

ANSC 446 / IB 416
Population Genetics
Final Exam, December 17, 2009

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 40 lizards and homozygous in 20 lizards.

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

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

- (9) 2. Coat color in horses is determined by multiple alleles. A complete Black horse (C1 black horse with black mane and tail) is dominant to a Bay horse (C2 brown horse with black legs, mane and tail) and a Mahogany Bay. A Bay is dominant to a Mahogany Bay (C3 brown horse with black roots, legs, mane, and tail). Your sample has 3000 horses (Black, Bay, and Mahogany Bay).

Color	Observed Number
Black	480
Bay	1470
Mahogany Bay	1050

Estimate the allele frequencies for C1, C2, and C3.

- (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
A and A
A and B
O and B

Assign the four babies to their correct parents.

- (9) 4. A survey in one state finds that the proportion of newborn infants who have the recessive autosomal disease cystic fibrosis is 1 in 2500.

(3) a) What is the estimated frequency of this disease allele?

(3) b) What proportion of individuals would be carriers of the disease?

(3) c) Assuming a random-mating population, what proportion of matings would be between two carriers?

- (6) 5. For the addax antelope, a population size of 1600 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 1600, 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?

(8) 6. What are the similarities and differences between the multi-regional and the “out of Africa” hypotheses of modern human origins? Which is favored by genetic evidence?

(5) 7. What does Kimura’s Neutral Theory claim? What does Ohta’s Nearly Neutral Model say about selection and drift in large versus small populations?

(5) 8. Assume the probability of a child being born a boy is 0.52. What is the probability that a family with four children would have two boys and two girls?

(9) 9. What’s *different* between a cladogram, a phylogram and a chronogram?

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

0.2 A_1B_1 , 0.2 A_1B_2 , 0.1 A_2B_1 , and 0.5 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 .3, how much gametic disequilibrium is expected after 4 more generations of random matings?

(3) c. How far apart are loci A and B in map units (i.e., in centiMorgans)?

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

(18) 11. 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.

(3) a. May be run using the Jukes-Cantor model

(3) b. Uses a distance matrix

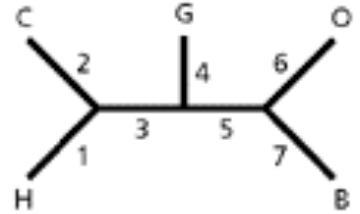
(3) c. Uses a clustering algorithm

(3) d. Places operational taxonomic units at external nodes

(3) e. Can be used with mtDNA sequences

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

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



(3) a. How many OTUs?

(3) b. How many internal branches?

(3) c. What numbers are next to internal branches?

(3) d. How many branches total?

(3) e. How many terminal nodes?

(3) f. How many internal nodes?

(3) g. Name one number or letter at a terminal node.

(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 **1**, 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?

- (16) 13. Assume that the fitness values are 0.8, 1.0 and 0.7 for genotypes A_1A_1 , A_1A_2 , and A_2A_2 , respectively.
- (3) a. What are the values for the selection coefficients s_1 and s_2 ?
- (3) b. What is this type of fitness relationship among genotypes called?
- (3) c. What is the equilibrium frequency for A_2 ?
- (3) d. For the A locus, at what allele frequencies will the genetic load be minimized?
- (4) e. Four isolated populations have initial allele frequencies for A_2 of 0.0, 0.45, 0.50 and 1.0. At what frequency will allele A_2 stabilize in each of these four populations?
- (6) 14. At a biallelic autosomal locus, a deleterious additive allele with a selection coefficient of 0.4 is found at a frequency of 0.3. Assuming random mating, what will be the frequency of the allele in the next generation?

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

a. Coefficient of inbreeding

b. Genetic drift:

c. Homoplasy:

d. Fisher's fundamental theorem of natural selection:

e. Wahlund effect:

f. Heuristic method:

g. Operational taxonomic unit, **OTU**:

h. Lineage sorting:

i. Vicariance:

j. Epistasis:

k. Genetic hitchhiking:

l. Selective sweep:

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

- a. Darwinian (positive) selection:
- b. Outgroup:
- c. Founder effect:
- d. Cline:
- e. Quantitative trait:
- f. Heterozygote advantage:
- g. Test of neutrality (include description):

(14) 17. In the pedigree on the right, CA1 and CA2 are outbred.

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

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

(8) 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?

