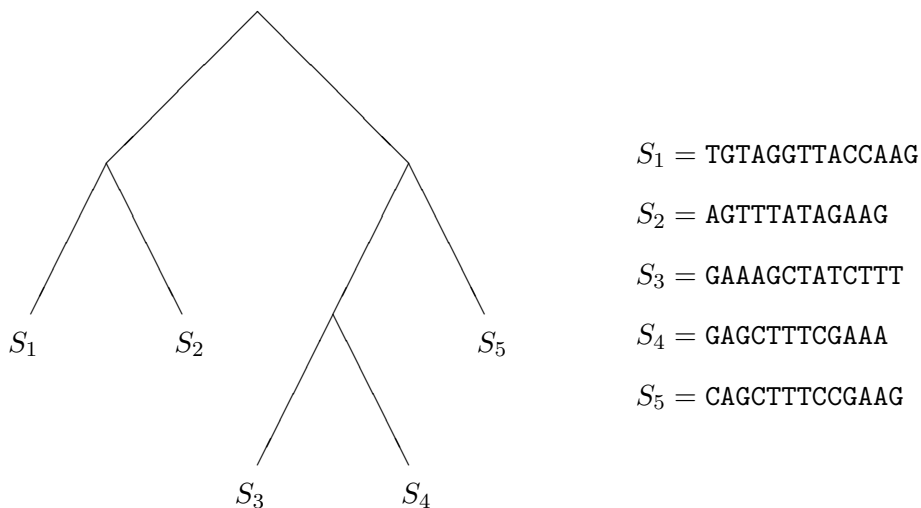


Algorithms in Genome Research
Winter 2016/2017

Exercises

Number 4, Discussion: 2016 December 16

1. What kind of signals does one typically expect in non-protein coding DNA regions?
Are there differences between prokaryotes and eukaryotes?
2. Remember the details of the algorithm from the Sequence Analysis class that allows to find maximal repeats using a suffix tree. (If you did not attend that class, you can find the details of the algorithm in Section 7.12.1 of Dan Gusfield's book *Algorithms on Strings, Trees, and Sequences*, Cambridge University Press 1997.)
 - (a) Explain the main idea to efficiently test for left-maximality.
 - (b) Try and discuss how a suffix tree could be used to find *tandem repeats*, i.e. repeats where both copies follow each other immediately.
3. What is the application scenario of phylogenetic footprinting?
4. Find all phylogenetic footprints of length $k = 4$ with a parsimony score of at most $d = 2$ in the following tree T :



(Hint: You may implement the algorithm or try it manually. The latter should not take longer than 30 minutes.)