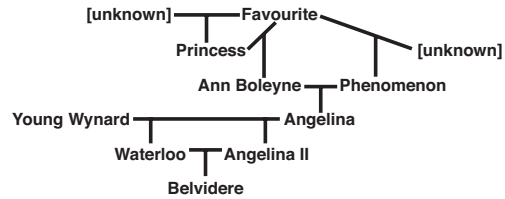
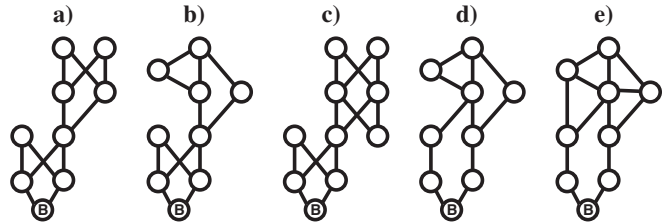


Correct answers in red

1. Sewall Wright first developed the method for calculating inbreeding coefficients from pedigrees in the early 1920's. This is a small part of his large pedigree for "The Duchess family of Shorthorns as bred by Thomas Bates". This breed of cattle was developed in 1700's-1800's by many generations of inbreeding and artificial selection. Apparently, Favourite was a favorite for breeding.



Which path diagram matches the pedigree of Belvidere? (Hint: note that Belvidere's parents are full siblings.) **b**



correct

2. Over time, natural selection can cause populations to lose variation if less fit alleles are eliminated. You suspect that natural selection has reduce variation in the global population of flu viruses during the 2004 flu season. The easiest way to see if genetic variation was lost is to see how \_\_\_\_\_ changes throughout the flu season.

- a.  $H_e$
- b.  $\mu$
- c.  $s$
- d.  $N$
- e.  $m$

Genetic variation is most easily quantified as  $H_e$ .

3. Which of the following is true about populations that are variable, and subject only to drift?
- a. A population undergoing drift will always lose its most rare allele.
  - b. All populations undergoing drift eventually become monomorphic.
  - c.  $p$  will steadily increase, generation after generation.
  - d.  $H_o$  will fluctuate over time, but eventually  $H_o$  will equal 1.0
  - e. The frequency of each allele and each genotype will remain constant over time.

a) is wrong because sometimes a rare allele can become common and eventually drift to fixation. For example, an allele at a frequency of 0.05 has a 5% chance of becoming fixed by drift.

d) is wrong because eventually  $H_o = 0$ . (If the population is fixed for one allele, there are no heterozygotes.)

4. What is the equilibrium frequency of allele A in a one-way mutation model with  $\mu = 1 \times 10^{-6}$ ?
- a. 0
  - b.  $1 \times 10^{-36}$
  - c.  $1 \times 10^{-12}$
  - d.  $1 \times 10^{-6}$
  - e. 0.999999

In the one way mutation model, the whole population will become fixed for  $a$ .

5. You conduct a test for Hardy Weinberg genotype frequencies. If your calculated test statistic is greater than the critical value of 3.84, what can you conclude?
- The null hypothesis of natural selection on this gene is accepted.
  - The null hypothesis of natural selection on this gene is rejected.
  - The null hypothesis of nonrandom mating is accepted.
  - The null hypothesis of random mating, no natural selection, no mutation, no drift, no gene flow is accepted.
  - The null hypothesis of random mating, no natural selection, no mutation, no drift, no gene flow is rejected.
6. Natural selection can most easily maintain more than one allele if
- the homozygous dominant genotype has the highest fitness.
  - the homozygous dominant genotype has the same fitness as the heterozygote.
  - the recessive genotype has the highest fitness.
  - heterozygotes have the lowest fitness.
  - heterozygotes have the highest fitness.
7. The “heritability” of a trait is
- the genetic variance divided by the total phenotypic variance.
  - the genetic variance divided by the environmental variance.
  - {genetic variance + environmental variance} divided by the environmental variance.
  - the genetic variance plus the environmental variance.
  - the genetic variance.
- Definition from lecture 18.
8. Zygotes in a population are not in Hardy Weinberg frequencies. How can you distinguish between inbreeding and assortative mating?
- know the rules for mate choice in the adults
  - look at genotype frequencies at many genes on different chromosomes
  - examine mating pedigrees for many different individuals in the population
  - A and B only
  - A, B and C would all distinguish between inbreeding and assortative mating  
a) and c) focus on the definitions of inbreeding and assortative mating. b) is true because inbreeding will affect all genes, while assortative mating affects only the gene that codes for the mating phenotypes. This question was on practice exam 2C #15.
9. For one species to diverge genetically and evolve into two species, it is most important that
- mutation rates in one species become zero.
  - the expected heterozygosity in one species is zero.
  - gene flow between the two species decreases to zero.
  - the fitness of one species drops to zero.
  - the selective coefficients for one species drop to zero.

See gene flow lecture.

10. Marsh tulips exist in two kinds of habitats: the edges of lakes, and in drier areas. Pollen is dispersed among all populations by bees. One gene with controls leaf thickness and resistance to drying:

*TT* tulips have thin leaves and survive best in wet areas and worst in dry areas.

*tt* tulips have thick leaves and survive best in dry areas, worst at lake edges.

*Tt* heterozygotes have leaves of intermediate thickness and have intermediate survival at each site.

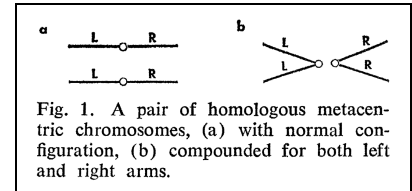
This situation is best described with a model that includes

- island model gene flow, and different incomplete dominance models for each habitat.
- island model gene flow, and different overdominance models for each habitat.
- island model gene flow, and the same underdominance model for each habitat.
- island model gene flow, and different underdominance models for each habitat.
- one way gene flow, and different underdominance models for each habitat.

<u>Genotype</u>	<u>Fitness in lake edges</u>	<u>Fitness in dry areas</u>
TT	Best	Worst
Tt	Intermediate	Intermediate
tt	Worst	Best

11. In 1972, Foster et al. suggested in the journal *Science* that compound chromosomes could be used to control natural insect populations.

For example, lab colonies of a pest mosquito would be created with compound chromosomes. (Individuals with two compound chromosomes survive just as well as individuals with two normal chromosomes.)



Males from the colony would be released into the wild. (Remember that only female mosquitoes feed.) Some wild females with normal chromosomes would mate with the released males. The offspring of these matings would have one normal copy of every chromosome and one compound copy, and would not survive.

In summary, Foster et al. suggested that \_\_\_\_\_ could be used to control pest insects.

- random genetic drift
- the basic Hardy Weinberg model
- inbreeding
- elevated mutation rates
- underdominance**

This example was used in lecture, and is in the Freeman text.

12. On the television show "LOST", 56 survivors of a plane crash are stranded indefinitely on a remote island. Assume there is drift only (i.e., they begin randomly mating, that there is no more immigration, no mutations, no natural selection, and that they can't build a raft to escape). If the frequency of blood type allele  $I_o$  is 0.714, what are the chances that someday the entire island has only blood type O (genotype  $I_oI_o$ )?

- 0.357%
- 0.714%
- 40%
- 71.4%**
- 100%

The probability that an allele will be fixed is equal to its frequency.

13. For the same 56 survivors, how many individuals are expected to have blood type O in the next generation?  $f(I_O) = 0.714$  now; assume random mating, and that the population size stays constant at 56 people.)
- about 23
  - about 29
  - about 36
  - about 40
  - about 51

Blood type O is genotype  $I_O I_O$ .

$$f(I_O)^2 = 0.510 \quad 0.510 * 56 = 28.55 \text{ people}$$

14. For the same island with  $f(I_O) = 0.714$  now, imagine now that 5 new plane crash survivors show up every 50 years (forever). The new immigrants are all coming from Australia, where  $f(I_O)$  is 0.2 and does not change. Assuming only immigration every 50 years (no drift, no mutation, no natural selection, random mating), where will  $f(I_O)$  eventually stabilize?
- Eventually, the island will stabilize either at  $f(I_O) = 1.0$  or at  $f(I_O) = 0.0$
  - Eventually, the island will stabilize at  $f(I_O) = 0.0$
  - Eventually, the island will stabilize at  $f(I_O) = 0.2$
  - Eventually, the island will stabilize at  $f(I_O) = 0.457$
  - Eventually, the island will stabilize at  $f(I_O) = 0.714$

This is a one way migration model. The island is continually inundated with Australians. Remember that  $p = p^*$  at equilibrium in the one way migration model.

- 
15. Which of the following is FALSE?

- Polymorphism can be maintained in some models with nonrandom mating only.
- Polymorphism can be maintained in some models with mutation only.
- Polymorphism can be maintained in some models with drift only.
- Polymorphism can be maintained in some models with migration only.
- Polymorphism can be maintained in some models with natural selection only.

Polymorphism can be maintained in models with nonrandom mating only, in the 2-way mutation model, in some migration models, and in the overdominance model.

16. 60% of San Diego citizens have normal earlobes, which are dominant to attached earlobes. If we assume random mating, what is the frequency of the attached earlobe allele?
- 0.16
  - 0.36
  - 0.40
  - 0.63
  - 0.77

$$40\% \text{ have attached earlobes} = q^2$$
$$q = \sqrt{0.40} = 0.63$$

17. Tay Sachs disease is usually first diagnosed by age 1, and almost always fatal by age 4. Natural selection on this gene is best characterized as
- sexual selection
  - fertility selection
  - gametic selection
  - fatality selection
  - viability selection
18. The mutation rate from allele *B* to allele *C* is  $1 \times 10^{-8}$  per generation. Genotypes *BB* and *BC* have no noticeable effects, but individuals with genotype *CC* are sterile. At this time,  $f(BB) = 0.95$ ,  $f(BC) = 0.04$ , and  $f(CC) = 0.01$ . If random mating is assumed, at equilibrium, what is the frequency of individuals with the sterile genotype *CC*?
- 0
  - $1 \times 10^{-64}$
  - $1 \times 10^{-8}$
  - $1 \times 10^{-4}$
  - $1 \times 10^{-2}$

A model with one way mutation and complete dominance. Since all *CC* individuals are sterile,  $w = 0$  for *CC*, and  $s = 1$ .

From the formula sheet,  $q^{\wedge} = \text{sqrt}(\mu/s)$

$$q^{\wedge} = \text{sqrt}(1 \times 10^{-8} / 1.0) = 0.0001 \quad q^2 = 1 \times 10^{-8}$$

19. In humans, femur length is best characterized as a
- mendelian trait
  - continuous trait
  - conspecific trait
  - meristic trait
  - threshold trait
20. The total phenotypic variance of a trait is made up of
- genetic differences among individuals only.
  - a genetic component and an allelic component.
  - a genetic component and an environmental component.
  - a genetic component and a mutational component.
  - a genetic component, an allelic component and a mutational component.

21. There is a species of field mouse that lives on old lava fields in Arizona, as well as the surrounding desert scrub. Coat color is controlled by a single gene under natural selection. (Mice with black coats match the black lava better, and can avoid visual predators.) What is the relative fitness of the blond genotype on the lava?

Genotype	Color	Lifetime survival on lava flows	Avg. # offspring on lava flows for surviving mice
<i>KK</i>	black	75% survive	2.4
<i>Kk</i>	black	75% survive	2.4

$kk$

blond

25% survive

2.4

- a. 0.125
  - b. 0.25
  - c. 0.33
  - d. 0.60
  - e. 2.5
- = 0.6 / 1.8

22. A lava field population of mice from the previous question begins with  $f(K) = 0.5$ . If there is no drift, no mutation, random mating and no immigration, what is the equilibrium frequency of the  $K$  allele?

- a. 0.0
- b. 0.25
- c. 0.33
- d. 0.60
- e. 1.00

At equilibrium, the full dominance selection model goes to fixation for the dominant allele.

---

23. What is the relationship between Mendelian genetics and quantitative genetics?

- a. The traits that Mendel studied (e.g., pea color and seed shape) are quantitative (polygenic) traits.
- b. When Mendelian traits are part of gene pools, forces such as migration, natural selection and drift convert them into quantitative traits.
- c. Mendelian traits become quantitative traits when a new species is formed.
- d. Quantitative traits are determined entirely by environmental factors, so they cannot be studied using Mendelian tools such as breeding experiments.
- e. Quantitative traits are usually controlled by many genes, and each gene behaves according to the rules of Mendelian genetics.

24. A model with both drift and gene flow ...

- a. can be used for situations in which Hardy Weinberg equilibrium applies.
- b. was first developed by Charles Darwin to explain descent with modification.
- c. is used to estimate how much gene flow is actually occurring in natural populations.
- d. shows that divergence among populations increases as gene flow increases.
- e. reaches an equilibrium predicted by the variables  $s$  and  $t$ .

See lecture notes. Answer d is exactly the opposite: more gene flow means less divergence. This question was on practice Exam 2B #30.

25.  $p = f(A) = 0.5$  in a population with random mating. Calculate  $p$  after one generation of selection based on the following data:

Genotype	Survival rate
AA	0.85
Aa	0.95
aa	0.05

- 0.29
- 0.36
- 0.64
- 0.89
- 0.95

$$w_{AA} = 0.895; w_{Aa} = 1.0; w_{aa} = 0.0526$$

$$\text{assuming random mating, } \bar{w} = 0.224 + 0.5 + 0.013 = 0.737$$

$$p' = p(qw_{Aa} + pw_{AA}) / \bar{w} = 0.5(0.5 \cdot 1.0 + 0.5 \cdot 0.895) / 0.737 = 0.5 \cdot (0.948) / 0.737$$

$$p' = 0.643$$

Questions 26-27 concern the 20 individuals on the right that were captured from a natural population of weasels.

Genotype	Number in sample
DD	10
Dd	2
dd	8

26. What is  $H_o$ ?

- 0.05
- 0.10
- 0.20
- 0.495
- 0.8

27. How inbred is the average weasel in this population?

- The average weasel has an inbreeding coefficient of 0.1
- The average weasel has an inbreeding coefficient of 0.2
- The average weasel has an inbreeding coefficient of 0.8
- The average weasel has an inbreeding coefficient of 1.8
- The average weasel is not inbred.

$$H_e = 2(0.55)(0.45) = 0.495$$

$$F = 1 - (H_o / H_e) = 1 - (0.1 / 0.495) = 0.8$$

28. A fire sweeps through a population of the wildflower *Ipomopsis aggregata* ("scarlet gilia"). It decreases the population size from 10,000 seeds in the soil to 500 seeds in the soil. Seeds that carried a dominant heat shock protein mutation survived better. How did this fire affect the genome of this flower?

- Drift was increased for all genes, and there was natural selection (complete dominance) on the heat shock protein.
- Drift was decreased for all genes, and there was natural selection (complete dominance) on the heat shock protein.

- c. Drift was decreased for all genes, and there was natural selection (underdominance) on the heat shock protein.
- d. Drift was decreased for all genes, inbreeding was increased, and there was natural selection (underdominance) on the heat shock protein.
- e. Drift was increased for all genes, inbreeding was increased, and there was natural selection (underdominance) on the heat shock protein.

There is nothing about inbreeding in this example.

Questions 29-30 concern the 64 individuals on the genetic data in this table.

<u>Genotype</u>	<u>Number in sample</u>
AA	43
BB	3
AB	10
AC	8

29. What is the frequency of allele *B*?

- a. 0.102
- b. 0.125
- c. 0.160
- d. 0.203
- e. 0.250
- = (6+10) / (2\*64)

30. What is the expected heterozygosity for this population?

- a. 0.000
- b. 0.203
- c. 0.281
- d. 0.305
- e. 0.320
- =  $1 - (0.8125)^2 - (0.125)^2 - (0.0625)^2$

31. The most common allele for human apolipoprotein E called  $\epsilon 2$ . (Other alleles are named  $\epsilon 3$ ,  $\epsilon 4$ , etc.) The genotype at this locus determines (to some extent) one's risk for elevated plasma cholesterol and triglyceride levels, for atherosclerosis. A random survey of 661 individuals finds these genotypes:

486 of  $\epsilon 2\epsilon 2$

152 of  $\epsilon 2\epsilon 3$

23 of  $\epsilon 3\epsilon 3$

Does this locus depart from Hardy-Weinberg frequencies? (For 1 degree of freedom  $\chi^2 > 3.84$  is significant.)

- a. Yes.  $\chi^2 = 3188.4$
- b. Yes.  $\chi^2 = 893.5$
- c. Yes.  $\chi^2 = 6.23$
- d. No.  $\chi^2 = 0.47$
- e. No.  $\chi^2 < 0$

<u>Observed</u>	<u><math>\epsilon 2\epsilon 2</math></u>	<u><math>\epsilon 2\epsilon 3</math></u>	<u><math>\epsilon 3\epsilon 3</math></u>	<u>Sum</u>
	486	152	23	80

Allele frequencies:

A

a



