CS481: Bioinformatics Algorithms

Can Alkan

EA224

calkan@cs.bilkent.edu.tr

http://www.cs.bilkent.edu.tr/~calkan/teaching/cs481/

Outline

- DNA Sequence Comparison
- Change Problem
- Manhattan Tourist Problem
- Longest Paths in Graphs
- Sequence Alignment
- Edit Distance
- Longest Common Subsequence Problem
- Dot Matrices

DNA sequence comparison

- Gene similarities between two genes with known and unknown function alert biologists to some possibilities
- Computing a similarity score between two genes tells how likely it is that they have similar functions
- Dynamic programming is a technique for revealing similarities between genes
- The ***Change Problem*** is a good problem to introduce the idea of dynamic programming

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 $c = (c_1, c_2, \ldots, c_d)$, in a decreasing order of value ($c_1 > c_2 > \ldots > c_d$)

Output: A list of d integers $i_1, i_2, \ldots, i_d$ such that

$$c_1 i_1 + c_2 i_2 + \ldots + c_d i_d = M$$

and $i_1 + i_2 + \ldots + i_d$ is minimal

Change Problem: Example

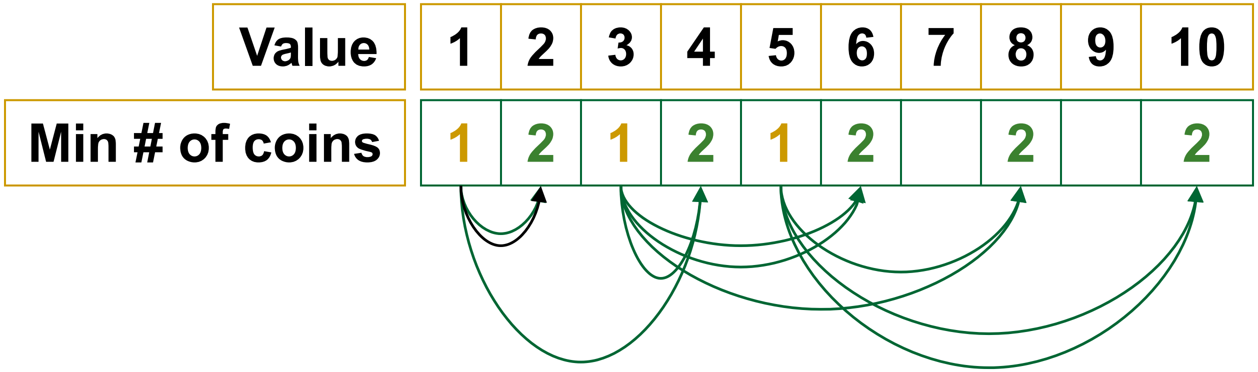
Given the denominations 1, 3, and 5, what is the minimum number of coins needed to make change for a given value?

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?



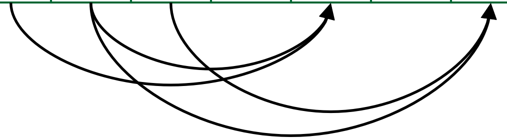
Value	1	2	3	4	5	6	7	8	9	10
Min # of coins	1	2	1	2	1	2		2		2

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:

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

Change Problem: Recurrence (cont'd)

Given the denominations c: c_1, c_2, …, c_d, the recurrence relation is:

$$\text{minNumCoins}(M) = \text{min of} \begin{cases} \text{minNumCoins}(M-c_1) + 1 \\ \text{minNumCoins}(M-c_2) + 1 \\ \dots \\ \text{minNumCoins}(M-c_d) + 1 \end{cases}$$

Change Problem: A Recursive Algorithm

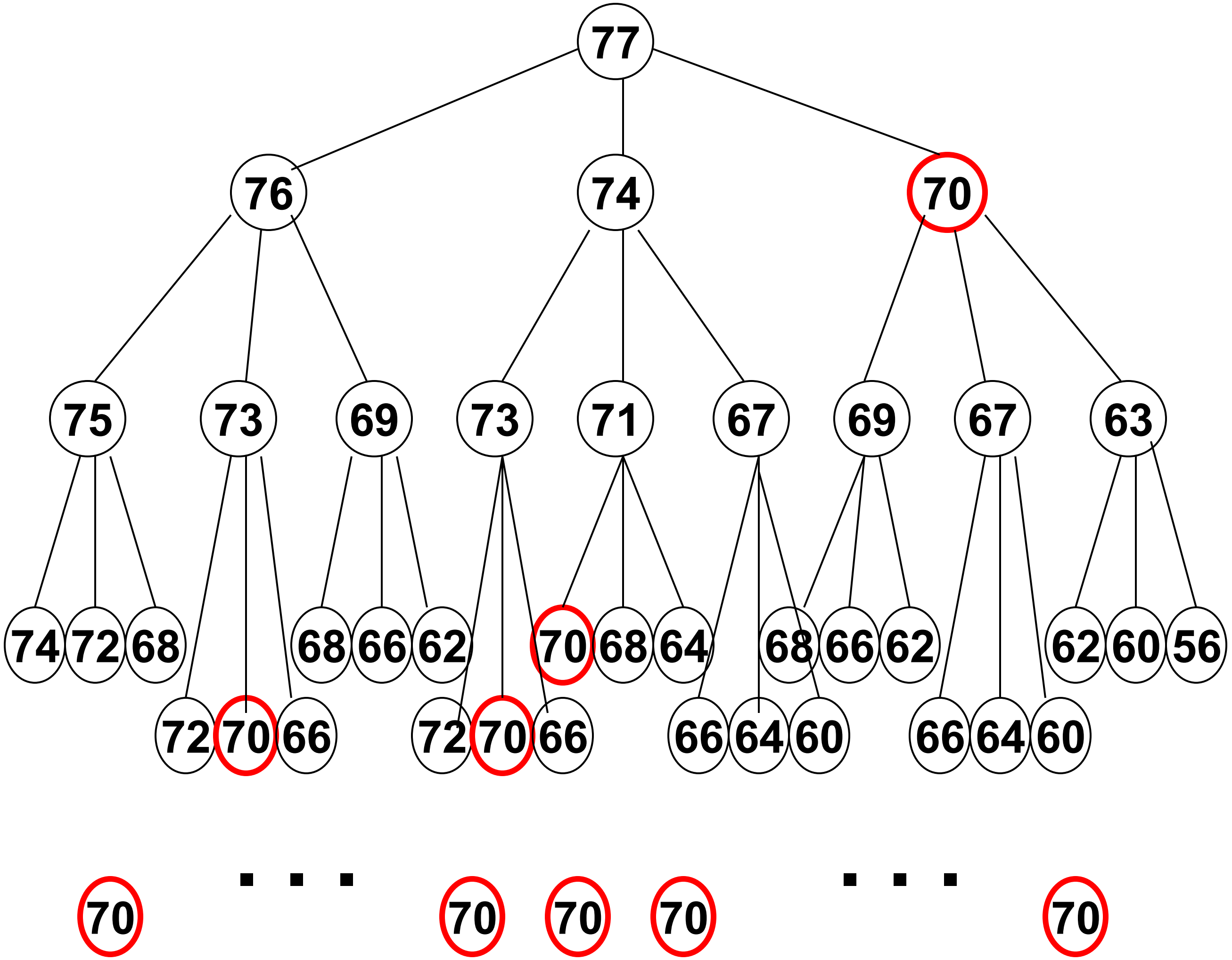
```
RecursiveChange(M,c,d)
  if $M = 0$
    return 0
  bestNumCoins ← infinity
  for $i$ ← 1 to $d$
    if $M \geq c_i$
      numCoins ← RecursiveChange($M - c_i$ , c, d)
      if $numCoins + 1 < bestNumCoins$
        bestNumCoins ← $numCoins + 1$
  return bestNumCoins
```

RecursiveChange Is Not Efficient

- It recalculates the optimal coin combination for a given amount of money repeatedly

- i.e., $\boldsymbol{M}$ = 77, $\boldsymbol{c}$ = (1,3,7):
  - Optimal coin combo for 70 cents is computed **9** times!

The RecursiveChange Tree



We Can Do Better

- We’re re-computing values in our algorithm more than once

- Save results of each computation for 0 to ***M***

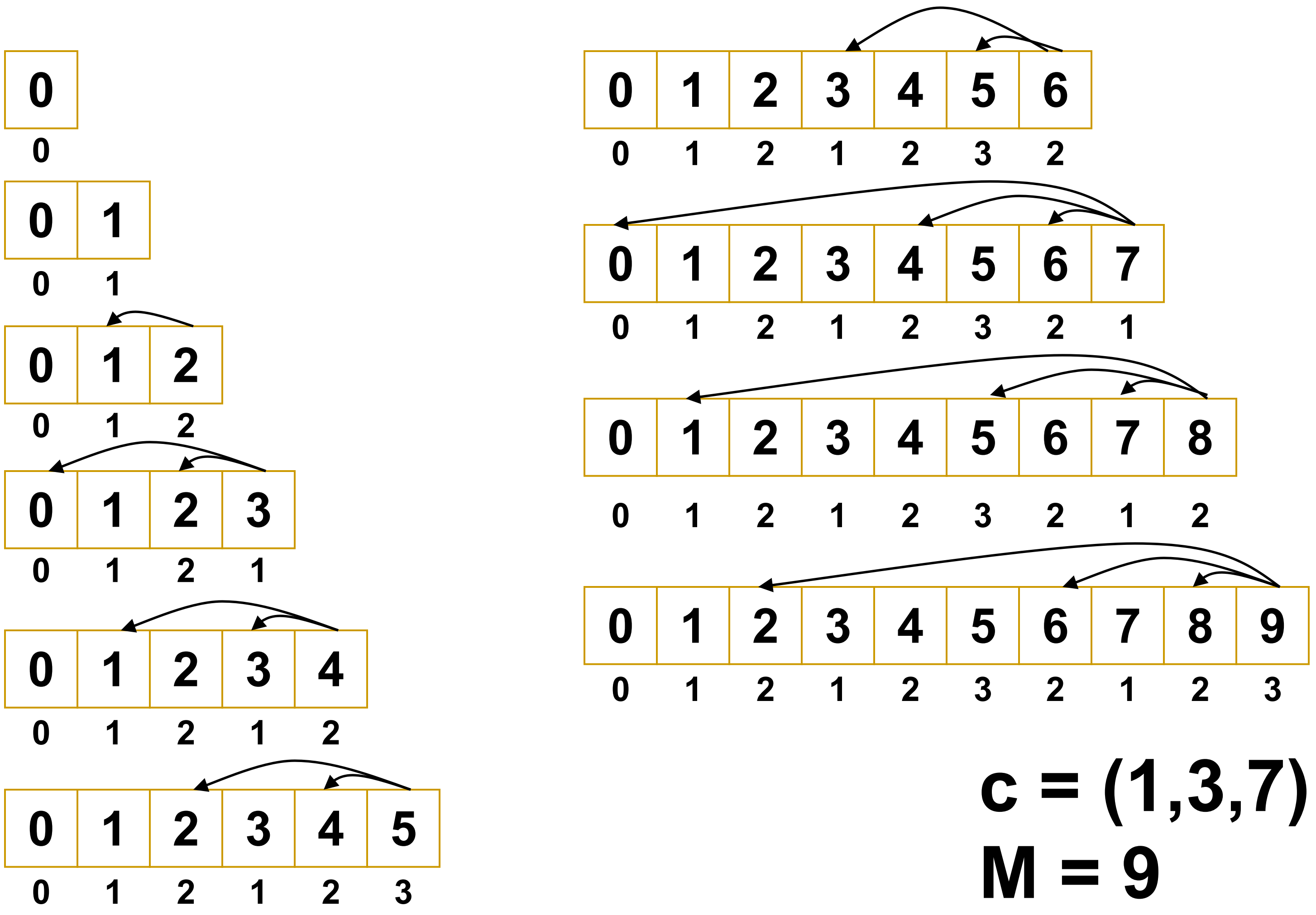
- This way, we can do a reference call to find an already computed value, instead of re-computing each time

- Running time ***M********d***, where ***M*** is the value of money and ***d*** is the number of denominations

The Change Problem: Dynamic Programming

```
DPChange(M,c,d)
  $bestNumCoins_0 \leftarrow 0$
  for $m \leftarrow 1$ to $M$
    $bestNumCoins_m \leftarrow$ infinity
    for $i \leftarrow 1$ to $d$
      if $m \geq c_i$
        if $bestNumCoins_{m - c_i} + 1 < bestNumCoins_m$
          $bestNumCoins_m \leftarrow bestNumCoins_{m - c_i} + 1$
  return $bestNumCoins_M$
```

DPChange: Example



0	
0	

0	1
0	1

0	1	2
0	1	2

0	1	2	3
0	1	2	1

0	1	2	3	4
0	1	2	1	2

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

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

0	1	2	3	4	5	6	7
0	1	2	1	2	3	2	1

0	1	2	3	4	5	6	7	8
0	1	2	1	2	3	2	1	2

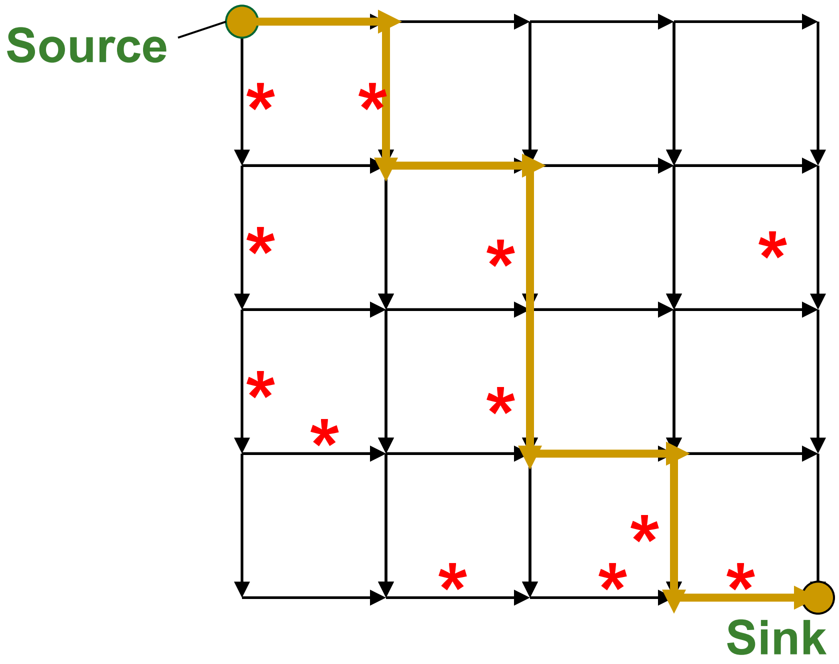
0	1	2	3	4	5	6	7	8	9
0	1	2	1	2	3	2	1	2	3

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)

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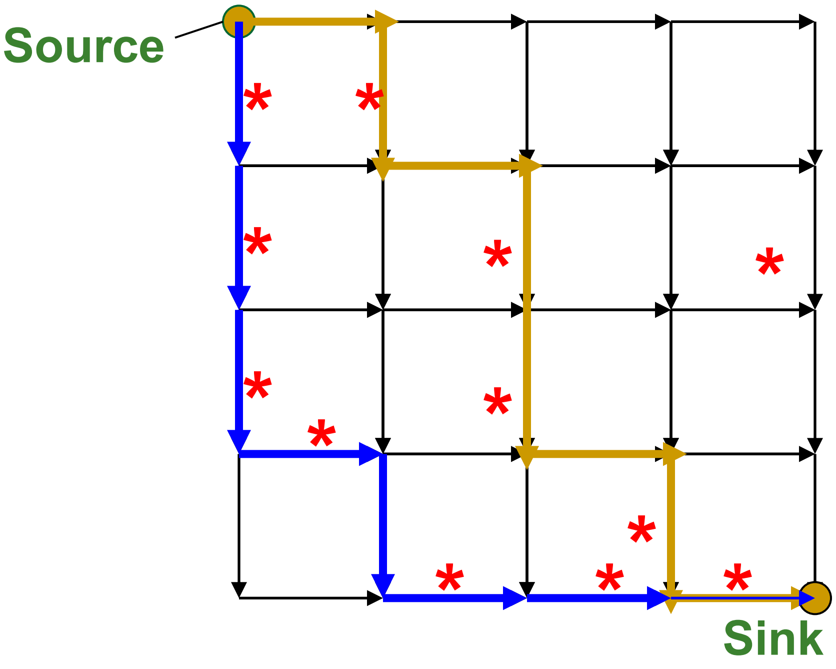


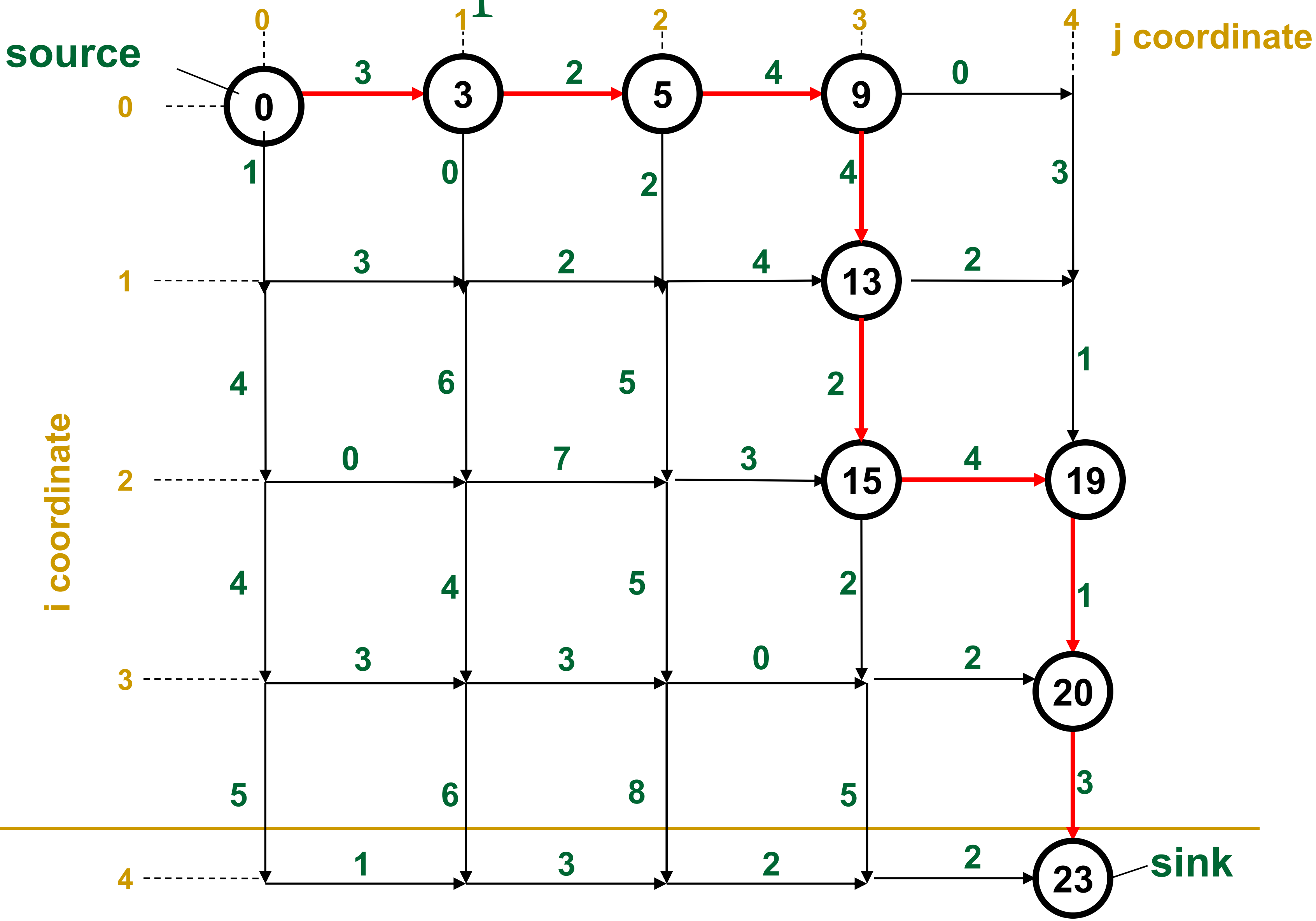
Manhattan Tourist Problem: Formulation

Goal: Find the longest path in a weighted grid.

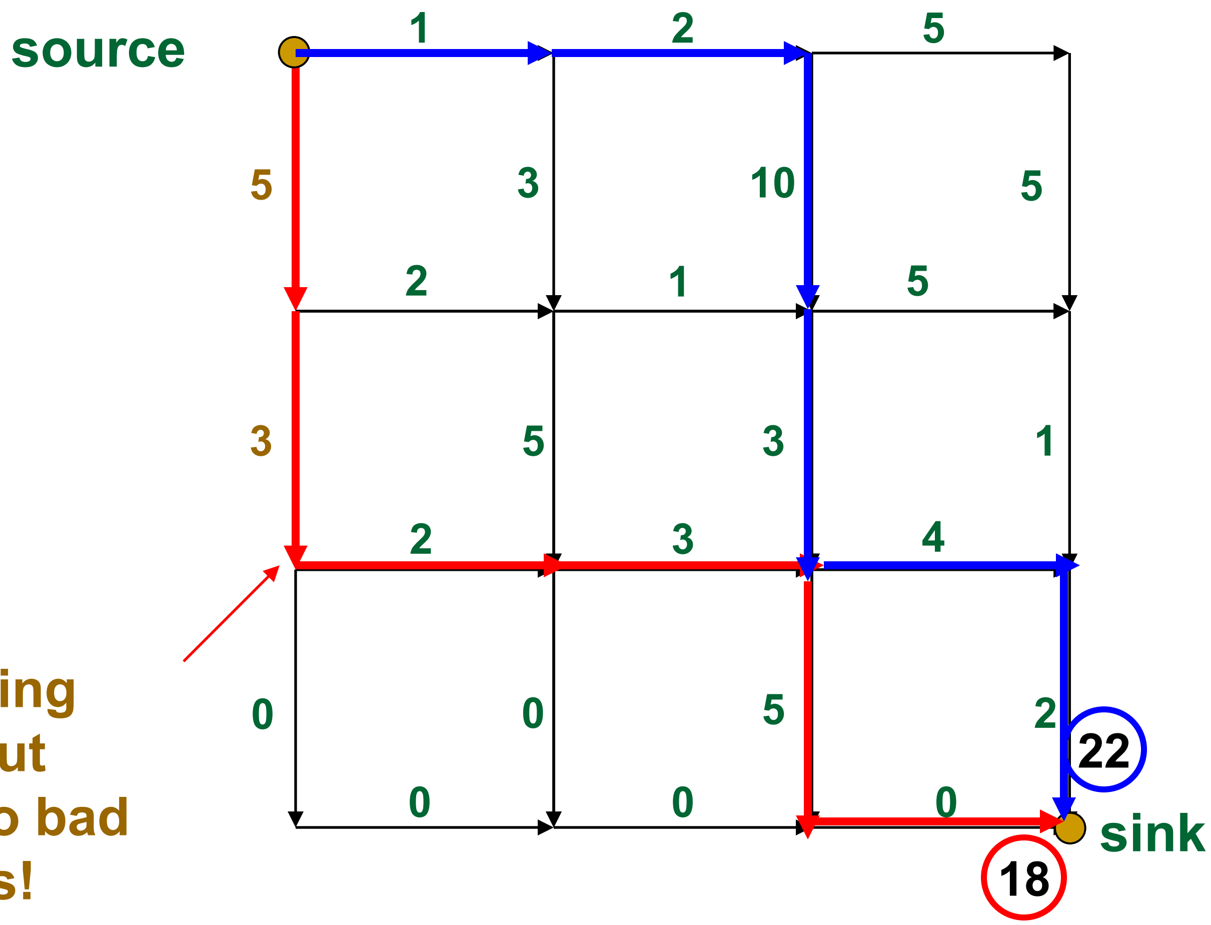
Input: A weighted grid G with two distinct vertices, one labeled “source” and the other labeled “sink”

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

MTP: An Example



MTP: Greedy Algorithm Is Not Optimal



promising start, but leads to bad choices!

MTP: Simple Recursive Program

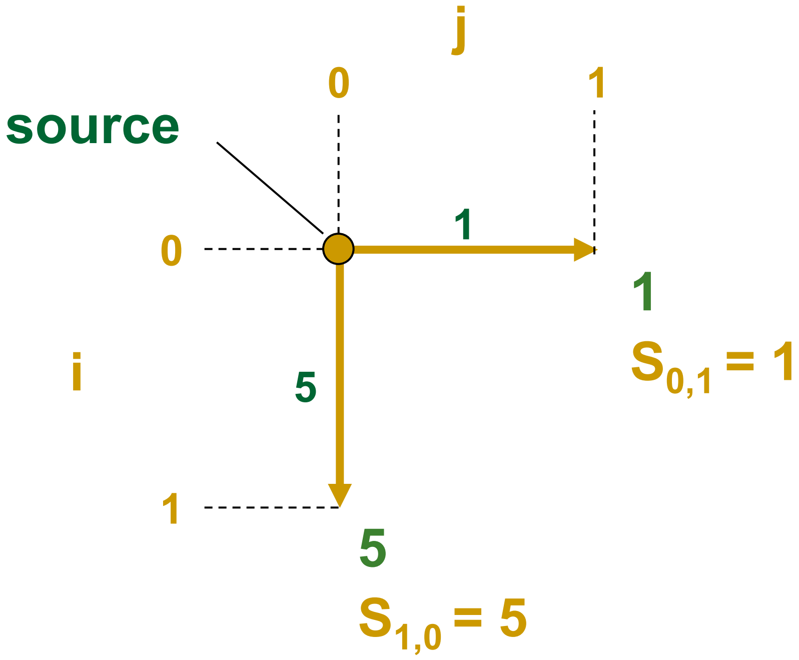
```
MT(n,m)
   if n=0  or m=0
      return MT(n,m)
   x ← MT(n–1,m)+
                length of the edge from (n– 1,m) to (n,m)
   y ← MT(n,m–1)+
                length of the edge from (n,m–1) to (n,m)
   return max{x,y}
```

MTP: Simple Recursive Program

```
MT(n,m)
   x ← MT(n-1,m)+
                length of the edge from (n– 1,m) to (n,m)
   y ← MT(n,m-1)+
                length of the edge from (n,m-1) to (n,m)
   return min{x,y}
```

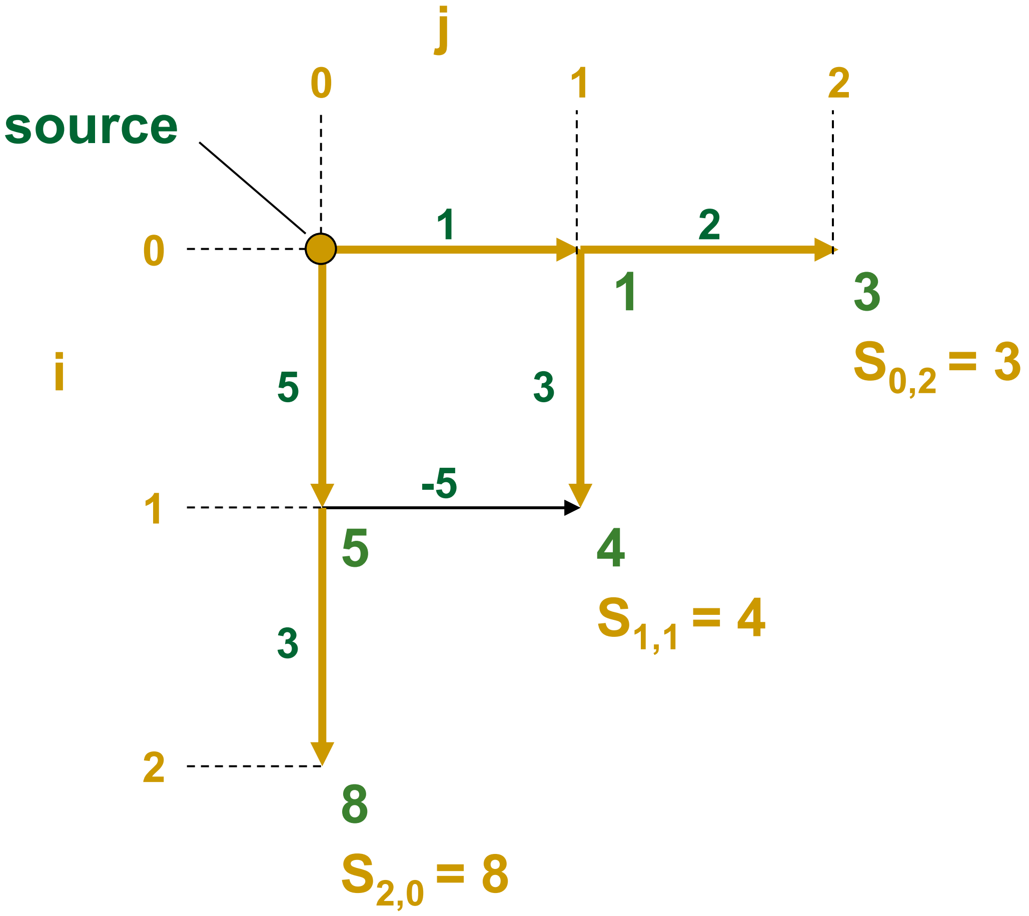
What’s wrong with this approach?

MTP: Dynamic Programming

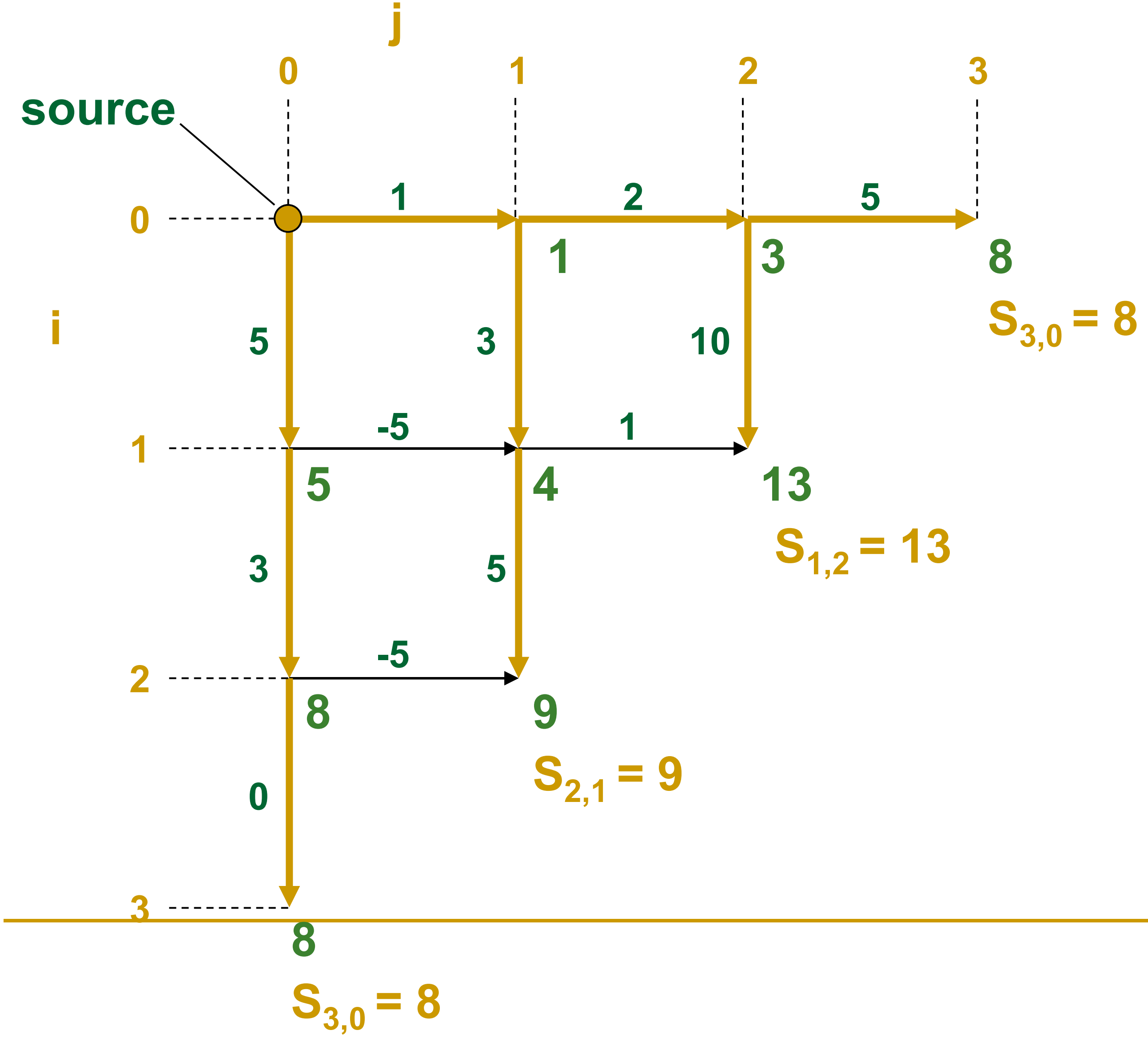


- Calculate optimal path score for each vertex in the graph
- Each vertex's score is the maximum of the prior vertices score plus the weight of the respective edge in between

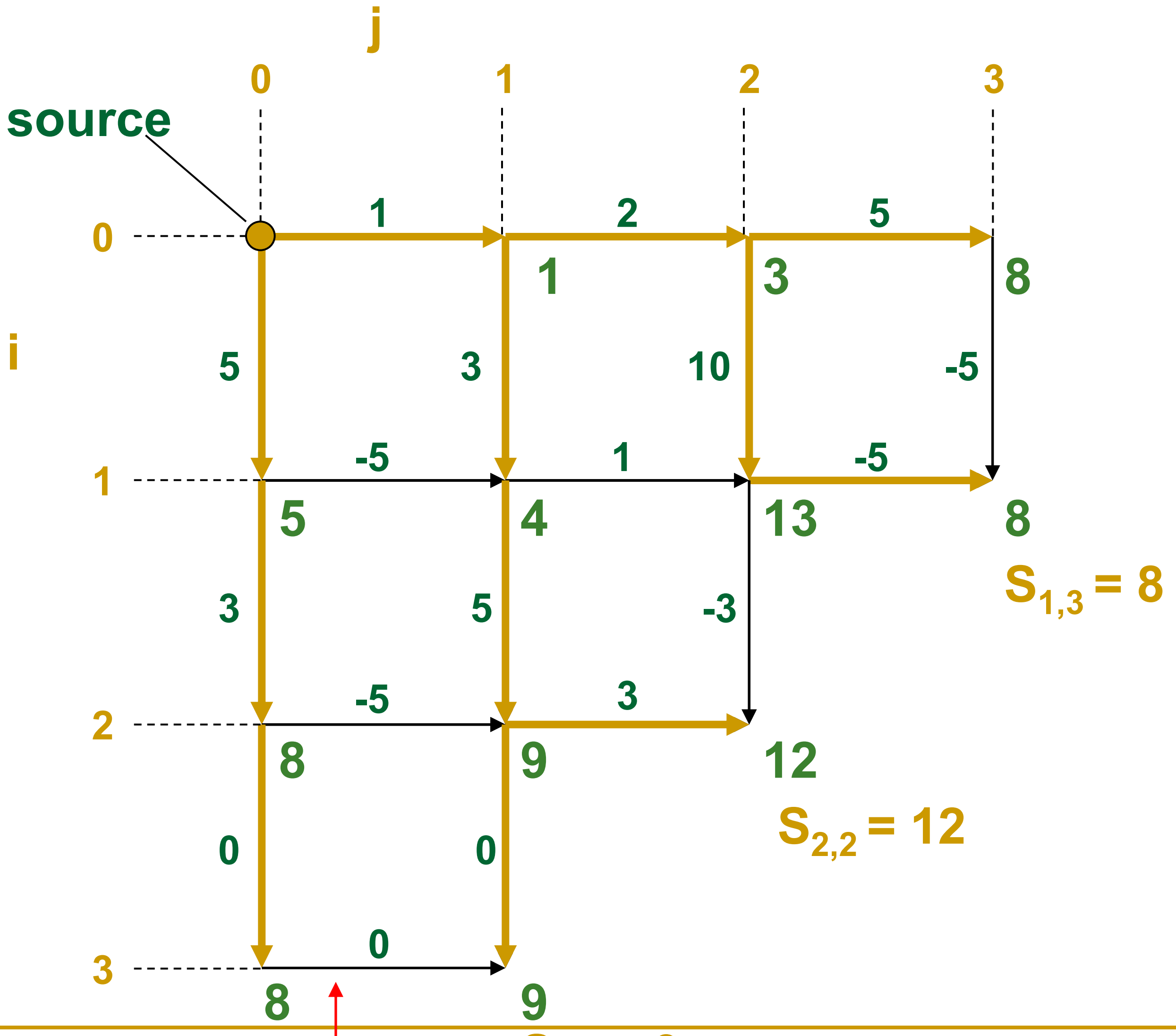
MTP: Dynamic Programming (cont'd)



MTP: Dynamic Programming (cont'd)



MTP: Dynamic Programming (cont'd)



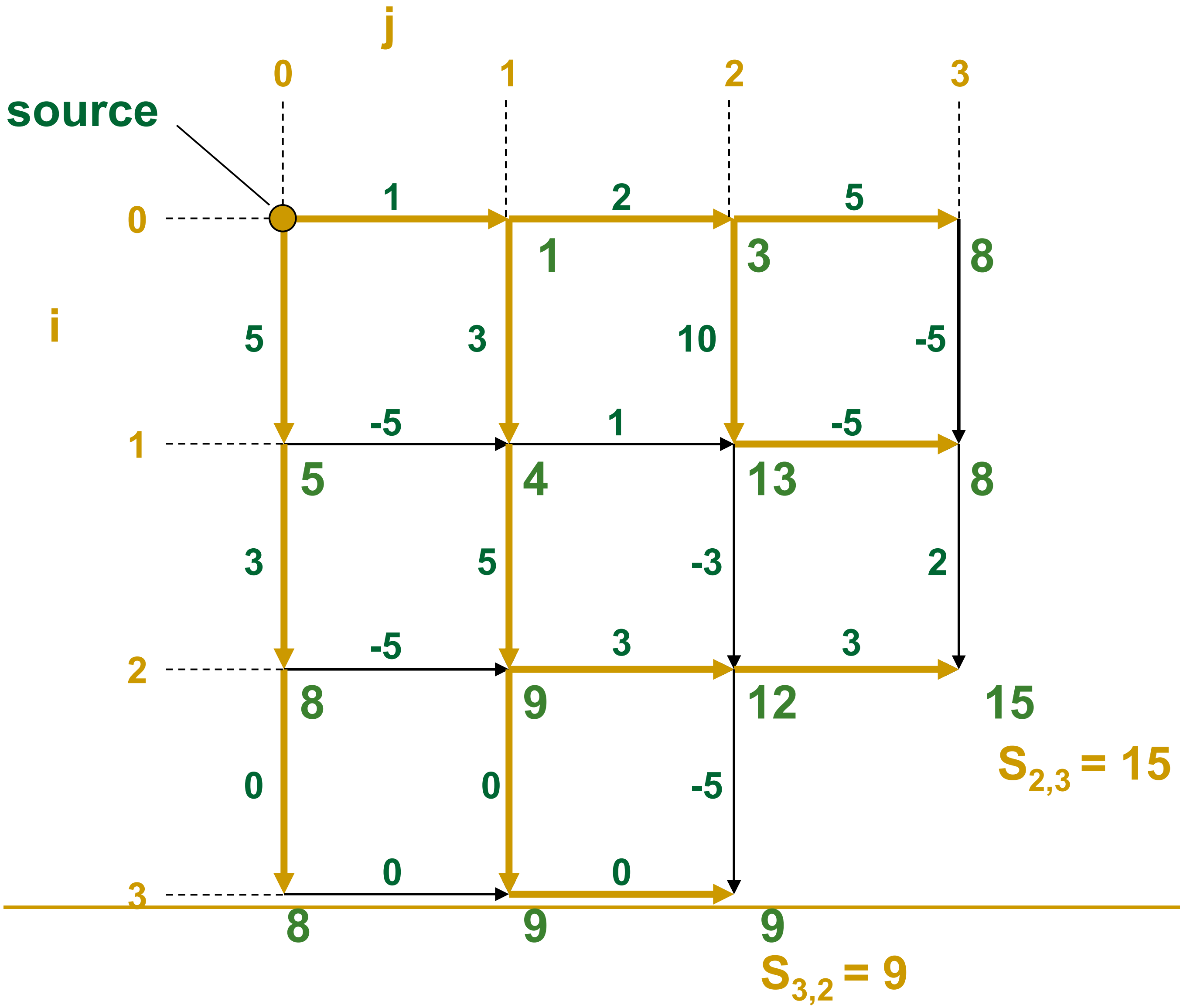
$S_{1,3} = 8$

$S_{2,2} = 12$

$S_{3,1} = 9$

greedy alg. fails!

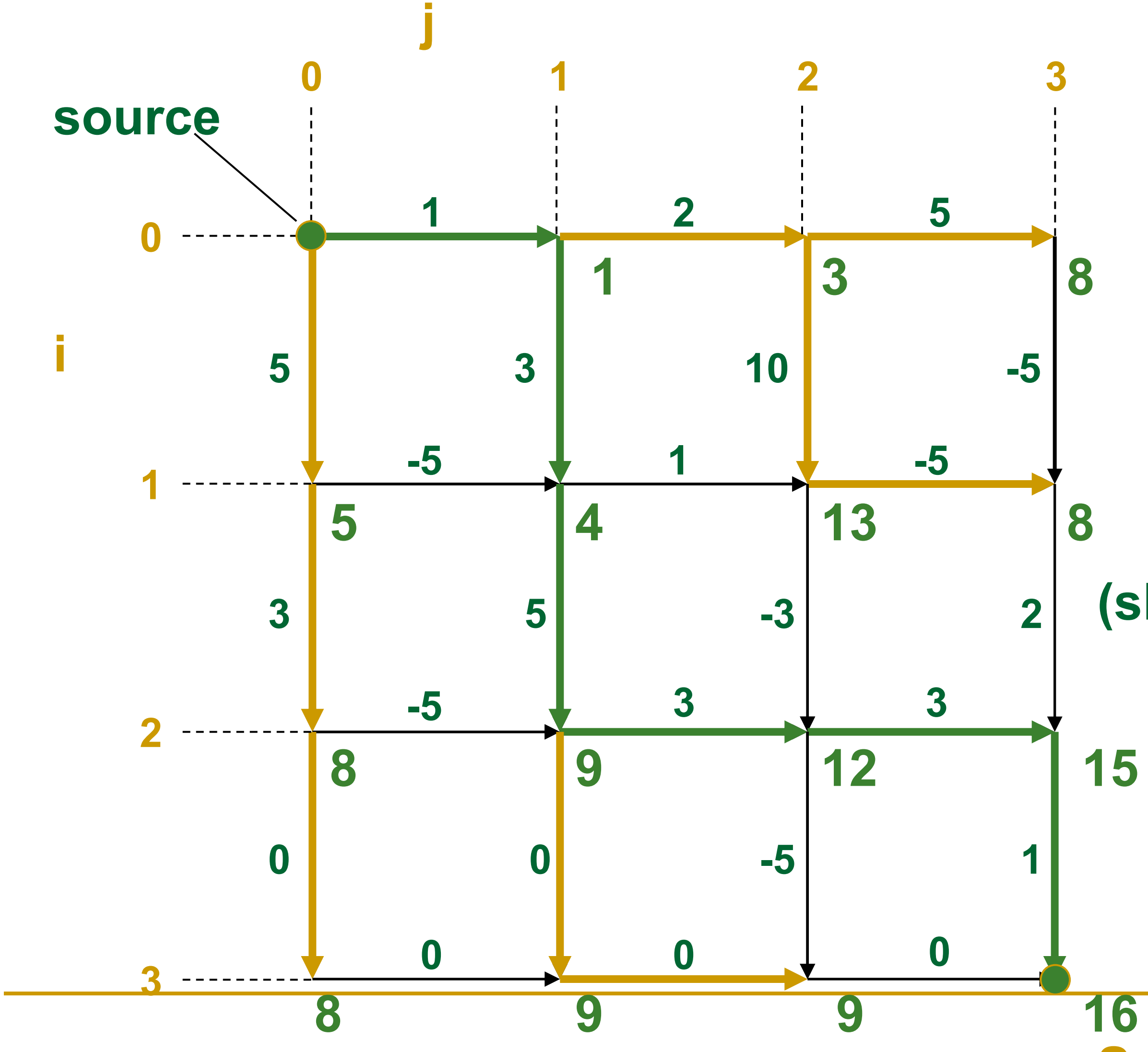
MTP: Dynamic Programming (cont'd)



$S_{2,3} = 15$

$S_{3,2} = 9$

MTP: Dynamic Programming (cont'd)



Done!

(showing all back-traces)

$S_{3,3} = 16$

MTP: Recurrence

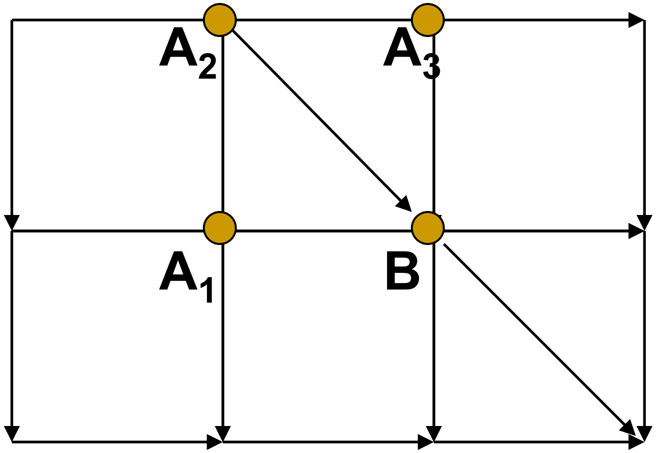
Computing the score for a point (i,j) by the recurrence relation:

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

The running time is n x 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:

$$s_B = \max\text{ of } \begin{cases} s_{A1} + \text{weight of the edge } (A_1, B) \\ s_{A2} + \text{weight of the edge } (A_2, B) \\ s_{A3} + \text{weight of the edge } (A_3, B) \end{cases}$$

Manhattan Is Not A Perfect Grid (cont'd)

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

$$s_x = \begin{array}{c} \textbf{max} \\ \textbf{of} \end{array} \left\{ \begin{array}{r} s_y + \textbf{weight of vertex } (y, x) \textbf{ where} \\ y \in \textbf{Predecessors}(x) \end{array} \right.$$

- 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

- Try to find such order for a directed cycle

DAG: Directed Acyclic Graph

- Since Manhattan is not a perfect regular grid, we represent it as a DAG

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:

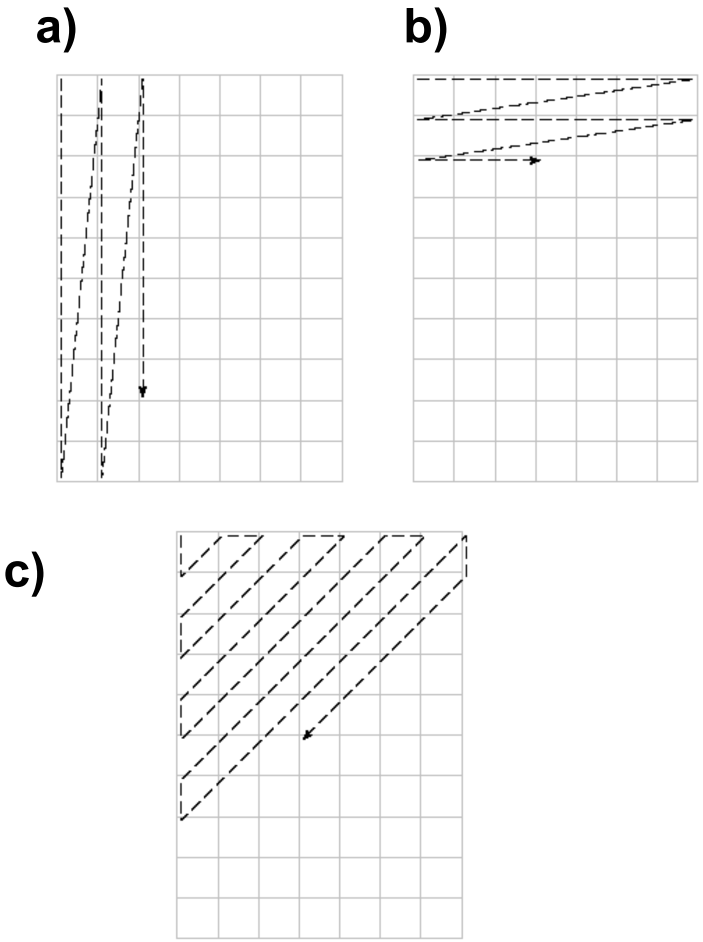
$$s_v = \max \text{ of } \begin{cases} s_{u_1} + \text{weight of edge from } u_1 \text{ to v} \\ s_{u_2} + \text{weight of edge from } u_2 \text{ to v} \\ s_{u_3} + \text{weight of edge from } u_3 \text{ to v} \end{cases}$$

<u>In General</u>:

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

Traversing the Manhattan Grid

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



ALIGNMENT

Alignment: 2 row representation

Given 2 DNA sequences v and w:

v : ATCTGAT m = 7
w : TGCATA 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

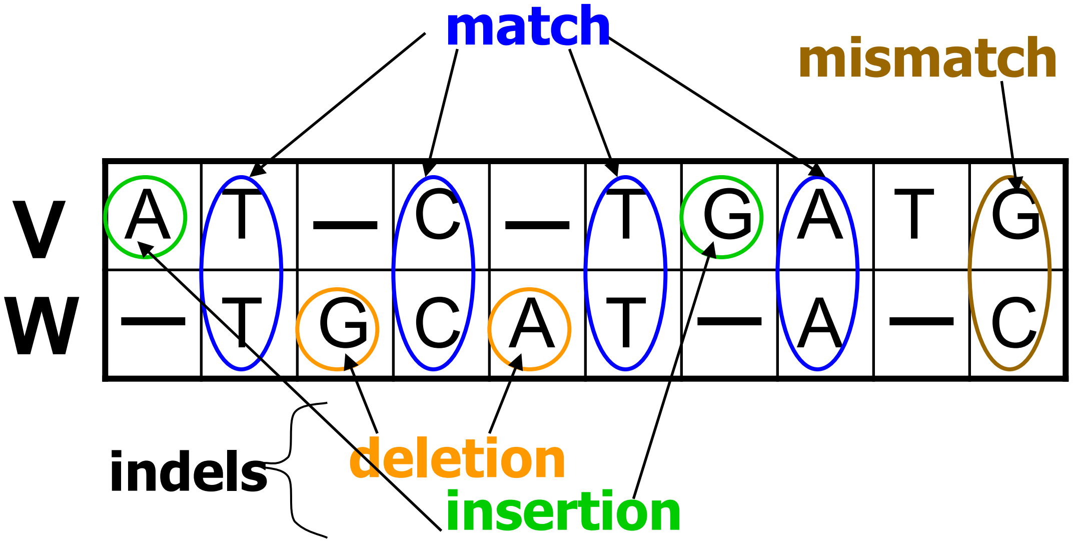
5 matches 2 insertions 2 deletions

Aligning DNA Sequences

V = ATCTGATG n = 8

W = TGCATAC m = 7

4 matches
1 mismatch
2 insertions
2 deletions



V	A	T	—	C	—	T	G	A	T	G
W	—	T	G	C	A	T	—	A	—	C

Longest Common Subsequence (LCS) – Alignment without Mismatches

- Given two sequences

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

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

$$v\text{: } 1 \le i_1 < i_2 < \ldots < i_t \le m$$

and a sequence of positions in

$$w\text{: } 1 \le j_1 < j_2 < \ldots < j_t \le n$$

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)→(1,0)→(2,1)→(2,2)→(3,3)→(3,4)→(4,5)→(5,5)→(6,6)→(7,6)→(8,7)

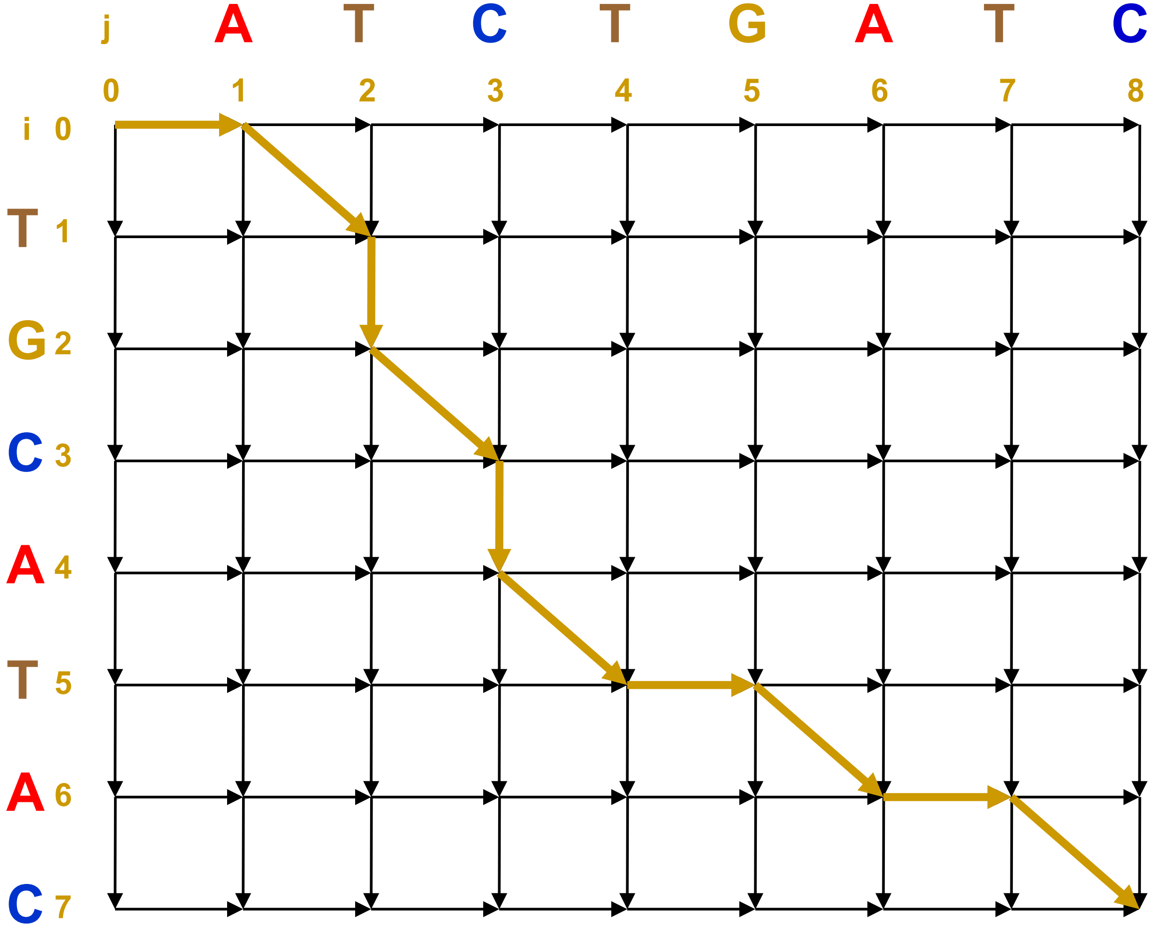
Matches shown in red

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

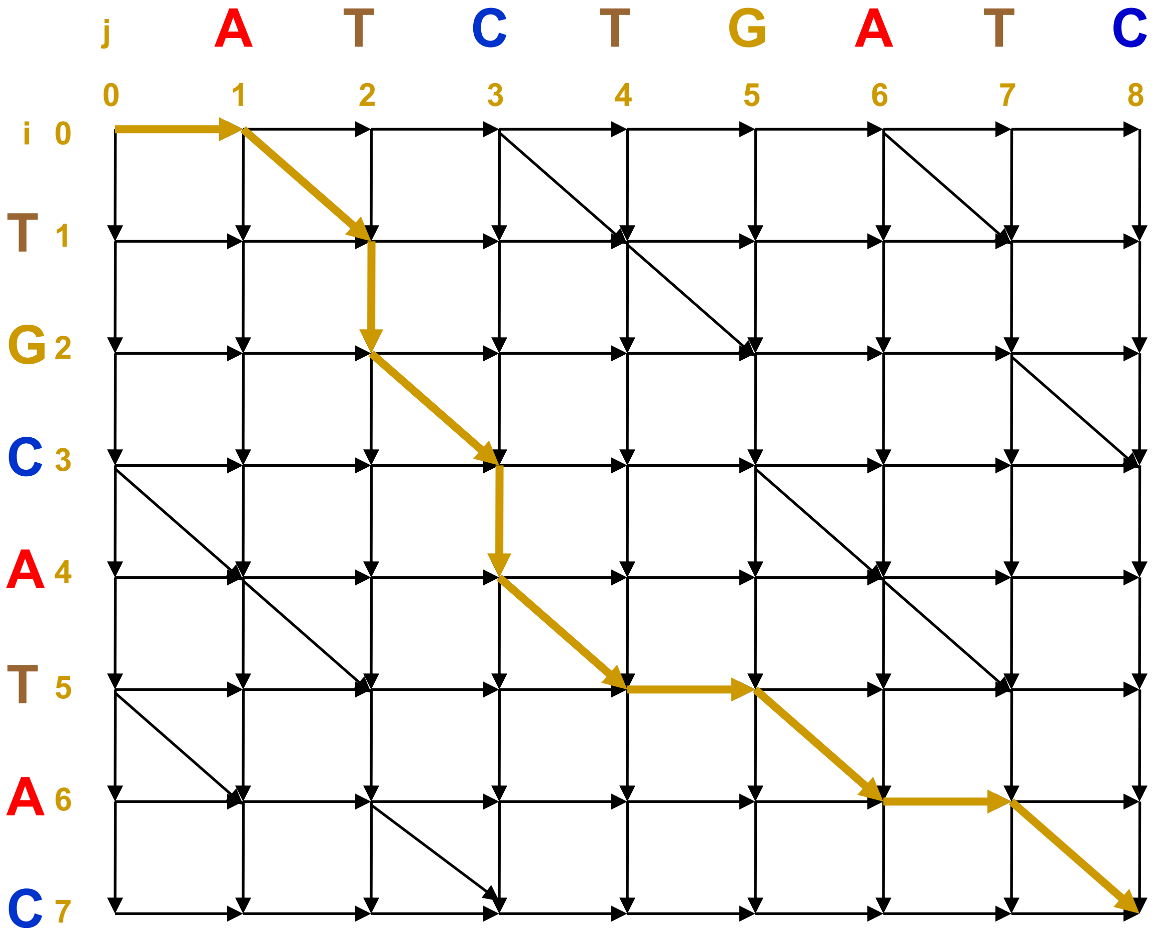
positions in w: $1 < 3 < 5 < 6 < 7$

Every common subsequence is a path in 2-D grid

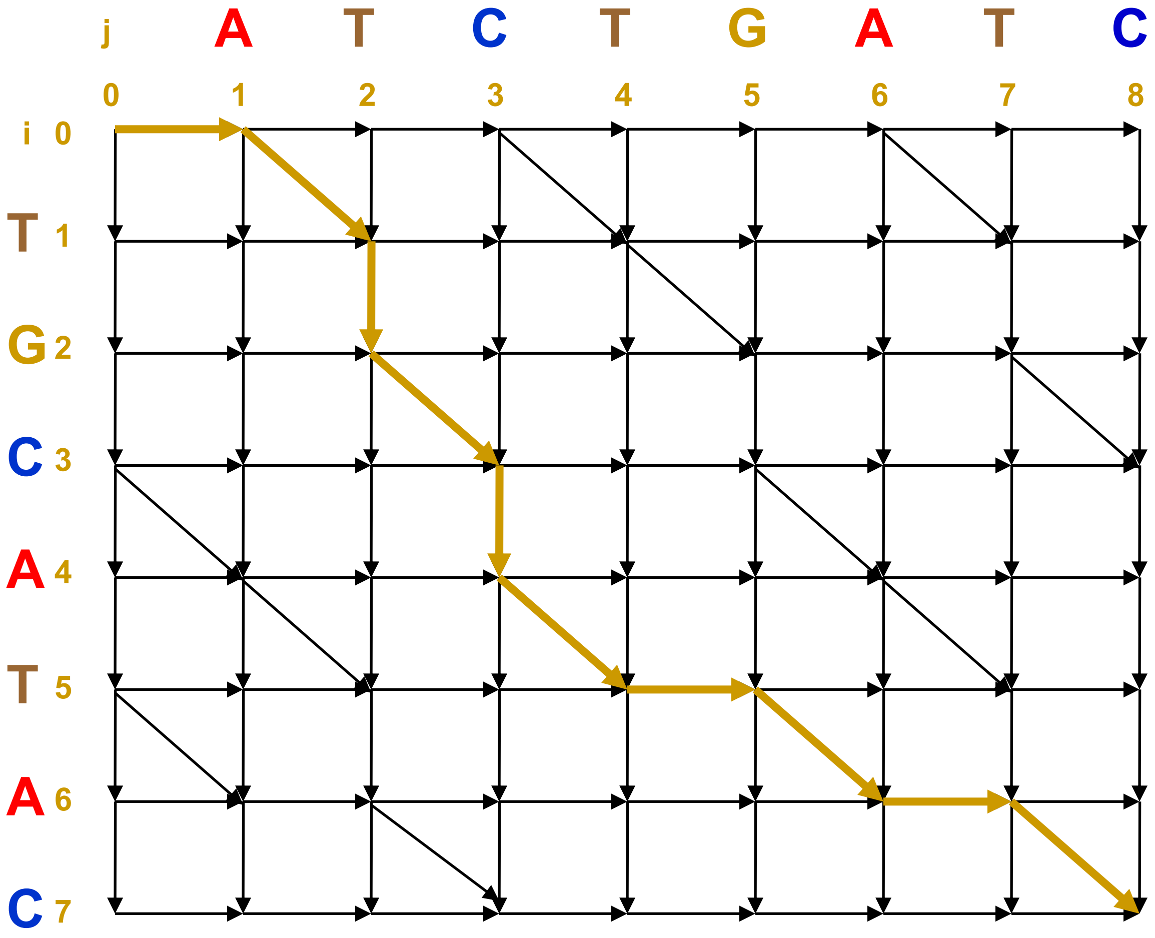
LCS Problem as Manhattan Tourist Problem



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: $v_1 \ldots v_i$

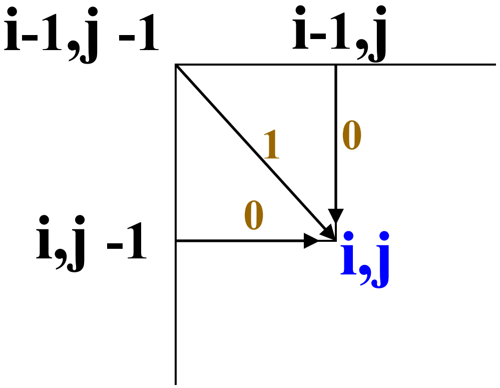
and w_j = prefix of w of length j: $w_1 \ldots w_j$

The length of LCS(v_i,w_j) is computed by:

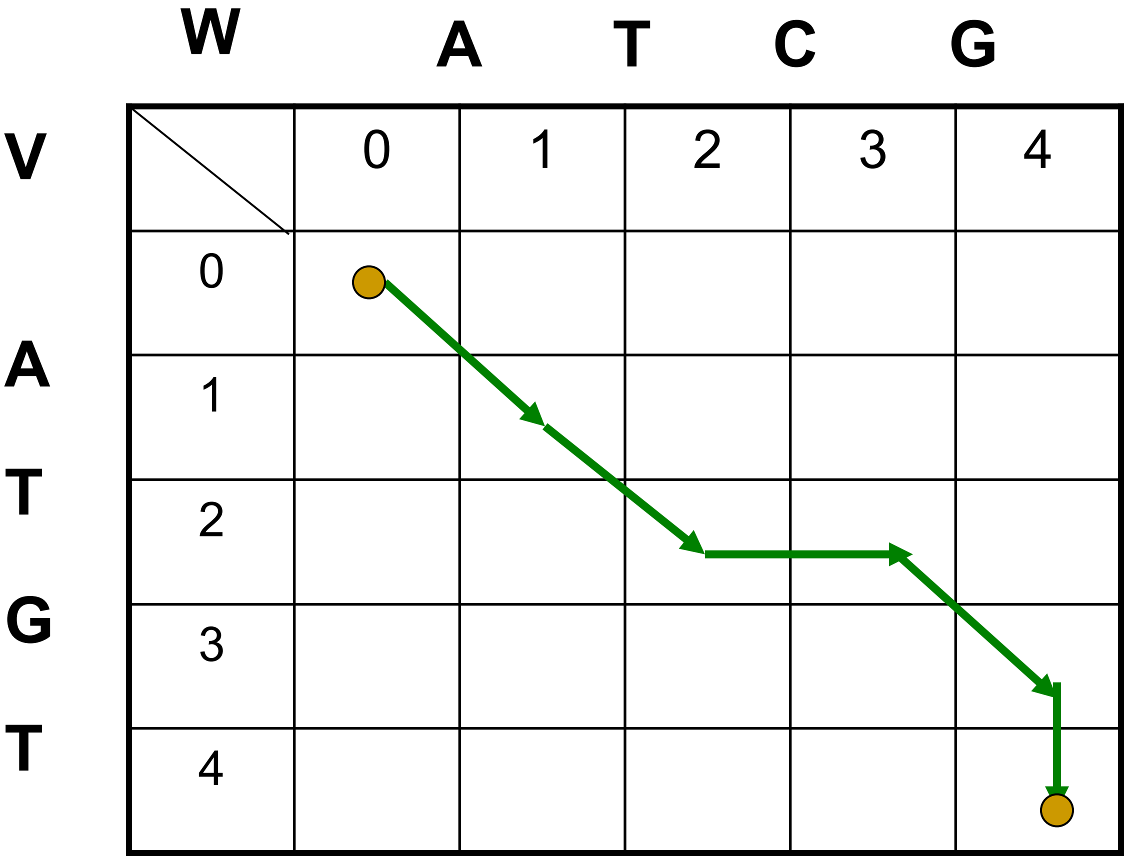
$$s_{i,\,j} = \max \begin{cases} s_{i-1,\,j} \\ s_{i,\,j-1} \\ s_{i-1,\,j-1} + 1 \text{ if } v_i = w_j \end{cases}$$

Computing LCS (cont'd)

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



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
```

DISTANCE BETWEEN STRINGS

Aligning Sequences without Insertions and Deletions: Hamming Distance

Given two DNA sequences v and w :

v : ATATATAT
w : TATATATA

- **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 :  ATATATAT--
w :  --TATATATA
```

- **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 → w

Edit Distance vs Hamming Distance

Hamming distance always compares i^{-th} letter of v with i^{-th} letter of w

```
v = ATATATAT
    | | | | | | | |
w = TATATATA
```

Hamming distance:

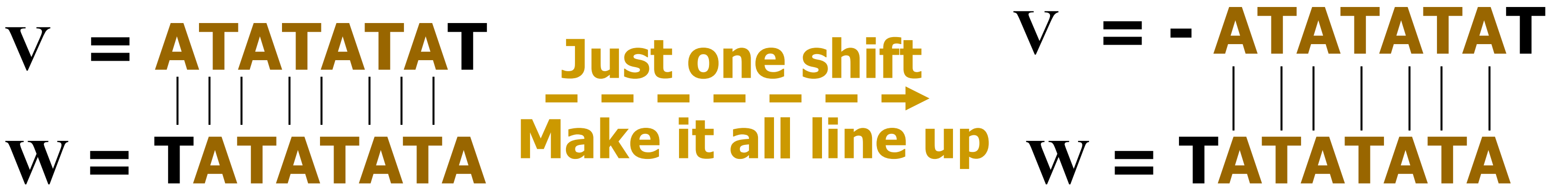
d(v, w)=8

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

Edit distance may compare i-th letter of v with j-th letter of w



```
v = ATATATAT
    ||||||||
w = TATATATA
```

Just one shift

Make it all line up

```
v = - ATATATAT
       |||||||
w =   TATATATA
```

Hamming distance: $d(v, w)=8$

Computing Hamming distance is a trivial task

Edit distance: $d(v, w)=2$

Computing edit distance is a non-trivial task

Edit Distance vs Hamming Distance

Hamming distance always compares
i-th letter of v with
i-th letter of w

```
v = ATATATAT
    ||||||||
w = TATATATA
```

Hamming distance:
d(v, w)=8

Edit distance may compare
i-th letter of v with
j-th 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 → (delete last T)
TGCATA → (delete last A)
TGCAT → (insert A at front)
ATGCAT → (substitute C for 3rd G)
ATCCAT → (insert G before last A)
ATCCGAT (Done)

Edit Distance: Example

TGCATAT → ATCCGAT in 5 steps

TGCATAT → (delete last T)
TGCATA → (delete last A)
TGCAT → (insert A at front)
ATGCAT → (substitute C for 3rd G)
ATCCAT → (insert G before last A)
ATCCGAT (Done)

What is the edit distance? 5?

Edit Distance: Example (cont'd)

TGCATAT → ATCCGAT in 4 steps

TGCATAT → (insert A at front)

ATGCATAT → (delete 6th T)

ATGCATA → (substitute G for 5th A)

ATGCGTA → (substitute C for 3rd G)

ATCCGAT (Done)

Edit Distance: Example (cont'd)

TGCATAT → ATCCGAT in 4 steps

TGCATAT → (insert A at front)

ATGCATAT → (delete 6th T)

ATGCATA → (substitute G for 5th A)

ATGCGTA → (substitute C for 3rd G)

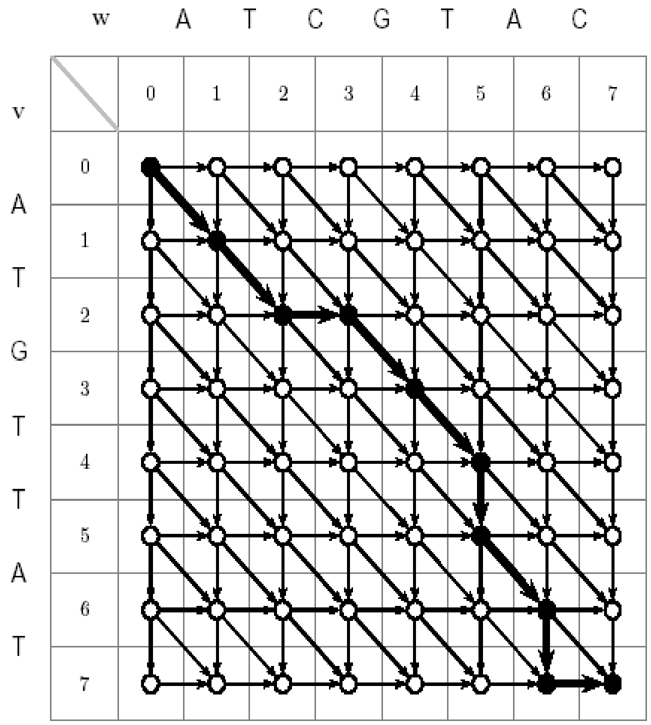
ATCCGAT (Done)

Can it be done in 3 steps???

The Alignment Grid

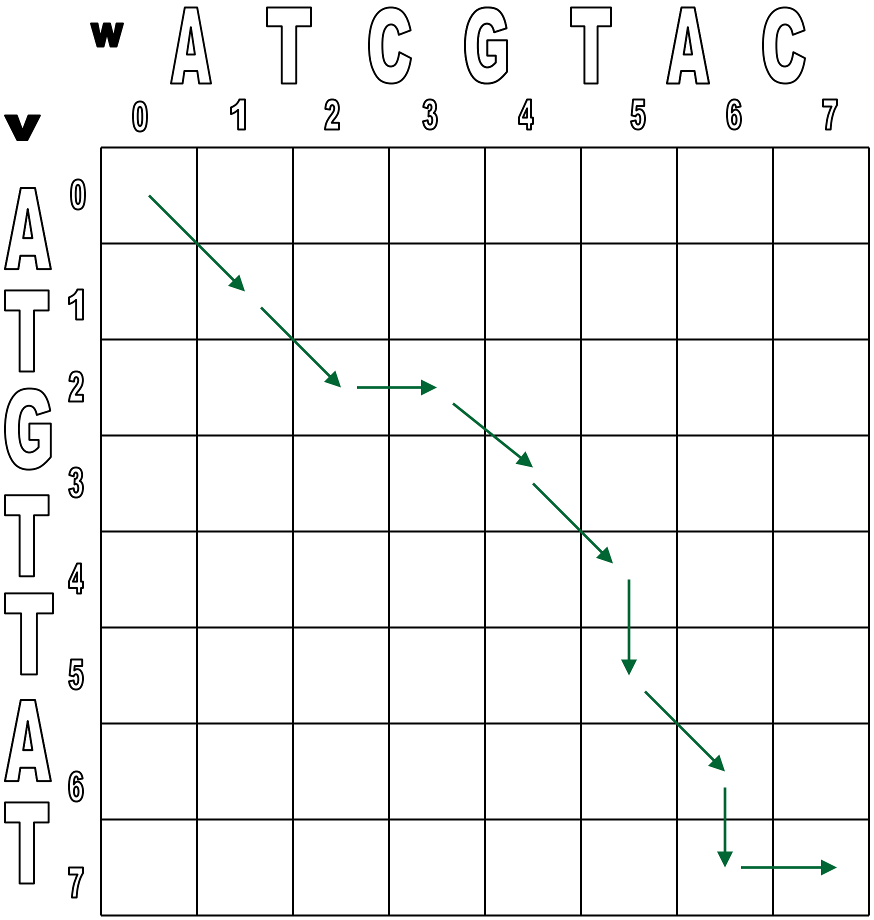
- Every alignment path is from source to sink

```
        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
```



```
↘  ↘  →  ↘  ↘  ↓  ↘  ↓  →
A  T  -  G  T  T  A  T  -
A  T  C  G  T  -  A  -  C
```

Alignment as a Path in the Edit Graph

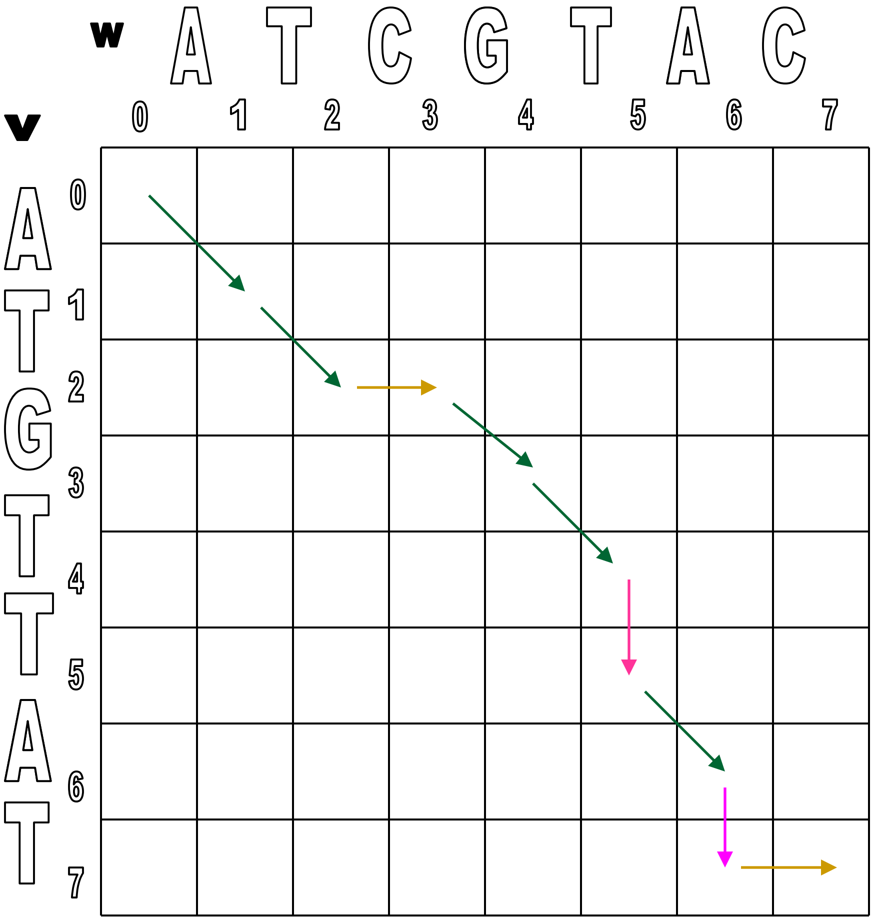


0	1	2	2	3	4	5	6	7	7
	A	T	_	G	T	T	A	T	_
	A	T	C	G	T	_	A	_	C
0	1	2	3	4	5	5	6	6	7

- 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)

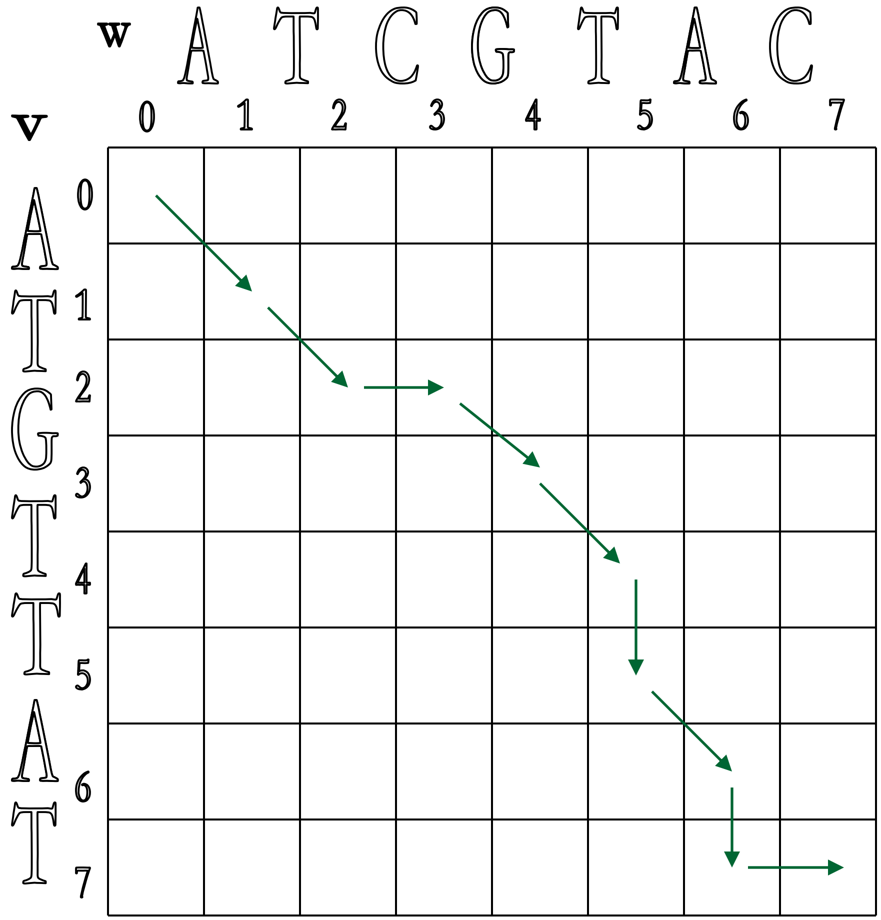


↓ and → represent indels in v and w with score 0.

↘ represent matches with score 1.

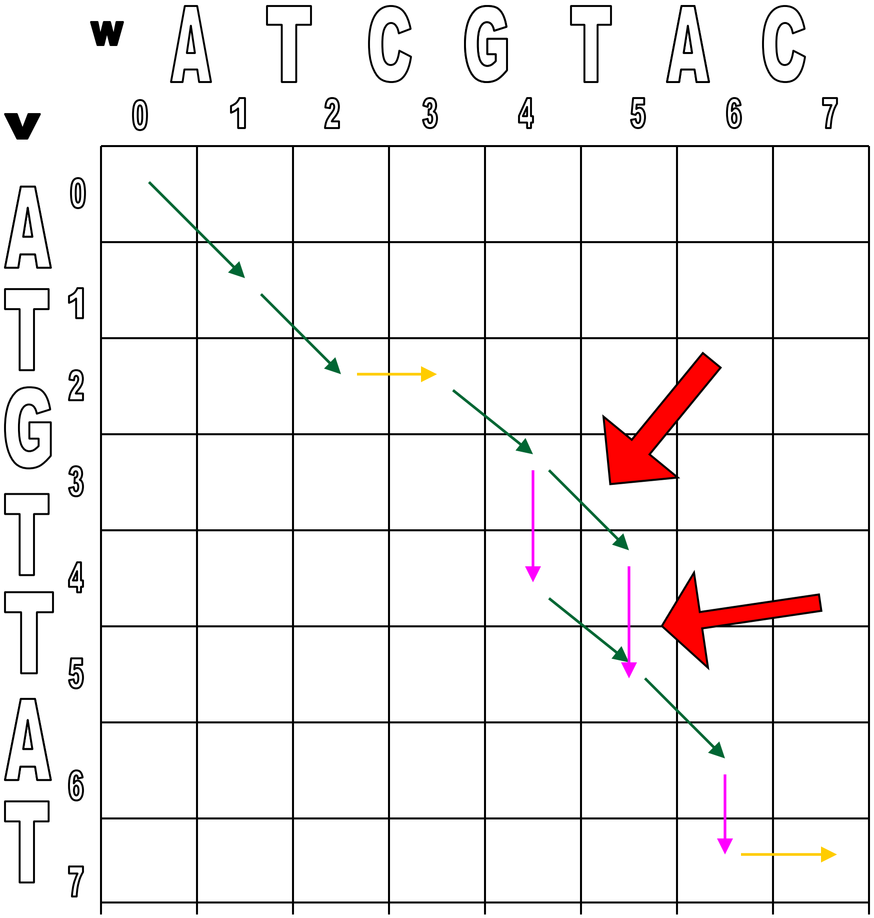
- The score of the alignment path is 5.

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

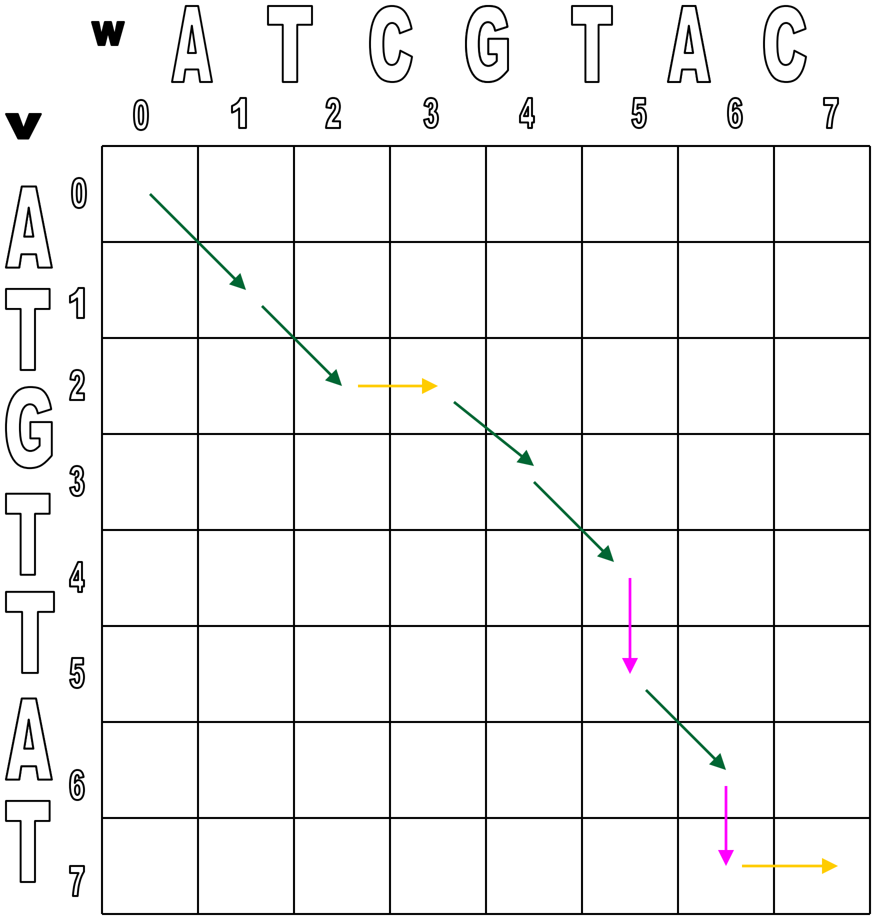
0122345677

v= AT_GTTAT_

w= ATCG_TA_C

0123445667

Alignment as a Path in the Edit Graph



```
      0122345677
v=    AT_GTTAT_
w=    ATCGT_A_C
      0123455667
```

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

Alignment: Dynamic Programming

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

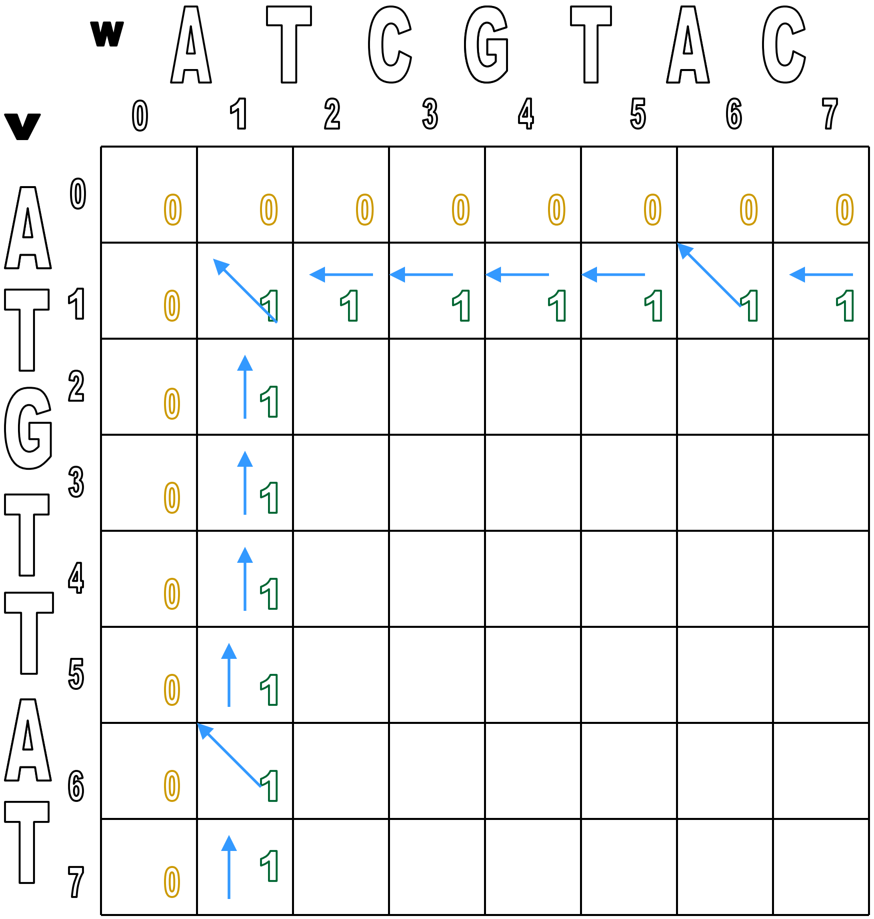
Dynamic Programming Example

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

Initialize 1st row and 1st column to be all zeroes.

Or, to be more precise, initialize 0th row and 0th 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
	0	0	0	0	0	0	0	0	0
A	1	0	1	1	1	1	1	1	1
T	2	0	1						
G	3	0	1						
T	4	0	1						
T	5	0	1						
A	6	0	1						
T	7	0	1						

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

Alignment: Backtracking

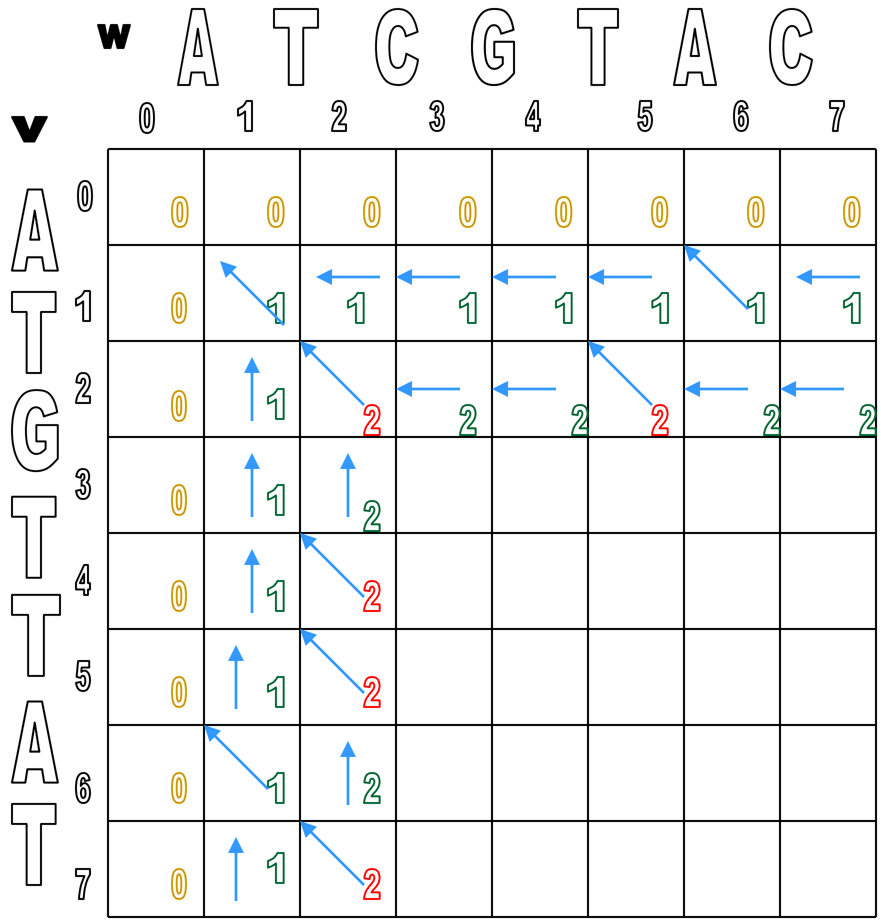
Arrows ↖ ↑ ← show where the score originated from.

↑ if from the top

← if from the left

↖ if $v_i = w_j$

Backtracking Example



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

Find a match in row and column 2.

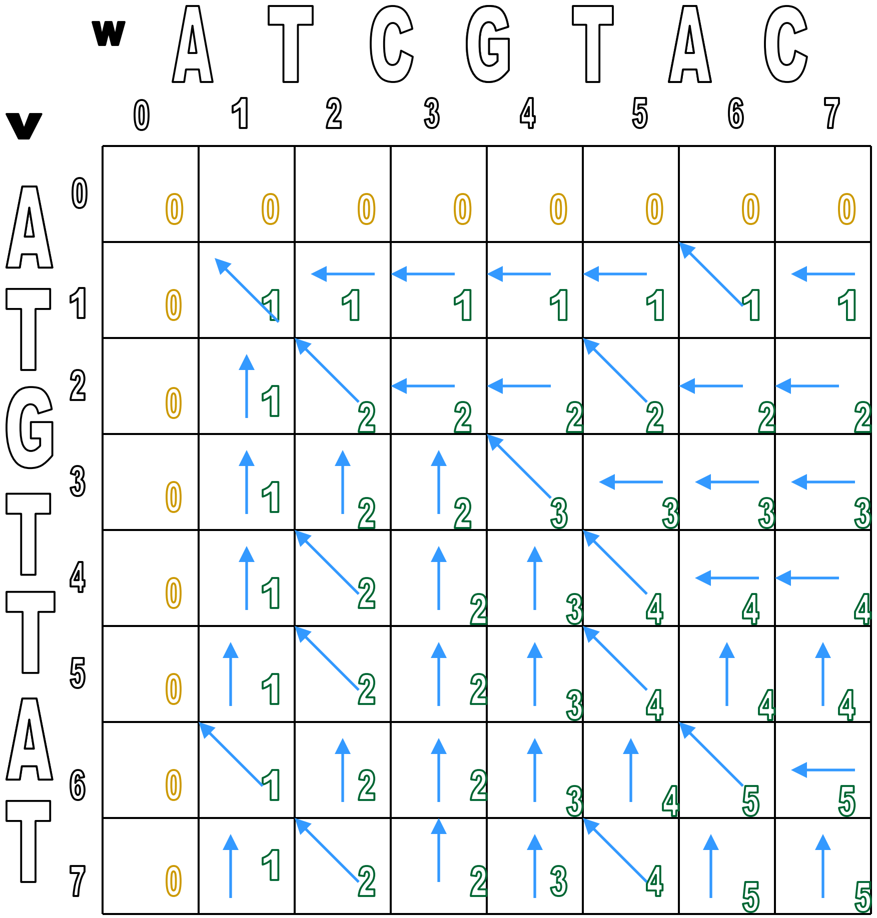
i=2, j=2,5 is a match (T).

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



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

Continuing with the dynamic programming algorithm gives this result.

Alignment: Dynamic Programming

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

Alignment: Dynamic Programming

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

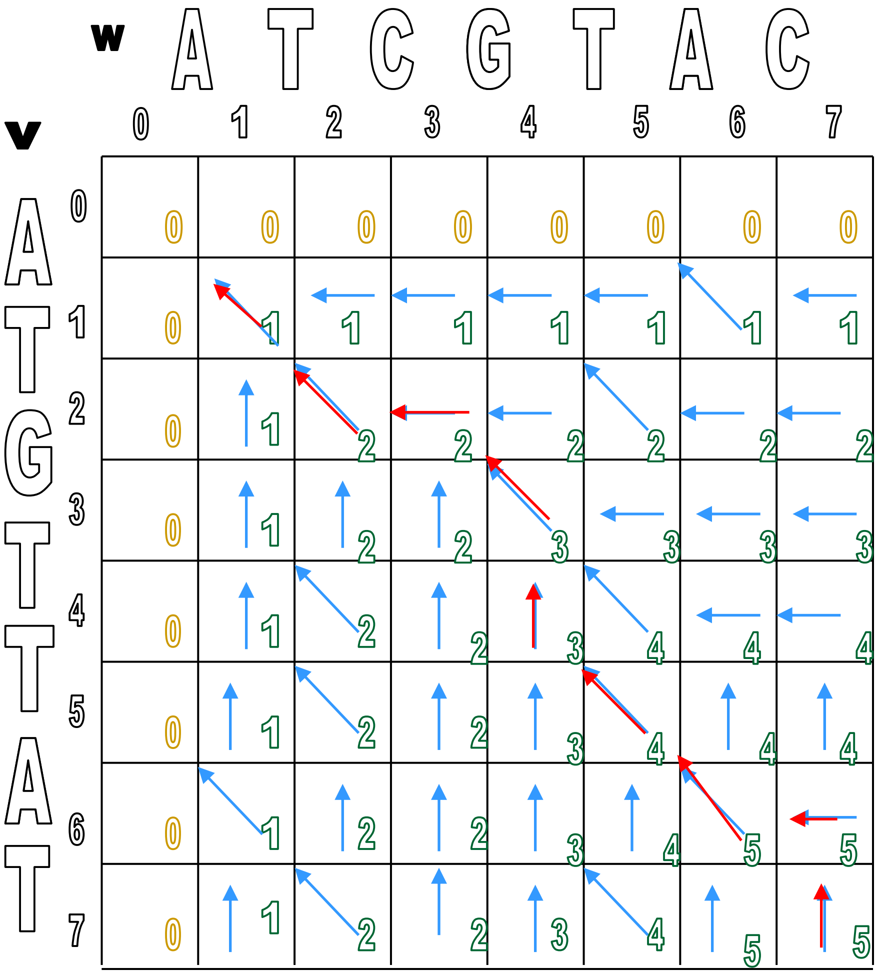
This recurrence corresponds to the Manhattan Tourist problem (three incoming edges into a vertex) with all horizontal and vertical edges weighted by zero.

LCS Algorithm

```
LCS(v,w)
    for $i \leftarrow 1$ to $n$
        $s_{i,0} \leftarrow 0$
    for j ← 1 to $m$
        $s_{0,j} \leftarrow 0$
    for $i \leftarrow 1$ to $n$
        for $j \leftarrow 1$ to $m$
            $s_{i,j} \leftarrow \max\begin{cases} s_{i-1,j} \\ s_{i,j-1} \\ s_{i-1,j-1} + 1, \text{ if } v_i = w_j \end{cases}$
            $b_{i,j} \leftarrow \begin{cases} \text{“ } \uparrow \text{ “} & \text{if } s_{i,j} = s_{i-1,j} \\ \text{“ } \leftarrow \text{ “} & \text{if } s_{i,j} = s_{i,j-1} \\ \text{“ } \nwarrow \text{ “} & \text{if } s_{i,j} = s_{i-1,j-1} + 1 \end{cases}$
    return ($s_{n,m}$, $\boldsymbol{b}$)
```

Now What?

- 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



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

Printing LCS: Backtracking

```
PrintLCS(b,v,$i$,$j$)
    if  $i = 0$ or $j = 0$
        return
    if $b_{i,j}$ = “ $\nwarrow$ “
         PrintLCS(b,v,$i-1$,$j-1$)
         print $v_i$
    else
        if $b_{i,j}$ = “ $\uparrow$ “
           PrintLCS(b,v,$i-1$,$j$)
        else
           PrintLCS(b,v,$i$,$j-1$)
```

LCS Runtime

- It takes O(nm) time to fill in the nxm dynamic programming matrix.

QUIZ 1

DNA mapping

$\Delta \boldsymbol{X} = \{0,1,2,3,3,5,5,7,8,8,10,12,13,13,15,16\}$

Use the partial digest algorithm to find *X*