Problem Set 11

1. In class, we looked at sequence variation for the cytochrome B gene in different human populations.
    - **a.** Of the total number of variable sites, changes at which codon position contributed to most of the sequence variation in the data? (1 pt)
    - **b.** Explain why this result is expected under the neutral theory of molecular evolution (3 pts)

2. Why is the rate of fixation of neutral mutations (μ) independent of population size? (4 pts)

3. If most mutations are deleterious (i.e. alleles of negative effect) and have a low probability of fixation, you would expect positive alleles to have a high probability of fixation given the fitness advantage that they engender to the individual carrying the allele.
    - **a.** Why is the rate of fixation for positive alleles so low according to the neutral theory? (3 pts)
    - **b.** Which evolutionary process governs the rate of fixation for alleles with positive or negative effects? For neutral alleles? (2 pts)

4. Compare the % sequence divergence observed in two genes in a pair of salamander species. The histone protein requires a precise structure to function properly, while the structure of the zinc finger gene depends on only a few key amino acids. You can assume that most of the observed variation in these genes has no effect on fitness.
    - **a.** Fill in the blanks below with >, < or = to indicate the relative divergence expected in these comparison. (3 pts)

3rd codon positions in the histone gene	________	1st codon positions in histone gene
3rd codon positions in the histone gene	________	3rd codon positions in the zinc finger gene
1st codon positions in the histone	________	1st codon positions in the zinc finger gene

    - **b.** Explain the reasoning that you used in filling in the blanks above. (3 pts)
    - **c.** Suppose that you discover a gene in which most mutations that change the protein sequence <u>increase</u> fitness. How would you expect the rate of divergence at 1st codon positions in the gene under positive selection compare to the rate of divergence at 1st codon positions in the histone and zinc finger genes? Why? (3 pts)
    - **d.** How would you expect the rate of divergence at 1st codon positions to compare to the rate of divergence at 3rd codon positions in the gene under positive selection? Why? (3 pts)

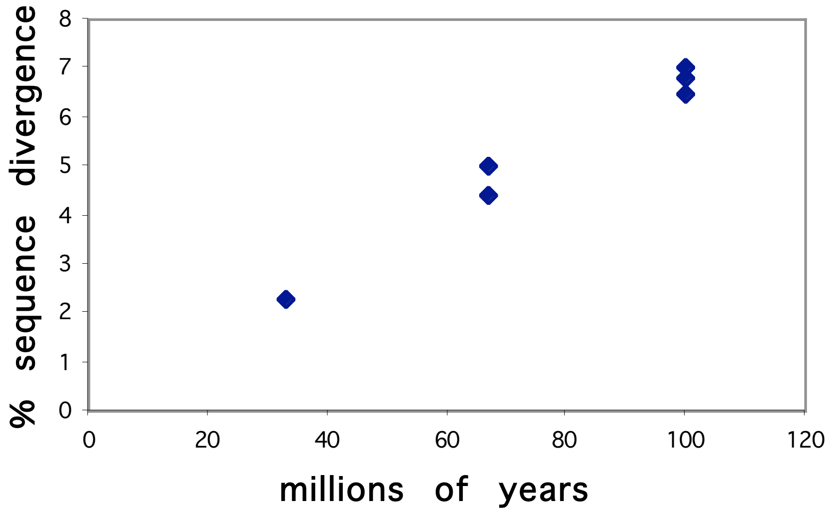
5. Suppose that the neutral mutation rate is measured to be 3×10^{-9} in a gene encoding a milk protein and as 1×10^{-9} in a gene encoding a DNA binding protein.
    - **a.** Give two biological explanations for why the neutral mutation rate could be higher in the milk gene. (4 pts)
    - **b.** How could you distinguish between these two explanations? (4 pts)

6. Molecular clock estimates (calibrated using the bird-mammal divergence) for the age of major groups of placental mammals suggests that these groups radiated more than 100 million years ago. This conflicts with the fossil evidence that major lineages of mammals diverged from each other after the non-avian dinosaurs went extinct 65 million years ago.
    - **a.** Assuming that the molecular clock dates are correct, describe two ways you could explain the gap in the fossil record. (4 pts)
    - **b.** Assuming that the current understanding of the fossil record is correct, give a specific explanation of what could have changed at the molecular level to cause the inflated estimates of divergence times. (4 pts)

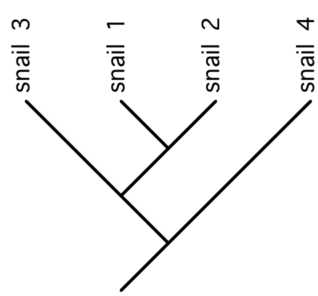
7. When calibrating a molecular clock, explain why it is important to do each of the following:

- **a.** Use data from the same gene region for the calibration of the clock and for comparisons of taxa whose divergence dates are being estimated. (3 pts)
- **b.** Use data for the calibration from taxa that are as closely related as possible to the taxa whose divergences dates are being estimated. (3 pts)

8. The following graphs % sequence divergence in the cytochrome *b* gene versus estimated divergence time for a small (hypothetical) clade of snails.



- **a.** You discover that the cytochrome *b* sequence of a species of shell-less snail is only 3.5% divergent from snail species 1's cytochrome *b* gene. Estimate when the most recent common ancestor of the shell-less snail and species 1 lived. (**Be sure to show your work!**) (3 pts)
- **b.** The tree below shows the relationships among the shelled species used to produce the graph above. Add the shell-less snail to the tree of species used in a way that is consistent with your answer in **a**. (3 pts)



9. One of the major events in the evolutionary history of life was the diversification of complex, multicellular animals into the (basic phyla). Prior to the middle Cambrian (ca. 540 million years ago), there are almost no fossils that are identifiable as members of living phyla. In the middle Cambrian, a wide array of phyla appear in the fossil record. The traditional interpretation of the fossil record is that animal phyla diversified rapidly (i.e. more or less at the same time) in the early Cambrian. How can this hypothesis be tested? (I realize this is an open-ended question—you need to explain all of the major steps in using a molecular clock to test this hypothesis). (7 pts)