

3.8 Exercises

1. Solution 1.

- a. Using the Fitch-Hartigan algorithm gives parsimony score 3 for both trees.

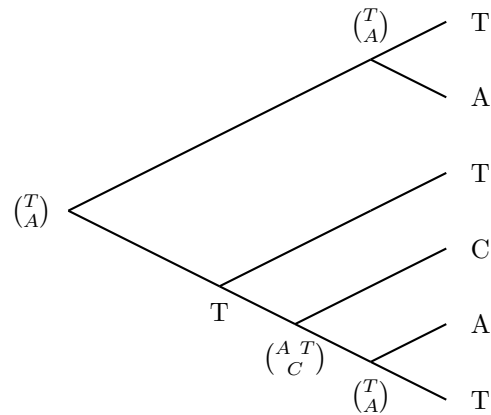


Figure 3.1: $ps(T_1) = 3$

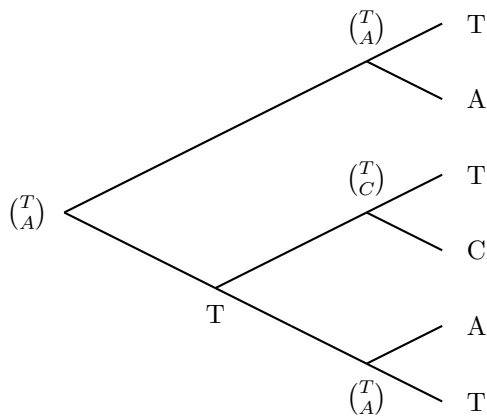
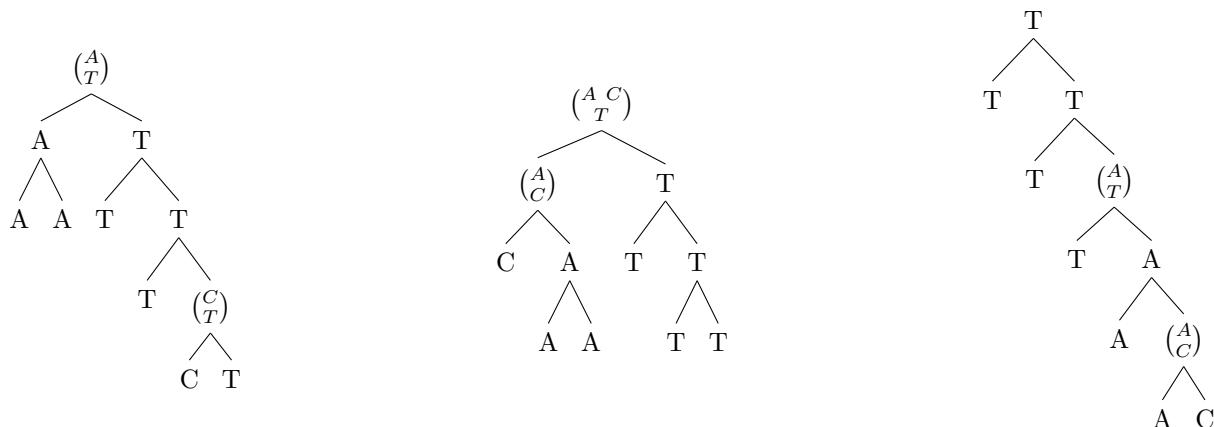
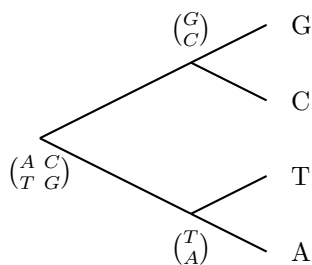


Figure 3.2: $ps(T_2) = 3$

- b. The parsimony score for these three trees is 2.
 c. Since the root would be labelled at worst with all four nucleotides, there can be at most 3 state changes on any tree.

2. Solution 2.

- a. The parsimony score for the left tree is 7 and for the right one is 8.
 b. Since the third tree has parsimony score 10, then T_1 is the most parsimonious.

Figure 3.3: $ps(T) = 2$ for all three treesFigure 3.4: $PS(T) = 3$

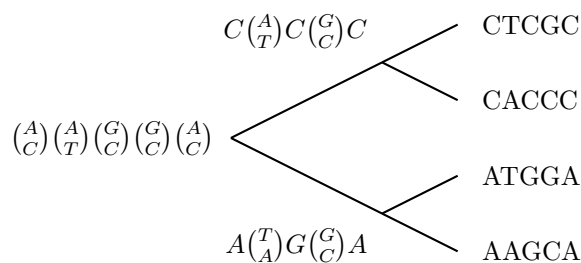
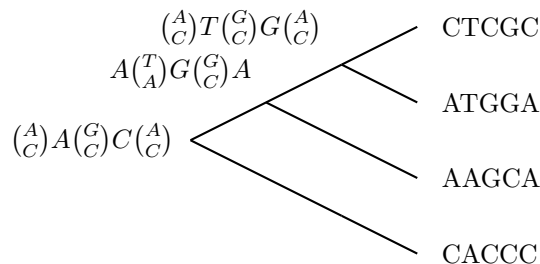
3. Consider the following sequences from four taxa.

	1	
	123456789012345	
S_1 :	AATCGCTGCTCGACC	
S_2 :	AAATGCTACTGGACC	
S_3 :	AAACGTTACTGGAGC	
S_4 :	AATCGTGGCTCGATC	

- Which sites are informative? **Be careful! Informative requires two bases to occur at least twice.**
- Use the informative sites to determine parsimony scores for the three possible unrooted trees relating the taxa. Which is the most parsimonious?
- If S_4 is known to be an outgroup, use your answer to (b) to give a rooted tree relating S_1 , S_2 , and S_3 .

Solution 3.

- By definition of an informative site, we can see that sites 3, 6, 8, 11 are informative.
- T_3 is the most parsimonious.
- Since T_3 is the most parsimonious, so the following tree is the good choice for a rooted tree relating S_1 , S_2 , and S_3 .

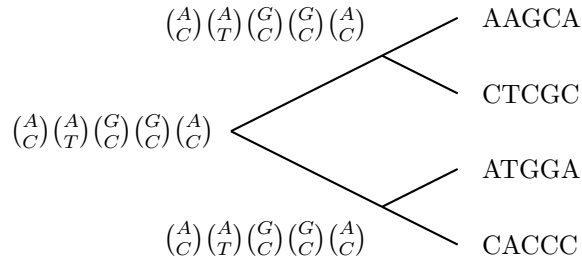
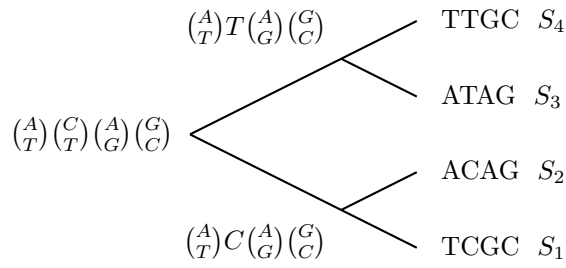
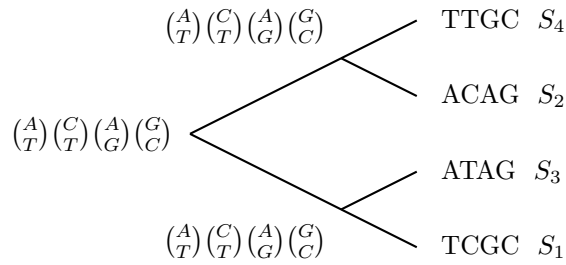
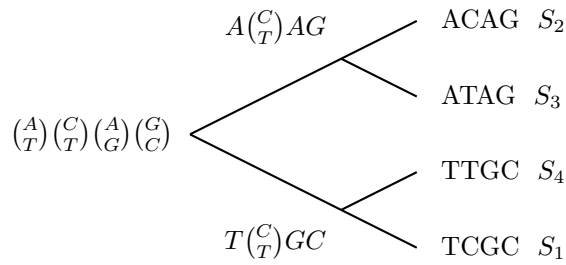
Figure 3.5: $ps(T_1) = 7$ Figure 3.6: $ps(T_2) = 8$

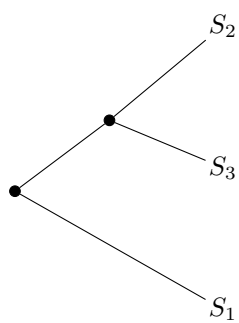
4. Show that if χ is an informative character on a set X of n taxa (so $n \geq 4$), then there exist two phylogenetic X -trees T_1, T_2 with $ps_\chi(T_1) \neq ps_\chi(T_2)$.

Proof. Suppose that χ is an informative character on a set $X = \{A, B, C, D\}$ such that takes on state T to a, b and A to c, d . Now consider two trees $T_1 = ((a, b), (c, d))$ and $T_2 = ((a, d)(b, c))$. We observe that the parsimony score for T_1 is 1 and for T_2 is 2. Then there exists two phylogenetic X -trees T_1, T_2 with $ps_\chi(T_1) \neq ps_\chi(T_2)$. \square

5. For the character and first tree in Figure 3.12, calculate the parsimony score, labeling the interior vertices according to the Fitch-Hartigan algorithm. Then show that the second tree requires exactly the same number of base changes, even though it is not consistent with the way you labeled the interior vertices on the first tree. (The moral of this problem is that naively interpreting the Fitch-Hartigan algorithm will not produce all minimal extensions of a character.)

SOLUTION: The parsimony score for both of them is 3.

Figure 3.7: $ps(T_3) = 10$ Figure 3.8: $ps(T_1) = 7$ Figure 3.9: $ps(T_2) = 8$ Figure 3.10: $ps(T_3) = 5$

Figure 3.11: *Rooted tree*