

1. Which of the following populations are in Hardy-Weinberg equilibrium? (To answer the question, carry out a statistical test of this hypothesis).

Pop'n	<u>Genotype</u>		
	AA	Aa	aa
1	25	50	25
2	10	80	10
3	40	20	40

Answer: The critical value of X^2 for 1 df is 3.84. We reject the null hypothesis (of HW eq'b) if this value is exceeded.

#1. Accept

#2. Reject

#3. Reject

2. For problem 1, for those populations which deviate significantly from H-W expectation, suggest an explanation consistent with the observed deviations.

Pop #2: heterozygote excess, due possibly to overdominant selection

Pop #3: heterozygote deficiency, due possibly to underdominant selection

3. For genotypes with the following fitnesses and frequencies at birth

Genotype	AA	Aa	aa
Birth Freq'cy	p^2	$2pq$	q^2
Fitness	1	1	$1-s$

a. What is the freq'cy of AA individuals in the adult population?

Answer: $p^2 / (p^2 + 2pq + q^2(1-s))$

b. What is the frequency of the A allele in the adult population?

Answer: $p' = (p^2 + pq) / (p^2 + 2pq + q^2(1-s))$
 $= p / (p^2 + 2pq + q^2(1-s))$
 $= p / (1 - sq^2)$

c. What is the mean fitness of the population?

Answer: $p^2 + 2pq + q^2(1-s) = 1 - sq^2$

4. Consider a locus with 2 alleles, A and a. A is dominant, and selection is working against the recessive homozygote. The frequency of A in two successive generations is 0.4875 and 0.5. What is the value of s, the selection coefficient against the aa genotype?

Answer:

The described fitness scheme is as follows:

Genotype	AA	Aa	aa
Birth Freq'cy	p^2	$2pq$	q^2
Fitness	1	1	$1-s$

Using $p' = p / (1 - sq^2)$ and substituting $p' = 0.5$ and $p = 0.4875$ and $q = 1 - p$, $s = 0.095$ (approx.)

5. Listed below are adult genotype frequencies for a locus with two alleles. The polymorphism is maintained by heterozygote advantage, due to differences in survival (not reproduction). What are the fitnesses (and selection coefficients) of the two homozygotes, relative to a fitness of 1 for the heterozygote?

Genotype	$A_1 A_1$	$A_1 A_2$	$A_2 A_2$
Adult Freq'cy	1/6	2/3	1/6

Answer:

Assuming equilibrium, because the homozygous genotypes are equally frequent, they must have equal fitness ($s = t$). When $s = t$, both alleles will be maintained at equal frequency ($p = q = 1/2$ at equilibrium).

From this, we can obtain the frequencies of each genotype at birth, according to the HW model as (in the above order) 1/4, 1/2 and 1/4.

The frequency of $A_1 A_1$ after selection is

$$1/4(1-s) / \bar{w} = 1/6$$

$$\bar{w} = 1/4 * (1-s) + 1/2 * 1 + 1/4 * (1-t) = 1 - s/4 - t/4 = 1 - s/2$$

(using the fact that $s = t$)

Substituting this value for \bar{w} and solving for s , $s = 1/2$.

Assigned Problems, Ch. 6:

1. No selection, no mutation, no genetic drift (chance variation in allele frequencies from one generation to the next), no migration, random mating.

Selection, mutation, migration and genetic drift change genotype and allele frequencies.

Non-random mating changes genotype frequencies.

#3a. Migration followed by natural selection. The frequency of the T allele is likely to increase rapidly.

- b. Migration followed by natural selection. The frequency of the T allele may increase, but only slowly, and perhaps not at all, due to the rarity of the T allele and the weakness of selection.
- c. Frequency-dependent selection. The frequency of small males is likely to gravitate toward a stable equilibrium frequency, at which small and large males have identical fitness.
- d. Underdominance. One allele will very likely go to fixation, and the other allele will be lost. Which allele is lost is likely to depend on where the initial allele frequencies are, relative to the unstable equilibrium point.
- e. Heterozygote superiority, or overdominance. The frequency of the m allele is likely to gravitate toward a stable equilibrium frequency.

#4. The younger women were used to estimate the genotype and thus allele frequencies before selection (for resistance to kuru).

#5. The HW (or random mating) model says nothing about the expected frequency of alleles. It simply allows prediction of the frequencies of different genotypes given the allele frequencies, under a set of assumptions including random mating.

#6.	Obs'd #	Exp'd #
SS	1194	1194
Ss	526	526
ss	<u>58</u>	<u>58</u>
	1778	1778

The expected numbers were determined by

- A. calculating the frequency of S as $(2 \cdot 1194 + 526) / (2 \cdot 1778)$, the percentage of S alleles in the sample.
- B. Using $p = \text{freq}(S)$ to calculate the expected genotype frequencies according to the HW model
- C. Multiplying the expected frequencies by 1778

A chi-square with one degree of freedom finds that the deviation of the observed from the expected numbers is zero, indicating the population is in HW equilibrium.

To determine whether the next generation is in equilibrium, you would need the numbers of each genotype in that generation.

#7. These small changes are likely due to genetic drift. The easiest way to reduce this effect is to use a larger population size.

#8. When females are rarer, females will be able to find mates more easily than will males and females will have a selective advantage. Parents that produce mostly females will have more grand-offspring, compared to parents that produce mostly males. When males are rare, males will find mates more easily, will have a selective advantage, and their parents will produce more grand-offspring. This is an example of frequency-dependent selection, and is thought to maintain the 50:50 sex ratio seen in most species.