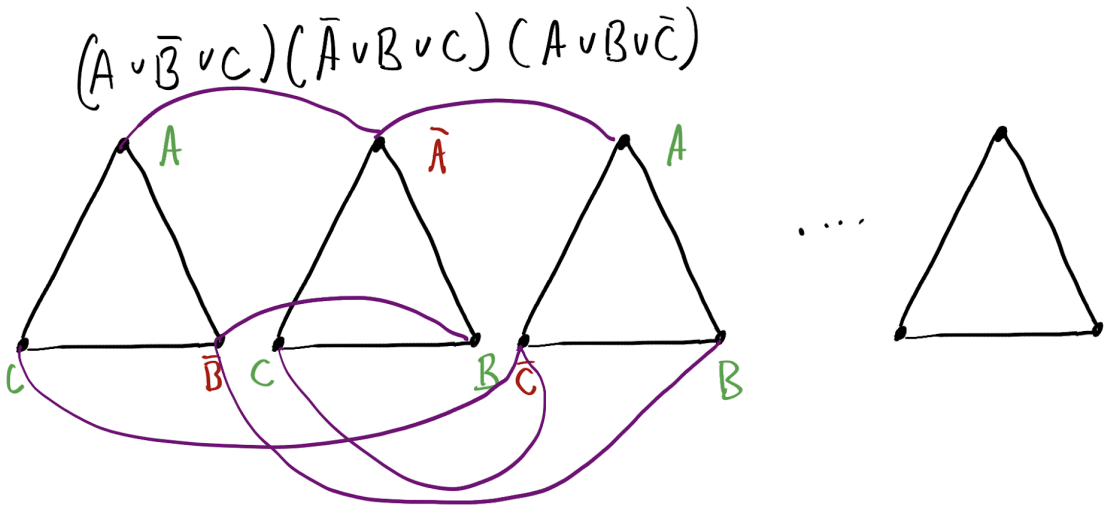
Independent set is NP-complete.

1. It is in NP.
2. It is hard for NP.

To show that it is hard for NP, we will show

$$\text{3-SAT} \underset{P}{\leq} \text{Independent Set}$$

Given variables $x_1, x_2, ..., x_n$, and clauses $c_1, c_2, ..., c_k$, we will create a graph.



Vertex Cover

A vertex cover is a subset of vertices such that every edge is incident to at least one vertex from the set.

Optimization version: given a graph, find a minimum number of vertexes to form a vertex coveFindVertexCoverr.

Decision version: given a graph, see if you can form a vertex cover with ℓ vertices or less.

Theorem

1. It is in NP
2. It is hard for NP

To show that it is hard for NP, we will show $\text{Independent Set} \underset{P}{\leq} \text{Vertex Cover}$.

If you have an independent set of a graph, the nodes that are not in the independent set are in the vertex cover. The reverse is also true.

So, if you just set $\ell = |V| - k$, with the same graph, that is the independent set problem solved using the vertex covering algorithm.

Algorithm

To find a vertex cover of size k, consider all subsets of vertices of size k. Check if it is a vertex cover.

This will about be

$$\binom{n}{k} \approx O(n^k)$$

Alternatively, if you take every edge, you can try each vertex connected to that edge.

This takes about $T(k) = 2T(k-1) + O(n)$ time, so $\Theta(n2^k)$ time.

$O(n2^k)$ is “fixed parameter tractable”.

This means that it is $O(f(k)n^\ell)$

There is another algorithm that takes $\Theta(kn + 1.274^k)$ and another that takes $\Theta(k^2 2^k + m + n)$.

Planar Graph

A graph is planar if you can draw it so that no two edges cross.

Two examples of nonplanar graphs:

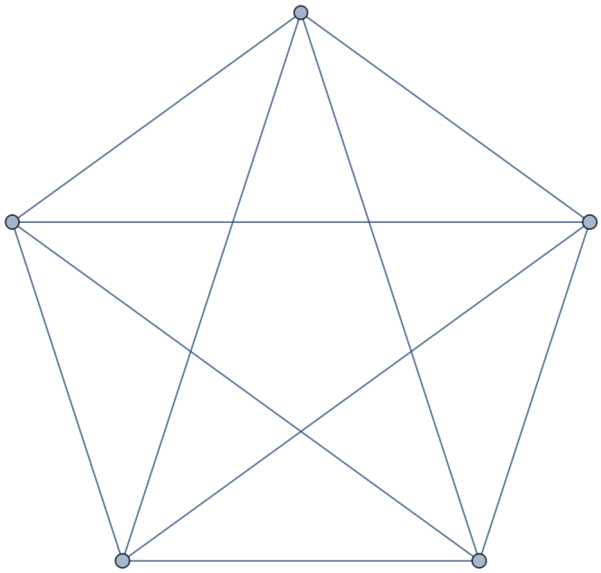


Figure 1: K5 Graph

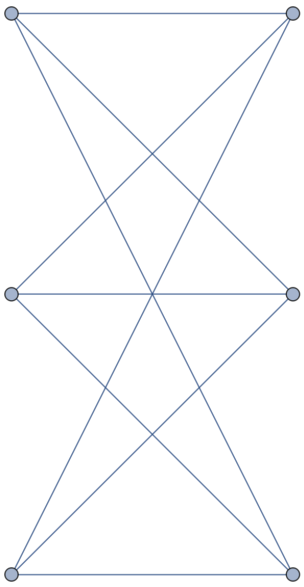


Figure 2: K3, 3 Graph

For coloring a planar graph, 2 coloring is easy, 3 coloring is NP-complete, but 4 coloring is also easy.

Kuratowski’s Theorem

A graph is planar iff K_5 or $K_{3,3}$ are not embedded.

This may sound simple, but this also means that you have to check if there is path between each of the 5 or 6 vertices.

This are called homomorphic graphs. For example, the following graphs are homomorphic: