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# CS481: Bioinformatics Algorithms

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# The Change Problem

Goal: Convert some amount of money  $M$  into given denominations, using the fewest possible number of coins

Input: An amount of money  $M$ , and an array of  $d$  denominations  $c = (c_1, c_2, \dots, c_d)$ , in a decreasing order of value ( $c_1 > c_2 > \dots > c_d$ )

Output: A list of  $d$  integers  $i_1, i_2, \dots, i_d$  such that
$$c_1 i_1 + c_2 i_2 + \dots + c_d i_d = M$$
and  $i_1 + i_2 + \dots + i_d$  is minimal

# Change Problem: Example

Given the denominations 1, 3, and 5, what is the minimum number of coins needed to make change for a given value?


Value	1	2	3	4	5	6	7	8	9	10
Min # of coins	1		1		1					

**Only one coin is needed to make change for the values 1, 3, and 5**

# Change Problem: Example (cont'd)

Given the denominations 1, 3, and 5, what is the minimum number of coins needed to make change for a given value?

Value	1	2	3	4	5	6	7	8	9	10
Min # of coins	1	2	1	2	1	2		2		2




**However, two coins are needed to make change for the values 2, 4, 6, 8, and 10.**

# Change Problem: Example (cont'd)

Given the denominations 1, 3, and 5, what is the minimum number of coins needed to make change for a given value?

Value	1	2	3	4	5	6	7	8	9	10
Min # of coins	1	2	1	2	1	2	3	2	3	2



**Lastly, three coins are needed to make change for the values 7 and 9**

# Change Problem: Recurrence

This example is expressed by the following recurrence relation:

$$\text{minNumCoins}(M) = \min \text{ of } \left\{ \begin{array}{l} \text{minNumCoins}(M-1) + 1 \\ \text{minNumCoins}(M-3) + 1 \\ \text{minNumCoins}(M-5) + 1 \end{array} \right.$$

# Change Problem: Recurrence (cont'd)

Given the denominations  $c$ :  $c_1, c_2, \dots, c_d$ , the recurrence relation is:

$$\text{minNumCoins}(M) = \min \text{ of } \left\{ \begin{array}{l} \text{minNumCoins}(M - c_1) + 1 \\ \text{minNumCoins}(M - c_2) + 1 \\ \dots \\ \text{minNumCoins}(M - c_d) + 1 \end{array} \right.$$

# Change Problem: A Recursive Algorithm

1. RecursiveChange(*M, c, d*)
2.     if  $M = 0$
3.         return 0
4.      $bestNumCoins \leftarrow \text{infinity}$
5.     for  $i \leftarrow 1$  to  $d$
6.         if  $M \geq c_i$
7.              $numCoins \leftarrow \text{RecursiveChange}(M - c_i, c, d)$
8.             if  $numCoins + 1 < bestNumCoins$
9.                  $bestNumCoins \leftarrow numCoins + 1$
10.     return  $bestNumCoins$

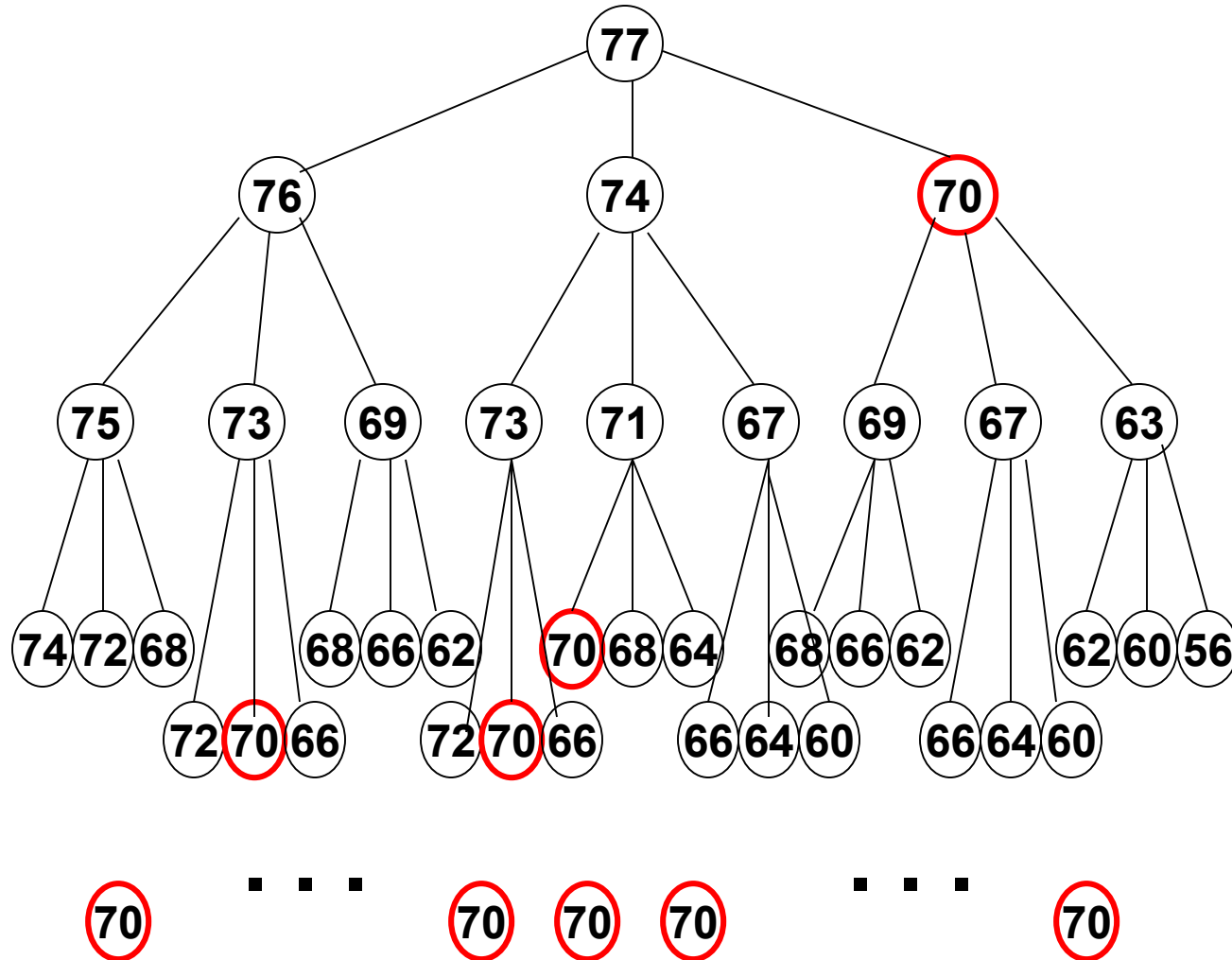


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# RecursiveChange Is Not Efficient

- It recalculates the optimal coin combination for a given amount of money repeatedly
- i.e.,  $M = 77$ ,  $c = (1, 3, 7)$ :
  - Optimal coin combo for 70 cents is computed **9** times!

# The RecursiveChange Tree



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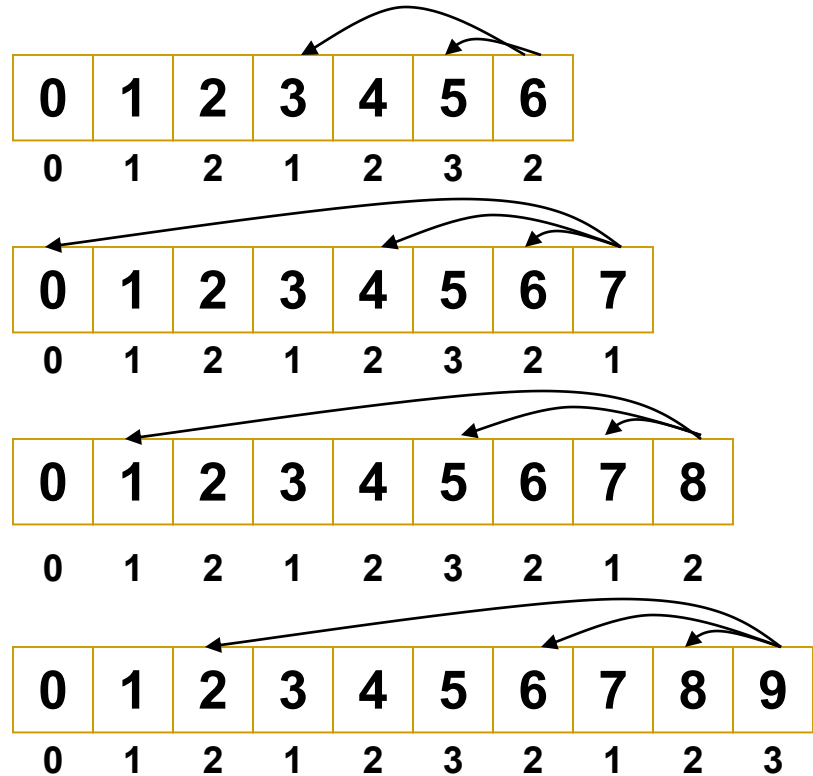
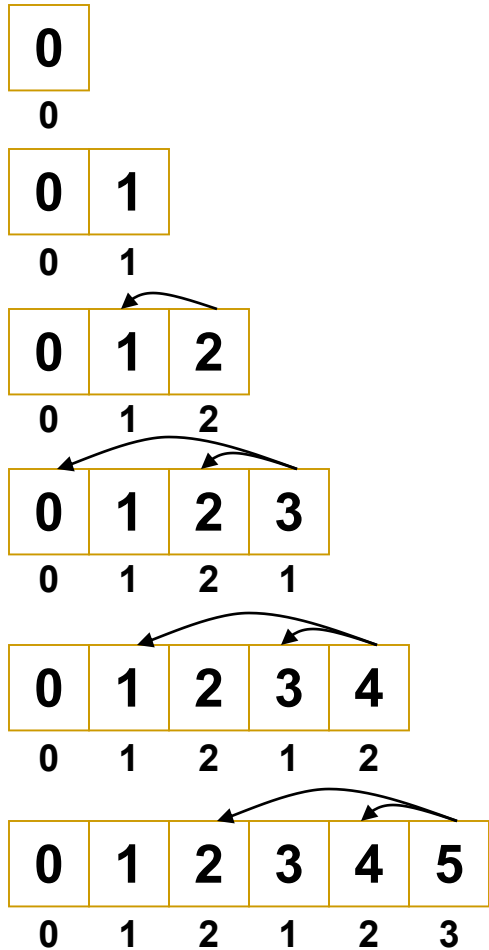
# We Can Do Better

- We're re-computing values in our algorithm more than once
  - Save results of each computation for 0 to  $M$
  - This way, we can do a reference call to find an already computed value, instead of re-computing each time
  - Running time  $M * d$ , where  $M$  is the value of money and  $d$  is the number of denominations
-

# The Change Problem: Dynamic Programming

1. DPChange(M, c, d)
2.   bestNumCoins<sub>0</sub>  $\leftarrow$  0
3.   for m  $\leftarrow$  1 to M
4.     bestNumCoins<sub>m</sub>  $\leftarrow$  infinity
5.     for i  $\leftarrow$  1 to d
6.       if m  $\geq$  c<sub>i</sub>
7.         if bestNumCoins<sub>m - c<sub>i</sub></sub> + 1 < bestNumCoins<sub>m</sub>
8.         bestNumCoins<sub>m</sub>  $\leftarrow$  bestNumCoins<sub>m - c<sub>i</sub></sub> + 1
9.   return bestNumCoins<sub>M</sub>

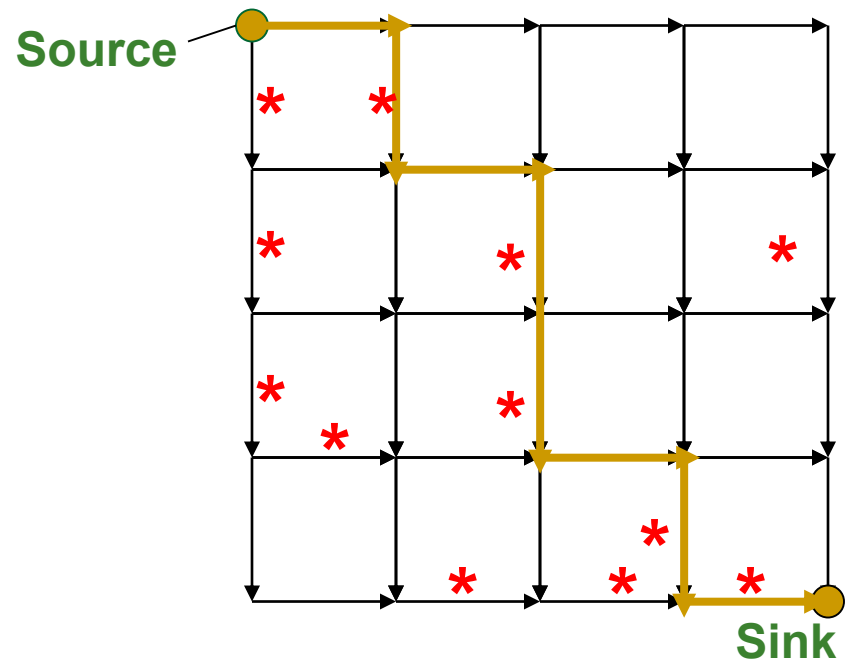
# DPChange: Example



**c = (1,3,7)**  
**M = 9**

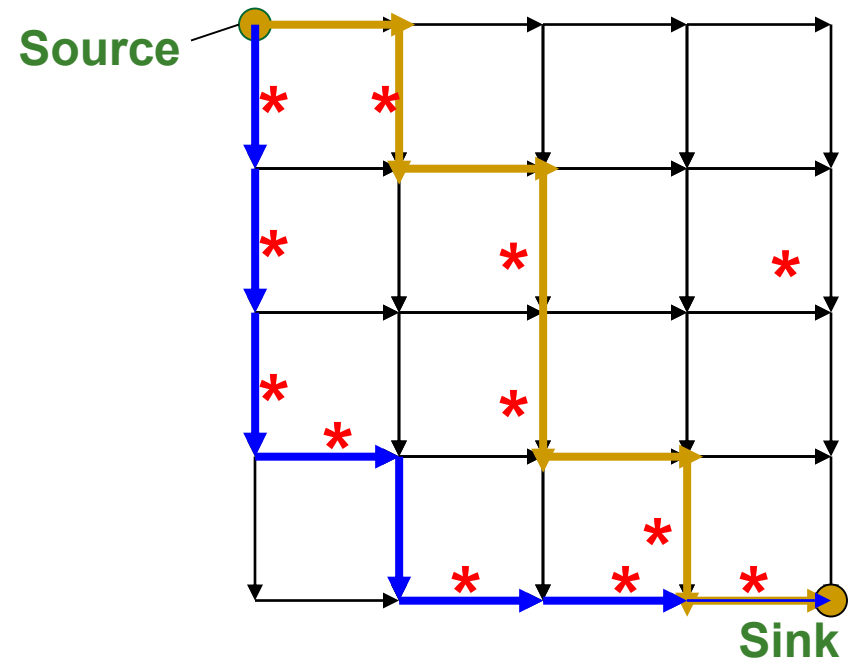
# Manhattan Tourist Problem (MTP)

Imagine seeking a path (from source to sink) to travel (only eastward and southward) with the most number of attractions (\*) in the Manhattan grid



# Manhattan Tourist Problem (MTP)

Imagine seeking a path (from source to sink) to travel (only eastward and southward) with the most number of attractions (\*) in the Manhattan grid



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# Manhattan Tourist Problem: Formulation

Goal: Find the longest path in a weighted grid.

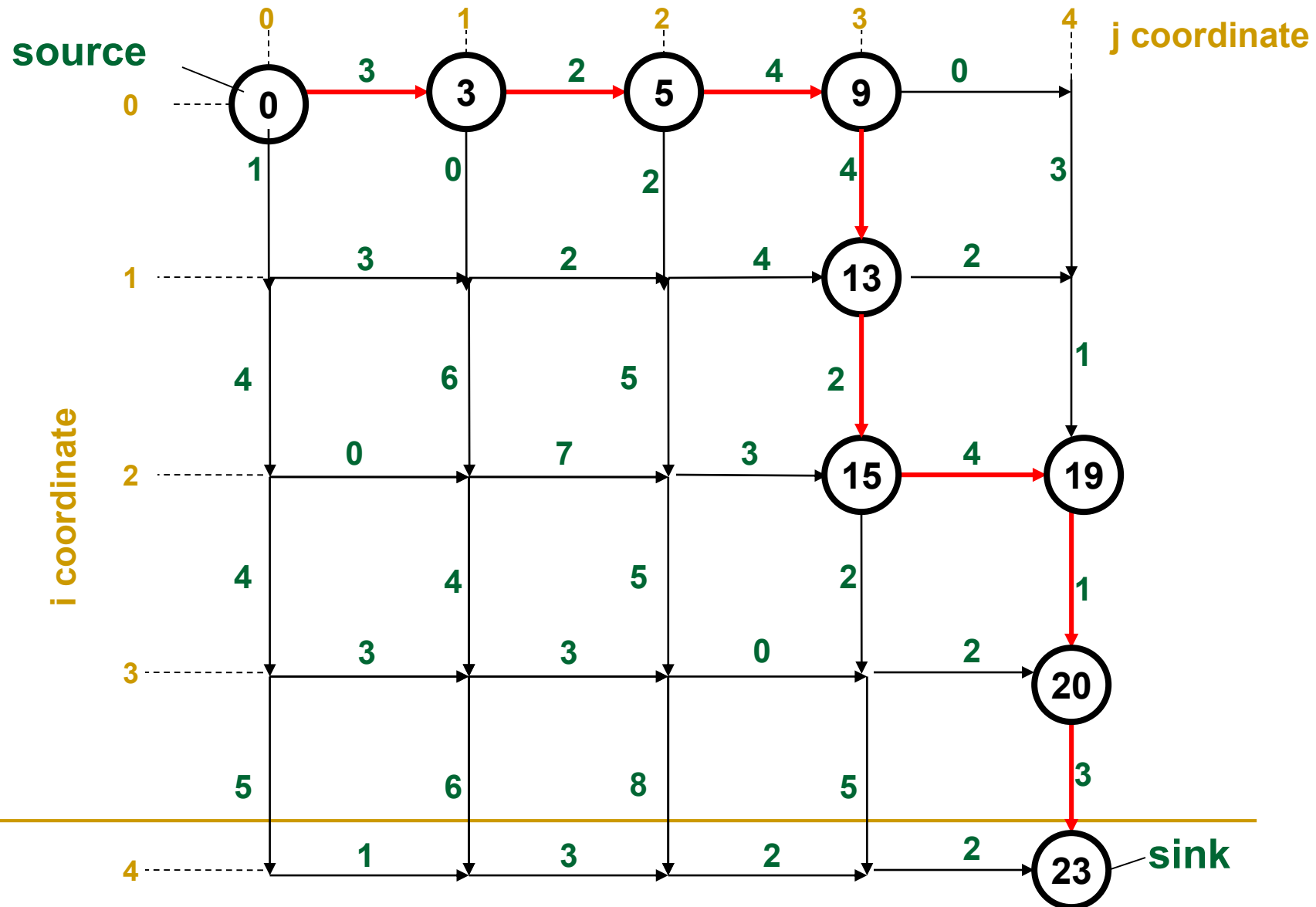
Input: A weighted grid  $G$  with two distinct vertices, one labeled “source” and the other labeled “sink”

Output: A longest path in  $G$  from “source” to “sink”

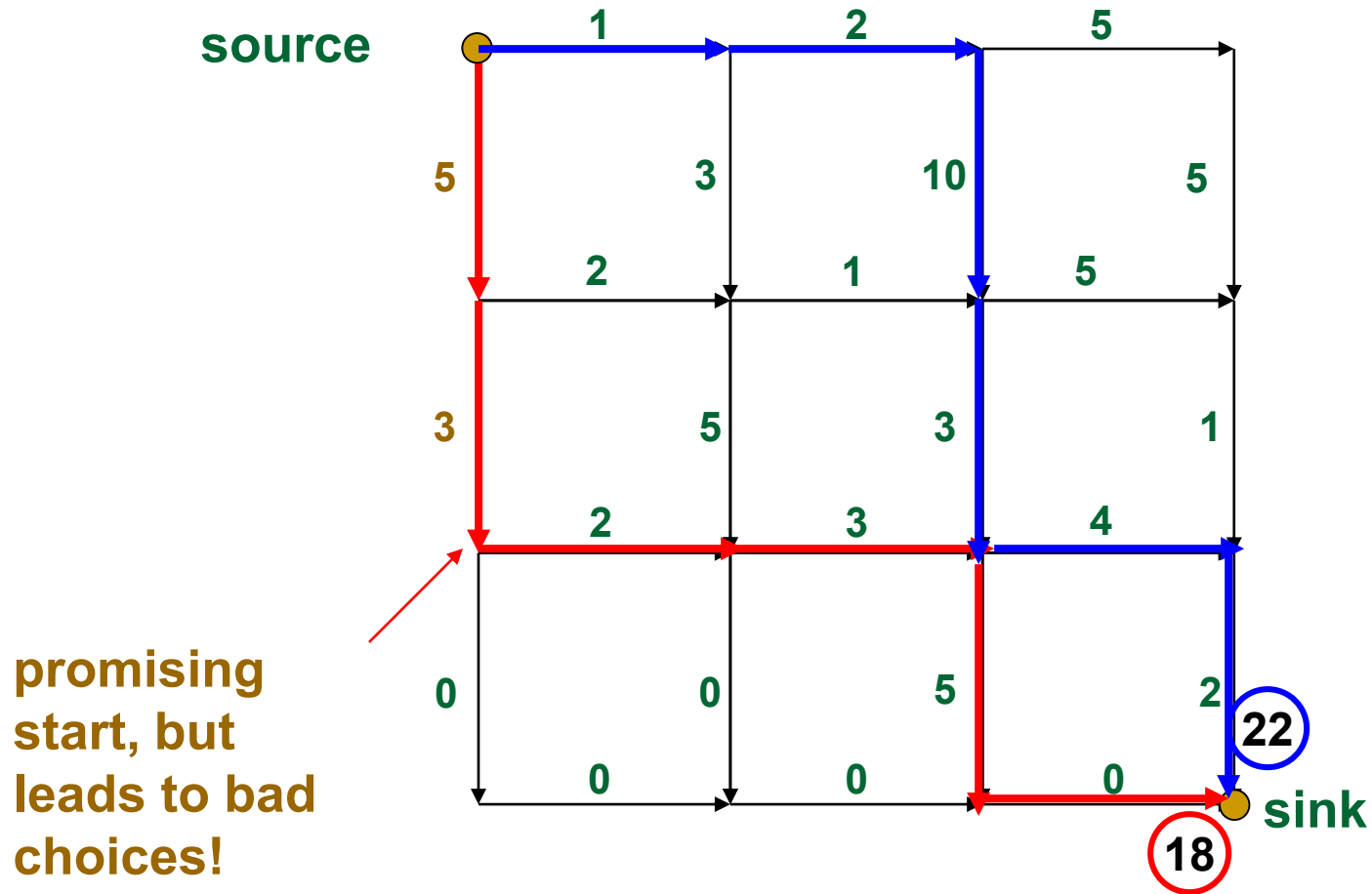
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# MTP: An Example



# MTP: Greedy Algorithm Is Not Optimal



# MTP: Simple Recursive Program

MT(n,m)

if  $n=0$  or  $m=0$

return MT(n,m)

$x \leftarrow \text{MT}(n-1, m) +$

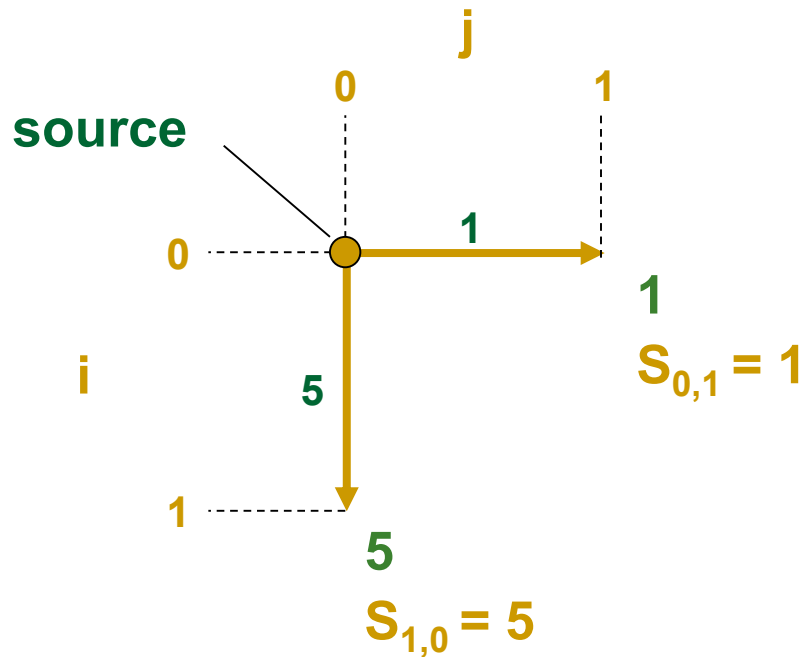
length of the edge from  $(n-1, m)$  to  $(n, m)$

$y \leftarrow \text{MT}(n, m-1) +$

length of the edge from  $(n, m-1)$  to  $(n, m)$

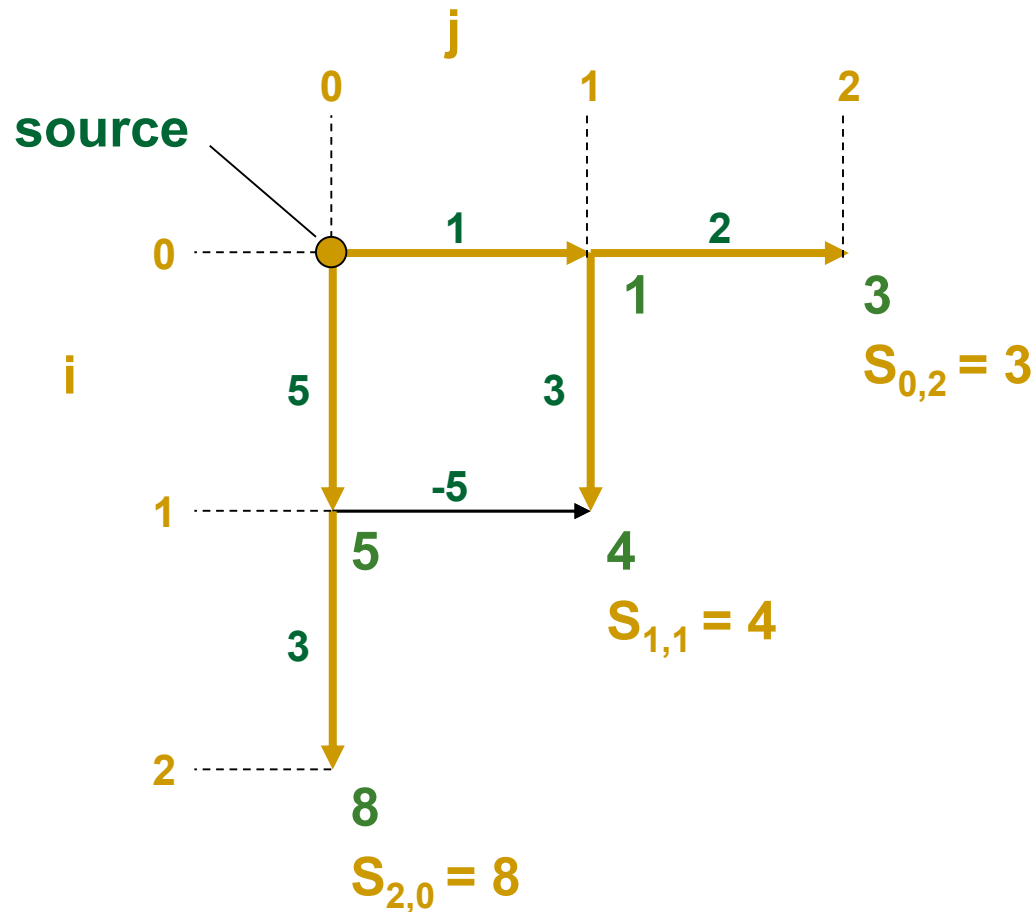
return  $\max\{x, y\}$

# MTP: Dynamic Programming

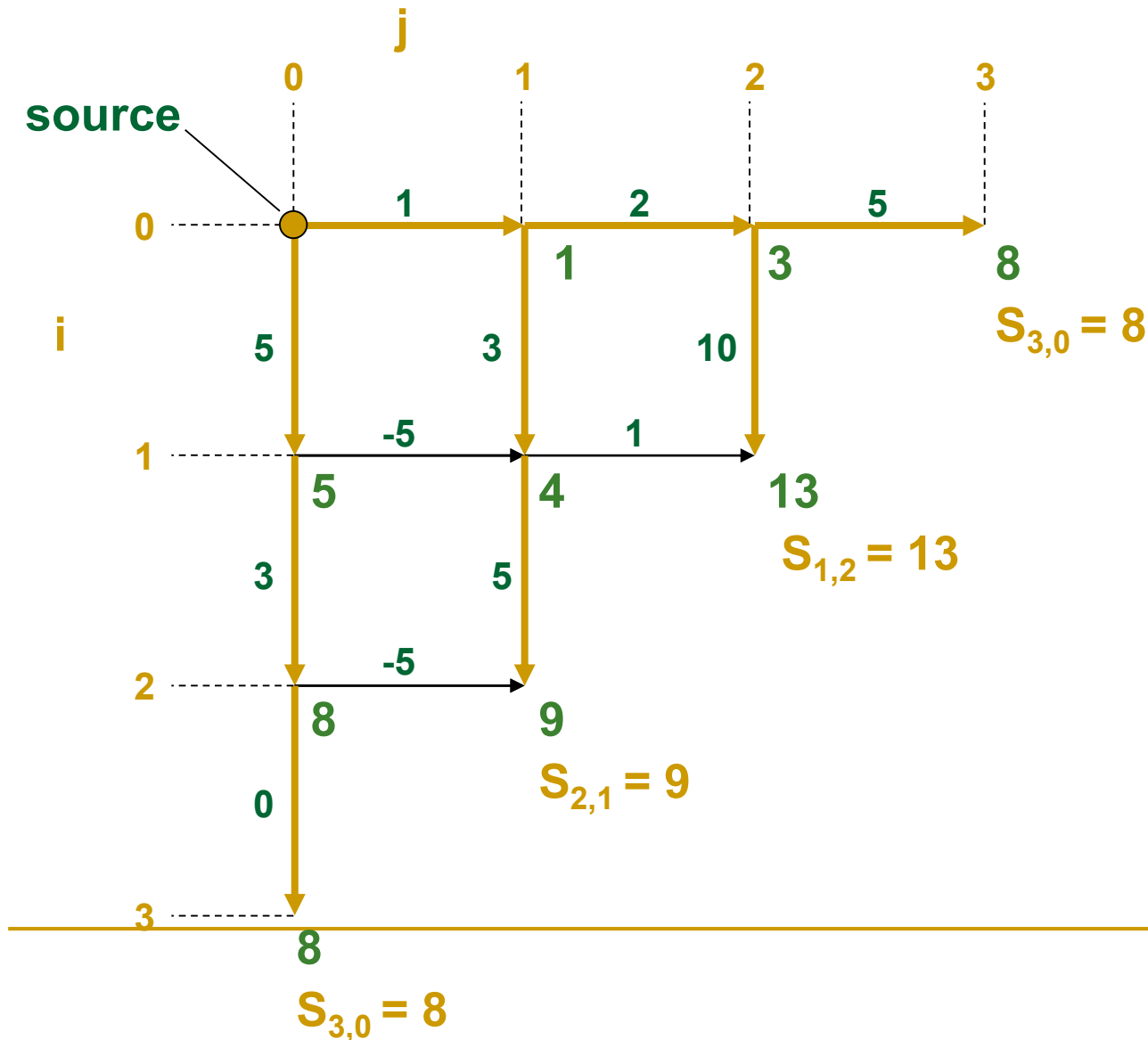


- Calculate optimal path score for each vertex in the graph
- Each vertex's score is the maximum of the prior vertices score plus the weight of the respective edge in between

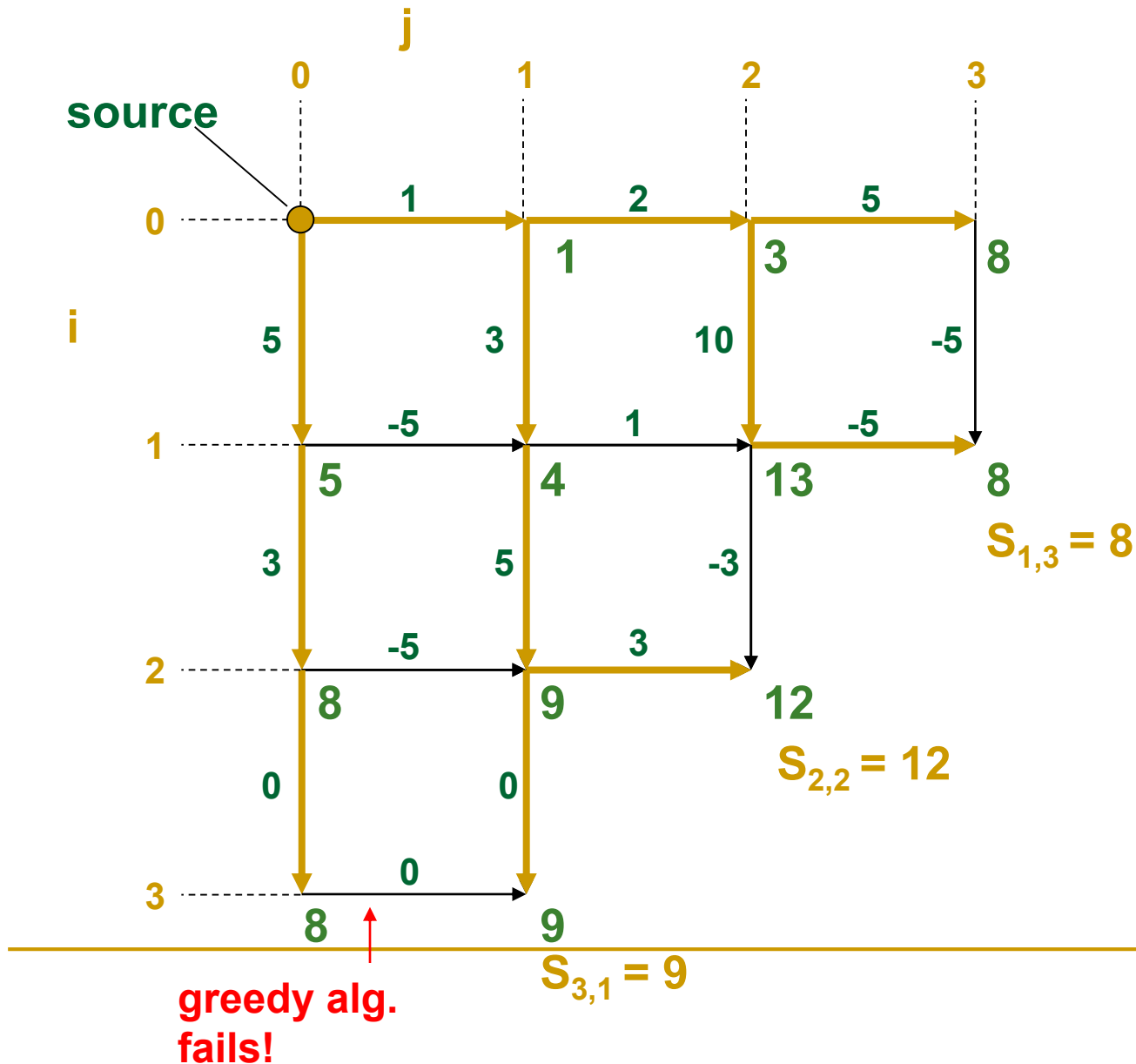
# MTP: Dynamic Programming (cont'd)



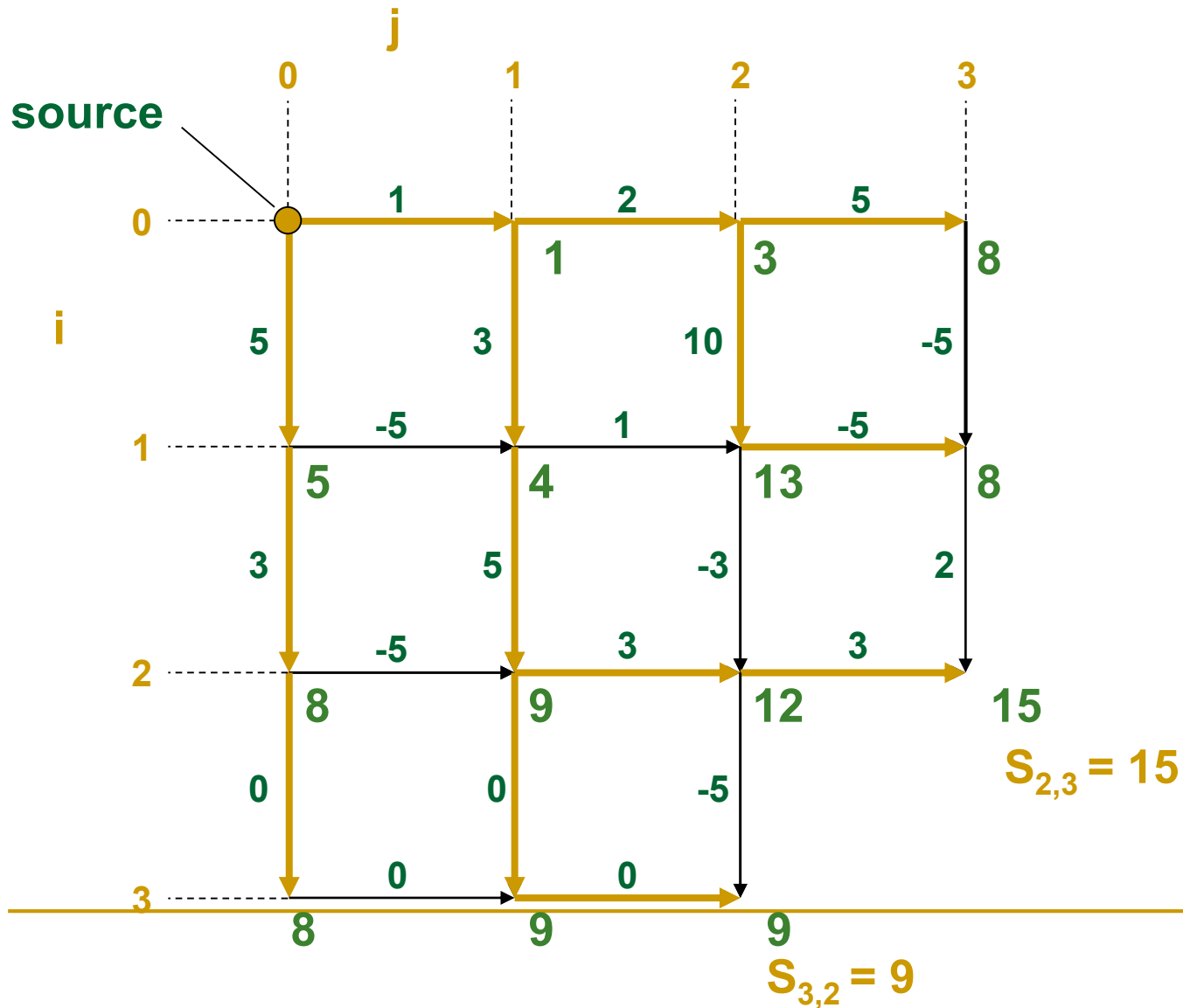
# MTP: Dynamic Programming (cont'd)



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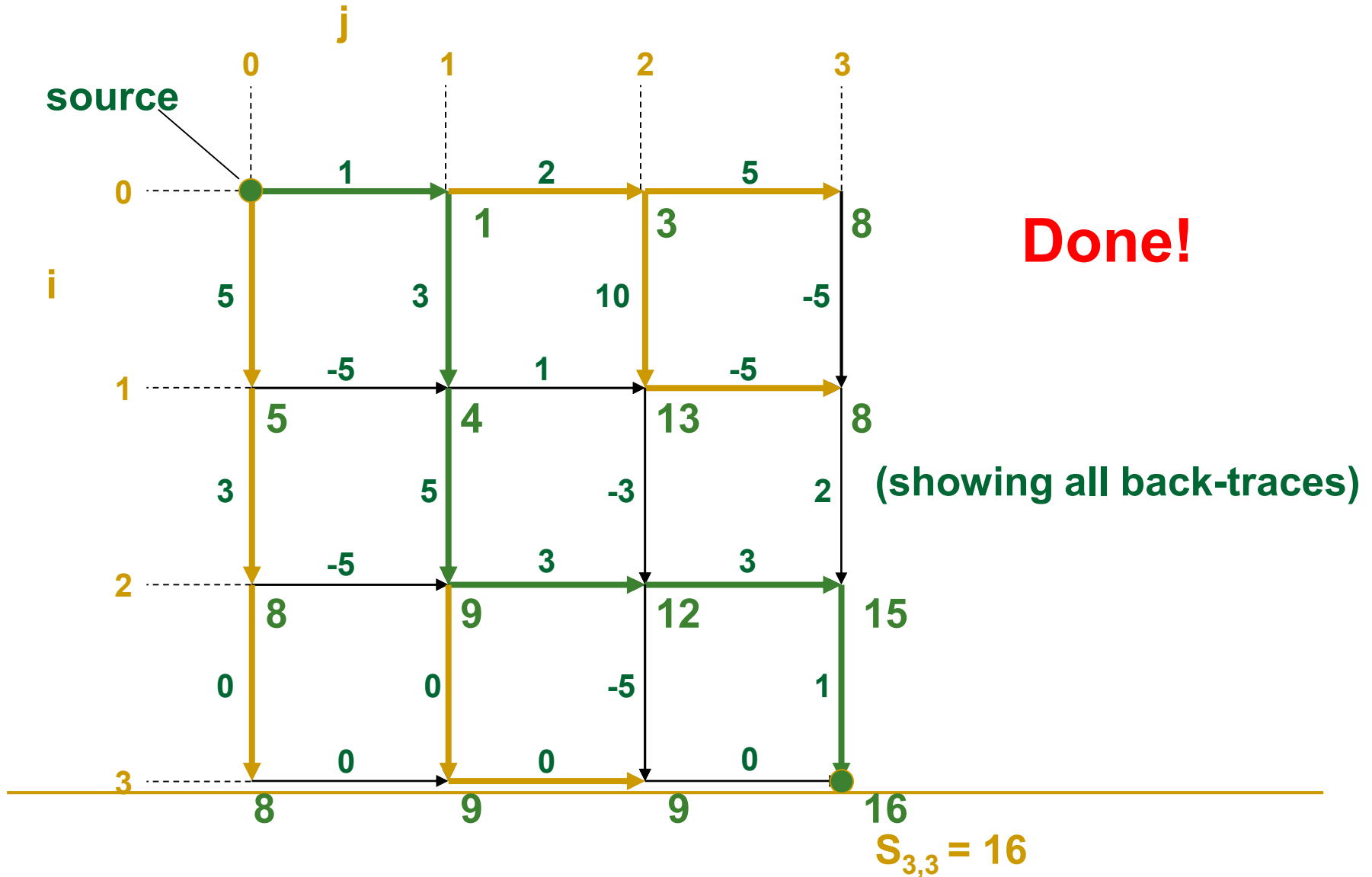


# MTP: Dynamic Programming (cont'd)





# MTP: Dynamic Programming (cont'd)



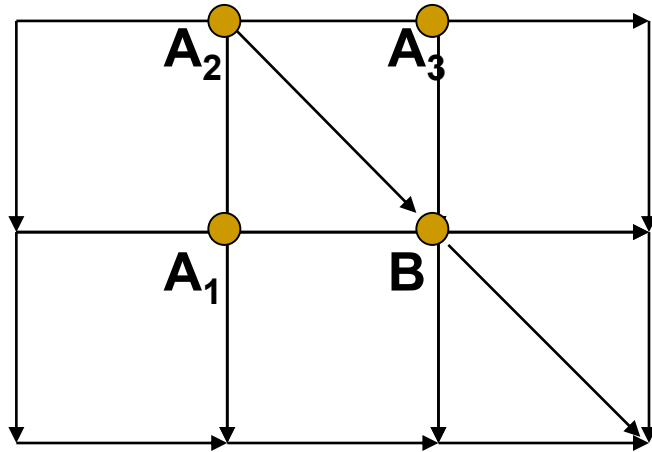
# MTP: Recurrence

Computing the score for a point (i,j) by the recurrence relation:

$$s_{i,j} = \max \begin{cases} s_{i-1,j} + \text{weight of the edge between } (i-1, j) \text{ and } (i, j) \\ s_{i,j-1} + \text{weight of the edge between } (i, j-1) \text{ and } (i, j) \end{cases}$$

The running time is  $n \times m$  for a  $n$  by  $m$  grid  
( $n$  = # of rows,  $m$  = # of columns)

# Manhattan Is Not A Perfect Grid



What about diagonals?

- The score at point B is given by:

$$s_B = \max_{\text{of}} \begin{cases} s_{A_1} + \text{weight of the edge } (A_1, B) \\ s_{A_2} + \text{weight of the edge } (A_2, B) \\ s_{A_3} + \text{weight of the edge } (A_3, B) \end{cases}$$

## Manhattan Is Not A Perfect Grid (cont'd)

Computing the score for point  $x$  is given by the recurrence relation:

$$s_x = \max_{\text{of}} \left\{ s_y + \text{weight of vertex } (y, x) \text{ where } y \in \text{Predecessors}(x) \right.$$

- Predecessors ( $x$ ) – set of vertices that have edges leading to  $x$
- The running time for a graph  $G(V, E)$  ( $V$  is the set of all vertices and  $E$  is the set of all edges) is  $O(E)$  since each edge is evaluated once

# Traveling in the Grid

- The only hitch is that one must decide on the order in which visit the vertices
- By the time the vertex  $x$  is analyzed, the values  $s_y$  for all its predecessors  $y$  should be computed – otherwise we are in trouble.
- We need to traverse the vertices in some order
- Since Manhattan is not a perfect regular grid, we represent it as a DAG

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# Longest Path in DAG Problem

- Goal: Find a longest path between two vertices in a weighted DAG
  - Input: A weighted DAG  $G$  with source and sink vertices
  - Output: A longest path in  $G$  from source to sink
-

# Longest Path in DAG: Dynamic Programming

- Suppose vertex  $v$  has indegree 3 and predecessors  $\{u_1, u_2, u_3\}$
- Longest path to  $v$  from source is:

$$s_v = \max_{\text{of}} \begin{cases} s_{u_1} + \text{weight of edge from } u_1 \text{ to } v \\ s_{u_2} + \text{weight of edge from } u_2 \text{ to } v \\ s_{u_3} + \text{weight of edge from } u_3 \text{ to } v \end{cases}$$

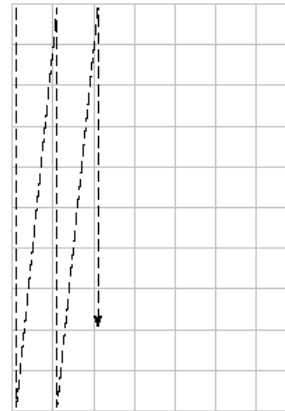
In General:

$$s_v = \max_u (s_u + \text{weight of edge from } u \text{ to } v)$$

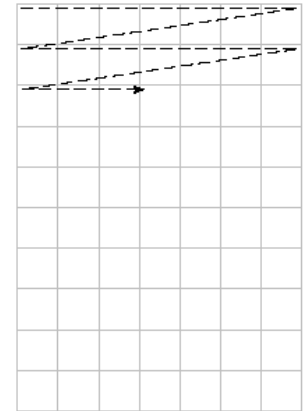
# Traversing the Manhattan Grid

- **3 different strategies:**
  - **a) Column by column**
  - **b) Row by row**
  - **c) Along diagonals**

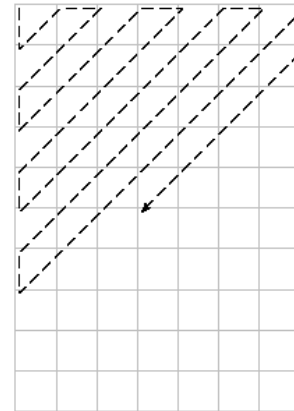
a)



b)



c)





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# ALIGNMENT

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# Alignment: 2 row representation

Given 2 DNA sequences v and w:

v : A T C T G A T      m = 7  
w : T G C A T A      n = 6

Alignment : 2 \* k matrix ( k > m, n )

letters of v	A	T	--	G	T	T	A	T	--
letters of w	A	T	C	G	T	--	A	--	C

5 matches

2 insertions

2 deletions

# Aligning DNA Sequences

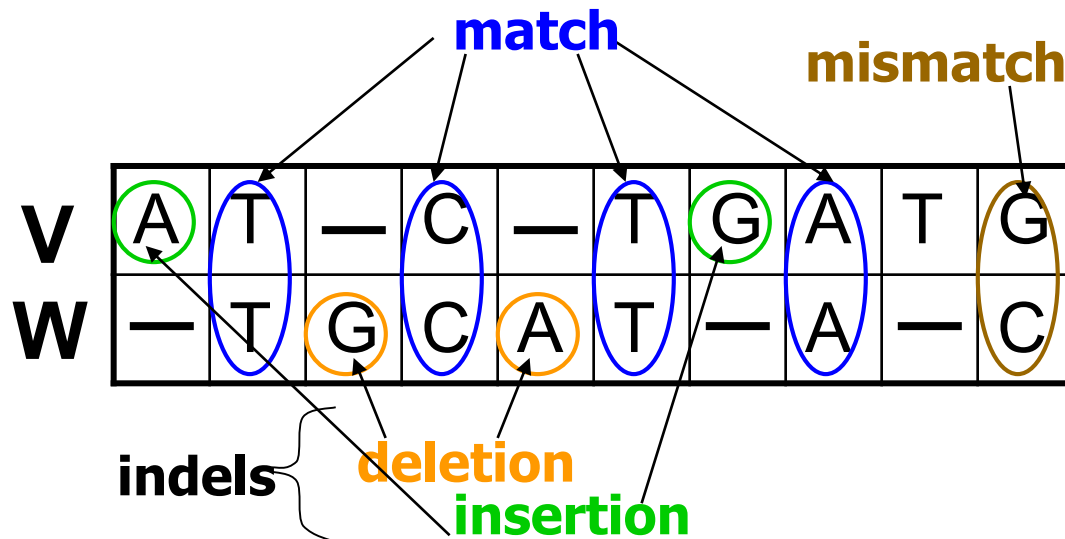
**V = ATCTGATG**

**n = 8**

**W = TGCATAC**

**m = 7**

**4 matches**  
**1 mismatch**  
**2 insertions**  
**3 deletions**



# Longest Common Subsequence (LCS) – Alignment without Mismatches

- Given two sequences

$$v = v_1 v_2 \dots v_m \text{ and } w = w_1 w_2 \dots w_n$$

- The LCS of  $v$  and  $w$  is a sequence of positions in

$$v: 1 \leq i_1 < i_2 < \dots < i_t \leq m$$

and a sequence of positions in

$$w: 1 \leq j_1 < j_2 < \dots < j_t \leq n$$

such that  $i_t$ -th letter of  $v$  equals to  $j_t$ -letter of  $w$  and  $t$  is maximal

# LCS: Example

i coords:	0	1	2	2	3	3	4	5	6	7	8
elements of v	A	T	--	C	--	T	G	A	T	C	
elements of w	--	T	G	C	A	T	--	A	--	C	
j coords:	0	0	1	2	3	4	5	5	6	6	7

$(0,0) \rightarrow (1,0) \rightarrow (2,1) \rightarrow (2,2) \rightarrow (3,3) \rightarrow (3,4) \rightarrow (4,5) \rightarrow (5,5) \rightarrow (6,6) \rightarrow (7,6) \rightarrow (8,7)$

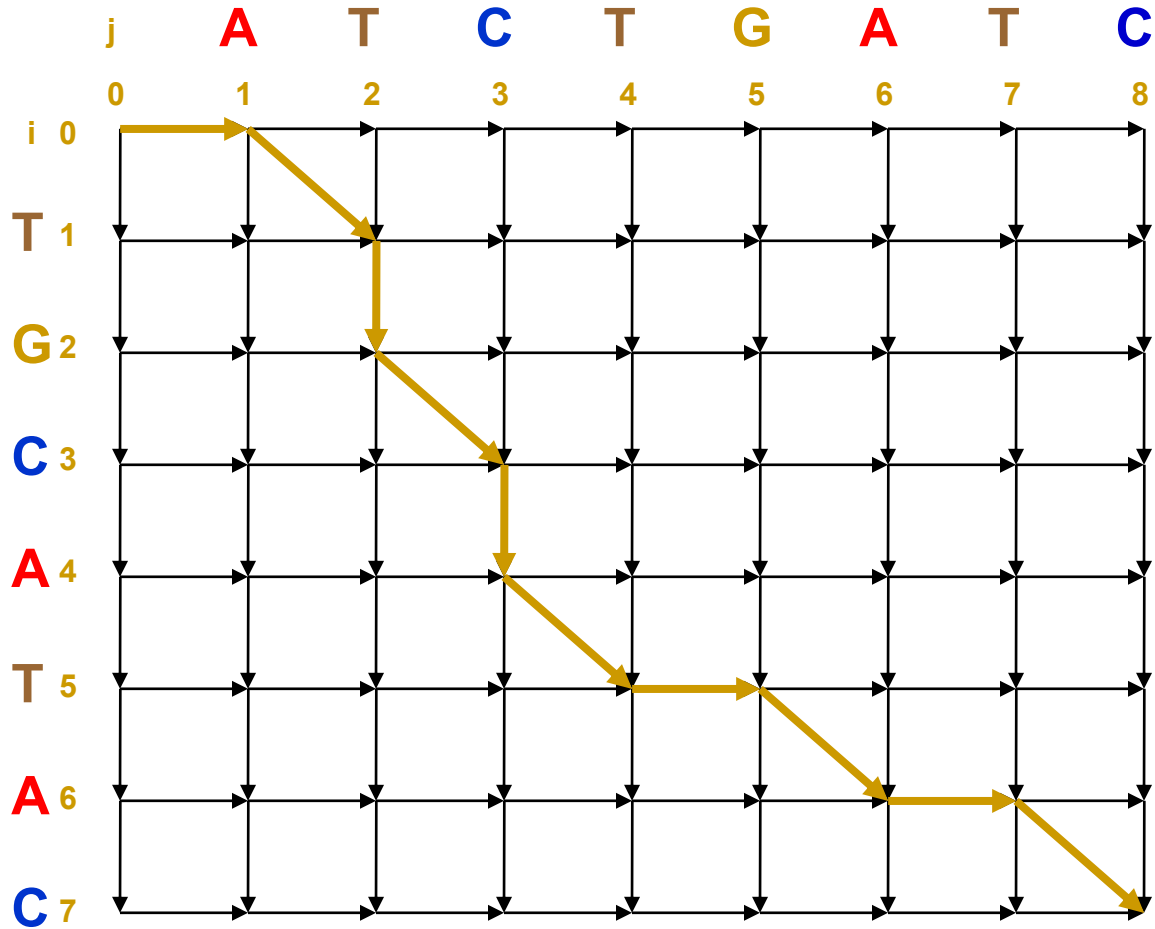
Matches shown in  
red

positions in v:  $2 < 3 < 4 < 6 < 8$

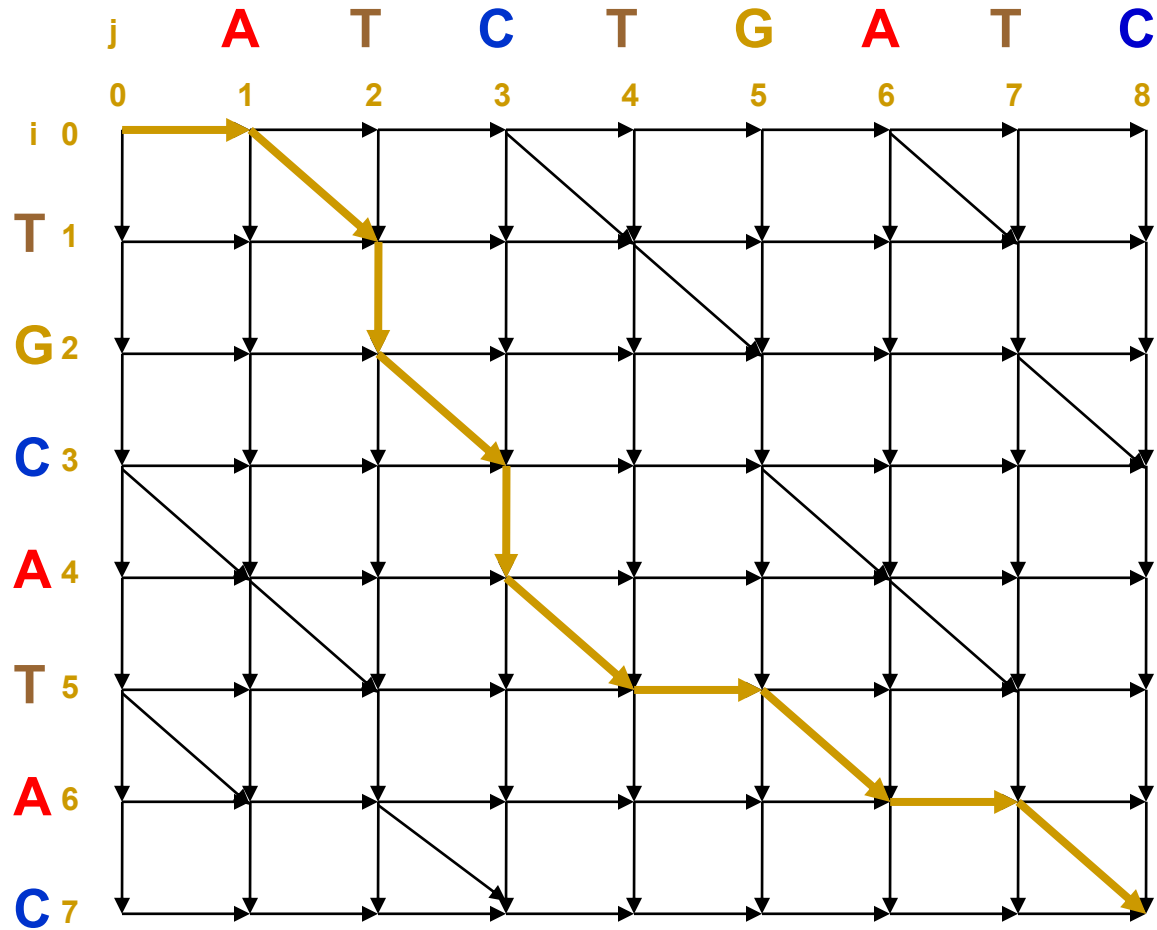
positions in w:  $1 < 3 < 5 < 6 < 7$

**Every common subsequence is a path in 2-D grid**

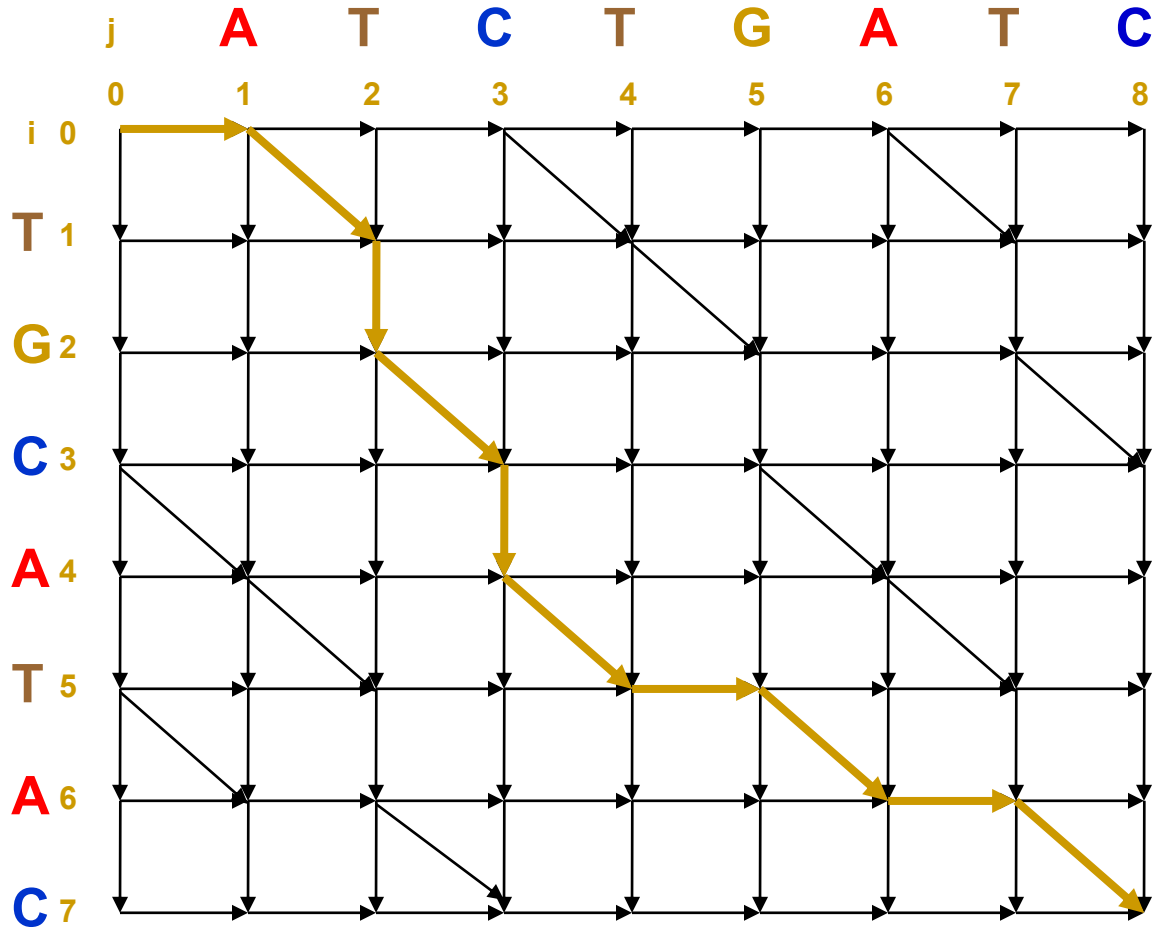
## LCS Problem as Manhattan Tourist Problem



# Edit Graph for LCS Problem



# Edit Graph for LCS Problem



Every path is a common subsequence.

Every diagonal edge adds an extra element to common subsequence

**LCS Problem:**  
Find a path with maximum number of diagonal edges



# Computing LCS

Let  $v_i$  = prefix of  $v$  of length  $i$ :  $v_1 \dots v_i$

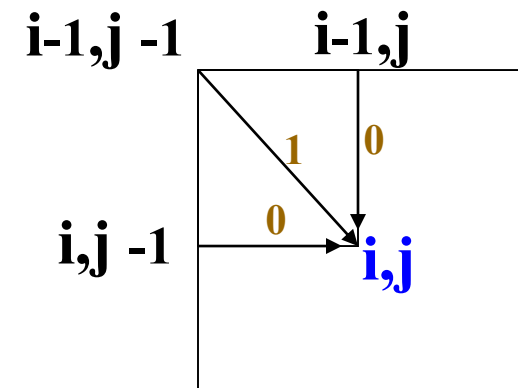
and  $w_j$  = prefix of  $w$  of length  $j$ :  $w_1 \dots w_j$

The length of  $\text{LCS}(v_i, w_j)$  is computed by:

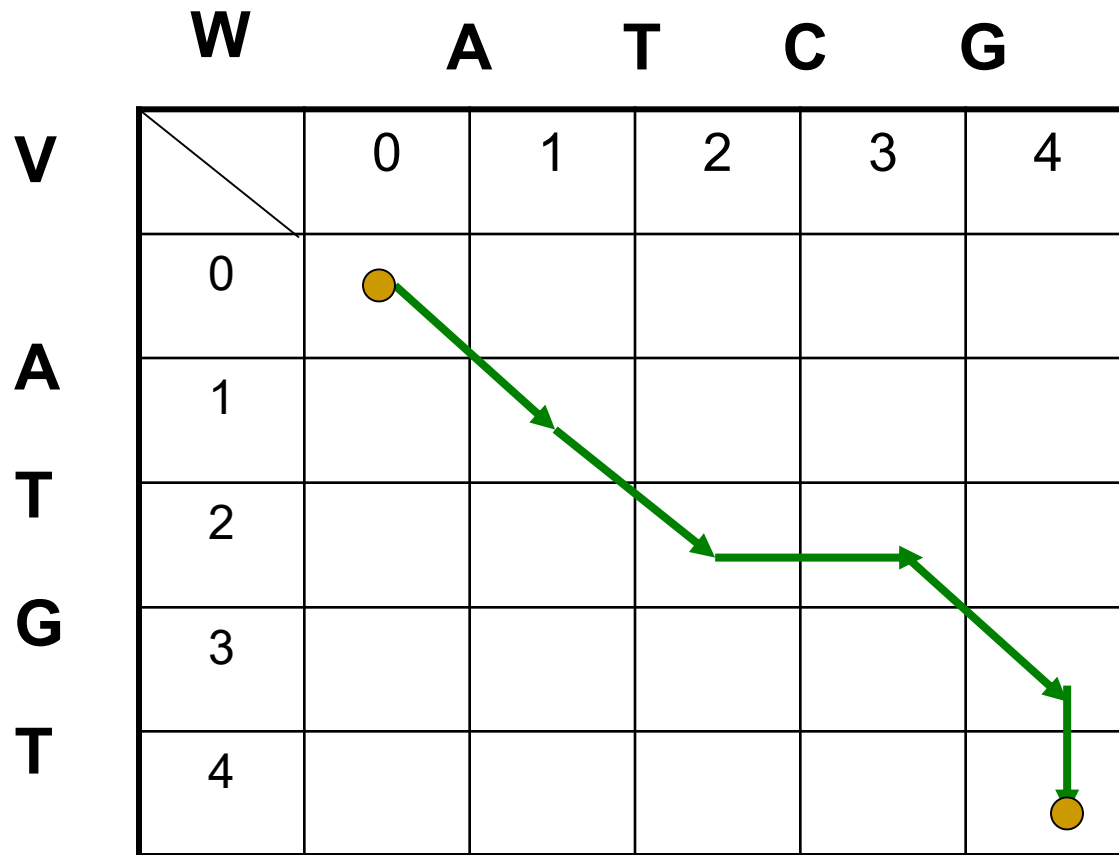
$$s_{i,j} = \max \begin{cases} s_{i-1,j} \\ s_{i,j-1} \\ s_{i-1,j-1} + 1 \text{ if } v_i = w_j \end{cases}$$

# Computing LCS (cont'd)

$$s_{i,j} = \text{MAX} \begin{cases} s_{i-1,j} + 0 \\ s_{i,j-1} + 0 \\ s_{i-1,j-1} + 1, \end{cases} \quad \text{if } v_i = w_j$$



# Every Path in the Grid Corresponds to an Alignment



↘ ↘ → ↘ ↓  
0 1 2 2 3 4  
V = A T - G T  
| | |  
W = A T C G -  
0 1 2 3 4 4

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# **DISTANCE BETWEEN STRINGS**

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# Aligning Sequences without Insertions and Deletions: Hamming Distance

**Given two DNA sequences  $v$  and  $w$  :**

**$v$  : A T A T A T A T**

**$w$  : T A T A T A T A**

- **The Hamming distance:  $d_H(v, w) = 8$  is large but the sequences are very similar**

# Aligning Sequences with Insertions and Deletions

**By shifting one sequence over one position:**

**v : A T A T A T --**  
**w : -- T A T A T A**

- **The edit distance:  $d_H(v, w) = 2$ .**
- **Hamming distance neglects insertions and deletions in DNA**

# Edit Distance

Levenshtein (1966) introduced **edit distance** between two strings as the minimum number of elementary operations (insertions, deletions, and substitutions) to transform one string into the other

$d(v,w)$  = MIN number of elementary operations  
to transform  $v \rightarrow w$

# Edit Distance vs Hamming Distance

**Hamming distance**

**always compares**

**$i$ -th letter of  $v$  with**

**$i$ -th letter of  $w$**

$V = \text{ATATATAT}$   
          | | | | | | | |  
 $W = \text{TATATATA}$

**Hamming distance:**

**$d(v, w) = 8$**

**Computing Hamming distance  
is a trivial task.**



# Edit Distance vs Hamming Distance

**Hamming distance**

**always compares**

**$i$ -th letter of  $v$  with**

**$i$ -th letter of  $w$**

$V = \text{ATATATAT}$

$W = \text{TATATATA}$

**Just one shift**  
**Make it all line up**

**Hamming distance:**

$$d(v, w) = 8$$

Computing Hamming distance  
is a **trivial** task

**Edit distance**

**may compare**

**$i$ -th letter of  $v$  with**

**$j$ -th letter of  $w$**

$V = - \text{ATATATAT}$

$W = \text{TATATATA}$

**Edit distance:**

$$d(v, w) = 2$$

Computing edit distance  
is a **non-trivial** task

# Edit Distance vs Hamming Distance

**Hamming distance  
always compares**

**i<sup>th</sup> letter of v with  
i<sup>th</sup> letter of w**

V = **ATATATAT**  
      | | | | |  
W = **TATATATA**

**Hamming distance:**

$$d(v, w) = 8$$

**Edit distance  
may compare**

**i<sup>th</sup> letter of v with  
j<sup>th</sup> letter of w**

V = - **ATATATAT**  
          | | | | |  
W = **TATATATA**

**Edit distance:**

$$d(v, w) = 2$$

(one insertion and one deletion)

**How to find what j goes with what i ???**

# Edit Distance: Example

TGCATAT → ATCCGAT in 5 steps

TGCATAT<sup>T</sup> → (delete last <sup>T</sup>)

TGCAT<sup>A</sup> → (delete last <sup>A</sup>)

TGCAT → (insert <sup>A</sup> at front)

<sup>A</sup>T<sup>C</sup>CAT → (substitute <sup>C</sup> for 3<sup>rd</sup> <sup>G</sup>)

AT<sup>C</sup>CAT → (insert <sup>G</sup> before last A)

ATCC<sup>G</sup>AT (Done)

# Edit Distance: Example

TGCATAT → ATCCGAT in 5 steps

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TGCAT → (insert <sup>A</sup> at front)

<sup>A</sup>T<sup>C</sup>CAT → (substitute <sup>C</sup> for 3<sup>rd</sup> <sup>G</sup>)

AT<sup>C</sup>CAT → (insert <sup>G</sup> before last A)

ATCC<sup>G</sup>AT (Done)

**What is the edit distance? 5?**

# Edit Distance: Example (cont'd)

TGCATAT → ATCCGAT in 4 steps

TGCATAT → (insert **A** at front)

**A**TGCATAT → (delete 6<sup>th</sup> **T**)

ATGC**A**TA → (substitute **G** for 5<sup>th</sup> **A**)

AT**G**CGTA → (substitute **C** for 3<sup>rd</sup> **G**)

AT**C**CGAT (Done)

# Edit Distance: Example (cont'd)

TGCATAT → ATCCGAT in 4 steps

TGCATAT → (insert **A** at front)

**A**TGCATAT**T** → (delete 6<sup>th</sup> **T**)

ATGC**A**TA → (substitute **G** for 5<sup>th</sup> **A**)

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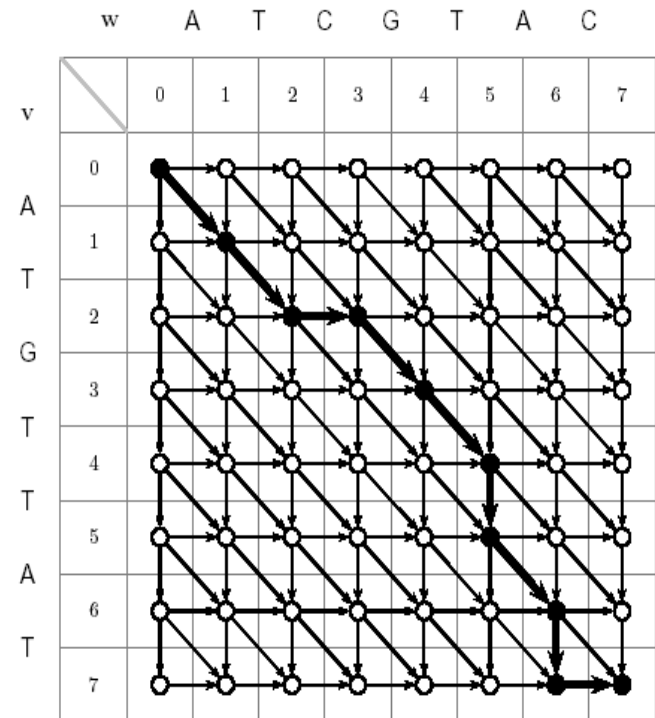
AT**C**CGAT (Done)

Can it be done in 3 steps???

# The Alignment Grid

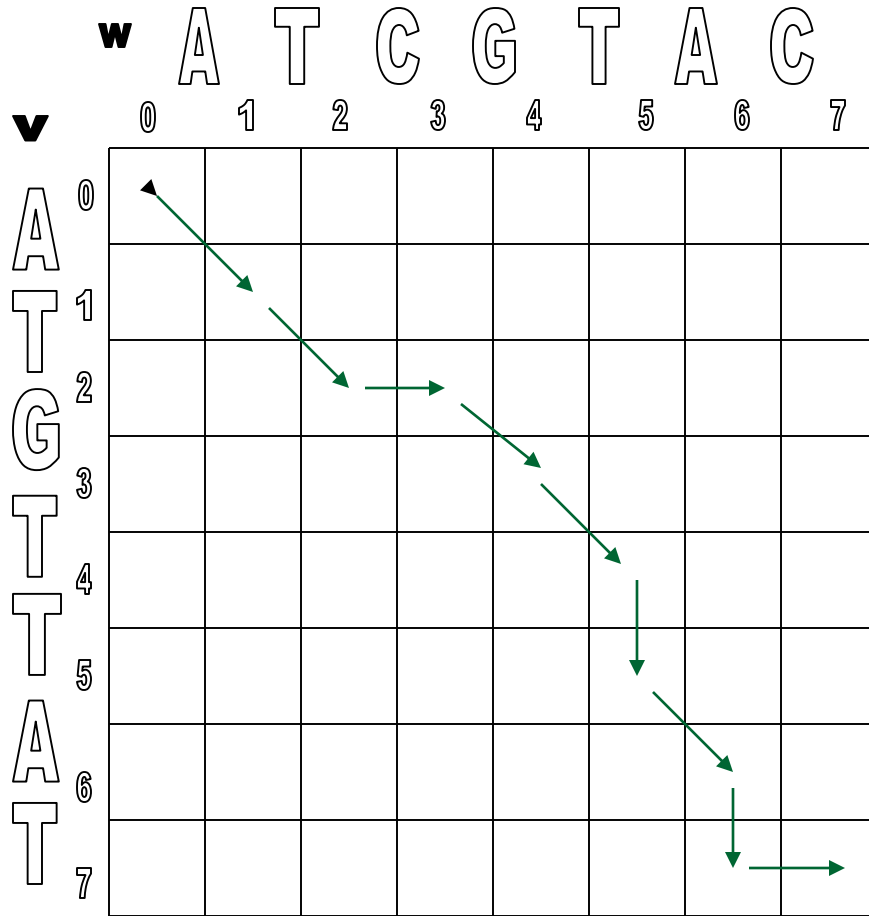
- Every alignment path is from source to sink

	0	1	2	2	3	4	5	6	7	7
v =		A	T	-	G	T	T	A	T	-
w =		A	T	C	G	T	-	A	-	C
	0	1	2	3	4	5	5	6	6	7



$\swarrow$	$\swarrow$	$\rightarrow$	$\swarrow$	$\swarrow$	$\downarrow$	$\swarrow$	$\downarrow$	$\rightarrow$
A	T	-	G	T	T	A	T	-
A	T	C	G	T	-	A	-	C

# Alignment as a Path in the Edit Graph



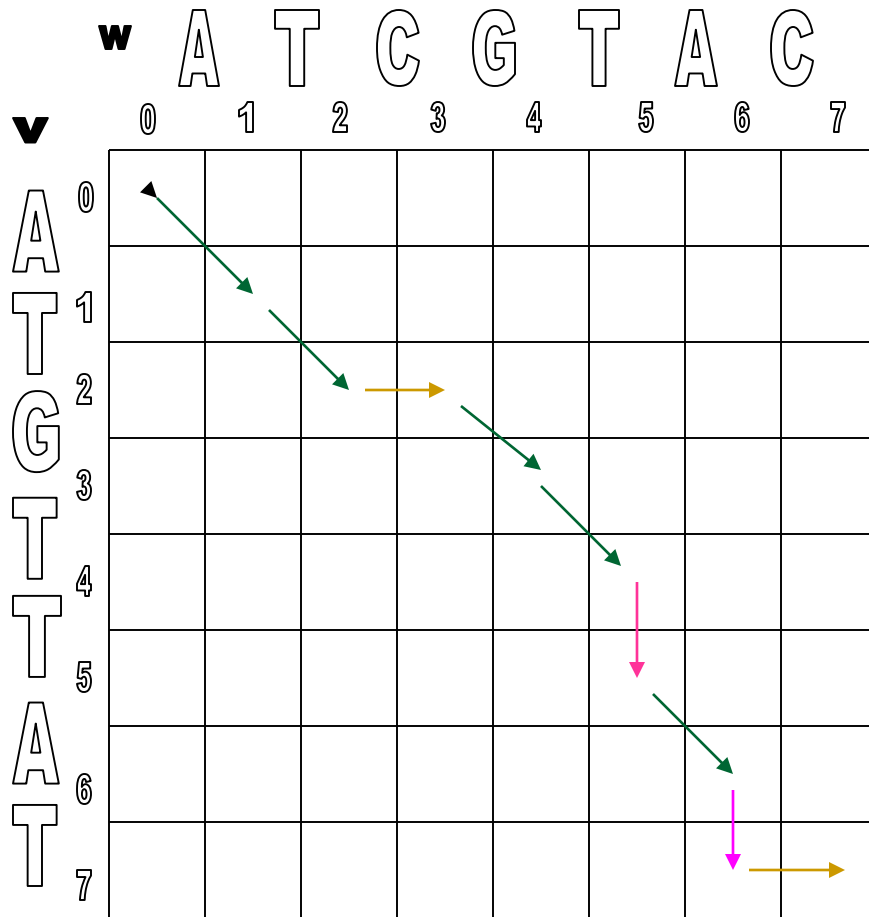
0	1	2	2	3	4	5	6	7	7
	A	T	_	G	T	T	A	T	_
	A	T	C	G	T	_	A	_	C
0	1	2	3	4	5	5	6	6	7

**- Corresponding path -**

(0,0) , (1,1) , (2,2), (2,3),  
(3,4), (4,5), (5,5), (6,6),  
(7,6), (7,7)



# Alignments in Edit Graph (cont'd)

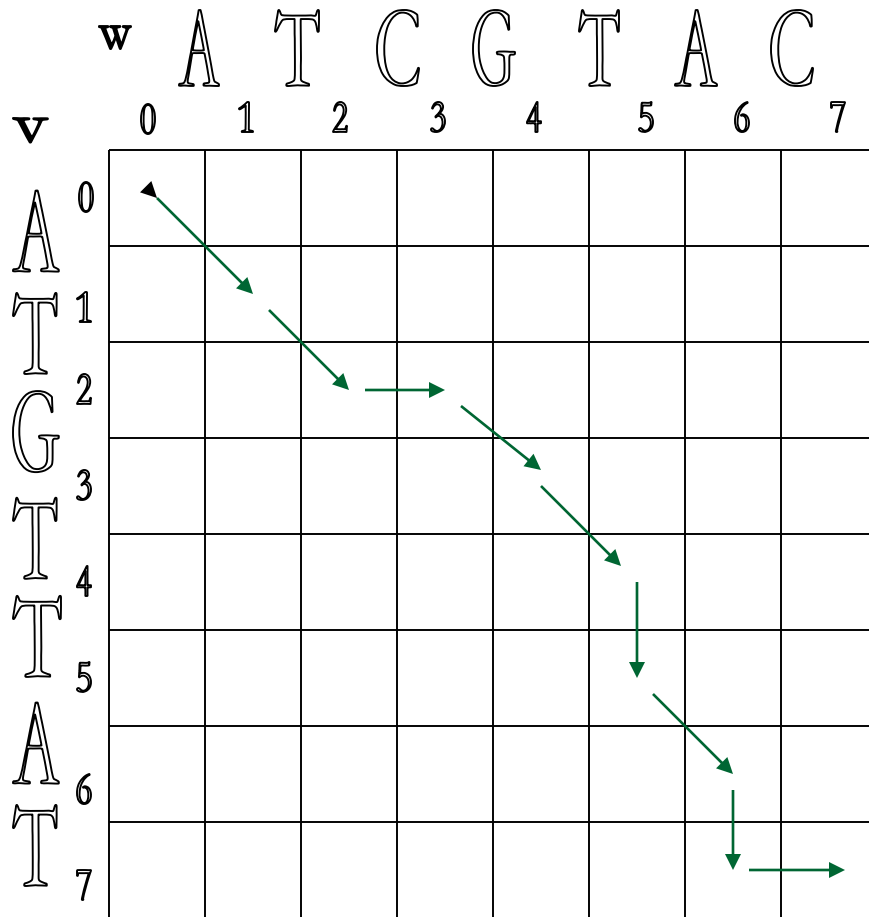


↓ and → represent indels in **v** and **w** with score 0.

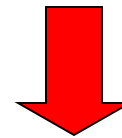
↘ represent matches with score 1.

- The score of the alignment path is 5.

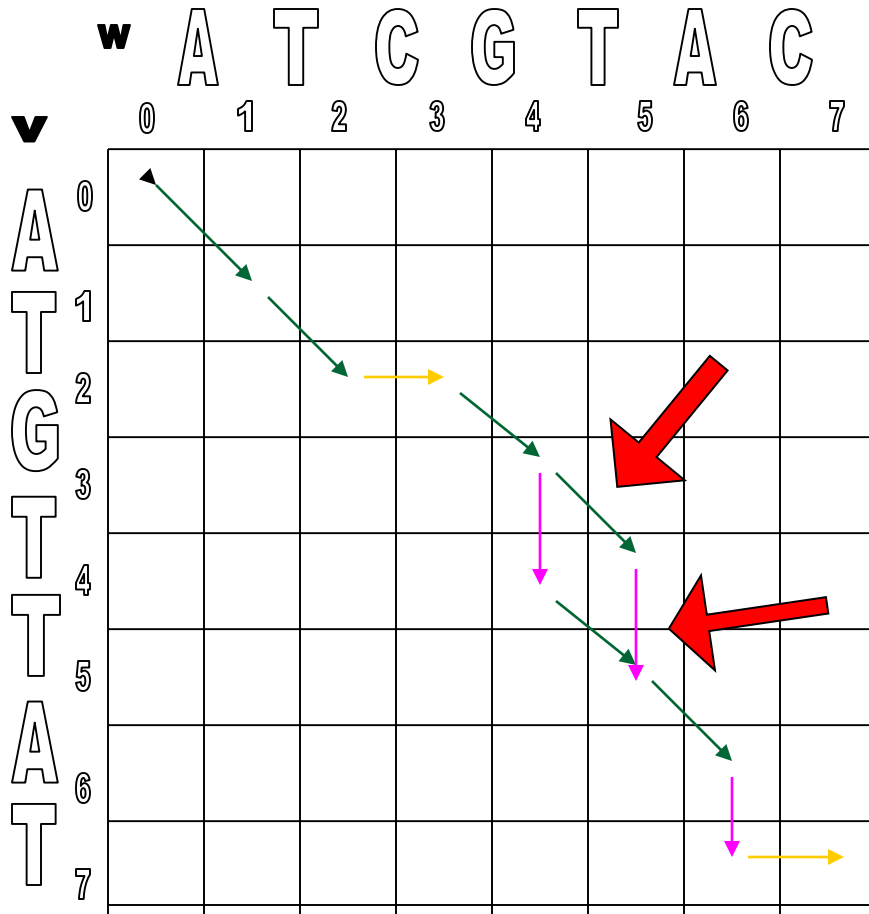
# Alignment as a Path in the Edit Graph



Every path in the edit graph corresponds to an alignment:



# Alignment as a Path in the Edit Graph



## Old Alignment

0122345677

v= AT\_GTTAT\_

w= ATCGT\_A\_C

0123455667

## New Alignment

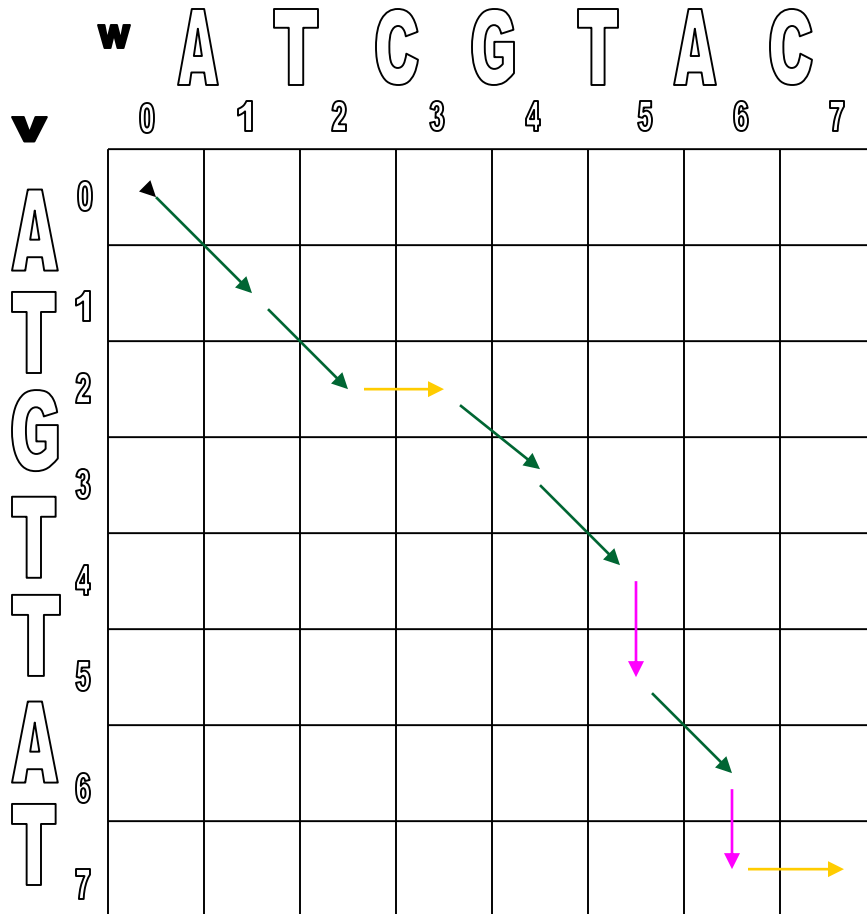
0122345677

v= AT\_GTTAT\_

w= ATCG\_TA\_C

0123445667

# Alignment as a Path in the Edit Graph



012**2**34**5**6**7**7

V= AT\_G**T**TAT\_

W= AT**C**GT\_**A**\_C

012**3**45**5**6**6**7

(0,0) , (1,1) , (2,2), **(2,3)**,  
(3,4), (4,5), **(5,5)**, (6,6),  
**(7,6)**, **(7,7)**

# Alignment: Dynamic Programming

$$s_{i,j} = \max \begin{cases} s_{i-1,j-1} + 1 & \text{if } v_i = w_j \quad \swarrow \\ s_{i-1,j} & \downarrow \\ s_{i,j-1} & \rightarrow \end{cases}$$

# Dynamic Programming Example

		w							
		A	T	C	G	T	A	C	
v	0	0	0	0	0	0	0	0	0
	A	0							
	T	0							
	G	0							
	T	0							
	T	0							
	A	0							
	T	0							

**Initialize 1<sup>st</sup> row and 1<sup>st</sup> column to be all zeroes.**

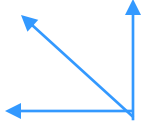
**Or, to be more precise, initialize 0<sup>th</sup> row and 0<sup>th</sup> column to be all zeroes.**

# Dynamic Programming Example

		w							
		A	T	C	G	T	A	C	
v		0	1	2	3	4	5	6	7
A	0	0	0	0	0	0	0	0	0
T	1	0	1	1	1	1	1	1	1
G	2	0	1						
T	3	0	1						
T	4	0	1						
T	5	0	1						
A	6	0	1						
T	7	0	1						

$$S_{i,j} = \max \begin{cases} S_{i-1,j-1} & \leftarrow \text{value from NW} + 1, \text{ if } v_i = w_j \\ S_{i-1,j} & \leftarrow \text{value from North (top)} \\ S_{i,j-1} & \leftarrow \text{value from West (left)} \end{cases}$$

# Alignment: Backtracking

Arrows  show where the score originated from.



if from the top



if from the left



if  $v_i = w_j$



# Backtracking Example

		<b>w</b>							
		A T C G T A C							
		0	1	2	3	4	5	6	7
<b>v</b>	A	0	0	0	0	0	0	0	0
	T	0	1	1	1	1	1	1	1
	G	0	1	2	2	2	2	2	2
	T	0	1	2					
	T	0	1	2					
	T	0	1	2					
	A	0	1	2					
	T	0	1	2					

Find a match in row and column 2.

$i=2, j=2,5$  is a match (T).

$j=2, i=4,5,7$  is a match (T).

Since  $v_i = w_j$ ,  $s_{i,j} = s_{i-1,j-1} + 1$

$$s_{2,2} = [s_{1,1} = 1] + 1$$

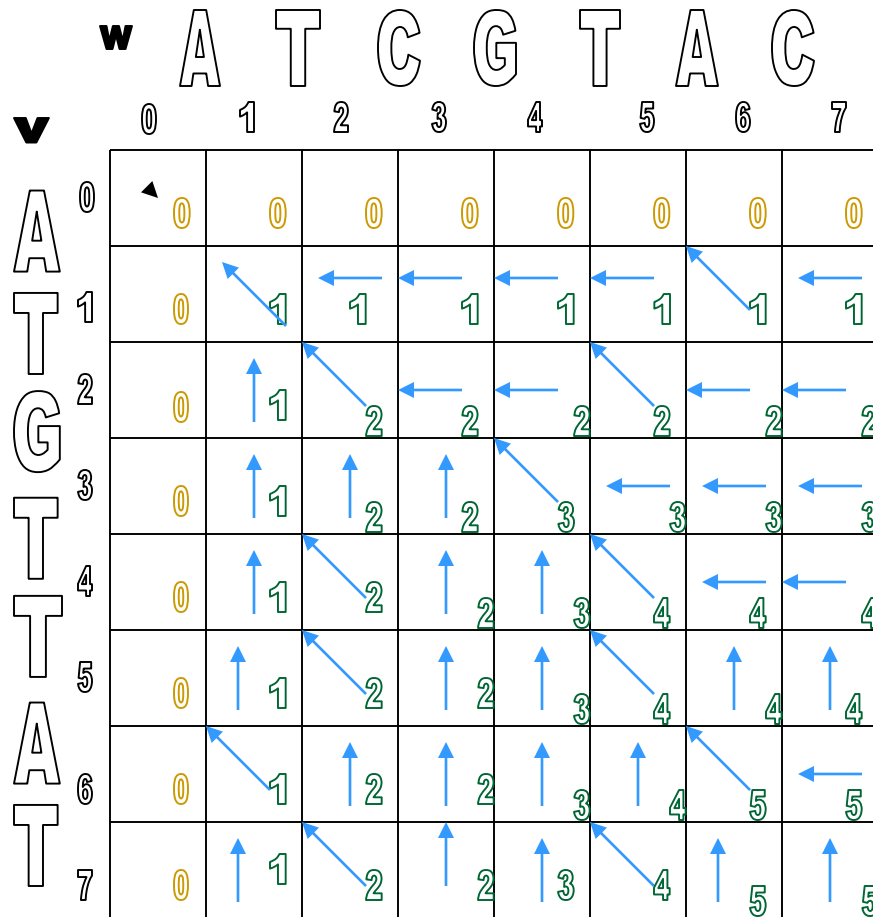
$$s_{2,5} = [s_{1,4} = 1] + 1$$

$$s_{4,2} = [s_{3,1} = 1] + 1$$

$$s_{5,2} = [s_{4,1} = 1] + 1$$

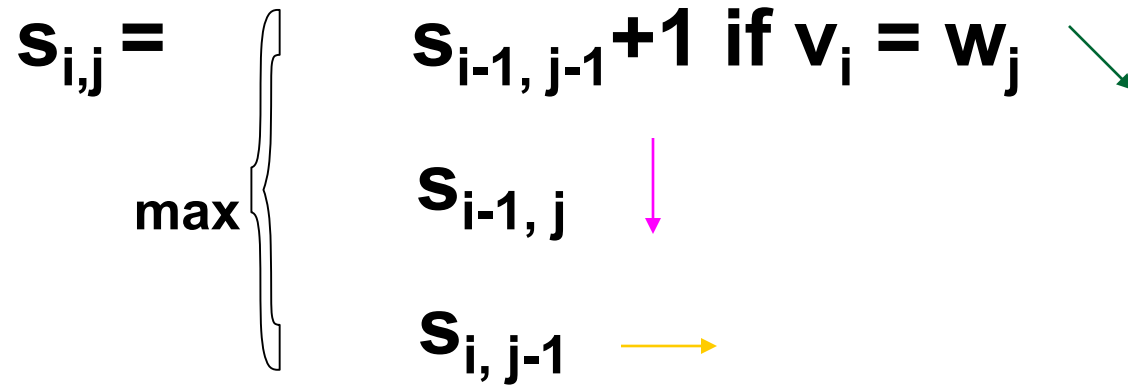
$$s_{7,2} = [s_{6,1} = 1] + 1$$

# Backtracking Example



**Continuing with the dynamic programming algorithm gives this result.**

# Alignment: Dynamic Programming

$$s_{i,j} = \max \begin{cases} s_{i-1,j-1} + 1 & \text{if } v_i = w_j \\ s_{i-1,j} \\ s_{i,j-1} \end{cases}$$


# Alignment: Dynamic Programming

$$s_{i,j} = \max \begin{cases} s_{i-1,j-1} + 1 & \text{if } v_i = w_j \quad \searrow \\ s_{i-1,j} + 0 & \quad \downarrow \\ s_{i,j-1} + 0 & \quad \rightarrow \end{cases}$$

This recurrence corresponds to the Manhattan Tourist problem (three incoming edges into a vertex) with all horizontal and vertical edges weighted by zero.

# LCS Algorithm

## 1. Levenshtein(v,w)

2.     for  $i \leftarrow 1$  to  $n$

3.          $s_{i,0} \leftarrow 0$

4.     for  $j \leftarrow 1$  to  $m$

5.          $s_{0,j} \leftarrow 0$

6.     for  $i \leftarrow 1$  to  $n$

7.         for  $j \leftarrow 1$  to  $m$

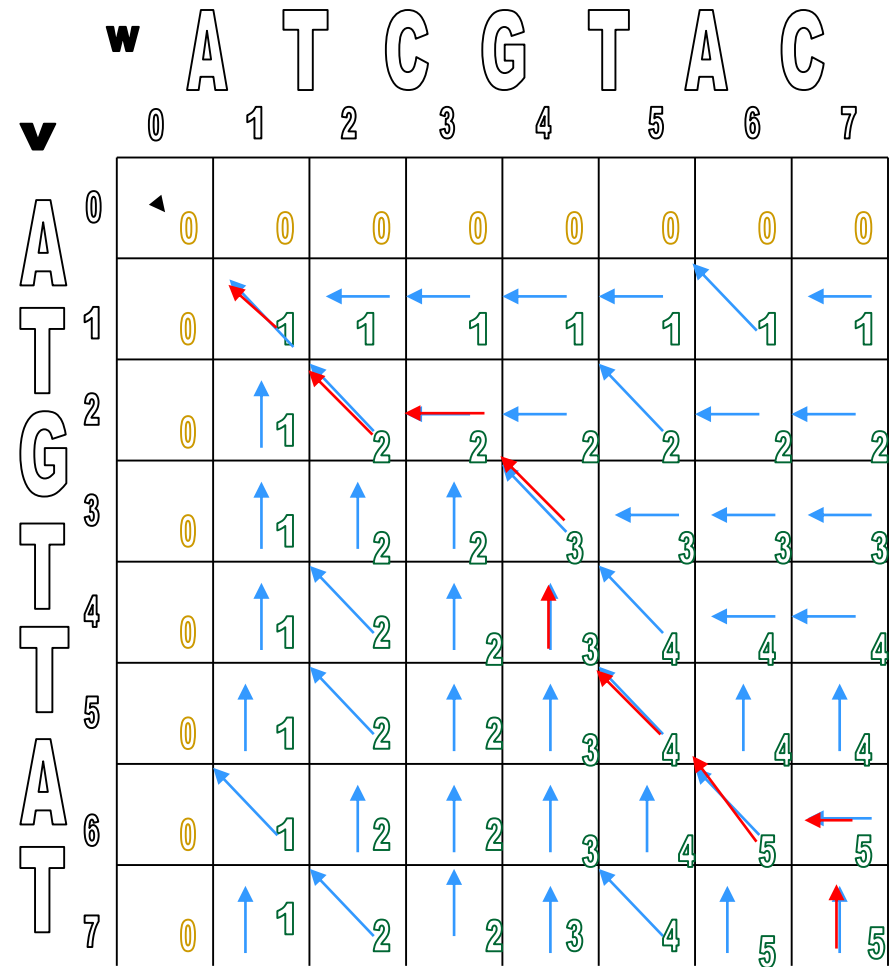
8.              $s_{i,j} \leftarrow \max \left\{ \begin{array}{l} s_{i-1,j} \\ s_{i,j-1} \\ s_{i-1,j-1} + 1, \text{ if } v_i = w_j \end{array} \right.$

9.              $b_{i,j} \leftarrow \begin{cases} \text{“} \uparrow \text{“} & \text{if } s_{i,j} = s_{i-1,j} \\ \text{“} \leftarrow \text{“} & \text{if } s_{i,j} = s_{i,j-1} \\ \text{“} \swarrow \text{“} & \text{if } s_{i,j} = s_{i-1,j-1} + 1 \end{cases}$

10.             return  $(s_{n,m}, b)$

# Now What?

- $\text{LCS}(v, w)$  created the alignment grid
- Now we need a way to read the best alignment of  $v$  and  $w$
- Follow the arrows backwards from sink



# Printing LCS : Backtracking

```
1.  PrintLCS (b,v,i,j)
2.      if  $i = 0$  or  $j = 0$ 
3.          return
4.      if  $b_{i,j} = \nwarrow$ 
5.          PrintLCS (b,v,i-1,j-1)
6.          print  $v_i$ 
7.      else
8.          if  $b_{i,j} = \uparrow$ 
9.              PrintLCS (b,v,i-1,j)
10.         else
11.             PrintLCS (b,v,i,j-1)
```

# LCS Runtime

- It takes  $O(nm)$  time to fill in the  $n \cdot m$  dynamic programming matrix.