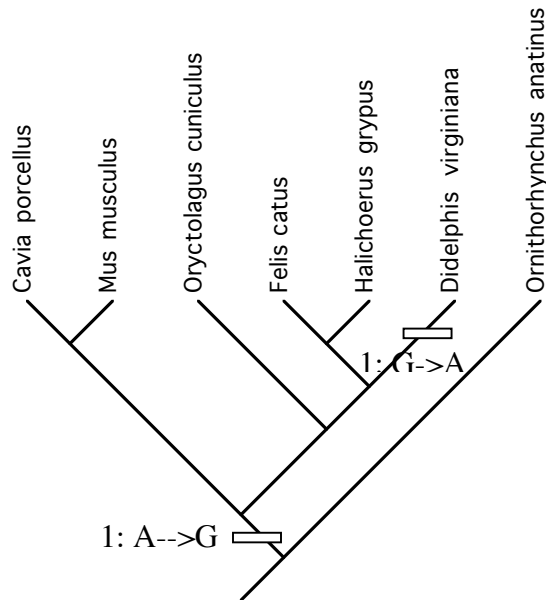


Problem Set 10

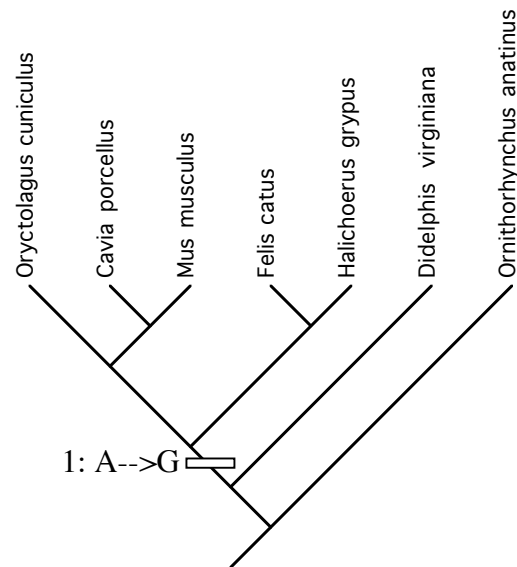
1. The table below shows 12 variable sites from the 12S Ribosomal RNA gene for a small set of mammalian species.

taxon/character	1	2	3	4	5	6	7	8	9	10	11	12
Felis_catus (cat)	G	T	C	A	T	G	C	C	C	C	T	C
Halichoerus_grypus (seal)	G	C	C	A	T	G	C	C	C	C	T	C
Oryctolagus_cuniculus (rabbit)	G	T	T	G	C	G	A	C	C	T	T	A
Cavia_porcellus (guinea pig)	G	T	T	G	C	A	A	A	T	T	T	A
Mus_musculus (mouse)	G	A	T	G	T	A	C	C	T	T	T	A
Didelphis_virginiana (opossum)	A	A	T	T	T	G	T	T	C	T	C	C
Ornithorhynchus_anatinus (platypus)	A	A	C	T	T	G	T	A	C	T	C	C

- a. For each tree, show how many evolutionary steps are required to explain the data above. Be sure to clearly mark where **every character changes and what the change is** (see my example for character 1). (Note that there is another equally parsimonious reconstruction for character 1. When we're interested in phylogeny inference, it's important to find one of the most parsimonious reconstructions, but we don't need to find all of them.) (12 pts)



Tree 1 Total Length _____



Tree 2 Total Length _____

- b. Which tree is a better hypothesis of evolutionary relationships? (2 pts)
 c. Identify a synapomorphy for the rabbit + mouse + guinea pig clade. (Say which character, and which character state). (2 pts)
 d. Changing the placement of the root (= rerooting) a phylogenetic tree does not change the number of steps in the tree. Explain why this is the case, and how we are able to choose among this set of trees of equal length. (4 pts)

- f. Describe two general kinds of effects that the difference in placement of the root has on our understanding of evolutionary history. For each effect give a specific example from this data set, assuming that the outgroup were actually *Oryctolagus*. (6 pts)
2. You are constructing a data matrix to use in determining the relationships within a group of beetles. One feature that catches your attention is a spine that is found on the legs of some species.
- Under what condition would the spines in these taxa be homologous? (2 pts)
 - What are two aspects of the spines that you would examine in order to determine whether or not they are in fact homologous? (2 pts)
 - Is function generally a good indicator of homology? Why or why not? (2 pts)
3. Why would it be incorrect to have a character called malleus with two states, present and absent, and to code the malleus as present in mammals but absent in reptiles? (4 pts)
4. Identify three general kinds of assumptions that are made in phylogenetic analysis. For each kind of assumption, describe one way in which the assumption could be tested. (12 pts)
5. It is sometimes assumed that the method of parsimony will tend to group more similar taxa, but this is not the case. Use the example below to explain why similarity is not necessarily a good indication of relatedness. (The relationships among 4 taxa, A, B, C, and D, are shown. Each bar indicates a change in a character. The number indicates the character that changed.)
- What is the most closely related pair of taxa in the tree below? (2 pts)
 - How many of the 6 characters have the same state in this pair of taxa? (2 pts)
 - Which pair of taxa are most similar? (2 pts)
 - How closely related is this pair of taxa? (2 pts)
 - Explain why only shared derived similarities (i.e. synapomorphies), not all kinds of similarities, are a good indication of relatedness. (4 pts)

