

# Livestock Breeding and Genomics - Solution 6

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## Problem 1: Parent Offspring Breeding Values

As shown in the course notes, the breeding value  $u_i$  of animal  $i$  can be decomposed into the average of the parent breeding values plus a mendelian sampling term ( $m_i$ ). This means

$$u_i = \frac{1}{2}u_s + \frac{1}{2}u_d + m_i$$

where animal  $i$  has parents  $s$  and  $d$ . The mendelian sampling term  $m_i$  is the deviation of the single breeding value  $u_i$  from the parent average breeding value. Because  $m_i$  is modelled as a deviation, it follows that for a large number ( $N$ ) of offspring from parents  $s$  and  $d$ , the average over all mendelian sampling terms must be 0.

### Your Task

Show that the average mendelian sampling term over a large number of offspring is 0 using a single locus model for the following cases.

**Case 1: Homozygous and Heterozygous Parents** Parent  $s$  with genotype  $G_1G_1$  and parent  $d$  with genotype  $G_1G_2$

**Case 2: Homozygous and Heterozygous Parents** Parent  $s$  with genotype  $G_2G_2$  and parent  $d$  with genotype  $G_1G_2$

**Case 3: Heterozygous Parents** Both parents  $s$  and  $d$  have genotype  $G_1G_2$

### Solution

**Case 1: Homozygous and Heterozygous Parents** Parent  $s$  with genotype  $G_1G_1$  and parent  $d$  with genotype  $G_1G_2$ . The average breeding value of parents  $s$  and  $d$  is

$$\frac{1}{2}(u_s + u_d) = \frac{1}{2}(2q\alpha + (q - p)\alpha) = \frac{3}{2}q\alpha - \frac{1}{2}p\alpha$$

Offspring of parents  $s$  and  $d$  will either be homozygous  $G_1G_1$  or heterozygous both with probability of 1/2. For a homozygous offspring  $i$ , the mendelian sampling term  $m_i$  can be computed as

$$m_i = u_i - \frac{1}{2}[u_s + u_d] = 2q\alpha - \frac{1}{2}[2q\alpha + (q - p)\alpha] = 2q\alpha - \left[\frac{3}{2}q\alpha - \frac{1}{2}p\alpha\right] = \frac{1}{2}q\alpha + \frac{1}{2}p\alpha = \frac{1}{2}\alpha$$

For a heterozygous offspring  $j$ , the mendelian sampling term  $m_j$  is computed as

$$m_j = u_j - \frac{1}{2} [u_s + u_d] = (q - p)\alpha - \left[ \frac{3}{2}q\alpha - \frac{1}{2}p\alpha \right] = -\frac{1}{2}q\alpha - \frac{1}{2}p\alpha = -\frac{1}{2}\alpha$$

Because homozygous and heterozygous offspring occur with equal probability, the average mendelian sampling term over a large number of offspring of parents  $s$  and  $d$  is

$$\frac{1}{2} * \frac{1}{2}\alpha + \frac{1}{2} * \left(-\frac{1}{2}\alpha\right) = 0$$

**Case 2: Homozygous and Heterozygous Parents** Parent  $s$  with genotype  $G_2G_2$  and parent  $d$  with genotype  $G_1G_2$ . The average breeding value of parents  $s$  and  $d$  is

$$\frac{1}{2} (u_s + u_d) = \frac{1}{2} (-2p\alpha + (q - p)\alpha) = \frac{1}{2}q\alpha - \frac{3}{2}p\alpha$$

Offspring of parents  $s$  and  $d$  are either homozygous  $G_2G_2$  or heterozygous both with probability  $1/2$ . For a homozygous offspring  $i$ , the mendelian sampling term  $m_i$  is computed as

$$m_i = u_i - \frac{1}{2} [u_s + u_d] = -2p\alpha - \left[ \frac{1}{2}q\alpha - \frac{3}{2}p\alpha \right] = -\frac{1}{2}p\alpha - \frac{1}{2}q\alpha = -\frac{1}{2}\alpha$$

For a heterozygous offspring  $j$ , the term  $m_j$  is computed as

$$m_j = u_j - \frac{1}{2} [u_s + u_d] = (q - p)\alpha - \left[ \frac{1}{2}q\alpha - \frac{3}{2}p\alpha \right] = \frac{1}{2}q\alpha + \frac{1}{2}p\alpha = \frac{1}{2}\alpha$$

Because homozygous and heterozygous offspring occur both with equal probability, the average mendelian sampling term over a large number of offspring is

$$\frac{1}{2} * \left(-\frac{1}{2}\alpha\right) + \frac{1}{2} * \frac{1}{2}\alpha = 0$$

**Case 3: Heterozygous Parents** Both parents  $s$  and  $d$  have genotype  $G_1G_2$ . Both parents  $s$  and  $d$  are heterozygous and have therefore the same genotype and the same breeding value. Hence the average breeding value of the parents is also the same which is

$$\frac{1}{2} [u_s + u_d] = (q - p)\alpha$$

Offspring of parents  $s$  and  $d$  will be homozygous  $G_1G_1$  or  $G_2G_2$  both with probability  $1/4$  or heterozygous with probability  $1/2$ . For offspring  $i$  with genotype  $G_1G_1$ , the mendelian sampling term  $m_i$  is

$$m_i = u_i - \frac{1}{2} [u_s + u_d] = 2q\alpha - [(q - p)\alpha] = \alpha$$

For offspring  $j$  with genotype  $G_1G_2$ , the mendelian sampling term  $m_j$  is

$$m_j = 0$$

For offspring  $k$  with the genotype  $G_2G_2$ , the mendelian sampling term  $m_k$  is

$$m_k = u_k - \frac{1}{2} [u_s + u_d] = -2p\alpha - [(q - p)\alpha] = -\alpha$$

In the computation of  $m_i$ ,  $m_j$  and  $m_k$ , the definition of the allele substitution effect was used. The average mendelian sampling term over a large number of offsprings of parents  $s$  and  $d$  corresponds to

$$\frac{1}{4} * \alpha + \frac{1}{2} * 0 + \frac{1}{4} * (-\alpha) = 0$$