

# 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
TAGCTATCACGACCGCGGTCGATTGCCCGAC
```

- Resulting alignment:

```
-AGGCTATCACCTGACCTCCAGGCCGA--TGCCC---
TAG-CTATCAC--GACCGC--GGTCGATTGCCCGAC
```

- Also for Machine Translation, Information Extraction, Speech Recognition

# Edit Distance

The minimum edit distance between two strings is

the minimum number of edits

- Insertion
- Deletion
- Substitution

needed to transform one to other.

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 is 2 (Levenshtein)

- Distance between them is 8

# MED app1: Alignment in Computational Biology

- Given a sequence of bases

```
AGGCTATCACCTGACCTCCAGGCCGATGCCC  
TAGCTATCACGACCGCGGTCGATTGCCCCGAC
```

- An alignment:

```
-AGGCTATCACCTGACCTCCAGGCCGA--TGCCC---  
TAG-CTATCAC--GACCGC--GGTCGATTGCCCCGAC
```

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

# MED app2: 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

# MED computation

For two strings

- $X$  of length  $n$
- $Y$  of length  $m$

$D(i, j)$ : the edit distance between  $X[1..i]$  and  $Y[1..j]$

$X[1..i]$ : the first  $i$  characters of  $X$  and

$Y[1..j]$ : the first  $j$  characters of  $Y$

- The edit distance between  $X$  and  $Y$  is thus  $D(n, m)$
- **Dynamic programming:** A tabular computation of  $D(n, m)$

# MED computation

- Initialization

$$D(i, 0) = i$$

$$D(0, j) = j$$

- Recurrence Relation:

For each  $i = 1 \dots M$

For each  $j = 1 \dots N$

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

- Termination:

$D(N, M)$  is distance




# 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

# Edit distance table

N	9									
O	8									
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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 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

# 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

# MED with BACKTRACE

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

# MED+BACKTRACE

- Base conditions:

$$D(i, 0) = i$$

$$D(0, j) = j$$

Termination:

$D(N, M)$  is distance

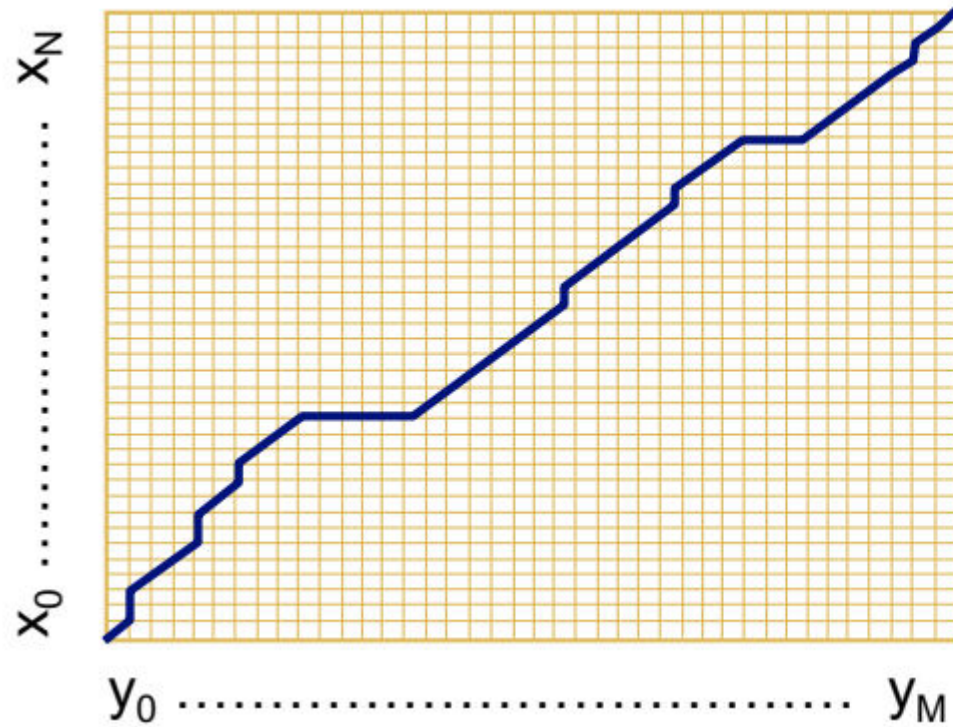
- Recurrence Relation:

For each  $i = 1 \dots M$

For each  $j = 1 \dots N$

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

# 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

# Performance

- Time:

$O(nm)$

- Space:

$O(nm)$

- Backtrace

$O(n+m)$



# Weighted MED

Some errors are more frequent than others.

## Confusion matrix for spelling errors

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

- Initialization:

$$D(0,0) = 0$$

$$D(i,0) = D(i-1,0) + \text{del}[x(i)]; \quad 1 < i \leq N$$

$$D(0,j) = D(0,j-1) + \text{ins}[y(j)]; \quad 1 < j \leq M$$

- Recurrence Relation:

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

- Termination:

$D(N,M)$  is distance