Livestock Breeding and Genomics - Exercise 5

Peter von Rohr

2018-10-26

Prediction of Breeding Values Using the Regression Method

We are using the dataset shown in Table 1 for this exercise. For the animals listed in Table 1, the weaning weight (in 100kg) was observed as phenotypic records. The following parameters are associated with the observed data

- The population mean is assumed to be equal to the average of all observations: $\mu = 2.5$
- The phenotypic variance is assumed to correspond to the empirical variance from the observations and corresponds to $\sigma_p^2 = 0.1014$
- The heritability is assumed to be $h^2 = 0.25$
- The genetic-additive variance can be computed as $\sigma_a^2 = h^2 * \sigma_p^2 = 0.25 * 0.1014 = 0.0254$

Table 1: Example Data Set To Predict Breeding Values

Animal	Sire	Weaning Weight
12	1	2.61
13	1	2.31
14	1	2.44
15	1	2.41
16	1	2.51
17	1	2.55
18	1	2.14
19	1	2.61
20	2	2.34
21	2	1.99
22	2	3.10
23	2	2.81
24	2	2.14
25	2	2.41
26	3	2.54
27	3	3.16

Problem 1: Own performance

Compute the predicted breeding values and the reliabilities for the animals listed in Table 1. Compare the ranking of the animals according to their phenotypic values and according to their predicted breeding values. Compare the reliabilities of the predicted breeding values.

Problem 2: Predicted Breeding Values Based on Progeny Records

Compute the predicted breeding values and the reliabilities for the sires based on the progeny records. We are assuming that all progeny for a given sire are half-sibbs. Compare the ranking of the sires according to the average progeny performance values and according to the predicted breeding values.