

**Quiz 1**

You may use any books, notes, or references, but you must work independently of other people, inside or outside of the course: **you are on your honor to do so.**

To keep the amount of writing under control, please confine the answers to the space provided (but write clearly and large enough to see!); outlines are fine. You of course may type the answer if you want, following the same space constraint (no smaller than 10 pt. font). Include literature citations (author and year are enough) where you use them.

1.(9 points) Briefly describe each of the following morphometric methods, and their possible uses in systematics:

a) Bivariate plot

b) Procrustes analysis

c) Thin-plate spline

2.(6 points) You have just overheard an argument about reconstructing relationships between a pheneticist, cladist, and an evolutionary biologist. Briefly compare and contrast each individual's position.

3. (5 points) How is it possible that branch lengths on a tree produced using UPGMA may not agree with branch lengths calculated directly from the distance matrix?

4. (5 points) What is the difference between divisive and agglomerative clustering methods? Give one example of each.

5. (20 points) What are the general attributes of a "good" taxonomic character? Give: a) A list with a few-sentence explanation of each criterion; b) An indication of particular problems faced by morphological and DNA-sequence data for each criterion.

6. (5 points) You have constructed a tree using the parsimony criterion and a second tree using the largest clique found in your data by compatibility analysis. Why might your two trees have different topologies?

7. (10 points) Briefly define the following terms:

DNA hybridization

Step matrix

Manhattan distance

Retention index

transversion

character weighting

epistemology

The alternating sister group rule

Dollo parsimony

Median state rule

8. (20 points) Briefly contrast the following pairs of terms (Use diagrams if they help):

maximum likelihood vs. maximum parsimony

Strict consensus trees vs. majority-rule consensus trees

transformational vs. taxic homology

Lundberg rooting vs. outgroup rooting

decay index vs. bootstrap support

9. (10 points) Quantitative, continuous characters are an initially attractive set of potential characters that seem often to contain phylogenetic signal. Discuss why they are so difficult to use. When can they be included in an analysis? How?

10. (10 pts.) In which one of the following cases is the maximum parsimony method most likely to be inconsistent (i.e., not converging on the correct tree as more data are added). Why? What properties of data make the problem worse?