Matrix Chain Multiplication

The input to the following algorithm is $p = (p_0, \ldots, p_n)$, where $p_{i-1} \times p_i$ is the dimension of A_i .

• s[i,j] is the best place to split the computation of $A_{i..j}$ to $A_{i..k}A_{k+1..j}$.

Matrix-Chain-Order(p)

```
n \leftarrow length[p] - 1
    for i \leftarrow 1 to n do
          m[i,j] \leftarrow 0
    for l \leftarrow 2 to n do
4
          for i \leftarrow 1 to n - l + 1 do
5
                i \leftarrow i + l - 1
6
                m[i,j] \leftarrow \infty
7
                for k \leftarrow i to j-1 do
8
                      q \leftarrow m[i, k] + m[k+1, j] + p_{i-1}p_kp_i
9
                      if q < m[i,j]
10
                          then m[i,j] \leftarrow q
11
                                  s[i,j] \leftarrow k
12
```

13 **return** m and s

Running time: $O(n^3)$

• Key point: the same information (m[i,j]) gets reused over and over.

Computing an optimal solution

Matrix-Chain-Order computes the best place to split and the optimal number of scalar multiplications.

• From s[i,j], it's easy to compute how to multiply

M-CHAIN-MULTIPLY(A, s, i, j)

```
1 if j > i

2 then X \leftarrow \text{M-CHAIN-MULTIPLY}(A, s, i, s[i, j])

3 Y \leftarrow \text{M-CHAIN-MULTIPLY}(A, s, s[i, j] + 1, j)

4 return MATRIX-MULTIPLY(X, Y)

5 else return A_i
```

Get the right answer by calling M-Chain-Multiply (A, s, 1,

Longest Common Subsequence

Given two sequences, we want to find there longest common subsequence. This is a problem that comes up, for example, in gene sequencing (if we want to compare to genomes).

Formally, if $Z = (z_1, \ldots, z_k)$ is a subsequence of $X = (x_1, \ldots, x_m)$ if there exist i_1, \ldots, i_k such that $i_1 < \ldots < i_k$ and $z_j = x_{i_j}$.

Example: The longest common subsequence of (A, A, B, C, A, A, D, A) and (A, C, B, C, A, B, D, C, A) is (A, B, C, A, D, A).

• There can be at most 3 A's in the lcs, so this is the best we can do.

The brute force approach to finding LCS of X and Y is to consider all subsequences of X and see which ones are subsequences of Y.

• The number of subsequences of X is exponential in length(X).

We can do better using dynamic programming.

Characterizing an LCS

Given a sequence $X = (x_1, \ldots, x_m)$, if $i \leq m$, let $X_i = (x_1, \ldots, x_i)$.

Theorem: Suppose that $Z = (z_1, \ldots, z_k)$ is an lcs for $X = (x_1, \ldots, x_m)$ and $Y = (y_1, \ldots, y_n)$.

- 1. If $x_m = y_n$, then $z_k = x_m = y_n$ and Z_{k-1} is an lcs for X_{m-1} and Y_{n-1} .
- 2. If $x_m \neq y_n$ and $z_k \neq x_m$, then Z is an lcs for X_{m-1} and Y_n .
- 3. If $x_m \neq y_n$ and $z_k \neq y_n$, then Z is an lcs for X and Y_{n-1} .

Therefore, an lcs for X and Y contains within it an lcs for two smaller sequences.

• We can find LCS(X, Y) by first finding $LCS(X_i, Y_j)$ for all the prefixes of X and Y.

Solving LCS Recursively

Let c[i, j] the length of an lcs of X_i and Y_j .

$$c[i,j] = \begin{cases} 0 & \text{if } i = 0 \text{ or } j = 0 \\ c[i-1,j-1] + 1 & \text{if } i,j > 0, \ x_i = y_j \\ \max(c[i-1,j],c[i,j-1]) & \text{if } i,j > 0, \ x \neq y_j \end{cases}$$

LCS-LENGTH(X, Y)

```
1 \quad n \leftarrow length[X]
2 \quad m \leftarrow length[Y]
3 for i \leftarrow 1 to m do
4 	 c[i,0] \leftarrow 0
5 for j \leftarrow 0 to n do
         c[0,j] \leftarrow 0
7
   for i \leftarrow 1 to m do
         for j \leftarrow 1 to n do
               if x_i = y_i
9
                  then c[i,j] \leftarrow c[i-1,j-1] + 1
10
                  else c[i,j] \leftarrow \max(c[i-1,j],c[i,j-1])
11
12 return c
```

Running time (and space): O(nm)

Printing out an LCS

```
PRINT-LCS(c, X, i, j)

1 if i = 0 or j = 0

2 then return

3 if c[i - 1, j] = c[i, j]

4 then PRINT-LCS(c, X, i - 1, j)

5 else if c[i, j - 1] = c[i, j]

6 then PRINT-LCS(c, X, i, j - 1)

7 else PRINT-LCS(c, X, i, j - 1)

8 print x_i
```

Greedy Algorithms

One approach to an optimization problem: make the choice that currently looks best.

- Sometimes this greedy approach is a bad idea
 you can get caught in a trap
- Other times it works remarkably well.

Kruskal's algorithm for MST can be viewed as a greedy algorithm:

• Choose the edge of least weight that buys you something

So can Prim's algorithm:

• Choose the edge of least weight that extends the current tree and buys you something.

And so can Dijkstra's algorithm:

• Choose the node not yet chosen which is closest to the source.

Activity Selection

Suppose that we have a set $S = \{1, ..., n\}$ of proposed *activities* that need to use the same resource

- only one can be active at a time
 - example: scheduling classes in a lecture hall
- Activity i has a start time s_i and a finish time f_i .

Problem: choose the maximum set of mutually compatible activities

• Don't want activities whose start-finish times overlap

Basic idea: keep choosing an activity as long as it's compatible with the ones you've already chosen.

• The actual algorithm suggests a particular way to choose.

Order the activities by increasing finish time:

$$f_1 \leq f_2 \leq \ldots \leq f_n$$

• This pre-processing step takes time $O(n \log n)$

Assume the algorithm gets as input the sequence s of start times and the sequence f of finish times (in sorted order):

Greedy-Activity-Selector(s, f)

Clearly this gives a set of compatible activities.

It's also efficient:

• After preprocessing, run in time $\Theta(n)$.

But why is it correct?

Theorem: Greedy-Activity-Selector chooses a maximum set of mutually compatible activities.

Proof: By strong induction on n, the number of activities in S.

Base case: clearly OK if S = 1.

Inductive step: First show that there is a maximum set that includes activity 1 (the one with earliest finish time).

Let A be a maximum set and let k be the activity in A with earliest finish time.

- If k = 1, we're done.
- If not, let $B = A \{k\} \cup \{1\}$. The activities in B must be mutually compatible
 - \circ activity 1 can't overlap with anything, since its finish time is earlier than k's
- \bullet Thus, B is a maximum set that includes 1.

If A is a maximum set of mutually compatible activities in $S = \{1, ..., n\}$ and $1 \in A$, then $A - \{1\}$ is a maximum set of mutually compatible activities in $S' = \{i \in S : s_i \geq f_1\}.$

 \bullet S' consists of activities that start after 1 ends.

Now by induction, the algorithm produces a maximum set on S'.

• But the action of algorithm on S' is exactly the same as the action of the algorithm on S after choosing 1.

Greedy vs. Dynamic Programming

A greedy algorithm works only if making the greedy choice gives an optimal solution:

- That works in some cases, but not always.
- The hard part is often showing that it works

Example:

- The θ -1 $knapsack\ problem$: there are n items
 - \circ Item i has value v_i and weight w_i .

You can put at most W pounds into a knapsack. Which items do you take?

- For each item, you either take it or leave it (0-1)
- The fractional knapsack problem: same setup, but now you can take part of an item.
 - This means you have more flexibility

Key point:

• There's a greedy algorithm for the fractional knapsack problem, but not for the 0-1 knapsack problem For the fractional knapsack problem:

- First sort the items by value/pound (v_i/w_i)
- Pick the most valuable items that you can fit in, then the next one, etc., until there's no more room.
- Then put in as much of the last item as you can to get to weight W.
 - This is OK since you can take fractions of an item.

This approach doesn't work for the 0-1 knapsack problem:

- Suppose there are three items and the knapsack can hold 50 pounds:
 - o Item 1 weighs 10 lb. and is worth \$60
 - o Item 2 weighs 20 lb. and is worth \$100
 - o Item 3 weighs 30 lb. and is worth \$120
- Item 1 is the most valuable, but the optimal solution is $\{2,3\}$.

You can use dynamic programming to solve the 0-1 knapsack problem.

Huffman Codes

Suppose you have a large file, where only 6 different characters appear

- Not all characters appear equally often
- How do we represent the characters so as to get greatest compression?
 - Compression is critical in transmitting data over a modem
 - There are *lots* of coding algorithms

Assume each character is represented as a binary string. Example:

```
a = 000000 b = 000001 ... z = 011010 , = 011011 ...
```

Is this a good encoding?

- This is a *fixed-length* code: all characters encoded by a 6-bit code word
- It's a better idea to use a variable-length code
- Greater frequency \Rightarrow shorter code word
 - Modern coding algorithms (based on Ziv-Lempel) adaptively choose length of code word

Prefix Code

If one code is a prefix of another, then decoding is harder

• if e is 0 and a is 01, when you see 0, is it an e or the beginning of an a.

It is best to assume a prefix code

• no codeword is the prefix of another codeword.

Decoding is simple with a prefix code:

- Keep running along string until you have a complete codeword, and continue
 - Note: this is a greedy decoding algorithm
- E.g., suppose e = 0, a = 10, b = 110
 - then 00110100 = eebae