

# Algorithms and Datastructures

Levenshtein distance, Dynamic programming

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Introduction

Edit distance



## **Edit distance:**

- Measurement for similarity of two words / strings
- Algorithm for efficient calculation
- General principle: dynamic programming

# Introduction

## Motivation: Error tolerant string comparison





eyjafjallajökull

eyjafjallajökull - der unaussprechliche vulkanfilm

eyjafjallajökull film

eyjafjallajökull trailer

[Weitere Informationen](#)

### Ergebnisse für **eyjafjallajökull**

Stattdessen suchen nach: [ejafjatlajökuk](#)

#### Eyjafjallajökull – Wikipedia

[de.wikipedia.org/wiki/Eyjafjallajökull](https://de.wikipedia.org/wiki/Eyjafjallajökull)

Der Name **Eyjafjallajökull** (isländisch für „Inselberge-Gletscher“) rührt von den so genannten Landeyjar (dt. Landinseln) her. Das sind felsige Erhebungen, ...

Name - Der Gletscher - Der Vulkan unter dem Gletscher - Eruptionsgeschichte





#### Eyjafjallajökull - Der unaussprechliche Vulkanfilm Film 2014 ...

[www.kino.de/Filme](http://www.kino.de/Filme)



31.07.2014 - **Eyjafjallajökull** - Der unaussprechliche Vulkanfilm, Irwitzige Komödie um ein verfeindetes Ex-Ehepaar, das wegen der Asche des isländischen ...

#### Bilder zu eyjafjallajökull

Unangemessene Bilder melden



Weitere Bilder zu eyjafjallajökull



### Eyjafjallajökull

Gletscher in Island

Der Eyjafjallajökull, zu deutsch Eyjaföll-Gletscher, ist der sechstgrößte Gletscher Islands. Er liegt an der äußersten Südküste, westlich des Gletschers Mýrdalsjökull in der Gemeinde Rangárþing eystra, die größte Höhe beträgt 1651 m.

[Wikipedia](#)

**Letzte Eruption:** April 2010

**Höhe:** 1.666 m

**Fläche:** 100 km²

**Prominenz:** 1.051 m

**Erstbesteiger:** Sveinn Pálsson

### A lot of applications where similar string are searched:

- Duplicates in databases:

Hein Blöd     27568 Bremerhaven

Hein Bloed    27568 Bremerhafen

Hein Doof     27478 Cuxhaven

- Product search:

memory stik

- Websearch:

eyjaföllajaküll

uniwersität verien 2017

- Bioinformatics: Similarity of DNA-sequences

### Search of similar proteins:

- BLAST (**B**asic **L**ocal **A**lignment **S**earch **T**ool)
- Alignment  $\hat{=}$  Edit distance
- Changed life-science completely

### Google-Scholar entry:

[HTML] Gapped **BLAST** and **PSI-BLAST**: a new generation of protein database search programs

SF Altschul, TL Madden, AA Schäffer... - Nucleic acids ..., 1997 - Oxford Univ Press

Abstract The **BLAST** programs are widely used tools for searching protein and DNA databases for sequence similarities. For protein comparisons, a variety of definitional, algorithmic and statistical refinements described here permits the execution time of the ...

Zitiert von: **58805** Ähnliche Artikel Alle 135 Versionen Zitieren Speichern

## Definition of edit distance: (*Levenshtein-distance*)

- Let  $x$ ,  $y$  be two strings
- Edit distance  $ED(x, y)$  of  $x$  and  $y$ :  
The minimal number of operations to transform  $x$  into  $y$ 
  - Insert a character
  - Replace a character with another
  - Delete a character

# Edit distance

## Example

1 2 3 4 5

DOOF



BOOF



BLOF



BLOEF



BLOED

replace(1, B)

replace(2, L)

insert(4, E)

replace(5, D)

ED=4

1 2 3 4 5

B LOED



B LOEF



B LOF



BOOF



DOOF

replace(5, F)

delete(4)

replace(2,  $\emptyset$ )

replace(1, D)

ED=4



## Notation:

- $\varepsilon$  is the empty string
- $|x|$  is the length of the string  $x$  (number of characters)
- $x[i..j]$  is the slice of  $x$  from  $i$  to  $j$  where  $1 \leq i \leq j \leq |x|$



## Trivial facts:

- $ED(x, y) = ED(y, x)$

- $ED(x, \varepsilon) = |x|$

- $ED(x, y) \geq \text{abs}(|x| - |y|)$

$$\text{abs}(x) = \begin{cases} x & \text{if } x \geq 0 \\ -x & \text{else} \end{cases}$$

- $ED(x, y) \leq ED(x[1..n-1], y[1..m-1]) + 1 \quad n = |x|, m = |y|$

### Solutions based on examples:

- From VERIEN to FERIEEN?
- From MEXIKO to AMERIKA?
- From AAEBEAAABEAREEEAEBA to RBEAAEEBAAAEBBAEAE?
- Searching biggest substrings can yield the solution but doesn't have to

### Recursive approach:

- Dividing in two halves? Not a good idea:

$$ED(\text{GRAU}, \text{RAUM}) = 2 \quad \text{but} \quad ED(\text{GR}, \text{RA}) + ED(\text{AU}, \text{UM}) = 4$$

- Finding “smaller” sub problems?  
Let's try it!

## Terminology:

- Let  $x, y$  be two strings
- Let  $\sigma_1, \dots, \sigma_k$  be a sequence of  $k$  operations where  $k = \text{ED}(x, y)$  for  $x \rightarrow y$  (transform  $x$  into  $y$ )  
(We do not know this sequence but we assume it exists)

## Terminology:

- We only consider **monotonous** sequences:

The position of  $\sigma_{i+1}$  is  $\geq$  the position of  $\sigma_i$  where we only allow the positions to be equal on a delete operation

1 2 3 4 5

DOOF



replace(1, B)

BOOF



replace(2, L)

BLOF



insert(4, E)

BLOEF



replace(5, D)

BLOED

1 2 3 4 5 6 7

SAUDOOF



delete(1)

AUDOOF



delete(1)

UDOOF



delete(1)

DOOF



insert(4, O)

DOOOF

## Terminology:

- **Lemma:** For any  $x$  and  $y$  with  $k = \text{ED}(x, y)$  exists a **monotonous** sequence of  $k$  operations for  $x \rightarrow y$
- **Intuition:** The order of our sequence is not relevant (Therefore we can also sort them monotonously)

1	2	3	4	5
D	O	O	F	

B L O E D

1	2	3	4	5	6	7
S	A	U	D	O	O	F

D O O O F

### Consider the last operation:

- Solve **blue** part recursively

DOOF

↓↓↓↓

BLOE

↓ insert

BLOED

Figure: Case 1a

DOOF

↓↓↓↓↓

BLOEDF

↓ delete

BLOED

Figure: Case 1b

DOOF

↓↓↓↓↓

BLOEF

↓ replace

BLOED

Figure: Case 1c

### Consider the last operation:

- Solve **blue** part recursively

W I N T E R



S O M M E R

↓ nothing

S O M M E R

### Display of solution:

- Alignment

- Example:

—	—	—	B	L	O	E	D
S	A	U	B	L	O	E	D

**Figure:** Case 2



### Dynamic programming:

- Instances of Bellman's principle of optimality:
  - Shortest paths
  - Edit distance



**Figure:** Richard Bellman  
(1920 - 1984)

- Optimal solutions consist of optimal partial solutions
  - Shortest paths: Each partial path has to be optimal
  - Edit distance: Each partial alignment has to be optimal

$\bar{S}$	$\bar{A}$	$\bar{U}$	B		L	O	E	D	E	R
S	A	U	B		L	O	E	D	-	-

- Always solvable through dynamic programming  
(Caching of optimal partial solutions)

## Case analysis:

- We consider the last operation  $\sigma_k$ 
  - $\sigma_1, \dots, \sigma_{k-1}: x \rightarrow z$  and  $\sigma_k: z \rightarrow y$   
Example:

$x = \text{DOOF}, z = \text{SAUBLOEF}, y = \text{SAUBLOED}$

- Let  $n = |x|, m = |y|, m' = |z|$
- We note  $m' \in \{m-1, m, m+1\}$       why?

## Case analysis:

- Case 1:  $\sigma_k$  does something at the outer end:
  - Case 1a:  $\sigma_k = \text{insert}(m' + 1, y[m])$  [then  $m' = m - 1$ ]
  - Case 1b:  $\sigma_k = \text{delete}(m')$  [then  $m' = m + 1$ ]
  - Case 1c:  $\sigma_k = \text{replace}(m', y[m])$  [then  $m' = m$ ]
- Case 2:  $\sigma_k$  does nothing at the outer end:
  - Then  $z[m'] = y[m]$  and  $x[n'] = z[m']$  and with that  
 $\sigma_1, \dots, \sigma_{k-1}: x[1..n-1] \rightarrow y[1..m-1]$  and  $x[n] = y[m]$

## Case analysis:

- Case 1a (insert):  $\sigma_1, \dots, \sigma_{k-1}: x \rightarrow y[1..m-1]$
- Case 1b (delete):  $\sigma_1, \dots, \sigma_{k-1}: x[1..n-1] \rightarrow y$
- Case 1c (replace):  $\sigma_1, \dots, \sigma_{k-1}: x[1..n-1] \rightarrow y[1..m-1]$
- Case 2 (nothing):  $\sigma_1, \dots, \sigma_k: x[1..n-1] \rightarrow y[1..m-1]$

## This results in the recursive formula:

- For  $|x| > 0$  and  $|y| > 0$  is  $ED(x, y)$  the minimum of
  - $ED(x, y[1..m-1]) + 1$  and
  - $ED(x[1..n-1], y) + 1$  and
  - $ED(x[1..n-1], y[1..m-1]) + 1$  if  $x[n] \neq y[m]$
  - $ED(x[1..n-1], y[1..m-1]) + 0$  if  $x[n] = y[m]$
- For  $|x| = 0$  is  $ED(x, y) = |y|$
- For  $|y| = 0$  is  $ED(x, y) = |x|$

```
def edit_distance(x, y):  
    if len(x) == 0:  
        return len(y)  
    if len(y) == 0:  
        return len(x)  
  
    ed1 = edit_distance(x, y[:-1]) + 1  
    ed2 = edit_distance(x[:-1], y) + 1  
    ed3 = edit_distance(x[:-1], y[:-1])  
    if x[-1] != y[-1]:  
        ed3 += 1  
  
    return min(ed1, ed2, ed3)
```

### Recursive program:

- The algorithm results in the following recursive formular:

$$\begin{aligned}T(n, m) &= T(n-1, m) + T(n, m-1) + T(n-1, m-1) + 1 \\&\geq T(n-1, m-1) + T(n-1, m-1) + T(n-1, m-1) \\&= 3 \cdot T(n-1, m-1)\end{aligned}$$

- This results in  $T(n, n) \geq 3^n$

⇒ The runtime is at least exponential

## Dynamic programming:

- We create a table with all possible combination of substrings and save calculated entries
- This results in a runtime and space consumption of  $O(n \cdot m)$

## Visualization on the next slide:

- Operations always refer to the last position (indices are omitted)
- We also display the replaced character on a `replace` operation to visualize operations without costs  
 $\Rightarrow \text{repl}(\text{A}, \text{A})$





### **Fast algorithm:**

We can determine the **edit distance** for all combination of partial strings from the top left to bottom right.



## How to get the sequence of operations?

- We save at each recursion the most efficient previous entry (the **highlighted arrows** in our image)
- There can be **more than one** arrows to the three previous entries
- If we follow the highlighted path from  $(n, m)$  to  $(1, 1)$  we get the optimum operations to transform  $x$  into  $y$ 
  - If we can follow **more than one path** there exist more than one ideal **sequence**



## General principle:

- Recursive computation of ...
  - ... the same reoccurring partial problems
  - ... a limited number of partial problems
- Computation of the solutions for all partial problems
- In a order that unsolved partial problems consist of already solved partial problems
- The “path” to our solution normally gets computed while searching the best solution
- Dijkstra algorithm is basically dynamic programming!

### Additional applications:

- *Edit distance*: global alignment with  $O(n^2)$  space and time consumption
- But: Model for deletion unrealistic
  - In evolution larger pieces are more likely
  - delete operation: first gap expensive (e.g. 2), remaining are cheaper (e.g. 0.5)

			B	L	O	E	D
$\bar{S}$	$\bar{A}$	$\bar{U}$	B	L	O	E	D

- Solution in  $O(n^3)$  time or  $O(n^2)$  affine

$O(n^2)$  space consumption might be problematic:

### **Hirschberg algorithm:**

- Divide-and-conquer approach
- $O(n)$  space and  $O(n^2)$  time consumption



- Sequencing:  $O(n^2)$  is too much
- Index: suffixtree, suffixarray, burrow-wheeler-transform



## ■ General

[CRL01] Thomas H. Cormen, Ronald L. Rivest, and Charles E. Leiserson.

**Introduction to Algorithms.**

MIT Press, Cambridge, Mass, 2001.

[MS08] Kurt Mehlhorn and Peter Sanders.

Algorithms and data structures, 2008.

<https://people.mpi-inf.mpg.de/~mehlhorn/ftp/Mehlhorn-Sanders-Toolbox.pdf>.

## ■ **Dynamic programming**

[Wik] [Dynamic programming](https://en.wikipedia.org/wiki/Dynamic_programming)

`https:`

`//en.wikipedia.org/wiki/Dynamic_programming`

## ■ **Edit distance**

[Wik] [Levenshtein distance](https://en.wikipedia.org/wiki/Levenshtein_distance)

`https:`

`//en.wikipedia.org/wiki/Levenshtein_distance`