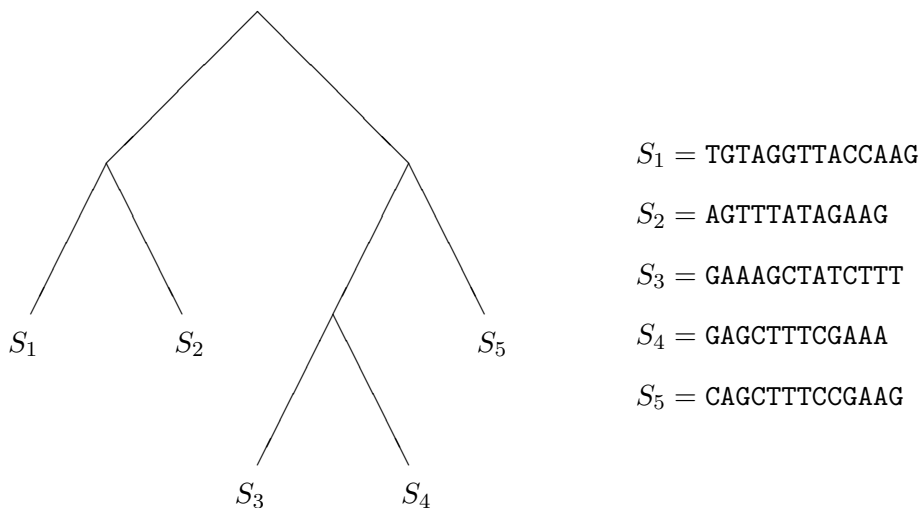


Algorithms in Genome Research  
Winter 2010/2011

Exercises

Number 1, Discussion: 2010 November 05

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.)