ANSC 446 / IB 416
Population Genetics
Exam 1
Sept. 22, 2006

Name ______________________

(5 pages) Show your work to earn partial credit for incomplete answers.

(12) 1. 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

(8) a) Estimate the allele frequencies for C1, C2, and C3.

Answer: $P_{C3} = \sqrt{1050/3000} = \sqrt{.35} = .59160798 \sim .5916$

$$P_{C2} = \left[\frac{(1470 + 1050)}{3000}\right]^{1/2} - (.35)^{1/2} = (.84)^{1/2} - (.35)^{1/2} = .32490716 \sim .3249$$

$P_{C1} = 1 - (.59160798 + .32490716) = .08348486 \sim .0835$

~~(4) b) Estimate the variance of the allele frequency for C1.~~

$\cancel{\textbf{Answer: } V(\hat{P}_{C1}) = \frac{1 - (\hat{P}_{C2} + \hat{P}_{C3})^2}{4N} = \frac{1 - .84}{4(3000)} = \frac{.16}{12000} = .00001333}$

Potentially useful chi square critical values.	
Degrees of freedom	P value = .05
1	3.84
2	5.99
3	7.81
4	9.49

(12) 2. Dwarf mice caused by Congenital Hypothyroidism is an autosomal-recessive condition found in one of 4000 neonates.

(6) a) Assuming random mating, what is the frequency of heterozygotes? (4 decimals please)

Answer: $q = (1/4000)^{.5} = .01581139 \sim .0158$

$f(het) = 2pq = 2(1-q)(q) = 2(q - q^2) = 2\{(1/4000)^{.5} - (1/4000)\} = 2\{sqrt(.00025) - .00025\}$
$= 2(.1581139 - .00025) = 2(.1556139) = .03112278 \sim .0311$

~~(6) b) What is the standard deviation of the frequency of the dwarf allele for a population of 1000 males and 1000 females?~~

~~**Answer: $V(q) = (1-q^2) / 4N = (1 - 1/4000)/ 4(1000 + 1000) = (1- .00025) / 8000$**~~
~~**$= .99975 / 8000 = .00012497$**~~
~~**$SE(q) = sqrt(V(q)) = sqrt(.00012497) = .01117894 \sim .0112$**~~

(12) 3. Three genotypes for Citrullinemia, labeled as normal, heterozygotes, and affected, have been identified in cattle.

(6) a) Among 8 offspring born from matings between heterozygous individuals, what is the probability that 1 offspring is normal, 4 offspring are heterozygotes and 3 offspring are affected?

Answer: Nn x Nn yields ¼ NN, ½ Nn and ¼ nn offspring at birth. The probability of this particular combination of offspring would be estimated from the multinomial expansion.

$\{8! / [1!*4!*3!]\}*\{[(1/4)^1]*[(1/2)^4]*[(1/4)^3]\} = \{280\}(.25)(.0625)(.015625) = .06835938 \sim .0684$

(6) b) If the offspring were not observed until one month of life, only normal and heterozygous offspring would have survived to then. Among the 5 surviving offspring, what is the probability that 1 offspring is normal and 4 offspring are heterozygotes?

Answer: At one month of age, Nn x Nn yields 1/3 NN and 2/3 Nn and zero nn offspring. The binomial expansion can be used to answer this question.

$\{5! / [1!*4!]\}*\{[(1/3)^1]*[(2/3)^4]\} = \{5\}\{(1/3)(.19753086)\} = .32921811 \sim .3292$

The multinomial expansion can also be used to answer this question.

$\{5! / [1!*4!*0!]\}*\{[(1/3)^1]*[(2/3)^4]*[0^0]\} = \{5\}\{(1/3)(.19753086)\} = .32921811 \sim .3292$

(8) 4. Albinism is observed among Hopi Native Americans who are homozygous for the albinism allele. Among the Hopi, the probability is .8 that a normal pigmented individual is homozygous for the normal allele. An albino father (aa) has had four normally pigmented children with a normal pigmented mother (A_).

(2) a) What is(are) the genotype(s) of the children?

Answer: Aa

(6) b) What is the probability that the mother is homozygous for the normal allele? (4 decimals please)

Answer: P(mother is AA / 4 Aa children)

$$= \left\{ \frac{P(\text{ 4 Aa children / aa x AA}) \, P(\text{aa x AA})}{P(\text{ 4 Aa children / aa x AA}) \, P(\text{aa x AA}) + P(\text{ 4 Aa children / aa x Aa}) \, P(\text{aa x Aa})} \right\}$$

= {(1) (.8)} / { 1 (.8) + $(1/2)^4$ (.2) = .8 / .90440125 = .88456313 ~ .8846

(10) 5. A population survey for a microsatellite locus in a *Drosophila* population resulted in the following numbers of different genotypes.

A_1A_1	A_1A_2	A_1A_3	A_2A_2	A_2A_3	A_3A_3
5	6	24	30	203	232

(6) a) Calculate the allele frequencies for all the alleles.

Answer: p_{A1} = [5 +1/2(6) + ½(24)]/500 = 20/500 = .04

p_{A2} = [30 + ½ (6 + 203)]/ 500 = 134.5/500 = .269

p_{A3} = [232 + ½ (24 + 203)]/ 500 = 345.5/500 = .691

~~(4) b) Estimate the standard deviation of the A_3 allele frequency.~~

~~**Answer:**~~ $$Sd\left(\hat{P}_{A_3}\right) = \sqrt{\frac{\hat{P}_3\left(1-\hat{P}_3\right)}{2N}} = \sqrt{\frac{.691(1-.691)}{2(500)}} = .0146$$

(8) 6. An x-linked recessive trait is present in 20 percent of the males in a population at equilibrium.

(4) a) What is the frequency of the trait in females?

Answer: $q^2 = (.2)^2 = .04$

(4) b) What is the expected frequency of carrier females?

Answer: 2pq = 2(.8)(.2) = .32

(14) 7. Assume that the following mtDNA sequences were found in three different individuals.

AATGGAGACTTT
ATTCCAGATTAA
AAAGGAGACTTT

(2) a) How many sites are available and analyzed?

Answer: 12

(2) b) How many sites are segregating?

Answer: 7

(2) c) What proportion of nucleotide sites differ in the sample?

Answer: 7/12 = .5833

(2) d) How many pairwise comparisons are possible for this sample?

Answer: $\frac{S(S-1)}{2} = \frac{3(3-1)}{2} = 3$

(6) e) Estimate nucleotide diversity.

Answer: $\pi = \left(\frac{1}{3}\right)\left(\frac{1}{12}\right)[6+1+7\ ]$ = 14 / (3)(12) = .3889

$$\pi = \left(\frac{2}{s(s-1)}\right)\left(\frac{1}{N}\right)[\pi 12 + \pi 13 + \pi 23]$$

(24) 8. Two populations of elephants were sampled and found to have the following allele frequencies for two SNP sites:

	Site 1		Site 2	
	G	C	G	A
60 African Elephants	.05	.95	.30	.70
140 Indian Elephants	.35	.65	.45	.55

(4) a) Estimate the mean allele frequency of G at Site 1.

Answer $\bar{P} = \frac{60(.05) + 140(.35)}{200} = 52/200 = .26$

(4) b) Estimate variance of allele frequency of G at Site 1.

Answer: $\hat{V}(P) = [60/200](.05)^2 + [140/200](.35)^2 - (.26)^2$

$= .00075 + .08575 - .0676 = .0189$

(4) c) Calculate the X^2 value to determine whether these populations of elephants are significantly different at Site 1.

Answer: $X^2 = \frac{2(200)(.0189)}{(.26)(.74)} = 7.56 / .1924 = 39.29313929 \sim 39.29$

(8) d) Calculate genetic identify and its three components for Site 1.

Answer: $Jxy = \sum_{i=1}^{n} P_{ix} \bullet P_{iy} = (.05)(.35) + (.95)(.65) = .635$

$Jx = \sum_{i=1}^{n} P^2_{ix} = (.05)^2 + (.95)^2 = .8125$

$Jy = \sum_{i=1}^{n} P^2_{iy} = (.35)^2 + (.65)^2 = .545$

$I = \frac{Jxy}{(Jx\ Jy)^{1/2}} = \frac{.635}{((.8125)(.545))^{1/2}} = \frac{.635}{.6654} = .95425356 \sim .9543$

(4) e) Estimate the standard genetic distance between the two elephant populations at Site 1.

Answer: $D = -\ln(I) = -\ln(.95425356) = .04682586 \sim .0486$