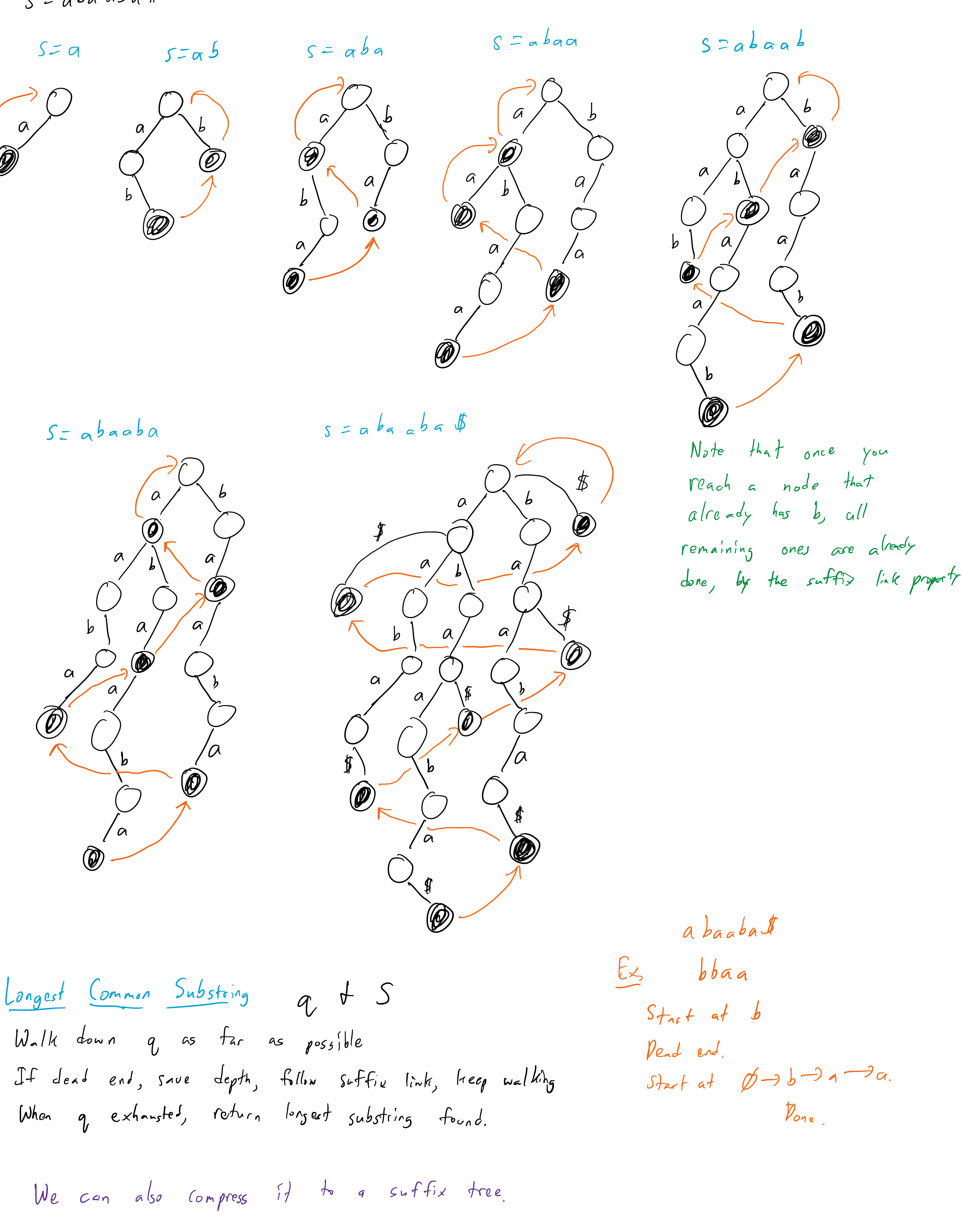
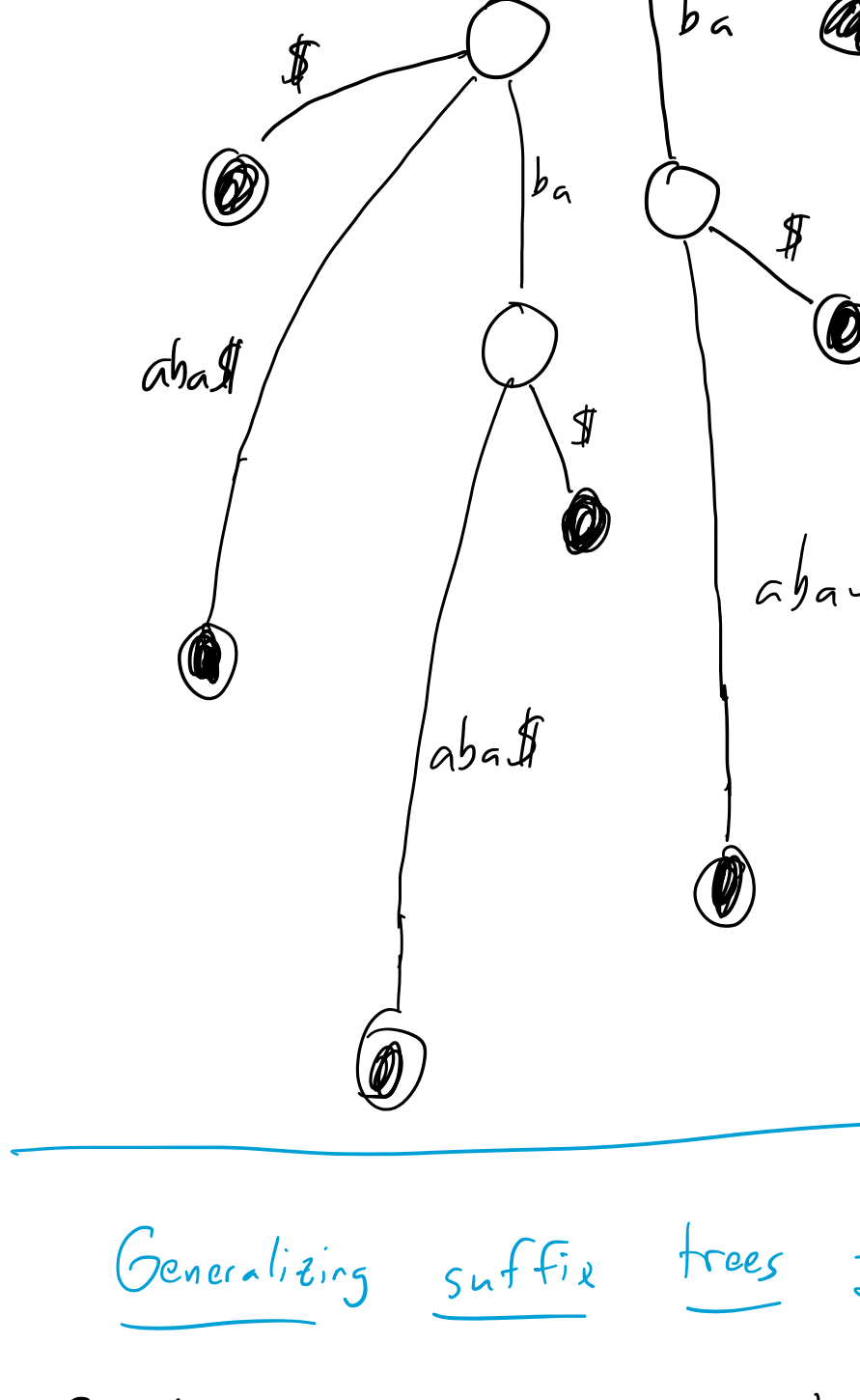


Last time we learned about suffix tries & trees.
 Let's remind ourselves of suffix trie construction.
 We build it up while walking the string from left to right.



We can also compress it to a suffix tree.

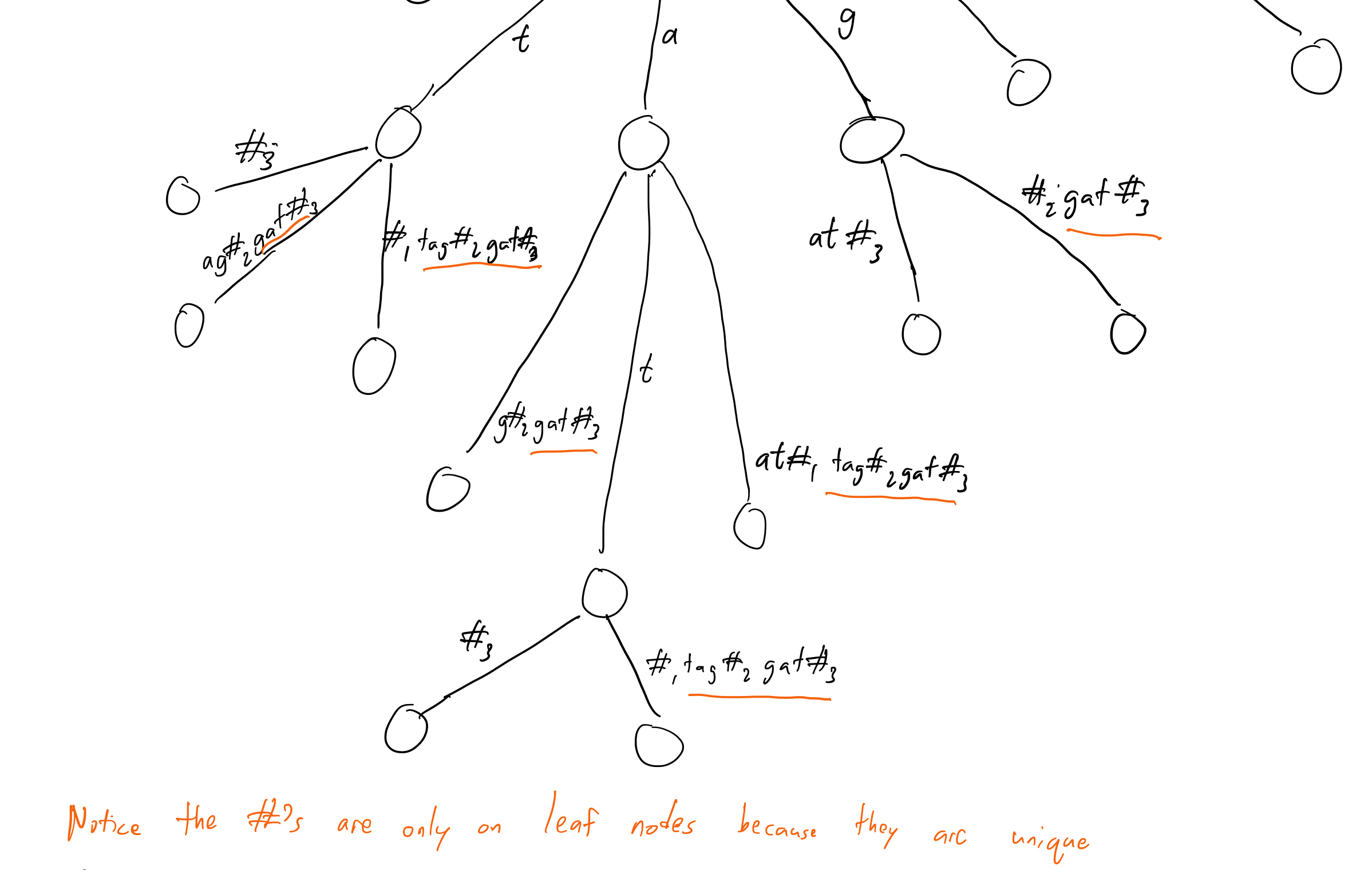


Generalizing suffix trees to multiple strings (GST)

Goal: represent set of strings $P = \{S_1, S_2, \dots, S_m\}$

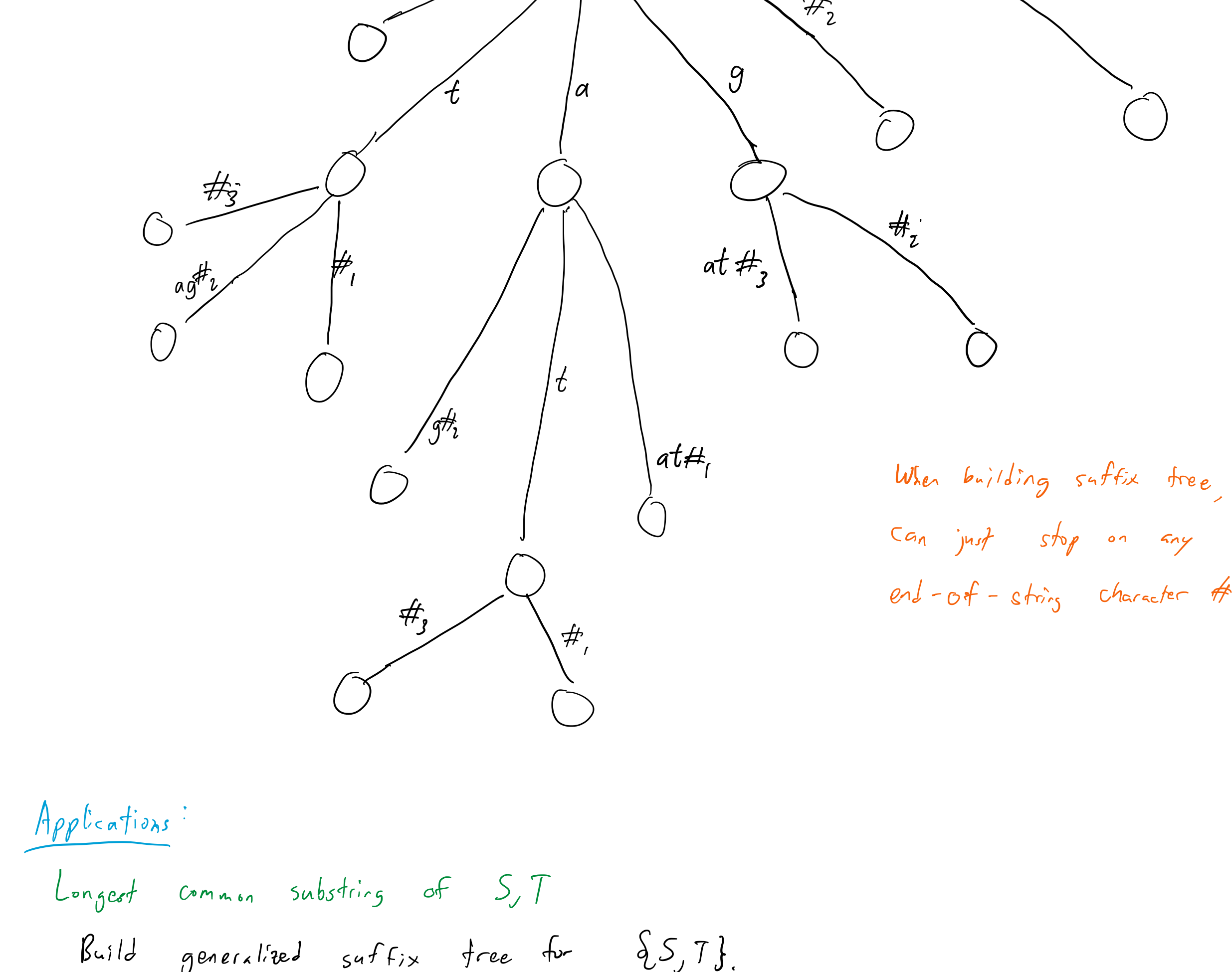
Ex: aat, tag, gat

Sol. build suffix tree for aat# tag# gat#



Notice the #s are only on leaf nodes because they are unique

Remove any text after first # on leaf.



When building suffix tree, can just stop on any end-of-string character #.

Applications:

Longest common substring of S, T

Build generalized suffix tree for $\{S, T\}$.

Find deepest node that has descendants from both strings

(containing both $\#_1$ & $\#_2$)

Determine strings in database $\{S_1, \dots, S_m\}$ that contain query q .

Build GST.

Follow path for q .

If we end at node u , traverse the tree below u & exit if $\#_2$ is found.

Longest Common Extension at i, j

Given strings S & T , want to find longest substring of S starting at i

that matches a substring of T starting at j .

S T

Ex AAAATTTT CCCC GGGG TTTT CCCC GGGG AAAA

$i=9$ $i=5$

Can solve by walking on both strings until mismatch, but we want to do this faster by preprocessing.

Sol. Build GST for S, T . $O(|S| + |T|)$ time.

Preprocess tree so that lowest common ancestors can be found in constant time

We are not covering LCA in 1531, but exists complicated data structure that takes $O(|S| + |T|)$ time to build initially.

In 1531/02613, we take for granted this LCA data structure

Create array mapping suffix numbers to leaf nodes. $O(|S| + |T|)$ time.

Given query (i, j) :

Find leaf nodes for i, j . $O(1)$

Return string of LCA for i, j . $O(1)$



Using LCE to find palindromes

Maximal even palindrome at pos. i : the longest string to the left & right

such that left half = reverse of right half.

S i Ex. GATTAG

$nnnn = reverse(nnnn)$

Goal: find all maximal even palindromes.

Construct $S^r = reverse(S)$. $O(|S|)$

S^r $n-i$

Preprocess S & S^r so LCE queries take $O(1)$ time. $O(|S|)$

$LCE(i, n-i) = \text{length of longest palindrome centered at } i$

for i :

Compute $LCE(i, n-i)$

$O(1)$ $O(1)$ $O(1)$

k-mismatch using LCE

Given long reference string T , & a short string P , check

if $\exists$ a k -mismatch of P starting at pos i of T .

k substitutions of characters in P to be exact match.

P T

$j=1$ pos in P

$c=0$ # mismatches so far

Repeat until $c > k$:

$j = j + LCE(i, j) + 1$ $O(1)$ to get $LCE(i, j)$

$i = i + LCE(i, j) + 1$ matched all of P

If $j \geq |P| + 1$, return True.

$c = c + 1$

return False

Finding all k -mismatches takes $O(k \cdot |T|)$ time

Suffix arrays

Suffix trees are $O(n)$ space, but the constant is large.

(≈ 20 bytes per char in good implementation)

10 Gb genome = 200 GB to store.

Suffix arrays are more efficient even than suffix trees & do most of the same ops.

Idea: Sort all suffixes of string lexicographically & keep the indices.

$S = catcat\$$

1 catcat\$

2 atcat\$

3 tcat\$

4 tcat\$

5 cat\$

6 at\$

7 t\$

8 \$

sorted

8 \$

6 at\$

2 atcat\$

5 cat\$

1 catcat\$

7 t\$

4 tcat\$

3 tcat\$

Search substring by binary search of suffixes.

Confusing is easy because all suffixes starting with "at" are next to each other.

App: k-mer counting for all k-mers.

Only keep indices & original str S .

Construction: $O(n^2 \log n)$ by sorting suffixes, where each comparison takes $O(n)$ time.

But better $O(n)$ algorithms such as building suffix tree.

$\Sigma = \{a, c, g, t\}$

$S = catcat\$$

12345678

If edges sorted lexicographically, leaf labels are exactly suffix array