

Population Genetics
Problem Set 10

1. What are the similarities and differences between the multi-regional and the “out of Africa” hypotheses of modern human origins?
2. What are the similarities and differences between a cladogram, a phylogram and a chronogram?
3. What is the difference between a hard and a soft polytomy on a tree?
4. What are the similarities and differences between monophyly, paraphyly and polyphyly?
5. What characteristics is one searching for in choosing a distance correction method?

6. Give the best definition for the following terms:

- a. Phenetics:
- b. Cladistics:
- c. True tree:
- d. Operational taxonomic unit, **OTU**:
- e. Internal node of a tree:
- f. Root of a tree:
- g. Outgroup:
- h. Tree topology:
- i. Plesiomorphy:
- j. Apomorphy:
- k. **Autapomorphy**:
- l. Homology:
- m. Homoplasy:
- n. Lineage sorting:
- o. Dot plot:
- p. Heuristic method:
- q. Long branch attraction:
- r. Pseudoreplicates:

7. What are two ways to classify phylogenetic methods; name four commonly used methods and where they fall into these two classifications.

8. Which of the following generally apply to the following methods: Neighbor Joining (NJ), minimum evolution (ME), maximum parsimony (MP) or maximum Likelihood (ML)? Write NJ, ME, MP and/or ML if the phrase applies.

- May be used to produce a cladogram or phylogram
- Bootstrap support may be calculated using pseudoreplicates
- May be used to analyze either mtDNA or nuclear sequences
- May be used to examine if clades are reciprocally monophyletic
- Can handle outgroup sequences
- Requires an accurate alignment of sequences
- May have internal and external nodes
- Places operational taxonomic units at external nodes
- May be used to draw a tree with rectangular shape
- May be rooted or unrooted
- Generates a distance matrix
- Calculates the probability of the data given a hypothesis
- Of the 4 methods listed, considered the most computationally intensive
- May be run using the Jukes-Cantor model
- May be run using the Kimura-2-Parameter model
- Ideally tries to examine all possible trees
- May use a heuristic search across tree space
- May generate more than one optimal tree
- May produce a tree with a polytomy
- Uses a clustering algorithm to produce a single resolved tree
- Of the 4 methods listed, the least computationally intensive
- Guaranteed to generate the true evolutionary history for the sequences