Stat 551

Homework 2

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1

(a) First, recall that $\sum_i p_i \alpha_i = 0$, or, in the bi-allelic case, $p\alpha_1 + q\alpha_2 = 0$. Using this, we have

$$\begin{aligned}
2pq(\alpha_1 - \alpha_2)^2 &= 2pq(\alpha_1^2 - 2\alpha_1\alpha_2 + \alpha_2^2) \\
&= 2pq\alpha_1^2 - 4pq\alpha_1\alpha_2 + 2pq\alpha_2^2 \\
&= 2p(1-p)\alpha_1^2 - 4pq\alpha_1\alpha_2 + 2q(1-q)\alpha_2^2 \\
&= 2p\alpha_1^2 - 2p^2\alpha_1^2 - 4pq\alpha_1\alpha_2 + 2q\alpha_2^2 - 2q^2\alpha_2^2 \\
&= 2(p\alpha_1^2 + q\alpha_2^2) - 2p^2\alpha_1^2 - 4pq\alpha_1\alpha_2 - 2q^2\alpha_2^2 \\
&= 2(p\alpha_1^2 + q\alpha_2^2) - 2(p^2\alpha_1^2 + 2pq\alpha_1\alpha_2 + q^2\alpha_2^2) \\
&= 2(p\alpha_1^2 + q\alpha_2^2) - 2(\underbrace{p\alpha_1 + q\alpha_2}_{0})^2 \\
&= 2(p\alpha_1^2 + q\alpha_2^2)
\end{aligned}$$

(b) Denoting β_{ij} the breeding value of an individual with genotype A_iA_j, we wish to find $\mathrm{Cov}(\beta, \delta)$, the covariance between breeding values and the dominance effects at a bi-allelic locus.

$$\mathrm{Cov}(\beta, \delta) = \mathbb{E}[\beta\delta] - \mathbb{E}[\beta]\mathbb{E}[\delta]$$

but as we showed in class, $\mathbb{E}[\delta] = 0$. Therefore, we have

$$\begin{aligned}
\mathrm{Cov}(\beta, \delta) &= \mathbb{E}[\beta\delta] \\
&= p^2\beta_{11}\delta_{11} + 2pq\beta_{12}\delta_{12} + q^2\beta_{22}\delta_{22} \\
&= p^2\left(2q\left[a + d(q-p)\right]\right)\left(-2q^2d\right) + 2pq\left((q-p)\left[a + d(q-p)\right]\right)(2pqd) + q^2\left(-2p\left[a + d(q-p)\right]\right)\left(-2p^2d\right) \\
&= \left(-4p^2q^3d + 4p^2q^2(q-p)d + 4p^3q^2d\right)(a + d(q-p)) \\
&= \left(-4p^2q^3d + 4p^2q^3d - 4p^3q^2d + 4p^3q^2d\right)(a + d(q-p)) \\
&= 0
\end{aligned}$$

2

(a) The mean trait value is given by

$$\begin{aligned}
\mu_G &= 1.2p^2 + 1.6 \times 2pq + 0.7q^2 \\
&= 1.2p^2 + 3.2p(1-p) + 0.7(1-p)^2 \\
&= 1.2p^2 + 3.2p - 3.2p^2 + 0.7(1 - 2p + p^2) \\
&= 1.2p^2 + 3.2p - 3.2p^2 + 0.7 - 1.4p + 0.7p^2 \\
&= -1.3p^2 + 1.8p + 0.7
\end{aligned}$$

Maximizing, we have

$$\begin{aligned}\frac{\partial \mu_G}{\partial p} &= -2.6p + 1.8 \\ \Rightarrow p^* &= \frac{9}{13} \approx 0.692\end{aligned}$$

So the frequencies that maximize the mean trait value are $p = \frac{9}{13} \approx 0.692$ (the frequency for A_1) and $q = \frac{4}{13} \approx 0.308$ (the frequency for A_2).
The maximum mean trait value is then

$$\begin{aligned}\mu_G &= 1.2p^2 + 1.6 \times 2pq + 0.7q^2 \\ &\approx 1.323\end{aligned}$$

(b) The minimum mean trait value is obtained when $p = 0$. This is when the allele frequency of A_1 is 0 and the allele frequency of A_2 is 1, yielding a mean trait value of 0.7.

(c) Using our additive model, we have $a = 0.25$ and $d = 0.65$, yielding, when we use $p = p^* \approx 0.692$,

$$\begin{aligned}\alpha_1 &= q\,(a + d(q-p)) = 0 \\ \alpha_2 &= -p\,(a + d(q-p)) = 0\end{aligned}$$

so the additive effects are both 0, and therefore the breeding values and additive variance component are all also 0.

(d) The dominance effects at the locus are

$$\begin{aligned}\delta_{11} &= -2q^2 d \approx -0.123 \\ \delta_{12} &= 2pqd \approx 0.277 \\ \delta_{22} &= -2p^2 d \approx -0.623\end{aligned}$$

which yield a dominance variance component of

$$\sigma_D^2 = (2pqd)^2 \approx 0.0767$$