Minimum Edit Distance

Definition of Minimum Edit Distance

How similar are two strings?

Spell correction

- The user typed “graffe”

  Which is closest?

  - graf
  - graft
  - grail
  - giraffe

- Computational Biology
  - Align two sequences of nucleotides

```
AGGCTATCACCTGACCTCCAGGCCGATGCCC
TAGCTATCACGACCGCGGTCGATTTGCCCGAC
```

  - Resulting alignment:

```
-AGGCTATCACCTGACCTCCAGGCCGA--TGCCC---
TAG-CTATCAC--GACCGC--GGTCGATTTGCCCGAC
```

- Also for Machine Translation, Information Extraction, Speech Recognition

Edit Distance

The minimum edit distance between two strings

Is the minimum number of editing operations

- Insertion
- Deletion
- Substitution

Needed to transform one into the other

Minimum Edit Distance

Two strings and their **alignment**:

```
I N T E * N T I O N
| | | | | | | | | |
* E X E C U T I O N
```

Minimum Edit Distance

```
I N T E * N T I O N
| | | | | | | | | |
* E X E C U T I O N
d s s   i s
```

If each operation has cost of 1

- Distance between these is 5

If substitutions cost 2 (Levenshtein)

- Distance between them is 8

Alignment in Computational Biology

Given a sequence of bases

AGGCTATCACCTGACCTCCAGGCCGATGCCC
TAGCTATCACGACCGCGGTCGATTTGCCCGAC

An alignment:

-**AG**G**CTATCAC**CT**GACC**T**C**CA**GG**C**CGA**--**TGCCC**---
T**AG**-**CTATCAC**--**GACC**G**C**--**GG**T**CGA**TT**TGCCC**GAC

Given two sequences, align each letter to a letter or gap

Other uses of Edit Distance in NLP

Evaluating Machine Translation and speech recognition

```
R Spokesman confirms    senior government adviser was appointed
H Spokesman said    the senior            adviser was appointed
              S      I              D                        I
```

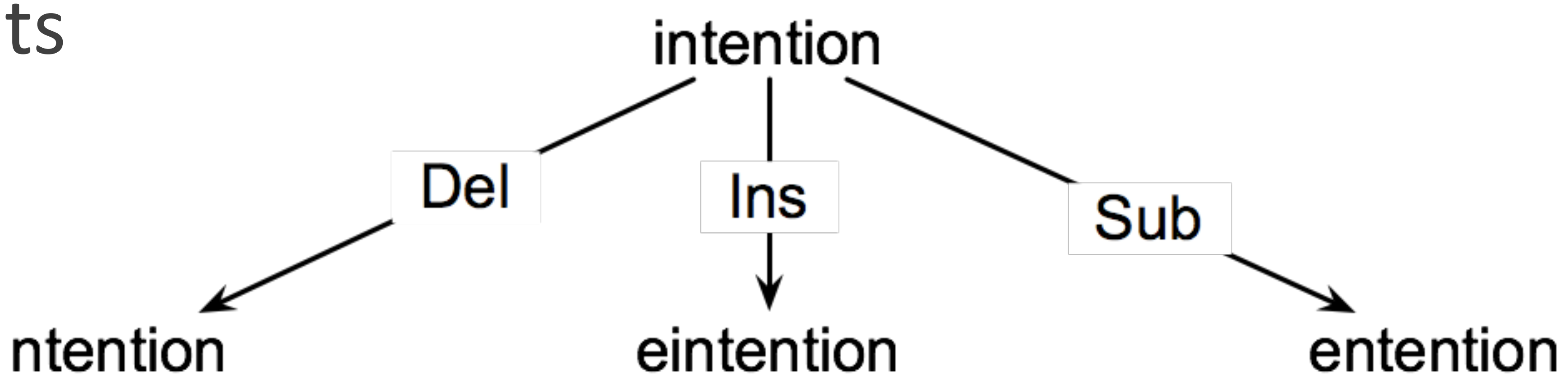
Named Entity Extraction and Entity Coreference

- IBM Inc. announced today
- IBM profits
- Stanford Professor Jennifer Eberhardt announced yesterday
- for Professor Eberhardt…

How to find the Min Edit Distance?

Searching for a path (sequence of edits) from the start string to the final string:

- **Initial state**: the word we're transforming
- **Operators**: insert, delete, substitute
- **Goal state**: the word we're trying to get to
- **Path cost**: what we want to minimize: the number of edits



Minimum Edit as Search

But the space of all edit sequences is huge!

- We can’t afford to navigate naïvely
- Lots of distinct paths wind up at the same state.
  - We don’t have to keep track of all of them
  - Just the shortest path to each of those revisted states.

Defining Min Edit Distance

For two strings

- X of length *n*
- Y of length *m*

We define D(*i*,*j*)

- the edit distance between X[1..*i*] and Y[1..*j*]
  - i.e., the first *i* characters of X and the first *j* characters of Y
- The edit distance between X and Y is thus D(*n*,*m*)

Minimum Edit Distance

Definition of Minimum Edit Distance

Computing Minimum Edit Distance

Dynamic Programming for Minimum Edit Distance

Dynamic programming: A tabular computation of D(*n,m*)

Solving problems by combining solutions to subproblems.

Bottom-up

- We compute D(i,j) for small *i,j*
- And compute larger D(i,j) based on previously computed smaller values
- i.e., compute D(*i,j*) for all *i* (0 < *i* < n) and *j* (0 < j < m)

Defining Min Edit Distance (Levenshtein)

Initialization

```
    D(i,0) = i
    D(0,j) = j
```

Recurrence Relation:

```
    For each i = 1…M
        For each j = 1…N
```

$$D(i,j) = \min \begin{cases} D(i-1,j) + 1 \\ D(i,j-1) + 1 \\ D(i-1,j-1) + \begin{cases} 2; & \text{if } X(i) \neq Y(j) \\ 0; & \text{if } X(i) = Y(j) \end{cases} \end{cases}$$

Termination:

```
 D(N,M) is distance
```

The Edit Distance Table

N	9									
O	8									
I	7									
T	6									
N	5									
E	4									
T	3									
N	2									
I	1									
#	**0**	1	2	3	4	5	6	7	8	9
	#	E	X	E	C	U	T	I	O	N

The Edit Distance Table

N	9									
O	8									
I	7									
T	6									
N	5									
E	4									
T	3									
N	2									
I	1									
#	**0**	1	2	3	4	5	6	7	8	9
	#	E	X	E	C	U	T	I	O	N

$$D(i,j) = \min \begin{cases} D(i-1,j) + 1 \\ D(i,j-1) + 1 \\ D(i-1,j-1) + \begin{cases} 2; & \text{if } S_1(i) \neq S_2(j) \\ 0; & \text{if } S_1(i) = S_2(j) \end{cases} \end{cases}$$

Edit Distance

$$D(i,j) = \min \begin{cases} D(i-1,j) + 1 \\ D(i,j-1) + 1 \\ D(i-1,j-1) + \begin{cases} 2; & \text{if } S_1(i) \neq S_2(j) \\ 0; & \text{if } S_1(i) = S_2(j) \end{cases} \end{cases}$$

N	9									
O	8									
I	7									
T	6									
N	5									
E	4									
T	3									
N	2									
I	1									
#	**0**	1	2	3	4	5	6	7	8	9
	#	E	X	E	C	U	T	I	O	N

The Edit Distance Table

N	9	8	9	10	11	12	11	10	9	**8**
O	8	7	8	9	10	11	10	9	8	9
I	7	6	7	8	9	10	9	8	9	10
T	6	5	6	7	8	9	8	9	10	11
N	5	4	5	6	7	8	9	10	11	10
E	4	3	4	5	6	7	8	9	10	9
T	3	4	5	6	7	8	7	8	9	8
N	2	3	4	5	6	7	8	7	8	7
I	1	2	3	4	5	6	7	6	7	8
#	**0**	1	2	3	4	5	6	7	8	9
	#	E	X	E	C	U	T	I	O	N

Minimum Edit Distance

Computing Minimum Edit Distance

Minimum Edit Distance

Backtrace for Computing Alignments

Computing alignments

Edit distance isn't sufficient

- We often need to **align** each character of the two strings to each other

We do this by keeping a "backtrace"

Every time we enter a cell, remember where we came from

When we reach the end,

- Trace back the path from the upper right corner to read off the alignment

Edit Distance

$$D(i,j) = \min \begin{cases} D(i-1,j) + 1 \\ D(i,j-1) + 1 \\ D(i-1,j-1) + \begin{cases} 2; & \text{if } S_1(i) \neq S_2(j) \\ 0; & \text{if } S_1(i) = S_2(j) \end{cases} \end{cases}$$

N	9									
O	8									
I	7									
T	6									
N	5									
E	4									
T	3									
N	2									
I	1									
#	**0**	1	2	3	4	5	6	7	8	9
	#	E	X	E	C	U	T	I	O	N

MinEdit with Backtrace

n	9	↓ 8	↙←↓ 9	↙←↓ 10	↙←↓ 11	↙←↓ 12	↓ 11	↓ 10	↓ 9	↙ **8**
o	8	↓ 7	↙←↓ 8	↙←↓ 9	↙←↓ 10	↙←↓ 11	↓ 10	↓ 9	↙ **8**	← 9
i	7	↓ 6	↙←↓ 7	↙←↓ 8	↙←↓ 9	↙←↓ 10	↓ 9	↙ **8**	← 9	← 10
t	6	↓ 5	↙←↓ 6	↙←↓ 7	↙←↓ 8	↙←↓ 9	↙ **8**	← 9	← 10	←↓ 11
n	5	↓ 4	↙←↓ 5	↙←↓ 6	↙←↓ 7	↙←↓ **8**	↙←↓ 9	↙←↓ 10	↙←↓ 11	↙↓ 10
e	4	↙ 3	← 4	↙← **5**	← **6**	← 7	←↓ 8	↙←↓ 9	↙←↓ 10	↓ 9
t	3	↙←↓ 4	↙←↓ **5**	↙←↓ 6	↙←↓ 7	↙←↓ 8	↙ 7	←↓ 8	↙←↓ 9	↓ 8
n	2	↙←↓ **3**	↙←↓ 4	↙←↓ 5	↙←↓ 6	↙←↓ 7	↙←↓ 8	↓ 7	↙←↓ 8	↙ 7
i	**1**	↙←↓ 2	↙←↓ 3	↙←↓ 4	↙←↓ 5	↙←↓ 6	↙←↓ 7	↙ 6	← 7	← 8
#	**0**	1	2	3	4	5	6	7	8	9
	#	**e**	**x**	**e**	**c**	**u**	**t**	**i**	**o**	**n**

Adding Backtrace to Minimum Edit Distance

Base conditions:

```
D(i,0) = i          D(0,j) = j
```

Termination:

```
D(N,M) is distance
```

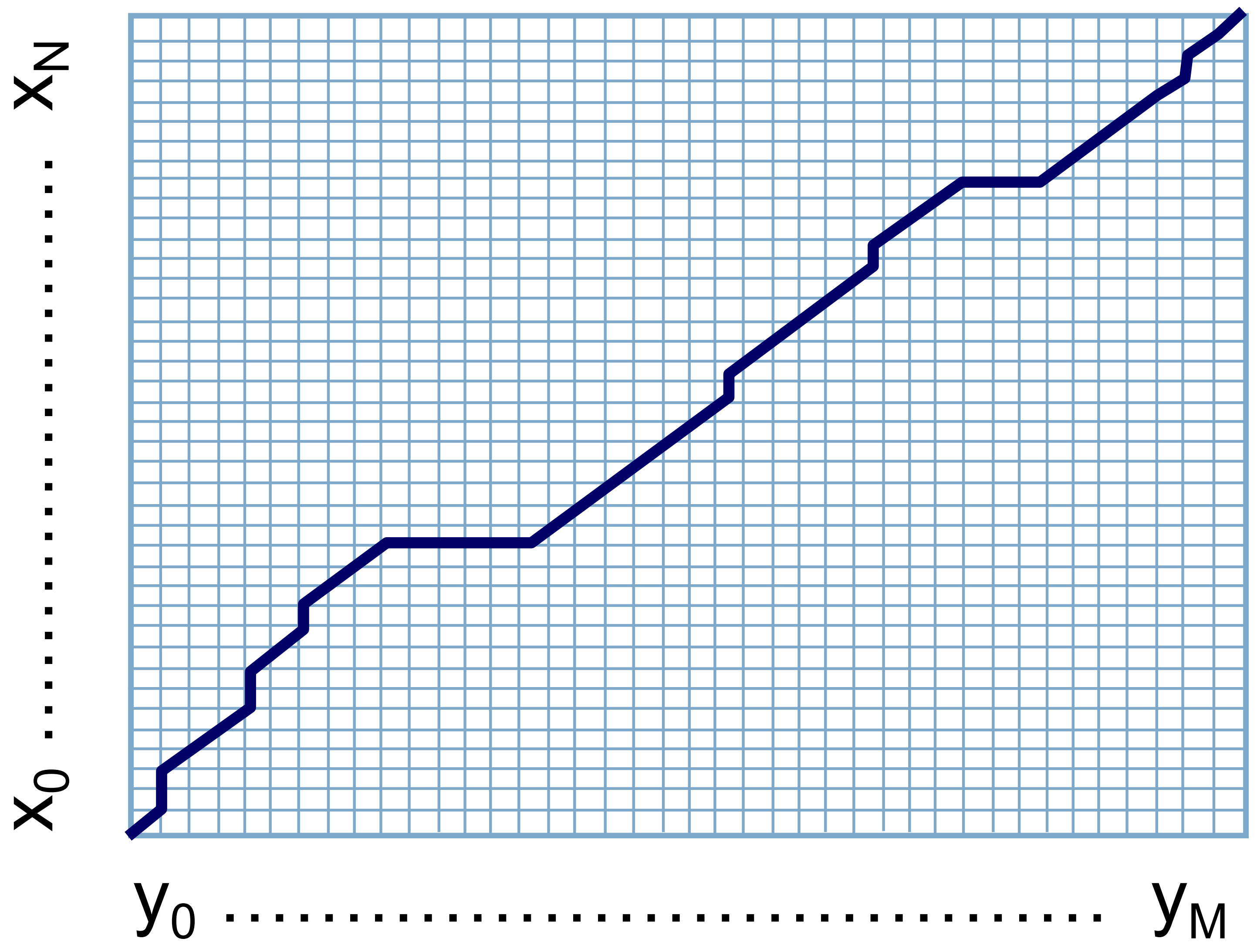
Recurrence Relation:

```
For each  i = 1…M
     For each  j = 1…N
```

$$D(i,j) = \min \begin{cases} D(i-1,j) + 1 & \text{deletion} \\ D(i,j-1) + 1 & \text{insertion} \\ D(i-1,j-1) + \begin{cases} 2; & \text{if } X(i) \neq Y(j) \quad \text{substitution} \\ 0; & \text{if } X(i) = Y(j) \end{cases} \end{cases}$$

$$ptr(i,j) = \begin{cases} \text{LEFT} & \text{insertion} \\ \text{DOWN} & \text{deletion} \\ \text{DIAG} & \text{substitution} \end{cases}$$

The Distance Matrix



Every non-decreasing path

from (0,0) to (M, N)

corresponds to
an alignment
of the two sequences

An optimal alignment is composed
of optimal subalignments

SLIDE ADAPTED FROM SERAFIM BATZOGLOU WITH PERMISSION

Result of Backtrace

Two strings and their **alignment**:

```
I N T E * N T I O N
| | | | | | | | | |
* E X E C U T I O N
```

Performance

Time:

$O(nm)$

Space:

$O(nm)$

Backtrace

$O(n+m)$

Minimum Edit Distance

Backtrace for Computing Alignments

Minimum Edit Distance

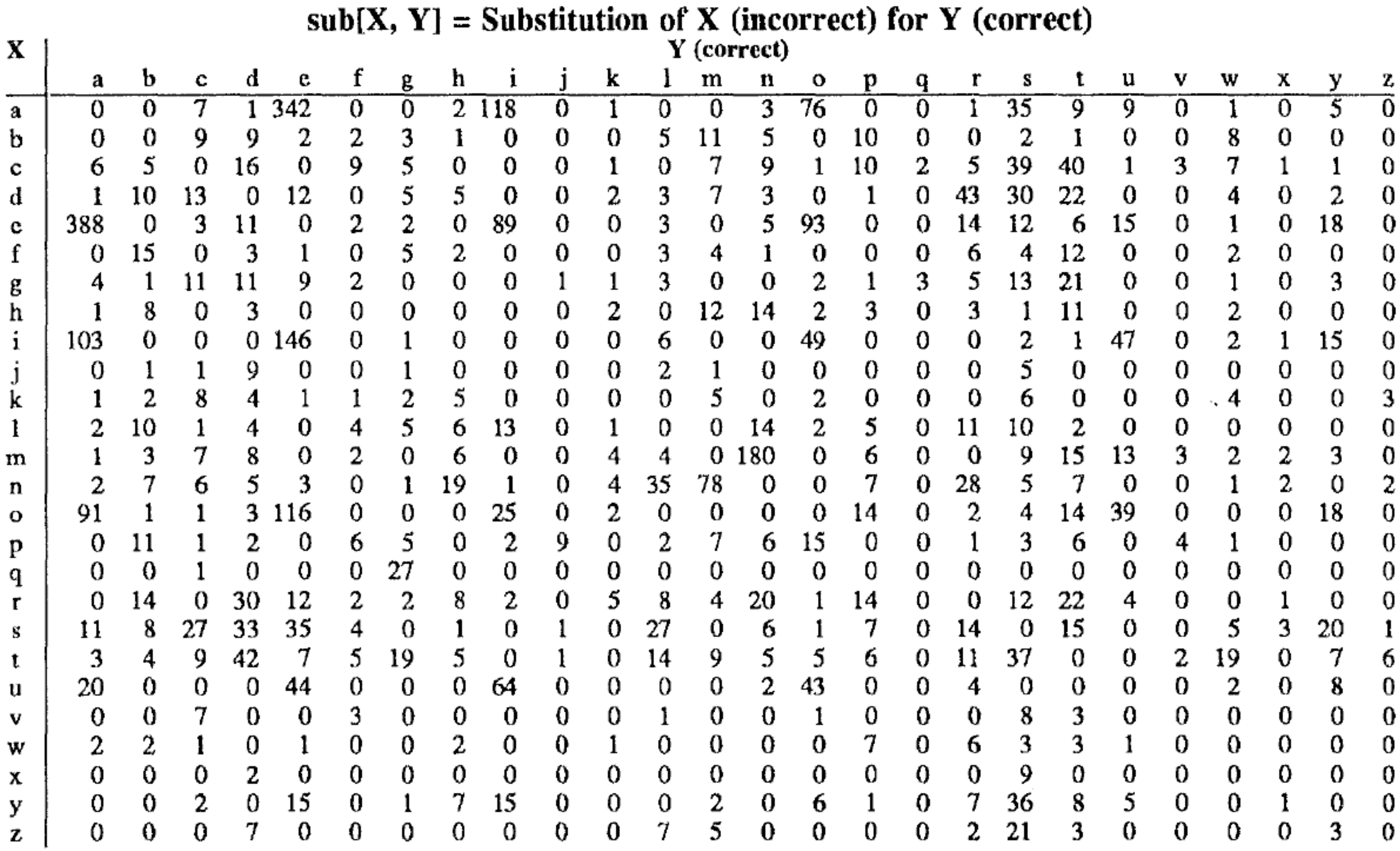
Weighted Minimum Edit Distance

Weighted Edit Distance

Why would we add weights to the computation?

- Spell Correction: some letters are more likely to be mistyped than others
- Biology: certain kinds of deletions or insertions are more likely than others

Confusion matrix for spelling errors



sub[X, Y] = Substitution of X (incorrect) for Y (correct)

X	Y (correct)																									
	a	b	c	d	e	f	g	h	i	j	k	l	m	n	o	p	q	r	s	t	u	v	w	x	y	z
a	0	0	7	1	342	0	0	2	118	0	1	0	0	3	76	0	0	1	35	9	9	0	1	0	5	0
b	0	0	9	9	2	2	3	1	0	0	0	5	11	5	0	10	0	0	2	1	0	0	8	0	0	0
c	6	5	0	16	0	9	5	0	0	0	1	0	7	9	1	10	2	5	39	40	1	3	7	1	1	0
d	1	10	13	0	12	0	5	5	0	0	2	3	7	3	0	1	0	43	30	22	0	0	4	0	2	0
e	388	0	3	11	0	2	2	0	89	0	0	3	0	5	93	0	0	14	12	6	15	0	1	0	18	0
f	0	15	0	3	1	0	5	2	0	0	0	3	4	1	0	0	0	6	4	12	0	0	2	0	0	0
g	4	1	11	11	9	2	0	0	0	1	1	3	0	0	2	1	3	5	13	21	0	0	1	0	3	0
h	1	8	0	3	0	0	0	0	0	0	2	0	12	14	2	3	0	3	1	11	0	0	2	0	0	0
i	103	0	0	0	146	0	1	0	0	0	0	6	0	0	49	0	0	0	2	1	47	0	2	1	15	0
j	0	1	1	9	0	0	1	0	0	0	0	2	1	0	0	0	0	0	5	0	0	0	0	0	0	0
k	1	2	8	4	1	1	2	5	0	0	0	0	5	0	2	0	0	0	6	0	0	0	4	0	0	3
l	2	10	1	4	0	4	5	6	13	0	1	0	0	14	2	5	0	11	10	2	0	0	0	0	0	0
m	1	3	7	8	0	2	0	6	0	0	4	4	0	180	0	6	0	0	9	15	13	3	2	2	3	0
n	2	7	6	5	3	0	1	19	1	0	4	35	78	0	0	7	0	28	5	7	0	0	1	2	0	2
o	91	1	1	3	116	0	0	0	25	0	2	0	0	0	0	14	0	2	4	14	39	0	0	0	18	0
p	0	11	1	2	0	6	5	0	2	9	0	2	7	6	15	0	0	1	3	6	0	4	1	0	0	0
q	0	0	1	0	0	0	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
r	0	14	0	30	12	2	2	8	2	0	5	8	4	20	1	14	0	0	12	22	4	0	0	1	0	0
s	11	8	27	33	35	4	0	1	0	1	0	27	0	6	1	7	0	14	0	15	0	0	5	3	20	1
t	3	4	9	42	7	5	19	5	0	1	0	14	9	5	5	6	0	11	37	0	0	2	19	0	7	6
u	20	0	0	0	44	0	0	0	64	0	0	0	0	2	43	0	0	4	0	0	0	0	2	0	8	0
v	0	0	7	0	0	3	0	0	0	0	0	1	0	0	1	0	0	0	8	3	0	0	0	0	0	0
w	2	2	1	0	1	0	0	2	0	0	1	0	0	0	0	7	0	6	3	3	1	0	0	0	0	0
x	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0
y	0	0	2	0	15	0	1	7	15	0	0	0	2	0	6	1	0	7	36	8	5	0	0	1	0	0
z	0	0	0	7	0	0	0	0	0	0	0	7	5	0	0	0	0	2	21	3	0	0	0	0	3	0

Weighted Min Edit Distance

Initialization:

```
  D(0,0) = 0
  D(i,0) = D(i-1,0) + del[x(i)];    1 < i ≤ N
  D(0,j) = D(0,j-1) + ins[y(j)];    1 < j ≤ M
```

Recurrence Relation:

$$D(i,j) = \min \begin{cases} D(i-1,j) + del[x(i)] \\ D(i,j-1) + ins[y(j)] \\ D(i-1,j-1) + sub[x(i),y(j)] \end{cases}$$

Termination:

```
D(N,M) is distance
```

Where did the name, dynamic programming, come from?

…The 1950s were not good years for mathematical research. [the] Secretary of Defense …had a pathological fear and hatred of the word, research…

I decided therefore to use the word, “**programming**”.

I wanted to get across the idea that this was dynamic, this was multistage… I thought, let’s … take a word that has an absolutely precise meaning, namely **dynamic**… it’s impossible to use the word, **dynamic**, in a pejorative sense. Try thinking of some combination that will possibly give it a pejorative meaning. It’s impossible.

Thus, I thought dynamic programming was a good name. It was something not even a Congressman could object to.”

Richard Bellman, “Eye of the Hurricane: an autobiography” 1984.

Minimum Edit Distance

Weighted Minimum Edit Distance

Minimum Edit Distance

Minimum Edit Distance in Computational Biology

Sequence Alignment

AGGCTATCACCTGACCTCCAGGCCGATGCCC

TAGCTATCACGACCGCGGTCGATTTGCCCGAC

-**AG**G**CTATCAC**CT**GACC**T**C**CA**GG**C**CGA**--**TGCCC**---

T**AG**-**CTATCAC**--**GACC**G**C**--**GG**T**CGA**TT**TGCCC**GAC

Why sequence alignment?

Comparing genes or regions from different species

- to find important regions
- determine function
- uncover evolutionary forces

Assembling fragments to sequence DNA

Compare individuals to looking for mutations

Alignments in two fields

In Natural Language Processing

- We generally talk about distance (minimized)
  - And weights

In Computational Biology

- We generally talk about similarity (maximized)
  - And scores

The Needleman-Wunsch Algorithm

Initialization:

```
  D(i,0) = -i * d
  D(0,j) = -j * d
```

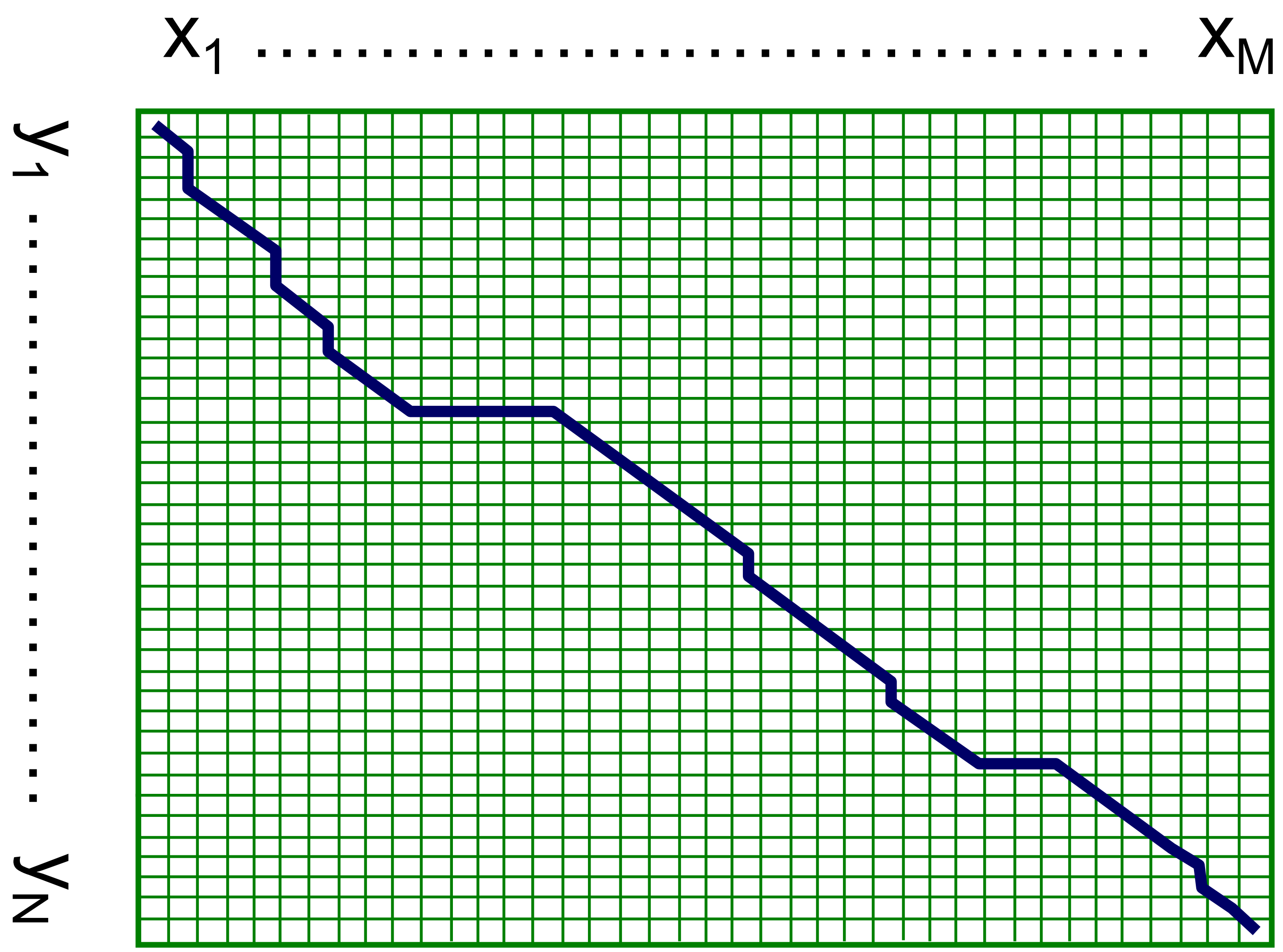
Recurrence Relation:

$$D(i,j) = \min \begin{cases} D(i-1,j) - d \\ D(i,j-1) - d \\ D(i-1,j-1) + s[x(i),y(j)] \end{cases}$$

Termination:

```
D(N,M) is distance
```

The Needleman-Wunsch Matrix



(Note that the origin is at the upper left.)

SLIDE ADAPTED FROM SERAFIM BATZOGLOU WITH PEMISSION

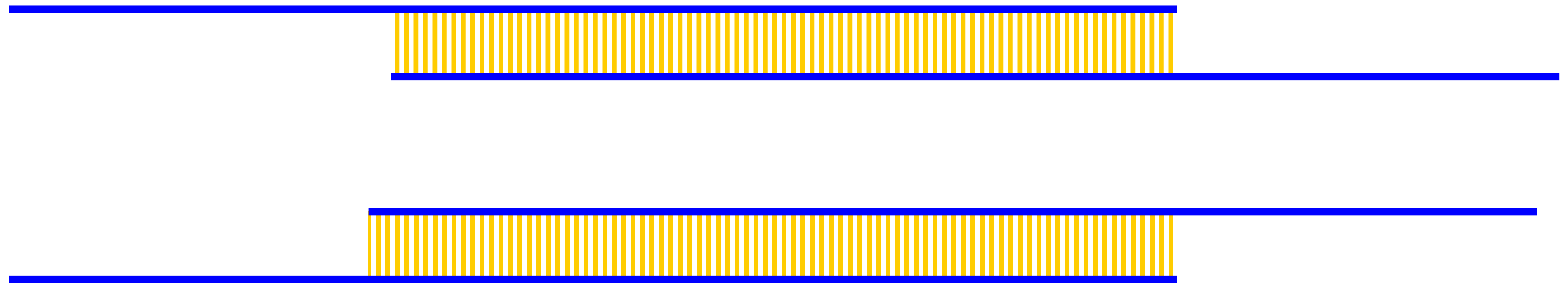
A variant of the basic algorithm:

Maybe it is OK to have an unlimited # of gaps in the beginning and end:

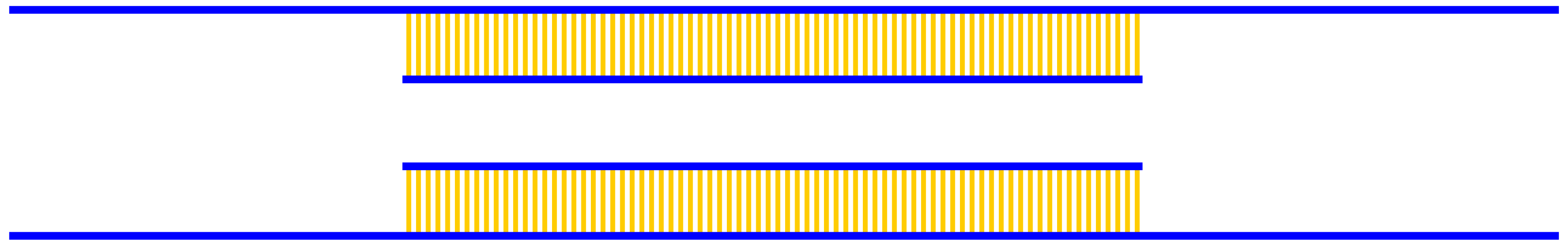
```
----------CTATCACCTGACCTCCAGGCCGATGCCCCTTCCGGC
GCGAGTTCATCTATCAC--GACCGC--GGTCG--------------
```

- If so, we don't want to penalize gaps at the ends

Different types of overlaps

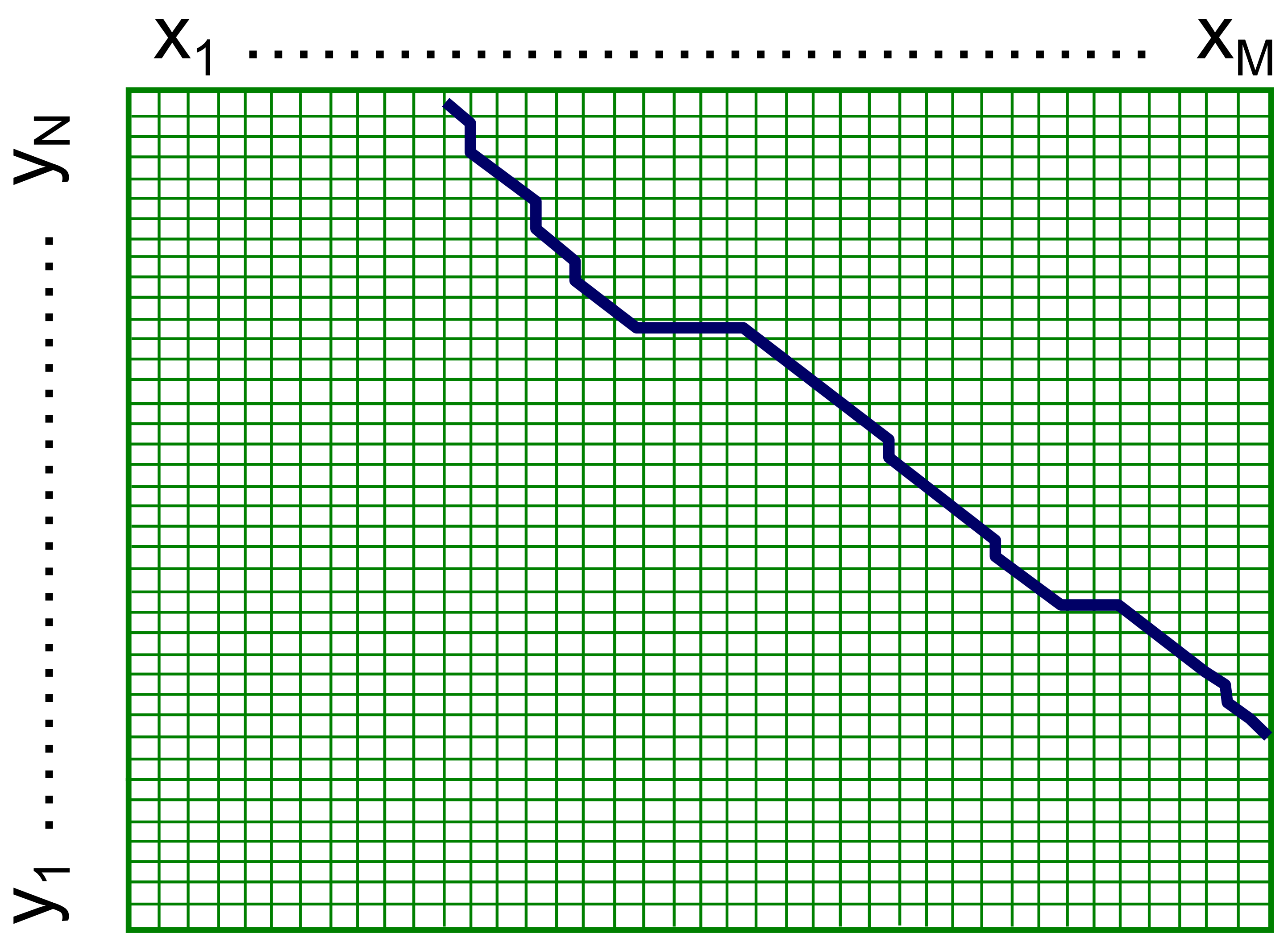


Example:
2 overlapping“*reads*” from a sequencing project



Example:
Search for a mouse gene within a human chromosome

The Overlap Detection variant



Changes:

1. Initialization

```
For all i, j,
    F(i, 0) = 0
    F(0, j) = 0
```

2. Termination

$$F_{OPT} = \max \begin{cases} \max_i F(i, N) \\ \max_j F(M, j) \end{cases}$$

SLIDE FROM SERAFIM BATZOGLOU WITH PERMISSION

The Local Alignment Problem

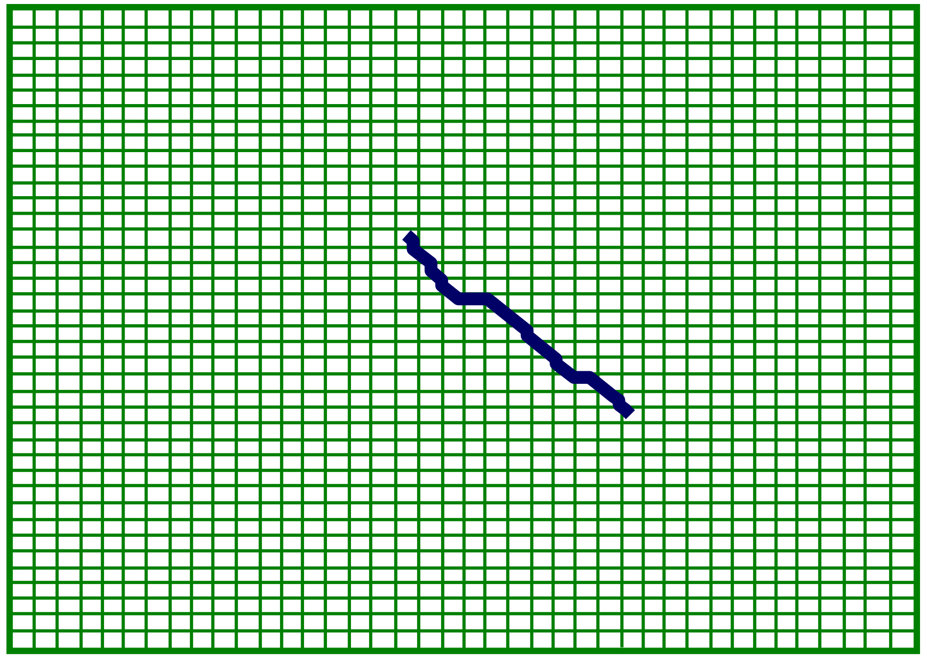
Given two strings $x = x_1 \ldots\ldots x_M$,

$y = y_1 \ldots\ldots y_N$

Find substrings x', y' whose similarity (optimal global alignment value) is maximum

x = aaaacccccggggtta

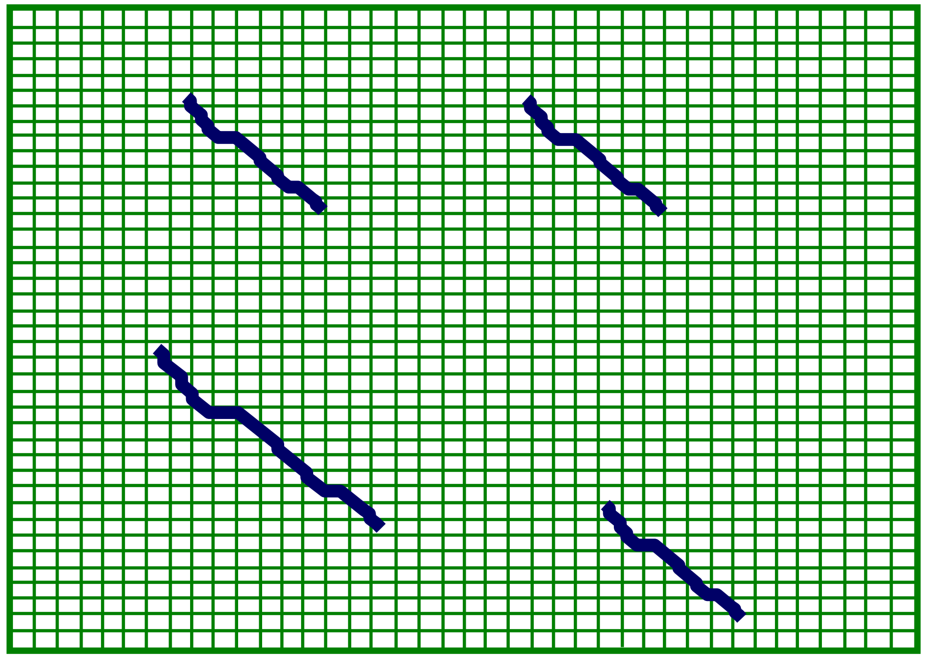
y = ttcccgggaaccaacc



SLIDE FROM SERAFIM BATZOGLOU WITH PERMISSION

The Smith-Waterman algorithm

Idea: Ignore badly aligning regions



Modifications to Needleman-Wunsch:

Initialization:

$$F(0, j) = 0$$

$$F(i, 0) = 0$$

Iteration:

$$F(i, j) = \max \begin{cases} 0 \\ F(i-1, j) - d \\ F(i, j-1) - d \\ F(i-1, j-1) + s(x_i, y_j) \end{cases}$$

SLIDE FROM SERAFIM BATZOGLOU WITH PERMISSION

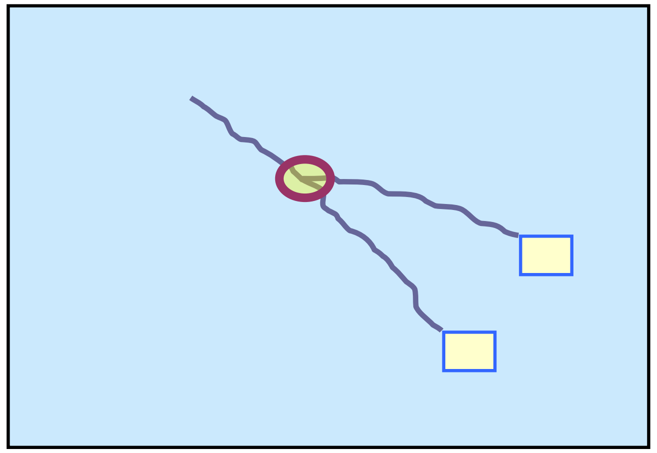
The Smith-Waterman algorithm

Termination:

1. If we want the best local alignment…

$$F_{OPT} = \max_{i,j} F(i, j)$$

Find F_{OPT} and trace back



2. If we want all local alignments scoring > t

?? For all i, j find F(i, j) > t, and trace back?

Complicated by overlapping local alignments

Local alignment example

X = ATCAT

Y = ATTATC

Let:

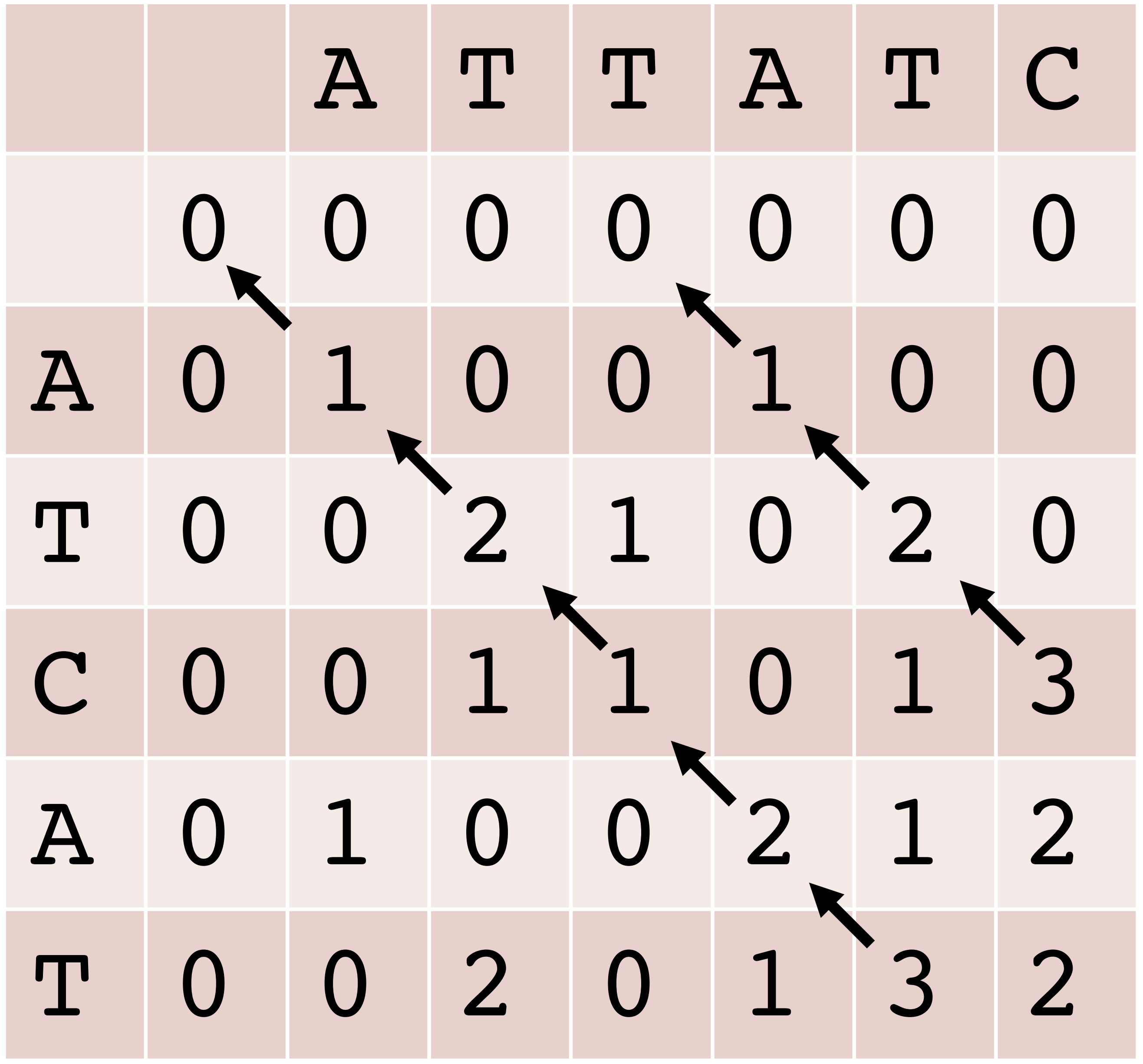
m = 1 (1 point for match)

d = 1 (-1 point for del/ins/sub)

		A	T	T	A	T	C
	0	0	0	0	0	0	0
A	0						
T	0						
C	0						
A	0						
T	0						

Local alignment example

```
X = ATCAT
Y = ATTATC
```

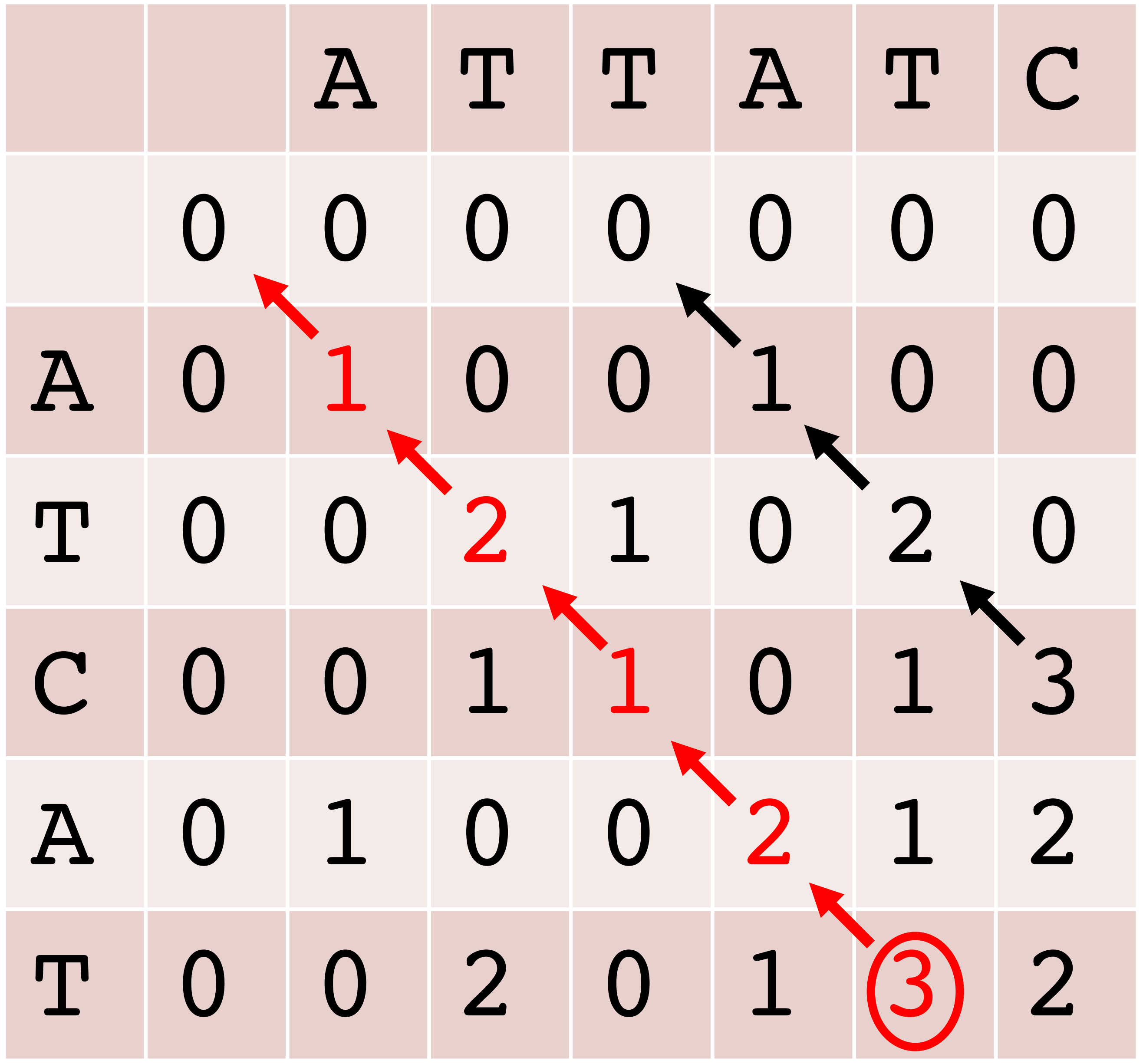


		A	T	T	A	T	C
	0	0	0	0	0	0	0
A	0	1	0	0	1	0	0
T	0	0	2	1	0	2	0
C	0	0	1	1	0	1	3
A	0	1	0	0	2	1	2
T	0	0	2	0	1	3	2

Local alignment example

X = **ATCAT**

Y = **ATTAT**C

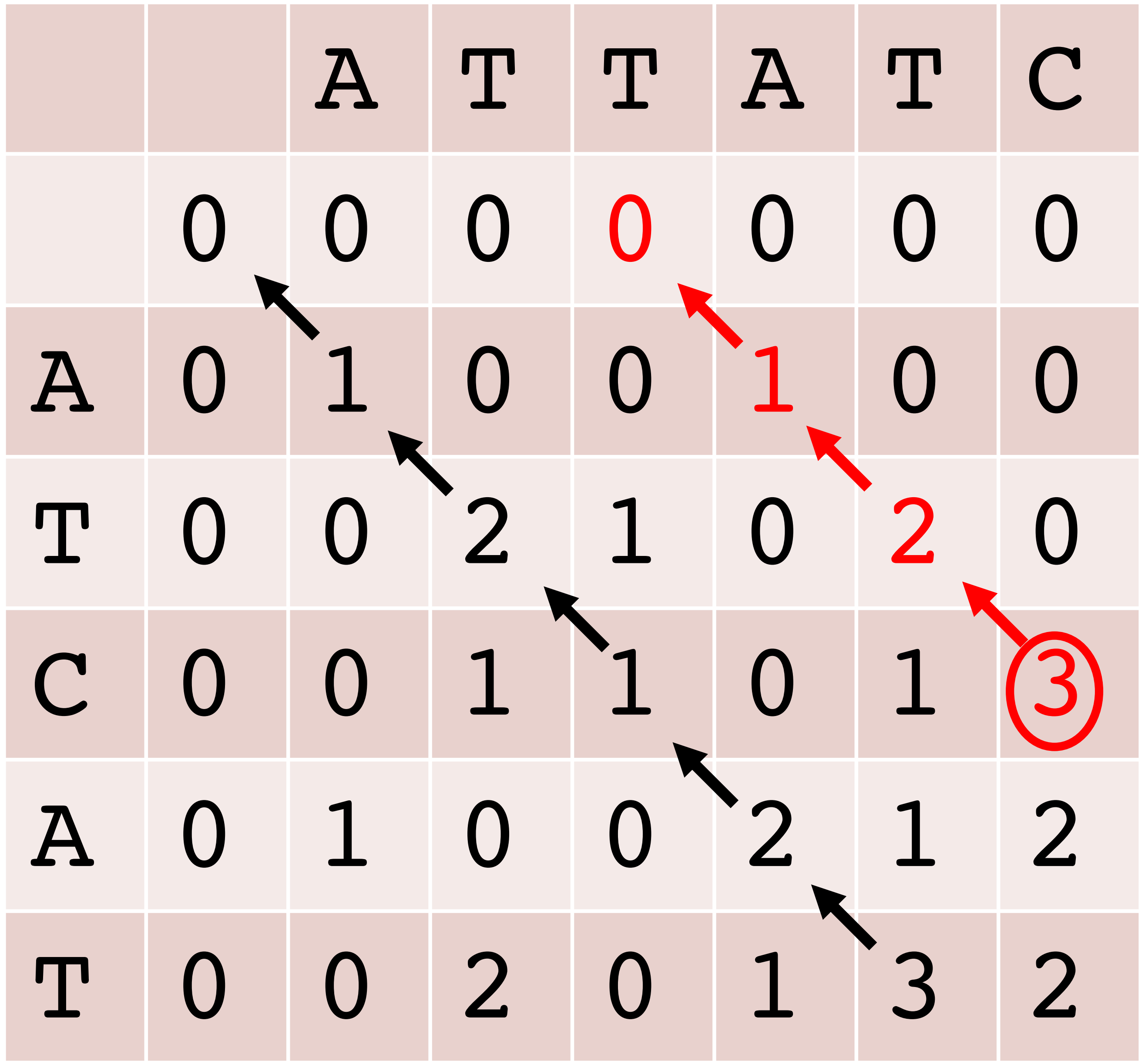


		A	T	T	A	T	C
	0	0	0	0	0	0	0
A	0	1	0	0	1	0	0
T	0	0	2	1	0	2	0
C	0	0	1	1	0	1	3
A	0	1	0	0	2	1	2
T	0	0	2	0	1	3	2

Local alignment example

X = **ATC**AT

Y = ATT**ATC**



		A	T	T	A	T	C
	0	0	0	0	0	0	0
A	0	1	0	0	1	0	0
T	0	0	2	1	0	2	0
C	0	0	1	1	0	1	3
A	0	1	0	0	2	1	2
T	0	0	2	0	1	3	2

Minimum Edit Distance

Minimum Edit Distance in Computational Biology