Practice Problems for Population Genetics

1) As part of a class project, we have been tracking the frequency of two different color morphs (zigzag and monochrome) of salamanders on Hanover College's campus. These organisms are diploid and the alleles that confer dorsal color pattern are not associated with the sex chromosomes. We know that dorsal color pattern is regulated by a single locus with two alleles (Z and z). The allele conferring the zigzag pattern is completely dominant to the allele that confers monochrome color. In an initial study, we find 376 monochrome salamanders and 119 with the zigzag pattern. We then genotype them and discover 47 are homozygous dominant and 72 are heterozygous.

ZZ	47
Zz	72
zz	376
	495

a. What is the frequency of the two alleles in this population?

$$P = P^2 + \tfrac{1}{2}(2pq)$$
$$= \frac{47}{495} + \frac{1}{2}\left(\frac{72}{495}\right)$$
$$= 0.095 + 0.073$$

$$\boxed{f(Z) = P = 0.168}$$
$$q = 1 - 0.168$$
$$\boxed{f(z) = q = 0.832}$$

b. What is the expected frequency of each genotype in this population?

$$f(ZZ) = p^2$$
$$= 0.168^2$$
$$\boxed{f(ZZ) = 0.028}$$

$$f(Zz) = 2pq$$
$$= 2(0.168)(0.832)$$
$$\boxed{f(Zz) = 0.2796}$$

$$f(zz) = q^2$$
$$= 0.832^2$$
$$\boxed{f(zz) = 0.692}$$

c. What is the expected number of individuals of each genotype in this population?

$$\#ZZ = P^2 \times N$$
$$= 0.028 \times 495$$
$$\boxed{\#ZZ = 13.9}$$

$$\#Zz = 2pq \times N$$
$$= 0.2796 \times 495$$
$$\boxed{\#Zz = 138.4}$$

$$\#zz = q^2 \times N$$
$$= 0.692 \times 49$$
$$\boxed{\#zz = 342.5}$$

d. Is this population evolving? How do you know? Conduct a statistical test to verify whether your assertion is correct.

These #s are different than the observed values - & the pop is likely evolving.

$$\chi^2 = \sum \frac{(O-E)^2}{E} = \frac{(47-13.9)^2}{13.9} + \frac{(72-138.4)^2}{138.4} + \frac{(376-342.5)^2}{342.5} =$$
$$= 78.8 + 31.86 + 3.28 = \boxed{113.94}$$

DF = # catagories - 1

= 3 - 1

$\boxed{DF = 2}$

$\boxed{P < 0.001}$

- our chi square Value is very large & $P < 0.001$
- We reject the Null which says the observed & expected Values are similar
- B/c Obs + Exp values are different, we can conclude our pop is not in HWE & is therefore evolving

2) Suppose we follow up the previous study with a mark-recapture study to assess the fitness advantage of the various genotypes. After marking the salamanders we collected previously, we recapture 66 monochrome salamanders and 9 salamanders with zigzags. 2 of these are homozygous dominant and 7 are heterozygous.

Overall surv rate is 75/495 = 0.152

a. What is the survival rate for each genotype?

Genotype	Collected/Marked	Recaught (O)	Expected if HWE	Surv Rate
ZZ	47	2	0.152 × 47 = 7.12	2/7.12 = 0.28
Zz	72	7	10.9	7/10.9 = 0.64
zz	376	66	57.2	66/57.2 = 1.154
	495	75		

b. Calculate the selection and dominance coefficients for the salamanders in this population

-First have to calc relative fitness

Surv Rate	Relative Fitness	Formula
0.28	0.28/1.154 = 0.243	$W_{ZZ} = 1-s$
0.64	0.64/1.154 = 0.55	$W_{Zz} = 1-hs$
1.154	1.154/1.154 = 1	$W_{zz} = 1$

$0.243 = 1 - s$

$s = 1 - 0.243$

$\boxed{s = 0.76}$

$\frac{0.55}{0.76} = \frac{1}{0.76} - \frac{h(0.76}{0.76}$

$0.72 = 1.316 - h$

c. What is the population mean fitness given the allele frequencies you actually observed in the original sample?

$h = 1.316 - 0.7$

$\boxed{h = 0.596}$

$$\bar{W} = p^2(W_{AA}) + 2pq(W_{Aa}) + q^2(W_{aa})$$

$$= \frac{47}{495}(0.243) + \frac{72}{495}(0.55) + \frac{376}{495}(1)$$

$$\bar{W} = 0.023 + 0.08 + 0.76$$

$$\boxed{\bar{W} = 0.863}$$

3) Chupacabras have a gene that codes for incisors that hook outwards forming a scythe-like structure. Animals with this trait use it to slash the necks of unsuspecting sleeping humans at night and lick up their blood. If they are Homozygous recessive they have the scythe-like tooth. The other two genotypes have needle-like incisors that suck the blood from their victims (happy Halloween!). We (courageously) sample a population of Chupacabra's and find that 70 individuals out of 200 have the scythe-like tooth. What is the frequency of the remaining two genotypes in our population and how many individuals in our sample likely have each genotype?

ss - scythe #

70

Ss - Vampire

SS - Vampire

$q^2 = 70$

$q = \sqrt{\frac{70}{200}}$

$\boxed{q = 0.59}$

$p = 1 - 0.59$

$\boxed{p = 0.41}$

$f(Ss) = 2pq = 2(0.41)(0.59)$

$\boxed{f(Ss) = 0.48}$

$f(SS) = p^2 = 0.41^2$

$\boxed{f(SS) = 0.17}$

$\#SS = p^2 \times N$

$= 0.17 \times 200$

$\boxed{\#SS = 33.62}$

$\#Ss = 2pq \times N$

$= 0.48 \times 200$

$\boxed{\#Ss = 96}$

4) Domestic rabbits have a gene that codes for floppy or straight ears. Bunnies that are homozygous dominant have straight ears. Heterozygous bunnies have ears that stick off to the side and are neither floppy or straight, and homozygous recessive bunnies have floppy ears. We sample the bunnies on our rabbit farm and find that out of 200, 15% have floppy ears, 47% have intermediate ears, and 38% have straight ears.

a. What are the frequencies of our alleles on the farm?
b. If the allele coding for straight ears mutates to the other allele at a rate of 0.001, and the allele coding for floopy ears mutates to the other allele at a rate of 0.00001, what will the new allele frequencies be after one generation?
c. Given these mutation rates, will they cause the allele frequencies to reach 1 and 0 respectively or will they reach an equilibrium? Explain.
d. What is the equilibrium frequency for the two alleles?
e. How many generations will it take to reach this frequency?

Phenotype	freq
Straight ears (FF)	0.38
Side ears (Ff)	0.47
Floppy ears (ff)	0.15

Allele Freq

$p = p^2 + \frac{1}{2}(2pq)$

$= 0.38 + \frac{1}{2}(0.47)$

$\boxed{p = 0.615 = f(F)}$

$p + q = 1$

$0.615 + q = 1$

$q = 1 - 0.615$

$\boxed{q = 0.385 = f(f)}$

$F \xrightarrow{mut} f = 0.001 = u$

$f \xrightarrow{mut} F = 0.00001 = v$

$P_{t+1} = P_t(1-u) + (1-P_t)v$

$P_{t+1} = 0.615(1-0.001) + (1-0.615)(0.00001)$

$P_{t+1} = 0.6144 + 3.85 \times 10^{-6}$

$P_{t+1} = 0.6144$

New allele frequencies after a generation of mutational Δ

$\boxed{f(F) = 0.6144}$

$\boxed{f(f) = 1 - 0.6144 = 0.3856}$

- Eventually an equilibrium will be reached. We are loosing F alleles & they are becoming f alleles. Eventually the loss of F to mutation is counterbalanced by the sheer # of f alleles + the relatively low # of F alleles

- Equilibrium frequency is calculated

$$\hat{P} = \frac{V}{u+V} = \frac{0.00001}{0.001 + 0.00001} = \boxed{0.0099 = \text{equilib freq of } F}$$

$$\boxed{\begin{aligned} \text{equilib freq of } f &= 1 - 0.0099 \\ &= 0.9901 \end{aligned}}$$

- How many generations?
  - frequency of F changes $0.615 - 0.6144 = 6 \times 10^{-4}$ each generatio

$$\# \text{Gen} = \frac{\text{Orig Freq}}{\Delta \text{ per gen}} = \frac{0.615}{6 \times 10^{-4}} = \boxed{1025 \text{ generations}}$$