Livestock Breeding and Genomics - Solution 11

Peter von Rohr

2023-11-24

Problem 1: Inbreeding Coefficient

Because of very low amounts of harvested corn and grains at the end of the 18th century in central Europe, many farmers were forced to leave their contry and find a new home in the USA. In 1810 a group of farmers took a population of about 200 animals and moved to the US. After the arrival, the group formed 4 subgroups and settled in the states of Wisconsin, Virginia, Texas and California. The animals were equally partitioned to the subgroups. After the partion into the subpopulations, the animals were bred independently in the four different lines. In 1960, semen from bulls of the partitioned subpopulations was re-imported to Europe.

Assumptions

- Although, cattle does not follow the same mode of inheritance as the organism shown in the lecture, the computations as shown in the lecture can be used as an approximation.
- The ratio of the number of female animals to the total population size can be assumed to be 0.5.
- In contrast to the size N of the subpopulations that was assumed to be the number of individuals, here N is the number of female animals in a given subpopulation.
- The generation interval can be assumed to be 10 years.

Your Task:

- Compute the inbreeding coefficient F_t for the bulls from which semen was re-imported back into Europe.

Solution

From the lecture the inbreeding coefficient (F_t) can be computed as

$$F_t = 1 - (1 - \Delta F)^t$$

with ΔF corresponding to $1/(2N)$ where N is the number of female animals in any of the subpopulations. The variable t corresponds to the number of generations. Inserting all the quantities in

$$F_t = 1 - (1 - 0.02)^{15} = 0.2614$$

Problem 2: Inbreeding Depression

Use the same assumptions as in Problem 1 and compute the inbreeding depression caused by the inbreeding coefficient computed in Problem 1 at two different genetic loci.

a. Locus A is purely additive with a genotypic value of $a = 25$. Hence the genotypic value of the heterozygous genotype is in the middle between the values of the two homozygous genotypes. In other words, the quantity $d = 0$. The minor allele frequency (MAF) of the positive allele of locus A is $p = 0.1$

b. Locus B where the valud of the heterozygous genotypes $B_1 B_2$ is 10 units above the mean of the homozygous genotypes, hence you can set the quantity $d = 10$. The minor allele frequency of the positive allele of locus B is $p = 0.05$.

Solution

In the general the inbreeding depression is computed as

$$M_0 - M_F = 2d\bar{p}\bar{q}F$$

a. For an additive locus, $d = 0$ and hence the inbreeding depression for that locus is 0.

b. For locus B, the inbreeding depression is

$$M_0 - M_F = 2 * 10 * 0.05 * (1 - 0.05) * 0.2614309 = 0.2484$$

Problem 3: Genetic additive Variance

Compute the between-line, the within-line and the total genetic variance for the population described in Problem 1 and the locus A of Problem 2a.

Solution

The different variance components can be computed as shown by the following ANOVA (analysis of variance) table.

Source	Variance
Between lines	$2FV_G$
Within lines	$(1 - F)V_G$
Total	$(1 + F)V_G$

The variance V_G corresponds to the genetic additive variance in the base population and is computed as

$$V_G = 2p_0 q_0 a^2 = 2 * 0.1 * (1 - 0.1) * 25^2 = 112.5$$

The three variance components are computed using the inbreeding coefficient and V_G

Source	Variance	Values
Between lines	$2FV_G$	58.82195
Within lines	$(1 - F)V_G$	83.08902
Total	$(1 + F)V_G$	141.91098