

## Concept Test #2

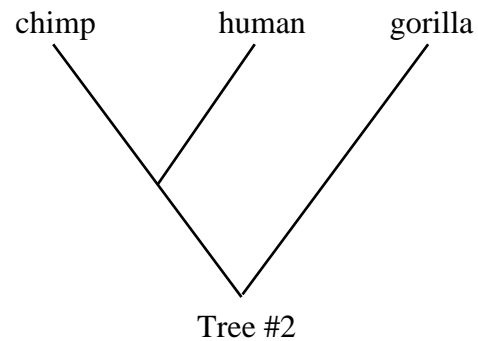
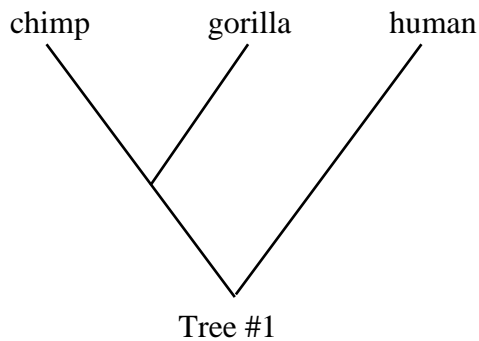
Please type answers to the following questions on separate sheets of paper (single spaced). We have indicated at the beginning of each question the maximum length of your answer and the point value. **Do not** exceed the space limit indicated. You may consult your books and lecture notes, but please don't discuss the test with anyone other than your TA. Due **Dec. 13** at 4 PM outside of Corson Hall Rm. 343. (75 points total)

Question 1. (1/2 page max, 8 points)

Describe the importance of mass extinctions in shaping current diversity. Use either the end-Permian extinction or the end-Cretaceous (K/T) extinction as an example. For the one you choose, roughly what percentage of species went extinct? What caused the extinction? Can species "adapt" to mass extinctions? If so, how? If not, why not?

Question 2. (1/4 page, 6 points)

The following are two trees representing two different hypotheses for the relationships among humans, chimps, and gorillas. Describe in words what each tree represents. What type of data support each tree? Is the evidence for one tree stronger?

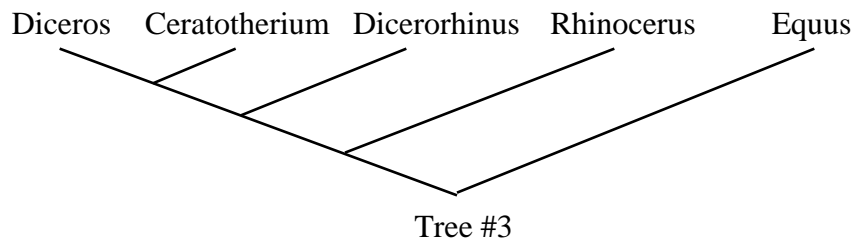
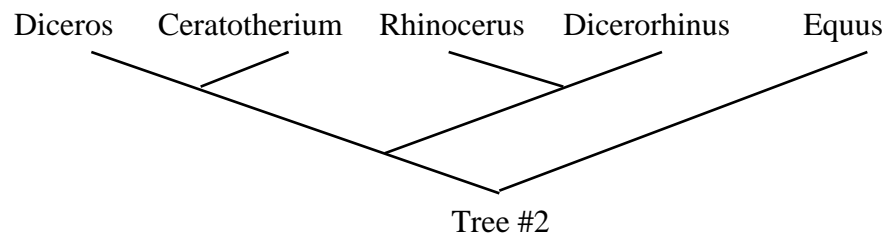
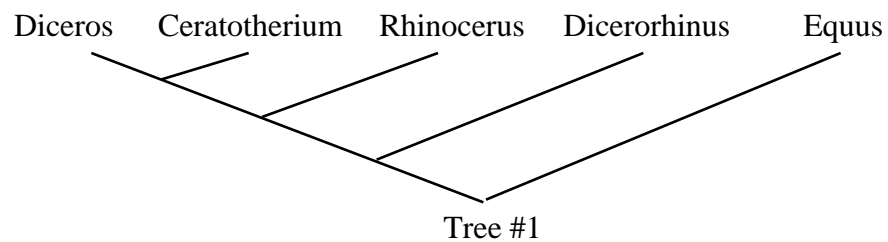


Question 3. (1/2 page plus drawings, 12 points)

Four genera of rhinoceroses are extant: two in Asia (India/Java and Sumatra) and two in Africa. These taxa are remnants of a much more diverse radiation. One of the Asian genera (*Rhinoceros*) has a single horn. In contrast, the second Asian genus (*Dicerorhinus*) and the two African genera (*Diceros* and *Ceratotherium*) have two horns. Mitochondrial DNA sequence data for these taxa and an outgroup are shown below. Detach this page and staple it to your typed answers.

Genus	Nucleotide Site						
	1	2	3	4	5	6	7
Rhinoceros	G	G	C	A	G	T	T
Dicerorhinus	G	C	G	T	C	T	T
Diceros	C	C	G	T	G	A	T
Ceratotherium	C	C	G	T	G	A	T
Equus (outgroup)	G	C	C	A	C	T	A

- Identify all potential synapomorphies by circling them on the matrix above.
- Plot the character state changes on the three phylogenetic hypotheses shown below (e.g. for character 1 changing from G to C mark 1:G → C). Assume that the same character state can evolve in multiple lineages, but that reversals DO NOT occur. On each phylogeny, indicate homoplasious character states (mark these with asterisks). Which is the most parsimonious tree? What does parsimony mean?



- c) Map horn number (1 or 2) on the tips of the most parsimonious tree. Is the 2-horned or 1-horned character state ancestral? Why?
- d) Does the most parsimonious phylogeny show the Asian genera to be sister taxa? Are the African genera sister taxa? Why?
- e) Use your most parsimonious tree to make a reasonable hypothesis regarding the biogeographic history of these taxa.
- f) Some systematists would like to place the two Asian genera into one subfamily and the two African genera into a second subfamily. Would such a classification system be cladistically correct? Why or why not? If not, what classification would you suggest?

Question 4. (1/2 page, 12 points)

Choose two species concepts from those we have discussed. Apply your species concepts to **one** of the following two scenarios. Your answer should include a justification for the species concepts you used and a conclusion as to how many species you believe are actually present.

**Scenario #1: *Ensatina* salamanders**

In southern California just east of San Diego there are two distinct forms of *Ensatina* salamanders, which do not interbreed where they overlap. *E. klauberi* has a blotchy dark color pattern whereas *E. eschscholtzii*, is more uniformly lightly pigmented. The blotchy salamanders are found inland along the Sierra Nevada mountains which delimit the east side of the San Joaquin Valley. . The smooth salamanders can be traced west to the coast and north along the Coastal Range mountains marking the west side of the San Joaquin Valley. In northern California and Oregon, the mountain ranges meet and only one form of salamander (*E. oregonensis*) is found. There is a continuous set of intermediate salamander populations along the mountains, all connected by gene flow. This is an example of a species ring.

**Scenario #2: *Quercus* oak trees**

Many of the oaks in North America exhibit a high degree of gene flow with other oak species while also maintaining distinct morphologies across their geographic ranges. One example is *Quercus macrocarpa*, the bur oak, which is one of the most majestic broad-leaf trees in the United States, with individuals that can live 400 years or more. It is readily distinguished by deeply lobed leaves and an acorn with a fringed rim around the cup. The species ranges from Canada south to Texas and from the Dakotas east. In Quebec, *Q. macrocarpa* has a high degree of gene flow with *Q. bicolor*, a morphologically distinct form. In fact, you can safely assume that *Q. macrocarpa* in Quebec exchanges more genes with local *Q. bicolor* than it does with *Q. macrocarpa* in Texas at the other end of the range.

Question 5. (1/3 page plus figure, 12 points)

Pairs of taxa	Percent Sequence Difference in Protein X	Age of Fossil Common Ancestor (million years)
1-2	5	10
3-4	20	20
5-6	10	???

Use the above data on the percent sequence difference in protein X, which is relatively conserved, to estimate how long ago taxa 5 and 6 split from each other. Draw a graph. What is the rate of this molecular clock? A fourth pair of taxa are estimated to have diverged 100 million years ago, and differ in the coding sequence of this protein by 30 percent. Is that a greater or smaller proportion change than you would expect given the other data? What might account for this? If you have another pair of taxa and you would like to know when they diverged, what kind of gene would you use?

Question 6. (1/2 page plus figures, 12 points)

Gould and Lewontin are highly critical of the adaptationist programme - the tendency to propose "adaptive stories" to explain organismal traits. It is clear that some organismal traits are indeed adaptations. However it is often difficult to prove that this is the case. Consider the following situation: six closely related species of pond-dwelling insects living in the eastern United States. The larvae can only survive in the water, and adults can only survive brief periods away from water, as might happen during dispersal. Three of the species are flightless and live in large lakes that are permanent habitats. The other three have massive wing muscles, can fly, and live in temporary pools of water that dry up in the summer.

Why do you think that large wing muscles might be viewed as an adaptation to living in temporary habitats -or conversely why might small wing muscles be viewed as an adaptation to living in permanent habitats? How would knowing the phylogenetic relationships among the six species help you in determining whether large/small wing muscles is an adaptation? Draw two phylogenetic trees: one supporting the adaptive hypothesis and one suggesting that the association between flight ability and temporary habitats is not adaptive. Briefly explain your trees. If you found a seventh species that lives in the permanent ponds and has large wing muscles but does not fly, how would that influence your interpretation?

Question 7. (1/3 page, 7 points)

Under strict neutrality the rate of substitution of new mutants is equal to the mutation rate ( $k = \mu$ ). What is meant by a substitution? What is so surprising about this result? Explain this result intuitively.

Question 8. (1/4 page, 6 points)

The figure shows a cross-section of rock strata containing both sedimentary and igneous rocks. The igneous rocks have all been aged and are shown to the nearest million years ago (MYA). An igneous intrusion is shown in black. Briefly describe the geological history shown in this cross-section. Give the narrowest possible age ranges of layers A and B.

