Exercises for population genetics

June 21, 2010

A model of assortative mating

The Hardy-Weinberg law assumes random mating. Often, however, mating is non-random with respect to phenotype or genotype. The following model is based on O'Donald (1960; Heredity 15: 389).

Assume a diploid locus with genotypes AA, Aa and aa. The genotype frequencies in the population are ϕ_{AA}, ϕ_{Aa} and ϕ_{aa}, respectively. The allele frequencies are $p = \phi_{AA} + \phi_{Aa}/2$ for the A allele and $q = \phi_{aa} + \phi_{Aa}/2$ for the a allele. Furthermore, assume that, with probability α, females mate with males having the same genotype as themselves. With probability $1 - \alpha$, they mate randomly (which may include matings with an identical genotype).

Exercise 1. Write down recursions for the change in genotype frequencies due to this mating scheme, using the fact that the offspring produced by random mating follow the Hardy-Weinberg law.

Answer

$$\begin{aligned} \phi'_{AA} &= \alpha(\phi_{AA} + \phi_{Aa}/4) + (1-\alpha)p^2 \\ \phi'_{Aa} &= \alpha\phi_{Aa}/2 + (1-\alpha)2pq \\ \phi'_{aa} &= \alpha(\phi_{aa} + \phi_{Aa}/4) + (1-\alpha)q^2. \end{aligned} \tag{1}$$

Exercise 2. Show that the above mating scheme does not alter allele frequencies.

Answer:

$$\begin{aligned} p' &= \phi'_{AA} + \phi'_{Aa}/2 \\ &= \alpha(\phi_{AA} + \phi_{Aa}/2) + (1-\alpha)(p^2 + p(1-p)) \\ &= \alpha p + (1-\alpha)p = p. \end{aligned} \tag{2}$$

Exercise 3. What is the frequency of heterozygotes at equilibrium?

Answer:

$$\begin{aligned}\phi_{Aa}^* &= \alpha\phi_{Aa}^*/2 + (1-\alpha)2pq \\ \phi_{Aa}^* &= 2pq\frac{1-\alpha}{1-\alpha/2}.\end{aligned} \tag{3}$$

Exercise 4. The "heterozygote deficiency index" $I = 1 - \phi_{Aa}/2pq$ is a measure for the degree of reproductive isolation between the two homozygote genotypes. What is this value at equilibrium, and what does this mean?

Answer:

$$I^* = \frac{\alpha}{2-\alpha}. \tag{4}$$

I^* increases with α and reaches 1 for $\alpha = 1$. That is, if mating occurs only within genotypic groups, heterozygotes are eventually eliminated (because, each generation, half of their offspring are homozygotes), and the two homozygotes can be seen as independent species.

Exercise 5. In a variant of this model, let's assume that assortative mating is based on phenotypes instead of genotypes, and that AA and Aa individuals are phenotypically identical (i.e. allele A is dominant). Show that the new recursion for the heterozygote frequency is

$$\phi'_{Aa} = \alpha\frac{2p\phi_{Aa}}{2p+\phi_{Aa}} + (1-\alpha)2pq \tag{5}$$

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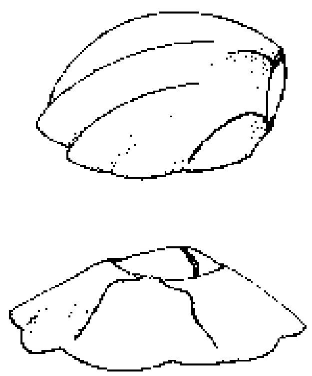
Answer:

$$\begin{aligned}\phi'_{Aa} &= \alpha\frac{\phi_{AA}\phi_{Aa} + \phi_{Aa}^2/2}{\phi_{AA}+\phi_{Aa}} + (1-\alpha)2pq \\ &= \alpha\frac{\phi_{Aa}(\phi_{AA}+\phi_{Aa}/2)}{\phi_{AA}+\phi_{Aa}/2+\phi_{Aa}/2} + (1-\alpha)2pq \\ &= \alpha\frac{p\phi_{Aa}}{p+\phi_{Aa}/2} + (1-\alpha)2pq\end{aligned} \tag{6}$$

The environmental threshold model

Quantitative genetics typically is concerneed with continuous traits. One way to include discrete traits into this framework is via the so-called threshold model, which assumes that an all-or-nothing trait is expressed if an underlying continuous trait exceeds a threshold. This model is appropriate for discrete traits that do not follow simple Mendelian rules. Here, we will focus on a variant of this model that deals with phenotypic responses to environmental stimuli.

Many species possess facultative responses against predators, which are only deployed if predators are actually present. For example, some barncacles develop into a bent morph when exposed to chemical cues from a predatory snail (Lively 1986, Evolution 67: 858).



Here, we assume that the defense is either present or absent, but that the induction threshold (the predator density necessary to trigger induction) is a quantitative trait, which is determined by many genes and is normally distributed in the population. At a given predator density, the defended morph will have either higher or lower fitness than the non-defended one (depending on the costs and benefits of the defense), so in general, the induction threshold will be subject to selection. The evolution of the mean induction threshold can be modeled by the breeder's equation, $R = h^2 S$. Doing so requires calculating the selection differential S, which we will do in the following.

Exercise 6. Assume that, before selection, the induction threshold z is normally distributed with mean $\bar{z} = \mu$ and variance σ^2. An individual expresses the defense if predator density $P > z$. Let undefended individuals have fitness $w_u(P)$ and defended individuals fitness $w_d(P)$. Note that both fitness values are (unspecified) functions of P. We will need the mean values of z for defended and undefended individuals, which are given by

$$\begin{aligned} \bar{z}_u &= \frac{\int_P^\infty z f_\mu(z)dz}{\int_P^\infty f_\mu(z)dz} = \mu + \frac{\sigma^2 f_\mu(P)}{1-d(P)} \\ \bar{z}_d &= \frac{\int_{-\infty}^P z f_\mu(z)dz}{\int_{-\infty}^P f_\mu(z)dz} = \mu - \frac{\sigma^2 f_\mu(P)}{d(P)} \end{aligned} \tag{7}$$

where $f_\mu(.)$ is a normal distribution with mean μ and variance σ^2, and $d(P) = \int_{-\infty}^P f_\mu(z)dz$ is the proportion of defended prey. Calculate the selection differential S.

Answer:

$$\begin{aligned} S &= \frac{w_u(P)}{\bar{w}(P)}(1-d(P))\bar{z}_u + \frac{w_d(P)}{\bar{w}(P)}d(P)\bar{z}_d - \mu \\ &= \frac{1}{\bar{w}(P)}\left[(1-d(P))w_u(P)\left(\mu + \frac{\sigma^2 f_\mu(P)}{1-d(P)}\right) + d(P)w_d(P)\left(\mu - \frac{\sigma^2 f_\mu(P)}{d(P)}\right)\right] - \mu \\ &= \frac{1}{\bar{w}(P)}\left[\mu((1-d(P))w_u(P) + d(P)w_d(P)) + (w_u(P) - w_d(P))\sigma^2 f_\mu(P)\right] - \mu \\ &= \frac{w_u(P) - w_d(P)}{\bar{w}(P)}\sigma^2 f_\mu(P). \end{aligned} \tag{8}$$

where $\bar{w}(P) = (1-d(P))w_u(P) + d(P)w_d(P)$ is the mean fitness for a given predator density. If P is constant, this means that μ will evolve to $\pm\infty$. However, if P is variable, the mean induction threshold will tend to increase when P is low and decrease when P is high.