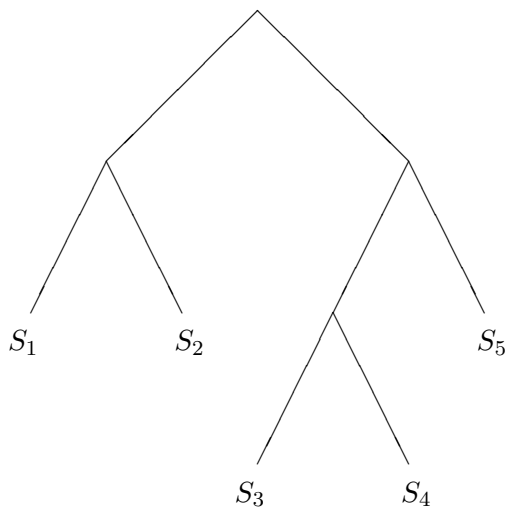


Algorithms in Genome Research
Winter 2005/2006

Exercises

Sheet 5, Discussion 05.01.2006

1. What kind of signals does one typically expect in non-coding DNA regions?
Are there differences between prokaryotes and eukaryotes?
2. What is the application scenario of phylogenetic footprinting?
3. Find all phylogenetic footprints of length $k = 4$ with a parsimony score of at most $d = 2$ in the following tree T :



$S_1 = \text{TGTAGGTTACCAAG}$

$S_2 = \text{AGTTTATAGAAG}$

$S_3 = \text{GAAAGCTATCTTT}$

$S_4 = \text{GAGCTTTCGAAA}$

$S_5 = \text{CAGCTTTCGAAG}$

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