AP Biology – Spring 2019 Edward R. Murrow High School
Exam 1 Review Sheet Mr. Sprague

Format:

Section I 21 multiple choice questions
Section II 1 essay question and 3 short free response questions

Reading: Hillis chapters 15, 16, 17, concept 19.1, and appendix B (section on sample populations) (and all readings from Semester I: Hillis chapters 1–14 and 41)

Concepts to Review:

- EVERYTHING FROM SEMESTER I

- Mechanisms of Evolution
  - Understand the term *evolution*.
  - Understand how each of the following mechanisms of evolution work: *mutation*, *gene flow*, *genetic drift*, *natural selection*, and *sexual selection*.
  - Be able to explain how the *founder effect* can occur from genetic drift.
  - Be able to explain and give examples of the differences between *directional*, *disruptive*, and *stabilizing selection*.
  - Be able to explain how the frequency of a phenotype could change through selection, including: *genetic variation*, *overpopulation*, *competition*, and *differential survival and reproduction*.
  - Be able to use the Hardy-Weinberg equilibrium equation to calculate allele frequencies (proportion of *A* vs. *a*) and genotype frequencies (proportion of individuals with *AA* vs. *Aa* vs. *aa*) in a population.
  - Be able to discuss the assumptions of the Hardy-Weinberg equilibrium equation and why those assumptions are unrealistic in real life.

- Speciation
  - Understand the term *speciation*.
  - Be able to explain the difference between *allopatric speciation* and *sympatric speciation*, and be able to give some examples of each.
  - Be able to explain the term *polyploidy* and the role of polyploidy in the speciation of plants.
  - Understand the term *hybridization*, be able to explain how *prezygotic isolation mechanisms* and *postzygotic isolation mechanisms* prevent hybridization between species, and be able to give some examples of each type of mechanism.

- Phylogeny
  - Understand the terms *convergent evolution*, *adaptive radiation*, and *horizontal (lateral) transfer*.
  - Be able to explain what *homologous structures* are and how they are evidence of common ancestry.
  - Be able to explain what *analogous structures* are and how they are evidence of convergent evolution.
  - Be able to read a *phylogenetic tree* (also called a *cladogram*) and identify a *monophyletic group*.
  - Be able to construct a phylogenetic tree based on data on shared traits, DNA, or amino acid sequences.
  - Be able to use the principle of *parsimony* to evaluate how well a phylogenetic tree fits the data it is based on.
  - Be able to explain how a *molecular clock* is used to determine how long ago certain groups of species diverged.
  - Be able to describe the *Three Domain System* of classification.
  - Be able to compare *bacteria*, *archaea*, and *eukarya*, and describe some characteristics of a universal common ancestor for all three domains.

- Statistics
  - Be able to understand what the terms *population mean*, *sample mean*, *standard deviation*, and *standard error of the mean* represent, as well as how these terms are related.
  - Be able to make inferences about the amount of variation in a population and how much overlap exists between different populations given data on sample means and standard errors.

Overarching Questions to Consider:

Suggestion: Answer all of these questions in writing, then compare answers with a classmate. I promise that taking the time to do so will be well worth it and much more useful then memorizing facts and definitions.

1. What kind of changes in a population would be considered *evolutionary* changes? What is the time frame for evolution?
2. What is the difference between evolution and natural selection? How can you have evolution without natural selection? How can you have natural selection without evolution?
3. Why is Hardy-Weinberg equilibrium a useful model for studying populations? What are the shortcomings of the model? How do the assumptions of the model relate to evolution?
4. What is a gene? What is an allele? How is a genotype different from a gene? How is a genotype different from an allele? Why is it easier to estimate the q^2 of a population than it is to estimate q? Why is it easier to estimate the q^2 of a population than it is to estimate p^2?
5. What are some ways that biologists define a species? Why are these definitions problematic?
6. What kinds of data would an evolutionary biologist use to construct a cladogram? How do each of these data sets show evidence of evolutionary relationships? What are the advantages and disadvantages of using different types of data sets to investigate evolutionary relationships?
7. What is the difference between divergent evolution and convergent evolution? Why is divergent evolution so much easier (and thus, more common) than convergent evolution? How does this connect to the parsimony principle? How does this connect to homologous and analogous structures?
8. What does it mean for a gene to be conserved? Why is it useful to study conserved genes?
9. What is horizontal transfer? Why does it make constructing phylogenetic trees for prokaryotes challenging?
10. What was the common ancestor of bacteria, archaea, and eukaryotes like? (List as many traits as you can.) What evidence supports your claim?
11. Why are statistics needed when analyzing biological data? What does the SEM tell us?
12. How can biologists make accurate inferences about the frequency of phenotypes in a population even when we only sample a very small portion of the overall population? What should we look for when taking our samples to minimize the amount of error in our generalization?

Practice Exam Questions:

Visit the course website and click on the "Multiple Choice Practice" link. Complete all practice questions for the relevant chapters and check your work against the answer key. Note: these items are password protected.