

BIOL/COMP 327
Assignment 1
Wednesday, October 12, 2005
All problems are of equal value.

1. In an ternary (or trichotomous) rooted phylogenetic tree each of the internal nodes has 3 children.
 - (a) How many different rooted ternary phylogenetic trees are there with 3 species, 4 species, 5 species?
 - (b) Draw all of the possible rooted ternary 5 species trees.
 - (c) In an rooted ternary phylogenetic tree with m internal nodes, how many edges does it have? how many species or leaves? (What we want here is an expression involving m .)
2. The distance between each of the five species, a, b, c, d, and e, are given in the following table:

	a	b	c	d	e
a	0	9	8	7	8
b	9	0	3	6	7
c	8	3	0	5	6
d	7	6	5	0	3
e	8	7	6	3	0

- (a) Use UPGMA to reconstruct the phylogenetic tree of the species. Include the edge lengths predicted by the tree.
- (b) Verify that the distances form an additive metric and reconstruct the additive tree they are derived from. Include the edge lengths predicted by the tree.
- (c) Compare your answers under the two reconstructions.

PLEASE TURN OVER FOR QUESTION 3

3. In standard parsimony analysis with characters with two states, 0 representing absence of a feature and 1 representing presence of a feature, a change from 0 to 1 is the same as a change from 1 to 0. Camin and Sokal (1965) introduced a variation on the standard parsimony analysis where changes from 0 to 1 are possible but changes from 1 to 0 are not possible.
 - (a) What possible biological justification might there be for introducing this measure of parsimony? Can you think of a situation involving DNA sequence data where such a measure might make sense?
 - (b) Give an example where standard parsimony and Camin-Sokal parsimony give different results, i.e., present situation where they would reconstruct different trees.
 - (c) Describe an efficient algorithm for computing Camin-Sokal parsimony on a rooted binary phylogenetic tree where the leaves are labeled. What is the approximate running time of your algorithm?