Quiz 1
    You may use any books, notes, or references, but you must work independently of other people.
    To keep the amount of writing under control, <u>please confine the answers to the space provided</u> (but write clearly and large enough to see!); outlines are fine.

1. (10 points) Compare and contrast three sequence alignment methods; be sure to discuss them in terms of their advantages, limitations, and under what circumstances they would be best implemented.

2. (10 points) Discuss appropriate and inappropriate circumstances for the use of DNA data for taxon identification and taxon delimitation. What do you think are the realistic possibilities and drawbacks for a global, all-species, DNA barcoding enterprise.

3. (10 points) Explain the relationship between the intent & function of the current nomenclatural codes (ICZN & ICBN) and phylogenetic hypotheses. What are the arguments pro and con for moving to the Phylocode for dealing with phylogenetic classification?

4. (20 points) In terms of all possible characters one might envisage, describe the attributes of the imaginary perfect matrix of phylogenetic characters. Be sure to describe the qualities these characters would have in terms character analysis and their distribution on resulting trees.

5. (10 points) What are some differences between land-plant development and vertebrate development? How can ontogenetic information be used in phylogenetic inference?

6. (10 points) How can you deduce the ancestral character state of a given character for a clade? What data would you need?

7. (30 points: 5 points each) Briefly contrast the following pairs of terms (Use diagrams if they help)

orthology vs. paralogy

shape vs. size in morphometrics

morphological vs. molecular characters

Manhattan vs. Euclidian distance

Biological species concept vs. phylogenetic species concept

ordering vs. polarity of character states