

# CS 577 - Dynamic Programming

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TopHat Join Code: 524741



# DYNAMIC PROGRAMMING

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Richard Bellman

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## Why “Dynamic Programming”?

Reasons for the name:

- In the 1950s, “programming” was about “planning” rather than coding.
- “Dynamic” is exciting – Air Force director didn’t like research and wanted pizzazz.
- “Dynamic” sounds better than “linear” (Re: rival Dantzig).

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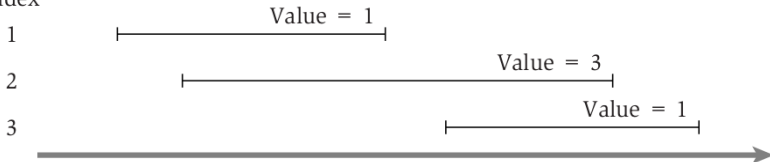
## What is it?

- Your new favourite algorithmic technique.
- Extreme Divide and Conquer
- Many sub-problems, but not quite brute-force.
- Dynamic in that it calculates a bunch of solutions from the “smallest” to the “largest”.

# WEIGHTED INTERVAL SCHEDULING

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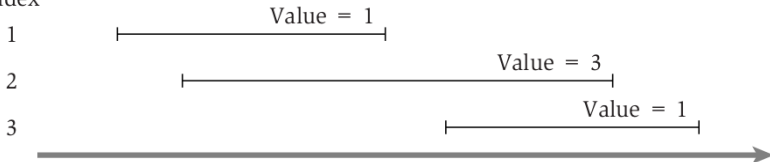


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- Requests:  $\sigma = \{r_1, \dots, r_n\}$

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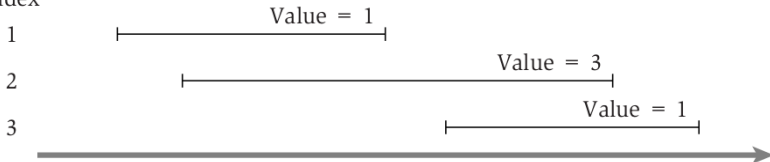
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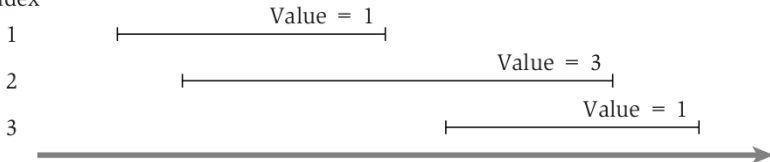


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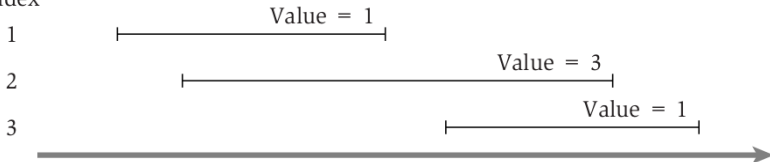


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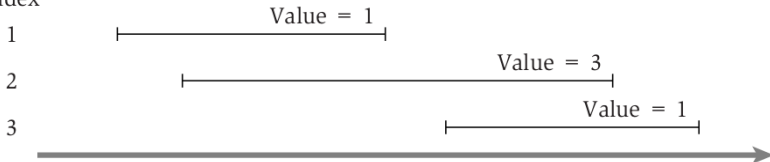
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TH1: What is the value of the FF heuristic?

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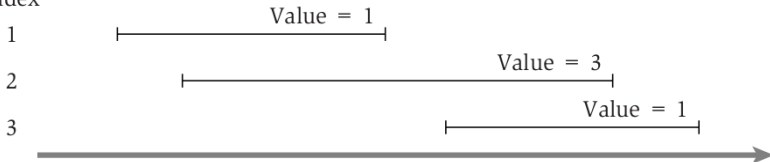
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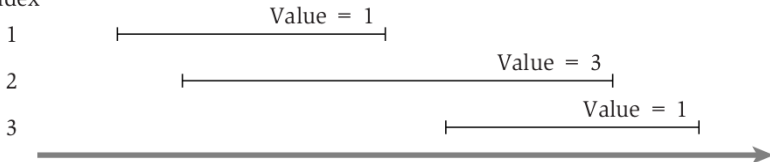
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## Recursive Procedure

- 1 Assume  $\sigma$  ordered by finish time (asc).

## Proof of optimality.



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## Recursive Procedure

- ❶ Assume  $\sigma$  ordered by finish time (asc).
- ❷ Find the optimal value in sorted  $\sigma$  of first  $j$  items:
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  - ②  $\text{OPT}(j) = \max(\text{OPT}(j-1), \text{OPT}(i) + v_j)$

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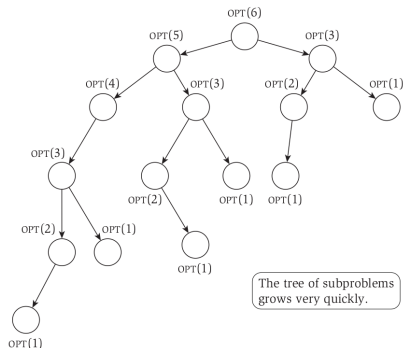
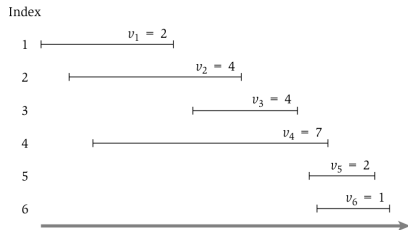
**Inductive step:**

- By ind hyp, we have opt for  $j-1$  and opt for  $i$ .
- FF assures the dichotomy that the last interval is either in the solution or not.
- Take the max of whether or not a given interval is included.



# CONSIDER THE RECURSION

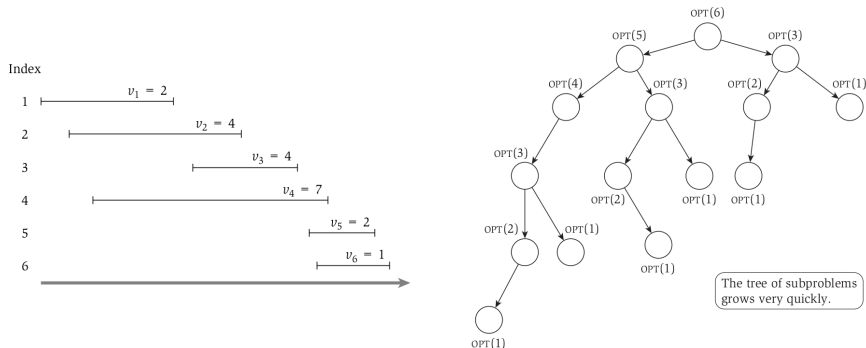
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The tree of subproblems grows very quickly.

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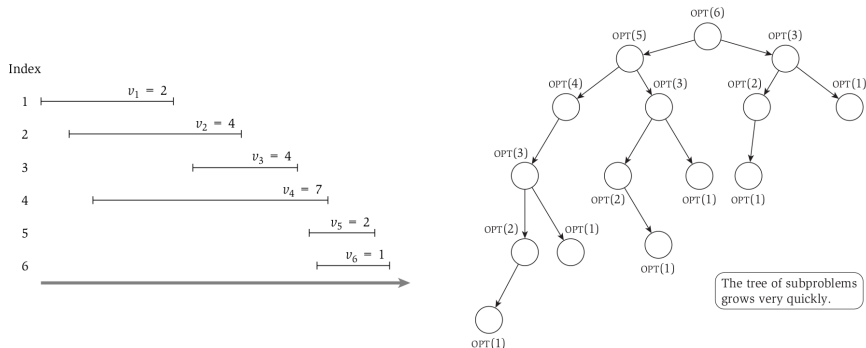
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TH3: What is the asymptotic number of recursive calls with  $n$  jobs?

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$$\text{OPT}(j) = \max(\text{OPT}(j-1), \text{OPT}(i) + v_j)$$



TH3: What is the asymptotic number of recursive calls with  $n$  jobs?  $O(2^n)$



# MEMOIZING THE RECURSION

## Memoization

- Not a typo.
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## Basic Technique

- Calculate once: store the value in array and retrieve for future calls.
- Can be implemented recursively, but tends to be more natural as an iterative process.

# DYNAMIC PROGRAM SOLUTION

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**Algorithm:** WEIGHTINTDP

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Sort  $\sigma$  by finish time

$m[0] := 0$

**for**  $j = 1$  *to*  $n$  **do**

    | Find index  $i$

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- We understand how loops work.
- NO Pseudocode.

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- DP algorithms are formulaic.
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## We want:

- Definitions required for algorithm to work
- Description of matrix
- Bellman Equation
- Location of solution, order to populate the matrix

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## Location of solution, order to populate

- The maximum value of a compatible schedule for the  $n$  jobs is found at  $m[n]$ . Populate from 1 to  $n$ .

# ANALYZE THE ALGORITHM

## DP Solution

- $\sigma$  sorted by finish time, ascending order.
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- Preprocessing:



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- Preprocessing:
  - Sorting jobs:  $O(n \log n)$ .

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  - Number of cells: TopHat 4

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- Preprocessing:
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  - Number of cells:  $O(n)$

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- Populate the matrix:
  - Number of cells:  $O(n)$
  - Cost per cell: TopHat 5

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Overall: TopHat 6

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Overall:  $O(n^2)$  linear search,  $O(n \log n)$  binary search



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## What about the schedule $S$ ?

Trace back from the optimal value:

- Job  $j$  is part of the optimal schedule from 1 to  $j$  iff  $v_j + \text{OPT}(i) \geq \text{OPT}(j-1)$

# BASIC DP OUTLINE

## Algorithm Template

- Preprocessing of data
- Populate the matrix:
  - Iterate over the cells in the correct order.
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- ❶ There are only a polynomial number of subproblems.
- ❷ The solution to the larger problem can be efficiently calculated from the subproblems.
- ❸ Natural ordering of the subproblems from “smallest” to “largest”.

# LONGEST INCREASING SUBSEQUENCE



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## Problem

- Given an integer array  $A[1..n]$ .
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  - puddles: subsequence, substring (contiguous)
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TH1: For an array of length  $n$ , how many subsequences?

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## Problem

- Given an integer array  $A[1..n]$ .
- Find the longest increasing subsequence. That is, let  $i$  be a sequence of indexes, we have  $A[i_k] < A[i_{k+1}]$  for all  $k$ .

## Subsequence

- For a sequence  $A$ , a subsequence  $S$  is a subset of  $A$  that maintains the same relative order.
- Ex: I like watching the puddles gather rain.
  - puddles: subsequence, substring (contiguous)
  - late train: subsequence, not substring (not contiguous)

TH1: For an array of length  $n$ , how many subsequences?  $2^n$

# RECURSIVE APPROACH

---

**Algorithm:** LIS

---

**Input** : Integer  $k$ , and array of integers  $A[1..n]$ .

**Output:** Return length of LIS where every value  $> k$ .

Exo: Complete the algorithm

---

## RECURSIVE APPROACH

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**Input** : Integer  $k$ , and array of integers  $A[1..n]$ .

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**else if**  $A[1] \leq k$  **then**

**return** LIS( $k, A[2..n]$ )

**else**

$skip := \text{LIS}(k, A[2..n])$

$take := \text{LIS}(A[1], A[2..n]) + 1$

**return**  $\max\{skip, take\}$

**end**

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## RECURSIVE APPROACH

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TH2: For an array  $A[1..n]$ , how would you find the length of the LIS using the LIS( $\cdot$ ) algorithm?



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TH2: For an array  $A[1..n]$ , how would you find the length of the LIS using the LIS( $\cdot$ ) algorithm? LIS( $-\infty, A[1..n]$ )

## RECURSIVE APPROACH

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TH3: Run time of the algorithm for a length  $n$  array?

## RECURSIVE APPROACH

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## RECURSIVE APPROACH

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TH4: How many distinct recursive calls for a length  $n$  array?

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$O(n^2)$

# DYNAMIC PROGRAM FOR LIS

## Description of matrix

TH5: Number of dimensions of array?

# DYNAMIC PROGRAM FOR LIS

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2D array  $L$ , where  $L[i, j]$  is the maximum LIS of  $A[j..n]$  with every item  $> A[i], i < j$ .



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## Solution and populating $L$

- Solution in  $L[0][1]$ ; add  $A[0] = -\infty$ .
- Populate  $j$  from  $n$  to  $1$ ;  $i$  from  $0$  to  $j-1$  or  $j-1$  to  $0$ .

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- TH6: Run time:

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- Run time:  $O(n^2)$

# SUBSET AND KNAPSACK

# SUBSET PROBLEM

## Problem Definition

- A single machine that we can use for time  $W$ .

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- Decreasing weights: TopHat D1

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- Increasing weights: TopHat D2

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## 1D Approach

- if  $n \notin S$ , then  $v[n] = v[n - 1]$

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To solve  $v[n]$ , we need to consider:

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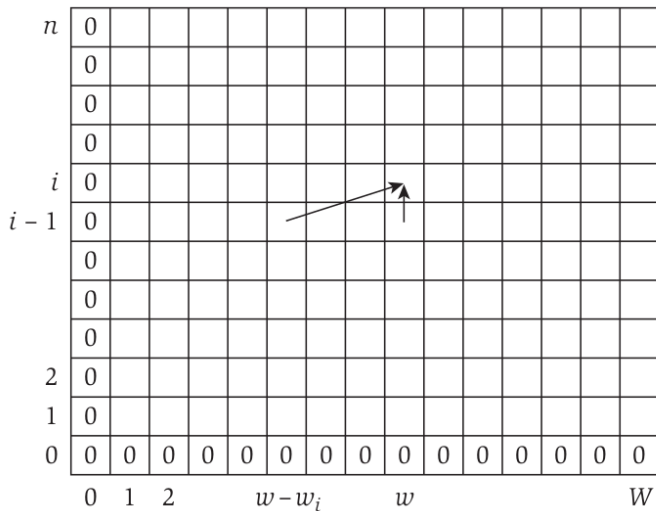
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TH7: Running time to populate the matrix:  $O(nW)$

TH8: Is this polynomial? No, *pseudo-polynomial* because of  $W$  which is unbounded.

# SUBSET VISUALIZATION

Matrix Visualization:



# SUBSET VISUALIZATION

Example Run:

$W = 6$ , items  $w_1 = 2$ ,  $w_2 = 2$ ,  $w_3 = 3$

3							
2							
1							
0	0	0	0	0	0	0	0
	0	1	2	3	4	5	6

**Initial values**



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Initial values

3							
2							
①	0	0	2	2	2	2	2
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Filling in values for  $i = 1$

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Filling in values for  $i = 1$

3							
②	0	0	2	2	4	4	4
1	0	0	2	2	2	2	2
0	0	0	0	0	0	0	0
	0	1	2	3	4	5	6

Filling in values for  $i = 2$

# SUBSET VISUALIZATION

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3							
2							
1							
0	0	0	0	0	0	0	0
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Initial values

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2							
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	0	1	2	3	4	5	6

Filling in values for  $i = 1$

3							
②	0	0	2	2	4	4	4
1	0	0	2	2	2	2	2
0	0	0	0	0	0	0	0
	0	1	2	3	4	5	6

Filling in values for  $i = 2$

3							
2	0	0	2	2	4	4	4
③	0	0	2	3	4	5	5
1	0	0	2	2	2	2	2
0	0	0	0	0	0	0	0
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Filling in values for  $i = 3$

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How can we recover the subset itself?

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TH9: Running time of recovery of subset:  $O(n)$

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- You are a thief with a knapsack that can carry  $W$  weight of goods.

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- Each item has a value:  $v_1, v_2, \dots, v_n$ .

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- A set of items:  $1, 2, \dots, n$ .
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- Each item has a value:  $v_1, v_2, \dots, v_n$ .
- What is the subset  $S$  of items to steal that maximizes  $\sum_{i \in S} v_i$  with the constraint that  $\sum_{i \in S} w_i \leq W$ ?

EXERCISE: SOLVE THIS WITH DP IN  $O(nW)$ .

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## DP Solution

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  - $i$ : Item indices from 0 to  $n$ .
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- Solution value:  $v[n, W]$ .



# EDIT DISTANCE

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## Problem

Minimum number of letter

- insertions: adding a letter,
- deletions: removing a letter,
- substitutions: replacing a letter

to change string  $A[1..m]$  to string  $B[1..n]$ .

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to change string  $A[1..m]$  to string  $B[1..n]$ .

Ex: TUESDAY  $\rightarrow$  THUESDAY  $\rightarrow$  THURSDAY

Or, align and count mismatched letters

T UESDAY

THURSDAY

# RECURSIVE APPROACH

## Smaller Subproblems

- Let  $A[1..m]$  and  $B[1..n]$  be the 2 input strings.
- What is the edit distance for  $A[1..i]$  and  $B[1..j]$ :

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  - Substitution:  $\text{Edit}(i, j) = \text{TH2}$

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  - Substitution:  $\text{Edit}(i, j) = \text{Edit}(i - 1, j - 1) + 1$ .

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  - $i = 0$ :  $\text{Edit}(i, j) = j$ .
  - $j = 0$ :  $\text{Edit}(i, j) = i$ .

# DYNAMIC PROGRAM FOR EDIT DISTANCE

Description of matrix

TH4: Number of dimensions of array?

# DYNAMIC PROGRAM FOR EDIT DISTANCE

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TH4: Number of dimensions of array? 2

# DYNAMIC PROGRAM FOR EDIT DISTANCE

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2D array  $E$ , where  $E[i, j]$  is the edit distance for  $A[1..i]$  and  $B[1..j]$ .

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$$E[i, j] = \begin{cases} i, & \text{if } j = 0 \\ j, & \text{if } i = 0 \\ \min\{E[i, j-1] + 1, E[i-1, j] + 1, \\ \quad E[i-1, j-1] + A[i] \neq B[j]\}, & \text{otherwise} \end{cases}$$

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### Solution and populating $L$

- Solution in TopHat 5
- Set  $E[0, j] = j$ ;  $E[i, 0] = i$ ; populate from 1 to  $n$ , 1 to  $m$ .

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- Solution in  $E[m, n]$
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- TH6: Run time:



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- Run time:  $O(mn)$

# SPACE SAVINGS

## Bellman Equation

$$E[i, j] = \begin{cases} i, & \text{if } j = 0 \\ j, & \text{if } i = 0 \\ \min\{E[i, j-1] + 1, E[i-1, j] + 1, \\ \quad E[i-1, j-1] + A[i] \neq B[j]\}, & \text{otherwise} \end{cases}$$

## How much space do we need?

- Notice that  $E[i][j]$  depends on  $E[i, j-1]$ ,  $E[i-1, j]$ , and  $E[i-1, j-1]$ .
- We only need previous and current row of matrix for calculations.

# SHORTEST PATH

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## GOING NEGATIVE

### Problem Definition

We have a directed graph  $G = (V, E)$ , where  $|V| = n$  and  $|E| = m$  and a node  $s$  that has a path to every other node in  $V$ . For each edge  $e = (i, j)$ ,  $c_{ij}$  is the weight of the edge, and there are no cycles with negative weight.

- What is the shortest path from  $s$  to each other node?

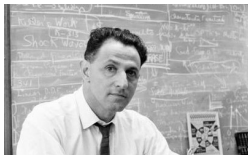
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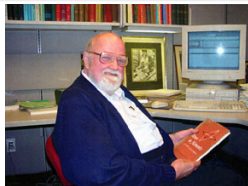
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Richard Bellman



L R Ford Jr.

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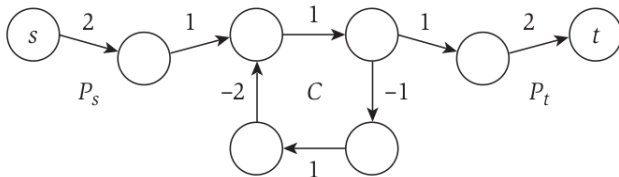
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- What is the shortest path from  $s$  to each other node?

Why no negative cycles?



# DIJKSTRA'S

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**Algorithm:** *Dijkstra's*

---

Let  $S$  be the set of explored nodes.

For each  $u \in S$ , we store a distance value  $d(u)$ .

Initialize  $S = \{s\}$  and  $d(s) = 0$

**while**  $S \neq V$  **do**

    Choose  $v \notin S$  with at least one incoming edge  
    originating from a node in  $S$  with the smallest

$$d'(v) = \min_{e=(u,v):u \in S} d(u) + \ell_e$$

    Append  $v$  to  $S$  and define  $d(v) = d'(v)$ .

**end**

**return**  $S$

---

# DIJKSTRA'S

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- Lose guarantee that minimum edge between  $S$  and  $V \setminus S$  is part of minimum path.

## Why not just boost all edges by max negative value plus a bit ( $\beta$ )?

- A path with  $x$  edges: Cost increases  $x \cdot \beta$ .
- Solution in new graph is not guaranteed to be optimal in original graph.

# BELLMAN-FORD

## Observation 1

*If  $G$  has no negative cycles, then there exists a shortest path from  $s$  to  $t$  that is simple, and has at most  $n - 1$  edges.*

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  - TH23: Where is the solution?



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TH24: Build the Bellman equation.

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$$M[i][v] = \min\{M[i - 1][v], \min_{w \in V}\{M[i - 1][w] + c_{vw}\}\},$$

where  $c_{vw} = \infty$  if no edge from  $v$  to  $w$ .

# BELLMAN-FORD ANALYSIS

$$M[i][v] = \min\{M[i-1][v], \min_{w \in V}\{M[i-1][w] + c_{vw}\}\}$$

## Worst Case: $n$ nodes

- TH25: # of Cells:

## BELLMAN-FORD ANALYSIS

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### Worst Case: $n$ nodes

- # of Cells:  $O(n^2)$ .

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### Worst Case: $n$ nodes

- # of Cells:  $O(n^2)$ .
- TH26: Cost per cell:



## BELLMAN-FORD ANALYSIS

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### Worst Case: $n$ nodes

- # of Cells:  $O(n^2)$ .
- Cost per cell:  $O(n)$ .
- Overall:  $O(n^3)$ .

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### Worst Case: $n$ nodes

- # of Cells:  $O(n^2)$ .
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### Worst Case: $n$ nodes, $m$ edges

- For each node  $v$ , we only need to consider outgoing edges to  $w$  (denoted by  $\eta_v$ ).
- For every node  $v$ , we need to do this calculation for  $0 \leq i \leq n-1$  lengths.

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## Worst Case: $n$ nodes, $m$ edges

- Overall:  $O\left(n \sum_{v \in V} \eta_v\right) = O(mn)$ .

## Space Saving: $O(n)$ .

- To build row  $i$ :
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- Recovery of actual path: An additional array  $first[v]$  that maintains the first hop from  $v$  to  $t$ .

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### Augmented Graph for Negative Cycle Finding

- Add a node  $t$  with an incoming edge from all other nodes with cost 0.
- Run Bellman-Ford from any node  $s$  to  $t$  until number of edges  $n$ .
- If, for some  $v$ ,  $M[n][v] \neq M[n-1][v]$ , then there is a negative cycle.

# DYNAMIC PROGRAMMING FOR GAMES

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## DP for Games

In many games, DP is a natural paradigm for an optimal strategy.

# COINS IN A LINE

## Players

Two players:



Alice  
(Player A)



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- Winner: Player with the max value at the end; winning player keeps the coins.



## GREEDY APPROACHES

### Largest Coin

TopHat D1: Give a counter-example.

## GREEDY APPROACHES

### Largest Coin

[1,3,6,3]

A: 3; [1,3,6]

B: 6; [1,3]

A: 6; [1]

B: 7; []

# GREEDY APPROACHES

## Largest Coin

## Even or Odd

[1,3,6,3,1,3]

A: 3; [1,3,6,3,1]

B: 1; [1,3,6,3]

A: 6; [1,3,6]

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A: 3; [1,3,6,3,1]

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A: 4; [3,6,3]

B: 4; [6,3]

A: 10; [3]

B: 7; []

# NATURAL DICHOTOMY

TH D2: What is the natural dichotomy?

# NATURAL DICHOTOMY

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- Two players: Assume that Bob will play optimally.



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- Solution: TH3

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- Runtime: TH4

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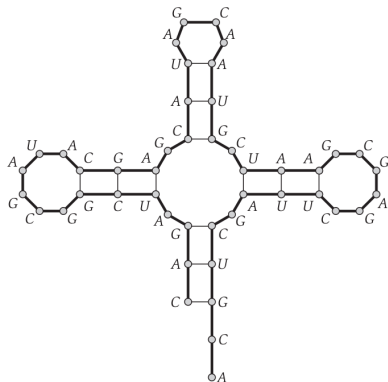
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- Proof of correctness: Strong induction on the cell population order..

# RNA SECONDARY STRUCTURE





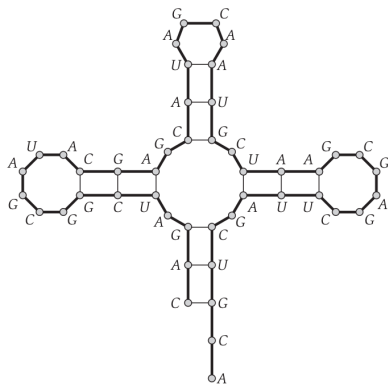
# RNA SECONDARY STRUCTURE



## Problem Definition

- RNA tends to loop back on itself, forming base pairs.
- RNA alphabet:  $\{A, C, G, U\}$ .
- Valid pairs:  $(A, U)$  or  $(C, G)$ .
- Input:  $n$  length string:  
 $B = b_1 b_2 \dots b_n$
- Output: Determine a secondary structure with maximum number of base pairs.

## RNA SECONDARY STRUCTURE



## Secondary Structure

$S = \{(i, j)\}$ , where  $i < j$  and  $i, j \in \{1, \dots, n\}$ , such that:

- ❶ No Sharp turns:  $i < j - d$  for some constant  $d$ .
- ❷ All pairs are valid.
- ❸  $S$  is a matching: no base appears more than once.
- ❹ Non-crossing: For any  $(i, j), (i', j') \in S$ , we cannot have  $i < i' < j < j'$ .

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## 1D Approach

- 1D array  $m$ , where  $m[j]$  is the maximum # of pairs among:  
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  - Sub-problems:
    - 1 Max pairs in  $[i, t - 1]$ :  $m[i][t - 1]$ .

## SECOND DYNAMIC PROGRAMMING ATTEMPT

### 2D Approach

- 2D array  $m$ , where  $m[i][j]$  is the maximum # of pairs among:  $b_i b_{i+1} \dots b_j$ .
- No sharp turns:  $m[i][j] = 0$  for  $i \geq j - d$ .
- Solution:  $m[1][n]$ .

### Recursive Sub-problems

Dichotomy:

- ①  $j$  is not a pair:  $m[i][j] = m[i][j - 1]$ .
- ②  $j$  is paired with  $i \leq t < j - d$ 
  - $v_{ij}$  as indicator: 1 if valid pair, 0 otherwise
  - Non-crossing: No pairs between  $[i, t - 1]$  and  $[t + 1, j - 1]$ .
  - Sub-problems:
    - ① Max pairs in  $[i, t - 1]$ :  $m[i][t - 1]$ .
    - ② Max pairs in  $[t + 1, j - 1]$ :  $m[t + 1][j - 1]$ .

## SECOND DYNAMIC PROGRAMMING ATTEMPT

### 2D Approach

- 2D array  $m$ , where  $m[i][j]$  is the maximum # of pairs among:  $b_i b_{i+1} \dots b_j$ .

### Recursive Sub-problems

Dichotomy:

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- 2  $j$  is paired with  $i \leq t < j - d$ 
  - $v_{ij}$  as indicator: 1 if valid pair, 0 otherwise
  - Non-crossing: No pairs between  $[i, t - 1]$  and  $[t + 1, j - 1]$ .
  - Sub-problems:
    - 1 Max pairs in  $[i, t - 1]$ :  $m[i][t - 1]$ .
    - 2 Max pairs in  $[t + 1, j - 1]$ :  $m[t + 1][j - 1]$ .

TopHat 13: What is the Bellman equation?

## SECOND DYNAMIC PROGRAMMING ATTEMPT

### 2D Approach

- 2D array  $m$ , where  $m[i][j]$  is the maximum # of pairs among:  $b_i b_{i+1} \dots b_j$ .

### Recursive Sub-problems

Dichotomy:

- 1  $j$  is not a pair:  $m[i][j] = m[i][j - 1]$ .
- 2  $j$  is paired with  $i \leq t < j - d$ 
  - $v_{ij}$  as indicator: 1 if valid pair, 0 otherwise
  - Non-crossing: No pairs between  $[i, t - 1]$  and  $[t + 1, j - 1]$ .
  - Sub-problems:
    - 1 Max pairs in  $[i, t - 1]$ :  $m[i][t - 1]$ .
    - 2 Max pairs in  $[t + 1, j - 1]$ :  $m[t + 1][j - 1]$ .

$$m[i][j] = \max(m[i][j - 1], \max_{i \leq t < j - d} \{v_{tj} \cdot (1 + m[i][t - 1] + m[t + 1][j - 1])\})$$



# RNA SECONDARY STRUCTURE EXAMPLE

$$m[i][j] = \max \left( m[i][j-1], \max_{i \leq t < j-d} \{v_{tj} \cdot (1 + m[i][t-1] + m[t+1][j-1])\} \right)$$

- $B = \text{ACCGGUAGU}$  and  $d = 4$

i				
4				
3				
2				
1				
j	6	7	8	9

# RNA SECONDARY STRUCTURE EXAMPLE

$$m[i][j] = \max \left( m[i][j-1], \max_{i \leq t < j-d} \{v_{tj} \cdot (1 + m[i][t-1] + m[t+1][j-1])\} \right)$$

- $B = ACCGGUAGU$  and  $d = 4$

i				
4	0	0	0	
3	0	0		
2	0			
1				
j	6	7	8	9

# RNA SECONDARY STRUCTURE EXAMPLE

$$m[i][j] = \max \left( m[i][j-1], \max_{i \leq t < j-d} \{v_{tj} \cdot (1 + m[i][t-1] + m[t+1][j-1])\} \right)$$

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i				
4	0	0	0	0
3	0	0	1	
2	0	0		
1	1			
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$$m[i][j] = \max \left( m[i][j-1], \max_{i \leq t < j-d} \{v_{tj} \cdot (1 + m[i][t-1] + m[t+1][j-1])\} \right)$$

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4	0	0	0	0
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- $B = ACCGGUAGU$  and  $d = 4$

i				
4	0	0	0	0
3	0	0	1	1
2	0	0	1	1
1	1	1	1	
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- $B = ACCGGUAGU$  and  $d = 4$

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4	0	0	0	0
3	0	0	1	1
2	0	0	1	1
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- $B = \text{ACCGGUAGU}$  and  $d = 4$

i				
4	0	0	0	0
3	0	0	1	1
2	0	0	1	1
1	1	1	1	2
j	6	7	8	9

### Running Time

- # of cells: TH14
- Work per cell:

# RNA SECONDARY STRUCTURE EXAMPLE

$$m[i][j] = \max \left( m[i][j-1], \max_{i \leq t < j-d} \{v_{tj} \cdot (1 + m[i][t-1] + m[t+1][j-1])\} \right)$$

- $B = \text{ACCGGUAGU}$  and  $d = 4$

i				
4	0	0	0	0
3	0	0	1	1
2	0	0	1	1
1	1	1	1	2
j	6	7	8	9

## Running Time

- # of cells:  $O(n^2)$ .
- Work per cell:



# RNA SECONDARY STRUCTURE EXAMPLE

$$m[i][j] = \max \left( m[i][j-1], \max_{i \leq t < j-d} \{v_{tj} \cdot (1 + m[i][t-1] + m[t+1][j-1])\} \right)$$

- $B = \text{ACCGGUAGU}$  and  $d = 4$

i				
4	0	0	0	0
3	0	0	1	1
2	0	0	1	1
1	1	1	1	2
j	6	7	8	9

## Running Time

- # of cells:  $O(n^2)$ .
- Work per cell: TH15

## RNA SECONDARY STRUCTURE EXAMPLE

$$m[i][j] = \max \left( m[i][j-1], \max_{i \leq t < j-d} \{v_{tj} \cdot (1 + m[i][t-1] + m[t+1][j-1])\} \right)$$

- $B = \text{ACCGGUAGU}$  and  $d = 4$

i				
4	0	0	0	0
3	0	0	1	1
2	0	0	1	1
1	1	1	1	2
j	6	7	8	9

### Running Time

- # of cells:  $O(n^2)$ .
- Work per cell:  $O(n)$ .

# RNA SECONDARY STRUCTURE EXAMPLE

$$m[i][j] = \max \left( m[i][j-1], \max_{i \leq t < j-d} \{v_{tj} \cdot (1 + m[i][t-1] + m[t+1][j-1])\} \right)$$

- $B = \text{ACCGGUAGU}$  and  $d = 4$

i				
4	0	0	0	0
3	0	0	1	1
2	0	0	1	1
1	1	1	1	2
j	6	7	8	9

## Running Time

- # of cells:  $O(n^2)$ .
- Work per cell:  $O(n)$ .
- Overall:  $O(n^3)$ .

# SEQUENCE ALIGNMENT

# SEQUENCE ALIGNMENT

Scarites	C	T	T	A	G	A	T	C	G	T	A	C	C	A	-	-	-	A	A	T	A	T	T	A	C	
Carenum	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	A	-	T	A	C	-	T	T	T	A	C
Pasimachus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	T	A	T	A	G	T	T	T	A	C	
Pheropsofus	C	T	T	A	G	A	T	C	G	T	T	C	C	A	C	-	-	-	A	C	A	T	A	T	A	C
Brachinus armiger	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	T	A	T	A	T	T	C
Brachinus hirsutus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	T	A	T	A	T	A	C
Aptinus	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	C	A	T	T	A	C	
Pseudomorpha	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	C	A	A	T	A	C	

## Needleman–Wunsch Problem

- An alphabet  $S$ .
- Strings  $X = x_1x_2 \dots x_m$  and  $Y = y_1y_2 \dots y_n$  from  $S$ .
- A matching  $M = \{(i, j)\}$  of pairs without crossings, where  $i \in [1, m]$  and  $j \in [1, n]$ .

# SEQUENCE ALIGNMENT

Soarites	C	T	T	A	G	A	T	C	G	T	A	C	C	A	-	-	-	A	T	A	T	T	A	C		
Carenum	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	T	A	C	-	T	T	T	A	C	
Pasimachus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	T	A	A	G	T	T	T	T	A	C	
Pheropsophus	C	T	T	A	G	A	T	C	G	T	T	C	C	A	C	-	-	-	A	C	A	T	A	T	A	C
Brachinus armiger	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	T	A	T	A	T	T	C
Brachinus hirsutus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	T	A	T	A	T	A	C
Aptinus	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	C	A	T	T	A	T	C
Pseudomorpha	C	T	T	A	G	A	T	C	G	T	A	C	C	-	-	-	-	A	C	A	A	T	A	T	A	C

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- An alphabet  $S$ .
- Strings  $X = x_1x_2 \dots x_m$  and  $Y = y_1y_2 \dots y_n$  from  $S$ .
- A matching  $M = \{(i, j)\}$  of pairs without crossings, where  $i \in [1, m]$  and  $j \in [1, n]$ .
- Cost:
  - Gaps (unmatched indexes) have a cost of  $\delta$ .
  - For each symbol pair  $p, q \in S$ ,  $\alpha_{pq}$  is the matching cost.

# SEQUENCE ALIGNMENT

Scarites	C	T	T	A	G	A	T	C	G	T	A	C	C	A	-	-	-	A	A	T	A	T	T	A	C	
Carenum	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	A	-	T	A	C	-	T	T	T	A	C
Pasimachus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	T	A	T	A	G	T	T	T	A	C	
Pheropsophus	C	T	T	A	G	A	T	C	G	T	T	C	C	A	C	-	-	-	A	C	A	T	A	T	A	C
Brachinus armiger	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	T	A	T	A	T	T	C
Brachinus hirsutus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	T	A	T	A	T	A	C
Aptinus	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	-	A	C	A	T	T	A	C	
Pseudomorpha	C	T	T	A	G	A	T	C	G	T	A	C	C	-	-	-	-	A	C	A	A	T	A	T	A	C

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- An alphabet  $S$ .
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- Goal: Find the matching that minimizes the cost.

# SEQUENCE ALIGNMENT

Soarites	C	T	T	A	G	A	T	C	G	T	A	C	C	A	-	-	A	T	A	T	T	A	C			
Carenum	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	T	A	C	-	T	T	T	A	C	
Pasimachus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	T	A	T	A	G	T	T	T	A	C	
Pheropsophus	C	T	T	A	G	A	T	C	G	T	T	C	C	A	C	-	-	A	C	A	T	T	A	T	A	C
Brachinus armiger	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	T	A	T	A	T	T	T	C
Brachinus hirsutus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	T	A	T	A	T	T	A	C
Aptinus	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	C	A	T	T	A	T	A	C
Pseudomorpha	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	C	A	T	A	T	T	A	C

$$\delta = 3; \alpha_{pp} = 0; \alpha_{pq} = 1$$

TopHat Q16: What is the cost of the matching:

o-currance

occurrence

## Needleman–Wunsch Problem

- An alphabet  $S$ .
- Strings  $X = x_1x_2 \dots x_m$  and  $Y = y_1y_2 \dots y_n$  from  $S$ .
- A matching  $M = \{(i, j)\}$  of pairs without crossings, where  $i \in [1, m]$  and  $j \in [1, n]$ .
- Cost:
  - Gaps (unmatched indexes) have a cost of  $\delta$ .
  - For each symbol pair  $p, q \in S$ ,  $\alpha_{pq}$  is the matching cost.
- Goal: Find the matching that minimizes the cost.



# SEQUENCE ALIGNMENT

Soarites	C	T	T	A	G	A	T	C	G	T	A	C	C	A	-	-	A	T	A	T	T	A	C		
Carenum	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	T	A	C	-	T	T	T	A	C
Pasimachus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	T	A	T	A	G	T	T	T	A	C
Pheropsophus	C	T	T	A	G	A	T	C	G	T	T	C	C	A	C	-	-	A	C	A	T	T	A	C	
Brachinus armiger	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	T	A	T	T	T	C	
Brachinus hirsutus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	T	A	T	T	T	A	C
Aptinus	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	C	A	T	T	A	C	
Pseudomorpha	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	C	A	T	T	A	C	

$$\delta = 3; \alpha_{pp} = 0; \alpha_{pq} = 1$$

TopHat Q17: What is the cost of the matching:

o-curr-ance

occurre-nc

## Needleman–Wunsch Problem

- An alphabet  $S$ .
- Strings  $X = x_1x_2 \dots x_m$  and  $Y = y_1y_2 \dots y_n$  from  $S$ .
- A matching  $M = \{(i, j)\}$  of pairs without crossings, where  $i \in [1, m]$  and  $j \in [1, n]$ .
- Cost:
  - Gaps (unmatched indexes) have a cost of  $\delta$ .
  - For each symbol pair  $p, q \in S$ ,  $\alpha_{pq}$  is the matching cost.
- Goal: Find the matching that minimizes the cost.

# SEQUENCE ALIGNMENT

Soarites	C	T	T	A	G	A	T	C	G	T	A	C	C	A	A	-	-	A	A	T	A	T	T	A	C	
Carenum	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	A	-	T	A	C	-	T	T	T	A	C
Pasimachus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	T	A	T	A	G	T	T	T	A	C	
Pheropsophus	C	T	T	A	G	A	T	C	G	T	T	C	C	A	C	-	-	A	C	A	T	A	T	A	C	
Brachinus armiger	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	T	A	T	T	T	A	C	
Brachinus hirsutus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	T	A	T	T	T	A	C	
Aptinus	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	C	A	T	T	A	C		
Pseudomorpha	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	C	A	T	T	A	C		

$$\delta = 1; \alpha_{pp} = 0; \alpha_{pq} = 4$$

TopHat Q18: What is the cost of the matching:

o-currance

occurrence

## Needleman–Wunsch Problem

- An alphabet  $S$ .
- Strings  $X = x_1x_2 \dots x_m$  and  $Y = y_1y_2 \dots y_n$  from  $S$ .
- A matching  $M = \{(i, j)\}$  of pairs without crossings, where  $i \in [1, m]$  and  $j \in [1, n]$ .
- Cost:
  - Gaps (unmatched indexes) have a cost of  $\delta$ .
  - For each symbol pair  $p, q \in S$ ,  $\alpha_{pq}$  is the matching cost.
- Goal: Find the matching that minimizes the cost.

# SEQUENCE ALIGNMENT

Soarites	C	T	T	A	G	A	T	C	G	T	A	C	C	A	-	-	A	A	T	A	T	T	A	C	
Carenum	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	T	A	C	-	T	T	T	A	C
Pasimachus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	T	A	T	A	G	T	T	T	A	C
Pheropsophus	C	T	T	A	G	A	T	C	G	T	T	C	C	A	C	-	-	A	C	A	T	A	T	A	C
Brachinus armiger	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	T	A	T	T	T	A	C
Brachinus hirsutus	A	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	T	A	T	T	T	A	C
Aptinus	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	C	A	T	T	A	C	
Pseudomorpha	C	T	T	A	G	A	T	C	G	T	A	C	C	A	C	-	-	A	C	A	T	T	A	C	

$$\delta = 1; \alpha_{pp} = 0; \alpha_{pq} = 4$$

TopHat Q19: What is the cost of the matching:

o-curr-ance

occurre-nce

## Needleman–Wunsch Problem

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- Strings  $X = x_1x_2 \dots x_m$  and  $Y = y_1y_2 \dots y_n$  from  $S$ .
- A matching  $M = \{(i, j)\}$  of pairs without crossings, where  $i \in [1, m]$  and  $j \in [1, n]$ .
- Cost:
  - Gaps (unmatched indexes) have a cost of  $\delta$ .
  - For each symbol pair  $p, q \in S$ ,  $\alpha_{pq}$  is the matching cost.
- Goal: Find the matching that minimizes the cost.

# DESIGNING NEEDLEMAN–WUNSCH ALGORITHM

## Basic Dichotomy

In optimal alignment  $M$ , either  $(m, n) \in M$  or  $(m, n) \notin M$ .

# DESIGNING NEEDLEMAN–WUNSCH ALGORITHM

## Basic Dichotomy

In optimal alignment  $M$ , either  $(m, n) \in M$  or  $(m, n) \notin M$ .

## Lemma 1

*Let  $M$  be any alignment of  $X$  and  $Y$ . If  $(m, n) \notin M$ , then either the  $m$ th position of  $X$ , or the  $n$ th position of  $Y$  is not matched in  $M$ .*

# DESIGNING NEEDLEMAN–WUNSCH ALGORITHM

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In optimal alignment  $M$ , either  $(m, n) \in M$  or  $(m, n) \notin M$ .

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## Proof.



# DESIGNING NEEDLEMAN–WUNSCH ALGORITHM

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## Proof.

- By way of contradiction, assume that



# DESIGNING NEEDLEMAN–WUNSCH ALGORITHM

## Basic Dichotomy

In optimal alignment  $M$ , either  $(m, n) \in M$  or  $(m, n) \notin M$ .

## Lemma 1

*Let  $M$  be any alignment of  $X$  and  $Y$ . If  $(m, n) \notin M$ , then either the  $m$ th position of  $X$ , or the  $n$ th position of  $Y$  is not matched in  $M$ .*

## Proof.

- By way of contradiction, assume that  $(m, n) \notin M$ , and  $(m, j), (i, n) \in M$  for  $i < m$  and  $j < n$ .





# DESIGNING NEEDLEMAN–WUNSCH ALGORITHM

## Basic Dichotomy

In optimal alignment  $M$ , either  $(m, n) \in M$  or  $(m, n) \notin M$ .

## Lemma 1

*Let  $M$  be any alignment of  $X$  and  $Y$ . If  $(m, n) \notin M$ , then either the  $m$ th position of  $X$ , or the  $n$ th position of  $Y$  is not matched in  $M$ .*

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- By way of contradiction, assume that  $(m, n) \notin M$ , and  $(m, j), (i, n) \in M$  for  $i < m$  and  $j < n$ .
- Contradicts the non-crossing requirement.



# DESIGNING NEEDLEMAN–WUNSCH ALGORITHM

## Key Concepts for Optimality

In an optimal alignment  $M$ , at least one of the following is true:

- ❶  $(m, n) \in M$ ; or
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- TH20: How many dimensions for the matrix?

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  - TH21: Build the Bellman equation.

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  - Runtime: TH22

# DESIGNING NEEDLEMAN–WUNSCH ALGORITHM

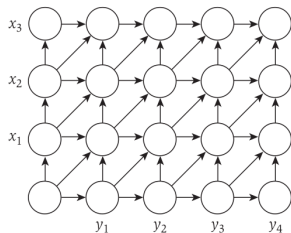
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  - Runtime:  $O(mn)$ .



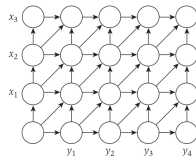
# GRAPHING THE ALGORITHM



## Theorem 2

Let  $f(i, j)$  denote the minimum cost of a path from  $(0, 0)$  to  $(i, j)$  in  $G_{XY}$ . Then,  $\forall i, j$   $f(i, j) = A[i][j]$ .

# GRAPHING THE ALGORITHM



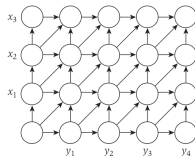
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Proof.



# GRAPHING THE ALGORITHM



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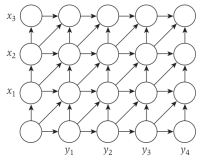
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## GRAPHING THE ALGORITHM



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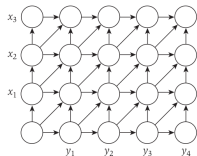
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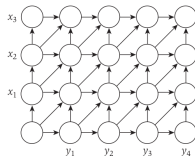
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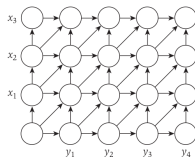
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- Base case:  $i + j = 0$ . We have  $f(0, 0) = 0 = A[0][0]$ .
- Induction hypothesis: The claim holds for all pairs  $(i', j')$  such that  $i' + j' < i + j$ .



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- Inductive step:

$$\begin{aligned} f(i, j) &= \min\{\alpha_{x_i y_j} + f(i-1, j-1), \delta + f(i-1, j), \delta + f(i, j-1)\} \\ &= \min\{\alpha_{x_i y_j} + A[i-1][j-1], \delta + A[i-1][j], \delta + A[i][j-1]\} \\ &= A[i, j] \end{aligned}$$

□

## SEQUENCE ALIGNMENT EXAMPLE

$$A[i][j] = \min\{\alpha_{x_i y_j} + A[i-1][j-1], \delta + A[i-1][j], \delta + A[i][j-1]\}$$

- “mean” vs “name”

- $\delta = 2; \alpha = \begin{cases} 0 & \text{if same letter} \\ 3 & \text{if vowel to consonant} \\ 1 & \text{otherwise} \end{cases}$

n					
a					
e					
m					
-					
	-	n	a	m	e



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n	8	6	5	4	6
a	6	5	3	5	5
e	4	3	2	4	4
m	2	1	3	4	6
-	0	2	4	6	8
	-	n	a	m	e

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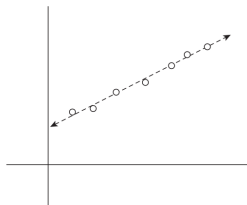
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# LEAST SQUARES

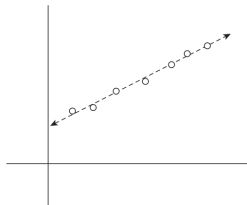
# SEGMENTED LEAST SQUARES



## Problem Setup

- Set of  $n$  points:  $P := \{(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)\}$  on the plane.
- Suppose  $x_1 < x_2 < \dots < x_n$ .
- Find  $L : y = ax + b$  that minimizes:  
$$\text{Error}(L, P) = \sum_{i=1}^n (y_i - ax_i - b)^2 .$$

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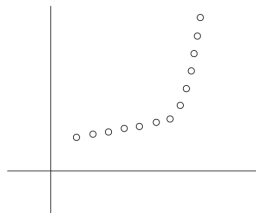
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## Problem Formulation

- Partition the points (by  $x$ ) into contiguous subsets.
- Minimize the sum of  $\text{Error}(L, p_i) + C$  for all subsets, where  $C$  is a fixed cost per subset.

# SEGMENTED LEAST SQUARES



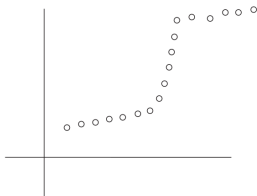
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- Number of cells:  $O(n)$ .
- Work done for cell  $j$ : TH11

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- Overall:  $O(n^2)$ .

# MAX SUBARRAY\*

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Given an array  $A$  of integers, find the contiguous subarray of  $A$  of maximum sum.

## Exercise – Teams of 3 or so

- Solve the problem in  $\Theta(n^2)$ .
- Solve the problem in  $O(n \log n)$ .
- Prove correctness and complexity.

## PART 1: GIVE A $\Theta(n^2)$ SOLUTION.

---

**Algorithm:** CHECKALLSUBARRAYS

---

**Input** : Array  $A$  of  $n$  ints.

**Output:** Max subarray in  $A$ .

Let  $M$  be an empty array

```
for  $i := 1$  to  $\text{len}(A)$  do  
    for  $j := i$  to  $\text{len}(A)$  do  
        if  $\text{sum}(A[i..j]) > \text{sum}(M)$  then  
             $M := A[i..j]$   
        end  
    end  
end  
return  $M$ 
```

---

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**end**

**end**

**end**

**return**  $M$

---

### Analysis

- Correct: Checks all possible contiguous subarrays.



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      |  $M := A[i..j]$ 
    end
  end
end
return  $M$ 
```

---

### Analysis

- Correct: Checks all possible contiguous subarrays.
- Complexity:
  - Re-calculating the sum will make it  $O(n^3)$ . Key is to calculate the sum as you iterate.
  - For each  $i$ , check  $n - i + 1$  ends. Overall:

$$\sum_{i=1}^n i = \frac{n(n+1)}{2} = \Theta(n^2)$$

## PART 2: GIVE AN $O(n \log n)$ SOLUTION.

---

**Algorithm:** MAXSUBARRAY

---

**Input** : Array  $A$  of  $n$  ints.

**Output:** Max subarray in  $A$ .

$A_1 := \text{MAXSUBARRAY}(\text{Front-half of } A)$

$A_2 := \text{MAXSUBARRAY}(\text{Back-half of } A)$

$M := \text{MIDMAXSUBARRAY}(A)$

**return** *Array with max sum of  $\{A_1, A_2, M\}$*

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## PART 2: GIVE AN $O(n \log n)$ SOLUTION.

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**return** *Array with max sum of  $\{A_1, A_2, M\}$*

---

---

**Algorithm:** MIDMAXSUBARRAY

---

**Input** : Array  $A$  of  $n$  ints.

**Output:** Max subarray that crosses midpoint  $A$ .

$m := \text{mid-point of } A$

$L := \text{max subarray in } A[i, m-1] \text{ for } i = m-1 \rightarrow i$

$R := \text{max subarray in } A[m, j] \text{ for } j = m \rightarrow n$

**return**  $L \cup R$  // subarray formed by combining  $L$  and  $R$ .

---

## PART 2: GIVE AN $O(n \log n)$ SOLUTION.

---

**Algorithm:** MAXSUBARRAY

---

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**return** Array with max sum of  $\{A_1, A_2, M\}$

---

### Analysis

- Correctness: By induction,  $A_1$  and  $A_2$  are max for subarray and  $M$  is max mid-crossing array.
- Complexity: Same recurrence as MERGESORT.

# MAX SUBARRAY

## Problem

Given an array  $A$  of integers, find the contiguous subarray of  $A$  of maximum sum.

## Exercise – Teams of 3 or so

- Solve the problem in  $\Theta(n^2)$ .
- Solve the problem in  $O(n \log n)$ .
- Prove correctness and complexity.
- **With dynamic programming, solve the problem in  $O(n)$ !**

## PART 3: GIVE AN $O(n)$ SOLUTION.

### DP Solution

- 1D array  $s$ , where  $s[i]$  contains the value of the max subarray ending at  $i$ . ( $O(n)$  cells)
- Bellman equation:  $s[i] = \max(s[i - 1] + A[i], A[i])$ . ( $O(1)$  time)
- Solutions is:  $\max_j \{s[j]\}$ . ( $O(n)$  time)

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- Or, trace back from max value at index  $j$  until  $s[i] = A[i]$ .

# APPENDIX

# REFERENCES

<i>Scaphites</i>	G	T	T	G	T	C	C	-	-	-	T	T	T	C
<i>Caranum</i>	G	T	T	G	T	C	C	-	-	-	T	T	T	C
<i>Palaeosinhuus</i>	T	T	T	G	T	C	C	-	-	-	T	T	T	C
<i>Phoropapilio</i>	G	T	T	G	T	C	C	-	-	-	T	T	T	C
<i>Brachinus armiger</i>	T	T	T	G	T	C	C	-	-	-	T	T	T	C
<i>Brachinus hirsutus</i>	G	T	T	G	T	C	C	-	-	-	T	T	T	C
<i>Apilinus</i>	G	T	T	G	T	C	C	-	-	-	T	T	T	C
<i>Pseudosinhuus</i>	G	T	T	G	T	C	C	-	-	-	T	T	T	C



<https://brand.wisc.edu/web/logos/>

## IMAGE SOURCES II



[https://www.pngfind.com/mpng/mTJmbx\\_spongebob-squarepants-png-image-spongebob-cartoon](https://www.pngfind.com/mpng/mTJmbx_spongebob-squarepants-png-image-spongebob-cartoon)



[https://www.pngfind.com/mpng/xhJRmT\\_cheshire-cat-vintage-drawing-alice-in-wonderland](https://www.pngfind.com/mpng/xhJRmT_cheshire-cat-vintage-drawing-alice-in-wonderland)