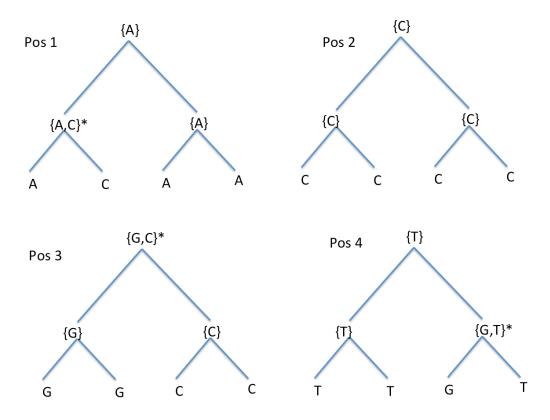
Exercises - Week 9

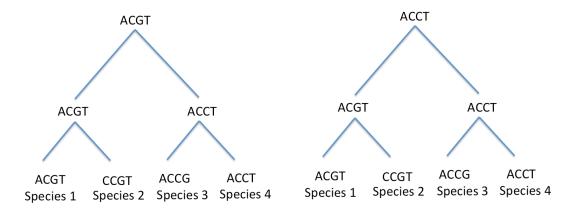
Genomics and bioinformatics

1 The Fitch's algorithm

Applying the Fitch's algorithm to each column separately, we find:

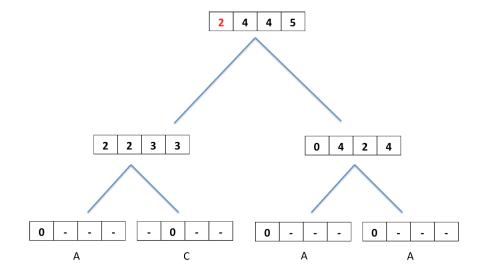


There are two assignments of the states to the internal nodes, with a parsimony length L(T) = 3.



2 The Sankoff's algorithm

Applying the Sankoff's algorithm to the first column of the MSA, we find:



The score of the tree is equal to the minimum of the root values, which is 2. This means that given the first column of the MSA and the substitution matrix M, one needs at least a penalty of 2 with respect to mutations to explain this tree.

3 The UPGMA algorithm

