# Fully-Compressed Suffix Trees

Luís M. S. Russo

CITI (FCT/UNL)
**lsr@di.fct.unl.pt**

O Gosto pela Matemática - Uma Década de Talentos

# Outline

# Pattern Matching Problem 29 min

**Problem (Exact Matching)**

*Find pattern $P$ in text $T$.*

**Example**

1. $T = acctgcgctagct$, $n = 13$, $\sigma = 4$
2. $acctgcgctagct$, $P = c$, $m = 1$, $occ = 5$
3. $acctgcgctagct$, $P = cct$, $m = 3$, $occ = 1$

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# Text Database Problems

27 min

**Problem (On-line Limitations)**

*On-line solutions are not viable for large text databases, $O(m + n)$.*

**Example (On-line scan)**

- Scanning 3Gb DNA sequences takes too long.
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- We need indexes that have $O(m + occ)$ time.
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# The Suffix Tree

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- Suffix trees have optimal $O(m + occ)$ performance.
- What is a suffix tree ?
- Gather the suffixes & build a tree.

## Example (Suffix Tree for *atttat*)

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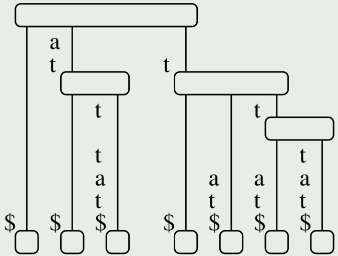

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- Searching means descending from the ROOT & reporting leaves bellow.
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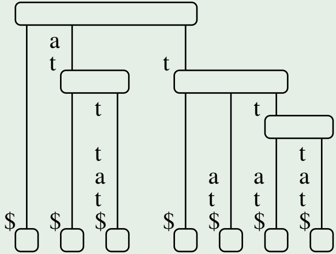

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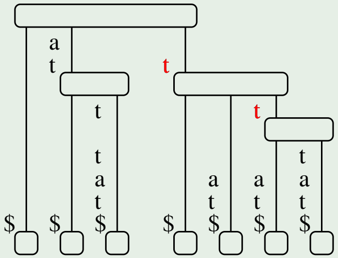

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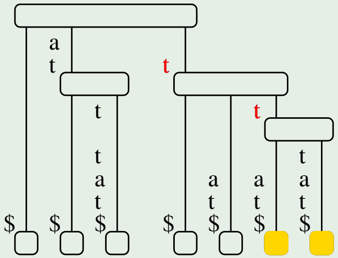

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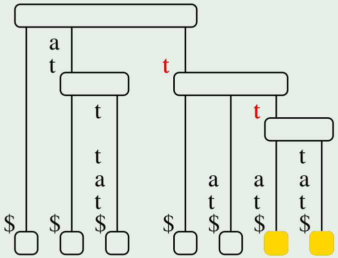

# Suffix Tree Representation 22 min

- Naive construction takes $O(n^2)$ space & time
- Efficient algorithms using pointers and amortized analysis take $O(n)$ space & time.

## Example (Suffix Tree for *atttat*)

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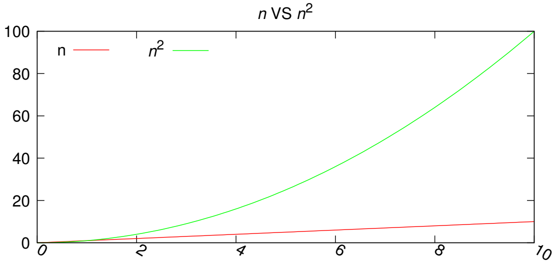
# What is the difference ? 20 min

There is no way to index 3Gb DNA with an $O(n^2)$ algorithm



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19 min

- Not going to explain Ukkonen's algorithm
- Key concept SLINK, always exists

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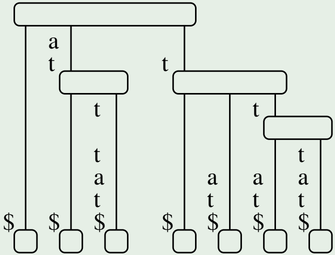

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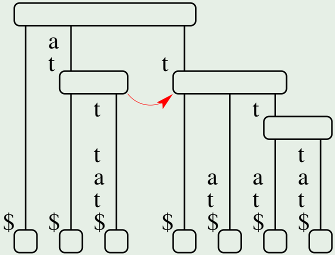

# Representation Problems

17 min

**Problem (Suffix Trees need too much space)**

*Pointer based representations require $O(n \log n)$ bits.*

- This is much larger than the indexed string, $n \log \sigma$ bits.
- State of the art implementations require $[8, 10] \times 8n$ bits.
- This is 48 Gb for 3 Gb of DNA, i.e. for the human genome.
- Modern representations use data compression techniques.
- Compressing the tree requires finding regularities.

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*Pointer based representations require $O(n \log n)$ bits.*

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# Lowest Common Ancestors 15 min

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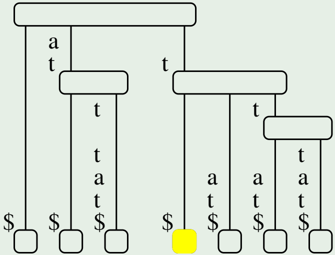

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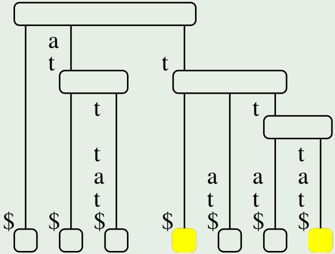

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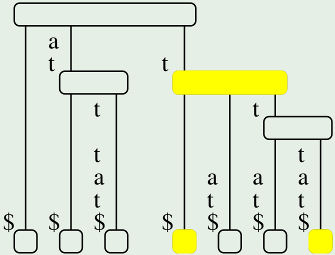

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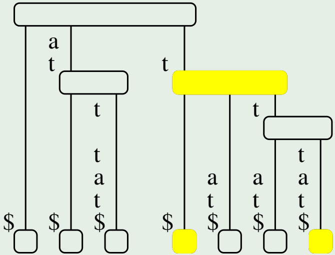

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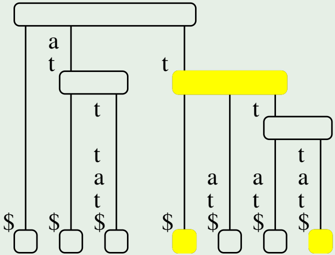


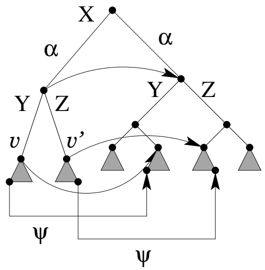
# LCA and SLINK

12 min

**Lemma**

*When* $\mathrm{LCA}(v, v') \neq \textsc{Root}$ *we have that:*

$$\textsc{SLink}(\mathrm{LCA}(v, v')) = \mathrm{LCA}(\textsc{SLink}(v), \textsc{SLink}(v'))$$

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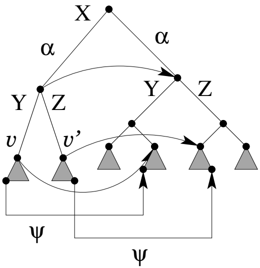


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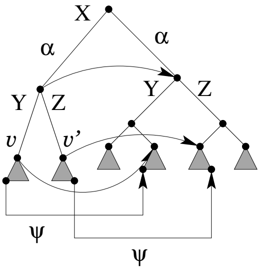


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# Fundamental lemma

10 min

**Lemma**

*If* $\text{SLINK}^r(\text{LCA}(v, v')) = \text{ROOT}$, *and let* $d = \min(\delta, r+1)$.
*Then* $\text{SDEP}(\text{LCA}(v, v')) =$

$$\max_{0 \leq i < d}\{i + \text{SDEP}(\text{LCSA}(\text{SLINK}^i(v), \text{SLINK}^i(v')))\}$$

**Proof.**

$$\begin{aligned}\text{SDEP}(\text{LCA}(v, v'))& \\ &= i + \text{SDEP}(\text{SLINK}^i(\text{LCA}(v, v'))) \\ &= i + \text{SDEP}(\text{LCA}(\text{SLINK}^i(v), \text{SLINK}^i(v'))) \\ &\geq i + \text{SDEP}(\text{LCSA}(\text{SLINK}^i(v), \text{SLINK}^i(v')))\end{aligned}$$

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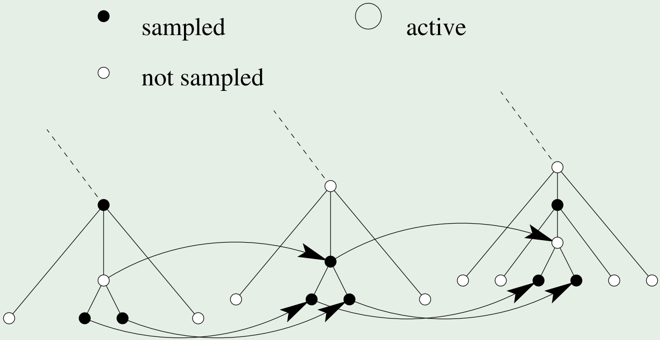
7 min

## Example ($\delta = 3$)



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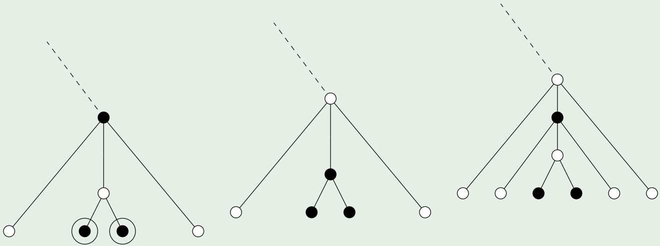

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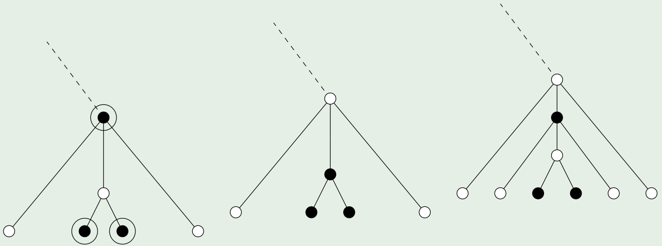

SDEP : 5

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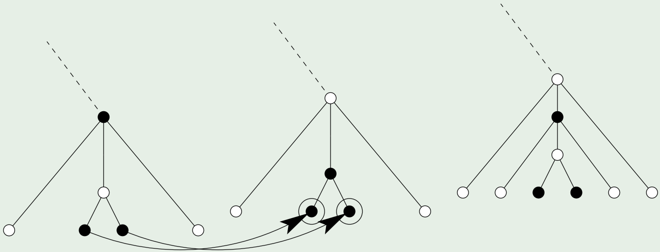

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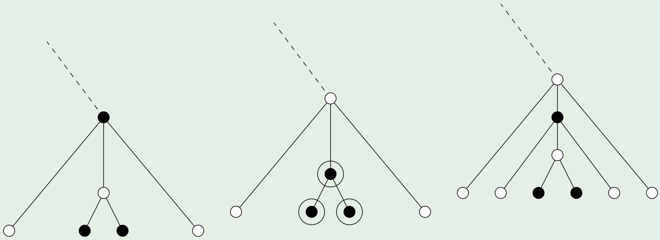

SDEP : 5 10

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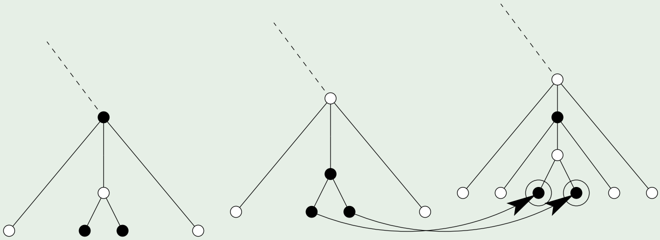

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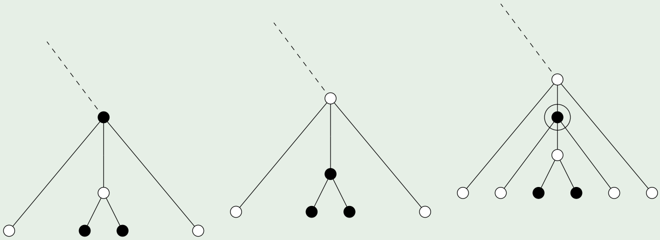

SDEP : 5 10 7

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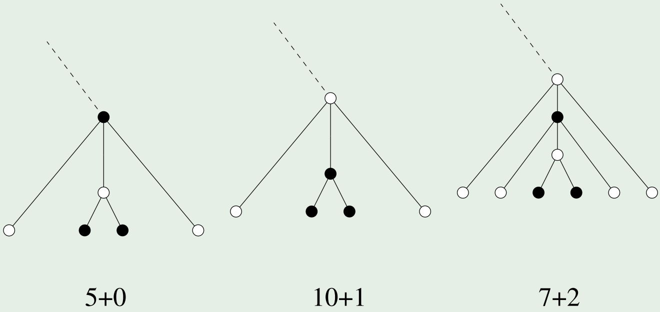

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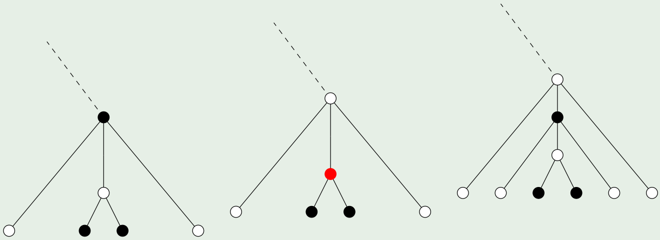


5+0

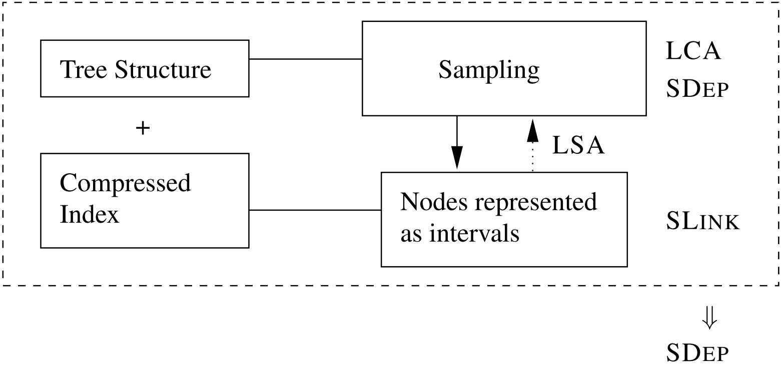
10+1

7+2

# Entangled Operations

6 min

Why is the lemma important ?



# Experimental Results

3 min

| Space in MBs | File | FCST | FFCST | LSA | LSAF | CST |
|---|---|---|---|---|---|---|
| Pitches | 53 | 44 | 134 | 43 | 50 | 214 |
| Proteins | 63 | 50 | 121 | 48 | 56 | 204 |
| DNA | 100 | 57 | 142 | 54 | 69 | 287 |
| XML | 100 | 55 | 198 | 52 | 67 | 316 |

| CHILD Operation | Pitches | Proteins | DNA | XML |
|---|---|---|---|---|
| FCST | 1.3E-2 | 3.4E-3 | 1.6E-3 | 8.7E-3 |
| FFCST | 9.4E-3 | 5.7E-3 | 7.2E-1 | 1.9E-2 |
| LSA | 7.6E-3 | 2.7E-3 | 2.E-3 | 9.7E-3 |
| LSAF | 1.3E-2 | 3.5E-3 | 1.6E-3 | 8.9E-3 |
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# Summary

2 min

We presented a representation of suffix trees that:

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