

Algorithms and Datastructures

Levenshtein distance, Dynamic programming

Albert-Ludwigs-Universität Freiburg



**UNI
FREIBURG**

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Bioinformatics Group / Department of Computer Science
Algorithms and Datastructures, February 2017

Introduction

Edit distance

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Edit distance:

Edit distance:

- Measurement for similarity of two words / strings

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- Algorithm for efficient calculation



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: [ejafatlajökuk](#)

Eyjafjallajökull – Wikipedia

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



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



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uniwersität verien 2017

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- Bioinformatics: Similarity of DNA-sequences

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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

Introduction

Edit distance

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

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Edit distance

Example



1 2 3 4 5
DOOF

BLOED

Edit distance

Example



1 2 3 4 5

DOOF



replace(1, B)

BOOF

BLOED

Edit distance

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BLOF

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⏟
ED=4

Edit distance

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BOOF



BLOF



BLOEF



BLOED

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Edit distance

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BOOF



BLOF



BLOEF



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⏟
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B LOED

DOOF

Edit distance

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BOOF



BLOF



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B LOED



B LOEF

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DOOF

Edit distance

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DOOF



BOOF



BLOF



BLOEF



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BOOF



BLOF



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B LOF



BOOF

DOOF

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Edit distance

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DOOF



BOOF



BLOF



BLOEF



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BOOF



DOOF

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BOOF



BLOF



BLOEF



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



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Recursive approach:

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Recursive approach:

- Dividing in two halves? Not a good idea:

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

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



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- 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)



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

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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

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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:

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- Solve **blue** part recursively

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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:

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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:

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- Instances of Bellman's principle of optimality:

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Figure: Richard Bellman
(1920 - 1984)

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- 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

Dynamic programming:

- Instances of Bellman's principle of optimality:
 - Shortest paths
 - Edit distance
- 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
- Always solvable through dynamic programming
(Caching of optimal partial solutions)



Figure: Richard Bellman
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 - $\sigma_1, \dots, \sigma_{k-1}: x \rightarrow z$ and $\sigma_k: z \rightarrow y$

Example:

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

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- Let $n = |x|$, $m = |y|$, $m' = |z|$

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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?



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 - Case 1c: $\sigma_k = \text{replace}(m', y[m])$ [then $m' = m$]
- Case 2: σ_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 $x[n] = y[m]$



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 - $ED(x[1..n-1], y) + 1$ and
 - $ED(x[1..n-1], y[1..m-1]) + 1$ if $x[n] \neq y[m]$

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

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
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```
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:

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- The algorithm results in the following recursive formular:

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

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⇒ The runtime is at least exponential



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- Operations always refer to the last position (indices are omitted)

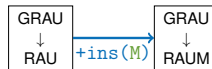
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Visualization on the next slide:

- 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
 $\Rightarrow \text{repl}(\text{A}, \text{A})$









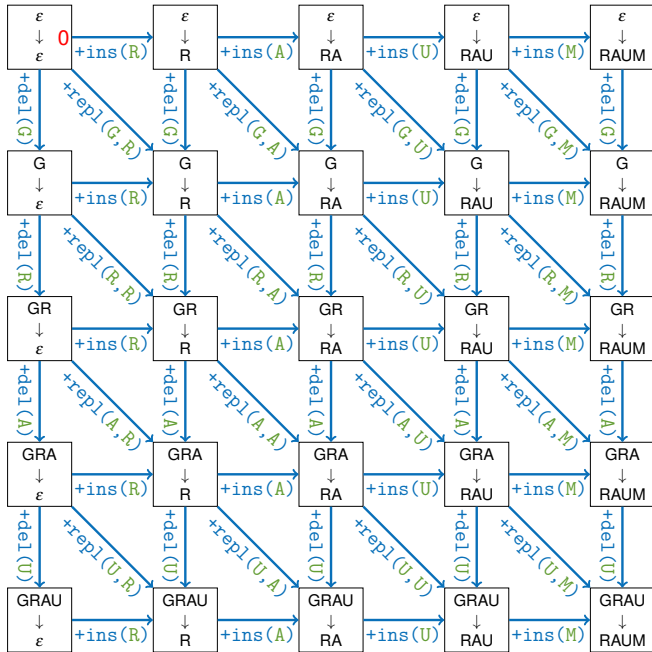






Fast algorithm:

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



















































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 - If we can follow **more than one path** there exist more than one ideal **sequence**



General principle:

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- 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:



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

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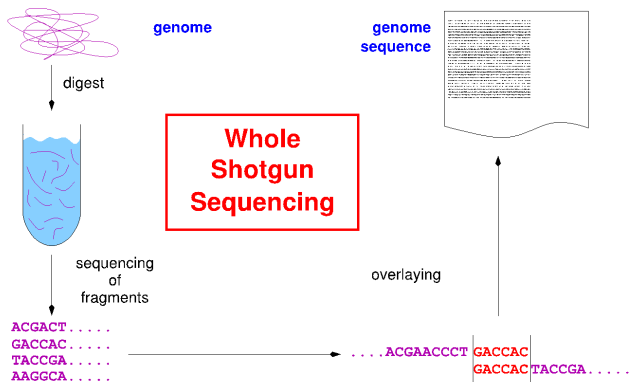
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Hirschberg algorithm:

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

Edit distance

Additional applications (III)





- Sequencing: $O(n^2)$ is too much



- 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.

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■ **Dynamic programming**

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

`https:`

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■ **Edit distance**

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

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