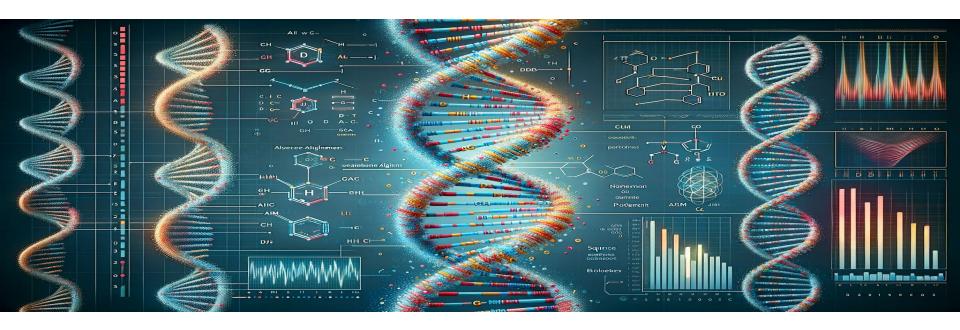
CSE7850/CX4803 Machine Learning in Computational Biology

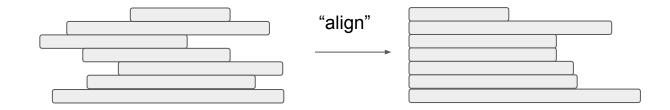


Lecture 3: Sequence Alignment

Yunan Luo

What is "alignment"





source

Alignment of protein/DNA sequences?

Given a set of sequences:

ACTCGCAATATGC
CTCCAATATGC
ATCGCTATATGC
ACTGATTAC
ACTCAATATGC
TCGAATATGC

Sequence alignment is not only about this:

ACTCGCAATATGC
CTCCAATATGC
ATCGCTATATGC
ACTGATTAC
ACTCAATATGC
TCGAATATGC

Sequence alignment is more like this:

ACTCGCAATATGC
-CTC-CAATATGC
A-TCGCTATATGC
ACT-G-ATTA--C
ACT--CAATATGC
--TCG-AATATGC

Any patterns?

Alignment of protein/DNA sequences?

Given a set of sequences:

ACTCGCAATATGC
CTCCAATATGC
ATCGCTATATGC
ACTGATTAC
ACTCAATATGC
TCGAATATGC

Sequence alignment is not only about this:

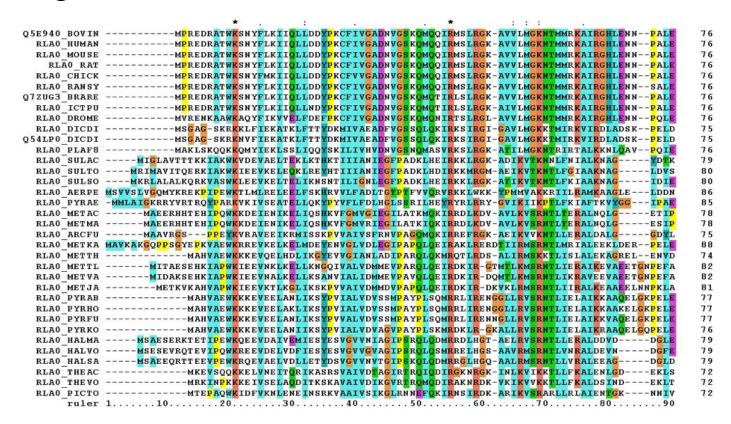
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CTCCAATATGC
ATCGCTATATGC
ACTGATTAC
ACTCAATATGC
TCGAATATGC

Sequence alignment is more like this:

ACTCGCAATATGC
-CTC-CAATATGC
A-TCGCTATATGC
ACT-G-ATTA--C
ACT--CAATATGC
--TCG-AATATGC

Any patterns?

A real alignment



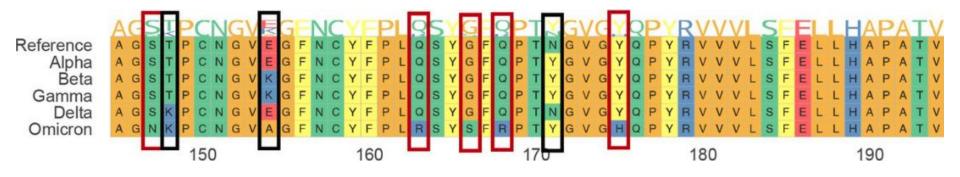
Why alignments?

Example #1: reconstructing phylogenetic tree of species Monotremata -Marsupialia -Xenarthra Insectivora -Rodentia -Lagomorpha Macroscelidea SEQUENCE_1 MADTTA - AGI -Scandentia SEQUENCE_2 MADTT - - AG Archonta Primates SEQUENCE_3 MAETTA - AGIIFY - Dermoptera Chiroptera SEQUENCE 4 MAESTAAAGLLFY-Pholidota SEQUENCE_5 MAESTA - AGLIFY Carnivora -Tubulidentata Cetacea

> - Artiodactyla - Perissodactyla - Hyracoidea - Proboscidea - Sirenia

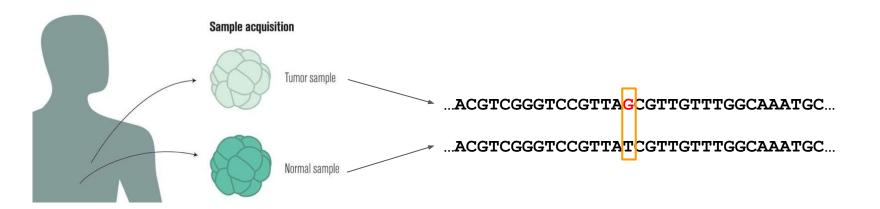
Why alignments?

Example #2: comparing different COVID-19 variants



Why alignments?

Example #3: identifying disease variants



"Goodness" of alignments

Given two sequences:

ATTTTCCC ATTTACGC

There are many possible alignments: which one is better?

ATTTTCCC ATTTACGC ATTT-TCCC ATTTA-CGC ATTTTCCC-----

Edit distance: the total number of substitutions, insertions and deletions needed to transform one sequence to another

"Goodness" of alignments

Given two sequences:

ATTTTCCC ATTTACGC

There are many possible alignments: which one is better?

ATTTTCCC ATTTACGC

Edit distance=2

ATTT-TCCC
ATTTA-CGC

Edit distance=3

ATTTTCCC-----

Edit distance=16

Edit distance: the total number of substitutions, insertions and deletions needed to transform one sequence to another

Edit distance (Levenshtein, 1966)

Elementary operations: insertion, deletions and substitutions of single characters



Vladimir I. Levenshtein (1935 - 2017)

Edit Distance problem: Given strings $\mathbf{v} \in \Sigma^{m}$ and $\mathbf{w} \in \Sigma^{m}$, compute the minimum number $d(\mathbf{v}, \mathbf{w})$ of elementary operations to transform \mathbf{v} into \mathbf{w} .

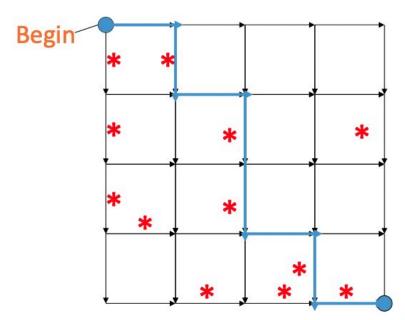
$$d(cat, car) = 1$$
 $d(cat, ate) = 2$ $d(cat, are) = 3$

How to compute the edit distance?

```
d( SYKVKLITPDGPIEFDCPDD,
    AYKVTLVTPEGKQELECPDD ) = ?
```

Manhattan Tourist Problem

A tourist in Manhattan
wants to visit the
maximum number of
attractions (*) by
traveling on a path (only
eastward and southward)
from start to end

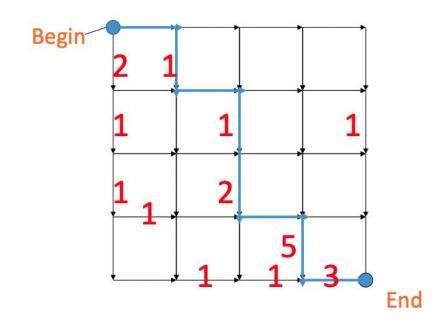


End

Manhattan Tourist Problem

A tourist in Manhattan
wants to visit the
maximum number of
attractions (*) by
traveling on a path (only
eastward and southward)
from start to end

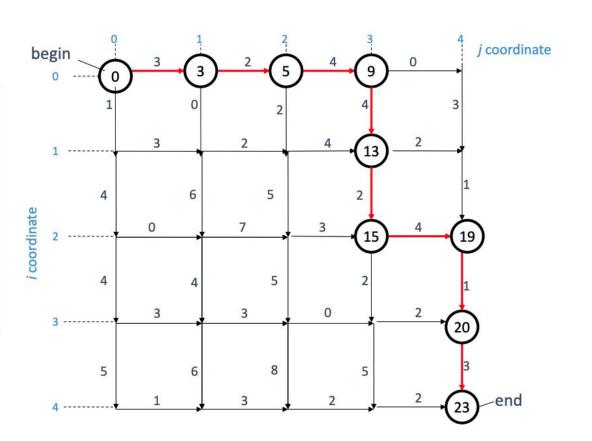
May be more than 1 attraction on a street. Add weights!



Manhattan Tourist Problem

Manhattan Tourist Problem (MTP):

Given a weighted, directed grid graph G with two vertices "begin" and "end", find the maximum weight path in G from "begin" to "end".

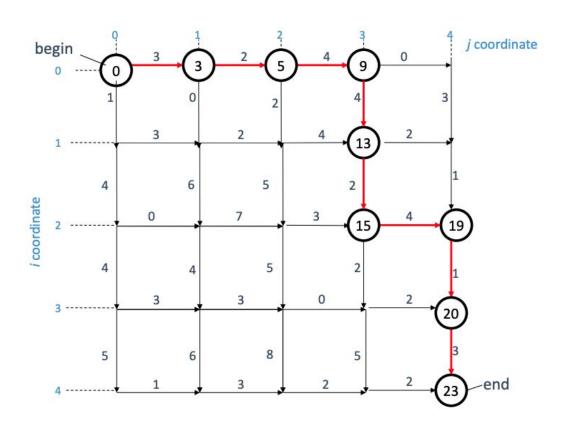


Solution - Exhaustive algorithm

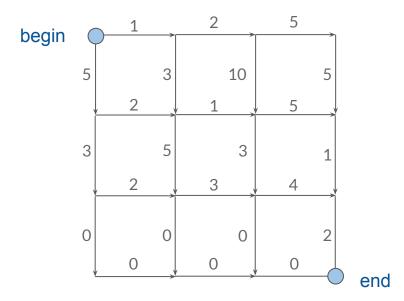
Check all paths

Question:

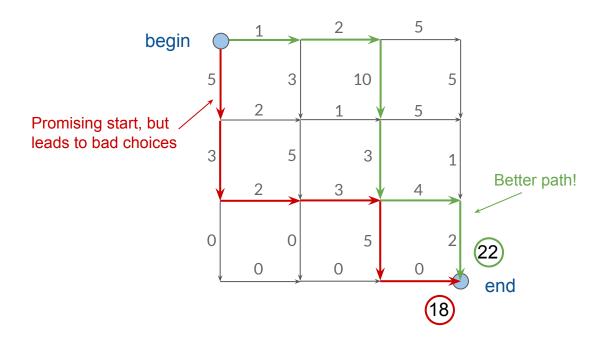
How many paths?



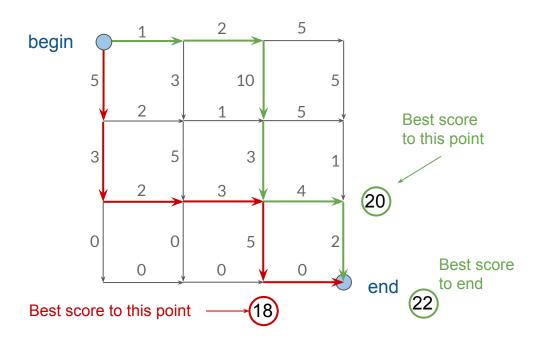
Solution - Greedy Algorithm



Solution - Greedy Algorithm



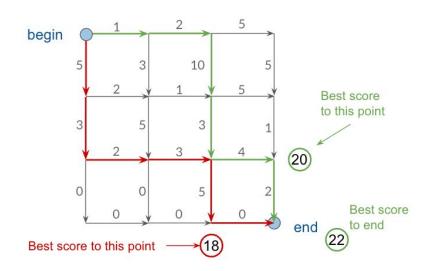
Optimal substructure



Optimal substructure

s[i, j] is the best score for path to coordinate (i, j)

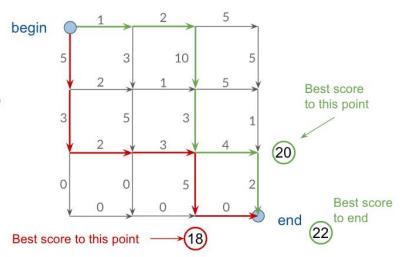
Question: What is the recurrence?



- w[(i-1,j),(i,j)] is weight of street between (i-1,j) and (i,j)
- w[(i, j-1), (i, j)] is weight of street between (i, j-1) and (i, j)

Optimal substructure

$$s[i,j] = \max \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ s[i-1,j] + w[(i-1,j),(i,j)] & \text{if } i > 0, \\ s[i,j-1] + w[(i,j-1),(i,j)] & \text{if } j > 0. \end{cases}$$

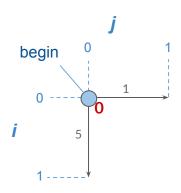


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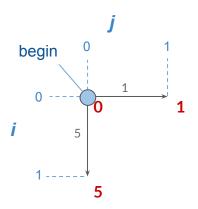
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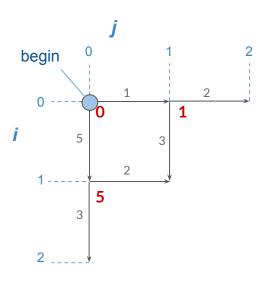
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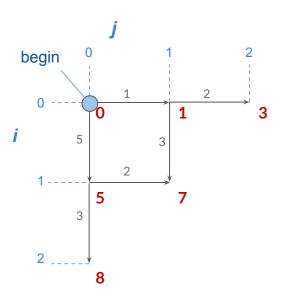
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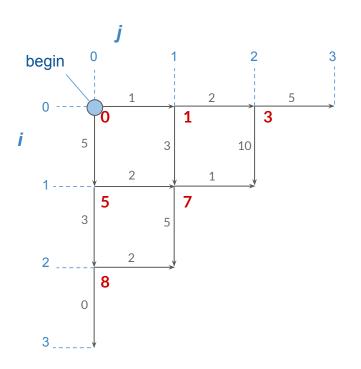
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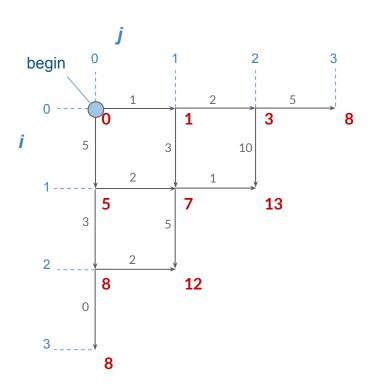
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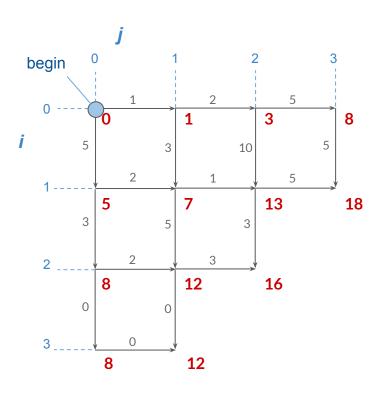
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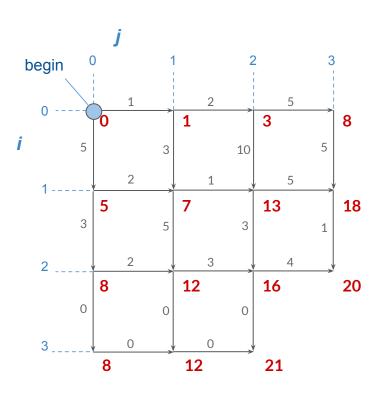
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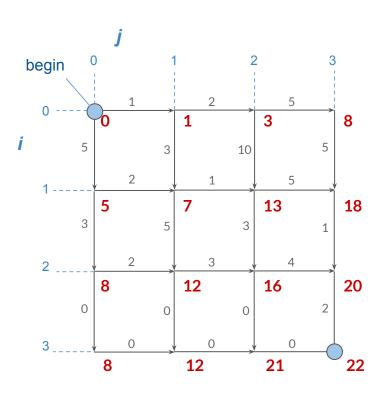
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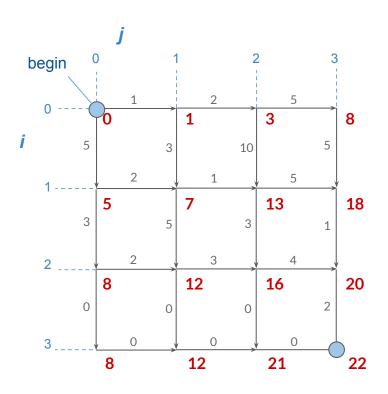
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Let *m* be the number of rows and *n* be the number of columns.

Running time: O(mn)

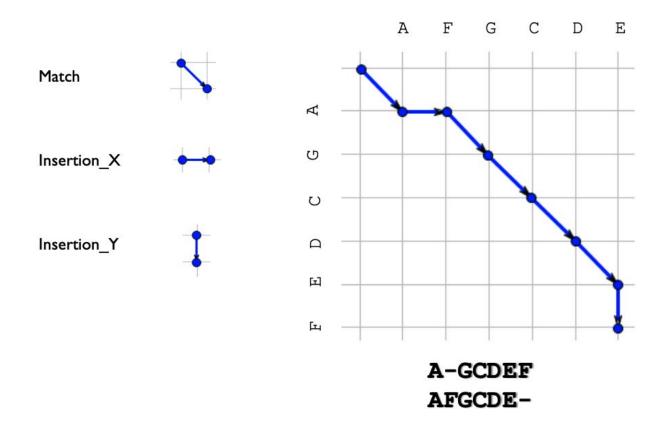
Recipe

1. Identify subproblems

2. Write down recursions

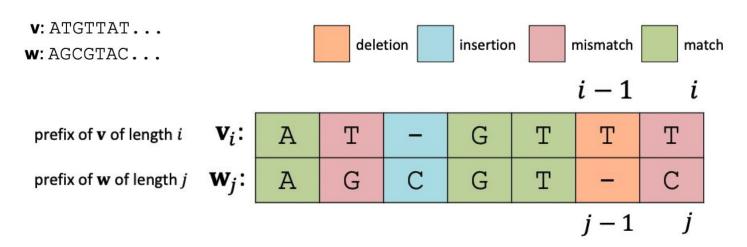
3. Make it dynamic-programming!

The edit distance problem



Compute edit distance

Edit Distance problem: Given strings $\mathbf{v} \in \Sigma^m$ and $\mathbf{w} \in \Sigma^n$, compute the minimum number $d(\mathbf{v}, \mathbf{w})$ of elementary operations to transform \mathbf{v} into \mathbf{w} .



Optimal substructure:

Edit distance obtained from edit distance of prefix of string.

Compute edit distance - Optimal substructure

d[i,j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

d[i,j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

Deletion: d[i, j] = ?

Extend by a character in v

| ••• | \mathbf{v}_i |
|-----|----------------|
| | 1 |

d[i, j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

Deletion: d[i,j] = d[i-1,j] + 1Extend by a character in **v**

| ••• | \mathbf{v}_i |
|-----|----------------|
| ••• | - |

d[i, j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

Deletion: d[i,j] = d[i-1,j] + 1Extend by a character in **v**

Insertion: d[i,j] = ?

Extend by a character in w

| ••• | \mathbf{v}_i |
|-----|----------------|
| ••• | 1 |



d[i, j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

Deletion: d[i,j] = d[i-1,j] + 1Extend by a character in **v**

v ...

Insertion: d[i, j] = d[i, j - 1] + 1

Extend by a character in ${\bf w}$



 \mathbf{v}_i

d[i, j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

Deletion: d[i,j] = d[i-1,j] + 1Extend by a character in **v**

Insertion: d[i,j] = d[i,j-1] + 1Extend by a character in **w**

Mismatch: d[i,j] = ?

Extend by a character in ${f v}$ and ${f w}$

| ••• | \mathbf{v}_i | | |
|-----|----------------|--|--|
| ••• | _ | | |





d[i, j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

> **Deletion:** d[i,j] = d[i-1,j] + 1Extend by a character in **v**

... **v**_i

Insertion: d[i,j] = d[i,j-1] + 1Extend by a character in **w** ... -... **w**_j

Mismatch: d[i,j] = d[i-1,j-1] + 1Extend by a character in \mathbf{v} and \mathbf{w} $egin{array}{c|c} \mathbf{w}_i & \mathbf{v}_i \\ \mathbf{w}_j & \mathbf{v}_j \end{array}$

d[i, j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

Deletion: d[i,j] = d[i-1,j] + 1

Extend by a character in ${f v}$

... **v**_i

Insertion: d[i, j] = d[i, j - 1] + 1

Extend by a character in w

... -... **w**_j

Mismatch: d[i,j] = d[i-1,j-1] + 1

Extend by a character in ${f v}$ and ${f w}$

 \mathbf{w}_i \mathbf{v}_i \mathbf{w}_j

Match: d[i,j] = ?

Extend by a character in **v** and **w**

... **v**_i

d[i, j] is the edit distance of \mathbf{v}_i and \mathbf{w}_j , where \mathbf{v}_i is prefix of \mathbf{v} of length i and \mathbf{w}_j is prefix of \mathbf{w} of length j

Deletion: d[i,j] = d[i-1,j] + 1

Extend by a character in ${f v}$

... **v**_i

 $\textbf{Insertion:}\ d[i,j] = d[i,j-1] + 1$

Extend by a character in w

... -... **w**_j

Mismatch: d[i,j] = d[i-1,j-1] + 1

Extend by a character in ${\bf v}$ and ${\bf w}$

 \mathbf{w}_i \mathbf{v}_i \mathbf{w}_j

Match: d[i,j] = d[i-1,j-1]

Extend by a character in ${\boldsymbol v}$ and ${\boldsymbol w}$

... **v**_i

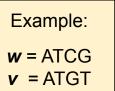
Compute edit distance - Recurrence

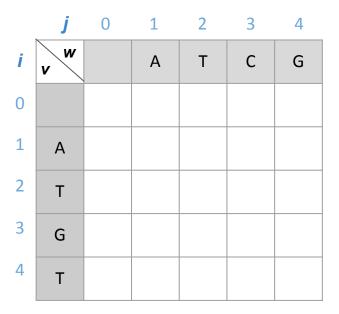
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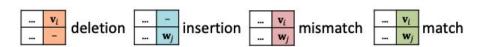
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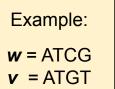
$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

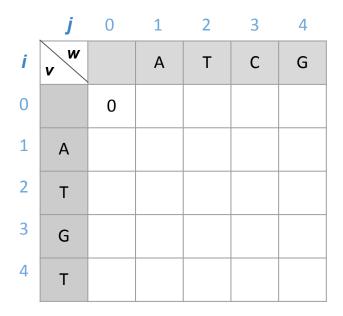






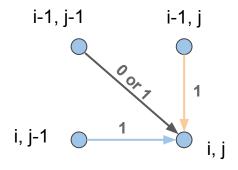
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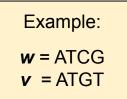


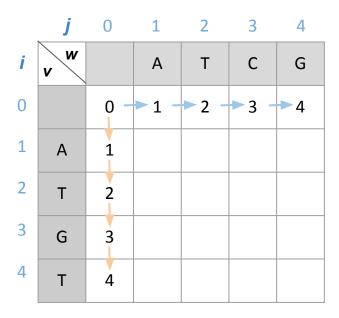


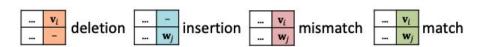


$$d[i,j] = \min egin{cases} 0, & ext{if } i = 0 ext{ and } j = 0, \ d[i-1,j]+1, & ext{if } i > 0, \ d[i,j-1]+1, & ext{if } j > 0, \ d[i-1,j-1]+1, & ext{if } i > 0, j > 0 ext{ and } v_i
eq w_j, \ d[i-1,j-1], & ext{if } i > 0, j > 0 ext{ and } v_i = w_j. \end{cases}$$

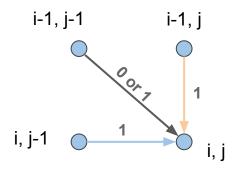


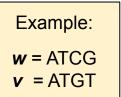


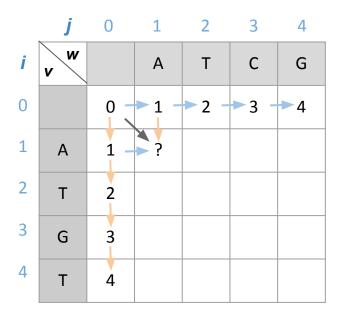




$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

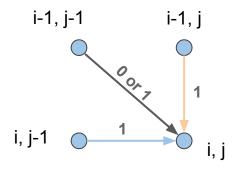


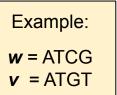


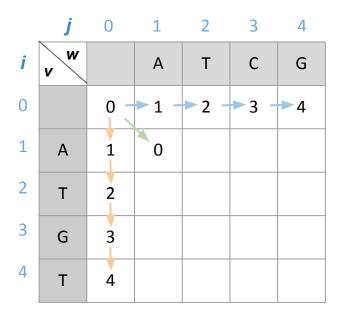




$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

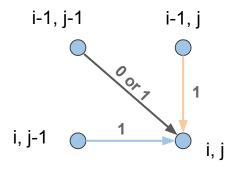


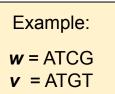


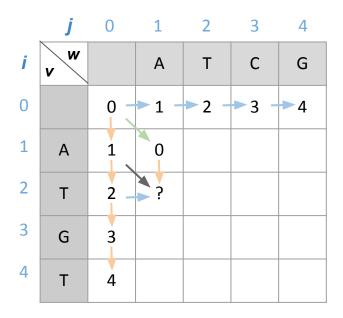




$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

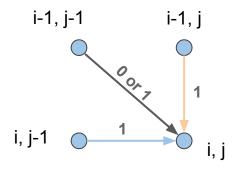


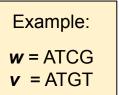


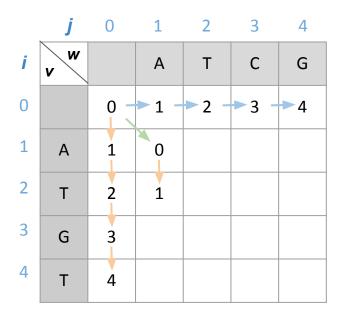




$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

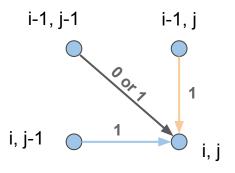


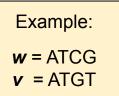


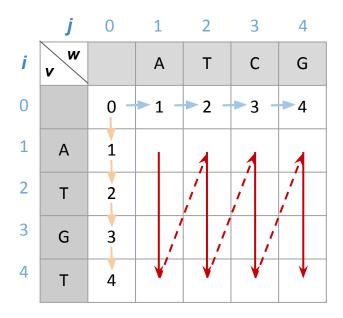


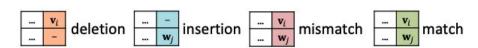


$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

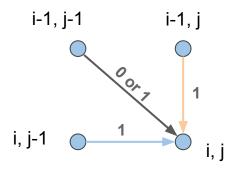


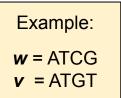


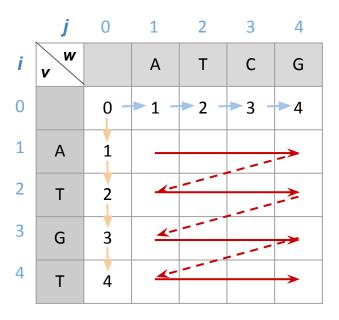




$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

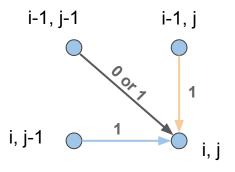


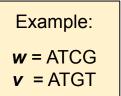


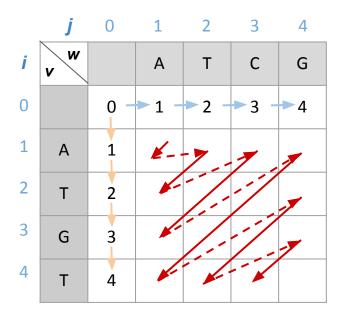




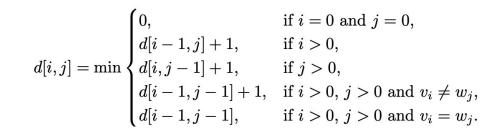
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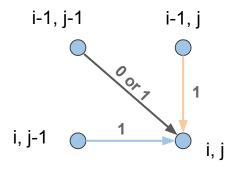


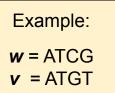


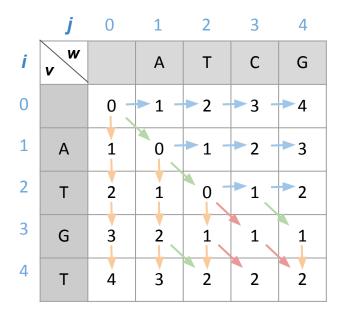






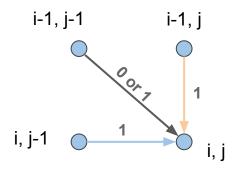


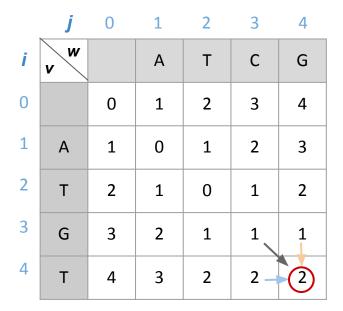




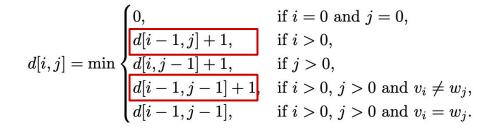


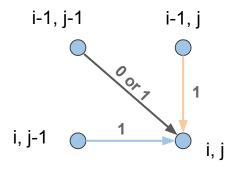
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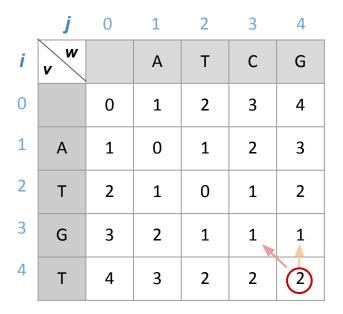


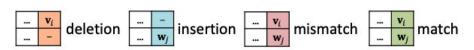




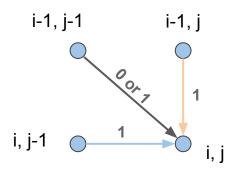


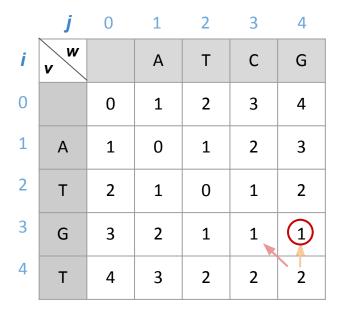






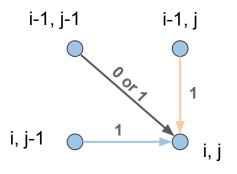
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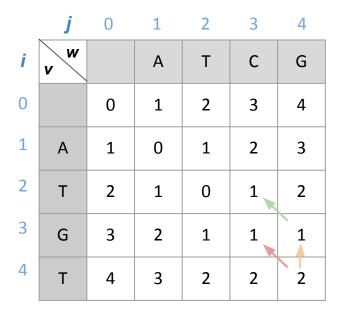






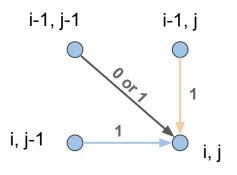
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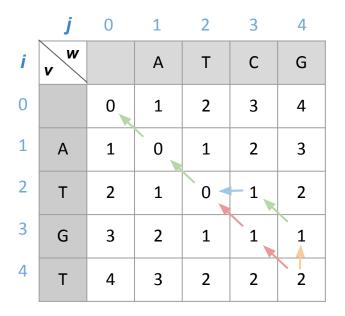






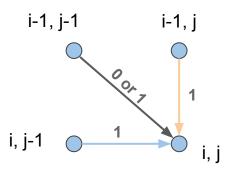
$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$







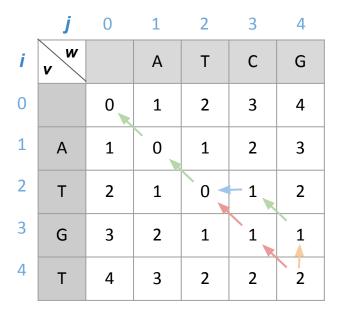
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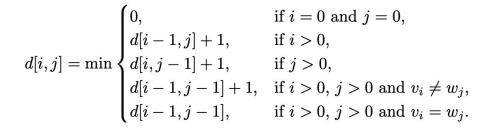
Backtrace algorithm

Base conditions: Termination: D(i,0) = iD(0,j) = jD(N,M) is distance Recurrence Relation: For each i = 1...Mach j = 1...N $D(i,j) = min \begin{cases} D(i-1,j) + 1 & \text{deletion} \\ D(i,j-1) + 1 & \text{insertion} \\ D(i-1,j-1) + 1; & \text{if } X(i) \neq Y(j) & \text{substituti} \\ 0; & \text{if } X(i) = Y(j) & \text{match} \end{cases}$ For each j = 1...Nsubstitution ptr(i,j)= DOWN deletion substitution match

Output the alignment



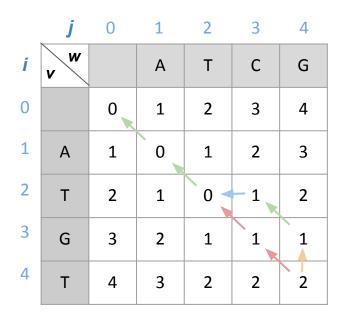




| А | Т | - | G | Т |
|---|---|---|---|---|
| A | Т | С | G | - |

| АТ | | G | Т | |
|----|---|---|---|--|
| A | Т | С | G | |

Computing edit distance -- Running time





$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

For each $(m + 1) \times (n + 1)$ entry:

- 3 addition operations
- · 1 comparison operation
- 1 minimum operation

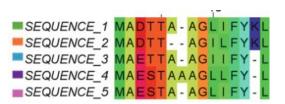
Running time: O(mn) time

Conclusions

Sequence alignment

- Algorithm for alignment
 - Edit distance
 - Dynamic programming

- Find the optimal alignment
 - Backtrace



$$d[i,j] = \min \begin{cases} 0, & \text{if } i = 0 \text{ and } j = 0, \\ d[i-1,j]+1, & \text{if } i > 0, \\ d[i,j-1]+1, & \text{if } j > 0, \\ d[i-1,j-1]+1, & \text{if } i > 0, j > 0 \text{ and } v_i \neq w_j, \\ d[i-1,j-1], & \text{if } i > 0, j > 0 \text{ and } v_i = w_j. \end{cases}$$

| | j | 0 | 1 | 2 | 3 | 4 |
|---|----|---|---|---|-------------------|---|
| i | vw | | А | Т | С | G |
|) | | 0 | 1 | 2 | 3 | 4 |
| | Α | 1 | 0 | 1 | 2 | 3 |
| | Т | 2 | 1 | 0 | - 1 _{**} | 2 |
| | G | 3 | 2 | 1 | 1 | 1 |
| | Т | 4 | 3 | 2 | 2 | 2 |