

# Livestock Breeding and Genomics - Solution 12

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2023-12-01

## Problem 1: Accuracy of Predicted Breeding Values

Use the dataset given below to predict breeding values for the response variable `Weight` using a BLUP animal model. The model contains `Herd` as fixed effect and `BreastCircumference` as regression covariate. Compute reliabilities ( $B\%$ ) for all predicted breeding values.

### Hints

- The phenotypic variance  $\sigma_p^2$  can be computed from the variance of the weight values given in the dataset.
- Heritability ( $h^2$ ) is assumed to be 0.25 for the trait `Weight`.

### Data

The dataset is available from

```
## https://charlotte-ngs.github.io/lbgfs2023/data/beef_data_blup.csv
```

### Solution

- Read the data

```
tbl_beef <- readr::read_delim(s_beef_data_path, delim = ",")
```

```
## Rows: 15 Columns: 6
## -- Column specification -----
## Delimiter: ","
## dbl (6): Animal, Sire, Dam, BreastCircumference, Herd, Weight
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

- Specify the linear mixed effects model

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

with vectors  $y$ : observations,  $\beta$ : fixed regression coefficient of `BreastCircumference` and fixed herd-effects,  $u$ : random breeding values,  $e$ : random residuals. Matrix  $X$  links covariates and fixed effects to observations and matrix  $Z$  related breeding values to observations.

Expected values of the random components are

$$E \begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} X\beta \\ 0 \\ 0 \end{bmatrix}$$

Variance-Covariance matrices of the random components are

$$\text{var} \begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} V & ZG & R \\ GZ^T & G & 0 \\ R & 0 & R \end{bmatrix}$$

with  $R = I * \sigma_e^2$ ,  $G = A\sigma_u^2$  and  $V = ZGZ^T + R$ . Matrix  $A$  is the numerator relationship matrix based on the pedigree and  $\sigma_e^2$  and  $\sigma_u^2$  are given variance components.

- Setup the mixed model equations (MME)

Mixed model equations for BLUE of  $\beta$  and BLUP of  $u$  are given by

$$\begin{bmatrix} X^T X & X^T Z \\ Z^T X & Z^T Z + \lambda * A^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^T y \\ Z^T y \end{bmatrix}$$

Information from data are inserted to the MME. Start with matrix  $X$

```
matX <- model.matrix(lm(Weight ~ 0 + BreastCircumference + as.factor(Herd), data = tbl_beef))
attr(matX,"assign") <- NULL
attr(matX,"contrasts") <- NULL
dimnames(matX) <- NULL
```

For matrix  $Z$ , we have to complete the pedigree

```
vec_fnd_sire <- setdiff(tbl_beef$Sire, tbl_beef$Animal)
vec_fnd_sire <- vec_fnd_sire[!is.na(vec_fnd_sire)]
vec_fnd_dam <- setdiff(tbl_beef$Dam, tbl_beef$Animal)
vec_fnd_dam <- vec_fnd_dam[!is.na(vec_fnd_dam)]
vec_fnd <- c(vec_fnd_sire, vec_fnd_dam)
n_nr_fnd <- length(vec_fnd)
n_nr_obs <- nrow(tbl_beef)
matZ <- cbind(matrix(rep(0, n_nr_fnd*n_nr_obs), nrow = n_nr_obs),
               diag(nrow = n_nr_obs))
```

The inverse numerator relationship  $A^{-1}$  is computed based on the pedigree

```
n_nr_ani <- n_nr_fnd + n_nr_obs
ped <- pedigreeemm::pedigree(sire = c(rep(NA, n_nr_fnd), tbl_beef$Sire),
                             dam = c(rep(NA, n_nr_fnd), tbl_beef$Dam),
                             label = c(1:n_nr_ani))
matA_inv <- as.matrix(pedigreeemm::getAInv(ped = ped))
```

```
## 'as(<dtMatrix>, "dtCMatrix")' is deprecated.
## Use 'as(., "CsparseMatrix")' instead.
## See help("Deprecated") and help("Matrix-deprecated").
```

The coefficient matrix and the right-hand-sides of the MME are

```
lambda <- (1-n_h2_weight) / n_h2_weight
mat_coef <- rbind(cbind(crossprod(matX), crossprod(matX, matZ)),
                  cbind(crossprod(matZ, matX), crossprod(matZ) + lambda * matA_inv))
vec_y <- tbl_beef$Weight
mat_rhs <- rbind(crossprod(matX, vec_y),
                 crossprod(matZ, vec_y))
mat_sol <- solve(mat_coef, mat_rhs)
mat_sol
```

```
##           [,1]
## 8.732302e+00
## -1.068146e+03
## -1.083529e+03
## -1.101438e+03
## 1  1.313321e+00
## 2 -2.114677e+00
## 3  1.524946e-01
## 4  2.757089e-01
## 5 -6.930179e-01
## 6 -1.594902e-01
## 7  2.757169e-01
## 8  9.499436e-01
## 9  8.854023e-01
## 10 6.245173e-01
## 11 8.252461e-01
## 12 1.478646e+00
## 13 5.187407e-01
## 14 4.999237e-01
## 15 -1.838960e+00
## 16 -3.993777e-02
## 17 -1.157909e+00
## 18 -2.820549e+00
## 19 -1.219582e+00
## 20 1.775756e+00
## 21 1.325188e+00
## 22 1.405062e+00
## 23 5.855898e-01
```

- Get estimates of fixed effects and predictions of breeding values from solutions of MME

Estimates for the fixed effects are:

```
n_nr_sol <- nrow(mat_sol)
n_nr_fix <- n_nr_sol - n_nr_ani
mat_sol[1:n_nr_fix,]
```

```
##
##      8.732302 -1068.145601 -1083.529349 -1101.438311
```

Predicted breeding values are:

```
mat_sol[(n_nr_fix + 1):n_nr_sol,]
```

```
##           1           2           3           4           5           6           7           8
##  1.31332085 -2.11467663  0.15249457  0.27570891 -0.69301795 -0.15949022  0.27571692  0.94994357  0.8
##           10           11           12           13           14           15           16           17
##  0.62451727  0.82524613  1.47864635  0.51874075  0.49992374 -1.83895972 -0.03993777 -1.15790882 -2.8
##           19           20           21           22           23
## -1.21958208  1.77575637  1.32518772  1.40506154  0.58558977
```

- Compute accuracies from inverse of coefficient matrix of MME

The above computed coefficient matrix corresponds to the simplified version. The prediction error variance is obtained from the inverse of the general form of the coefficient matrix. To get from the simplified to the general form, we have to divide by  $\sigma_e^2$ .

```
var_p <- var(tbl_beef$Weight)
var_e <- (1-n_h2_weight) * var_p
mat_coef_gen <- mat_coef / var_e
mat_coef_inv <- solve(mat_coef_gen)
mat_C22 <- mat_coef_inv[(n_nr_fix + 1):n_nr_sol, (n_nr_fix + 1):n_nr_sol]
vec_diag_C22 <- diag(mat_C22)
vec_inb <- pedigreeemm::inbreeding(ped = ped)
vec_ui <- n_h2_weight * var_p * (1+vec_inb)
vec_Bi <- 1 - vec_diag_C22 / vec_ui
```

The reliabilities (B%) of all animals in the pedigree are

```
100 * vec_Bi
```

```
##           1           2           3           4           5           6           7           8           9           10
##  5.069176  7.966395  6.562853 10.749386 13.928471  9.250136  8.756655 10.145390 16.738259 15.252424
##           12           13           14           15           16           17           18           19           20           21
##  9.417269 16.598186 16.746823 13.976110 16.080150 16.596515 16.892141 12.029691 21.305430 17.693402
##           23
## 16.180493
```