

1. 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 hormone receptor 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.

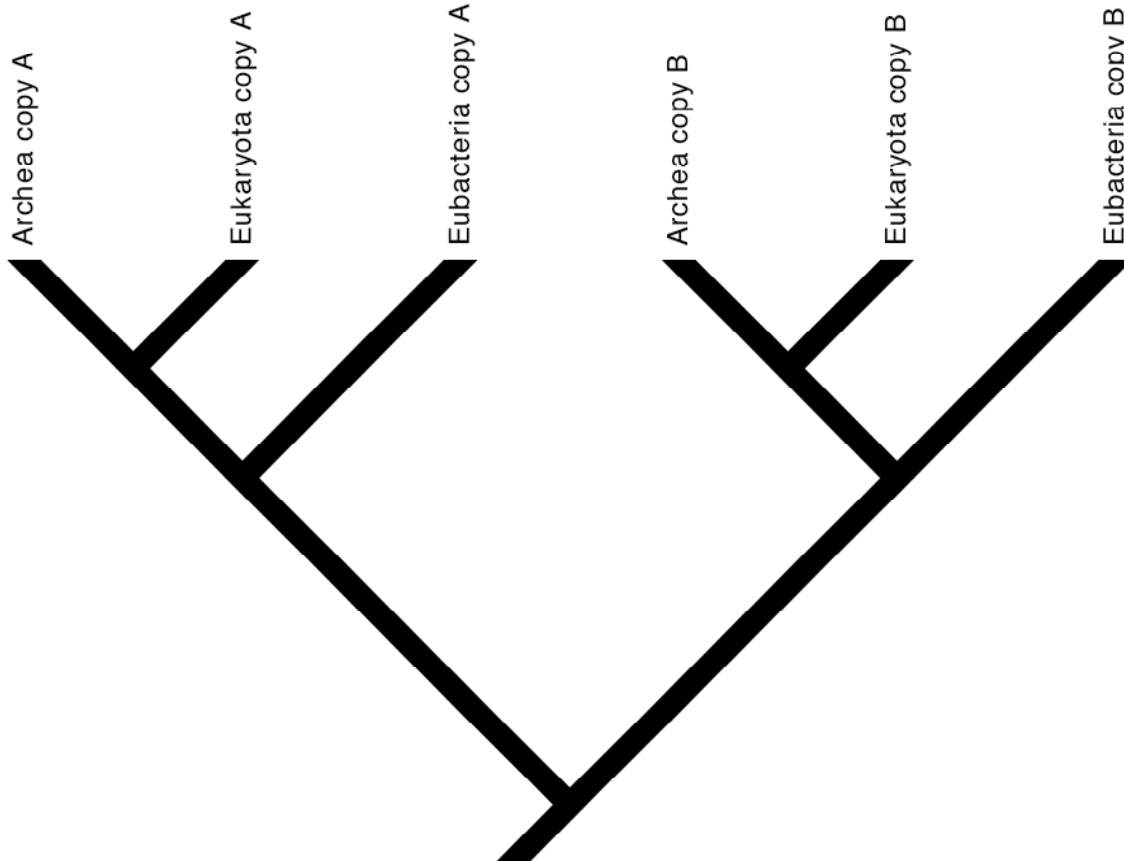
3rd codon positions in the histone gene
 3rd codon positions in the histone gene
 1st codon positions in the histone

1st codon positions in histone gene
 3rd codon positions in the hormone receptor gene
 1st codon positions in the hormone receptor gene

- b. Explain the reasoning that you used in filling in the blanks above.
- c. Suppose that you discover a gene in which most mutations that change the protein sequence increase 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 hormone receptor genes? Why?
- 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?

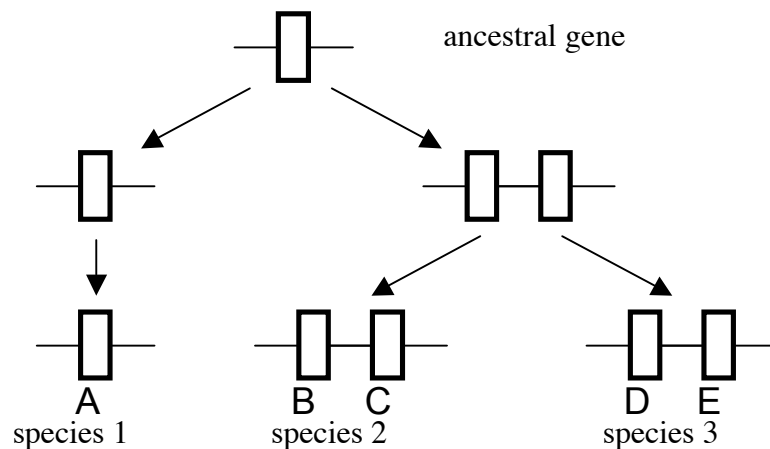
2. Why is the rate of fixation of neutral mutations (μ) independent of population size?
3. In order to root the tree of life an outgroup is required. Obviously, the entire tree of life isn't going to have an outgroup; all life is part of the ingroup. Scientists circumvented this problem by using duplicate genes that are present in all three major domains of life. The following questions refer to the tree below.
 - a. Label on the tree where the duplication event took place that produced copy A and copy B.
 - b. Label on the tree where speciation events occurred.
 - c. Circle the part of the tree that is acting as the root for gene copy A. Circle the part of the tree that is acting as the root for gene copy B.
 - d. Circle on the tree the most recent common ancestor of gene copy A. Circle on the tree the most recent common ancestor of gene copy B.

e. The tree below is a phylogenetic tree showing the relationships of different genes to each other. Based on this gene tree what would the phylogenetic tree depicting the relationships between these three taxa look like?



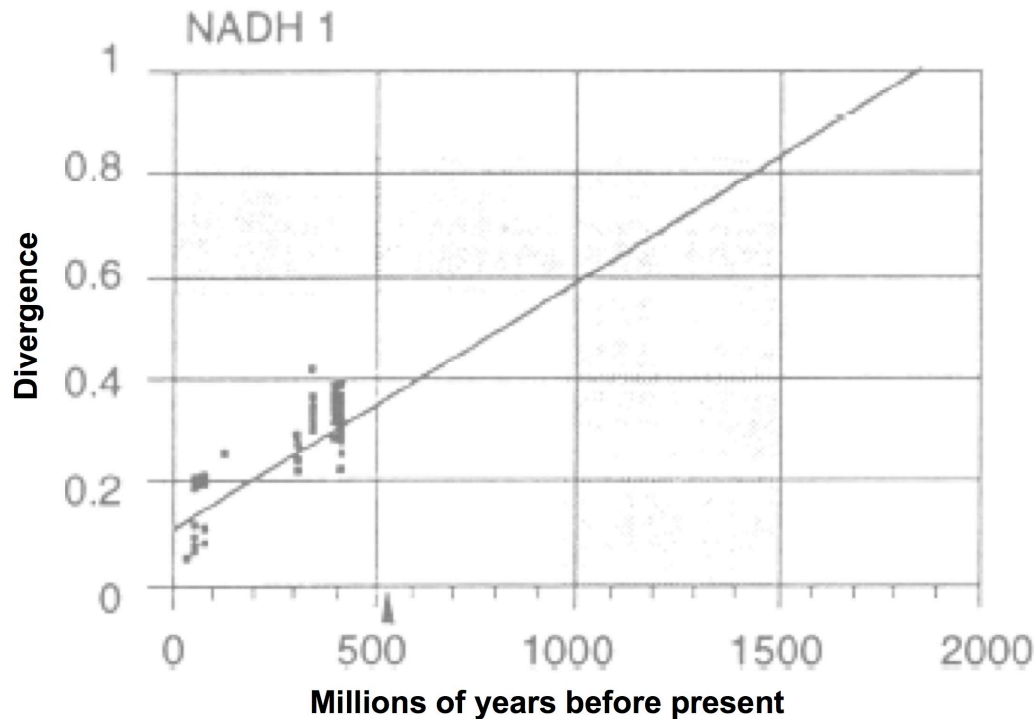
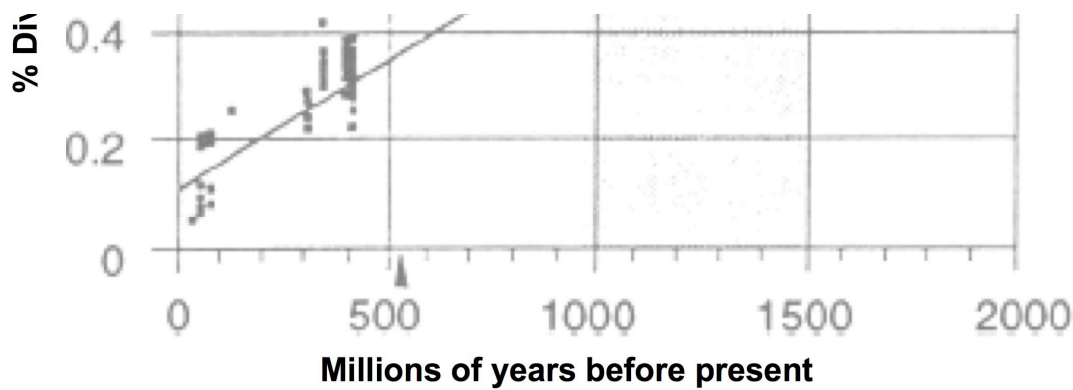
4. The diagram below shows the evolutionary history that generated five copies (labeled A-E) of a single ancestral gene in three species.

history of gene duplication and speciation



a. Draw a phylogenetic tree showing the evolutionary relationships among the five genes (A-E).

5. Although Samoan fruit bats (*Pteropus samoensis*) and Anetian fruit bats (*P. anetianus*) are more closely related to each other than either are to Tongan fruit bats (*P. tonganus*), the protein sequence of the Pap2L gene in *P. anetianus* is more similar to *P. tonganus* than it is to *P. samoensis*. Mutants for the Pap2L gene in *P. samoensis* are unable to detect papaya groves when foraging at night, whereas *P. samoensis* individuals with normal Pap2L can detect papaya from long distances after dark.
 - a. Identify one prediction of the neutral theory that is violated in this scenario.
 - b. What might have caused Pap2L divergence in *P. samoensis*, and what sort of evidence would you use to support your claim? (Think about, but don't talk about, our discussion of the FoxP2 gene)
6. Lynn Margulis put forth the endosymbiotic theory in 1970 in her important work, "The Origin of Eukaryotic Cells", providing a plausible explanation for the existence of organelles in eukaryotic cells.
 - a. Provide two examples of endosymbiotic events and describe the evidence that supports the validity of the occurrence of each.
 - b. What basic advantages does this type of mutualistic association provide for each of the partners involved?
7. While investigating the evolutionary dynamics of a particular gene in a lineage a researcher discovers that synonymous and non-synonymous sites are evolving at close to the same rate. This surprised the researcher because this gene is known to have an important function and mutants for this gene normally have low fitness.
 - a. Why is the researcher surprised that synonymous and non-synonymous sites are evolving at similar rates?
 - b. What is the expected dN/dS ratio for a gene under purifying selection?



The researchers discovered a 65 % divergence between protostomes and deuterostomes.

- a. How long ago does this molecular clock suggest protostomes and deuterostomes diverged from each other?
 - b. The fossil record, on the other hand, suggests that protostomes and deuterostomes diverged no earlier than 600 million years ago. The molecular clock method predicts that the amount of sequence divergence is equal to the rate of sequence change \times time since divergence. Assuming that protostomes and deuterostomes did diverge from each other within the last 600 million years, how might you explain the estimates derived using the molecular clock approach? Clue: think about how they calibrated the clock. How might this bias the results?
9. Three hypotheses have been presented regarding the relationship of the Ediacaran fauna to modern fauna.
- H1: The Ediacaran fauna include ancestors or close relatives of modern phyla.
- H2: The Ediacaran fauna represent a separate experiment in animal life, but are closely related to animals.

H3: The Ediacaran fauna are only distantly related to animals and shouldn't be considered part of the animal kingdom.

Two representatives of Ediacaran organisms are shown below. The first, *Fractofusus andersoni*, shows bilateral symmetry. The second, *Tribrachidium*, shows 3-fold symmetry.



Tribrachidium

Fractofusus andersoni

For each hypothesis, place *Fractofusus* and *Tribrachidium* on the tree somewhere that would support the hypothesis. Two important innovations in the animal kingdom have been included on the tree.

