Livestock Breeding and Genomics - Solution 12

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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 σ_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, β: 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

$$E \left[\begin{array}{c} y \\ u \\ e \end{array}\right] = \left[\begin{array}{c} X\beta \\ 0 \\ 0 \end{array}\right]$$

Variance-Covariance matrices of the random components are

$$var \left[\begin{array}{c} y \\ u \\ e \end{array}\right] = \left[\begin{array}{ccc} V & ZG & R \\ GZ^T & G & 0 \\ R & 0 & R \end{array}\right]$$

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 σ_e^2 and σ_u^2 are given variance components.

- Setup the mixed model equations (MME)

Mixed model equations for BLUE of β and BLUP of u are given by

$$\left[\begin{array}{lr} X^TX & X^TZ \\ Z^TX & Z^TZ + \lambda * A^{-1} \end{array}\right] \left[\begin{array}{c} \hat{\beta} \\ \hat{u} \end{array}\right] = \left[\begin{array}{c} X^Ty \\ Z^Ty \end{array}\right]$$

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 <- pedigreemm::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 <- pedigreemm::getAInv(ped = ped)
```

```
## 'as(<dtTMatrix>, "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]
##  [1,]  8.732302e+00
##  [2,] -1.068146e+03
##  [3,] -1.083529e+03
##  [4,] -1.101438e+03
##  [5,]  1.313321e+00
##  [6,] -2.114677e+00
##  [7,]  1.524946e-01
##  [8,]  2.757089e-01
##  [9,] -6.930179e-01
## [10,] -1.594902e-01
## [11,]  2.757169e-01
## [12,]  9.499436e-01
## [13,]  8.854023e-01
## [14,]  6.245173e-01
## [15,]  8.252461e-01
## [16,]  1.478646e+00
## [17,]  5.187407e-01
## [18,]  4.999237e-01
## [19,] -1.838960e+00
## [20,] -3.993777e-02
## [21,] -1.157909e+00
## [22,] -2.820549e+00
## [23,] -1.219582e+00
## [24,]  1.775756e+00
## [25,]  1.325188e+00
## [26,]  1.405062e+00
## [27,]  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,]
```

```
## [1]     8.732302 -1068.145601 -1083.529349 -1101.438311
```

Predicted breeding values are:

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

```
##  [1]  1.31332085 -2.11467663  0.15249457  0.27570891 -0.69301795 -0.15949022
##  [7]  0.27571692  0.94994357  0.88540227  0.62451727  0.82524613  1.47864635
## [13]  0.51874075  0.49992374 -1.83895972 -0.03993777 -1.15790882 -2.82054922
## [19] -1.21958208  1.77575637  1.32518772  1.40506154  0.58558977
```

- Compute accuracies from inverse of coefficient matrix of MME