### Bioinformatics I

WS 15/16

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 $\begin{array}{c|cccc} 1 & 2 & \sum (6+2) \\ \hline & & & \\ & & &$ 

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(Abgabe am 14. December 2015)

# Theoretical Assignment - Suffix tree construction and application

a - Suffix tree construction

i

If one uses the naive approach to construct the suffix tree of "CTAGTAGCAG", the result would look like Figure 1.

ii

- b Main data table of WOTD
- c Suffix tree application

## Theoretical Assignment - Runtime and space complexity of suffix trees

a

Assume a text T of length n with n times the letter "a". If one build a suffix tree for T using WOTD, each node will have just one c-group with all remaining suffixes in it. So evaluating the root node, one has to compute the longest common prefix of n suffixes, of n-1 suffixes for the second node and so on. In each c-group the shortest suffix is of length 1, so for each node  $\overline{u}$  there are just  $|R_a{\{\overline{u}\}}|$  numbers of comparisons.

Since T is of length n this will lead to an overall runtime of  $\sum_{i=1}^{n} i = \frac{1}{2}n(n+1)$ , which is in  $O(n^2)$ .  $\square$ 

### b

Suffix links are defined as an auxiliary edge that point from branching node  $\overline{bw}$  to the branching node  $\overline{w}$ , if it exists and to the root otherwise. If we now defined a suffix link, such that it points into the other direction (i.e. from branching node  $\overline{w}$  to branching node  $\overline{bw}$ ) gives us an efficient method to find maximal unique matches. If we now find a branching node that indicates a unique match (for definition see script) and there is a suffix link that point to another branching node, we know that the current branching node is not a maximal unique match (because it is not left

maximal). So we just have to follow the suffix links until we reach a branching node without an outgoing suffix link and we have found a maximal unique match.

C

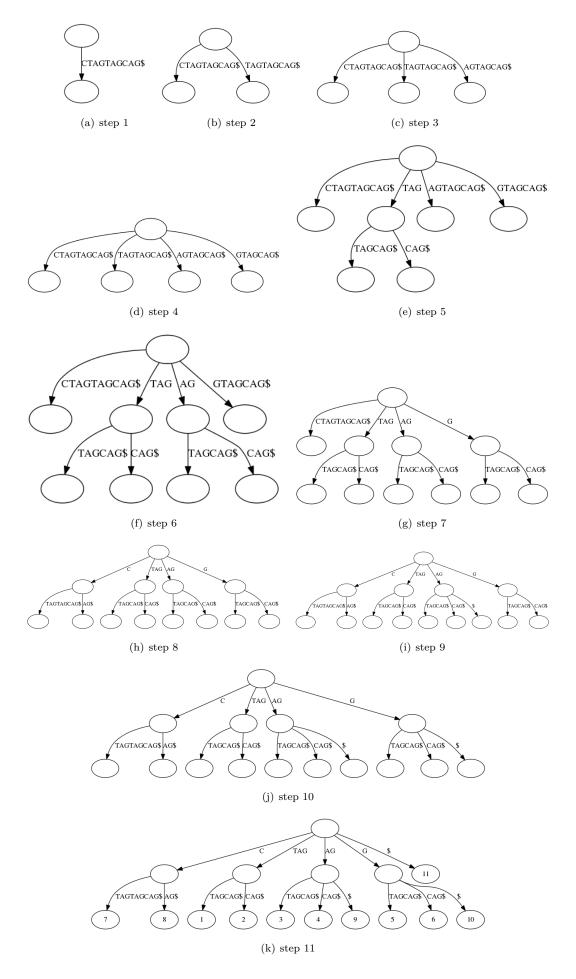


Figure 1: All steps of the naive implementation of suffix tree construction for the string "CTAGTAGCAG".