CSE 421 Intro to Algorithms Winter 2001

Sequence Alignment

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Sequence Alignment

- What
- Why
- A Simple Algorithm
- Complexity Analysis
- A better Algorithm: "Dynamic Programming"

Sequence Similarity: What

GGACCA

TACTAAG TCC-AAT

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Sequence Similarity: Why

- Diff
- RCS
- Molecular Bio

Similar sequences often have similar origin or function

Similarity often recognizable after 108 -109 years

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Terminology

- String: ordered list of letters TATAAG
- Prefix: consecutive letters from front empty, T, TA, TAT, ...
- Suffix: ... from end empty, G, AG, AAG, ...
- Substring: ... from ends or middle empty, TAT, AA, ...
- Subsequence: ordered, nonconsecutive

TT, AAA, TAG, ...

Sequence Alignment

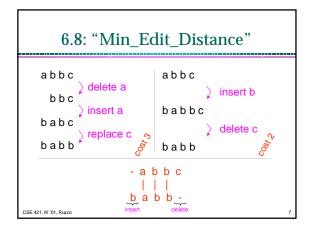
acbcdb ac--bcdbcadbd - c a d b - d -

Defn: An alignment of strings S, T is a pair of strings S', T' (with spaces) s.t.

(1) |S'| = |T'|, and

(|S| = "length of S")

(2) removing all spaces leaves S, T



Alignment Scoring

```
acbcdb
                     - b c d b
cadbd
              - c a d b - d -
              -1 2 -1 -1 2 -1 2 -1
              Value = 3*2 + 5*(-1) = +1
```

- The score of aligning (characters or spaces) x & y is $\sigma(x,y)$.
- *Value* of an alignment = $\sum_{i=1}^{S} \sigma(S'[i], T'[i])$
- An optimal alignment: one of max value

Optimal Alignment: A Simple Algorithm

for all subseqs A of S, B of T s.t. |A| = |B| do align A[i] with B[i], $1 \le i \le |A|$ align all other chars to spaces compute its value S = abcd A = cd $T = wxyz \quad B = xz$ -abc-d a-bc-d

retain the max

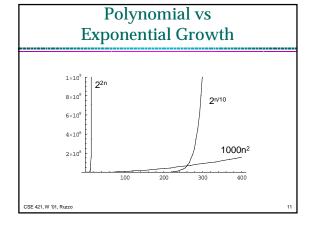
end

output the retained alignment

Analysis

- Assume |S| = |T| = n
- Cost of evaluating one alignment: ≥ n
- How many alignments are there: $\geq \binom{2n}{n}$ pick n chars of S,T together say k of them are in S match these k to the k unpicked chars of T
- Total time: $\geq n^{2n}$
- E.g., for n = 20, time is $> 2^{40}$ operations

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Candidate for Dynamic **Programming?**

- Common Subproblems?
 - » Plausible: probably re-considering alignments of various small substrings unless we're careful.
- Optimal Substructure?
 - » Plausible: left and right "halves" of an optimal alignment probably should be optimally aligned (though they obviously interact a bit at the interface).

Optimal Substructure (In More Detail)

- Optimal alignment ends in 1 of 3 ways:
 - » last chars of S & T aligned with each other
 - » last char of S aligned with space in T
 - » last char of T aligned with space in S
 - » (never align space with space; $\sigma(-, -) \ge 0$)
- In each case, the rest of S & T should be optimally aligned to each other

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Optimal Alignment in O(n²) via "Dynamic Programming"

- Input: S, T, |S| = n, |T| = m
- Output: value of optimal alignment

Easier to solve a "harder" problem:

$$\begin{split} V(i,j) = & \text{ value of optimal alignment of} \\ S[1], & \ldots, S[i] \text{ with } T[1], & \ldots, T[j] \\ & \text{ for all } 0 \leq i \leq n, \, 0 \leq j \leq m. \end{split}$$

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General Case

$$\begin{bmatrix} \bigcap_{n = 1}^{\infty} S[i] \\ \bigcap_{n = 1}^{\infty} T[j] \end{bmatrix} \begin{bmatrix} \bigcap_{n = 1}^{\infty} S[i] \\ \bigcap_{n = 1}^{\infty} I[i] \end{bmatrix}$$

$$\begin{bmatrix} \bigcap_{n = 1}^{\infty} S[i] \\ \bigcap_{n = 1}^{\infty} I[i] \end{bmatrix}$$

$$V(i,j) = \max \begin{cases} V(i-1,j-1) + \sigma(S[i],T[j]) \\ V(i-1,j) + \sigma(S[i],-1) \\ V(i,j-1) + \sigma(-1,T[j]) \end{bmatrix}$$

for all $1 \le i \le n$, $1 \le j \le m$.

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Base Cases

V(i,0): first i chars of S; all match spaces

$$V(i,0) = \sum_{k=1}^{i} \sigma(S[k],-)$$

V(0,j): first j chars of T; all match spaces

$$V(0, j) = \sum_{k=1}^{j} \sigma(-, T[k])$$

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	Misn Mato	natch = -1 ch = 2							
		j	0	1	2	3	4	5	
	i			С	а	d	b	d	←T
	0		0	-1	-2	-3	-4	-5	
	1	a	-1	-1	1				
	2	С	-2	1					Time =
	3	b	-3						O(mn)
	4	С	-4						
	5	d	-5						
	6	b	-6						
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Calculating One Entry

$$V(i,j) = \max \begin{cases} V(i-1,j-1) + \sigma(S[i],T[j]) \\ V(i-1,j) + \sigma(S[i],-) \\ V(i,j-1) + \sigma(-,T[j]) \end{cases}$$

$$V(i-1,j-1) \quad V(i-1,j-1) \quad V(i-1,j)$$
S[i] ...
$$V(i,j-1) \quad V(i,j-1) \quad V(i,j-1) \quad V(i,j-1) \quad V(i,j-1)$$

Finding Alignments: Trace Back									
	j	0	1	2	3	4	5		
<u>i</u>			С	a	d	b	d	←T	
0		0	- (1)	-2	-3	-4	-5		
1	а	(1)	-1	1	0	-1	-2		
2	С	-2	1	0	0	-1	-2		
3	g	-3	0	0	-1	2	1		
4	С	-4	-1	(1)	-1	(1),	1		
5	d	-5	-2	-2	1,	0	3		
6	b	-6	-3	-3	0	3	<u> </u>		
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Complexity Notes

- Time = O(mn), (value and alignment)
- Space = O(mn)
- Easy to get value in Time = O(mn) and Space = O(min(m,n))
- Possible to get value and alignment in Time = O(mn) and Space = O(min(m,n)) but tricky.

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