Dynamic Programming for Sequence Alignment

## An Important Algorithm Design Technique

Dynamic Programming Give a solution to a problem using smaller sub-problems, e.g. a recursive solution Useful when the same sub-problems show up again and again in the solution

## Sequence Similarity

GGACCA

TACTAAG

TCCAAT

## Sequence Similarity: What

GGACCA

T A C T A A G | : | : | | : T C C – A A T

## Sequence Similarity: Why

Most widely used comp. tools in biology New sequence always compared to sequence data bases

# Similar sequences often have similar origin or function

Recognizable similarity after 10<sup>8</sup> – 10<sup>9</sup> yr

not to mention:

- Unix "diff",
- module histories in version control systems,
- programming assignment pairs with sadly questionable evolutionary history,
- etc., etc., ...

## Terminology

String: ordered list of letters TATAAG Prefix: consecutive letters from front empty, T, TA, TAT, ...

Suffix: ... from end

empty, G, AG, AAG, ...

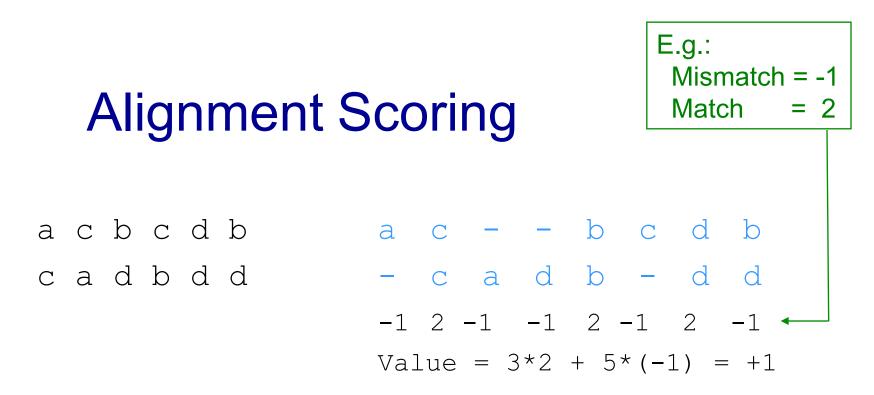
## Substring: ... from ends or middle empty, TAT, AA, ...

Subsequence: ordered, nonconsecutive TT, AAA, TAG, ...

## Sequence Alignment

acbcdb	acbcdb
/ \	
cadbd	- c a d b - d -

Defn: An alignment of strings S, T is a pair of strings S', T' (with spaces or '-') s.t.
(1) |S'| = |T'|, and (|S| = "length of S")
(2) removing all spaces leaves S, T



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

## Analysis of brute force

Assume |S| = |T| = nTime to evaluate one alignment: O(n)

How many alignments are there:

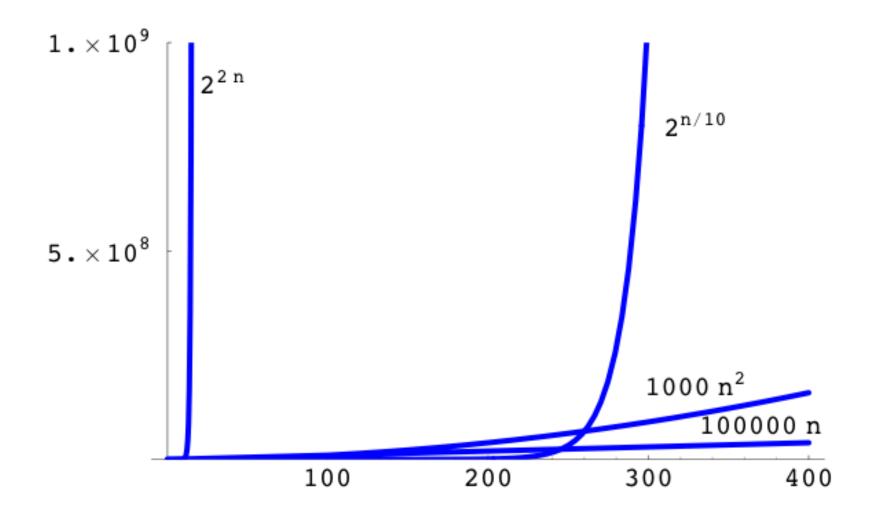
 $\sum_{k=0}^{n} \binom{n+k}{k} \binom{n}{k}$ 

e: S = abcde T = vwxyz --abc-de ab--c-de vw--xyz- --vwxyz-(two alignments, but same value)

Total time more than  $2^{2n}$ , for n > 3

E.g., for n = 20, time is >  $2^{40}$  >  $10^{12}$  operations

## Polynomial vs Exponential Growth



## Dynamic Programming Alg: The Key Idea

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;  $\sigma(-, -) < 0$ )

In each case, the *rest* of S & T should be optimally aligned to each other (else you could improve by doing so) Optimal Alignment in O(n<sup>2</sup>) via "Dynamic Programming"

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

Common: first solve for value of opt.

V(i,j) = value of optimal alignment ofS[1], ..., S[i] with T[1], ..., T[j] $for all 0 \le i \le n, 0 \le j \le m.$ 

### **Base Cases**

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

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

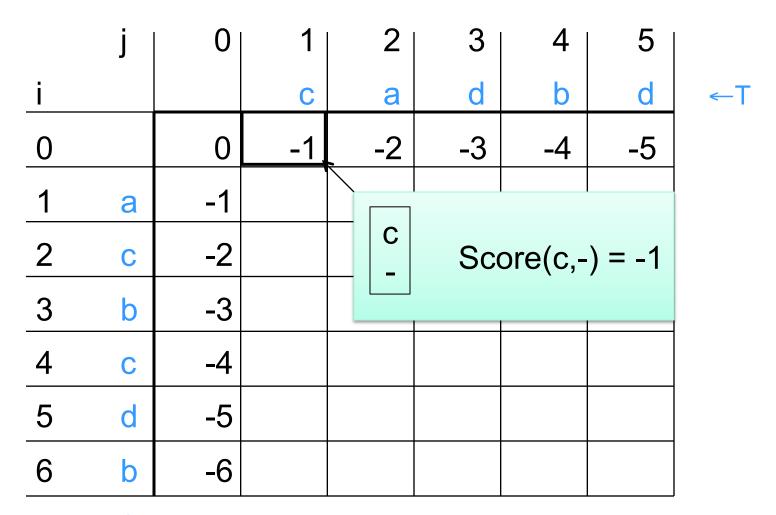
V(0,j): first j chars of T all match spaces  $V(0,j) = \sum_{k=1}^{j} \sigma(-,T[k])$ 

## **General Case**

Opt align of S[1], ..., S[i] vs T[1], ..., T[j]:  $\begin{bmatrix} \sim \sim \sim \sim T[j] \\ \sim \sim \sim \sim S[i] \end{bmatrix}, \begin{bmatrix} \sim \sim \sim \sim T[j] \\ \sim \sim \sim \sim -1 \end{bmatrix}, \text{ or } \begin{bmatrix} \sim \sim \sim \sim -1 \\ \sim \sim \sim \sim S[i] \end{bmatrix}$ Opt align of  $V(i,j) = \max \begin{cases} V(i-1,j-1) + \sigma(S[i],T[j]) \\ V(i-1,j) + \sigma(S[i], -) \\ V(i,j-1) + \sigma(-, T[j]) \end{cases}, \uparrow$ 

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

### Mismatch = -1 Match = 2

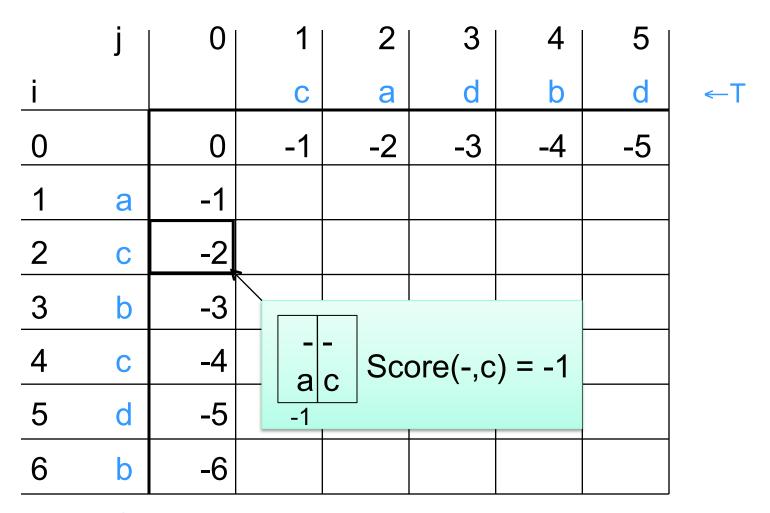


## $\begin{array}{ll} \text{Mismatch} = -1 \\ \text{Match} &= 2 \end{array}$

	j	0	1	2	3	4	5	
i			С	а	d	b	d	←T
0		0	-1	-2	-3	-4	-5	
1	а	-1						
2	С	-2						
3	b	-3	 _ a	Sc	Score(-,a) = -1			
4	С	-4					T	
5	d	-5						
6	b	-6						

#### 

## Example

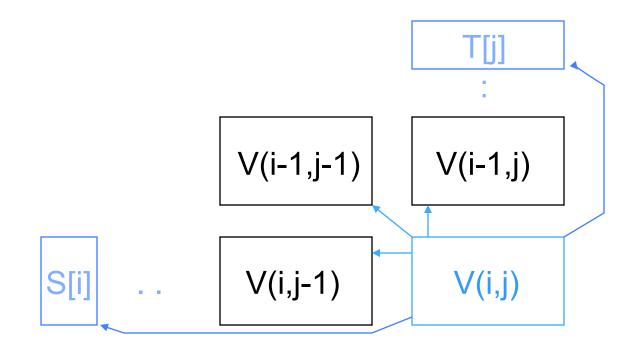


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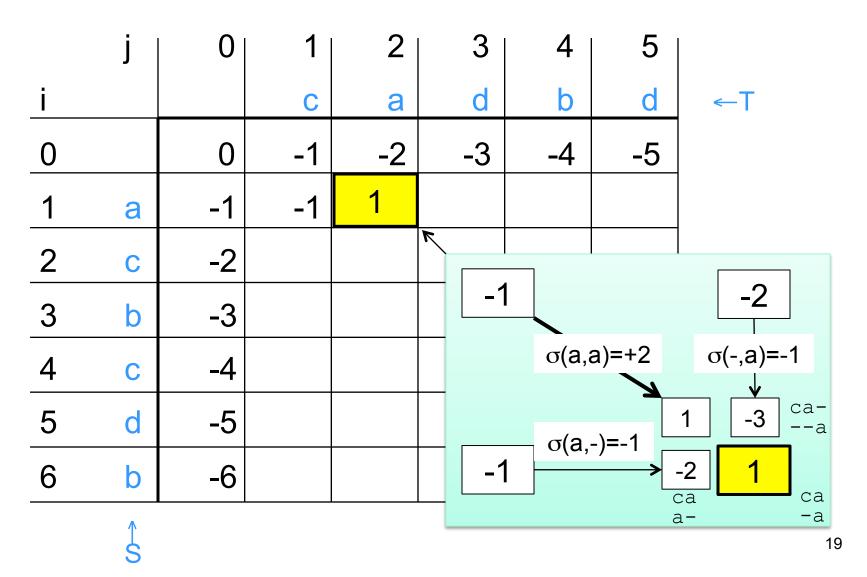
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## Calculating One Entry

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



#### Mismatch = -1 Match = 2



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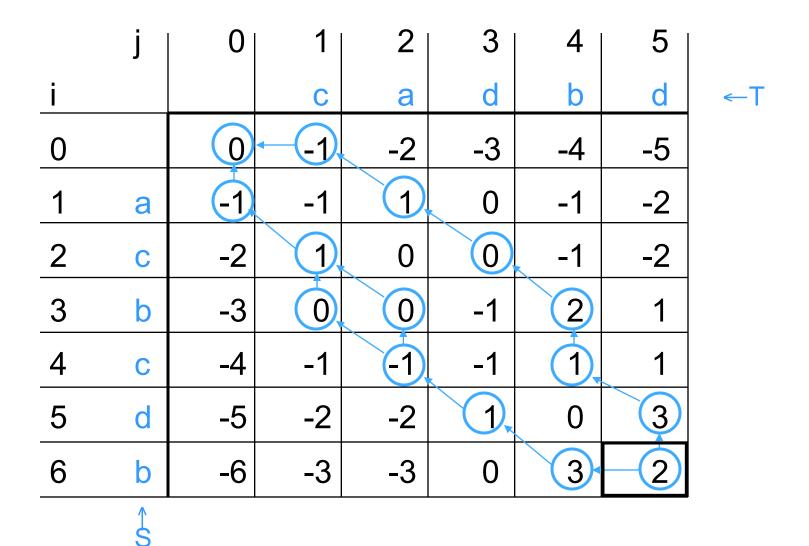
	j	0	1	2	3	4	5	
i			С	а	d	b	d	←T
0		0	-1	-2	-3	-4	-5	
1	а	-1	-1	1				
2	С	-2	1					Time =
3	b	-3						O(mn)
4	С	-4						
5	d	-5						
6	b	-6						

## $\begin{array}{ll} \text{Mismatch} = -1 \\ \text{Match} &= 2 \end{array}$

	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	0	-1	-2	
2	С	-2	1	0	0	-1	-2	
3	b	-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	2	

### Finding Alignments: Trace Back

Arrows = (ties for) max in V(i,j); 3 LR-to-UL paths = 3 optimal alignments



## **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.

## Summary

Sequence similarity has important

- Surprisingly simple scoring often works well in practice: score positions separately & add
- Simple "dynamic programming" algorithms can find *optimal* alignments under these assumptions in polynomial time (product of sequence lengths)

Keys to D.P. are to

- a) identify the subproblems (usually repeated/overlapping)
- b) be sure opt solutions to subproblems are needed for opt solution globally
- c) solve in a careful order; solve all small ones before needed by bigger ones
- d) build table with solutions to the smaller ones so bigger ones just need to do table lookups (*no* recursion, despite recursive formulation implicit in (a))