

## Final Exam Study Guide

The final exam will be held at 10:30 a.m. on Friday, May 2. The exam will consist of three sections: multiple choice, short answer, and problems. The exam will test your ability to apply concepts and solve problems, as well as your ability to recall specific facts and details. As you prepare for this exam, it will be helpful to review: lecture notes, problem sets, questions from discussion readings, and textbook reading assignments and questions (see readings handout). The final exam will include some comprehensive questions.

Approximately 33% of the points possible on this exam will be based on problems selected from those below.

1. The table below shows rates of nucleotide substitution between two related species for three different genes.

	Replacement rate ( $\times 10^9$ )	Silent-site rate ( $\times 10^9$ )	positive, negative, drift?
<b>Gene 1</b>	0.33	4.66	
<b>Gene 2</b>	2.79	2.81	
<b>Gene 3</b>	5.88	3.13	
<b>Pseudogene</b>	4.06		

- Based on these data, determine whether each gene is under positive selection, negative selection, or drift.
- Explain why silent-site and replacement substitutions provide information about whether a gene has experienced positive selection, negative selection, or drift.
- Pseudogenes are copies of genes that are no longer transcribed, so that they are now non-functional “junk DNA”. Predict the rate of silent-site substitutions for the pseudogene in the table above (the rate of replacement substitutions is given). Explain your prediction.

2. Red crossbills are small finches specialized for eating seeds out of cones of conifer trees. They fly thousands of kilometers each year in search of productive cone crops. Despite their mobility, crossbills have diverged into several “types” that differ in bill shape, body size, and vocalizations. Each type prefers to feed on a different species of conifer, and each species of conifer is only found in certain forests. Bill size and shape affects how efficiently a bird can open cones of a certain conifer species.

- Explain how a highly mobile animal such as the red crossbill could have diverged into different types in the absence of any geographic barrier.
- Describe a study you could use to test your ideas.
- If conifer species were not patchily distributed (i.e., in different forests), do you think crossbill speciation would occur more quickly or more slowly? Explain.

3. The table below shows imaginary sequences from the beta-casein gene – which encodes a milk protein – of four carnivores. Sites that differ in at least one of the groups are shown in bold (and are numbered in the table).

	2	7	14	19	24	30
Raccoon	<b>A</b> GTCCC <b>A</b> AGTGAAC <b>G</b> GAGACTATGG <b>T</b> TCCTAGGCACAAG					
Bear	ACTCCCTAGTGAAC <b>G</b> GAGACTATGG <b>C</b> TCCTACGCACAAG					
Sea lion	ACTCCCTAGTGAAG <b>G</b> GAGAT <b>T</b> TATGG <b>T</b> TCCTACGCACAAG					
Seal	ACTCC <b>A</b> AGTGAAC <b>G</b> GAGAT <b>T</b> TATGG <b>T</b> TCCTAGGCACAAG					

- Using this sequence data, construct the most parsimonious phylogeny of this group. Use raccoons as the outgroup.
- List all sites that are informative.
- Why are these sites informative?
- Suppose it were discovered that aquatic mammals show convergence in milk proteins – e.g., suppose a certain form of milk protein, with certain amino acid in key positions, is particularly beneficial for aquatic mammals. How would that affect your interpretation of the phylogeny you constructed above, based on milk casein data? Explain.

4. The table below shows genetic differences between a mtDNA gene (*cytochrome b*) of five species or subspecies of bears: polar bear (*Ursus maritimus*), Kodiak bear (*Ursus arctos middendorffi*), brown bear (*Ursos arctos*), grizzly bear (*Ursus arctos horribilis*), and black bear (*Ursus americanus*).

	Polar bear	Kodiak bear	Brown bear	Grizzly bear
Kodiak bear	0.030			
Brown bear	0.030	0.007		
Grizzly bear	0.003	0.027	0.027	
Black bear	0.094	0.100	0.100	0.090

- Which bears are most closely related? How can you tell?
- Use UPGMA to construct a phylogeny of this group.
- Based on this phylogeny, do you agree with the species status of these bears? Why or why not?

5. Suppose you are studying the development of monkeys, and you discover that monkeys have two (hypothetical) *Hox* genes that encode upper vs. lower trunk location. *Hox* gene *A* is expressed in the chest and shoulders, and *Hox* gene *B* in the abdomen and hips. Suppose you also discover that in monkeys a gene you call “*little*” is active in the posterior limb buds of all limbs, and is necessary for forming little fingers and little toes (rather than thumbs and big toes).

- a) Draw a sketch of what you think the limbs would look like if *Hox* genes *A* and *B* were switched with each other in a zygote.
- b) Would the resulting limbs have hands or feet? Where would there be big toes, little toes, thumbs, and little fingers?
- c) How about if *little* were knocked out? Explain your reasoning.