1. The data to the right come from a microsatellite study of two ring seal populations: one small population is isolated and landlocked in Lake Saimaa. The "marine" population consists of all seals in the open ocean. The alleles are named "195", "191", "189" … and so on. For example, the frequency of allele "189" in Lake Saimaa is 0.156. This locus is called "Hg8.10", and it is in a region of DNA that does not code for anything.

   Calculate H_e for Lake Saimaa.

   a. 0.132   b. 0.263   c. 0.737
   d. 0.844   e. 0.929

   $2pq = 2*0.156*0.844$

Locus/ allele	Saimaa	Marine
Hg8.10		
195	–	0.006
191	–	0.050
189	0.156	0.370
187	0.844	0.393
185	–	0.101
183	–	0.026
181	–	0.015
163	–	0.038

2. Which population is polymorphic for this gene?
   a. Lake Saimaa
   b. Marine
   c. both
   d. neither

3. Pituitary dwarfism is a caused by a homozygous recessive condition at the growth hormone gene GH1. The forward rate of mutation from the normal gene to the mutant form is 1×10^{-6}. The backward rate of mutation is so small that it can be ignored. If the frequency of the mutant allele is now 0.1000, what will it be in 1000 generations? Assume no natural selection or drift.
   a. 0.0000   b. 0.0999   c. 0.1000   d. 0.1009   e. 0.8991

   $p = 0.9, q = 0.1$

   $p_{1000} = 0.9 \, (1 - 1 \times 10^{-6})^{1000} = 0.8991$

   $q_{1000} = 1 - p_{1000} = 0.1009$

4. A brand new mutation has a 2% probability of eventually becoming fixed through the action of genetic drift alone. How big is the population? (Assume that the species is diploid.)
   a. 20   b. 25   c. 50   d. 100   e. 200

   prob. of fixation = frequency of the allele. A new mutation has a frequency of 1/2N.
   $0.02 = 1/2N$, so $N = 25$

5. **Tall Guys Get the Girls:** *Short Men Less Likely to Marry, Have Kids* by Rick Callahan, The Associated Press. Jan. 12, 2004 — If it seemed as if the tall guys got all the girls in high school, it wasn't your imagination. New research suggests taller men are more likely to marry and tend to have more children than short guys. What's behind the phenomenon — whether women prefer taller men or those men are simply more outgoing — is up for debate. But the numbers clearly stack up against shorter guys. Polish and British scientists studied the medical records of about 3,200 Polish men ages 25 to 60 and found that childless men were on average 1.2 inches shorter than men who had at least one child. Bachelors were about an inch shorter on average than married men. … The findings were published in Thursday's issue of the journal Nature.

This is an example of
a. inbreeding
b. positive assortative mating
c. viability selection
d. sexual selection
e. gametic selection

There is no information on nonrandom mating in this article. It states that taller men are more likely to mate. This is the definition of sexual selection.

6. The trait of interest in the last question (height) is a _____ trait.
a. Mendelian
b. pleiotropic
c. quantitative
d. meristic
e. threshold

Height in humans is a quantitative, continuous trait.

7. In a population of sea bass, 80 randomly surveyed individuals have genotypes as follows. 15 are *DD*, 36 are *Dd* and 29 are *dd*. Does this locus depart from Hardy-Weinberg frequencies? (For 1 degree of freedom $\chi^2 > 3.84$ is significant.)

a. Yes. $\chi^2 = 323.5$
b. Yes. $\chi^2 = 11.6$
c. No. $\chi^2 = 0.41$
d. No. $\chi^2 = 0.08$
e. No. $\chi^2 = 0.0051$

Observed	DD	Dd	dd	Sum
	15	36	29	80

Allele frequencies:	A	a
	0.413	0.588

Expected	AA	Aa	aa	Sum
Expected genotype freq	0.170	0.485	0.345	1.00
Expected genotype counts	13.6	38.8	27.6	80.00

Chi-sq. calc.	0.1414	0.1986	0.0697	**0.4097**

Chi-square = 0.4097

The chi square is less than the critical value. We accept the null hypothesis that the population is in H-W genotype frequencies.

8. Which microevolutionary force is acting on the sea bass population from the last question?
   a. inbreeding
   b. negative assortative mating
   c. mutation
   d. natural selection (overdominance)
   e. I accept the null hypothesis that none of these evolutionary forces are important.

9. A large African population of humans has no sickle cell anemia alleles. Then there is a single mutation in the gene pool from the normal allele to the sickle cell allele. (There are no more mutations.) This is an population in which 1) malaria is common, 2) mating is random and 3) there is no appreciable immigration or emigration. Based on what you know about sickle cell anemia from lecture, what would you expect in patterns of diversity <u>in newly fertilized zygotes</u>?
   a. H_o will reach a stable equilibrium between zero and one, and H_e will reach the same stable equilibrium.
   b. H_o will reach a stable equilibrium between zero and one, and H_e will reach a different stable equilibrium between zero and one.
   c. H_o will decrease to zero, and H_e will decrease to zero.
   d. H_o will decrease to zero, and H_e will increase to one.
   e. H_o will decrease to zero, and H_e will reach a stable equilibrium between zero and one.
   − SC anemia is an example of overdominance. At equilibrium, there will be two alleles in the population with frequencies greater than zero.
   − Therefore, $H_e = 2pq$ will be greater than zero at equilibrium. Remember that for two alleles, H_e is always defined as $2pq$ in every model.
   − Because there is random mating, $H_o = H_e$ at the time that zygotes are formed.

10. Many of the natural selection models have both stable and unstable equilibria. Imagine a model with incomplete dominance, 2 alleles and high selection coefficients. A population is sitting <u>very close</u> to the stable equilibrium. To move the population steadily away from this stable equilibrium, generation after generation, would require
    a. a single mutation.
    b. genetic drift.
    c. some inbreeding.
    d. negative assortative mating.
    e. None of these, because the population will almost certainly stay at or near the stable equilibrium.
That is the definition of a stable equilibrium!
The stable equilirbium is $p = 1.0$. If natural selection is strong, a single mutation will not matter because natural selection will eliminate that heterozygote. Drift will not move the population steadily away from the equilibrium; drift is a random process. Nonrandom mating will not increase the frequency of q, because there can only be very few Aa or aa if q is close to zero. The Aa or aa individuals created by any type of mating will have lowered fitness.

11. Normal *AA* individuals have a relative fitness of 1.0, heterozygous *Aa* individuals have a relative fitness of 0.95 and homozygous *aa* individuals have a relative fitness of 0.8. What are the selective coefficients h and s in this model?
    a. $h = 0.95, s = 0.8$
    b. $h = 0.05, s = 0.2$
    c. $h = 0.05, s = 0.8$
    d. $h = 0.25, s = 0.2$
    e. $h = 0.062, s = 0.2$

$1-s = 0.8$, so $s = 0.2$
$1-hs = 0.95$, substitute $s = 0.2$
$1-h(0.2) = 0.95$
$0.2h = 0.05$
$h = 0.25$

12. The model of natural selection in the previous question is
    a. full dominance
    b. partial dominance
    c. overdominance
    d. underdominance
    e. Domino's pizza dominance

13. There are 12 *AA* individuals, 5 *Aa* individuals and 15 *aa* individuals. What is the frequency of the *A* allele?
    a. 0.266   b. 0.375   c. 0.453   d. 0.531   e. 0.906
$= (24+5)/(24+10+30)$

14. Which of the following is <u>NOT</u> true about a population in Hardy-Weinberg equilibrium?
    a. allele frequencies do not change over time
    b. genotype frequencies do not change over time
    c. the population size is infinite
    d. every gene copy makes an identical contribution to the gene pool in the next generation
    e. mutations occur according to the one-way mutation model

15. Zygotes in a population are not in Hardy Weinberg frequencies. How can you distinguish between inbreeding and assortative mating?
    a. know the rules for mate choice in the adults
    b. look at genotype frequencies at many genes on different chromosomes
    c. examine mating pedigrees for many different individuals in the population
    d. A and B only
    e. A, B and C would all distinguish between inbreeding and assortative mating

16. Which of the following is <u>false</u> about mutations?
    a. The two-way (forward-backward) mutation model does not have a stable equilibrium.
    b. The one-way mutation model leads to a population with no heterozygosity.
    c. Mutations cause dramatic allele frequency changes only after many thousands of generations.
    d. Mutations provide the original source for all new alleles.
    e. Mutation and selection can balance each other to maintain polymorphism.

17. A monohybrid cross experiment is conducted. To determine whether the trait is controlled by one gene or by many genes, it is most useful to study
   a. the amount of variance in one of the two parental strains.
   b. the difference between the mean values of the two parental strains.
   c. the shape of both phenotypic distributions in the parental strains.
   d. the phenotypic distribution in the F1 generation.
   e. the phenotypic distribution in the F2 generation.

18. In a polymorphic population, which microevolutionary force(s) cause a <u>predictable</u> change in allele frequencies from one generation to the next?
   a. mutation
   b. natural selection
   c. drift
   d. A and B only
   e. A, B and C are true.
Drift causes unpredictable increases or decreases in allele frequencie from one generation to the next.

19. If $f(AA) = 1.0$, then
   a. The population may have gone through a recent bottleneck.
   b. The observed heterozygosity equals the expected heterozygosity.
   c. The gene is highly polymorphic.
   d. A and B only.
   e. A, B and C are true.
The observed heterozygosity equals the expected heterozygosity because if $p = 0$, then there are no heterozygotes and $H_e = 2pq = 0.0$

20. The Dunkers are a religious sect in rural Pennsylvania established by 27 families that emigrated from Germany in the mid-1700's. Since then, they have lived in small communities, intermarrying little with the surrounding population. The frequency of blood group A (genotypes $I_A I_A$ and $I_A I_O$) is 40-45% in Germany, 40-45% in Americans of German descent, <u>but 60% in the Dunkers</u>. (Consider "Germany", "Americans of German descent" and "Dunkers" to be three different populations.) This high frequency of the I_A allele in Dunkers is due primarily to
   a. Hardy-Weinberg equilibrium
   b. drift
   c. inbreeding
   d. mutation
   e. gene flow
This is a good example of a founder effect in a small population, with drift continuing after the founder effect. You cannot assume inbreeding because inbreeding by itself will not change allele frequencies. Inbreeding only changes genotype frequencies.

21. In a population of sharks, there is a base pair position at the top of the 3rd chromosome in which some individuals have "A" and some have "G". This could be possible in
    a. some models with gene flow only
    b. some models with natural selection only
    c. some models with mutation only
    d. A and B only
    e. **A, B and C**

All of these forces can maintain polymorphism in some cases.

22. $\overline{W}$ is defined as
    a. the average mutation rate from one allele to another.
    b. the total number of offspring in the entire population in one particular generation.
    c. the average relative fitness of all the individuals born in the population.
    d. the average absolute fitness for a particular allele.
    e. the average survivorship of homozygous *AA* individuals between zygote and adult.

23. In a field of daisies, half of the flowers with genotypes *gg* and *Gg* do not survive long enough to reproduce. All *GG* flowers survive to maturity. Of the mature flowers, *GG* produce on average 100 seeds, *Gg* 80 seeds and *gg* 20 seeds. What is the absolute fitness of genotype *Gg*?
    a. 20   b. 40   c. 50   d. 60   e. 80

= 0.5 * 80
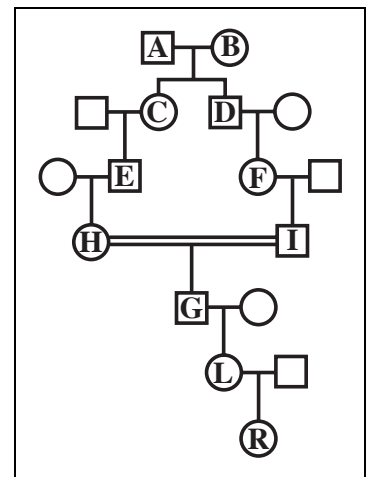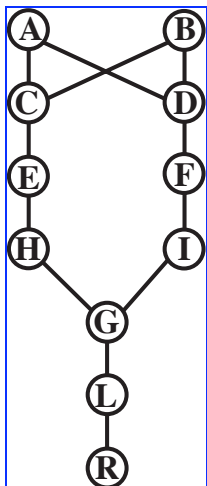
24. For the same daisies in the previous question, what is the relative fitness of genotype *gg*?
    a. 0.0   b. 0.1   c. 0.2   d. 1.0   e. 10

= (0.5 * 20) / (1.0 * 100)

25. On the TV show *Gilmore Girls*, I found out that Rory's great grandmother (*H* in the pedigree) was married to her second cousin. Rory is "R". What is the inbreeding coefficient for Rory's grandfather (*G* in the pedigree), assuming that individuals *A* and *B* are not inbred?
    a. 0.00195313   b. 0.00390625   c. 0.0078125
    d. 0.015625   e. 0.078125

$$f_G = \left(\tfrac{1}{2}\right)^6 \left(\tfrac{1}{2}\right)\left(1 + f_A\right) + \left(\tfrac{1}{2}\right)^6 \left(\tfrac{1}{2}\right)\left(1 + f_B\right) = \left(\tfrac{1}{2}\right)^7 \left(1 + 0\right) + \left(\tfrac{1}{2}\right)^7 \left(1 + 0\right) = \tfrac{1}{64} = 0.015625$$

On average, 1.6% of the genes in Rory's grandfather have two copies that are identical by descent, and those genes must be homozygous.

26. I have two large laboratory populations of *Drosophila*. There is random mating in each one, and no immigration. I know that one population went through a severe bottleneck 2 generations ago, and the other did not … but I forgot to label them. How could I figure out which population went through a bottleneck? There is only one correct answer.
    a. Estimate the frequency of red eyes and white eyes in each population. Then calculate allele frequencies assuming random mating. The population with the largest H_e went through a bottleneck.
    b. Collect 30 random flies from each population. Smash them. Conduct protein electrophoresis for all 60 flies at 20 loci. Calculate the summary statistic P. The population with the lower value of P went through a bottleneck.
    c. Collect 30 random flies from each population. Smash them. Visually examine the chromosomes under a microscope. The population with more mutant chromosomes went through a bottleneck.
    d. Collect 30 random flies from each population. Smash them. Record the genotypes at 20 different microsatellite loci. The population which fails a chi-square test for HW frequencies went through the bottleneck.
    e. Collect one female fly from each population for a detailed reproductive study. The fly that lays the fewest eggs is from the population that went through a bottleneck.

The population that went through a bottleneck will have lost variation at most of its loci; some genes will have become monomorphic if the bottleneck is severe. See examples at the end of lectures 10 and 13.

The chi-square test would be significant if there were too many or too few heterozygotes. If there is random mating in each population, this test will not be significant … even if variation is low from the bottleneck.

27. For alleles A and a, inbreeding would
    a. increase $f(aa)$ compared to HW expectations.
    b. increase $f(Aa)$ compared to HW expectations.
    c. increase H_o compared to HW expectations.
    d. A and B only.
    e. A, B and C are all true.

Inbreeding increase homozygotes and decreases heterozygotes.

28. Natural selection _____ the average population fitness over time.
    a. increases
    b. keeps constant
    c. decreases
    d. A and B are possible, depending on p and q.
    e. A, B and C are all possible, depending on p and q.

Natural selection almost always increases the population fitness in a <u>polymorphic</u> population, so I will give alternative credit for a). HOWEVER, if the population is on a stable or unstable equilibrium, then there will be no allele frequency changes and therefore no fitness changes. So d) is the correct answer.

29. For a large population, the heritability of a quantitative trait can be estimated by
    a. estimating how much of the total phenotypic variance is due to genetic differences between individuals.
    b. calculating Hardy Weinberg expectations for any particular gene.
    c. calculating its threshold value.
    d. estimating the mean phenotype of the population.
    e. estimating the variance of the heterozygotes.

30. If $p = 0.8$, we expect the frequency of *AA* to be _____ when mating is random.
    a. 0.04   b. 0.20   c. 0.32   d. 0.64   e. 0.80

31. There are 10 *BB* individuals and 5 *Bb* individuals. What is the observed frequency of the genotype *Bb?*
    a. 0.05   b. 0.17   c. 0.28   d. 0.33   e. 0.50

32. Lidicker and McCollum (1997) examined genetic variation in populations of sea otters (*Enhydra lutris*) in the eastern Pacific Ocean. Sea otters were distributed throughout this region before fur hunting nearly led to their local extinction. Along the central California coast only one population of 50 or fewer individuals is thought to have survived; this population was protected in 1911 and has grown to its current size of approximately 1500 otters. From this information, it is obvious that this population has gone through a _____, and is likely to have _____ genetic variation.
    a. migration event … high levels of
    b. bottleneck … lost some
    c. mutation … less fit
    d. threshold trait … normally distributed
    e. gene pool … Hardy Weinberg

33. In words, H_e is
    a. the proportion of all the genes in the genome that are polymorphic.
    b. the probability that if you pick two alleles randomly from a gene pool, they will be different.
    c. the probability that a new mutation will occur.
    d. the frequency of heterozygotes that you see in your sample.
    e. the probability that a particular allele will eventually become fixed by drift.