SARDIGNA CHIRCAS
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Artificial Intelligence for developers

8 weekend per diventare Machine Learning Specialist

Natural Language Processing

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Outline of the course

- Intro on AI, ML and NLP
- Text Processing
- Words and Corpora
- Lexical similarity
- Language Modeling
- Text Classification
- Semantic similarity
- Knowledge Graphs
- Intro to Large Language Models

Minimum Edit Distance

Lexical Similarity

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:

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

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

Other uses of Edit Distance in NLP

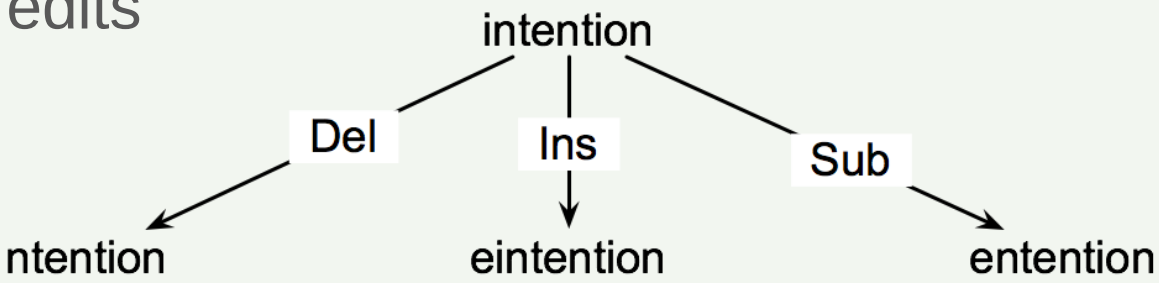
- Evaluating Machine Translation and speech recognition

```
R Spokesman confirms    senior government adviser was 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

Lexical Similarity

Computing the Minimum Edit Distance

Lexical Similarity

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

- Termination:

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

Minimum Edit Distance

Lexical Similarity

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

Computing the Minimum Edit Distance

Lexical Similarity

Backtrace for Computing Alignment

Lexical Similarity

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:

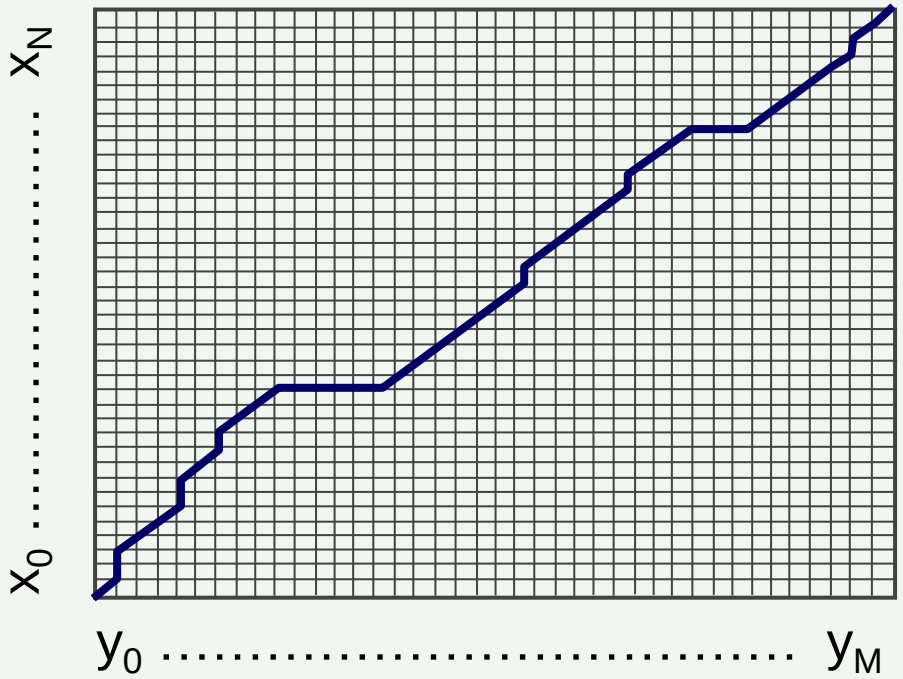
  `D(N,M) is distance`

- Recurrence Relation:

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

                LEFT     insertion
ptr(i,j)=       DOWN     deletion
                DIAG     substitution
```

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

  $O(n+m)$

Backtrace for Computing Alignment

Lexical Similarity

Weighted Minimum Edit Distance

Lexical Similarity

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


Tab
Caps Lock
Enter
Shift
Shift
Ctrl
Alt
Alt

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.

Weighted Minimum Edit Distance

Lexical Similarity

Applications to Computational Biology

Lexical Similarity

Sequence Alignment

```
AGGCTATCACCTGACCTCCAGGCCGATGCCC
TAGCTATCACGACCGCGGTCGATTTGCCCGAC
```

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

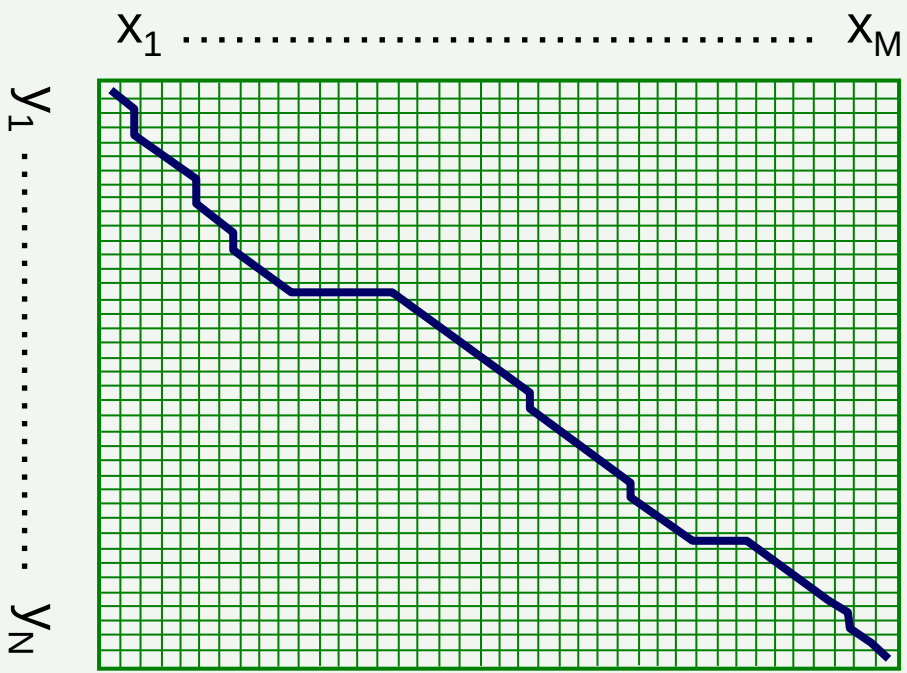
Why sequence alignment?

- 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 Matrix



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

Slide adapted from Serafim Batzoglou WITH PEMISSION

A variant of the basic algorithm:

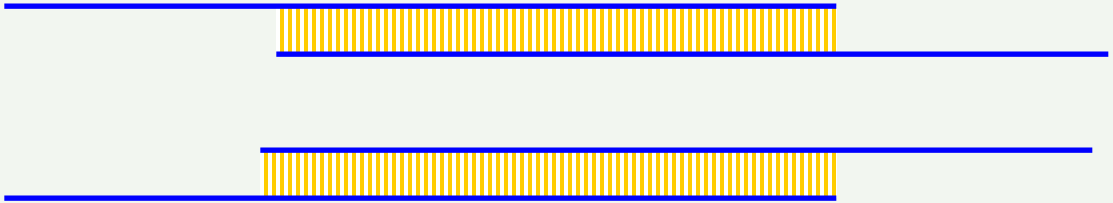
- Maybe it is OK to have an unlimited # of gaps in the beginning and end:

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

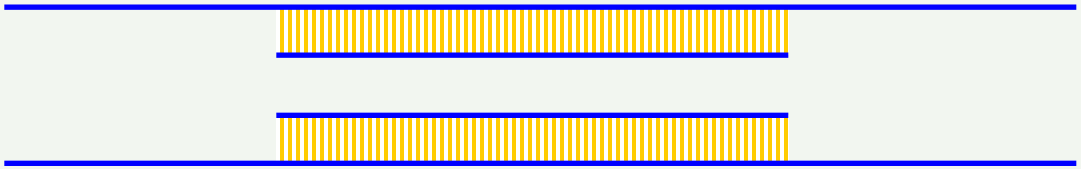
- If so, we don’t want to penalize gaps at the ends

Slide from Serafim Batzoglou WITH PERMISSION

Different types of overlaps



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



Example:
Search for a mouse gene within a human chromosome

Slide from Serafim Batzoglou WITH PERMISSION

Applications to Computational Biology

Lexical Similarity