

Livestock Breeding and Genomics - Exercise 4

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Problem 1: Prediction of Breeding Value and Reliability

Heifer Elsa has a weaning weight of 320 kg. The population mean of the same trait is at 250 kg. The heritability (h^2) of the trait weaning weight is assumed to be 0.45.

- What is the predicted breeding value \hat{a}_i for Elsa for weaning weight?
- Compute the reliability of \hat{a}_i from 1a)

Problem 2: Breeding Value Prediction Based on Repeated Observations

Besides the weaning weight Elsa has also an observation for her birth weight (52 kg) and some more repeated measures for her weight. We assume the heritability ($h^2 = 0.45$) to be the same as in Problem 1. The population mean for the repeated observations of the weight is 170 kg. The repeatability of the weight measurements is $t = 0.65$.

The following tables contains all observed values for the weight.

Measurement	Weight
1	52
2	82
3	112
4	141
5	171
6	201
7	231
8	260
9	290
10	320

- Predict the breeding value for Elsa based on the repeated weight records.
- What is the reliability for the predicted breeding value from 2a)?
- Compare the reliability from 2b) with the reliability from Problem 1.

Problem 3: Predicted Breeding Value and Confidence Interval

During the lecture, the concept of **reliability** (B) was introduced as a measure for the accuracy of a breeding value. The reliability corresponds to the squared correlation coefficient of the true breeding value (a) and the selection criterion (y). Hence

$$B = r_{a,y}^2$$

An alternative to the reliability, we can also use the standard deviation $\sqrt{\text{var}(\hat{a})}$ of the predicted breeding value to assess the accuracy of a predicted breeding value. This standard deviation of the predicted breeding values can be used to compute confidence intervals. These intervals indicate how accurate the predicted

breeding value is. A narrow confidence interval means that the predicted breeding value has a high accuracy. Each confidence interval is associated with an error probability. A very common value of an error probability is $\alpha = 0.05$. This leads to a 95%-confidence interval.

For a predicted breeding value \hat{a} the following procedure can be used to compute the 95%-confidence interval. So far, we have used the regression method to predict breeding values. With that method the predicted breeding value is expressed as a function of the phenotypic observations (y). In our model that links the true breeding values to the phenotypic observations, we have seen that the phenotypes (y) are random variables which follow a certain distribution. The normal distribution is a reasonable assumption for the distribution of the phenotypic observations. As a consequence the predicted breeding values follow also a normal distribution. This distribution has its center at the predicted breeding value and the variance ($var(\hat{a})$) can be computed with the prediction equation for a .

In problem 1 where the breeding value was predicted based on an own performance records, the standard deviation $\sqrt{var(\hat{a})}$ of the predicted breeding value can be computed as follows. We assume the phenotypic standard deviation for weaning weight is 20 kg.

$$\sqrt{var(\hat{a})} = \sqrt{var(b(y - \mu))} = b\sqrt{var(y)} = h^2\sqrt{var(y)} = 0.45 * 20 = 9$$

Based on the properties of the normal distribution 95% of the probability mass are within ± 1.96 standard deviations around the expected value. Therefore the lower (ug) and the upper (og) limits of the 95%-confidence interval are defined as

$$ug = \hat{a} - 1.96 * \sqrt{var(\hat{a})} = 31.5 \text{ kg} - 1.96 * 9 \text{ kg} = 13.86 \text{ kg}$$

$$og = \hat{a} + 1.96 * \sqrt{var(\hat{a})} = 31.5 \text{ kg} + 1.96 * 9 \text{ kg} = 49.14 \text{ kg}$$

Your Task

Compute the 95%-confidence interval for the predicted breeding values in Problem 2.

Problem 4: Response To Selection

Assuming that we select for the predicted breeding value based on repeated measures, the response to that selection schema per generation can be computed as

$$R = i * r_{a,\bar{y}}^2 * \sigma_{\bar{y}}$$

Compute the response to selection R for the results that you found in Problem 2. The selection intensity i can be assumed to be 1.4 and the phenotypic standard deviation is taken to be the same value as in Problem 3, $\sigma_y = 20$.