1. Consider a flower-color polymorphism in a normally outcrossing species of plan with allele (R) conferring red color and (r) conferring white. R is completely dominant to r. In a random sample of 250 individuals, 10 are scored as having white flowers.
    a. How might you estimate the frequencies of the two alleles at this locus?
    b. What assumptions need to be met to acquire such estimates?
    c. If these assumptions are met, what are the expected frequencies of the three genotypes in the population?
    d. How many of the remaining genotypes would you expect to find?

a) using one of the derivatives of the HW equation,

b) Random mating, No drift, No NS, No Gene flow
No mutation

	RR	Rr	rr
observed			10

* In this case we only have f(rr), so can't use the formulas $\left(P = P^2 + \frac{1}{2}2pq \text{ or } q = q^2 + \frac{1}{2}2pq\right)$

* But know $f(rr) = q^2$ so we can find q

$$q^2 = \frac{10}{250} = 0.04$$

$$\sqrt{q^2} = \sqrt{0.04}$$

$$\boxed{q = 0.2} \longrightarrow$$

$$P + q = 1$$

$$P + 0.2 = 1$$

$$\boxed{P = 0.8}$$

* Now that we have p + q

- we can calc the exp freq of each genotype (along w/ exp # of each genotype if I had asked for that)

$f(RR)$	$f(Rr)$	$f(rr)$
		$= q^2$
$= 0.8^2$	$= 2 \times 0.8 \times 0.2$	$= 0.2^2$
$\boxed{= 0.64}$	$\boxed{= 0.32}$	$\boxed{= 0.04}$

- If I had asked how many ind w/ each genotype

AA	Aa	aa
$p^2 \times N$	$2pq \times N$	$q^2 \times N$
$0.8^2 \times 250$	$2(0.8)(0.2) \times 250$	$0.2^2 \times 250$
$\boxed{160}$	$\boxed{80}$	$\boxed{10}$

2. Glaucoma occurs in individuals that have alleles D_4 and D_{17} (out of 20 different alleles in the population). If the frequency of these two alleles in the population is 0.0006 and 0.1, respectively, what is the probability that your new baby will possess this particular genotype? Assume that we do not know either parents genotype.

f (homozygote) = freq of allele × freq of allele

$= P_1 \times P_1$

$= P_1^2$

f (heterozygote) = freq of allele × freq of allele × 2

$= D_4 \times D_{17} \times 2$

$= 0.0006 \times 0.1 \times 2$

$f(D_4 D_{17}) = 0.00012$

$\boxed{\text{probability} = 0.012\%}$

3. Kettlewells (1973) classic mark-recapture study in England of industrial melanism in peppered moths (Biston betularia) demonstrated strong directional selection against the light colored phenotype. Since that time the levels of airborne pollutants have decreased. To test whether the level of selection has changed you conduct a similar experiment in North American moth species. Use the data from your mark-recapture experiment (given below) to answer the following questions. Assume that wing coloration is controlled by a single locus with two alleles (C and c) and that you can directly infer the underlying genotype of an individual by its color.

Dark wings = homozygote dominant
Medium wings = heterozygote
Light wings = homozygote recessive

Genotype	Marked Sample	Recaptures	expected	Surv Rate (O/E
CC	250	75	125	0.6
Cc	500	225	250	0.9
cc	250	200	125	1.6
Total	1000	500		

a) What is the survival rate for each genotype?

- To calculate the surv rate, first need to figure out how many we expected to recollect
- Remember to assume equal surv in all genotypes
- Since ½ of total surv, should expect ½ of each genotype

b) What are the selection and dominance coefficients?

- After calc surv rate, must scale each to 1.0 to give optimal genotype max fitness

CC $0.6/1.6 = 0.375$
Cc $0.9/1.6 = 0.5625$
cc $1.6/1.6 = 1.0$

- once fitness (absolute) scaled to 1.0
- use following formulas to calc s + h

$W_{cc} = 1-s$
$0.375 = 1-s$
$\boxed{0.625 = s}$

$W_{Cc} = 1-hs$
$0.5625 = 1-h(0.625)$
$\boxed{0.704 = h}$

$W_{cc} = 1.0$

c) Assuming the frequency of the dark allele in this population is freq (C) = p = 0.5 what is the population mean fitness?

if $p = 0.5$;
$p^2 = 0.25$
$2pq = 0.5$
$q^2 = 0.25$

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

$$= 0.25(1.0) + 0.5(0.5625) + 0.25(0.375)$$

$$\boxed{\bar{W} = 0.62375}$$

4. A population of lab mice has been bred in the lab for approximately 500 generations. This population consists of 3 morphs with that have different coat colors, with brown being homozygous dominant, gray being heterozygous, and white being homozygous recessive). The two alleles associated with these phenotypes are B and b, with B being completely dominant to b. The genotype frequencies of these morphs are BB = 0.27, Bb = 0.63, and bb = 0.1.
   a. Given the genotype frequencies what are the allele frequencies in this population?
   b. If the mutation rate of B to b is 0.000017 and b to B is 0.00032, what will the frequencies of each of these alleles be after 3 generations (assuming no other factor is influencing allele frequencies)?
   c. If these mutations rates don't change, will the allele frequenices continue to change in this population indefinitely? Why or why not?
   d. If these allele frequencies will not change indefinitely, what will each frequency be when back mutation finally counterbalances forward mutation?

BB	Bb	bb
0.27	0.63	0.1

* B/c we know freq (or #) of all genotypes, can use this formula

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

$$= 0.27 + \frac{1}{2}(0.63)$$

$$P = 0.585$$

$$\boxed{\begin{array}{l} f(b) = 0.415 \\ f(B) = 0.585 \end{array}}$$

* Remember, im asking for freq of b or B, not p + q. I would likely take a very nominal # of pts for not making this distinction

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

$$= .585(1-0.000017) + (1-.585)(0.00032)$$

$$= 0.584990055 \quad +$$

$$f(B)_{\text{first gen}} = 0.585122855$$

$$P_{t+2} = 0.585122855(1-0.000017) + (1-0.585122855)(0.00032)$$

$$0.5851129079$$

$$P_{t+2} = 0.5852456686$$

$$f(B)_{\text{2nd gen}}$$

$$P_{t+3} = 0.5852456686(1-0.000017) + (1-0.5852456686)(0.00032)$$

$$= 0.5852357194 \quad +$$

$$\boxed{0.5853684408}$$ after 3 Gens

c) Eventually allele freq will reach stable equilib

d) $$\hat{P} = \frac{v}{u+v} = \frac{0.00032}{0.000017 + 0.00032} = \boxed{0.9495548961}$$

equil freq of (B)

$$\boxed{\hat{q} = 0.0504451039}$$

Equilib freq of (b)