

BIOL 368, Fall 2008: Quiz 09/23/2008

25 points + 5 bonus + 5 for take-home. Max score 30.

Write your name at the top of each page. Don't forget to hand in your take-home portion, showing all your working, with your exam. (And make sure your name is on that as well.)

1. Give three conditions that must be met for the Hardy-Weinberg equilibrium to occur in a population. [3 points.]

Any three from:

- (a) **No mutation**
 - (b) **No selection**
 - (c) **Random mating**
 - (d) **No migration/gene flow**
 - (e) **Large population (implying no genetic drift).**
2. In the following equation, the terms w_{AA} , w_{Aa} and w_{aa} represent *fitness*:

$$\bar{w} = p^2 w_{AA} + 2pq w_{Aa} + q^2 w_{aa}$$

- (a) Give an example of a real-world measurement that might be used as a fitness parameter. [1 point.]
Must be an actual measurement, such as “number of offspring”, or “fraction surviving to adulthood.”
- (b) What is \bar{w} ? [1 point.]
Mean fitness of the population.

3. Give one circumstance in which genetic drift often plays a significant role in determining allele frequencies. [1 point.]

Small population size (or “bottleneck”).

4. Why do lethal alleles tend to persist in populations when they are recessive? [2 points.]

When they become rare, it is even *more* rare that heterozygotes will meet and have offspring with a (1/4) change of producing a homozygote recessive who dies. Thus the allele is almost immune from selection. [Must mention selection for full points.]

5. In class, I showed you that fitness is often represented using the following substitutions:

$$w_{AA} = 1 - s \quad w_{Aa} = 1 \quad w_{aa} = 1 - t \quad \bar{w} = 1 - p^2s - q^2t$$

in which case the non-trivial solution for the equilibrium frequency of the *A* allele is given by

$$\hat{p} = \frac{t}{s+t}$$

In one of your readings, the frequency of *Aa* carriers of the sickle-cell trait in some African tribes was reported as being as high as 40% (or 0.4). We know that *aa* genotypes have the sickle-cell *disease*, and die soon after birth. These two pieces of information are all you need to calculate *s* (a measure of how much more fit the *Aa* ‘carrier’ genotype is than the *AA* genotype, due to its resistance to malaria). Calculate *s* below. (*Hint: The information in the question gives you \hat{p} and *t*, but you won’t get it from any formulas. Just think carefully about what \hat{p} must be, given the genotype frequencies, and what a sensible value of *t* might be. Include your reasoning in your answer.*) [4 points.]

If *aa* individuals die, then a sensible value for w_{aa} is 0, in which case $t = 1$.

The fraction of *aa* genotypes in the population is approximately 0 (because they die very quickly). So if *Aa* are 40%, or 0.4, then *AA* must be 60%, or 0.6. This means that in the total pool of alleles, 80%, or 0.8 are *A* (all the 0.6 and half of the 0.4). This is \hat{p} .

We want to know *s*. If $\hat{p} = \frac{t}{s+t}$, then $s = \frac{t}{\hat{p}} - t = \frac{1}{0.8} - 1 = \frac{1-0.8}{0.8} = \frac{0.2}{0.8} = 0.25$.

6. (a) Here are the three compartments of the SIR (Susceptible, Infected, Recovered) disease model. Fill in the flow arrows for the version *with demography*, such as is suitable for a disease like chicken pox. Label the arrows with the rate terms, and then write the model below. [6 points.]

S

I

R

$$\frac{dS}{dt} = \mu - \beta SI - \mu S$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

- (b) Now you are going to construct a modified model for a hypothetical disease which is similar to chicken pox except for one thing: after getting the disease and recovering, individuals are immune for a while but then their immunity wears off and they become susceptible again. Draw the flowchart for this modified model (it will have all same pieces as in (a) above, *plus some extra*), and write the new equations, adding new terms as necessary. [4 points.]

S

I

R

$$\frac{dS}{dt} = \mu + \alpha R - \beta SI - \mu S$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

$$\frac{dR}{dt} = \gamma I - \alpha R - \mu R$$

7. (a) What name is given to R_0 ? [1 point.]

Basic reproductive rate.

- (b) Give a one-sentence description of R_0 . [2 points.]

The average number of new infections caused by a single infected individual in a large population of susceptibles.

or

The overall rate of infection divided by the overall rate of ‘not infection’ in population in which almost all individuals are susceptible.

8. [Bonus.] Calculate \hat{I} , the non-trivial equilibrium level of the disease in question 6. [Up to 5 points. Get as far as you can, and show your working. You will get credit for whatever you get right.]

First, do the easy one. Set $dI/dt = 0$.

$$0 = \beta SI - \gamma I - \mu I$$

Immediately this gives us the trivial solution of $I = 0$. But we can also rearrange to get

$$S = \frac{\gamma + \mu}{\beta}.$$

Alas, I is what we want, not S . So lets set $dR/dt = 0$:

$$0 = \gamma I - \alpha R - \mu R.$$

We can rearrange this to get

$$\gamma I = R(\alpha + \mu).$$

This still has R in it, so it’s not a final solution. But we know that $R = 1 - S - I$, and that $S = (\gamma + \mu)/\beta$. So we make the first substitution,

$$\gamma I = (1 - S - I)(\alpha + \mu),$$

then pull out the I term...

$$\gamma I = (1 - S)(\alpha + \mu) - I(\alpha + \mu)$$

...and move it to the other side:

$$\gamma I + I(\alpha + \mu) = (1 - S)(\alpha + \mu)$$

or

$$I(\gamma + \alpha + \mu) = (1 - S)(\alpha + \mu).$$

Finally we move the non- I stuff back back...

$$I = \frac{(1 - S)(\alpha + \mu)}{\gamma + \alpha + \mu}.$$

...and substitute our term for S :

$$I = \frac{(1 - \frac{\gamma + \mu}{\beta})(\alpha + \mu)}{\gamma + \alpha + \mu}.$$

This is a final solution because S is defined solely in terms of constants.