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 原本沒有的字，後來出現
  - Deletion 原本有的字，後來被刪除
  - Substitution 替換字
- 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

並不是拿到兩個字串就直接比
而是要適度的留白
試著找到一個編輯距離最小的對應法

- Given a sequence of bases

```
AGGCTATCACCTGACCTCCAGGCCGATGCCC
TAGCTATCACGACCGCGGTCGATTTGCCCGAC
```

- An alignment:

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

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

Other uses of Edit Distance in NLP

- Evaluating Machine Translation and speech recognition

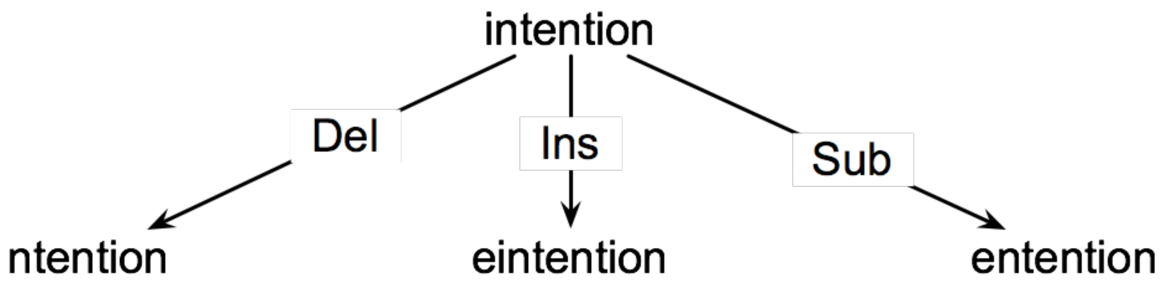
```
R Spokesman confirms     senior government adviser was shot
H Spokesman said     the senior            adviser was shot dead
                S     I                D                     I
```

- Named Entity Extraction and Entity Coreference
  - IBM Inc. announced today
  - IBM profits
  - Stanford President John Hennessy announced yesterday
  - for Stanford University President John Hennessy

IBM Inc和IBM只差一個字，所以可以說他們是一樣的字
下面這個例子也只差了President，所以可以說是一樣的字
這就是最小編輯距離的應用

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 不可能窮舉所有的可能
  - 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

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* ($0 < j < m$)

Dan Jurafsky

Defining Min Edit Distance (Levenshtein)

- Initialization

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

長度為i的句子x，和長度為0的句子y，編輯距離=i（i次deletion）

長度為0的句子x，和長度為i的句子y，編輯距離=i（i次insertion）

- Recurrence Relation:

```
For each  i = 1…M
    For each  j = 1…N
        D(i,j)= min { D(i-1,j) + 1
                    { D(i,j-1) + 1
                    { D(i-1,j-1) + { 2; if X(i) ≠ Y(j)
                                   { 0; if X(i) = Y(j)
```

- Termination:

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

D(i, j)的值，有三種可能

1. 原本D(i–1, j)，在x新增一個值
2. 原本D(i, j–1)，在y新增一個值
3. 原本D(i–1, j–1)，在x和y都加入一個值

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

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

向右：+1
向上：+1
右上：+2 or +0
向右或向上一定是insertion/deletion，所以只會是+1

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

找出兩個字串的最小編輯距離還不夠
還要找出這兩個義串應該要怎麼對應
才能得到最小編輯距離

Dan Jurafsky

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

Dan Jurafsky

MinEdit with Backtrace

向右：+1
向上：+1
右上：+2 or +0
要知道每一個值是從哪個方向來的
再一一遞迴到起點

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**	

```
ANS:
inte*ntion
#execution
```

Adding Backtrace to Minimum Edit Distance

- Base conditions:

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

  Termination:

  `D(N,M) is distance`

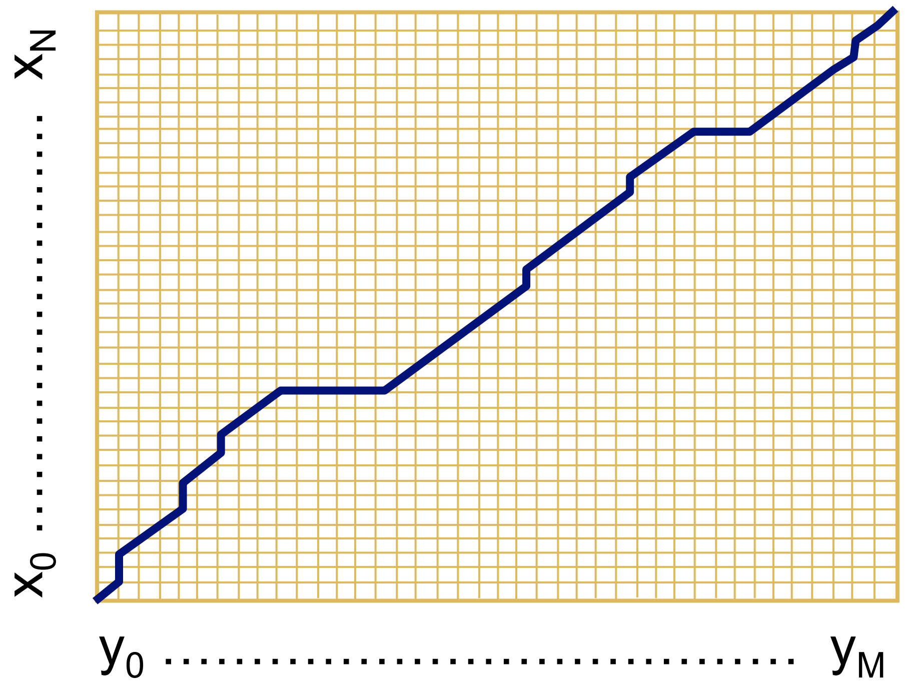
- Recurrence Relation:

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

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

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

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

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)

  `Matrix Size = n * m`

- Space:

  O(nm)

- Backtrace

  O(n+m)

Minimum Edit Distance

Backtrace for Computing Alignments

Minimum Edit Distance

Weighted Minimum Edit Distance

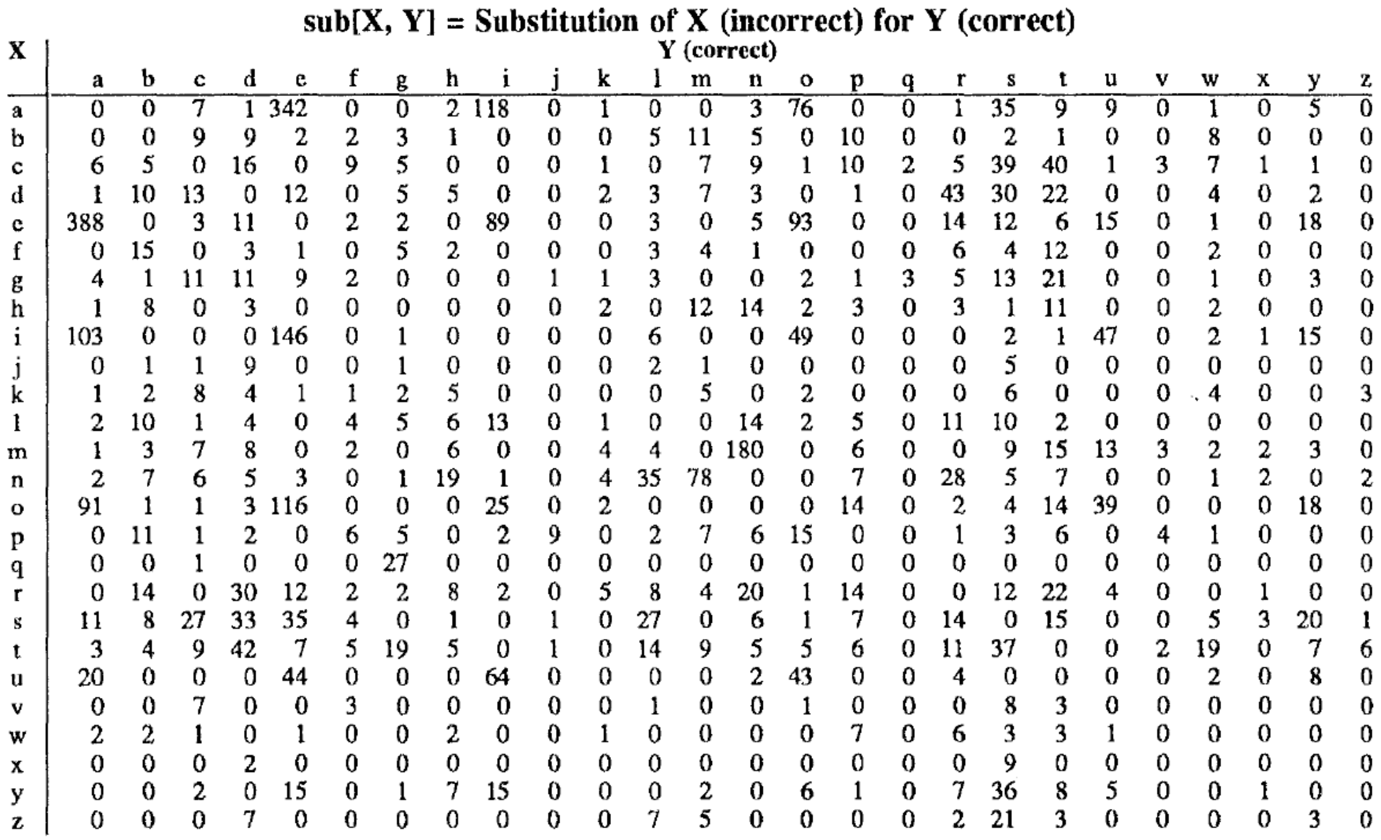
Weighted Edit Distance

- 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

有些字在鍵盤擺設上可能就在旁邊，比較容易打錯
這種錯誤就是比較能夠被容忍的

Dan Jurafsky

Confusion matrix for spelling errors



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

X	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

Y (correct)

~
`
!
1
@
2
#
3
$
4
%
5
^
6
&
7
*
8
(
9
)
0
—
-
+
=
Tab
Q
W
E
R
T
Y
U
I
O
P
{
[
}
]
Caps Lock
A
S
D
F
G
H
J
K
L
:
;
"
'
Enter
Shift
Z
X
C
V
B
N
M
<
,
>
.
?
/
Shift
Ctrl
Alt
Alt

Dan Jurafsky

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:

Weight

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

- 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
```

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

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
```

```
d: cost of insertion/deletion
s: cost of substitution from x(i) to y(j)
```

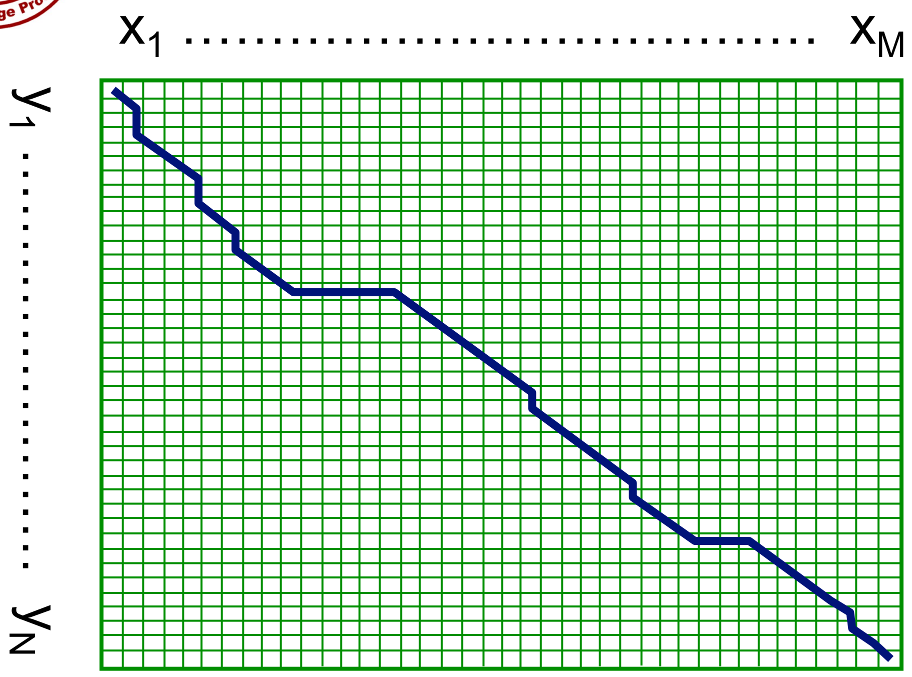
- Recurrence Relation:

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

- Termination:

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

The Needleman-Wunsch Matrix



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

Slide adapted from Serafim Batzoglou

A variant of the basic algorithm:

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

可能在整段基因當中
只有在某一個片段有大幅相近的現象
那我們只要擷取這個片段即可
不要過度懲罰前後補償的GAP

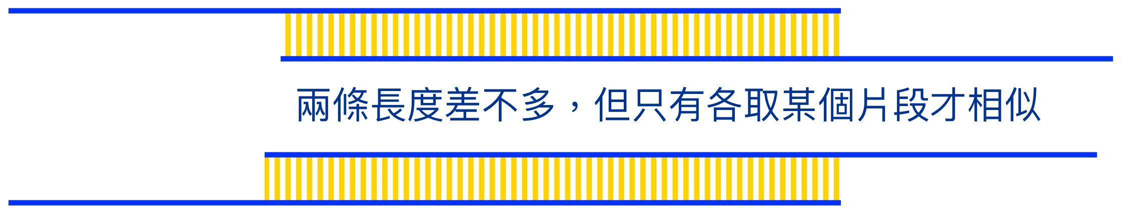
```
----------CTATCACCTGACCTCCAGGCCGATGCCCCTTCCGGC
GCGAGTTCATCTATCAC--GACCGC--GGTCG--------------
```

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

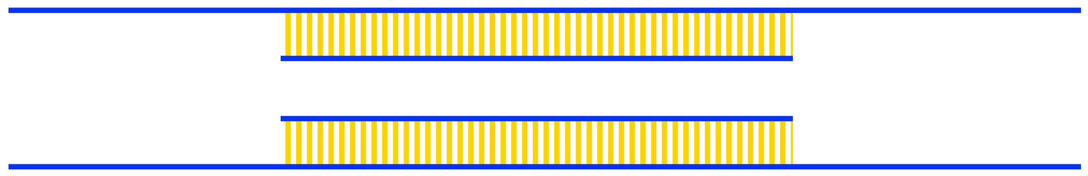
Slide from Serafim Batzoglou

Different types of overlaps

兩種Overlap



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

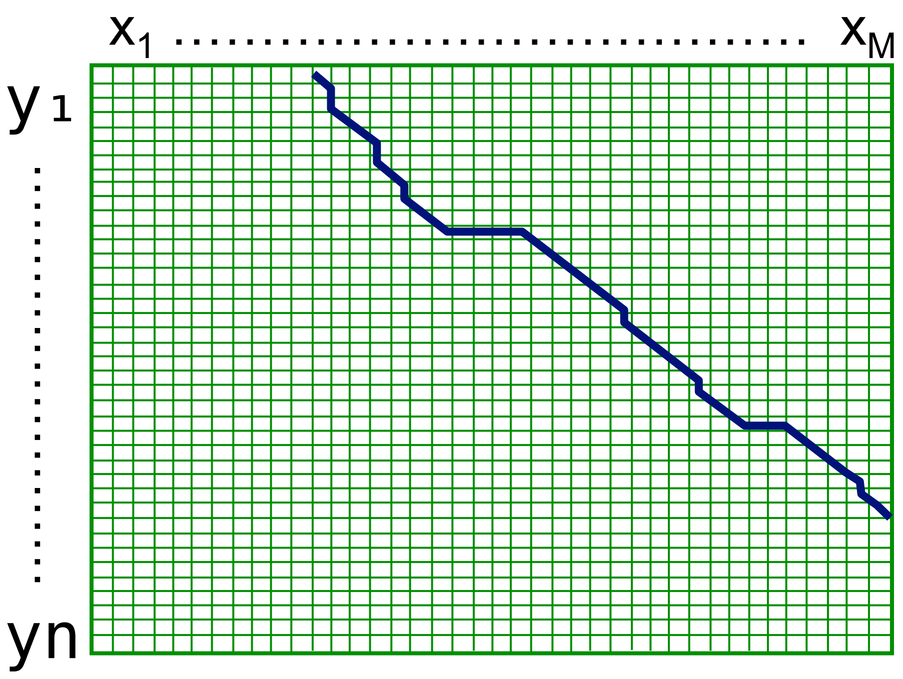


Example:
Search for a mouse gene within a human chromosome

Slide from Serafim Batzoglou

如何用演算法找出Overlap的部分？

The Overlap Detection variant



Slide from Serafim Batzoglou

Changes:

1. Initialization

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

2. Termination

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

The Local Alignment Problem

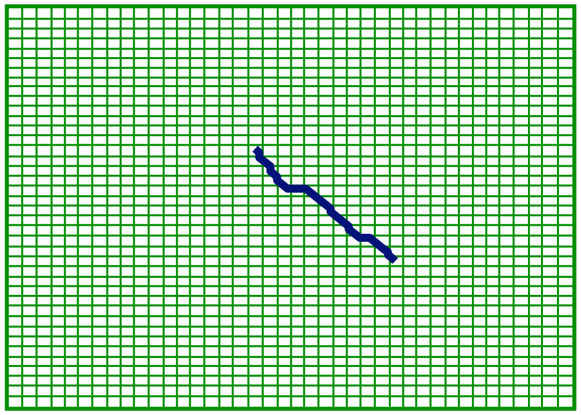
Given two strings $x = x_1......x_M$,

$y = y_1......y_N$

Find substrings x', y' whose similarity

(optimal global alignment value)

is maximum



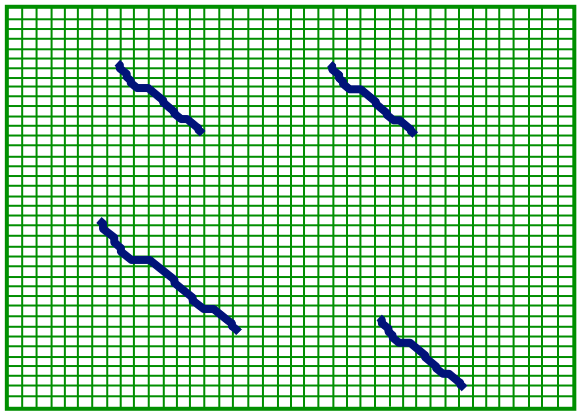
x = aaaac$\boxed{\text{cccggg}}$gtta

y = tt$\boxed{\text{cccggg}}$aaccaacc

Slide from Serafim Batzoglou

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

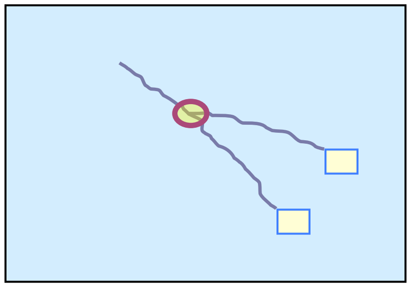
The Smith-Waterman algorithm

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

Slide from Serafim Batzoglou

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

Dan Jurafsky

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	$\boxed{3}$	2

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

Minimum Edit Distance

Minimum Edit Distance in Computational Biology