Livestock Breeding and Genomics - Solution 11

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2021-12-03

Data

```r
nr_animal <- 5
tbl_decomp <- tibble::tibble(Animal = c(1:nr_animal),
                             Sire = c(NA, NA, NA, 1, 4),
                             Dam = c(NA, NA, NA, 2, 3),
                             Trait = c(4.5, 2.9, 3.9, 3.5, 5.0))
tbl_decomp
```

```
## # A tibble: 5 x 4
##   Animal  Sire   Dam Trait
##    <int> <dbl> <dbl> <dbl>
## 1      1    NA    NA   4.5
## 2      2    NA    NA   2.9
## 3      3    NA    NA   3.9
## 4      4     1     2   3.5
## 5      5     4     3   5
```

Model

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

Components

```r
X = matrix(1, nrow = nr_animal, ncol = 1)
X
```

```
##      [,1]
## [1,]    1
## [2,]    1
## [3,]    1
## [4,]    1
## [5,]    1
```

```r
Z = diag(1, nrow = nr_animal)
Z
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    1    0    0    0
## [3,]    0    0    1    0    0
## [4,]    0    0    0    1    0
```

```
## [5,]    0    0    0    0    1
```

Pedigree

```r
ped = pedigreemm::pedigree(sire = tbl_decomp$Sire,
                           dam = tbl_decomp$Dam,
                           label = as.character(1:nr_animal))
Ainv <- as.matrix(pedigreemm::getAInv(ped = ped))
Ainv
```

```
##      1    2    3    4  5
## 1  1.5  0.5  0.0 -1.0  0
## 2  0.5  1.5  0.0 -1.0  0
## 3  0.0  0.0  1.5  0.5 -1
## 4 -1.0 -1.0  0.5  2.5 -1
## 5  0.0  0.0 -1.0 -1.0  2
```

MME

```r
xtx <- crossprod(X)
xtx
```

```
##      [,1]
## [1,]    5
```

```r
xtz <- crossprod(X, Z)
xtz
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    1    1    1    1
```

```r
ztx <- crossprod(Z, X)
ztx
```

```
##      [,1]
## [1,]    1
## [2,]    1
## [3,]    1
## [4,]    1
## [5,]    1
```

```r
ztz <- crossprod(Z)
ztz
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    1    0    0    0
## [3,]    0    0    1    0    0
## [4,]    0    0    0    1    0
## [5,]    0    0    0    0    1
```

```r
sigmae2 <- 40
sigmau2 <- 20
lambda <- sigmae2/sigmau2
lambda
```

```
## [1] 2
```

```
ztzainvlambda <- ztz + Ainv * lambda
ztzainvlambda
```

```
##    1  2  3  4  5
## 1  4  1  0 -2  0
## 2  1  4  0 -2  0
## 3  0  0  4  1 -2
## 4 -2 -2  1  6 -2
## 5  0  0 -2 -2  5
```

```
coef_mat <- rbind(cbind(xtx, xtz), cbind(ztx, ztzainvlambda))
coef_mat
```

```
##      1  2  3  4  5
##   5  1  1  1  1  1
## 1 1  4  1  0 -2  0
## 2 1  1  4  0 -2  0
## 3 1  0  0  4  1 -2
## 4 1 -2 -2  1  6 -2
## 5 1  0  0 -2 -2  5
```

```
y <- tbl_decomp$Trait
xty <- crossprod(X,y)
zty <- crossprod(Z,y)
rhs <- rbind(xty, zty)
rhs
```

```
##      [,1]
## [1,] 19.8
## [2,]  4.5
## [3,]  2.9
## [4,]  3.9
## [5,]  3.5
## [6,]  5.0
```

Solutions

```
sol <- solve(coef_mat, rhs)
sol
```

```
##          [,1]
##    3.92136986
## 1  0.20091324
## 2 -0.33242009
## 3  0.13150685
## 4 -0.05369863
## 5  0.24684932
```

Problem 1: Decomposition

From the lecture, we know how the predicted breeding value of animal $4 can be decomposed into different components. Verify this decomposition based on the solutions obtained above.

Solution

The decomposition is given as follows:

$$\hat{u}_4 = \frac{1}{6}\left[y_4 - \hat{\mu} + 2 * (\hat{u}_1 + \hat{u}_2) - \hat{u}_3 + 2\hat{u}_5\right]$$

This can be verified as follows

```
(tbl_decomp$Trait[4] - sol[1] + 2 * (sol[2]+sol[3]) - sol[4] + 2*sol[6])/6
```

```
## [1] -0.05369863
```

The breeding value of animal 4 is

```
sol[5]
```

```
## [1] -0.05369863
```

Problem 2: Reliabilities

Compute the reliabilities of all the predicted breeding values. The reliability B_i of the predicted breeding value for animal i is computed as

$$B_i = 1 - \frac{(C^{22})_{ii}}{var(u_i)}$$

```
C <- solve(coef_mat) * sigmae2
C
```

```
##                     1         2         3         4         5
##   15.726027 -6.849315 -6.849315 -6.301370 -9.260274 -9.369863
## 1 -6.849315 15.433790  2.100457  2.465753  8.493151  5.753425
## 2 -6.849315  2.100457 15.433790  2.465753  8.493151  5.753425
## 3 -6.301370  2.465753  2.465753 15.068493  3.013699  8.493151
## 4 -9.260274  8.493151  8.493151  3.013699 16.602740  9.698630
## 5 -9.369863  5.753425  5.753425  8.493151  9.698630 17.150685
```

The lower right corner C^{22} is

```
nr_fixed_effect <- ncol(X)
nr_sol <- nrow(sol)
C22 <- C[(nr_fixed_effect+1):nr_sol, (nr_fixed_effect+1):nr_sol]
C22
```

```
##           1         2         3         4         5
## 1 15.433790  2.100457  2.465753  8.493151  5.753425
## 2  2.100457 15.433790  2.465753  8.493151  5.753425
## 3  2.465753  2.465753 15.068493  3.013699  8.493151
## 4  8.493151  8.493151  3.013699 16.602740  9.698630
## 5  5.753425  5.753425  8.493151  9.698630 17.150685
```

The diagonal elements of C^{22}

```
C22ii <- diag(C22)
C22ii
```

```
##        1        2        3        4        5
## 15.43379 15.43379 15.06849 16.60274 17.15068
```

The reliabilities are

```r
B <- 1 - C22ii / sigmau2
B
```

```
##         1         2         3         4         5
## 0.2283105 0.2283105 0.2465753 0.1698630 0.1424658
```