All MBG Quiz answers

Quantitative Genetics W (University of Guelph)

Quizzes

Quiz 1

Question 1 *1 / 1 point*

If you are told 5.9% of the population suffers from a recessive condition, what is the frequency of the dominant allele (rounded to three decimal places)?
Answer:

0.757 ✓

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This is a circumstance where we have to estimate the frequency of the recessive allele as the square root of the frequency of the homozygous recessive genotype. When you use this estimation procedure, you are assuming Hardy-Weinberg equilibrium.

Question 2 *1 / 1 point*

In Labrador Retrievers, the coat colour is controlled by 2 loci. If we consider only the locus that controls the black or chocolate colours and we observe that of the 577 labs that are either black or chocolate, 239 of them are black and (577 - 239) are chocolate. What is the frequency of the recessive chocolate allele (two decimal places)?
Answer:

0.77 ✓

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In this case, we have to estimate the frequency of the chocolate allele because we do not know how many heterozygotes there are (they would be all black).

Question 3 *1 / 1 point*

Independent segregation is a test for linkage of loci. Suppose a researcher genotypes a population for alleles at two different loci. The results are: 62 individuals are **CT**, *373 individuals are* **Ct**, *66 individuals are* **cT** *and 82 individuals are* **ct** *What is the frequency of the* **t** *allele (two decimals)?*
Answer:

0.78 ✓

Question 4 *1 / 1 point*

If you are told 6.3% of the population suffers from a recessive condition, what is the frequency of the dominant allele (rounded to three decimal places)?
Answer:

0.749 ✓

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This is a circumstance where we have to estimate the frequency of the recessive allele as the square root of the frequency of the homozygous recessive genotype. When you use this estimation procedure, you are assuming Hardy-Weinberg equilibrium.

Question 5 *1 / 1 point*

If the recessive allele, **a**, *has a frequency of 0.18 how many* **AA** *individuals are there in a randomly mating population of 271 individuals? (rounded up to the nearest whole individual)*
Answer:

182 ✓

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*The frequency of the AA genotype is p^2 where p = 1 - q = 1 - f(a) . Out of a population of size n, p^2 of them will be p^2 * n*

Question 6 *1 / 1 point*

The Himalayan colour pattern in rabbits is controlled by a single locus with three alleles; **F** *for full colour,* **H** *for Himlalayan and* **A** *for albino. The* **F** *allele is dominant over the* **H** *and* **A** *alleles while the* **H** *allele is dominant over the* **A** *allele. If the number of individuals with the Himalayan colour pattern represent 36% of the population and the albinos represent 16% of the population, what is the frequency of the* **F** *allele? (rounded to 3 decimal places)*
Answer:

0.279 ✓

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You need to assume random mating to do this, there isn't any other way. The frequency of the **F** *allele is 1 - f(***H***) - f(***A***). f(***A***) = SQRT(f(AA)) and f (***H***) = SQRT(f(HH)+f(HA)+f(AA)) - SQRT(f(AA)).*

Question 7 *1 / 1 point*

Suppose you are told that the following observations were recorded on a population of 800 individuals: 200 individuals were observed to have the homozygous dominant phenotype and 400 individuals were observed to have the heterozygous phenotype. Is this population in Hard-Weinberg Equilibrium?

	1)	*No*
✓	*2)*	*Yes*

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*Test H / (PQ)**0.5 . If it equals 2 then you have HWE. The other tests are weaker.*
*Correct - Test H / (PQ)**0.5 and it is = 2 therefore it is HWE.*

Question 8 *1 / 1 point*

Determine the value of a test statistic to test the null hypothesis that a population with the following number of individuals is in Hardy-Weinberg equilibrium:
Number of TT individuals = 1324
Number of Tt individuals = 658
Number of tt individuals = 198

	1)	*0.433*
	2)	*5.1*
	3)	*0.0312*
	4)	*3.84*
✓	*5)*	*68.05*

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Correct. Well done.

Question 9 *1 / 1 point*

Based on your result from the question above, would this population be in Hardy Weinberg Equilibrium (with a 5% test)?

✓	*1)*	*No*

2) Yes

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Correct. The Chi-square statistic is well in excess of the critical value so we reject the null hypothesis and accept the alternate hypothesis that the population is **NOT** *in Hardy Weinberg Equilibrium.*

Question 10 *1 / 1 point*

You are told that in a population of 10,000 individuals, there were 1,764 matings recorded between heterozygous individuals and 882 matings recorded between homozygous dominant and homozygous recessive individuals. Is this population in Hardy-Weinberg equilibrium?

1) No

✓ 2) Yes

Quiz 2

Question 1

Suppose a researcher collects seeds and pollen (i.e. gametes) from a certain kind of plant. If 231 gametes are **AB**, *99 are* **Ab**, *154 are* **aB** *and 66 are* **ab**, *what is the frequency of the* **A** *and* **b** alleles (to 1 decimal place)?

✓ 1) f(A) = 0.6 and f(b) = 0.3

2) f(A) = 0.6 and f(b) = 0.2

3) f(A) = 0.5 and f(b) = 0.5

4) f(A) = 0.5 and f(b) = 0.3

Question 2 *1 / 1 point*

A researcher has calculated gametic frequencies for an experiment studying two loci and is quite confused by the results. Can you help the researcher by determining the coefficient of linkage disequilibrium from their data (to 2 decimal places)?
The data that they have are:
*f(***CE***) = 0.5872*
*f(***Ce***) = 0.1728*
*f(***cE***) = 0.1328*
*f(***ce***) = 0.1072*

1) d = 0.02

2) d = -0.04

3) d = 0.0

✓ 4) d = 0.04

5) d = -0.02

Question 3 *1 / 1 point*

If the coefficient of linkage disequilibrium is -0.03, what is the linkage phase?

✓ 1) Repulsion

2) Equilibrium

3) Coupling

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Correct, when d < 0, repulsion is the phase

Question 4 *1 / 1 point*

If we observe the following gametic frequencies and we know that the fraction of crossovers is 0.03, what is the coefficient of linkage disequilibrium in the next generation (to 4 decimal places)?
Number of **AB** *gametes = 148*
Number of **Ab** *gametes = 132*
Number of **aB** *gametes = 92*
Number of **ab** *gametes = 28*

1) *Next generation, d = 0.0243*

2) *Next generation, d = 0.0485*

✓ 3) *Next generation, d = -0.0485*

4) *Next generation d = 0*

5) *Next generation, d = 0.0122*

Question 5 *1 / 1 point*

With the following observed gametic frequencies, what would be the frequency of the **b** *allele at equilibrium?*

Number of **AB** *= 135*
Number of **Ab** *= 75*
Number of **aB** *= 45*
Number of **ab** *= 45*

1) *f(b) = 0.2*

2) *f(b) = 0.6*

3) *f(b) = 0.28*

✓ 4) *f(b) = 0.4*

5) *f(b) = 0.12*

Question 6 *1 / 1 point*

If d_0 (i.e. d for generation zero) is 0.07 and d_2 is 0.0252 , what is the fraction of crossovers (to 1 decimal place)?

1) *Fraction of crossovers, c = 0.6*

2) *Fraction of crossovers, c = 0*

✔ 3) *Fraction of crossovers, c = 0.4*

4) *Fraction of crossovers, c = 0.5*

5) *Fraction of crossovers, c = 0.2*

Question 7 *1 / 1 point*

If the coefficient of linkage disequilibrium at generation n (i.e. d_n) is observed to be -0.0050332 , the fraction of crossovers is observed to be 0.2 and the initial coefficient of linkage disequilibrium (i.e. d_0) was observed to be -0.03 , how many generations of random mating have occurred between d_0 and d_n; in other words, what is n (to the nearest whole generation)?

1) *n = 1*

✔ 2) *n = 8*

3) *n = 16*

4) *n = 6*

5) *n = 100*

Question 8 *1 / 1 point*

*As a result of genotyping two loci (**A** and **B**) in a large number of progeny of two heterozygous individuals, a researcher has determined that the gametes produced by one of the parents had the following frequencies:*
*f(**AB**) = 0.17,*
*f(**Ab**) = 0.17,*
*f(**aB**) = 0.26, and*
*f(**ab**) were the remainder.*
What is the coefficient of linkage disequilibrium (to two decimal places)?
Answer:

0.02 ✔

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The coefficient of linkage disequilibrium, d = ru-st where r = f(AB), s = f(Ab), t = f(aB) and u = f(ab).

Question 9 *1 / 1 point*

*After an exhaustive and expensive process to genotype individual spermatozoa for two loci, **C** and **D**, a bleary-eyed researcher has determined that, out of 1,000 spermatozoa, the following gametes were present:*
***CD**: 73*
***Cd**: 95*
***cD**: 96*
*and the remainder were **cd**.*
Your job is to help the now delirious researcher to figure out if these loci are in linkage disequilibrium by calculating the coefficient of linkage disequilibrium to two decimal places.
Answer:

0.04 ✔

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The coefficient of linkage disequilibrium, d = ru - st where r = f(CD) = number of CD / 1,000, s = f(Cd) = number of Cd / 1,000, t = f(cD) = number of cD / 1,000 and u = f(cd) = remainder / 1,000

Question 10 *1 / 1 point*

With the following observed gametic frequencies (which are in linkage disequilibrium), what is the frequency of the **AB** *gamete type at equilibrium?*
*f(***AB***) = 0.18*
*f(***Ab***) = 0.27*
*f(***aB***) = 0.25 and*
*f(***ab***) = the remainder.*

Answer:

0.19 ✓

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The frequency of the AB gamete type at equilibrium is the observed frequency minus the coefficient of linkage disequilibrium. So f(AB) at equilibrium = f(AB) observed – d

Question 11 *0 / 1 point*

The owner of a kennel is concerned about the possibility of a recessive condition in one of his prize male dogs. Suppose the recessive allele is known to have a frequency of 0.06 in the population. If the male dog is mated to 8 females each producing 5 puppies, what is the probability that his prize male will be detected as a carrier (to three decimal places)?
Answer:

0.782 ✗ **(0.704)**

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For this situation, you first need to figure out the frequency of the genotypes of the mates. Once that is figured out, then put those frequencies into the general detection of carriers equations.

Question 12 *1 / 1 point*

A Quarter Horse breeder has a stallion that they suspect may have had a parent that was dual registered in the paint herdbook. Although rare, it is possible for a solid coloured stallion to carry the lethal white overo allele. In order to test the stallion, the breeder arranges with a neighbour who has registered paint horses to breed all the paint mares for free for one year to see if the stallion is a carrier. Assuming all of the paint mares are heterozygous, what is the **percentage chance** *(express your answer as a percentage with one decimal place) that the Quarter Horse stallion is a carrier if he breeds 10 mares and produces no foals that die of Lethal White Overo Syndrome (Congenital Intestinal Aganglionosis)?*
Answer:

94.4 ✓

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All of the mares are the same genotype (heterozygous) so the result is 1-(0.75)^n but don't forget to mulitply by 100 and express it as a percentage (bolded in the question).

Question 13 *1 / 1 point*

A researcher samples gametes in two separate generations and observes the following results:
Generation 0:
Number of **GH** *= 195*
Number of **Gh** *= 45*
Number of **gH** *= 30*
Number of **gh** *= 30*

Generation 1:
Number of **GH** *= 192*
Number of **Gh** *= 48*
Number of **gH** *= 33*
Number of **gh** *= 27*

What will be the frequency of the **h** *allele at equilibrium?*

	1)	*f(h) = 0.0*
	2)	*f(h) = 0.2*
	3)	*f(h) = 0.5*
✓	*4)*	*f(h) = 0.25*

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Yes, the frequency of h stays the same every generation even though the genotypic frequencies are changing.

Question 14 *0 / 1 point*

If the phase of linkage disequilibrium is repulsion and the fraction of crossovers is 0.2, what will be the direction of change of the gametic frequencies after one generation of random mating if we are tracking two loci; **A** *and* **B***?*

- *1) f(AB) goes down, f(Ab) goes up, f(aB) goes up and f(ab) goes down*
- *2) f(AB) goes down, f(Ab) goes down, f(aB) goes up and f(ab) goes up*
- *3) f(AB) goes up, f(Ab) goes up, f(aB) goes down and f(ab) goes down*
- ✗ *4) No change*
- ➡ *5) f(AB) goes up, f(Ab) goes down, f(aB) goes down and f(ab) goes up*

Question 15 *0 / 1 point*

In practice, the fraction of crossovers, **c***, can equal zero based on observations with a fixed population size. However, in theory with an infinite population size, we can never completely rule out even a single crossover no matter how close two loci are to each other. So* **c** never theoretically equals zero.

Suppose we have two loci on a single human autosome. For easy calculations, assume the average chromosome in the human genome is 100 centimorgans long. A centimorgan is generally assumed to span approximately 1,000,000 bases in the human DNA sequence. Suppose we have a sufficiently large population and a single crossover event occurs between our two loci exactly in accordance with the probability that it would occur. What is the theoretical minimum number of offspring you would need to genotype in order to detect this one crossover event (assuming no genotyping errors)?

➡	*1)*	*100,000,000 random offspring*
	2)	*100,000 random offspring*
	3)	*100 random offspring*
✗	*4)*	*1,000,000 random offspring*
	5)	*1,000,000,000 random offspring*

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There are approximately 100 cM x 1,000,000 bases per cM = 100,000,000 bases on an average chromosome and you would have to genotype that many individuals to see that one single crossover for sure.

Quiz 3

Question 1 *1 / 1 point*

One common form of colour blindness in humans is caused by a recessive allele at a sex linked locus on the **X** *chromosome. We will denote the normal vision allele* **C+** *and the colour blind allele* **C***. The genotype is expressed by putting the colour blind allele in brackets beside the* **X** (for example X(C) X(C) is a homozygous colour blind female). If a woman with normal colour vision whose father was colour blind marries a man with normal colour vision whose father was also colour blind, what is the genotype of the woman's father?

✓ ◉	*1)*	*X(C) Y*
○	*2)*	*X(C+) Y*
○	*3)*	*X(C+) X(C)*

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Correct. The father must carry the recessive allele to be colour blind. Genotype = phenotype and none of the rest of the information is necessary.

Question 2 *1 / 1 point*

If selection favours heterozygotes and allele frequencies have reached equilibrium, what proportion of homozygous recessive individuals survive if 20% of the homozygous dominant individuals are eliminated each generation and the frequency of the dominant allele is 0.64

○	*1)*	*0.3556*
✓ ◉	*2)*	*0.6444*
○	*3)*	*0.1778*
○	*4)*	*0*
○	*5)*	*0.05625*

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Correct

Question 3 *1 / 1 point*

Suppose you have a population where the heterozygous individuals have twice as much fitness as the homozygous recessive individuals and half as much fitness as the homozygous dominant individuals. If the frequency of the dominant allele was 0.8 before selection, what is it after selection?

○	*1)*	*0.8352*
○	*2)*	*0.7752*
○	*3)*	*1.0000*
✓ ◉	*4)*	*0.8889*
○	*5)*	*0.8780*

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Correct. $s_1 = 0.5$ and $s_2 = 0.75$

Question 4 *1 / 1 point*

If selection favours heterozygotes and allele frequencies have reached equilibrium, what proportion of homozygous recessive individuals survive if 10% of the homozygous dominant individuals are eliminated each generation and the frequency of the dominant allele is 0.64

	1)	*0*
	2)	*0.1778*
	3)	*0.05625*
✓	*4)*	*0.8222*
	5)	*0.94375*

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Correct

Question 5 *1 / 1 point*

If a long term selection process results in no loss of alleles from a population, which genotype is preferred?

	1)	*homozygous dominant*
✓	*2)*	*Heterzygote*
	3)	*homozygous recessive*

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Correct. Allele frequencies reach equilibrium if selection is against both homozygotes

Question 6 *1 / 1 point*

If an original population has an allele with frequency 0.7 and a population size of 282 individuals and 60 individuals move from another population to join the original population and bring with them the same allele with frequency 0.5, what is the allele frequency in the new population (to two decimals - round to the nearest 0.01).

Answer:

0.66 ✓

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This is a migration situation. The most common challenge with these calculations is to figure out the migration rate, m, which is the number of migrating individuals divided by the new size of the population combining the original population PLUS the migrating individuals.

Question 7 *1 / 1 point*

A group of Andalusian (horse breed) stallions are imported carrying an allele frequency of 0.5. The existing Canadian population of Andalusians has an allele frequency of 0.8. A follow up study of the purebred Andalusian registration information shows that 39% of foals registered in Canada after the next breeding season were sired by one of these foreign sires. What is the allele frequency in the Canadian population (to two decimal places and round to the nearest 0.01)?

Answer:

0.74 ✓

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Some horse specific gender terms are in this question. Just in case, a stallion is a male horse and a mare is a female horse.

So, in this question you need to be careful about who is migrating. If foals are sired by foreign stallions it is the same as the stallions migrating. What about mares? Is there any mention of mares being imported? If not, there is no female migration. Since the question has some gender specific parameters, you need to use the formula that allows for different rates of migration between males and females. If you're not told about imported females then the original Canadian population of mares is unchanged.

Question 8 *1 / 1 point*

What proportion (to two decimal places - round to nearest 0.01) of a population **reproduce** *where:*
the frequency of the dominant allele is 0.7
24% of the heterozygotes are not sufficiently fit to reproduce and
45% of the homozygous recessive individuals are not sufficiently fit to reproduce?
Answer:

0.86 ✓

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Take the inventory of the information in the question. Be sure to differentiate between proportion that survive = fitness and proportion that do not survive/reproduce = s

The proportion of the overall population that survive is the total of the proportion of each genotype that survive.

Question 9 *1 / 1 point*

If an allele at a sex-linked locus in the domestic chicken has an allele frequency of 79% in males and 69% in females, what is the frequency of this allele in the population after many generations of random mating (as a percentage with one decimal place and rounded to the nearest 0.1%)?
Answer:

75.7 ✓

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*Don't forget poultry are birds and therefore the sex chromosome system is reversed. Males are "***ZZ***" and females are "***Z_***" so you can use the equation on the formula sheet but switch the males and females.*

Question 10 *1 / 1 point*

How many generations (rounded to the next whole generation) will it take for a lethal recessive allele to go from a frequency of 0.1 to a frequency of 0.05 in a random mating population (assuming nothing other than the recessive condition affects fitness)?
Answer:

10 ✓

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The number of generations, n, is defined as $1/q_n - 1/q_0$

Note that rounding is different for generations. If you calculate an answer that includes part of a generation, you **ALWAYS** *round* **UP** *to the* **nearest whole generation.** *The reason for this is that a partial generation of random mating is undefined because it isn't a random process.*

Question 11 *0 / 1 point*

This description applies to the **5** *questions from here to the end of the quiz.*

Marker assisted selection is a technique in which a marker locus is discovered close to a locus controlling a trait of interest (usually called a Quantitative Trait Locus or **QTL***).*
*Taking advantage of linkage disequilibrium between the marker locus and the QTL, breeders can select individuals as parents of the next generation on the basis of their marker genotype and know that the QTL genotype will also follow along. For example, if "***M***" is the marker locus and "***Q***" is the QTL, then the* **M** *allele*

can be assumed to be linked to the **Q** *allele and selecting individuals with the* **MM** *genotype is equivalent to selecting individuals for the* **QQ** *genotype,* **Mm** *to* **Qq** *and* **mm** *to* **qq**. *You can assume that the* **Q** *allele is a beneficial allele for the trait we are interested in. Your goal is to develop a selection strategy that will maximize the frequency of the linked beneficial allele when the only information available is on the marker genotype.* **The first question**... *What fitness levels would you assign to each of these three genotypes:* **MM**, **Mm** *and* **mm** *genotypes?*

1) *Fitness levels for each of the genotypes:*
MM = *0.5,*
Mm = *0.5, and*
mm = *0.*

2) *Fitness levels for each of the genotypes:*
MM = *1,*
Mm = *0, and*
mm = *0.*

3) *Fitness levels for each of the genotypes:*
MM = *0,*
Mm = *0.5, and*
mm = *1.*

4) *Fitness levels for each of the genotypes:*
MM = *1,*
Mm = *1, and*
mm = *0.*

5) *Fitness levels for each of the genotypes:*
MM = *1,*
Mm = *0.5, and*
mm = *0.*

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Fitness levels for each of the genotypes:
MM = *1,*
Mm = *0, and*
mm = *0.*
Then with **MM** *linked to* **QQ** *you will end up with only* **MM** *and therefore only* **QQ** *individuals and the frequency of the* **M** *and the linked* **Q** *alleles will be one in the selected individuals and in the next generation after they randomly mate.*

Question 12 *0 / 1 point*

Continuing with the strategy you started in the question above, what is the maximum **M** *and* **Q** *allele frequency you can achieve with the optimal strategy?*

1) *f(***M***) = f(***m***) = 0.5 and the linked f(***Q***) = f(***q***) = 0.5 along with it.*

2) *f(***M***) > f(***m***) and f(***m***) > 0 and the linked f(***Q***) > f(***q***) allele along with it.*

3) *f(***M***) = 1 and the linked f(***Q***) allele along with it.*

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In one generation, if you select all **MM** *individuals, the best possible result is to fix the* **M** *and therefore the* **Q** *allele.*

Question 13 *0 / 1 point*

Continuing along from the two questions above . . .

How do you know that the optimal strategy truly is the optimal strategy?

The maximum possible frequency of the marker allele is 1 and the optimal strategy achieved it.

The maximum possible frequency of the marker allele is 1 but it cannot be achieved in a single generation so any fitness level where the frequency of the good marker allele is increasing is an optimal strategy.

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The maximum possible allele frequency is 1. If you select all MM individuals you get f(M) = 1 in one generation and therefore it is the optimal strategy.

Question 14 *1 / 1 point*

Continuing on with our marker assisted selection theme from the three questions above...
Suppose recombination occurred between the "M" locus and the "Q" QTL locus. Since you can only "see" the genotypes for the "M" locus, can you tell if recombination occurs and, if so how?

1) *No, you can't tell if it happens because there is no way to see what is actually going on at the "Q" locus.*
2) *Yes you can tell if it happens by monitoring the selection response (change in phenotype) in each generation.*

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*Correct. The response in phenotype should be dramatic if the whole population becomes **MM** and a few recombinant individuals where **MM** becomes linked to **Qq** should stand out.*

Question 15 *1 / 1 point*

Still continuing our theme of marker assisted selection...
If recombination does occur between the marker locus "M" and the QTL "Q", what would be the best option to resume an effective marker assisted selection strategy?

1) *Abandon the marker locus completely and switch to more traditional means of selection.*
2) *Continue to use the original marker locus but somehow test the connection each generation to see how bad things are getting.*
3) *Search for another marker locus that is closer to the QTL so recombination is not as likely to occur.*

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Correct. Start over and find another, better marker locus to use.

Quiz 4

Question 1 *1 / 1 point*

If the effective population size is 60 individuals and there are 60 females in the population, how many males are there?

1)	*50*
2)	*40*
3)	*10*
4)	*20*
5)	*30*

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Correct.

Question 2 *1 / 1 point*

Inbreeding represents a _____ in heterozygosity. What goes in the blank?

✓	1)	*Decrease*
	2)	*Increase*
	3)	*Equililibrium*

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Correct

Question 3 *1 / 1 point*

If **A** *alleles are being created by mutation at a rate of 0.001% per generation and lost by mutation at a rate of 0.0025% per generation and yet the frequency of the* **A** *allele remains constant, what is the frequency of the* **A** allele?

✓	1)	*0.2857*
	2)	*1.0*
	3)	*0.7143*
	4)	*0.0*

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Correct. $p_E = v / (u+v)$

Question 4 *1 / 1 point*

If selection balances a mutation rate of 0.001 and selection works against the homozygous recessive genotype such that s = 0.2, what is the frequency of the recessive allele after many generations?

✓	1)	*0.07071*
	2)	*0.005*
	3)	*1.0*
	4)	*0.0*

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Correct. $q_E = SQRT(u / s)$

Question 5 *1 / 1 point*

Suppose as a breeder of Norfolk terriers, you are worried about the rate of inbreeding since the breed is small in number. You want to make sure the rate of inbreeding in your kennel stays below 6.25% per generation. If you have 10 females in your kennel, how few males can you get away with.

✓	1)	*3*
	2)	*2*
	3)	*2.5*
	4)	*1.5*

	5)	*3.5*

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Correct. Always round up.

Question 6 *1 / 1 point*

If you are going to allow a population of mice to randomly mate for 5 generations and you want to constrain inbreeding to 14.678481% after generation 5, how many males do you need if you have 20 females?

	1)	*50*
✓	*2)*	*5*
	3)	*8*
	4)	*2*
	5)	*10*

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Correct.

Question 7 *1 / 1 point*

If **A** *alleles are being created by mutation at a rate of 0.01% per generation and lost by mutation at a rate of 0.0025% per generation and yet the frequency of the* **A** *allele remains constant, what is the frequency of the* **A** allele?

✓	*1)*	*0.8*
	2)	*0.0*
	3)	*0.2*
	4)	*1.0*

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Correct. pE = v / (u+v)

Question 8 *1 / 1 point*

If the effective population size is 64 individuals and there are 80 females in the population, how many males are there?

	1)	*30*
✓	*2)*	*20*
	3)	*10*
	4)	*40*
	5)	*50*

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Correct.

Question 9 *1 / 1 point*

How much is the frequency of the homozygous dominant genotype increased in a population where f(A) = 0.61 and there are 20 individuals randomly mating (round to the nearest 0.0001)?
Answer:

0.0059 ✓

Question 10 *1 / 1 point*

If you observe a population to have an effective population size of 30 individuals, what is the level of inbreeding after 10 generations (rounded to the nearest 0.001)?
Answer:

0.155 ✓

Question 11 *0.01 / 1 point*

The vocabulary for the following five fill in the blank questions includes some of the following words/phrases:
equal, positive assortative, assortative, planned, randomly, non-random, reproductive technology, artificial insemination, AI, embryo transfer, ET, pairwise, at random

The effective population size calculation assumes that mates are chosen
___at random___ ✓ *(1%)*

Question 12 *0.01 / 1 point*

The effective population size calculation also assumes that matings are
___pairwise___ ✓ *(1%)*
and remain that way for life.

Question 13 *0.01 / 1 point*

When we use the (effective) population size to calculate inbreeding, we assume that all parents make a/an
___equal___ ✓ *(1%)*
contribution to the next generation.

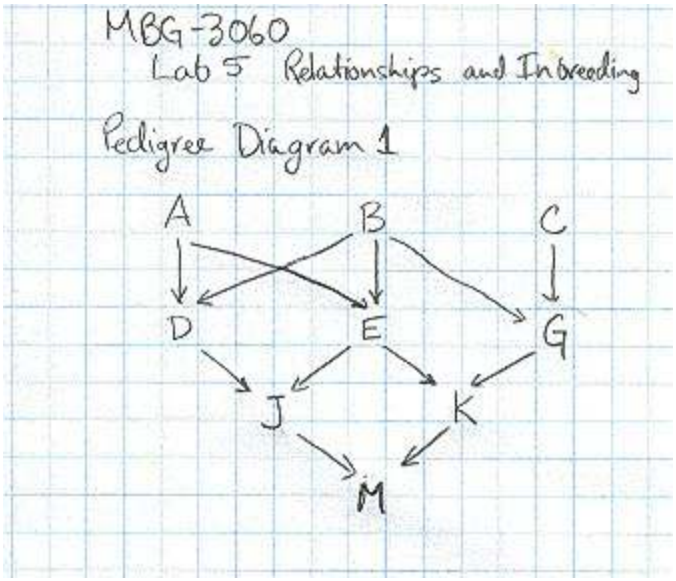
Question 14 *0.01 / 1 point*

To reduce the level of inbreeding in a small population, we can impose a system of
___assortative___ ✓ *(1%)*
mating.

Question 15 *0.01 / 1 point*

The effective population size can be altered without moving animals physically through the use of
___reproductive technology___ ✓ *(1%)*

Quiz 5



Image

Question 1 *1 / 1 point*

With respect to Pedigree Diagram 1, how many common ancestors are there for computing inbreeding in individual M?

✓ ◉	*1)*	*3*
○	*2)*	*1*
○	*3)*	*5*
○	*4)*	*2*
○	*5)*	*4*

View Feedback

Common ancestors are the individuals where we change directions on the arrows while following arrows backwards up the pedigree and forwards back down. Starting from parent J and tracing backwards and forwards to parent K, a common ancestor has to be an ancestor of both of J and K.
Yes indeed - individuals A, B and E

Question 2 *0 / 1 point*

With respect to Pedigree Diagram 1, how many unique paths are there in total from one parent of M to the other through all common ancestors?

○	*1)*	*2*
✗ ◉	*2)*	*4*
➡ ○	*3)*	*5*
○	*4)*	*1*

	5)	*3*

View Feedback

A unique path uses the common ancestor and other relatives only once, doesn't change direction more than once on the arrows and usually written with the common ancestor identified and the path stretching to each parent one either side from the common ancestor.
Sorry. Check out
J - D - **A** *- E - K*
J - D - **B** *- E - K*
J - D - **B** *- G - K*
J - E - **B** *- G - K*
J - **E** *– K*

Question 3 *0 / 1 point*

With respect to Pedigree Diagram 1, what is the level of inbreeding in individual M?

	1)	*3/32*
	2)	*1/8*
✗	*3)*	*7/32*
	4)	*1/16*
➡	*5)*	*1/4*

View Feedback

The paths are J-D-A-E-K contributing $(1/2)^{2+2+1}$
J-D-B-E-K contributing $(1/2)^{2+2+1}$
J-D-B-G-K contributing $(1/2)^{2+2+1}$
J-E-B-G-K contributing $(1/2)^{2+2+1}$
J-E-K contibuting $(1/2)^{1+1+1}$ *for a total of 1/4*

Sorry. The total is $(1/2)^5 + (1/2)^5 + (1/2)^5 + (1/2)^5 + (1/2)^3 = 1/4$

*The pathways are J-D-***A***-E-K where n + 1 = 5, J-D-***B***-E-K n + 1 = 5, J-E-***B***-G-K n + 1 = 5, J-D-***B***-G-K n + 1 = 5 and J-***E***-K n + 1 = 3.*

Question 4 *0 / 1 point*

With respect to Pedigree Diagram 1, if you were told that individuals A, B and C were not known to be related but did all come from a population of size 50, how much would this change your calculation of the inbreeding individual M?

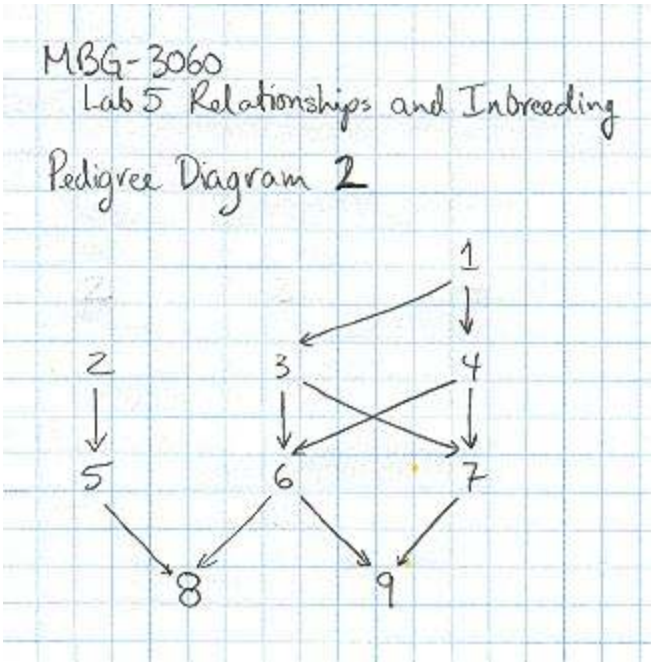
	1)	*0.006250*
	2)	*No change*
	3)	*0.003125*
✗	*4)*	*0.0025*
➡	*5)*	*0.00125*

View Feedback

Yes indeed F_A, F_B *and* F_C *are not zero anymore but increase to F = 1/2N = 0.01 However, C doesn't matter because it is not a common ancestor. Since A and B were not known to be related, then* F_E *is still*

assumed to be zero. Then, include in the formula $1/2^{n1+n2+1}$ $(1+F_{common\ ancestor})$
Sorry. F_A, F_B and F_C are not zero anymore but increase to F = 1/2N = 0.02 However, C doesn't matter because it is not a common ancestor. Since A and B were not known to be related, then F_E is still assumed to be zero.

Information



Image

Question 5 *1 / 1 point*

With respect to Pedigree Diagram 2, what is the additive genetic relationship between individuals 1 and 9?

	1)	*1/8*
	2)	*5/8*
✓	*3)*	*1/2*
	4)	*1/4*
	5)	*3/8*

View Feedback

Correct. One common ancestor (individual 1). 4 paths 1-3-6-9, 1-3-7-9, 1-4-6-9 and 1-4-7-9 each contributing $(1/2)^{0+3}$ = 1/8 for a total of 1/2

Question 6 *1 / 1 point*

With respect to Pedigree Diagram 1, what is the additive genetic relationship between individuals B and M?

	1)	*1/4*
	2)	*1/8*
	3)	*3/4*

	4)	3/8
✓	5)	1/2

View Feedback

Correct. One common ancestor (individual B). 4 paths B-D-J-M, B-E-J-M, B-E-K-M and B-G-K- M each contributing $(1/2)^{0+3}$ = 1/8 for a total of 1/2

Question 7 *1 / 1 point*

With respect to Pedigree Diagram 1, does the relationship between individuals B and M change if individuals A, B and C are inbred by 6.25% each? If so, by how much?

✓	1)	*Yes it changes by 0.03125*
	2)	*Yes it changes by 0.125*
	3)	*Yes it changes by 0.046875*
	4)	*Yes it changes by 0.0625*
	5)	*No, it does not change.*

View Feedback

Correct. One common ancestor (individual B). 4 paths B-D-J-M, B-E-J-M, B-E-K-M and B-G-K- M each contributing $(1/2)^{0+3}(1+F_B)$ = 1/8(1.0625) for a total of 0.53125 or a change of 0.03125

Question 8 *1 / 1 point*

With respect to the table below, what is the entry for the cell labelled "Fill In"? Note that the table border includes all the cells including the row and column labels that were outside the table as I draw them in class. Cells that are blank cannot be completed yet.

	- -	- -	A B	A C	A D
	A	B	C	D	E
A	1	0	1/2	3/4	7/8
B	0	1	1/2	1/4	1/8
C	½	1/2	1	3/4	5/8
D	¾	1/4	3/4	**Fill In**	
E	7/8	1/8	5/8		

	1)	1 + 3/8
	2)	1 + 1/8
	3)	1
	4)	1 + 1/16
✓	5)	1 + 1/4

View Feedback

Diagonal cells are 1 + 1/2(a_{AC})
Correct. 1 + 1/2(a_{AC})

Question 9 *1 / 1 point*

With respect to the table below, what is the entry for the cell labelled "Fill In"? Note that the table border includes all the cells including the row and column labels that were outside the table as I draw them in class. Cells that are blank cannot be completed yet.

	- -	- -	A B	A C	A D
	A	B	C	D	E
A	1	0	1/2	3/4	7/8
B	0	1	1/2	1/4	1/8
C	½	1/2	1	3/4	5/8
D	¾	1/4	3/4	From above	**Fill In**
E	7/8	1/8	5/8	**Fill In**	

- 1) 7/8
- 2) 1 + 1/4
- ✓ 3) 1

View Feedback

$1/2(a_{AD} + a_{DD})$
Correct = $1/2(a_{AD} + a_{DD})$

Question 10 *1 / 1 point*

With respect to the table below, what is the entry for the cell labelled "Fill In"? Note that the table border includes all the cells including the row and column labels that were outside the table as I draw them in class. Cells that are blank cannot be completed yet.

	- -	- -	A B	A C	A D
	A	B	C	D	E
A	1	0	1/2	3/4	7/8
B	0	1	1/2	1/4	1/8
C	½	1/2	1	3/4	5/8
D	¾	1/4	3/4	From above	From above
E	7/8	1/8	5/8	From above	**Fill In**

- ✓ 1) 1 + 3/8
- 2) 1
- 3) 1 + 1/4
- 4) 1 + 1/8

View Feedback

Diagonal cell = $1 + 1/2(a_{AD})$
Correct. Diagonal cell = $1 + 1/2(a_{AD})$

Question 11 *1 / 1 point*

As the degree of relatedness within a population increases, the level of inbreeding in that population also increases. As relatedness and inbreeding go up, individuals become more similar genetically and therefore genetic variability goes down. How would an increase in inbreeding and relatedness affect the variability we would see due to over-dominance?

1) *The variability would be unaffected because the proportion of heterozygous individuals would decrease and those individuals have the largest expression of phenotype.*

✓ 2) *The variability would decrease because the proportion of heterozygous individuals would decrease and those individuals have the largest expression of phenotype.*

3) *The variability would increase because the proportion of heterozygous individuals would decrease and those individuals have the largest expression of phenotype.*

View Feedback

Correct

Question 12 *1 / 1 point*

As the degree of relatedness within a population increases, the level of inbreeding in that population also increases. As relatedness and inbreeding go up, individuals become more similar genetically and therefore genetic variability goes down. How would an increase in inbreeding and relatedness affect the variability we would see due to incomplete dominance?

1) *The variability would increase somewhat because the proportion of heterozygous individuals would decrease and those individuals have a phenotype closer to one of the homozygotes.*

2) *The variability would be unaffected because the proportion of heterozygous individuals would decrease and those individuals have a phenotype closer to one of the homozygotes.*

✓ 3) *The variability would decrease somewhat because the proportion of heterozygous individuals would decrease and those individuals have a phenotype closer to one of the homozygotes.*

View Feedback

Correct

Question 13 *0 / 1 point*

As the degree of relatedness within a population increases, the level of inbreeding in that population also increases. As relatedness and inbreeding go up, individuals become more similar genetically and therefore genetic variability goes down. How would an increase in inbreeding and relatedness affect the variability we would see due to co-dominance?

1) *The variability would increase somewhat because the proportion of heterozygous individuals would decrease and those individuals have a phenotype between the homozygotes.*

✗ 2) *The variability would decrease somewhat because the proportion of heterozygous individuals would decrease and those individuals have a phenotype between the homozygotes.*

➡ 3) *The variability would be largely unaffected because the proportion of heterozygous individuals would decrease and those individuals have a phenotype between the homozygotes.*

View Feedback

The variability would be largely unaffected because the proportion of heterozygous individuals would decrease and those individuals have a phenotype between the homozygotes.

Question 14 *1 / 1 point*

As the degree of relatedness within a population increases, the level of inbreeding in that population also increases. As relatedness and inbreeding go up, individuals become more similar genetically and therefore genetic variability goes down. How would an increase in inbreeding and relatedness affect the variability we would see due to epistasis?

✓ 1) *The variability would increase or decrease somewhat or even stay the same because the proportion of heterozygous individuals would decrease but the epistatic interactions could occur amongst any combination of genotypes.*

2) *The variability would increase somewhat because the proportion of heterozygous individuals would decrease and the epistatic interactions would increase with it.*

3) *The variability would decrease somewhat because the proportion of heterozygous individuals would decrease and the epistatic interactions would decrease with it.*

View Feedback

Correct.

Question 15 *1 / 1 point*

As the degree of relatedness within a population increases, the level of inbreeding in that population also increases. As relatedness and inbreeding go up, individuals become more similar genetically and therefore genetic variability goes down. How would an increase in inbreeding and relatedness affect the variability we would see due to pleiotropy?

✓ 1) *The variability would increase or decrease somewhat or even stay the same because the proportion of heterozygous individuals would decrease but the pleiotropic interactions could occur amongst any combination of phenotypes.*

2) *The variability would increase somewhat because the proportion of heterozygous individuals would decrease and the pleiotropic interactions would increase with it.*

3) *The variability would decrease somewhat because the proportion of heterozygous individuals would decrease and the pleiotropic interactions would decrease with it.*

View Feedback

Correct.

Quiz 6

Question 1 *1 / 1 point*

Given the following group of Holstein cows and information on their milk yield, what is response in the next generation if you select the top 20% and the heritability of milk yield is 0.25? You may assume that "S" for the bulls is exactly the same as the "S" you determine for the cows so the response you calculate based on the best 20% of the cows is the overall response.

Cow ID	*Milk Yield (kg)*
Bossy	*9600*
Bessy	*8700*
Flossy	*9200*
Flo	*9100*
Winnie	*9800*
Flora	*9900*
Bell	*9100*
Ginger	*9500*
Popcorn	*9700*

Adele	9600

	1)	430 kg of milk
	2)	9420 kg of milk
	3)	53.75 kg of milk
✓	4)	107.5 kg of milk
	5)	50 kg of milk

View Feedback

Select Winnie and Flora for X_S = 9850 kg compared to a population average of 9420 kg so S = 430 kg and R = Sh^2 = 430 kg x 0.25 = 107.5 kg
Correct. Select Winnie and Flora for X_S = 9850 kg compared to a population average of 9420 kg so S = 430 kg and R = Sh^2 = 430 kg x 0.25 = 107.5 kg

Question 2 *1 / 1 point*

Given the following group of Holstein cows and information on their milk yield, what is increase in response in the next generation if you select the top 10% instead of the top 20% and the heritability of milk yield is 0.25? Likewise, here you can assume that the bulls also have the same "S" as the cows so the response you calculate based on "S" for the top 10% of the cows is the same as the overall response.

Cow ID	Milk Yield (kg)
Bossy	9600
Bessy	8700
Flossy	9200
Flo	9100
Winnie	9800
Flora	9900
Bell	9100
Ginger	9500
Popcorn	9700
Adele	9600

	1)	No change
	2)	120 kg of milk
	3)	60 kg of milk
✓	4)	12.5 kg of milk

View Feedback

Select only Flora this time and the response goes up to 120 kg of milk for a difference of 12.5 kg
Select only Flora this time and the response goes up to 120 kg of milk for a difference of 12.5 kg

Question 3 *1 / 1 point*

A researcher is tasked with finishing up a classical selection experiment with fruit flies to determine the response to selection for flying speed. Over the course of 20 generations of selection, the cumulative selection differential has been calculated to be 10 cm / second and the cummulative response has been calculated to be 2.5 cm / second. If the phenotypic standard deviation is 4 cm / second, what is the additive genetic variance?

		1)	*16 cm / second^2*
✓	●	*2)*	*4 cm / second^2*
		3)	*1 cm / second^2*
		4)	*2 cm / second^2*

View Feedback

Correct. First determine h^2 = R / S = 2.5 / 10 = 0.25. Then since $h^2 = \sigma_A^2 / \sigma_P^2$ and $\sigma_P^2 = 4^2$ then σ_A^2 = 0.25 x 4^2 = 4 cm/sec^2

Question 4 *1 / 1 point*

If you select the top 5% of your population, how much more selection response will you get than if you select the top 20% of your population?

		1)	*2.8882 x σ_P x h^2*
		2)	*Not enough information to determine.*
		3)	*2.063 x σ_P x h^2*
✓	●	*4)*	*0.663 x σ_P x h^2*
		5)	*1.400 x σ_P x h^2*

View Feedback

Correct. Find i from the table for 5% = 2.063 and for 20% = 1.4 and the difference is 0.663

Question 5 *1 / 1 point*

If you select the top 18% of individuals on the basis of their height from a population with an average height of 172 cm and a standard deviation of 5 cm, what is the height of the shortest individual in your selected group?

		1)	*179.29 cm*
		2)	*4.58 cm*
		3)	*172 cm*
✓	●	*4)*	*176.58 cm*

View Feedback

Correct. t from the table is 0.915 and t x σ_P + average = 176.58 cm

Question 6 *1 / 1 point*

If the average of a population in the progeny generation was 213 units, the average of the selected group was 275 units and the original population average was 169, what is the heritability of this trait (rounded to the nearest 0.01 and don't put the word "units" in the answer box)?
Answer:

0.42 ✓

Question 7 *1 / 1 point*

If the phenotypic standard deviation of a trait is 80, heritability is 0.38 and you select the top 10% of the population what is the response to selection (round to the nearest 0.01)?
Answer:

53.35 ✓

View Feedback

$R = i \times sigma_P \times h^2$

Question 8 *1 / 1 point*

If you select the top 10% of your population and observe a selection response of 17 units when the phenotypic standard deviation of a trait is 91, what is the heritability of the trait (round to the nearest 0.01)?
Answer:

0.11 ✓

View Feedback

$R = i \times sigma_P \times h^2$ so $h^2 = R / (i \times sigma_P)$

Question 9 *1 / 1 point*

In selecting for rapid growth of a particular type of grass for horse pastures, a researcher observes the selected group is 13 cm in height, the average of the population is 7 cm in height and the heritability of growth is 0.31. What is the average height of the plants in the next generation (rounded to the nearest 0.1 and don't put "cm" in the answer box)?
Answer:

8.9 ✓

Question 10 *1 / 1 point*

Following in Darwin's footsteps, you observe a wild population of finches. However, unlike Darwin you have a wide variety of quantitative genetics tools at your disposal. If you observe a response of 0.64 mm in beak length with a standard deviation of beak length equal to 0.83 mm and you suspect that 25% of the finches with the largest beaks are producing offspring, what is the heritability of beak length (rounded to the nearest 0.01)?
Answer:

0.61 ✓

View Feedback

$h^2 = R / (i \times \sigma_P$

Question 11 *0 / 1 point*

The response to selection calculation assumes several things. Which of the following options is the **most** *correct?*

1) *The generations are discrete.*

2) *Selected individuals randomly mate.*

3) *There are an equal number of males and females, pairwise mating.*

4) *All three of the above are correct.*

5) *Two out of the first three options are correct.*

Question 12 *1 / 1 point*

The degree of response to selection is a function of the superiority of the selected group and the heritability of the trait. If we want to improve selection response, we can do what to the superiority of the selected group?

1) *Increase the size of the selected group by including more individuals from the general distribution of the population.*

2) *Maintain the size of the selected group to prevent inbreeding.*

3) *Decrease the size of the selected group while increasing the difference between the selected group and the rest of the population.*

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Correct

Question 13 *1 / 1 point*

Selection response depends upon how well you pick animals and how heritable the trait is. Heritability is often considered to be fixed so improving selection response normally focuses on selecting. However, if you wanted to look at heritability as a source of more selection response which of the following is more correct?

1) *σ_A^2 remains fairly constant, h^2 must also remain fairly constant.*

2) *Although σ_A^2 remains fairly constant, h^2 can be improved by reducing σ_E^2 through more precise measurements or greater quality control.*

Question 14 *1 / 1 point*

In addition to selection differential and heritability, time can also be a factor in selection response. We can improve response in a fixed time by . . .

1) *Selecting animals later in life so they are more stable members of the population and more likely to contribute better progeny.*

2) *Selecting animals sooner in life and randomly mating them sooner to produce the newer generations sooner.*

3) *Not worrying about it. The generation interval for a species is constrained by the biology of the species and there isn't much that can be done about it.*

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Correct

Question 15 *0 / 1 point*

When making selection decisions, the size of the selected group can affect the potential for accumulating inbreeding. To avoid inbreeding and improve selection response even with a small selected group, one of these options would work better than the others...

1) *Select the best and smallest selected group you can get away with, mate the best to the best and avoid matings between relatives within this small group.*

2) *Avoid selecting any relatives so random mating cannot possibly result in an increase in inbreeding.*

✗ 3) *Select the best and smallest selected group you can get away with and avoid matings between relatives within this small group*

View Feedback

Select the best and smallest selected group you can get away with, mate the best to the best and avoid matings between relatives within this small group.

Quiz 7

Question 1 *1 / 1 point*

The Analysis of Variance table below was calculated from data on 5 sires with n matings per sire, each producing one progeny. Calculate the value for the the cell with the question mark.

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	?	5000	From below	From below
Error	15	From below	1000	σ_e^2
Total	From below	20000	n/a	n/a

1) sire d.f = 5

2) sire d.f = 20

✓ 3) sire d.f = 4

View Feedback

Correct.

Question 2 *1 / 1 point*

The Analysis of Variance table below was calculated from data on 5 sires with n matings per sire, each producing one progeny. Calculate the value for the the cell with the question mark.

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	From above	5000	?	From below
Error	15	From below	1000	σ_e^2
Total	From below	20000	n/a	n/a

✓ 1) MS Sire = 1250

2) MS Sire = 250

3) MS Sire = 1000

View Feedback

Correct. MS = SS / d.f.

Question 3 *1 / 1 point*

The Analysis of Variance table below was calculated from data on 5 sires with n matings per sire, each producing one progeny. Calculate the value for the the cell with the question mark.

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	From above	5000	From above	?
Error	15	From below	1000	σ_e^2
Total	From below	20000	n/a	n/a

✔ 1) EMS Sire = 4 $\sigma_s^2 + \sigma_e^2$

2) EMS Sire = 5 $\sigma_s^2 + \sigma_e^2$

3) EMS Sire = 20 $\sigma_s^2 + \sigma_e^2$

View Feedback

Correct

Question 4 1 / 1 point

The Analysis of Variance table below was calculated from data on 5 sires with n matings per sire, each producing one progeny. Calculate the value for the cell with the question mark.

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	From above	5000	From above	From above
Error	15	?	1000	σ_e^2
Total	From below	20000	n/a	n/a

✔ 1) SS error = 15000

2) SS error = 16000

3) SS error = 14000

View Feedback

Correct

Question 5 1 / 1 point

The Analysis of Variance table below was calculated from data on 5 sires with n matings per sire, each producing one progeny. Calculate the value for the cell with the question mark.

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	From above	5000	From above	From above
Error	15	From above	1000	σ_e^2
Total	?	20000	n/a	n/a

1) d.f. Total = 18

2) d.f. Total = 20

✔ 3) d.f. Total = 19

View Feedback

Correct.

Question 6 1 / 1 point

The Analysis of Variance table below was calculated from data on 10 sires with one mating per sire, each producing five progeny. What is heritability?

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	9	9000	1000	Calculate as part of h^2
Error	40	14000	350	σ_e^2
Total	49	23000	n/a	n/a

✓ 1) $h^2 = 0.5417$

2) $h^2 = 0.1066$

3) $h^2 = 0.8525$

View Feedback

Correct. This is case 2 with full sibs.

Question 7 *1 / 1 point*

To complete our exploration of ANOVA, let us consider the situation where we have 10 sires each mated to 5 dams and each mating produces 4 progeny. Calculate the value for the entry in the table below denoted by **?**

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	*9*	*450*	*?*	*From below*
Dam (Sire)	*From below*	*From below*	*12.5*	*From below*
Error	*150*	*1500*	*10*	σ_e^2
Total	*199*	*2450*	*n/a*	*n/a*

1) *45*

2) *25*

✓ 3) *50*

View Feedback

MS for sires is SS for sires / d.f. for sires = 50
Correct. MS for sires is SS for sires / d.f. for sires = 50

Question 8 *1 / 1 point*

To complete our exploration of ANOVA, let us consider the situation where we have 10 sires each mated to 5 dams and each mating produces 4 progeny. Calculate the value for the entry in the table below denoted by **?**

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	*9*	*450*	*From above*	*?*
Dam (Sire)	*From below*	*From below*	*12.5*	*From below*
Error	*150*	*1500*	*10*	σ_e^2
Total	*199*	*2450*	*n/a*	*n/a*

1) $\sigma_e^2 + 20\sigma_{Dam}^2 + 200\sigma_{Sire}^2$

2) $\sigma_e^2 + 10\sigma_{Dam}^2 + 20\sigma_{Sire}^2$

3) $\sigma_e^2 + 5\sigma_{Dam}^2 + 4\sigma_{Sire}^2$

4) $\sigma_e^2 + 4\sigma_{Dam}^2 + 10\sigma_{Sire}^2$

✓ 5) $\sigma_e^2 + 4\sigma_{Dam}^2 + 20\sigma_{Sire}^2$

View Feedback

Expected Mean Square for Sires is $\sigma_e^2 + n\sigma_{Dam}^2 + dn\sigma_{Sire}^2$
Correct. Expected Mean Square for Sires is $\sigma_e^2 + 4\sigma_{Dam}^2 + 20\sigma_{Sire}^2$

Question 9 *1 / 1 point*

To complete our exploration of ANOVA, let us consider the situation where we have 10 sires each mated to 5 dams and each mating produces 4 progeny. Calculate the value for the entry in the table below denoted by **?**

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	*9*	*450*	*From above*	*From above*
Dam (Sire)	*?*	*?*	*12.5*	*?*
Error	*150*	*1500*	*10*	σ_e^2
Total	*199*	*2450*	*n/a*	*n/a*

1) *d.f. Dams (sire) = 45, SS for Dams (sire) = 563 and EMS Dams (sire) = $\sigma_e^2 + 20\sigma_{Dams}^2$*

✓ 2) *d.f. Dams (sire) = 40, SS for Dams (sire) = 500 and EMS Dams (sire) = $\sigma_e^2 + 4\sigma_{Dams}^2$*

3) *d.f. Dams (sire) = 50, SS for Dams (sire) = 625 and EMS Dams (sire) = $\sigma_e^2 + 5\sigma_{Dams}^2$*

View Feedback

d.f. Dams (sire) = s(d - 1) = 40, SS for Dams (sire) = d.f. Dams x MS Dams = 500 and EMS Dams (sire) = $\sigma_e^2 + n\sigma_{Dams}^2 = \sigma_e^2 + 4\sigma_{Dams}^2$
Correct. d.f. Dams (sire) = 40, SS for Dams (sire) = 500 and EMS Dams (sire) = $\sigma_e^2 + 4\sigma_{Dams}^2$

Question 10 *1 / 1 point*

To complete our exploration of ANOVA, let us consider the situation where we have 10 sires each mated to 5 dams and each mating produces 4 progeny. Calculate h^2_{Sires}, h^2_{Dams} and h^2_{Both}

In case of differences in rounding, pick the solution below that is the closest to all 3 of your calculations. I wasn't nasty with the answers so the correct answer should be quite clear.

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Sire	*9*	*450*	*From above*	*From above*
Dam (Sire)	*From above*	*From above*	*12.5*	*From above*
Error	*150*	*1500*	*10*	σ_e^2

Total	199	2450	n/a	n/a

1) $h^2_{Sires} = 0.6061$, $h^2_{Dams} = 0.1616$ and $h^2_{Both} = 0.3838$

2) $h^2_{Sires} = 0.3$, $h^2_{Dams} = 0.2$ and $h^2_{Both} = 0.4$

✓ 3) $h^2_{Sires} = 0.6$, $h^2_{Dams} = 0.2$ and $h^2_{Both} = 0.4$

View Feedback

$\sigma_{Sire}^2 = 1.875$, $\sigma_{Dam}^2 = 0.625$ and $\sigma_P^2 = 12.5$, then $h^2_{Sires} = 0.6$, $h^2_{Dams} = 0.2$ and $h^2_{Both} = 0.4$
Correct. $h^2_{Sires} = 0.6$, $h^2_{Dams} = 0.2$ and $h^2_{Both} = 0.4$

Question 11 *0 / 1 point*

*Among the 3 cases of ANOVA for calculating heritability th*ere are 5 different ways to compute heritability. The ranking is determined by how close the calculation matches heritability. Any ties in ranking can be decided by considering the amount of information used in the calculation (more is better). Rank the 5 different ways of calculating heritability from best (1) to worst (5) using the matching system below.

✗ __2__ **(5)** *Worst*	**1.** *Case 3 Sires* $h^2 = 4\sigma_s^2 / \sigma_P^2$
✗ __1__ **(2)** *Very good*	**2.** *Case 1 Sires* $h^2 = 4\sigma_s^2 / \sigma_P^2$
✗ __3__ **(4)** *Not so good*	**3.** *Case 2 Sires* $h^2 = 2\sigma_s^2 / \sigma_P^2$
✗ __4__ **(1)** *Best*	**4.** *Case 3 Sires and Dams* $h^2 = 2(\sigma_s^2 + \sigma_{dams}^2) / \sigma_P^2$
✗ __5__ **(3)** *Good*	**5.** *Case 3 Dams* $h^2 = 4\sigma_{dams}^2 / \sigma_P^2$

Quiz 8

Question 1 *1 / 1 point*

You have calculated the repeatability of a trait to be 0.35. If an individual in the population has a phenotype of 52 units (from one observation) while the population averages 50 units, what is the expected phenotype of the individual with the next expression of that phenotype?

1) *51.3 units*

✓ 2) *50.7 units*

3) *52*

4) *50*

View Feedback

Correct. 1 - b times the population average + b times the individual's average

Question 2 *1 / 1 point*

You are given data for a population. The AA individuals average a phenotype of 150 units, the Aa individuals 130 units and the aa individuals 100 units. You discover that 64% of the individuals are AA, 32% are Aa and 4% are aa. You assume the population has been randomly mating and that differences in phenotype are due solely to the genotypes. Using the same population as the question directly above, what is the genotypic value of the AA genotype?

1) *-0.4 units*

2) *8.8 units*

✔ 3) 8.4 units

View Feedback

Correct. Calculate a = a + (q - p)d = 25 + (0.2 - 0.8)(5) = 22 units, then GV_{AA} = 2q(a - qd) = 2(0.2)(22 - 0.2(5)) = 8.4 units

Question 3 *1 / 1 point*

*Similar to the calculation of heritability from Analysis of Variance, w*e have also talked about using ANOVA to calculate repeatability. The ANOVA table below was calculated based on repeated measurements of birth weights of first and second born foals at a stable with 10 brood mares. What is the repeatability of birth weight from this dataset?

Source	d.f.	Sums of Squares	Mean Square	Expected Mean Square
Foal	*1*	*30*	*30*	$\sigma_e^2 + 10\sigma_{Foal}^2$
Mare	*9*	*540*	*60*	$\sigma_e^2 + 2\sigma_{Mare}^2$
Error	*9*	*180*	*20*	σ_e^2
Total	*19*	*750*	*n/a*	*n/a*

✔ 1) 0.5

2) 0.25

3) 0.75

View Feedback

Correct. r = σ_{Mare}^2 divided by (σ_e^2 + σ_{Mare}^2 where σ_{Mare}^2 = (MS Mare - MS Error)/2 and σ_e^2 = MS Error
Correct. r = σ_{Mare}^2 divided by (σ_e^2 + σ_{Mare}^2

Question 4 *0 / 1 point*

You have genotyped an entire population of lab mice for a single locus (let's label it B) that you have noticed have some interesting differences in size at a certain age. Based on your genotyping work, you calculate the average of the BB genotype to be 78 grams, the Bb genotype to be 45 grams and the bb genotype to be 24 grams. The frequency of the B allele is 0.73. What is the effect of the B allele in grams for this population (rounded to the nearest 0.01)?
Answer:

8.63 ✘ **(8.04)**

View Feedback

$a_1 = q[a+(q-p)d]$

Question 5 *1 / 1 point*

You have genotyped an entire population of lab mice for a single locus (let's label it B) that you have noticed have some interesting differences in size at a certain age. Based on your genotyping work, you calculate the average of the BB genotype to be 63 grams, the Bb genotype to be 50 grams and the bb genotype to be 20 grams. What is a in grams for this population (rounded to the nearest 0.1)?
Answer:

21.5 ✔

View Feedback

a = (average of BB - average of bb) / 2

Question 6 *1 / 1 point*

You have genotyped an entire population of lab mice for a single locus (let's label it B) that you have noticed have some interesting differences in size at a certain age. Based on your genotyping work, you calculate the

average of the BB genotype to be 75 grams, the Bb genotype to be 48 grams and the bb genotype to be 20 grams. What is d in grams for this population (rounded to the nearest 0.1)?
Answer:

0.5 ✓

View Feedback

d = Average of Bb - (Average of BB + Average of bb) / 2

Question 7 *1 / 1 point*
You have genotyped an entire population of lab mice for a single locus (let's label it B) that you have noticed have some interesting differences in size at a certain age. Based on your genotyping work, you calculate the average of the BB genotype to be 66 grams, the Bb genotype to be 52 grams and the bb genotype to be 25 grams. The frequency of the B allele is 0.80. What is the effect of the b allele in grams for this population (rounded to the nearest 0.01)?
Answer:

-13.28 ✓

View Feedback

$a_2 = -p[a+(q-p)d]$

Question 8 *1 / 1 point*
You have genotyped an entire population of lab mice for a single locus (let's label it B) that you have noticed have some interesting differences in size at a certain age. Based on your genotyping work, you calculate the average of the BB genotype to be 80 grams, the Bb genotype to be 32 grams and the bb genotype to be 25 grams. The frequency of the B allele is 0.73. What is the breeding value of the bb genotype in grams for this population (rounded to the nearest 0.01)?
Answer:

-53.92 ✓

View Feedback

$2a_2 = 2(-p)[a+(q-p)d]$

Question 9 *1 / 1 point*
You have genotyped an entire population of lab mice for a single locus (let's label it B) that you have noticed have some interesting differences in size at a certain age. Based on your genotyping work, you calculate the average of the BB genotype to be 76 grams, the Bb genotype to be 31 grams and the bb genotype to be 21 grams. The frequency of the B allele is 0.78. What is the breeding value of the BB genotype in grams for this population (rounded to the nearest 0.01)?
Answer:

16.41 ✓

View Feedback

$BV(BB) = 2a_1 = 2(q)[a+(q-p)d]$

Question 10 *1 / 1 point*
You have genotyped an entire population of lab mice for a single locus (let's label it B) that you have noticed have some interesting differences in size at a certain age. Based on your genotyping work, you calculate the average of the BB genotype to be 71 grams, the Bb genotype to be 40 grams and the bb genotype to be 22 grams. The frequency of the B allele is 0.65. What is the average effect of the B locus in grams for this population (rounded to the nearest 0.01)?
Answer:

26.45 ✓

View Feedback

$a = [a+(q-p)d]$

Question 11 *1 / 3 points*

Match the following types of selection to the model that is used to predict the response you would achieve

✖ __1__ **(3)**	*Hybrid model*		**1.** $R = Sh^2$
			2. $BV(BB) = 2a_1$
✔ __2__		*Finite locus model*	**3.** $R = 2a_1 + Sh^2$
✖ __3__ **(1)**		*Infinitesimal model*	

Question 12 *2 / 2 points*

Match the predicted genetic progress to the correct model type.

✔ __1__	*Infinitesimal model*	**1.** *Selection response is predicted to continue for many generations*
✔ __2__	*Finite locus model*	**2.** *Selection response is predicted to reach a plateau*

Quiz 9

Question 1 *1 / 1 point*

Referring to the SAS Statistical Analysis Output below, determine which factors were significant in the analysis of ovulation rate. Factors that were tested by SAS were the overall model, weight, IL1RN, NCOA1 and year.

MBG-3060 Sample QTL Detection SAS Output

This study looked at two markers contained within intronic regions of two genes,
IL1RN and NCOA1. These genes were selected as candidate genes for study due to their
roles in reproductive traits.

IL1RN: Interleukin 1 receptor antagonist is a gene encoding for a protein in the interleukin 1
cytokine family. This family of proteins is involved in modulating immune and inflammatory
response thereby playing a role in health traits. Maintaining pregnancy is a delicate
immunological process since the developing embryos are foreign proteins to the sow. We
studied this gene to see if immune function variability might be connected to improved
fertility.

NCOA1: Nuclear coactivator receptor 1 is a steriod and hormone receptor gene that encodes
for a product that binds to steroid and hormone receptor sites and stimulates transcription
activities for specific hormones. We were interested in this gene because it is involved in the
regulation of estrogen which is involved in female pig fertility.

Ovulation rates were collected on 174 sows by using a laparoscope to visually count the number of corpora lutea (ovulated follicles) on the surface of each sow's ovaries under general anesthetic. The experiment was conducted over 3 years so we included year in the model to eliminate any differences due to temporary environmental variation from year to year. Also, sows in the trial were different weights so we included weight in the model to adjust for differences in the size of the sow and therefore the size of the litter that she could be expected to carry. Alleles were coded as 1 and 2 so the genotypes are coded as 11, 12 and 22.

The GLM Procedure

Class Level Information

Class	Levels	Values
il1rn	3	11 12 22
ncoa1	3	11 12 22
yr	3	1 2 3

Number of observations 174
Dependent Variable: Ovulation Rate in Sows (OvRate)
Model: Ovulation Rate = Intercept + Sow Weight + Year + IL1RN + NCOA1 + Error

ANALYSIS OF VARIANCE - Overall Model

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	7	608.732665	86.961809	9.09	<.0001
Error	166	1588.577680	9.569745		
Corrected Total	173	2197.310345			

R-Square	Coeff Var	Root MSE	OvRate Mean
0.277035	17.83529	3.093500	17.34483

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Weight	1	289.0854193	289.0854193	30.21	<.0001
il1rn	2	40.2288497	20.1144248	2.10	0.1255
ncoa1	2	115.5178726	57.7589363	6.04	0.0029
yr	2	128.5863587	64.2931794	6.72	0.0016

Parameter		Estimate	Standard Error	t Value	Pr > |t|
Intercept		7.958601775	1.63030535	4.88	<.0001
Weight		0.054861330	0.00998167	5.50	<.0001
il1rn	11	0.206290233	0.80964454	0.25	0.7992
il1rn	12	-0.944039355	0.51874790	-1.82	0.0706
il1rn	22	0.000000000	.	.	.
ncoa1	11	2.469292581	0.74635056	3.31	0.0012
ncoa1	12	0.920452792	0.64035137	1.44	0.1525

```
ncoa1      22      0.000000000          .              .          .
yr         1       2.043315352       0.57667631       3.54       0.0005
yr         2       0.052588152       0.66419402       0.08       0.9370
yr         3       0.000000000          .              .          .

Note that the values above represented by a period "." cannot be estimated
because of the
number of degrees of freedom. These values are set to 0 by SAS and the other
values in the
same category are calculated as a difference from the one that is set to zero.

Least Squares Means

                OvRate          Standard
il1rn           LSMEAN             Error     Pr > |t|

11          18.1248997       0.7158005       <.0001
12          16.9745701       0.3833653       <.0001
22          17.9186095       0.4022295       <.0001

                OvRate          Standard
ncoa1           LSMEAN             Error     Pr > |t|

11          19.0120706       0.5106825       <.0001
12          17.4632308       0.3590225       <.0001
22          16.5427780       0.5854515       <.0001
```

1) *NCOA1*

2) *IL1RN*

3) *Year*

✓ 4) *Overall model, weight, NCOA1 and year.*

View Feedback

Compare the probability of a greater F-value (i.e. the p-value) for each of the overall model, weight, NCOA1 and year to "the usual 0.05" value. Each was less than 0.05 so each of these factors had a statistically significant effect on ovulation rate.
Correct. The probability of a greater F-value (i.e. the p-value) for each of the overall model, weight, NCOA1 and year was less than 0.05 so each of these factors had a statistically significant effect on ovulation rate.

Question 2 *0 / 1 point*

Refer to the SAS output sample from the previous question. Based on a t-test of the difference of a value from zero, which parameters were statistically significantly different from zero?

1) *NCOA1 11*

2) *Weight*

✗ 3) *IL1RN 11 and 12 genotypes and Year 2*

4) *The intercept*

5) *The intercept, weight, NCOA1 11 genotype and year 1*

View Feedback

Using the Pr > |t| column compare that probability to the usual value of 0.05. The intercept, weight, NCOA1 11 genotype and year 1 all had a Pr > |t| of less than 0.05
Oops. Using the Pr > |t| column, the intercept, weight, NCOA1 11 genotype and year 1 all had a Pr > |t| of less than 0.05

Question 3 *1 / 1 point*

Again referring to the SAS Output shown in the question above, the tables under the heading "Least Squares Means" provide the average Ovulation Rate (OvRate) phenotypes for each of the genotypes. The phenotype is measured in number of oocytes. Treating the NCOA1 marker locus as a QTL for which you can calculate allele effects, calculate **a**.

1) *0.6173 oocytes*

✓ 2) *1.2346 oocytes*

3) *-1.2346 oocytes*

4) *-0.3142 oocytes*

View Feedback

Correct. (19.0120706 - 16.542778) / 2

Question 4 *1 / 1 point*

Again referring to the SAS Output shown in the question above, the tables under the heading "Least Squares Means" provide the average Ovulation Rate (OvRate) phenotypes for each of the genotypes. The phenotype is measured in number of oocytes. Treating the NCOA1 marker locus as a QTL for which you can calculate allele effects, calculate **d**.

1) *-0.1571 oocytes*

2) *0.3142 oocytes*

3) *1.2346 oocytes*

✓ 4) *-0.3142 oocytes*

View Feedback

Correct. 17.4632308 - (19.0120706 + 16.542778) / 2

Question 5 *1 / 1 point*

Again referring to the SAS Output shown in the question above, the tables under the heading "Least Squares Means" provide the average Ovulation Rate (OvRate) phenotypes for each of the genotypes. The phenotype is measured in number of oocytes. Treating the NCOA1 marker locus as a QTL for which you can calculate allele effects and knowing that the "1" allele had a frequency of 0.62 in the population, calculate: **a** $\mathbf{a_1}$ *and* $\mathbf{a_2}$

1) *a = 0.6551 oocytes, a_1 = 0.2489 oocytes, and a_2 = -0.4061 oocytes*

2) *a = 1.3101 oocytes, a_1 = -0.4978 oocytes, and a_2 = 0.8122 oocytes*

✓ 3) *a = 1.3101 oocytes, a_1 = 0.4978 oocytes, and a_2 = -0.8122 oocytes*

4) *a = 1.3101 oocytes, a_1 = -0.8122 oocytes, and a_2 = 0.4978 oocytes*

View Feedback

$a = a + (q - p)d$, $a_1 = 2qa$, and $a_2 = -2pa$ and all have units of oocytes.
Correct.

Question 6 *1 / 1 point*

Again referring to the SAS Output shown in the question above, the tables under the heading "Least Squares Means" provide the average Ovulation Rate (OvRate) phenotypes for each of the genotypes. The phenotype is measured in number of oocytes. Treating the NCOA1 marker locus as a QTL for which you can calculate allele effects and knowing that the "1" allele had a frequency of 0.62 in the population, calculate the breeding value for each of the three NCOA1 marker genotypes.

- *1) $BV_{11} = 0.9956$ oocytes, $BV_{12} = 0.3144$ oocytes $BV_{22} = 1.6245$ oocytes*
- ✓ *2) $BV_{11} = 0.9956$ oocytes, $BV_{12} = -0.3144$ oocytes and $BV_{22} = -1.6245$ oocytes*
- *3) $BV_{11} = -0.9956$ oocytes, $BV_{12} = 0.3144$ oocytes and $BV_{22} = 1.6245$ oocytes*
- *4) $BV_{11} = 0.5265$ oocytes, $BV_{12} = -0.1663$ oocytes and $BV_{22} = -0.8590$ oocytes*

View Feedback

$BV_{11} = 2qa$ oocytes, $BV_{12} = (q - p)a$ oocytes and $BV_{22} = -2pa$ oocytes
Correct.

Question 7 *1 / 1 point*

*Again referring to the SAS Output shown in the question above, the tables under the heading "Least Squares Means" provide the average Ovulation Rate (OvRat*e) phenotypes for each of the genotypes. The phenotype is measured in number of oocytes. Treating the NCOA1 marker locus as a QTL for which you can calculate allele effects and knowing that the "1" allele had a frequency of 0.62 in the population, calculate the dominance deviation for each of the three NCOA1 marker genotypes.

- ✓ *1) $DD_{11} = 0.0907$ oocytes, $DD_{12} = -0.1480$ oocytes and $DD_{22} = 0.2416$ oocytes*
- *2) $DD_{11} = -0.0907$ oocytes, $DD_{12} = 0.1480$ oocytes and $DD_{22} = -0.2416$ oocytes*
- *3) $DD_{11} = 0.0454$ oocytes, $DD_{12} = -0.0740$ oocytes and $DD_{22} = 0.1208$ oocytes*

View Feedback

$DD_{11} = -2q^2d$ oocytes, $DD_{12} = 2pqd$ oocytes and $DD_{22} = -2p^2d$ oocytes
Correct.

Question 8 *1 / 1 point*

Again referring to the SAS Output shown in the question above, the tables under the heading "Least Squares Means" provide the average Ovulation Rate (OvRate) phenotypes for each of the genotypes. The phenotype is measured in number of oocytes. Treating the NCOA1 marker locus as a QTL for which you can calculate allele effects and knowing that the "1" allele had a frequency of 0.62 in the population, calculate the genotypic values for each of the three NCOA1 marker genotypes.

- *1) $GV_{11} = 0.6172$ oocytes, $GV_{12} = -0.3143$ oocytes and $GV_{22} = -0.6174$ oocytes*
- ✓ *2) $GV_{11} = 1.0863$ oocytes, $GV_{12} = -0.4624$ oocytes and $GV_{22} = -1.3829$ oocytes*
- *3) $GV_{11} = -0.6172$ oocytes, $GV_{12} = 0.3143$ oocytes and $GV_{22} = 0.6174$ oocytes*

View Feedback

$GV_{11} = BV_{11} + DD_{11} = 1.0863$ oocytes, $GV_{12} = BV_{12} + DD_{12} = -0.4624$ oocytes and $GV_{22} = BV_{22} + DD_{22} =$

-1.3829 oocytes
Correct

Question 9 *1 / 1 point*

Again referring to the SAS Output shown in the question above, the tables under the heading "Least Squares Means" provide the average Ovulation Rate (OvRate) phenotypes for each of the genotypes. The phenotype is measured in number of oocytes. Treating the NCOA1 marker locus as a QTL for which you can calculate allele effects and knowing that the "1" allele had a frequency of 0.62 in the population, calculate the additive genetic variation and dominance genetic variation at the NCOA1 marker locus.

1) $\sigma_A^2 = 0.0219$ oocytes^2 and $\sigma_D^2 = 0.2261$ oocytes^2

✓ 2) $\sigma_A^2 = 0.8086$ oocytes^2 and $\sigma_D^2 = 0.0219$ oocytes^2

3) $\sigma_A^2 = 0.0565$ oocytes^2 and $\sigma_D^2 = 0.0055$ oocytes^2

View Feedback

$\sigma_A^2 = 2pqa^2 = 0.2261$ oocytes^2 and $\sigma_D^2 = (2pqd)^2 = 0.0219$ oocytes^2
Correct.

Question 10 *1 / 1 point*

Given the following table of map distances in centimorgans, arrange the markers in the correct order. To make your life easier, start with M1 as the first marker. If this were a real dataset you wouldn't even know where to start!

Markers	M1	M2	M3	M4	M5
M1	0	4.6	1.1	7.2	5.8
M2	4.6	0	3.5	2.6	1.2
M3	1.1	3.5	0	6.1	4.7
M4	7.2	2.6	6.1	0	1.4
M5	5.8	1.2	4.7	1.4	0

1) M1 - M5 - M4 - M3 - M2

2) M1 - M4 - M2 - M3 - M5

3) M1 - M2 - M3 - M4 - M5

4) M1 - M3 - M2 - M4 - M5

✓ 5) M1 - M3 - M2 - M5 - M4

View Feedback

Correct. Use the distances from M1 to make it easy.

Question 11 *0 / 1 point*

Detecting QTL requires a number of pieces to fall into place. One of those pieces is to find a marker in close enough proximity to the QTL. Select the choice below that best describes an ideal marker.

An ideal marker will be one that is located within the coding or non-coding region of the gene that is suspected of creating the difference in phenotype.

✗ *An ideal marker will be one that is located near the gene that is suspected of creating the difference in phenotype.*

An ideal marker will be one that is located downstream (in a transcription sense) of the gene that is suspected of creating the difference in phenotype.

An ideal marker will be one that is located upstream (in a transcription sense) of the gene that is suspected of creating the difference in phenotype.

View Feedback

An ideal marker will be one that is located within the coding or non-coding region of the gene that is suspected of creating the difference in phenotype because if the marker is within the region of the actual gene, recombination between marker and gene is very, very, very, very, very, very . . . unlikely. Oops. An ideal marker will be one that is located within the coding or non-coding region of the gene that is suspected of creating the difference in phenotype.

Question 12 *1 / 1 point*

With any QTL used in a selection program, it is always a good idea to

1) *Don't worry about the marker allele - QTL allele linkage phase over time because we cannot control recombination.*
2) *Verify the marker allele - QTL allele linkage phase regularly over time.*
3) *Assume the marker allele - QTL allele linkage phase is maintained over time.*

View Feedback

Verify the marker allele - QTL allele linkage phase regularly over time to make sure M is still associated with Q and not q. Correct.

Question 13 *0 / 1 point*

Molecular and quantitative geneticists often use panels of markers to hunt for QTL so they can cover a wide area of the genome. Typically those analyses will be broken down to a chromosome by chromosome search for QTL, looking at all of the markers on a chromosome as an experimental unit. When multiple single nucleotide polymorphism (SNP) markers are available, it is better to

1) *Group markers into a haploid genotype based on parental inheritance and analyze the group of markers as a virtual single marker looking for an association with a QTL.*
2) *Analyze individual markers looking for associations with QTL for each marker and repeat the analysis as many times as there are markers on a chromosome.*
3) *Analyze individual markers looking for associations with QTL for each marker accounting for their linkage distances.*

View Feedback

Group markers into a haploid genotype based on parental inheritance and analyze the group of markers as a virtual single marker looking for an association with a QTL. A haploid covers a larger part of the genome and is therefore more accurate for obeserving crossover events than a single marker. Oops. Group markers into a haploid genotype based on parental inheritance and analyze the group of markers as a virtual single marker looking for an association with a QTL.

Question 14 *1 / 1 point*

All of the various methods of detecting QTL have one common aspect. Assuming a generic marker locus M with alleles M and m, which of the following is the most correct...

1) *All the methods are looking for a phenotypic difference in the heterozygotes resulting from matings between individuals with an MM genotype and individuals with an mm genotype.*
2) *All the methods are looking for a difference in phenotype between the individuals with an MM genotype versus an mm genotype.*
3) *All the methods are looking for a difference in selection response between the individuals with an MM genotype when they are selected as parents and mated versus when mm individuals are mated.*

View Feedback

All the methods are looking for a difference in phenotype between the individuals with an MM genotype versus an mm genotype. Correct.

Question 15 *0 / 1 point*

QTL detection and using QTL in marker assisted selection of livestock and companion animals or fine mapping of genes and eventually gene therapy or genetic counseling in humans is the state of the art in Quantitative Genetics research. This makes QTL detection as a field of research a . . .

1) *very dynamic area because allele frequencies can be dramatically altered which creates a need for a constant supply of new markers and new QTL.*

2) *very static area because once QTL are found all of the molecular genetic mechanisms are known and allele frequencies can be dramatically altered by rapid selection response quickly eliminating "bad" alleles and solving a genetic problem.*

View Feedback

very dynamic area because allele frequencies can be dramatically altered which creates a need for a constant supply of new markers and new QTL (and money!) very dynamic area because allele frequencies can be dramatically altered which creates a need for a constant supply of new markers and new QTL.

Quiz 10

Question 1 *0 / 1 point*

In a large random mating population, there is a single locus with alleles **A** *and* **a** *that you are interested in. You observe the frequency of the* **A** allele is 0.6.

If the homozygous recessive genotype has a fitness level of 50% in the current generation, what is the frequency of the homozygous recessive genotype among the progeny born in the next generation?

1) *0.1210*

2) *0.3478*

3) *0.4253*

4) *0.6522*

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Sorry, that is the allele frequency. $p_1 = p_0/(1-sq_0^2) = 0.6/(1-0.5(0.16)) = 0.6522$ *so* $q_1 = 0.3478$ *and* $q_1^2 = 0.1210 = f(aa)$

Question 2 *0 / 1 point*

In a large random mating population, there is a single locus with alleles **A** *and* **a** *that you are interested in. You observe the frequency of the* **A** *allele is 0.6.*
If the homozygous recessive genotype has a fitness level of 50% and the heterozygous genotype has a fitness level of 75% in the current generation, what is the frequency of the homozygous recessive genotype among the progeny born in the next generation?

1) *0.675*

2) *0.325*

3) *0.1056*

4) *0.4556*

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Sorry, that is the allele frequency. $p_1 = [p_0(1-s_1 q_0)]/[(1 - 2s_1p_0q_0 - s_2 q_0^2) = 0.675$ so $q_1 = 0.325$ and $q_1^2 = 0.1056 = f(aa)$

Question 3 *1 / 1 point*

Comparing the results for Questions 1 and 2, the difference between the two scenarios was the fitness of the genotypes. Which situation resulted in a greater decline of the **a** allele and why?

- ✔ 1) *The situation where selection acted on both the heterozygotes and homozygous recessive individuals resulted in the greatest decline of f(a) because this reduces the frequency of the* **a** *allele rather than just the* **aa** *genotype.*
- 2) *Both scenarios were equivalent. Neither produced a more rapid reduction in the allele or genotypic frequency.*
- 3) *The situation where selection acted on both the homozygous recessive individuals only resulted in the greatest decline because the frequency of the individuals who have two copies of the* **a** *allele was reduced and therefore a greater decline occurred by selecting against two copies at a time.*

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Correct. Working against the allele will always be faster than working against one genotype.

Question 4 *1 / 1 point*

As an organizer of the Triwizard Tournament, you are tasked with maintaing a dragon breeding program. Dragons require a substantial wingspan for flight so you have recorded the wingspans of 10 dragons as shown below. Select the top 20% of the population based on the phenotypes provided. Assume heritability of wingspan is 25% and that dragons can reproduce like earthworms and decide their own gender so you don't need to worry about gender in your selections. Calculate the response to selection and the narrowest wingspan that qualified for your selected group of dragons.

Individual	*Phenotype*	*Rank for Phenotype*
Smoky	*10.95*	*3*
Crispy	*4.94*	*6*
Crunchy	*8.92*	*4*
Sparky	*7.81*	*5*
Puff	*2.98*	*9*
Barney	*13.29*	*2*
Lance	*3.91*	*7*
Hubert	*3.05*	*8*
Elliot	*0.72*	*10*
Draconius	*17.59*	*1*

- 1) *Response is 3.86 metres and the minimum wingspan is 13.29 metres*
- 2) *Response is 2.006 metres and the minimum wingspan is 0.7 metres.*

	3)	*Response is 9.422 metres and the minimum wingspan is 13.29 metres.*
✓	4)	*Response is 2.006 metres and the minimum wingspan is 13.29 metres*

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Correct. Select the individuals ranked 1 and 2 (Draconius and Barney), their average wingspan is 15.44 m. The population mean is 7.416m. The R = S h^2 = (15.44 - 7.416) x 0.25 = 2.006 m

Question 5 *1 / 1 point*

As an organizer of the Triwizard Tournament, you are continuing with maintaing a dragon breeding program. Dragons require a substantial wingspan for flight so you have recorded the wingspans of 10 dragons as shown below. Select the top 10% of the population based on the phenotypes provided. Assume heritability of wingspan is 25% and that dragons can reproduce like earthworms and decide their own gender so you don't need to worry about gender in your selections. Calculate the response to selection and the narrowest wingspan that qualified for your selected group of dragons.

Individual	*Phenotype*	*Rank for Phenotype*
Smoky	*10.95*	*3*
Crispy	*4.94*	*6*
Crunchy	*8.92*	*4*
Sparky	*7.81*	*5*
Puff	*2.98*	*9*
Barney	*13.29*	*2*
Lance	*3.91*	*7*
Hubert	*3.05*	*8*
Elliot	*0.72*	*10*
Draconius	*17.59*	*1*

✓	1)	*Response is 2.544 metres and the minimum wingspan is 17.59 metres*
	2)	*Response is 4.398 metres and the minimum wingspan is 17.59 metres*
	3)	*Response is 9.960 metres and the minimum wingspan is 17.59 metres.*
	4)	*Response is 2.544 metres and the minimum wingspan is 0.7 metres.*

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Correct. Select the #1 ranked individual Draconius, his/her wingspan is 17.59 m. The population mean is 7.416m. The R = S h^2 = (17.59 - 7.416) x 0.25 = 2.544 m

Question 6 *1 / 1 point*

As an organizer of the Triwizard Tournament, you are continuing with maintaing a dragon breeding program. Dragons require a substantial wingspan for flight so you have recorded the wingspans of 10 dragons. You are tired of working with all the data so you calculate that the phenotypic variance is

25.491964. Using the new information, select the top 20% of the population based on the phenotypic variability. Assume heritability of wingspan is still 25% and that dragons can reproduce like earthworms and decide their own gender so you don't need to worry about gender in your selections. Calculate the response to selection and the narrowest wingspan that qualified for your selected group of dragons.

- ✓ 1) *Response is 1.7671 metres and the minimum wingspan is 11.67 metres*
- 2) *Response is 1.7671 metres and the minimum wingspan is 14.47 metres.*
- 3) *Response is 1.0609 metres and the minimum wingspan is 11.67 metres*

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Correct. i = 1.4 and t = 0.842 for p = 20%. Response is $i\sigma_p h^2$ = 1.4 x 5.0490 x 0.25 = 1.7671 m. Minimum phenotype is $t\sigma_p$ + mean = 0.842 x 5.0490 + 7.416 = 11.67 m

Question 7 *1 / 1 point*

As an organizer of the Triwizard Tournament, you are continuing with maintaing a dragon breeding program. Dragons require a substantial wingspan for flight so you have recorded the wingspans of 10 dragons. You are tired of working with all the data so you calculate that the phenotypic variance is 25.491964. Using the new information, select the top 10% of the population based on the phenotypic variability. Assume heritability of wingspan is still 25% and that dragons can reproduce like earthworms and decide which their own gender so you don't need to worry about gender in your selections. Calculate the response to selection and the narrowest wingspan that qualified for your selected group of dragons.

- 1) *Response is 1.6153 metres and the minimum wingspan is 13.88 metres*
- 2) *Response is 2.2152 metres and the minimum wingspan is 16.26 metres.*
- ✓ 3) *Response is 2.2152 metres and the minimum wingspan is 13.88 metres*

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Correct. i = 1.755 and t = 1.282 for p = 10%. Response is $i\sigma_p h^2$ = 1.755 x 5.0490 x 0.25 = 2.2152 m. Minimum phenotype is $t\sigma_p$ + mean = 1.282 x 5.0490 + 7.416 = 13.88 m

Question 8 *1 / 1 point*

*In questions 4, 5, 6 and 7 above you calculated response to selection for two diffe*rent scenarios two different ways. You should have different answers for each! Looking at those answers, what contributed to the difference in response between selecting 20% and 10%? Also, comparing the selection based on the data to the selection based on population variability, what contributed to the difference in response between the two situations?

- *1) Reducing the proportion selected increased the selection response because the average phenotype of the selected group increased.*
  ✓ 1) *2) The selection response was different between using the data and using the variability. This is due to the fact that the actual phenotypes are not normally distributed so assuming normality to use σ_p wasn't really a valid assumption.*
- *1) Reducing the proportion selected decreased the selection response because the average phenotype of the selected group changed.*
  2) *2) The selection response was different between using the data and using the variability. This is due to the fact that the actual phenotypes are not normally distributed so assuming normality to use σ_p wasn't really a valid assumption.*
- 3) *1) Reducing the proportion selected increased the selection response because the average phenotype of the selected group increased.*
  2) The selection response was the same when using the data and using the variability. This is due to the fact that the actual phenotypes are normally distributed so assuming normality to

use σ_p wasn't really a problem.

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Correct.

Question 9 *1 / 1 point*

A random sample of 10 individuals is drawn from a larger population of rabbits. These 10 individiuals are shown in the table below along with their phenotype which is their weight at 4 weeks of age. If the heritability of this trait is 0.30, calculate the response to selection based on selecting the top 4 individuals based on phenotype.

ID	Phenotype	Rank	Genotype
A	161.65	7	11
B	151.33	9	12
C	165.82	3	11
D	164.23	4	12
E	164.10	5	12
F	143.38	10	22
G	166.01	2	12
H	163.69	6	11
I	159.45	8	12
J	169.05	1	11

1) *The response to selection is 1.6220 grams.*

2) *The response to selection is 5.4065 grams.*

3) *The response to selection is 166.2775 grams*

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Correct.

Question 10 *1 / 1 point*

A random sample of 10 individuals is drawn from a larger population of rabbits. These 10 individiuals are shown in the table below along with their phenotype which is their weight at 4 weeks of age. If the heritability of this trait is 0.30 and the phenotypic standard deviation is 20.6110, calculate the response to selection based on selecting the top 40% of the individuals ignoring the actual phenotypes this time.

ID	Phenotype	Rank	Genotype
A	161.65	7	11
B	151.33	9	12
C	165.82	3	11
D	164.23	4	12
E	164.10	5	12
F	143.38	10	22
G	166.01	2	12
H	163.69	6	11
I	159.45	8	12
J	169.05	1	11

1) *The response to selection is 1.5644 grams*

✔ 2) *The response to selection is 5.9731 grams*

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Correct.

Question 11 *1 / 1 point*

Breeding values are normally computed as a selection tool. Suppose we continue to study a sample population of rabbits and genotype individuals for two alleles labelled "1" and "2". From those genotypes, you determine that the 4 week weight of the 11 individuals averages 169.97 grams, the 12 individuals average 161.47 and the 22 individuals average 138.97. You observe that there are 36% 11 individuals, 48% 12 individuals and 16% 22 individuals in the population. Calculate the breeding value of the 11 genotype, the dominance deviation for the 12 genotype and the genotypic value for the 22 genotype.

✔ 1) *BV_{11} = 11.28, DD_{12} = 3.36 and GV_{22} = -21.96 (all units grams).*

2) *BV_{11} = -2.82, DD_{12} = 3.36 and GV_{22} = 0.54 (all units grams).*

3) *BV_{11} = -16.92, DD_{12} = 3.36 and GV_{22} = 9.04 (all units grams).*

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a = 14.1, $a_1 = qa$ = 5.64, $a_2 = qa$ = -8.46, BV_{11} = 11.28, DD_{12} = 3.36 and GV_{22} = -21.96 (all units grams).
Correct.

Question 12 *1 / 1 point*

Using the genotype column in our now familiar data, select the top 40% of individuals based on genotype using information you computed from the question above. If these top 40% of individuals randomly mated and produced offspring, what would the the response to selection between the parent and progeny generations?

ID	Phenotype	Rank	Genotype
A	161.65	7	11
B	151.33	9	12
C	165.82	3	11
D	164.23	4	12
E	164.10	5	12
F	143.38	10	22
G	166.01	2	12
H	163.69	6	11
I	159.45	8	12
J	169.05	1	11

✔ 1) *The response is 11.28 grams*

2) *The response is 0 grams*

3) *The response is 9.04 grams*

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Correct. All progeny will be 11 so the response is BV_{11} - 0

Question 13 *1 / 1 point*

In questions 9, 10 and 12 above you calculated the response to selected when the top 40% of individuals were selected. Hopefully the resulting response to selection you calculated in each case was different (hint, hint). Using the phrases below, make the most appropriate match for each statement.

✓ __1__	*Question 9*
✓ __3__	*Question 12*
✓ __2__	*Question 10*

1. *Selection based on the infinitesimal model not assuming normality*

2. *Selection based on the infinitesimal model assuming normality*

3. *Selection based on the finite locus model not assuming normality*