

Longest Common Subsequences

Seminar 2

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1. Introduction

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1.1 What are LCS?

Notation

 $"LCS" = Longest \ Common \ Subsequence(s)$

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Example 1

 S_1 : A B A B B

Notation

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 $S_1:$ A B A B B $S_2:$ A A B A B

 \implies The LCS between S_1 and S_2 is **A B A B**

Notation

"LCS" = Longest Common Subsequence(s)

Example 1

 $S_1:$ A B A B B $S_2:$ A A B A B

 \implies The LCS between S_1 and S_2 is **A B A B**

NB: LCS may not be unique, A A B B also works.

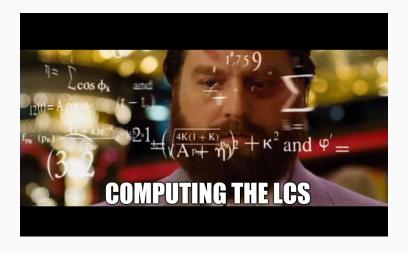
Example 2

What is the LCS of the following sequences ?

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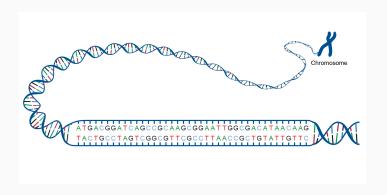


1. Introduction

1. Illitoduction

1.2 Why are we interested in LCS?

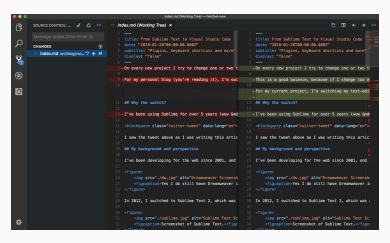
• Bioinformatics: Compare sequences of nucleotides (DNA)



- Bioinformatics: Compare sequences of nucleotides (DNA)
- Natural Language Processing: Compare texts



- Bioinformatics: Compare sequences of nucleotides (DNA)
- Natural Language Processing: Compare texts
- Computer Science: Detect differences in texts



2. How to find LCS?

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2.1 Step A: Building the table

Set-up

Let $S_1 = ABABB$ and $S_2 = AABAB$.

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• Make a table where S_1 and S_2 are the column and row names respectively.

	Α	В	Α	В	В
Α					
Α					
В					
Α					
В					

Set-up

Let $S_1 = ABABB$ and $S_2 = AABAB$.

- Make a table where S_1 and S_2 are the column and row names respectively.
- Add a row (resp. column) at the top (resp. left) of the table.
 Fill them with 0's.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0					
Α	0					
В	0					
Α	0					
В	0					

- If row and column names match, increment adjascent top-left-diagonal cell by 1.
- Else take the maximum of top and left cells.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0					
Α	0					
В	0					
Α	0					
В	0					

- If row and column names match, increment adjascent top-left-diagonal cell by 1.
- Else take the maximum of top and left cells.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0	1				
Α	0					
В	0					
Α	0					
В	0					

- If row and column names match, increment adjascent top-left-diagonal cell by 1.
- Else take the maximum of top and left cells.

	Ø	Α	В	А	В	В
Ø	0	0	0	0	0	0
Α	0	1	1			
Α	0					
В	0					
Α	0					
В	0					

- If row and column names match, increment adjascent top-left-diagonal cell by 1.
- Else take the maximum of top and left cells.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0	1	1	1		
Α	0					
В	0					
Α	0					
В	0					

- If row and column names match, increment adjascent top-left-diagonal cell by 1.
- Else take the maximum of top and left cells.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0	1	1	1	1	
Α	0					
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Ø	0	0	0	0	0	0
Α	0	1	1	1	1	1
Α	0					
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Ø	0	0	0	0	0	0
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Α	0	1				
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Ø	0	0	0	0	0	0
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Α	0	1	1			
В	0					
Α	0					
В	0					

- If row and column names match, increment adjascent top-left-diagonal cell by 1.
- Else take the maximum of top and left cells.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0	1	1	1	1	1
Α	0	1	1	2		
В	0					
Α	0					
В	0					

- If row and column names match, increment adjascent top-left-diagonal cell by 1.
- Else take the maximum of top and left cells.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0	1	1	1	1	1
Α	0	1	1	2	2	2
В	0					
Α	0					
В	0					

Start from top-left corner. Move left to right, line by line.

- If row and column names match, increment adjascent top-left-diagonal cell by 1.
- Else take the maximum of top and left cells.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0	1	1	1	1	1
Α	0	1	1	2	2	2
В	0	1	2	2	3	3
Α	0					
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	Ø	Α	В	А	В	В
Ø	0	0	0	0	0	0
Α	0	1	1	1	1	1
Α	0	1	1	2	2	2
В	0	1	2	2	3	3
Α	0	1	2	3	3	3
В	0	1	2	3	4	4

 \implies The length of the LCS is 4.

2. How to find LCS?

2.2 Step B: Crawling back up the table

From the table, deduce LCS by starting from the bottom-right cell. Compare cell value with values of top and left cells.

- If cell value ∈ {top cell value, left cell value}, move to the one with maximum value.
- Else, add character to LCS and move 1 cell diagonally top-left.

	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0	1	1	1	1	1
Α	0	1	1	2	2	2
В	0	1	2	2	3	3
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LCS: __ _ B

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	Ø	Α	В	Α	В	В
Ø	0	0	0	0	0	0
Α	0	1	1	1	1	1
Α	0	1	1	2	2	2
В	0	1	2	2	3	3
Α	0	1	2	3	3	3
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LCS: __ A B

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LCS: A B A B

3. Data analysis of LCS results

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3.1 Average LCS length

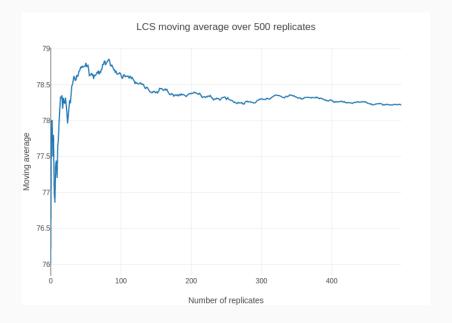
Question

Given two sequences of the same length, what percentage do they have in common?

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Given two sequences of the same length, what percentage do they have in common?

Answer: $\approx 80\%$



Superadditivity

Let L_n be the length of the LCS between two sequences of length n.

Proposition

 $(\mathbb{E}[L_n])_{n\geq 1}$ is a superadditive sequence, that is

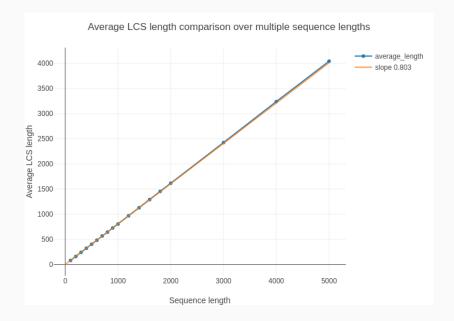
$$\mathbb{E}[L_{m+n}] \geq \mathbb{E}[L_m] + \mathbb{E}[L_n]$$

 S_1 : **A B A B** B S_2 : **A** A B **B B**

 S_1 : **A B A B** B S₃: **A** B S₂: **A** A **B** A B S₄: B **A**

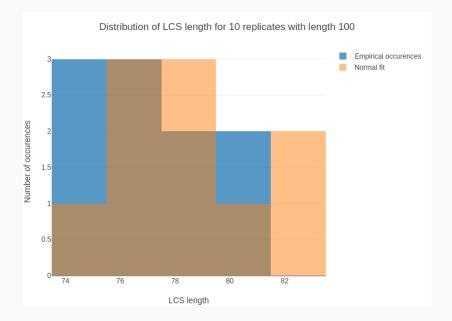
A B A B B A B A B

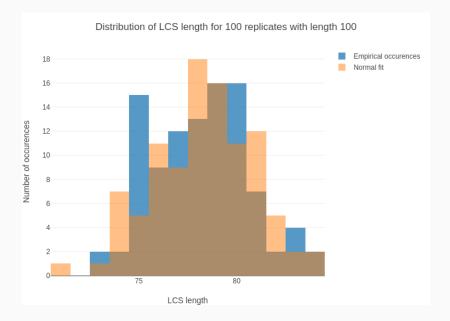
A B A B B A B A B

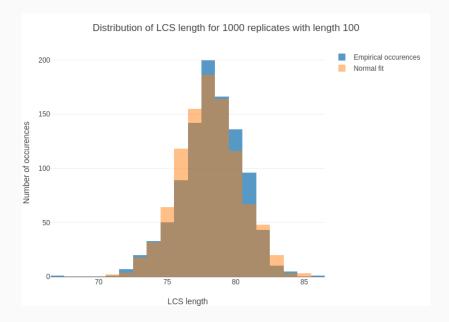


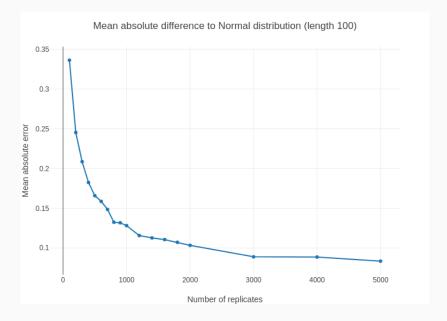
3. Data analysis of LCS results

3.2 Normal fit









Thank you

Questions?

https://github.com/jorislimonier/LCS