Advanced Data Structures for Sequence Analysis

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Let us have only a glimpse...

Preliminaries: Suffix Trees

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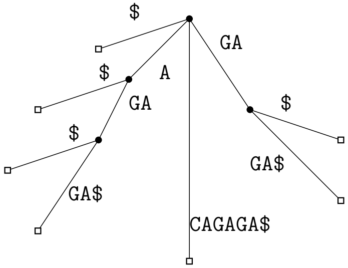
Let $T =$ `CAGAGA$`.



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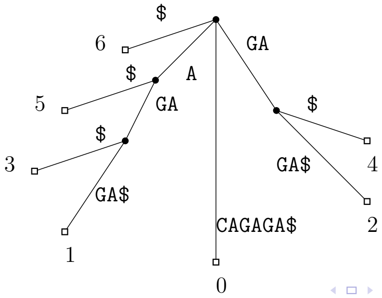

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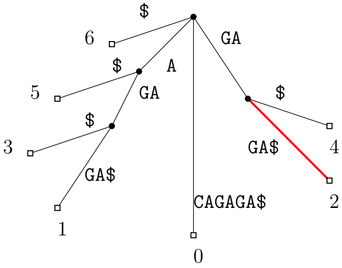

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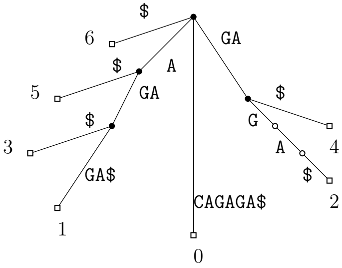

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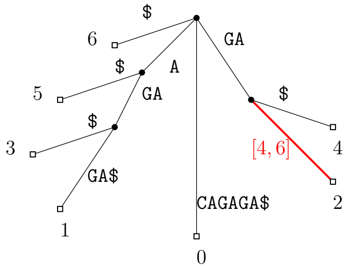

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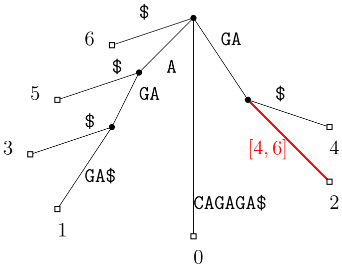

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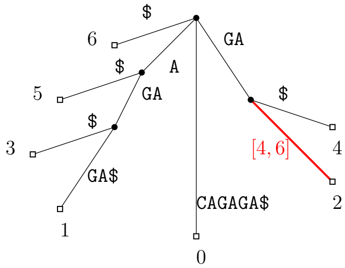

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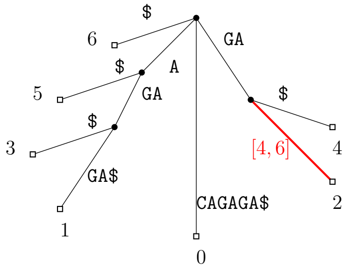

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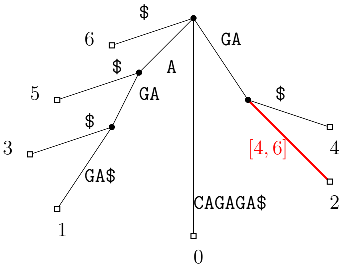

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Space linear in n: $O(n)$.

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In bioinformatics we usually have that $\Sigma = O(1)$.

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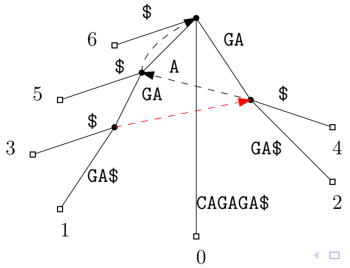
Let $T = \texttt{CAGAGA\$}$. $S_u = \texttt{AGA}$ and $S_v = \texttt{GA}$.



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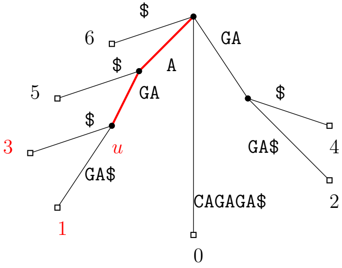

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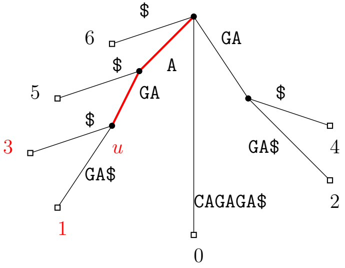

Traverse the subtree rooted at u with $S_u = P$.

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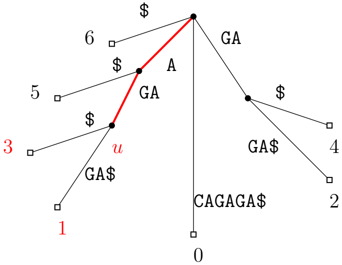

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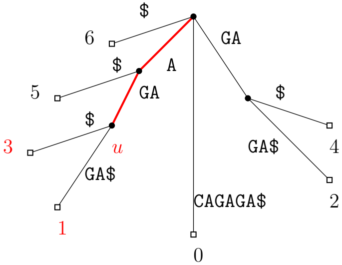

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Theorem

Exact string matching queries can be answered in $O(|P| + occ)$ time after $O(n)$ time preprocessing.

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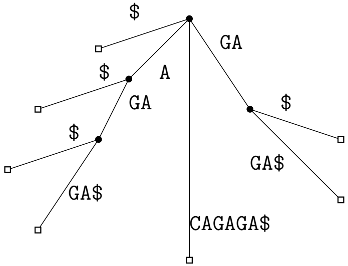

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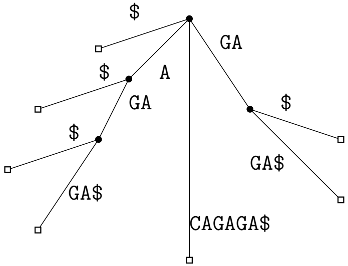

Every *locus* **(node, depth)** in the suffix tree represents a substring of the text and every substring is represented by some locus.

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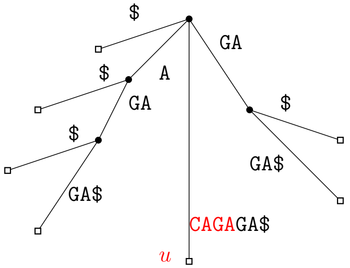
Let $T =$ CAGAGA\$. Locus $(u, 4)$ represents CAGA.



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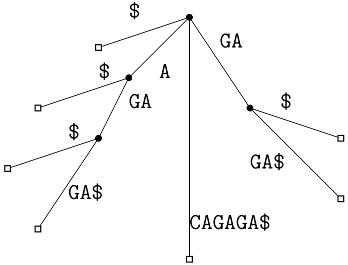

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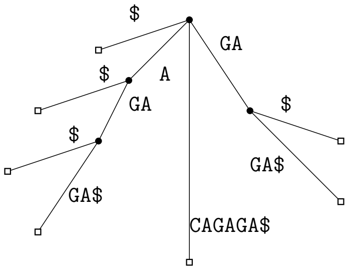

Count the number of distinct loci using a suffix tree traversal.

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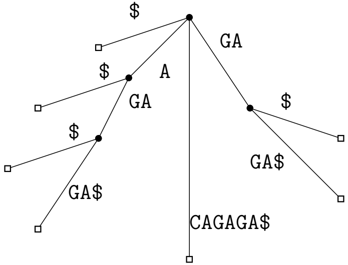

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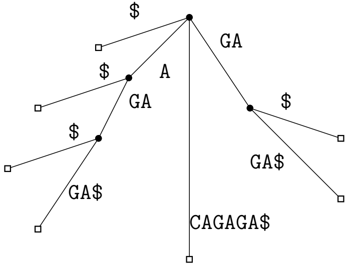

Theorem

The number of distinct substrings can be computed in $O(n)$ time.

Application 3: Longest repeating substring

INPUT: text T

OUTPUT: a longest string occurring at least twice

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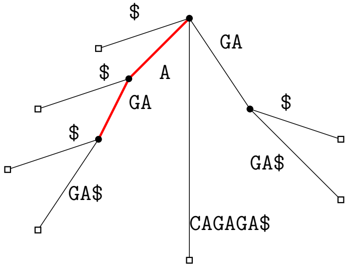
Let $T =$ CAGAGA\$. The answer is AGA.



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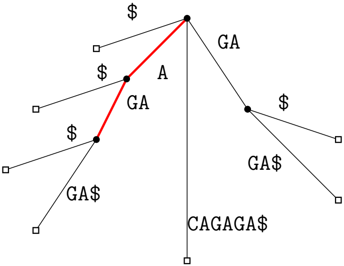

Find a deepest internal node using a traversal of the suffix tree.

Theorem

A longest repeating substring can be found in $O(n)$ time.

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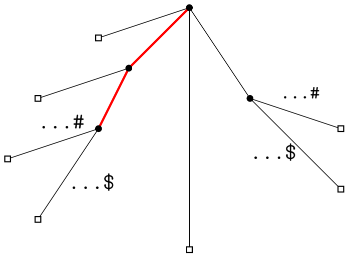

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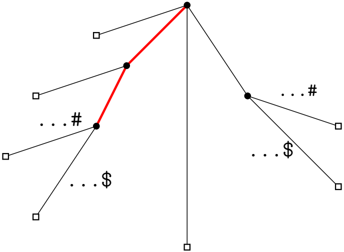

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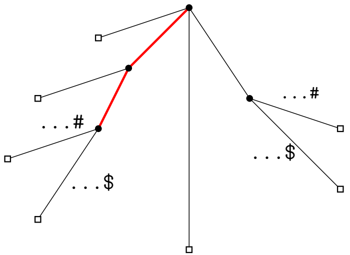

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Theorem

A longest common substring can be found in $O(n + |S|)$ time.

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QUERY: a text S; return the longest prefix of $S[i\,..]$ that is a substring of T, for all $i \in [0, |S|-1]$

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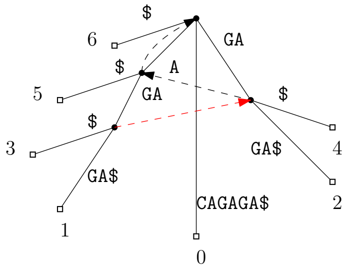

Scan S using the suffix tree of T.

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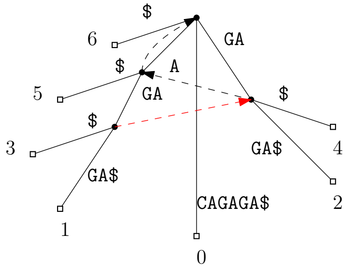

Spell $S[i\,..]$ as much as possible;

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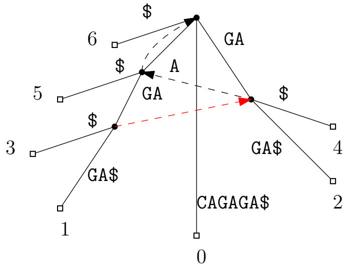

Spell $S[i\,..]$ as much as possible; say $S[i\,..\,j-1]$.

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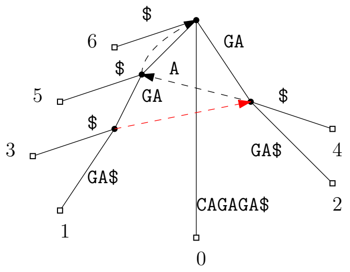

Mismatch at $S[i\,..\,j]$?

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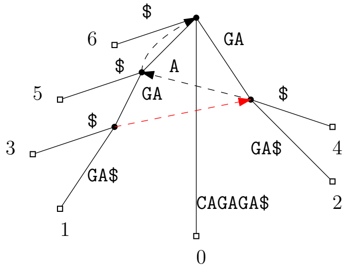

Mismatch at $S[i\,..\,j]$? Use suffix link as the failure transition!

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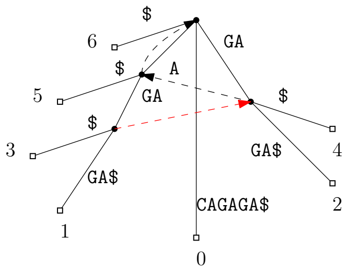

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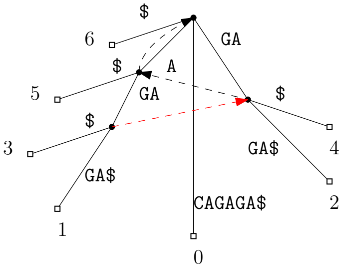

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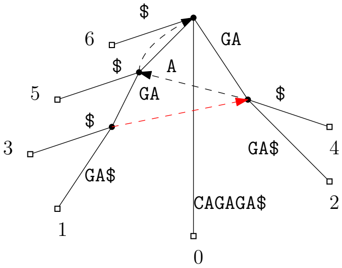

Theorem

Matching statistics of S with respect to T can be computed in $O(|S|)$ time after $O(n)$ time preprocessing.

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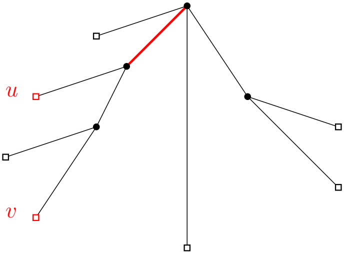
The lowest common ancestor (LCA) of two nodes u and v is the deepest node that is an ancestor of both u and v.



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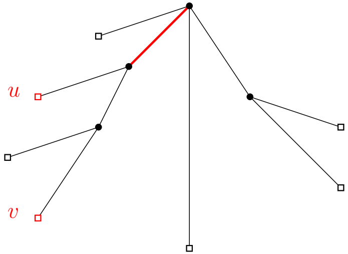
QUERY: a pair (i, j); return the longest common prefix of $T[i\,..]$ and $T[j\,..]$
The lowest common ancestor (LCA) of two nodes u and v is the deepest node that is an ancestor of both u and v.



Theorem (Bender and Farach-Colton, LATIN 2000)

Any tree of size $O(N)$ can be preprocessed in $O(N)$ time so that the LCA of any two nodes can be computed in $O(1)$ time.

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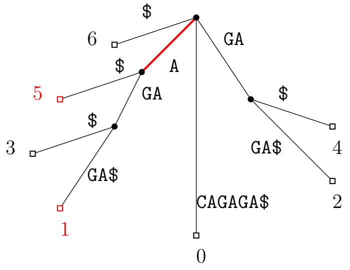
Let $T =$ CAGAGA\$. Let $(1, 5)$ be the query. The answer is A.



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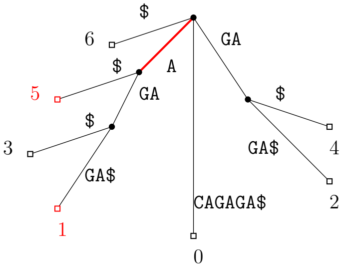

Theorem

Longest common prefix queries can be answered in $O(1)$ time after $O(n)$ time preprocessing.

Application 7: Longest palindromic substring

INPUT: text T
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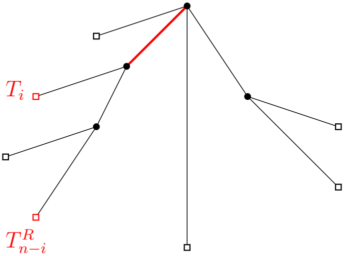

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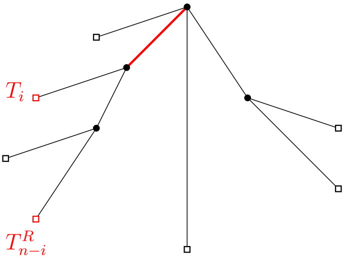

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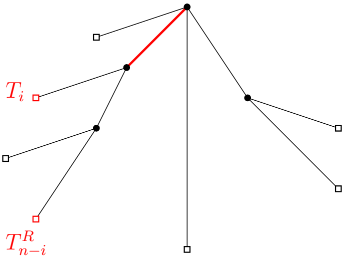

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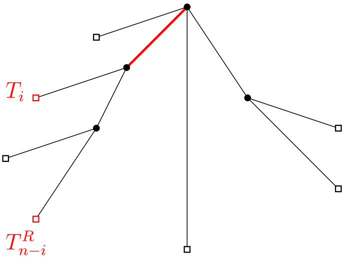

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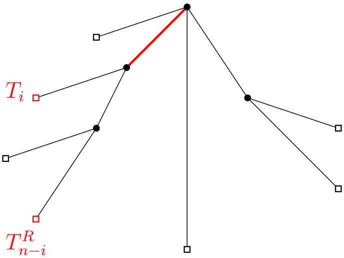

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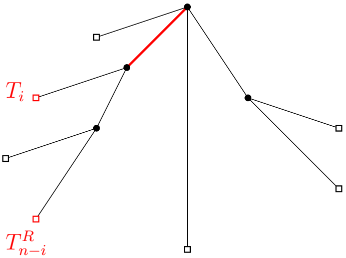

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Theorem

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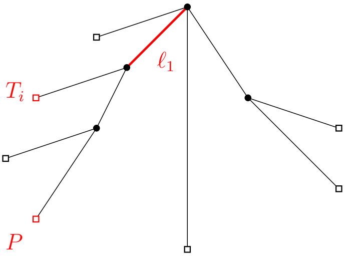

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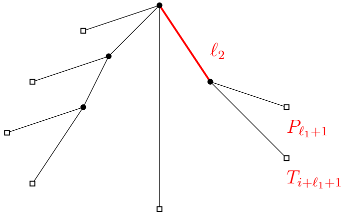

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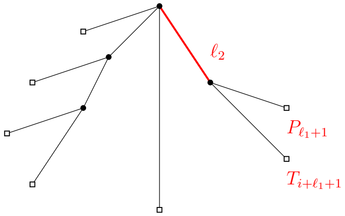

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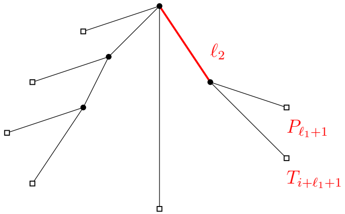

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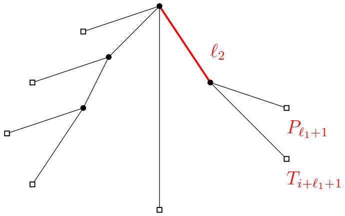

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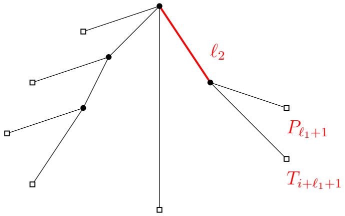

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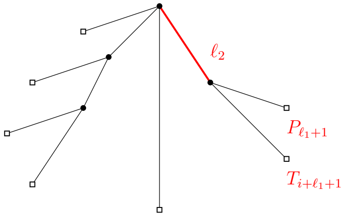

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Theorem (Landau and Vishkin, TCS 1986)

Approximate string matching can be solved in $O(kn)$ time.

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Let $T = \texttt{abbaabbbaaabab}$.

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Why do we care? LZ factorization is a basic and powerful technique for text compression (and string algorithms)!

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Theorem

LZ factorization can be computed in $O(n)$ time.

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OUTPUT: a shortest unique substring of T

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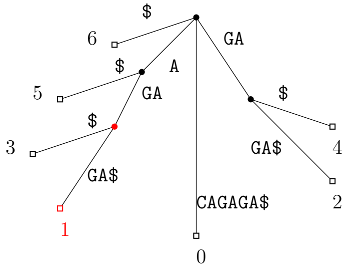

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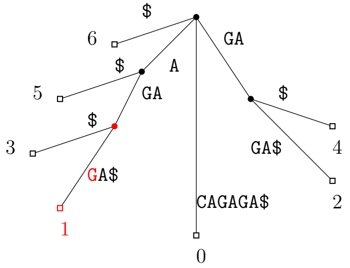

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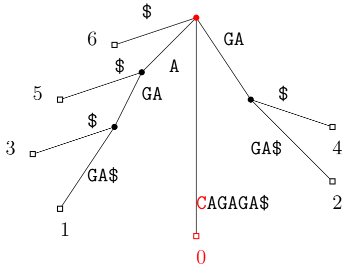
Let $T =$ CAGAGA\$. The shortest unique substring is C.



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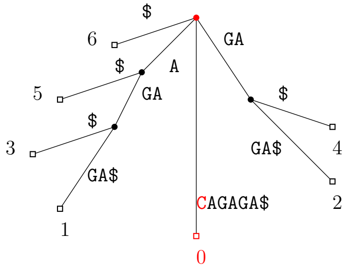

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Take-home message

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Thanks!