

Livestock Breeding and Genomics - Solution 8

Peter von Rohr

2020-11-13

Problem 1: Importance of Accuracy

The importance of the accuracy of predicted breeding values is different between livestock species and even between farmers within the same breeding organisation. When considering the selection response per year as a relevant criterion for comparing different selection strategies, there is a clear trade-off between accuracy of predicted breeding values and length of the generation interval. The selection response per year is defined as

$$\Delta_G = \frac{i * r_{u,\hat{u}} * \sigma_u}{L}$$

where i is the selection intensity, $r_{u,\hat{u}}$, σ_u is the genetic additive variance and L denotes the generation interval. Assume the values for i to be 1.4 and for σ to be 16. Compute the selection response Δ_G for the accuracies and the generation intervals given in the following table.

Accuracy	Generation Interval	Selection Response
0.45	2.0	
0.50	2.5	
0.55	3.0	
0.60	3.5	
0.65	4.0	
0.70	4.5	
0.75	5.0	
0.80	5.5	
0.85	6.0	
0.90	6.5	

Solution

We use the above given formula to compute Δ_G and fill out the table

Accuracy	Generation Interval	Selection Response
0.45	2.0	5.04
0.50	2.5	4.48
0.55	3.0	4.11
0.60	3.5	3.84
0.65	4.0	3.64
0.70	4.5	3.48
0.75	5.0	3.36
0.80	5.5	3.26
0.85	6.0	3.17

0.90

6.5

3.10

These results show that an increase in accuracy is not worth while to accept a longer generation interval, when looking at the selection response.

Problem 2: Decomposition of Predicted Breeding Values

Given is the following dataset.

Animal	Sire	Dam	Observation
1	NA	NA	20.09
2	NA	NA	11.32
3	NA	NA	16.40
4	1	2	20.25
5	4	3	11.49

Predict the breeding value for animal 4 once with the sire model and then with the animal model and see what is the difference between the two predicted breeding values based on the decomposition of the respective mixed model equation. The variances are given in the following table

Component	Variance
Residual	24
Additive Genetic	8
Sire	2

The residual variance-covariance matrix R is assumed to have a simple structure, meaning that we can write

$$R = I * \sigma_e^2$$

Solution

The breeding values for animal 4 is once estimated with a sire model and once with an animal model.

Sire Model The sire model for the given data set looks as follows

$$y = X\mu + Zs + e$$

Putting the information from the dataset into the model leads to

$$y = \begin{bmatrix} 20.09 \\ 11.32 \\ 16.4 \\ 20.25 \\ 11.49 \end{bmatrix}, X = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}, Z_s = \begin{bmatrix} 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 1 & 0 \\ 0 & 1 \end{bmatrix}, s = \begin{bmatrix} s_1 \\ s_4 \end{bmatrix}, e = \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \\ e_5 \end{bmatrix}$$

and μ is just a scalar parameter.

The mixed model equations for the sire model have the following structure

$$\begin{bmatrix} X^T X & X^T Z_s \\ Z_s^T X & Z_s^T Z_s + G_s^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mu} \\ \hat{s} \end{bmatrix} = \begin{bmatrix} X^T y \\ Z_s^T y \end{bmatrix}$$

Setting $G_s^{-1} = \lambda_s * A_s^{-1}$ with $\lambda_s = \sigma_e^2 / \sigma_s^2$ and A_s is the numerator relationship between the sires. Because we have 2 sires the matrix A_s will have dimension 2×2 . The diagonal elements are 1 and the offdiagonal element is derived from the covariance between s_1 and s_4 . From the pedigree, we know that 1 is the father of 4. For the covariance between s_1 and s_4 this means

$$\text{cov}(s_1, s_4) = \text{cov}(s_1, (\frac{1}{2}s_1 + e_4)) = \frac{1}{2}\text{cov}(s_1, s_1) = \frac{1}{2}\sigma_s^2$$

Hence

$$A_s = \begin{bmatrix} 1 & 0.5 \\ 0.5 & 1 \end{bmatrix}$$

The inverse A_s^{-1} is

$$A_s^{-1} = \begin{bmatrix} 1.33333333333333 & -0.666666666666667 \\ -0.666666666666667 & 1.33333333333333 \end{bmatrix}$$

Inserting the matrices into the mixed model equations

$$\begin{bmatrix} 5 & 1 & 1 \\ 1 & 17 & -8 \\ 1 & -8 & 17 \end{bmatrix} \begin{bmatrix} \hat{\mu} \\ \hat{s}_1 \\ \hat{s}_4 \end{bmatrix} = \begin{bmatrix} 79.55 \\ 20.25 \\ 11.49 \end{bmatrix}$$

When looking at the last equation, we can see that

$$1 * \hat{\mu} - 8 * \hat{s}_1 + 17 * \hat{s}_4 = y_5$$

Solving this for \hat{s}_4 leads to

$$\hat{s}_4 = \frac{1}{17} [y_5 - \hat{\mu} + 8\hat{s}_1]$$

The predicted breeding value of animal 4 depends on the observation y_5 of its progeny, the estimate of the global mean $\hat{\mu}$ and on the predicted breeding value of the sire of animal 4.

The numeric values of the solutions are given by

$$\begin{bmatrix} \hat{\mu} \\ \hat{s}_1 \\ \hat{s}_4 \end{bmatrix} = \begin{bmatrix} 15.9119 \\ 0.1705 \\ -0.1799 \end{bmatrix}$$

Animal Model

The animal model is given as

$$y = X\mu + Zu + e$$

Putting the information from the data into the model leads to

$$Z = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}, u = \begin{bmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \\ u_5 \end{bmatrix}$$

The other components are the same as in the sire model. The mixed model equations for the animal model have the following structure

$$\begin{bmatrix} X^T X & X^T Z \\ Z^T X & Z^T Z_s + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mu} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^T y \\ Z^T y \end{bmatrix}$$

The matrix G^{-1} is computed as $G^{-1} = \lambda * A^{-1}$ where $\lambda = \sigma_e^2 / \sigma_u^2 = 24/8 = 3$ and A corresponds to the numerator relationship matrix. Its inverse A^{-1} is

$$A^{-1} = \begin{bmatrix} 1.5 & 0.5 & 0 & -1 & 0 \\ 0.5 & 1.5 & 0 & -1 & 0 \\ 0 & 0 & 1.5 & 0.5 & -1 \\ -1 & -1 & 0.5 & 2.5 & -1 \\ 0 & 0 & -1 & -1 & 2 \end{bmatrix}$$

The mixed model equation are then

$$\begin{bmatrix} 5 & 1 & 1 & 1 & 1 & 1 \\ 1 & 5.5 & 1.5 & 0 & -3 & 0 \\ 1 & 1.5 & 5.5 & 0 & -3 & 0 \\ 1 & 0 & 0 & 5.5 & 1.5 & -3 \\ 1 & -3 & -3 & 1.5 & 8.5 & -3 \\ 1 & 0 & 0 & -3 & -3 & 7 \end{bmatrix} \begin{bmatrix} \hat{\mu} \\ \hat{u}_1 \\ \hat{u}_2 \\ \hat{u}_3 \\ \hat{u}_4 \\ \hat{u}_5 \end{bmatrix} = \begin{bmatrix} 79.55 \\ 20.09 \\ 11.32 \\ 16.4 \\ 20.25 \\ 11.49 \end{bmatrix}$$

When looking at the second but last equation in the mixed model equations, we get

$$\hat{\mu} - 3\hat{u}_1 - 3\hat{u}_2 + 1.5\hat{u}_3 + 8.5\hat{u}_4 - 3\hat{u}_5 = y_4$$

Solving for \hat{u}_4 gives

$$\hat{u}_4 = \frac{1}{8.5} [y_4 - \hat{\mu} + 3\hat{u}_1 + 3\hat{u}_2 - 1.5\hat{u}_3 + 3\hat{u}_5]$$

The numerical solution is

$$\begin{bmatrix} \hat{\mu} \\ \hat{u}_1 \\ \hat{u}_2 \\ \hat{u}_3 \\ \hat{u}_4 \\ \hat{u}_5 \end{bmatrix} = \begin{bmatrix} 15.9256 \\ 1.2782 \\ -0.9143 \\ -0.3638 \\ 0.498 \\ -0.5762 \end{bmatrix}$$

For the animal model, this shows that with the animal model all available information is used to predict the breeding value \hat{u}_4 . The following information is contained in the above equation

- own performance record y_4
- the estimate $\hat{\mu}$
- the predicted breeding values \hat{u}_1 and \hat{u}_2 of the parents
- the predicted breeding value \hat{u}_3 of the mate and
- the predicted breeding value \hat{u}_5 .

In contrast to that in the sire model the predicted breeding value \hat{s}_4 depends only on

- the performance record y_5 of the offspring
- the estimate $\hat{\mu}$
- the predicted breeding value \hat{s}_1 of the sire

With the sire model predicted breeding values depend on the performance records of progeny. Furthermore, the female side is not considered at all. These are the main differences between the two models.