Note that question 6 is optional. The exam can include question 6 and be marked out of 100, or exclude it and be marked out of 85. CLEARLY MARK YOUR PREFERENCE ON p7.

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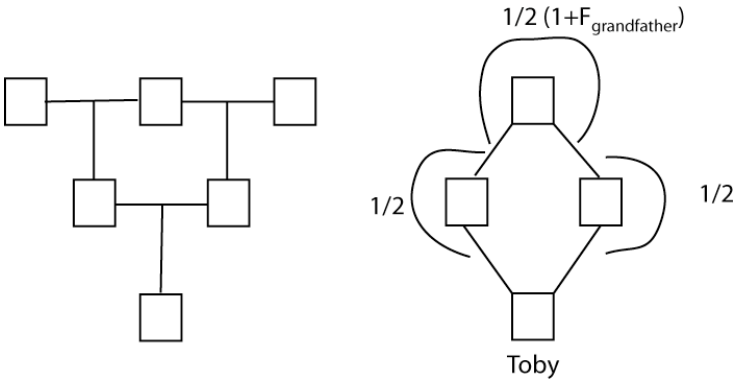
1. (6 points each) An individual babirusa named "Toby" in a zoo breeding program has the same grandfather on both sides, but two different grandmothers. The grandfather and grandmothers are unrelated, but the inbreeding coefficient of the grandfather is known to be 0.15, the paternal grandmother has inbreeding coefficient of 0.2, and the maternal grandmother has inbreeding coefficient of 0.1.

a. What is the inbreeding coefficient of Toby the babirusa?



$$F_{Toby} = (1/2)^3\left(1 + F_{grandfather}\right) = (1/2)^3(1 + 0.15) = 0.14375$$

b. The allele frequency at a particular neutral locus is 0.3 for the dominant allele. What is the chance that Toby has a dominant phenotype at this locus.

The phenotype frequency for a dominant phenotype is equal to the frequency of the dominant homozygote plus the frequency of heterozygotes. With inbreeding, the frequency of a homozygote is $p^2(1-F)+pF$ and the frequency of heterozygotes is $2p(1-p)(1-F)$. p is 0.3 and the inbreeding coefficient for Toby is 0.15, so the probability that he has a dominant phenotype is:

$$p^2(1-F)+pF+2p(1-p)(1-F) = 0.3^2(1-0.14375)+0.3(0.14375)+2(0.3)(0.7)(1-0.14375) = 0.4798$$

2. A *Drosophila* geneticist creates a new balancer chromosome which carries an allele making it lethal when homozygous. She starts a population with 50% individuals which are heterozygous for this balancer and another chromosome she calls *C* and 50% individuals heterozygous for the balancer and a chromosome she calls *D*. Chromosomes *C* and *D* differ only at one locus, at which they have different alleles. She then allows these flies to mate randomly for many generations at a large population size. Each surviving fly has the same expected number of offspring, but their probabilities of survival vary as given below:

Genotype	Survivorship probability
C/C	0.76
C/D	0.80
D/D	0.60
C/Balancer	0.50
D/ Balancer	0.59

Assume that the population is extremely large.

a. (5 points) What is the initial frequency of the balancer chromosome?

0.5 - -half of the initial chromosomes are the balancer.

b. (6 points) What is the equilibrium frequency of the balancer chromosome?

0 – The balancer chromosome has a low fitness on all background, and will be selected out of the population.

c. (6 points) What is the equilibrium frequency of chromosome *C*?

After the balancer is removed by selection, the *C* and *D* chromosomes display overdominance. Calculate the relative fitness by dividing by the heterozygote fitness, to get:

CC	CD	DD
0.76/0.80 = 0.95	0.80/0.80 = 1	0.60/0.80= 0.75
1-*s*= 0.95; *s* = 0.05		1-*t* = 0.75; *t* = *0.25*

$$\hat{p} = \frac{t}{s+t} = \frac{0.25}{0.05+0.25} = 0.8333$$

3. A population has 113 individuals with a variance in reproductive success of 2.5. It is fixed for the *fast* allele at its phosphoglucomutase (PGM) locus. A single individual heterozygous for the *slow* and *fast* alleles at PGM is introduced to this population, replacing one of the previous individuals. Assume that there are no selective differences between the *slow* and *fast* alleles, and that the population is maintained at this population size each generation.

a. (5 points) What is the heterozygosity at the PGM locus after this introduction?

$$p = \frac{1}{226} = 0.0044$$

$$2pq = 2(0.0044)(1-0.0044) = 0.0088$$

Note: I intended to ask for the expected heterozygosity. It is also correct to say that 1/113 of the population is heterozygous, or 0.00885.

b. (5 points) What is the probability that after one generation there will be no copies of the *slow* allele?

$$N_e = \frac{4N-2}{V+2} = \frac{4(113)-2}{2.5+2} = 100$$

$$\Pr[0] = \binom{200}{0}(0.0044)^0(1-0.0044)^{200} = 0.412$$

c. (7 points) What do we expect the heterozygosity to be after 5 generations?

$$N_e = \frac{4N-2}{V+2} = \frac{4(113)-2}{2.5+2} = 100$$

$$H_0 = 2(0.0044)(1-0.0044) = 0.00881$$

$$H_5 = H_0\left(1-\frac{1}{2N_e}\right)^5 = 0.00881\left(1-\frac{1}{200}\right)^5 = 0.00859$$

d. (3 points) Which model would tell us the probability of having no copies of the *slow* allele present after 5 generations?

Fisher-Wright model

4. (5 points each) A population of mice has a very large effective population size. It receive no migrants from other populations. At the *D* locus, the frequency of the *D* allele currently is 0.4. Mean numbers of offspring for the three genotypes at this locus are 2.0: 2.04: 2.08, for the *DD: Dd: dd* genotypes. Another locus in the same population, *G*, has an initial allele frequency of 0.2 for the *G* allele, and the *G* and *g* alleles on average have no effect on fitness. The *G* and *D* loci are on different chromosomes, and they start in linkage equilibrium.

a. What is the expected allele frequency of *d* after two generations?

The D locus has additive effects, so the change in allele frequency of *d* is given by $p' = \frac{w_d p}{\bar{w}}$, with $w_d = 1.02$. The *d* allele starts with frequency (1-0.4) = 0.6, therefore,

$$p_1 = \frac{1.02(0.6)}{1.02(0.6) + 0.4} = 0.6047$$

and

$$p_2 = \frac{1.02(0.6047)}{1.02(0.6047) + (1 - 0.6047)} = 0.6094$$

b. What is the expected allele frequency of *G* after two generations?

This locus is neutral, so on average the allele frequency won't change, so the expected frequency of ***G*** is 0.2.

c. What is the probability that both *D* and ***G*** fix in this population, after a long period of time has passed?

D is deleterious, and both alleles at this locus are common in a large population, therefore *D* is very, very unlikely to fix. Therefore the answer is approximately 0.

d. What is the probability that both *d* and *g* fix in this population, after a long period of time has passed?

d will fix with probability approximately 1. *g* will fix with probability equal to its initial allele frequency, or 0.8. Since these two are independent, the probability that both fix is 1 (0.8) = 0.8.

e. Assume that both *d* and *G* have fixed in the population. Which most likely fixed first?

Selection acts faster than drift in large populations, so *d* will fix faster than *G* on average.

5 a. (6 points) Studying a haploid species with non-overlapping generations, you observe that the allele frequency at a locus has changed from 0.50 to 0.6 in one generation. The population's size is 10^9, and there is no migration into this population. What is the relative fitness of the selectively favored allele?

Start from the allele frequency change due to haploid selection, $p' = \frac{wp}{\overline{w}}$, where $\overline{w} = pw + (1-p)$. In this case we can find $0.6 = \frac{w(0.5)}{w(0.5) + 0.5}$. Solving for *w* finds *w*= 1.5.

5 b. (5 points) Studying a diploid species with non-overlapping generations, you observe that the allele frequency at a locus has changed from 0.40 to 0.48 in one generation. The population's size is 10^9, and there is no migration into this population. Can you predict the equilibrium allele frequency at this locus? Why, or why not?

You can't predict its equilibrium allele frequency, because you can't tell from the information given whether the locus is overdominant (in which case there would be some equilibrium between 0.480 and 1) or if there is directional selection (in which case the equilibrium would be p = 1).

6. (*15 points OPTIONAL: Choose to answer and have exam marked of 100 points, or mark through with large X and have exam marked out of 85*)

What types of selection increase the amount of genetic variance within a population? Which decrease genetic variance? Why?