

**Molecular Evolution – 2010 (Instructor: Dr. Dan Graur)
Second Midterm Exam**

Name (print) _____

Name (sign) _____

Student ID# _____

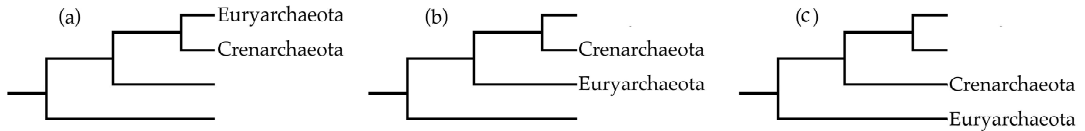
In True-or-False and multiple-choice questions, if you think there is more than one correct answer (or no correct answer), please write a note beside the question, explaining your concern. I will read your comments as long as the handwriting is legible. The same goes for the essay questions; I will read them as long as the handwriting is legible. Each True-or-False is worth 3 points.

1. **True or False.** Mutations in termination codons can cause gene elongation.
2. **True or False.** According to the endosymbiotic theory, mitochondrial genes are derived through the compartmentalization of nuclear genes.
3. **True or False.** Character data can always be converted into distance data.
4. **True or False.** Additive distances are always ultrametric.
5. **True or False.** In a rooted ultrametric tree with 4 OTUs (A, B, C, D), the distance between the root and A is equal to the distance between the root and C.
6. **True or False.** In a rooted additive tree with 4 OTUs (A, B, C, D), the distance between the root and A is equal to the distance between the root and C.
7. **True or False.** The Maximum Parsimony method of phylogenetic reconstruction uses distance matrices.
8. **True or False.** UPGMA produces ultrametric trees.
9. **True or False.** Neighbor-Joining produces ultrametric trees.
10. **True or False.** Humans (*Homo sapiens*) are the sister species to the two chimpanzee species (*Pan troglodytes* and *Pan paniscus*).

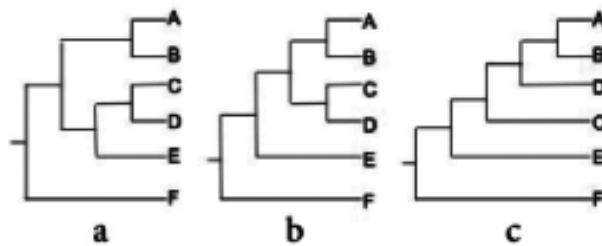
11. **True** or **False**. Within a monophyletic group it is possible to find paraphyletic groups.
12. **True** or **False**. All the people in the world constitute a monophyletic clade.
13. **True** or **False**. Long-branch attraction describes a problem in reconstructing phylogenetic trees that contain of a mixture of short and long terminal branches.
14. **True** or **False**. It is possible to explain unequal codon usage by invoking only mutations and genetic drift.
15. **True** or **False**. Parallelism produced identical amino-acid replacements in the lysozymes of cows, langurs (colobine monkeys), and humans.
16. **True** or **False**. Low K_A/K_S ratios indicate purifying selection.
17. **True** or **False**. High K_A/K_S ratios are frequently found in sex-related genes.
18. **True** or **False**. Rates of molecular evolution tend to correlate with generation times but not with metabolic rates.
19. **True** or **False**. Rates of molecular evolution tend to correlate with rates of morphological evolution.
20. **True** or **False**. In plants mitochondria have higher mutation rates than the nucleus.
21. **True** or **False**. Humans are a suitable outgroup for the tree of life.
22. **True** or **False**. The molecular clock hypothesis holds that the rate of evolution of a protein is roughly constant in all lineages as long as the protein maintains its original function.
23. **True** or **False**. Oogenesis produces the majority of mammalian mutations.
24. **True** or **False**. The weaker the functional constraint is on a protein, the slower its rate of evolution will be.
25. **True** or **False**. A multifurcation indicates that three or more species likely separated at the same time.

26. (3 points) Euryarchaeota and Crenarchaeota are the only taxa within Archaea. Which of the following trees is compatible with the paraphyly of Archaea? (Circle them.)

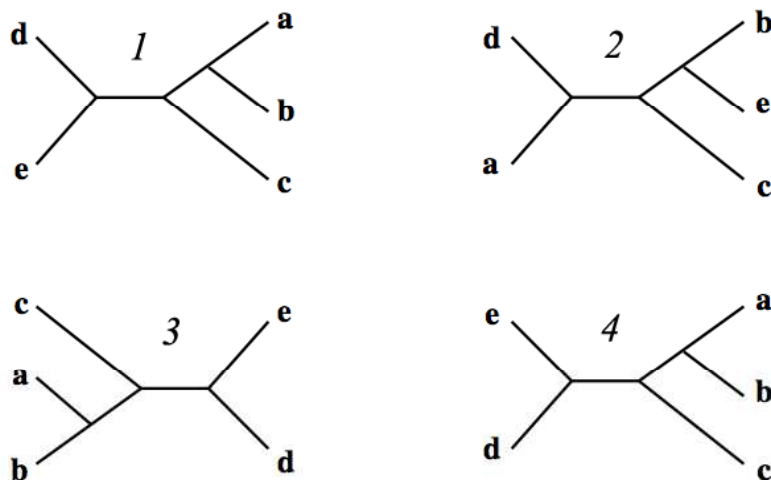
Answer: b & c



27. (3 points) SINE-1 is found in species A and B, but not in C, D, E, and F. SINE-2 is found in species C and D, but not in the other species. Which of the following rooted phylogenetic trees is supported by these findings? (circle them) Answer: a & b



28. (4 points) Which of the following topologies are identical? (Circle them.) Answer: 1, 3, & 4



29. (6 points) Present (name and **briefly** describe) two possible evolutionary scenarios leading to the emergence of new function (functional divergence) following gene duplication.

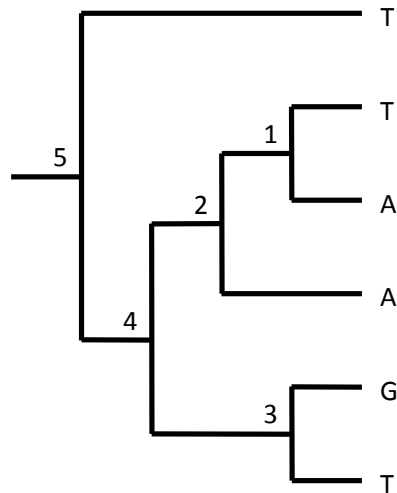
This question was canceled because we only briefly covered it in class. It will be covered in more depth later on in chapter 6.

30. (5 points) Using maximum parsimony reconstruct the ancestral nucleotide at the internal nodes of the following tree. If more than one nucleotide is possible, indicate which ones they are. (Fill in the blanks with your answers.)

We accepted two different answers for each node:

1 A 2 A 3 T 4 T 5 T

1 AT 2 A 3 GT 4 AGT 5 T



31. (4 points) Define homoplasy and give an example. The example can be an annotated figure.

a) Definition: A homoplasy is a character that is shared between two or more OTUs due to convergent or parallel evolution and not common ancestry.

b) Example: There were many possible answers: e.g. fins on sharks and whales; or independent but similar substitutions on a tree.