

ANSC 446 / IB 416
Population Genetics
Final Exam, December 15, 2008

Name _____

(5 pages) Please underline or indicate your answer. If rounding, use 3 significant digits. Show your work or describe your logic to earn partial credit for incomplete answers.

- (6) 1. An AFLP marker in xantusid lizards was found to be heterozygous in 50 lizards and homozygous in 10 lizards.

(3) a. Estimate the effective number of alleles at this marker.

(3) b. What does this estimate represent or mean?

- (14) 2. Assume that the following mtDNA sequences were found in four different individuals sampled from a population.

CATCGAGACTTGAGT
CTTCCAGATTTAAGC
CTTCCAGATTTAAGC
CATGGAGACTTGAGT

(3) a) How many sites are segregating?

(3) b) What proportion of nucleotide sites differ between the first and second sequences?

(3) c) How many transversions are present between the first and second sequences?

(5) d) Estimate the population nucleotide diversity from this sample.

- (6) 3. Four babies were born in a hospital on the same night, and their blood groups were later found to be O, A, B and AB. The four pairs of biological parents were:

O and O
AB and A
A and O
B and B

Assign the four babies to their correct parents.

- (15) 4. A population of 400 cattle is surveyed at a locus with two codominant alleles. The genotype A_1A_1 is found to be present in 60 cattle, A_1A_2 is present in 40 cattle, and A_2A_2 is present in 300 cattle.

(3) a. What are the genotype frequencies?

(3) b. What are the allele frequencies?

(3) c. What would be the genotype frequencies if the population were at Hardy-Weinberg equilibrium?

(3) d. Estimate the level of inbreeding (inbreeding coefficient) in the population.

(3) e. Assuming the population has equal numbers of males and females, what is the effective population size of this inbred population?

- (4) 5. At a biallelic autosomal locus, a deleterious allele with a dominance level of 0.2 and selection coefficient of 0.3 is found at a frequency of 0.1. Assuming random mating, what will be the frequency of the allele in the next generation?

- (6) 6. For the Arabian oryx, a population size of 734 is maintained in zoos. Assume that this population size is constant across generations.
- (3) a. Assuming that the effective population size equals the census size of 734, and assuming no selection or migration. How long will it take on average for a new neutral mutant allele to become fixed in this population?
- (3) b. For a new neutral mutation in this population, what is the probability that it will become fixed in the population?
- (4) 7. What is the difference between linkage disequilibrium and meiotic drive?
- (5) 8. What does Kimura's Neutral Theory claim? What does Ohta's Nearly Neutral Model say about selection and drift in large versus small populations?
- (4) 9. What are two proposed disadvantages and two proposed advantages for the evolution of sexual reproduction (and recombination).
- (6) 10. What's *different* between a cladogram, a phylogram and a chronogram?

(12) 11. Consider two loci (A and B) with two alleles each (A_1 , A_2 , B_1 , and B_2). A human population currently has the following gametic frequencies:

0.5 A_1B_1 , 0.2 A_1B_2 , 0.1 A_2B_1 , and 0.2 A_2B_2 .

(3) a) Estimate the current linkage (or gametic) disequilibrium.

(3) b) If the A and B loci are linked with recombination equal to .2, how much gametic disequilibrium is expected after 4 more generations of random matings?

(3) c. How far apart are loci A and B in terms of map units?

(3) d. How far apart would you expect them to be in terms of base pairs?

(24) 12. Which of the following generally apply to the following methods: Neighbor Joining (NJ), minimum evolution (ME), maximum parsimony (MP) or maximum likelihood (ML)? Write NJ, ME, MP and/or ML next to the phrase if the statement applies to the method.

(4) a. Requires an accurate alignment of sequences

(4) b. Uses a distance matrix

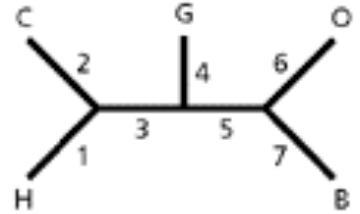
(4) c. Uses a clustering algorithm

(4) d. Compares optimality criteria across trees

(4) e. May conduct a heuristic search

(4) f. Bootstrap support may be calculated using pseudoreplicates

(26) 13. Consider the unrooted cladogram on the right: How many of the following elements are present on the tree?



(2) a. How many OTUs?

(2) b. How many internal branches?

(2) c. How many external branches?

(2) d. How many branches total?

(2) e. How many terminal nodes?

(2) f. How many internal nodes?

(2) g. How many nodes total?

(4) h. If the root were at position **3**, what would be the tree's topology (indicate the root)?

(4) i. If the root were at position **6**, what would be the tree's topology (indicate the root)?

(4) j. If in the tree at the top of the page, the letters B, C, G, H and O signify baboon, chimpanzee, gorilla, human and orang-utan, respectively, then what would a rooted tree look like that showed the true relationships among these species?

(12) 14. Assume that the fitnesses are 0.8, 1.0 and 0.7 for alleles A_1A_1 , A_1A_2 , and A_2A_2 , respectively.

(3) a. What is this type of fitness relationship among genotypes called?

(3) b. Calculate the mean fitness when $q = 0.1$.

(3) c. Is the mean fitness higher for any other allele frequency? Why or why not?

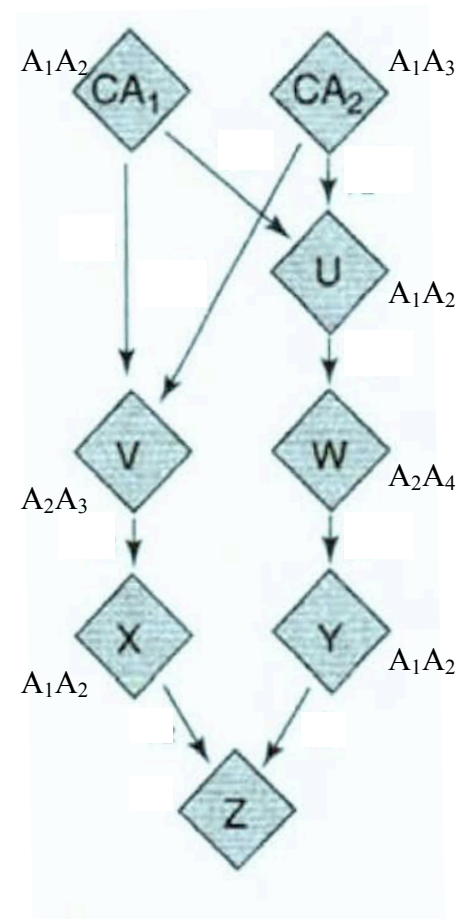
(3) d. What types of genes (or what region of the genome) would you expect to display this type of fitness relationship between homozygote and heterozygote genotypes?

(12) 15. In the pedigree on the right, CA1 and CA2 are outbred.

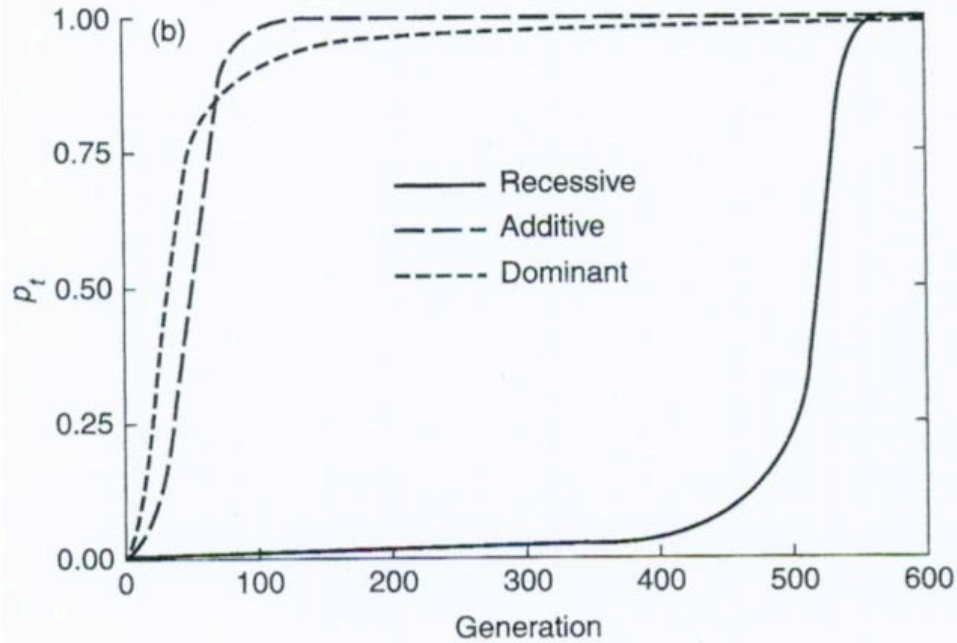
(3) a. What is the inbreeding coefficient for individual U?

(3) b. What is the inbreeding coefficient for individual Z?

(6) c. Genotypes are shown for the A locus for individuals included in the pedigree. What are the possible genotypes for individual Z to have at the A locus? Which of these would be identical by descent, and which have identity in state?



- (6) 16. The following Figure from Hedrick's text shows the rise in frequency for an allele at an initially low frequency ($p_0 = 0.01$) undergoing positive Darwinian selection ($s = 0.1$), in cases where the allele is recessive, dominant, or additive:



Given that the fitness value for an additive allele is exactly half way between the fitness of a dominant allele and the fitness of a recessive allele, why doesn't the curve showing increase in an additive allele fall exactly intermediate between the curve for a dominant and the curve for a recessive allele?

- (24) 17. Give the best definition for the following terms (2 points each):

- Coefficient of inbreeding, f
- Genetic drift:
- Continent-island model of migration:
- General model of migration:

e. Wahlund effect:

f. Cline:

g. Homoplasy:

h. Lineage sorting:

i. Vicariance:

j. Epistasis:

k. Genetic hitchhiking:

l. Selective sweep:

(14) 18. Name an **example** of each of the following (2 points each):

a. Darwinian (positive) selection:

b. Outgroup:

c. Plesiomorphy:

d. Autapomorphy:

e. Quantitative trait:

f. paraphyly:

g. polyphyly: