

# BIOB480/BIOE548 notes 9/24/2024

## Introduction

- Practice problems: another reason to read the book!
- Schedule change: out of town at a conference next week, so no class. Quiz 2 will be an open-book take home assignment due Thursday (but without the possibility of revisions). Thursday's coursework is TBD, but may involve a worksheet, or a video. Who knows! Will post updated syllabus and plan by EOD Thursday.
- Working on HW2, will have it and HW3 graded by end of week.

## Review:

Last class we discussed the impact of mutation on allele frequencies. Key models included the time in  $t$  generations required for allele frequencies to change from  $q_0$  to  $q_t$ :

$$t = \frac{(q_0 - q_t)}{q_0 q_t} = \frac{1}{q_t} - \frac{1}{q_0}$$

... the expected number of mutations in  $n$  genes given mutation rate  $\mu$ :

$$E(\text{no. mutations}) = \mu n$$

... the probability  $n$  genes *all* have mutations:

$$P(\text{all genes have mutations}) = \mu^n$$

... the probability there are *no* mutations in  $n$  genes:

$$P(\text{no genes have mutations}) = (1 - \mu)^n$$

... the frequency of allele  $A_1$  in the next generation given unidirectional mutation to  $A_2$  at rate  $\mu$ :

$$p_1 = p_0(1 - \mu)$$

... the change in frequency of  $A_1$  from generation  $p_0$  to  $p_1$  given unidirectional mutation rate  $\mu$ :

$$\Delta p = -\mu p_0$$

... the number of generations required to go from  $A_1$  allele frequency  $p_0$  to  $p_t$  given mutation rate  $u$ :

$$t = \frac{-\ln(p_0) - \ln(p_t)}{u}$$

... and the equilibrium allele frequencies of  $A_1$  and  $A_2$  given mutation in two directions:

$$\hat{p} = \frac{v}{u + v}; \quad \hat{q} = \frac{u}{u + v}$$

## Mutation-Selection Equilibrium

Next, we incorporate selection. Selection more or less inevitably act on the new mutations that are being continuously added to populations as the majority are deleterious (it's much easier to break something than improve it!). Intuitively, the overall change in the frequency of  $q$  will be equal to its change due to mutation and its change due to selection—a phenomenon known as **mutation-selection equilibrium**, or the balance between the addition of deleterious alleles by mutation and their removal by selection. For a deleterious recessive allele, this is :

$$\Delta q = \Delta q_{\text{mutation}} + \Delta q_{\text{selection}}$$

Assuming a model of simple dominance, we know that deleterious mutations increase as a product of their forward mutation rate ( $u$ ) and frequency ( $p$ ), and decrease at rate determined by the one locus selection models we covered last week ( $\frac{-spq^2}{1-spq^2}$ ). Therefore:

$$\Delta q = up - \frac{spq^2}{1-spq^2}$$

Since  $sq^2$  is an incredible small quantity for rare alleles, the denominator is essentially 1, so

$$\Delta q = up - spq^2$$

By definition, an equilibrium is when inputs (mutations) match outputs (alleles to selection) ( $\Delta q = 0$ ). When this is true,  $up \sim spq^2$ . We can divide both sides of the similarity by  $sp$  to isolate  $q^2$ :

$$0 \sim up + spq^2; \quad up \sim spq^2; \quad \frac{up}{sp} = \frac{u}{s} \sim q^2$$

We then take the square root of the right side of the equation to derive the equilibrium frequency of  $A_2$ :

$$\hat{q} \sim \sqrt{\frac{u}{s}}$$

In plain English, the equilibrium frequency of  $q$  will be the square root of the ratio of mutation from  $A_1$  to  $A_2$  to mutation from  $A_2$  to  $A_1$ . We further know that:

- The equilibrium only depends on the mutation rate and the selection coefficient
- Increased mutation rates will increase the frequency of  $A_2$
- Increased strength of selection against it will decrease it.

Two simple examples:

Q: What is the mutation-selection equilibrium for a recessive lethal allele if the forward mutation rate is  $3 \times 10^{-5}$ ?

A:

$$q \sim \sqrt{\frac{3 \times 10^{-5}}{1}} \sim 0.0054$$

Q: What is the mutation-selection equilibrium for a recessive deleterious allele if the forward mutation rate is  $1 \times 10^{-5}$  and the selection coefficient is 0.1?

A:

$$q \sim \sqrt{\frac{1 \times 10^{-5}}{0.1}} \sim 0.017$$

## Migration-selection equilibrium

In the same vein, we can model the counteracting forces of migration and selection. (Because mutation is rare and only changes allele frequencies very slowly, this will be more important for most scenarios discussed in class). The change in the frequency of allele  $q$  is going to be determined by the proportion of alleles in a population of interest that are contributed by migrants, a variable we call  $m$ , multiplied by the difference in the frequency of  $q$  in the migrant population and the local population:

$$\Delta q = m(q_m - q_0)$$

For example, if migrants are fixed (homogenous) for an allele that is absent from the focal population, and contribute 20% of alleles to the focal population, we expect a change in  $q$  of +0.2 in a single generation:

$$\Delta q = 0.2(1 - 0) = 0.2$$

By similar logic, the frequency of  $q$  in the generation 1 ( $q_1$ ) will be the sum of the product of  $m$  and  $q_m$  and the initial frequency of  $q$  and the proportion of alleles that are NOT migrants, which simplifies to the initial allele frequency plus the migration rate multiplied by the difference between the frequency of  $q$  in the migrant population and focal population:

$$q_1 = (1 - m)q_0 + mq_m = q_0 - mq_0 + mq_m = q_0 + m(q_m - q_0)$$

This gives us the basis for the derivation of  $\Delta q$  above:

$$\Delta q = q_1 - q_0 = (q_0 + m(q_m - q_0)) - q_0 = m(q_m - q_0)$$

As an example of its application, imagine a scenario in which we wish to estimate the migration rate of domestic dog alleles into a wild dog population. We will consider a locus that is *diagnostic* (fixed in one species or population and not the other), treat the new, hybrid population as  $q_0$ ,  $q_1$  as the initial allele frequency of “pure” wild dogs, and  $q_m$  as the allele frequency of domestic dogs:

wild dog	$q_0$	1
hybrid	$q_1$	0.78
dog	$q_m$	0

To do this need to isolate  $m$  from  $q_1 = q_0 + m(q_m - q_0)$ :

$$q_1 = q_0 + m(q_m - q_0) \quad q_1 - q_0 = m(q_m - q_0) \quad \frac{q_1 - q_0}{q_m - q_0} = m \quad m = \frac{0.78 - 1}{0 - 1} = 0.22$$

If migration and selection form an equilibrium allele frequency, what is it? This question is relevant to the analysis of clines and hybrid zones. We again consider the overall change in  $q$  to be the sum of the change in  $q$  due to opposing forces:

$$\Delta q = \Delta q_{\text{selection}} + \Delta q_{\text{migration}}$$