

Dynamic Programming: String Comparison

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Algorithmic Toolbox
Data Structures and Algorithms

Cystic Fibrosis

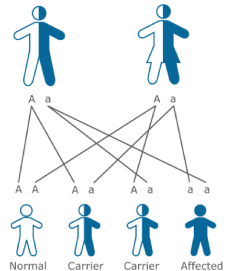
Cystic fibrosis (CF): An often fatal disease which affects the respiratory system and produces an abnormally large amount of mucus.

- Mucus is a slimy material that coats epithelial surfaces and is secreted into fluids such as saliva.



Approximately 1 in 25 Humans Carry a Faulty CF Gene

- When BOTH parent carry a faulty gene, there is a 25% chance that their child will have cystic fibrosis.
- In the early 1980s biologists hypothesized that CF is caused by mutations in an unidentified gene.



Where Is the Cystic Fibrosis Gene?

- In the late 1980s, biologists narrowed the search for the CF gene to a million nucleotide long region on chromosome 7.
- However, this regions contained many genes and it was unclear which of them was responsible for CF.



chromosome 7

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Hint 1: Cystic fibrosis involves sweet [secretion](#) with abnormally high sodium levels

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Hint 2: By that time biologists already knew the sequences of some genes responsible for secretion, e.g., **ATP binding proteins** act as transport channels responsible for [secretion](#)

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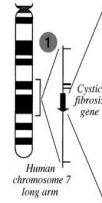
Hint 1: Cystic fibrosis involves sweet [secretion](#) with abnormally high sodium levels

Hint 2: By that time biologists already knew the sequences of some genes responsible for secretion, e.g., **ATP binding proteins** act as transport channels responsible for [secretion](#)

Hint 3: Should we search for genes in this region that are [similar](#) to known genes responsible for [secretion](#)?

Identifying the Cystic Fibrosis Gene

- BINGO: One of the genes in this region was **similar** to **ATP binding proteins** that act as transport channels responsible for **secretion**.



Hint 1: Cystic fibrosis involves sweet **secretion** with abnormally high sodium levels

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Hint 3: Should we search for genes in this region that are **similar** to known genes responsible for **secretion**?

Outline

- 1 The Alignment Game
- 2 Computing Edit Distance
- 3 Reconstructing an Optimal Alignment

The Alignment Game

A	T	G	T	T	A	T	A
A	T	C	G	T	C	C	

Alignment game: remove all symbols from two strings in such a way that the number of points is maximized:

Remove the 1st symbol from **both** strings:

- 1 point if the symbols match,

- 0 points if they don't match

Remove the 1st symbol from **one** of the strings:

- 0 points

The Alignment Game

A	T	G	T	T	A	T	A
A	T	C	G	T	C	C	
+1							

The Alignment Game

A	T	G	T	T	A	T	A
A	T	C	G	T	C	C	
+1	+1						

The Alignment Game

A	T	-	G	T	T	A	T	A
A	T	C	G	T	C	C		
+1	+1							

The Alignment Game

A	T	-	G	T	T	A	T	A
A	T	C	G	T	C	C		
+1	+1		+1					

The Alignment Game

A	T	-	G	T	T	A	T	A
A	T	C	G	T	C	C		
+1	+1		+1	+1				

The Alignment Game

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	C	
+1	+1		+1	+1				

The Alignment Game

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	C	
+1	+1		+1	+1				

The Alignment Game

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C
+1	+1		+1	+1				

The Alignment Game

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C
+1	+1		+1	+1				

The Alignment Game

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C
+1	+1		+1	+1				=4

Sequence Alignment

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C

Alignment of two strings is a two-row matrix:
1st row: symbols of the 1st string (in order)
interspersed by “-”
2nd row: symbols of the 2nd string (in order)
interspersed by “-”

Sequence Alignment

matches



A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C

Sequence Alignment

matches

mismatches

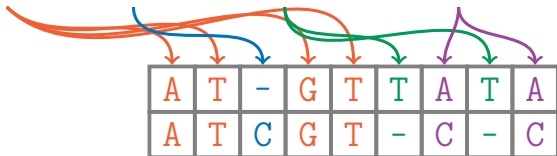


The diagram illustrates a sequence alignment between two DNA sequences. The top sequence is A T - G T T A T A and the bottom sequence is A T C G T - C - C. Arrows from the word 'matches' point to the first four columns (A-T, T-G, G-T, T-T), indicating identical base pairs. Arrows from the word 'mismatches' point to the last three columns (A-C, T-, A-C), indicating differences between the sequences. The hyphen in the top sequence at the sixth position indicates a gap.

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C

Sequence Alignment

matches insertions deletions mismatches



Alignment Score

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C

Alignment score: premium for every **match** ($+1$) and penalty for every **mismatch** ($-\mu$), **indel** ($-\sigma$).

Alignment Score

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C
+1	+1	-1	+1	+1	-1	+0	-1	+0

=1

Alignment score: premium for every **match** (+1) and penalty for every **mismatch** ($-\mu$), **indel** ($-\sigma$).

Example: $\mu = 0$ and $\sigma = 1$

Alignment Score

$$\text{\#matches} - \mu \cdot \text{\#mismatches} - \sigma \cdot \text{\#indels}$$

Optimal alignment

Input: Two strings, mismatch penalty μ , and indel penalty σ .

Output: An alignment of the strings maximizing the score.

Common Subsequence

A	T	-	G	T	T	A	T	A
A	T	C	G	T	-	C	-	C

Matches in an alignment of two strings
(ATGT) form their common subsequence

Longest common subsequence

Input: Two strings.

Output: A longest common subsequence of these strings.

Longest common subsequence

Input: Two strings.

Output: A longest common subsequence of these strings.

Maximizing the length of a common subsequence corresponds to maximizing the score of an alignment with $\mu = \sigma = 0$.

Edit distance

Input: Two strings.

Output: The minimum number of operations (insertions, deletions, and substitutions of symbols) to transform one string into another.

Edit distance

Input: Two strings.

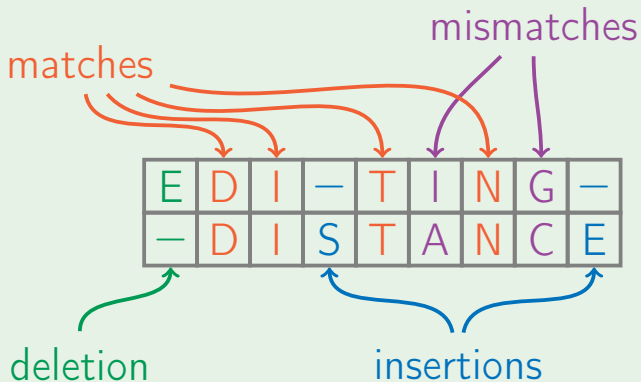
Output: The minimum number of operations (insertions, deletions, and substitutions of symbols) to transform one string into another.

The minimum number of insertions, deletions and mismatches in an alignment of two strings (among all possible alignments).

Example

E	D	I	-	T	I	N	G	-
-	D	I	S	T	A	N	C	E

Example



E	D	I	-	T	I	N	G	-
-	D	I	S	T	A	N	C	E

E	D	I	-	T	I	N	G	-
-	D	I	S	T	A	N	C	E

the total number of symbols in two strings=

E	D	I	-	T	I	N	G	-
-	D	I	S	T	A	N	C	E

the total number of symbols in two strings=

+2·#matches

+2·#mismatches

+1·#insertions

+1·#deletions

E	D	I	—	T	I	N	G	—
—	D	I	S	T	A	N	C	E

the total number of symbols in two strings=

$$\begin{array}{rcl}
 & +2 \cdot \text{\#matches} & \\
 +2 \cdot \text{\#matches} & & -1 \cdot \text{\#insertions} \\
 +2 \cdot \text{\#mismatches} & = & -1 \cdot \text{\#deletions} \\
 +1 \cdot \text{\#insertions} & & +2 \cdot \text{\#mismatches} \\
 +1 \cdot \text{\#deletions} & & +2 \cdot \text{\#insertions} \\
 & & +2 \cdot \text{\#deletions}
 \end{array}$$

E	D	I	-	T	I	N	G	-
-	D	I	S	T	A	N	C	E

the total number of symbols in two strings=

$$\begin{array}{rcl}
 +2 \cdot \# \text{matches} & +2 \cdot \# \text{matches} & \\
 +2 \cdot \# \text{mismatches} & -1 \cdot \# \text{insertions} & \\
 +1 \cdot \# \text{insertions} & -1 \cdot \# \text{deletions} & \\
 +1 \cdot \# \text{deletions} & +2 \cdot \# \text{mismatches} & \\
 & +2 \cdot \# \text{insertions} & \\
 & +2 \cdot \# \text{deletions} &
 \end{array}
 \left. \begin{array}{c} \\ \\ \\ \\ \\ \end{array} \right] \begin{array}{l} 2 \cdot \text{AlignmentScore} \\ (\mu = 0, \sigma = 1/2) \\ + \\ 2 \cdot \text{EditDistance} \end{array}$$

E	D	I	-	T	I	N	G	-
-	D	I	S	T	A	N	C	E

minimizing edit distance
=
maximizing alignment score

Outline

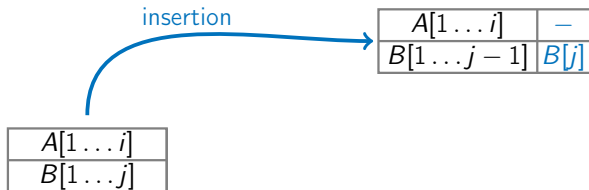
- 1 The Alignment Game
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$A[1 \dots i]$
$B[1 \dots j]$

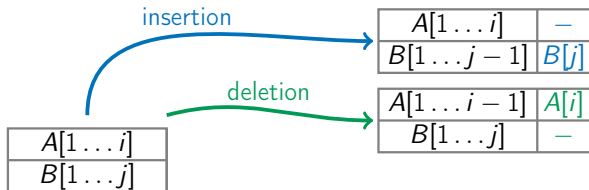
Given strings $A[1 \dots n]$ and $B[1 \dots m]$, what is an optimal alignment (an alignment that results in minimum edit distance) of an i -prefix $A[1 \dots i]$ of the first string and a j -prefix $B[1 \dots j]$ of the second string?

$A[1 \dots i]$
$B[1 \dots j]$

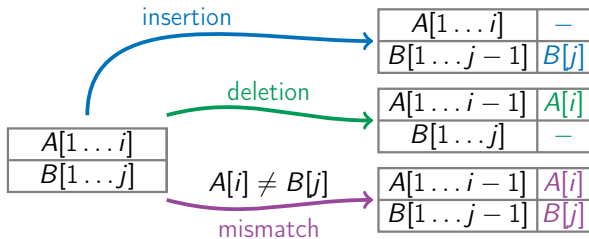
The last column of an optimal alignment is either



The last column of an optimal alignment is either
an **insertion**,

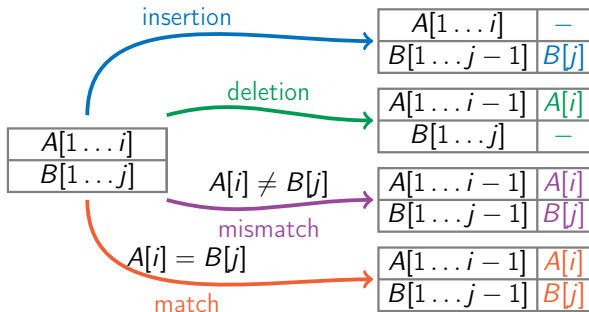


The last column of an optimal alignment is either
an insertion,
a deletion,



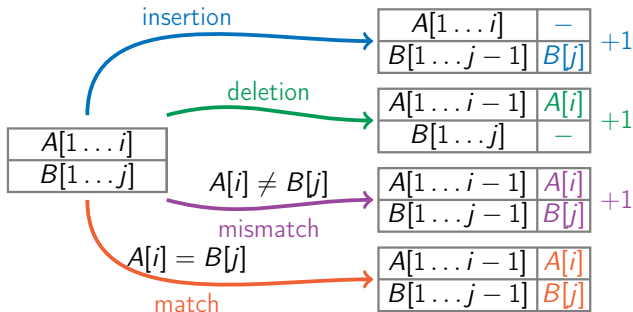
The last column of an optimal alignment is either

- an **insertion**,
- a **deletion**,
- a **mismatch**,



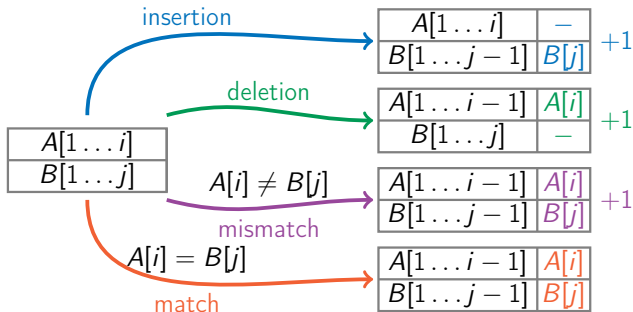
The last column of an optimal alignment is either

- an **insertion**,
- a **deletion**,
- a **mismatch**,
- or a **match**.

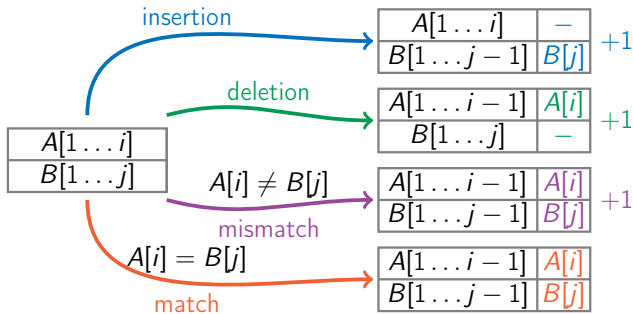


The last column of an optimal alignment is either
an **insertion**,
a **deletion**,
a **mismatch**,
or a **match**.

What is left (after the removal of the last column) is an **optimal** alignment of the corresponding two prefixes.



Let $D(i, j)$ be the edit distance of an i -prefix $A[1 \dots i]$ and a j -prefix $B[1 \dots j]$.



$$D(i, j) = \min \begin{cases} D(i, j-1) + 1 \\ D(i-1, j) + 1 \\ D(i-1, j-1) + 1 & \text{if } A[i] \neq B[j] \\ D(i-1, j-1) & \text{if } A[i] = B[j] \end{cases}$$

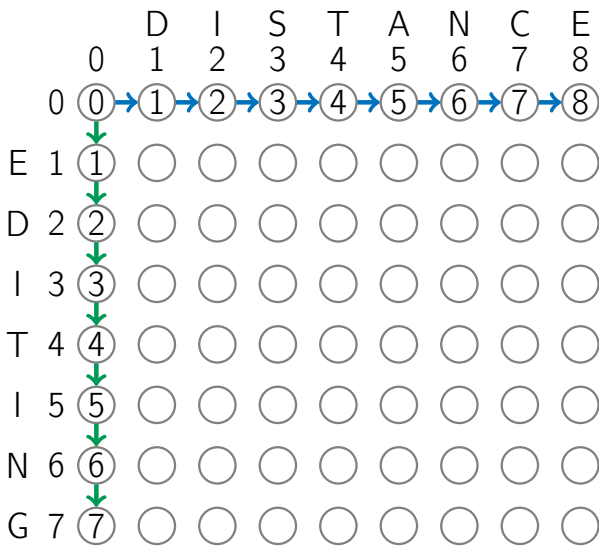
		<i>j</i>								
			D	I	S	T	A	N	C	E
		0	1	2	3	4	5	6	7	8
<i>i</i>	0	○	○	○	○	○	○	○	○	○
	E 1	○	○	○	○	○	○	○	○	○
	D 2	○	○	○	○	○	○	○	○	○
	I 3	○	○	○	○	○	○	○	○	○
	T 4	○	○	○	○	○	○	○	○	○
	I 5	○	○	○	○	○	○	○	○	○
	N 6	○	○	○	○	○	○	○	○	○
	G 7	○	○	○	○	○	○	○	○	○

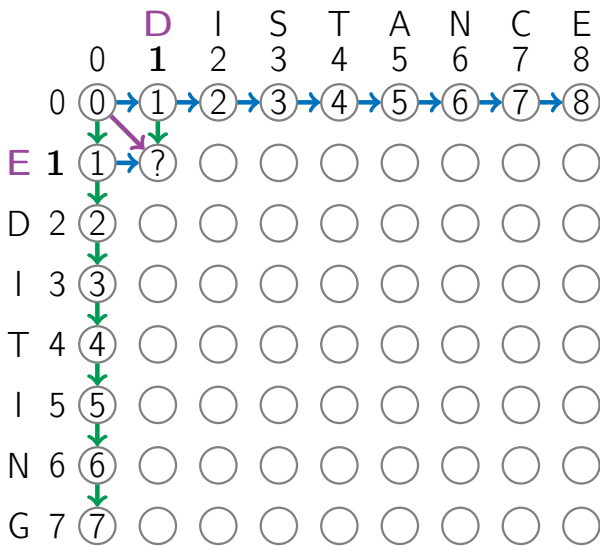
comparing $A[1 \dots n] = \text{EDITING}$
 and $B[1 \dots m] = \text{DISTANCE}$

		<i>j</i>								
			D	I	S	T	A	N	C	E
		0	1	2	3	4	5	6	7	8
0		○	○	○	○	○	○	○	○	○
E	1	○	○	○	○	○	○	○	○	○
D	2	○	○	○	○	○	○	○	○	○
I	3	○	○	○	○	○	○	○	○	○
<i>i</i> T	4	○	○	○	○	● $D(i,j)$	○	○	○	○
I	5	○	○	○	○	○	○	○	○	○
N	6	○	○	○	○	○	○	○	○	○
G	7	○	○	○	○	○	○	○	○	○

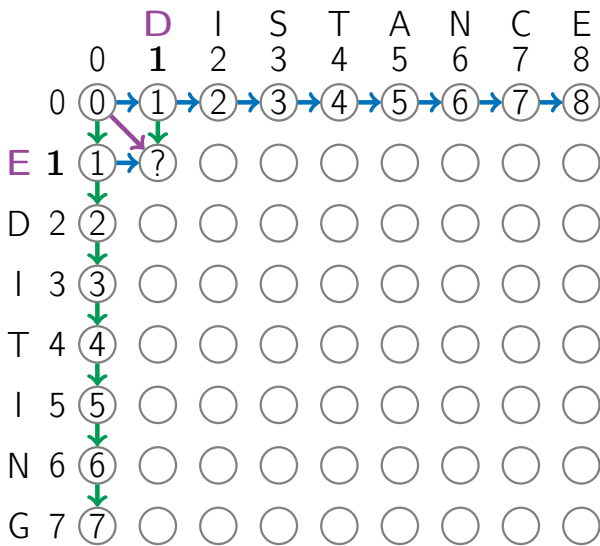
comparing $A[1 \dots n] = \text{EDITING}$
 and $B[1 \dots m] = \text{DISTANCE}$

		0	D 1	I 2	S 3	T 4	A 5	N 6	C 7	E 8
	0	0								
E	1	1								
D	2	2								
I	3	3								
T	4	4								
I	5	5								
N	6	6								
G	7	7								

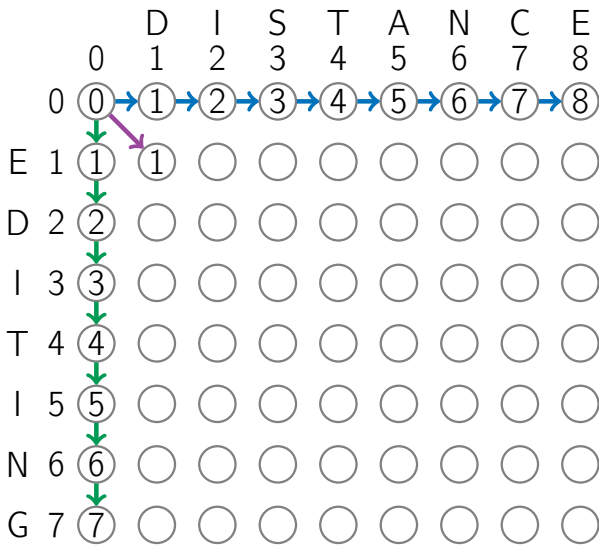


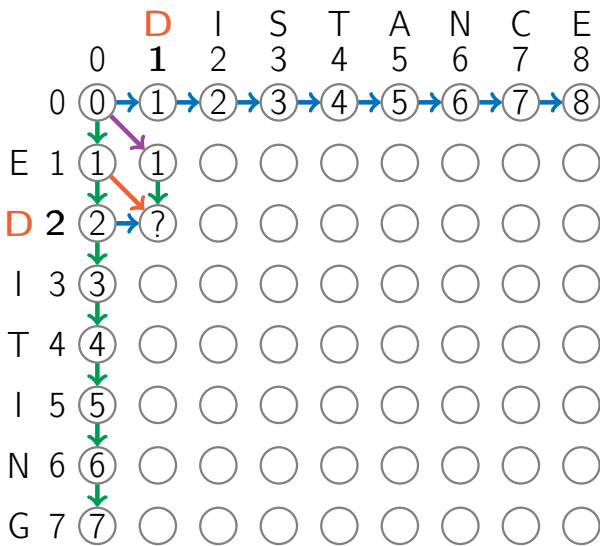


$$D(1, 1) = \min\{D(1, 0) + 1, D(0, 1) + 1, D(0, 0) + 1\}$$

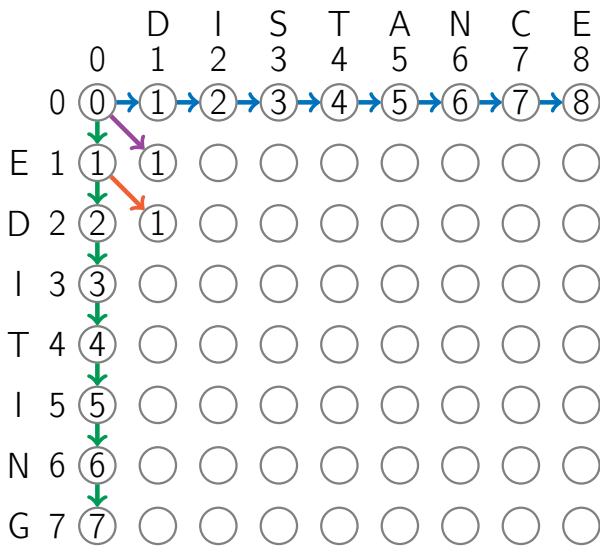


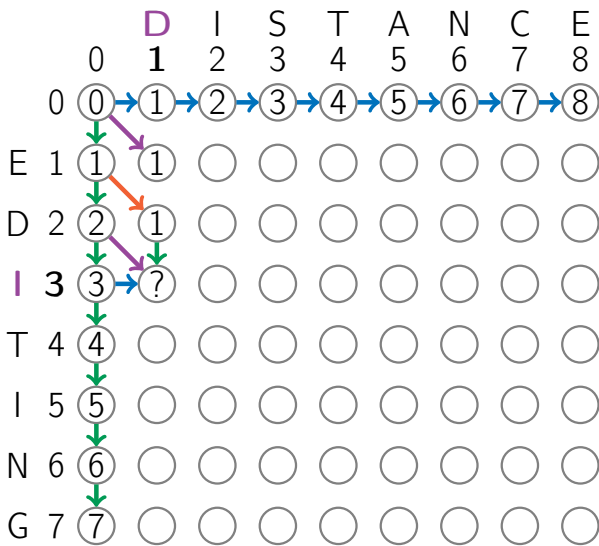
$$D(1, 1) = \min\{2, 2, 1\}$$



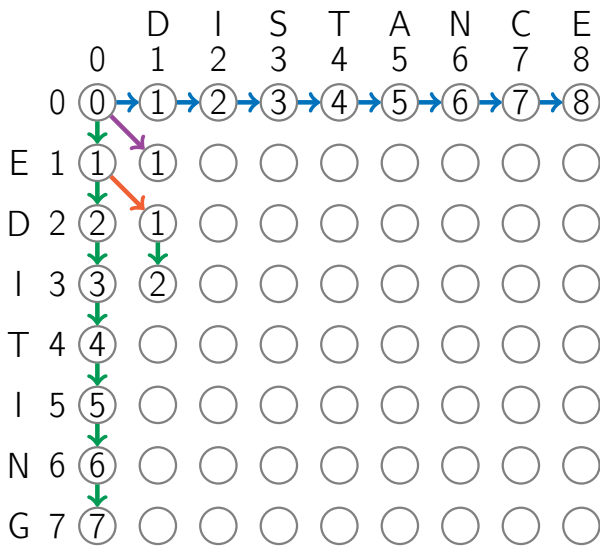


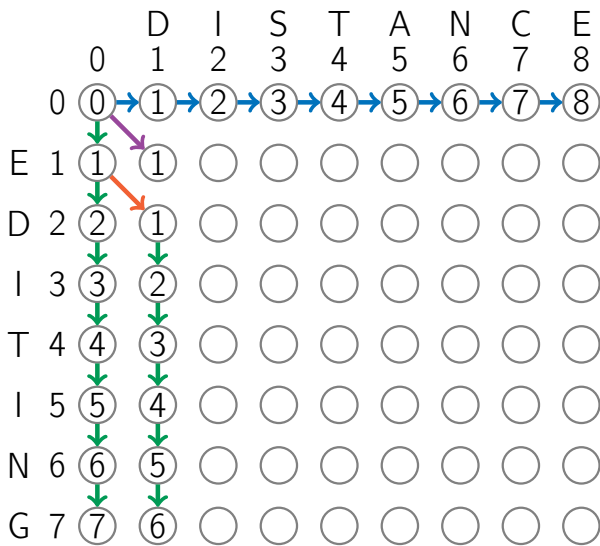
$$D(2, 1) = \min\{D(2, 0) + 1, D(1, 1) + 1, D(1, 0)\}$$

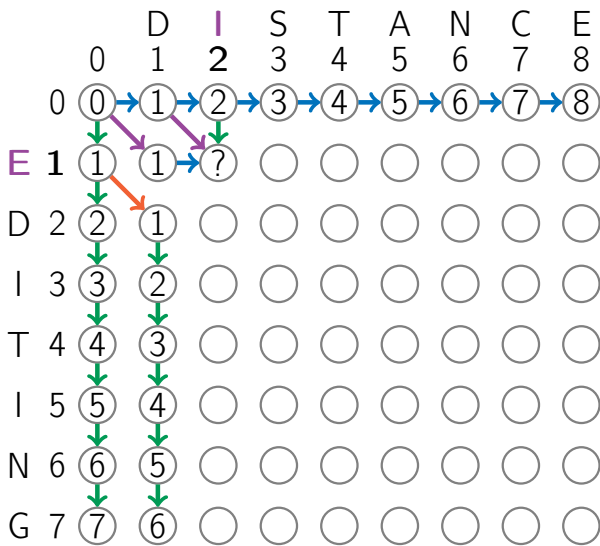




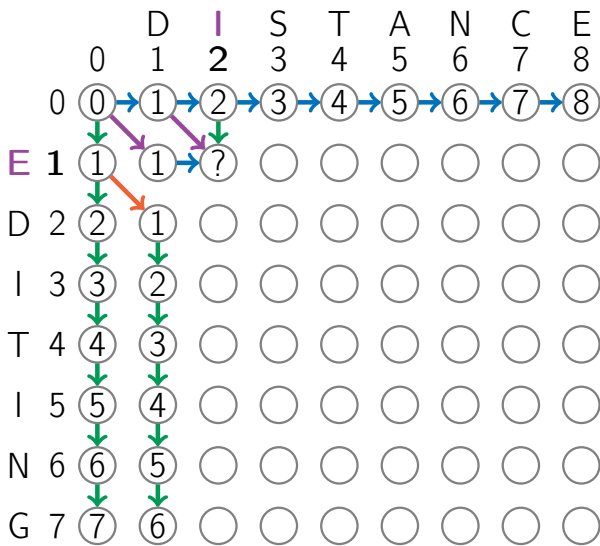
$$D(3, 1) = \min\{D(3, 0) + 1, D(2, 1) + 1, D(2, 0) + 1\}$$



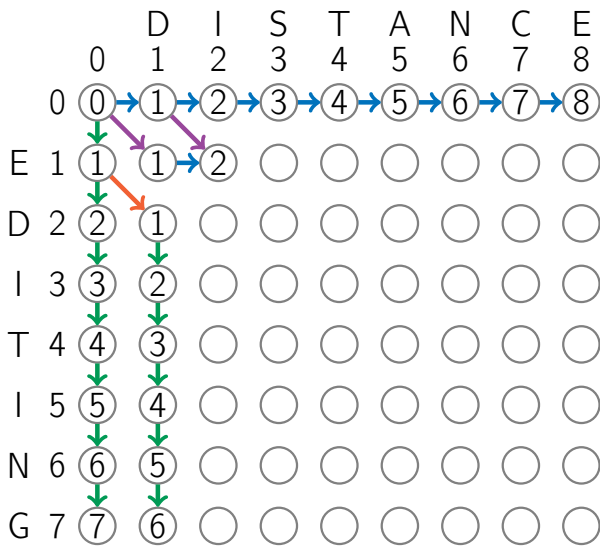


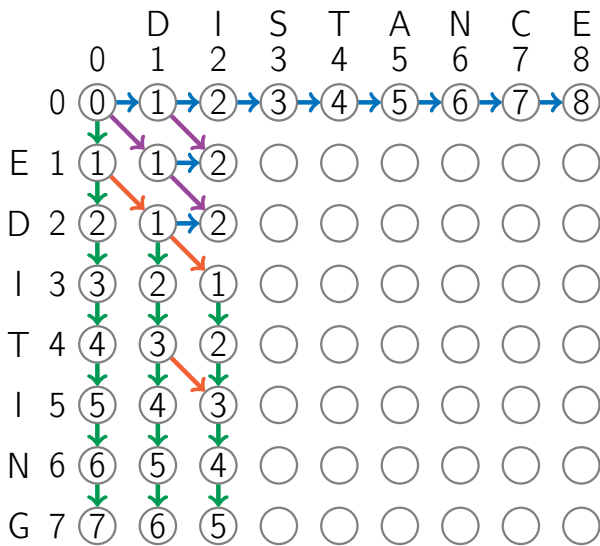


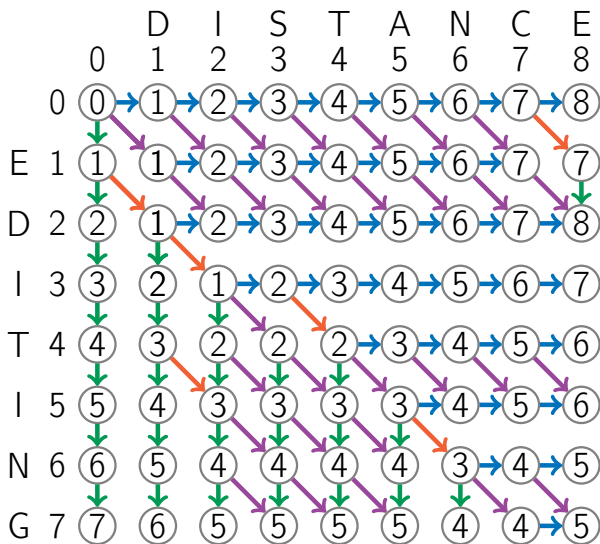
$$D(1, 2) = \min\{D(1, 1) + 1, D(0, 2) + 1, D(0, 1) + 1\}$$



$$D(1, 1) = \min\{2, 3, 2\}$$







EditDistance($A[1 \dots n], B[1 \dots m]$)

$D(i, 0) \leftarrow i$ and $D(0, j) \leftarrow j$ for all i, j

for j from 1 to m :

for i from 1 to n :

insertion $\leftarrow D(i, j - 1) + 1$

deletion $\leftarrow D(i - 1, j) + 1$

match $\leftarrow D(i - 1, j - 1)$

mismatch $\leftarrow D(i - 1, j - 1) + 1$

if $A[i] = B[j]$:

$D(i, j) \leftarrow \min(\textit{insertion}, \textit{deletion}, \textit{match})$

else:

$D(i, j) \leftarrow \min(\textit{insertion}, \textit{deletion}, \textit{mismatch})$

return $D(n, m)$

Outline

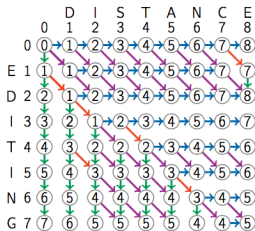
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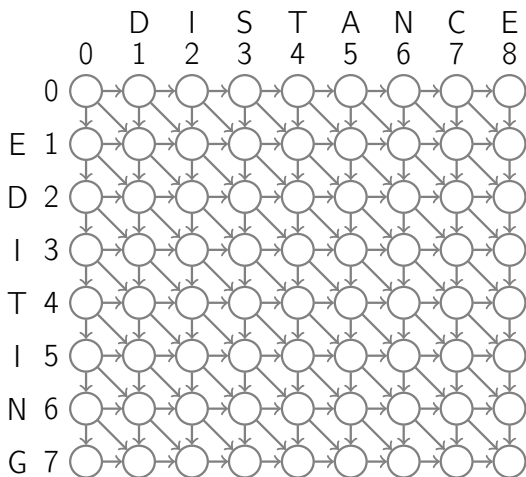
Optimal Alignment

- We have computed the edit distance, but how can we find an optimal alignment?

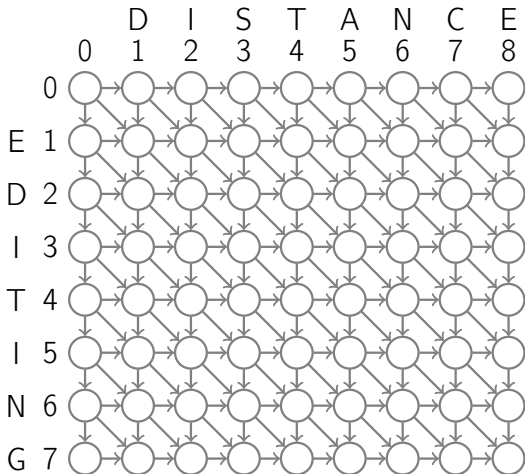
Optimal Alignment

- We have computed the edit distance, but how can we find an optimal alignment?
- The backtracking pointers that we stored will help us to reconstruct an optimal alignment.

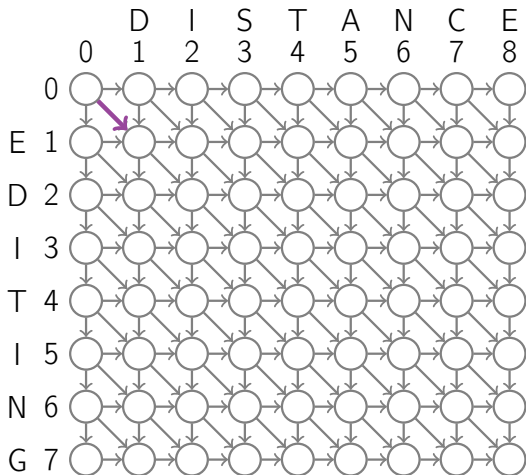




any path from
(0, 0) to (i, j)
spells an align-
ment of prefixes
 $A[1 \dots i]$ and
 $B[1 \dots j]$

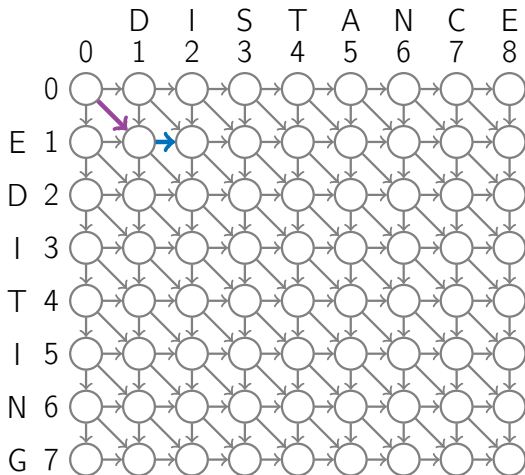


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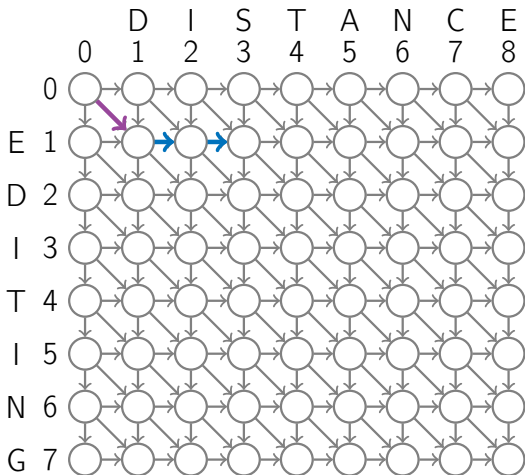


E
D

any path from
 $(0, 0)$ to (i, j)
 spells an alignment of prefixes
 $A[1 \dots i]$ and
 $B[1 \dots j]$

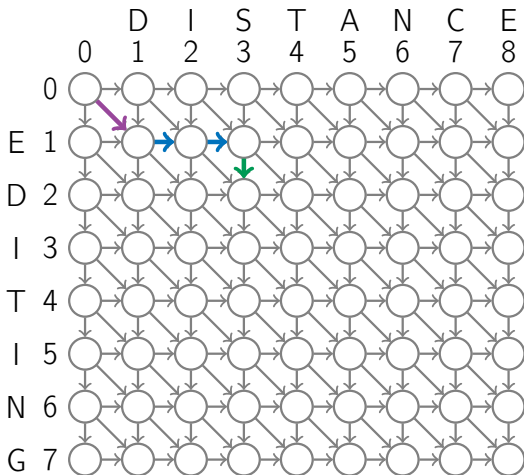


any path from
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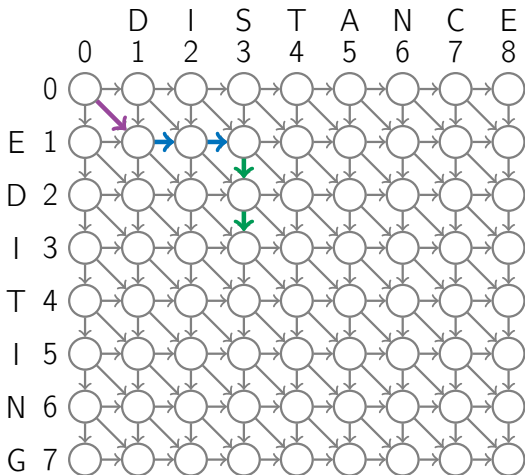
E	—	—
D	I	S

any path from
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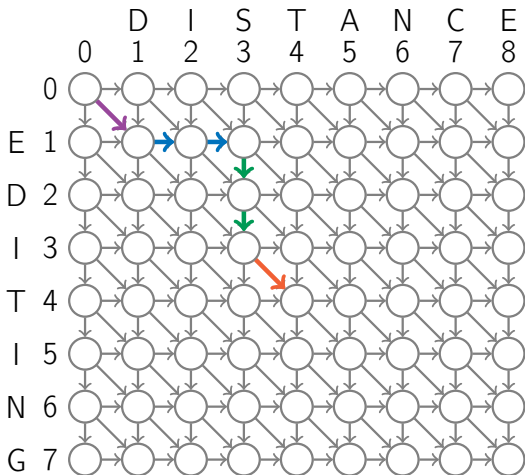
E	—	—	D
D	I	S	—

any path from
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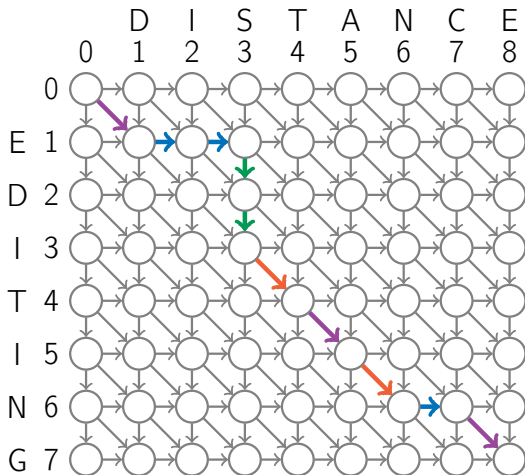
E	—	—	D	I
D	I	S	—	—

any path from
 $(0, 0)$ to (i, j)
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 ment of prefixes
 $A[1 \dots i]$ and
 $B[1 \dots j]$



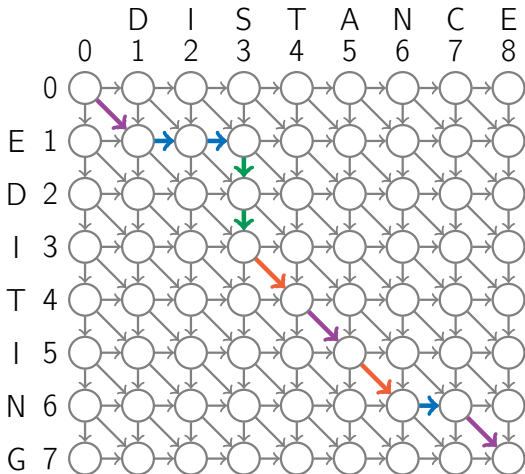
E	—	—	D	I	T
D	I	S	—	—	T

any path from
 $(0, 0)$ to (i, j)
 spells an align-
 ment of prefixes
 $A[1 \dots i]$ and
 $B[1 \dots j]$



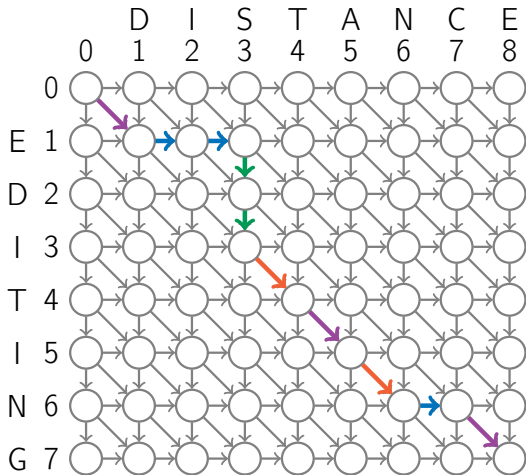
E	—	—	D	I	T	I	N	—	G
D	I	S	—	—	T	A	N	C	E

the constructed
path corresponds
to distance 8 and
is not optimal
(edit distance is 5)

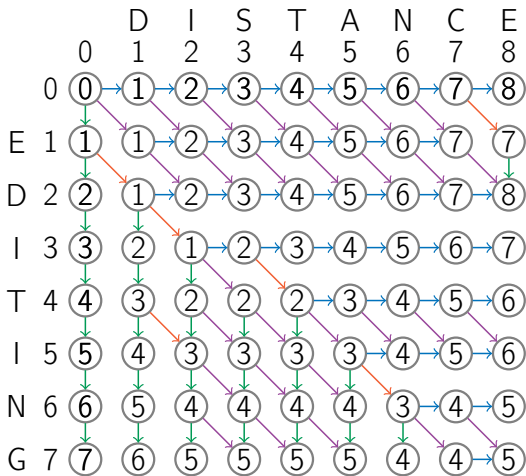


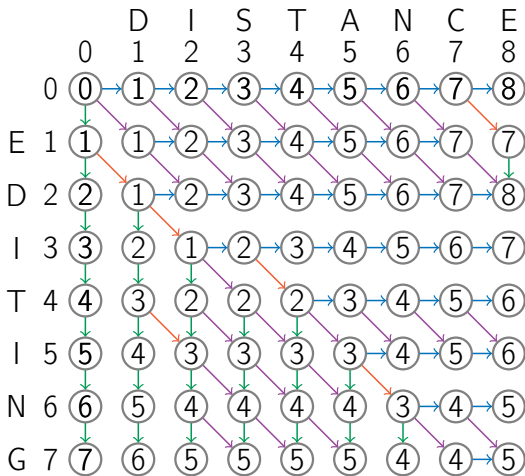
E	—	—	D	I	T	I	N	—	G
D	I	S	—	—	T	A	N	C	E

to construct an
optimal align-
ment we will use
the backtracking
pointers

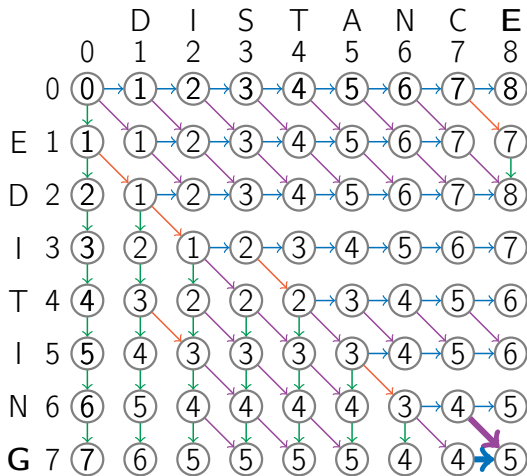


E	-	-	D	I	T	I	N	-	G
D	I	S	-	-	T	A	N	C	E

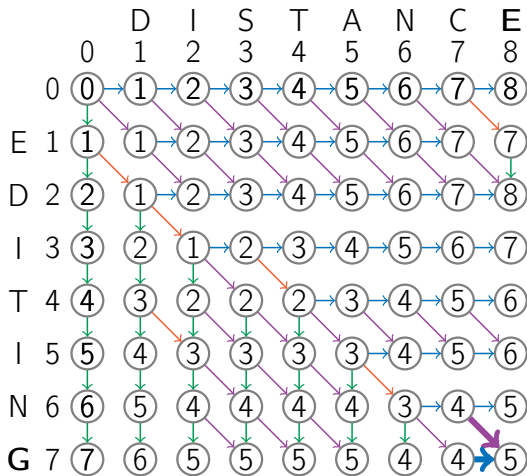




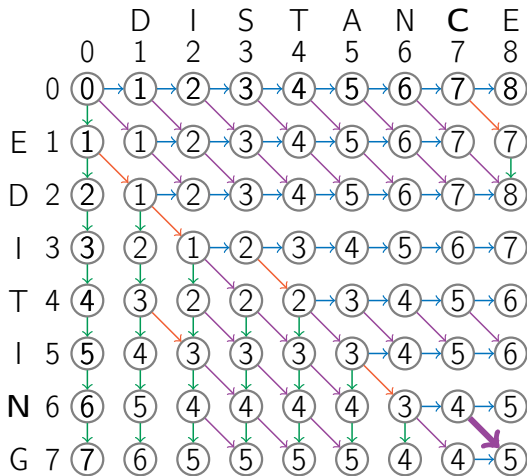
the edit distance
is 5



we arrived to the bottom right cell by moving along the backtracking pointers shown below

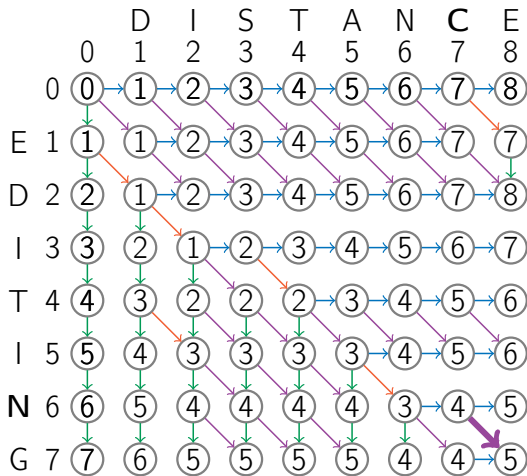


there exists an optimal alignment whose last column is a **mismatch** and an optimal alignment whose last column is an **insertion**



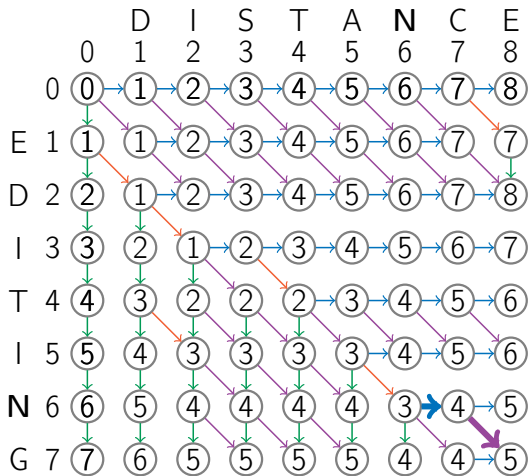
let's consider a
mismatch

G
E

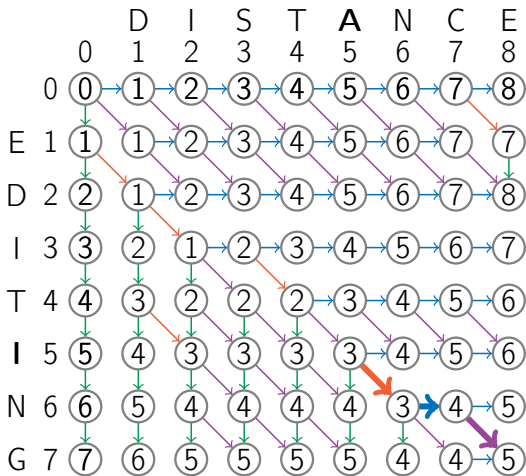


we continue in a similar fashion

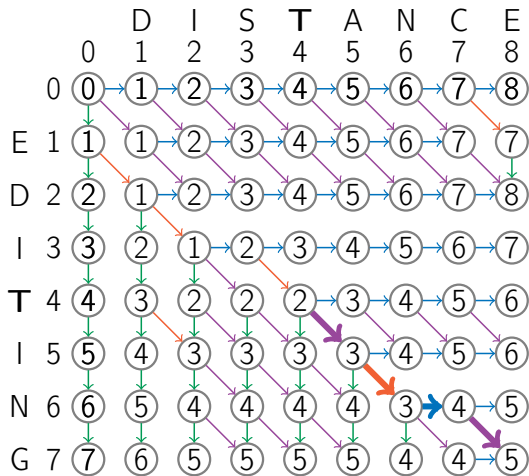
G
E



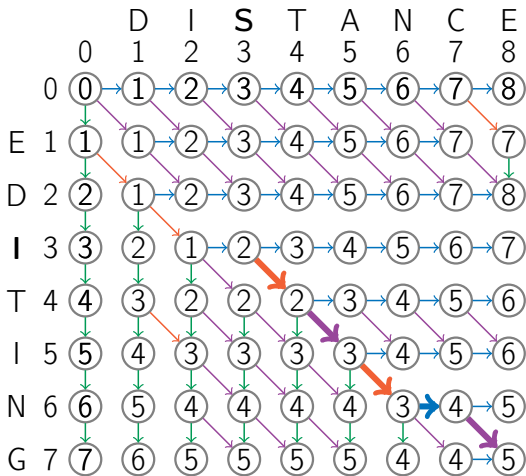
—	G
C	E



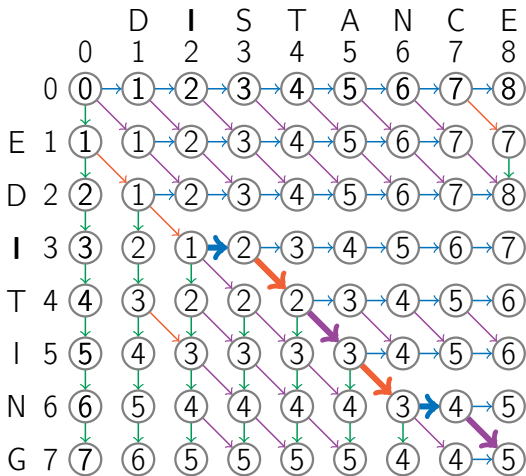
N	—	G
N	C	E



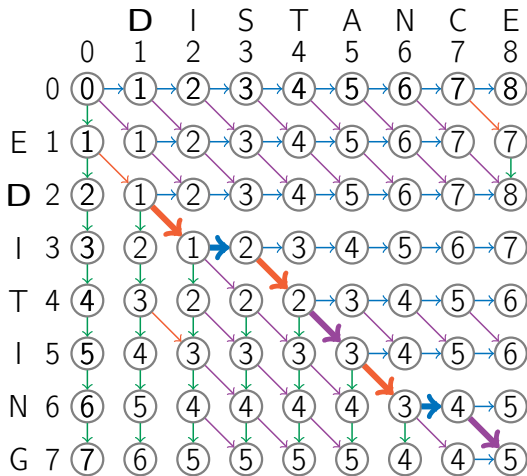
I	N	—	G
A	N	C	E



T	I	N	-	G
T	A	N	C	E

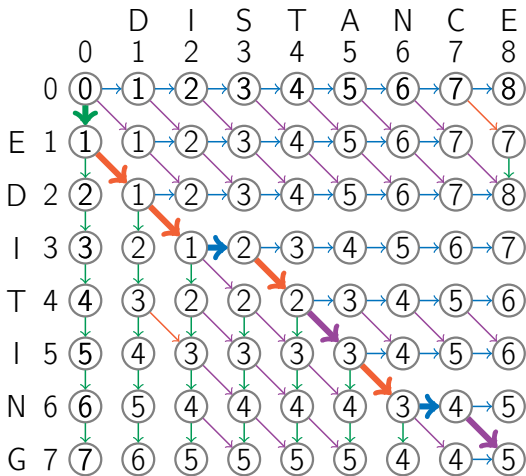


—	T	I	N	—	G
S	T	A	N	C	E



I	-	T	I	N	-	G
I	S	T	A	N	C	E





E	D	I	-	T	I	N	-	G
-	D	I	S	T	A	N	C	E

OutputAlignment(i, j)

```
if  $i = 0$  and  $j = 0$ :  
    return  
if  $\text{backtrack}(i, j) = \downarrow$ :  
    OutputAlignment( $i - 1, j$ )  
    print 

|        |
|--------|
| $A[i]$ |
| —      |

  
else if  $\text{backtrack}(i, j) = \rightarrow$ :  
    OutputAlignment( $i, j - 1$ )  
    print 

|        |
|--------|
| —      |
| $B[j]$ |

  
else:  
    OutputAlignment( $i - 1, j - 1$ )  
    print 

|        |
|--------|
| $A[i]$ |
| $B[j]$ |


```

OutputAlignment(i, j)

```
if  $i = 0$  and  $j = 0$ :  
    return  
if  $i > 0$  and  $D(i, j) = D(i - 1, j) + 1$ :  
    OutputAlignment( $i - 1, j$ )  
    print 

|        |
|--------|
| $A[i]$ |
| —      |

  
else if  $j > 0$  and  $D(i, j) = D(i, j - 1) + 1$ :  
    OutputAlignment( $i, j - 1$ )  
    print 

|        |
|--------|
| —      |
| $B[j]$ |

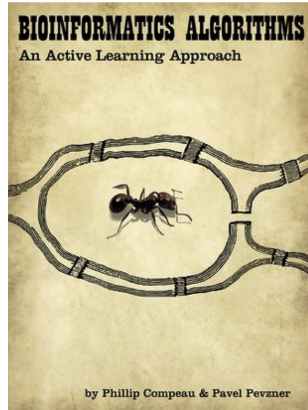
  
else:  
    OutputAlignment( $i - 1, j - 1$ )  
    print 

|        |
|--------|
| $A[i]$ |
| $B[j]$ |


```



Comparing Genes, Proteins, and Genomes MOOC (a part of Bioinformatics Specialization on Coursera)



Bioinformatics Algorithms textbook at bioinformaticsalgorithms.org (2nd two-volume edition was published in 2015)