# Livestock Breeding and Genomics - Solution 8

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# **Problem 1: Numerator Relationship Matrix**

Construct the numerator relationship matrix A for the following pedigree and verify the result using the function getA() from package pedigreemm.

 Table 1: Pedigree For Constructing Numerator Relationship Matrix

Sire	Dam
1	2
1	3
4	5
4	5
4	6
4	6
	1 1 4 4

# Solution

The numerator relationship is constructed using the following step-wise procedure. The following rules are used to compute the single elements.

- Case 1: If both parents s and d of animal i are known then
  - the diagonal element  $(A)_{ii}$  corresponds to:  $(A)_{ii} = 1 + F_i = 1 + \frac{1}{2}(A)_{sd}$  and
  - the offdiagonal element  $(A)_{ji}$  is computed as:  $(A)_{ji} = \frac{1}{2}((A)_{js} + \tilde{(A)}_{jd})$
  - because A is symmetric  $(A)_{ji} = (A)_{ij}$
- Case 2: If only one parent s is known and assumed unrelated to the mate

$$- (A)_{ii} = 1 - (A)_{ii} = (A)_{ii} = \frac{1}{2}((A)_{i})$$

$$-(A)_{ij} = (A)_{ji} = \frac{1}{2}((A)_{js})$$

• Case 3: If both parents are unknown

$$-(A)_{ii} = 1$$
  
-(A)...-(A)...

$$- (A)_{ij} = (A)_{ji} = 0$$

# Step 1

First, we extend the pedigree given in Table 1. All animals without parents are added at the top of the pedigree. This results in the matrix shown in Table 2.

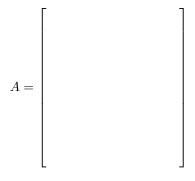
Animal	Sire	Dam
1	NA	NA
2	NA	NA
3	NA	NA
4	NA	NA
5	1	2
6	1	3

7	4	5
8	4	5
9	4	6
10	4	6

Because the pedigree in Table 2 is already ordered such that parents are before offspring, we can directly go to the next step.

#### Step 2

We start with an empty numerator relationship matrix A. The matrix A has dimensions  $10 \times 10$ 



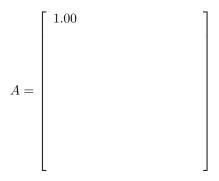
## Step 3

The single elements of A are computed according to the rules listed above.

The computation is started with animal 1. The first element is always the diagonal-element that corresponds to animal that we are currently looking at. For animal 1 the diagonal element is  $(A)_{11}$ . Because animal 1 has not parents, we are in case 3 for the diagonal element. If an animal has unknown parents, it also means that the animals's inbreeding coefficient  $F_i$  is 0. Hence

$$(A)_{11} = 1$$

Now we have the first element of our numerator relationship matrix.



#### Step 4

The next elements that need to be computed are the off-diagnoal element on row 1. Elements  $A_{12}$ ,  $A_{13}$  and  $A_{14}$  correspond to the additive genetic relationship between animal 1 and animals 2, 3 and 4. Because animals 2, 3 and 4 all have unknown parents, we are for all three elements in case 3, hence we can state

$$(A)_{12} = (A)_{13} = (A)_{14} = 0$$

For the remaining elements of the first row of A, the elements correspond to the additive genetic relationship between animal 1 and animals 5 to 10. Because animals 5 to 10 all have known parents, we have to use case 1 in the above formulated rules.

$$(A)_{15} = \frac{1}{2} ((A)_{11} + (A)_{12}) = \frac{1}{2} (1+0) = 0.5$$
$$(A)_{16} = \frac{1}{2} ((A)_{11} + (A)_{13}) = \frac{1}{2} (1+0) = 0.5$$
$$(A)_{17} = \frac{1}{2} ((A)_{14} + (A)_{15}) = \frac{1}{2} (0+0.5) = 0.25$$
$$(A)_{18} = \frac{1}{2} ((A)_{14} + (A)_{15}) = \frac{1}{2} (0+0.5) = 0.25$$
$$(A)_{19} = \frac{1}{2} ((A)_{14} + (A)_{16}) = \frac{1}{2} (0+0.5) = 0.25$$
$$(A)_{110} = \frac{1}{2} ((A)_{14} + (A)_{16}) = \frac{1}{2} (0+0.5) = 0.25$$

As a result, we have the first row of  ${\cal A}$ 

	1.00	0.00	0.00	0.00	0.50	0.50	0.25	0.25	0.25	0.25
A =										
71 —										
	L									-

# Step 5

Copy the first row to the first column

	1.00	0.00	0.00	0.00	0.50	0.50	0.25	0.25	0.25	0.25
	0.00									
	0.00									
	0.00									
4	0.50									
A =	0.50									
	0.25									
	0.25									
	0.25									
	$\begin{array}{c} 1.00\\ 0.00\\ 0.00\\ 0.00\\ 0.50\\ 0.50\\ 0.25\\ 0.25\\ 0.25\\ 0.25\\ 0.25\\ 0.25\\ \end{array}$									

# Step 6

Continue the same way with rows 2 to 10

## Verification

We first have to specify the pedigree, before being able to get the numerator relationship matrix

```
n_nr_animals <- 10
suppressPackageStartupMessages( library(pedigreemm) )
ped <- pedigree(sire = c(NA,NA,NA,1,1,4,4,4,4),</pre>
                dam = c(NA, NA, NA, NA, 2, 3, 5, 5, 6, 6),
                label = as.character(1:n_nr_animals))
mata ex8p1 verify <- getA(ped = ped)</pre>
mata_ex8p1_verify
## 10 x 10 sparse Matrix of class "dsCMatrix"
##
      [[ suppressing 10 column names '1', '2', '3' ... ]]
##
## 1 1.00 .
                         0.500 0.500 0.2500 0.2500 0.2500 0.2500
                     .
                .
                     .
           1.00 .
                         0.500 .
                                      0.2500 0.2500 .
## 2
      .
                1.00 .
                                0.500 .
## 3
                                                     0.2500 0.2500
      .
           .
                          .
                                             .
                   1.0 .
## 4
                                .
                                      0.5000 0.5000 0.5000 0.5000
                .
## 5 0.50 0.50 .
                         1.000 0.250 0.5000 0.5000 0.1250 0.1250
                     .
## 6
      0.50 .
                0.50 .
                         0.250 1.000 0.1250 0.1250 0.5000 0.5000
## 7 0.25 0.25 .
                     0.5 \ 0.500 \ 0.125 \ 1.0000 \ 0.5000 \ 0.3125 \ 0.3125
## 8 0.25 0.25 .
                     0.5 0.500 0.125 0.5000 1.0000 0.3125 0.3125
## 9 0.25 .
                0.25 \ 0.5 \ 0.125 \ 0.500 \ 0.3125 \ 0.3125 \ 1.0000 \ 0.5000
```

**##** 10 0.25 . 0.25 0.5 0.125 0.500 0.3125 0.3125 0.5000 1.0000

In the above result all elements which are 0 are represented by a dot.

# Problem 2: BLUP Animal Model

Use the following dataset to predict breeding values for all animals.

Animal	Sire	Dam	Herd	Observation
5	1	2	1	16.77
6	1	3	1	20.04
7	4	5	1	18.39
8	4	5	2	5.43
9	4	6	2	11.92
10	4	6	2	7.36

Table 3: Data for Animal Model

## Assumptions

- Random residuals are un-correlated and they all have equal variance  $\sigma_e^2$  which is assumed to be 24.
- The additive genetic variance  $\sigma_a^2$  is assumed to be 8.
- The pedigree is the same as in Problem 1. You can use solve() in R or pedigreemm::getAInv() to invert A.

## Your Tasks

- Specify all components including expected values and variances of the animal model using the information from the dataset.
- Set up mixed model equations
- Solve mixed model equations for estimates of fixed effects and for predicted breeding values

#### Solution

The animal model in general has the following form

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

where

- y vector of length n of observations
- $\beta$  vector of length p of unknown fixed effects
- $X \quad n \times p$  design matrix linking fixed effects to observations
- a vector of length q of unkown random breeding values
- $Z = n \times q$  design matrix linking breeding values to observations
- e vector of length n of unknown random residuals

The expected values of the fixed effects  $\beta$  are the fixed effects themselves, hence  $E(\beta) = \beta$ . The expected values of the random components are defined as

$$E(a) = 0$$
$$E(e) = 0$$
$$E(y) = X\beta$$

The variances of fixed effects are always 0. Based on the assumption of uncorrelated residuals, we know that  $var(e) = I\sigma_e^2$ . Because, we have an animal model, we also know that  $var(a) = A\sigma_a^2$  where A corresponds to the numerator relationship matrix. In summary, the variances of the random effects are

$$var(a) = G = A\sigma_a^2$$
$$var(e) = R = I\sigma_e^2$$
$$var(y) = ZGZ^T + R$$

Inserting the information from the dataset into the model gives the following results.

- Vector of observations
- $y = \begin{bmatrix} 16.77\\ 20.04\\ 18.39\\ 5.43\\ 11.92\\ 7.36 \end{bmatrix}$
- Herds as fixed effects. We have two herds, hence vector  $\beta$  has length p = 2. Component  $\beta_1$  will denote the effect of the first herd and component  $\beta_2$  the effect of the second herd.

$$X = \begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 0 & 1 \end{bmatrix}, \beta = \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix}$$

• Breeding values as random effects. In total, there are 10 animals in the pedigree and hence the length of the vector a is q = 10.

• The vector of random residuals is just

$$e = \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \\ e_5 \\ e_6 \end{bmatrix}$$

The solutions for  $\hat{\beta}$  and  $\hat{a}$  are obtained by solving the mixed model equations. The mixed model equations for the animal model and under the assumptions specified above are defined as

$$\left[\begin{array}{cc} X^T X & X^T Z \\ Z^T X & Z^T Z + \lambda * A^{-1} \end{array}\right] \left[\begin{array}{c} \hat{\beta} \\ \hat{a} \end{array}\right] = \left[\begin{array}{c} X^T y \\ Z^T y \end{array}\right]$$

The single components are computed as

$A^{-1} =$	$\begin{bmatrix} 2.0\\ 0.5\\ 0.5\\ 0.0\\ -1.0\\ 0.0\\ 0.0\\ 0.0\\ 0.0\\ 0.0 \end{bmatrix}$	$\begin{array}{c} 0.5 \\ 1.5 \\ 0.0 \\ 0.0 \\ -1.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \end{array}$	$\begin{array}{c} 0.5 \\ 0.0 \\ 1.5 \\ 0.0 \\ 0.0 \\ -1.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \end{array}$	$-1.0 \\ -1.0$	$-1.0 \\ 0.0 \\ 1.0 \\ 3.0 \\ 0.0 \\ -1.0 \\ -1.0 \\ 0.0$	$\begin{array}{c} 0.0 \\ -1.0 \\ 1.0 \\ 0.0 \\ 3.0 \\ 0.0 \\ 0.0 \\ -1.0 \end{array}$	$\begin{array}{c} 0.0\\ 0.0\\ -1.0\\ -1.0\\ 0.0\\ 2.0\\ 0.0\\ 0.0\\ 0.0\\ 0.0\\ 0.0\\ \end{array}$	$\begin{array}{c} 0.0 \\ -1.0 \\ 0.0 \\ 0.0 \\ 2.0 \\ 0.0 \end{array}$	$\begin{array}{c} 0.0 \\ -1.0 \\ 0.0 \\ -1.0 \\ 0.0 \\ 0.0 \\ 2.0 \end{array}$	$\begin{array}{c} 0.0 \\ 0.0 \\ 0.0 \\ -1.0 \\ 0.0 \\ -1.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 2.0 \end{array}$	
	L 0.0	0.0 X	0.0		0.0	-1.0	$\begin{array}{c} 0.0\\ 0.00\\ 0.00\\ 0.00\\ 16.77\\ 20.04\\ 18.39\\ 5.43\\ 11.92\\ 7.36\\ \end{array}$	0.0	0.0	2.0	]

Putting everything together into the mixed model equations leads to the following results

3.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	1.0	0.0	0.0	0.0		55.20
0.0	3.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	1.0		24.71
0.0	0.0	6.0	1.5	1.5	0.0	-3.0	-3.0	0.0	0.0	0.0	0.0		0.00
0.0	0.0	1.5	4.5	0.0	0.0	-3.0	0.0	0.0	0.0	0.0	0.0		0.00
0.0	0.0	1.5	0.0	4.5	0.0	0.0	-3.0	0.0	0.0	0.0	0.0		0.00
0.0	0.0	0.0	0.0	0.0	9.0	3.0	3.0	-3.0	-3.0	-3.0	-3.0	$\begin{bmatrix} \hat{\beta} \end{bmatrix}$	0.00
1.0	0.0	-3.0	-3.0	0.0	3.0	10.0	0.0	-3.0	-3.0	0.0	0.0	$\begin{vmatrix} \hat{a} \end{vmatrix} =$	16.77
1.0	0.0	-3.0	0.0	-3.0	3.0	0.0	10.0	0.0	0.0	-3.0	-3.0		20.04
1.0	0.0	0.0	0.0	0.0	-3.0	-3.0	0.0	7.0	0.0	0.0	0.0		18.39
0.0	1.0	0.0	0.0	0.0	-3.0	-3.0	0.0	0.0	7.0	0.0	0.0		5.43
0.0	1.0	0.0	0.0	0.0	-3.0	0.0	-3.0	0.0	0.0	7.0	0.0		11.92
0.0	1.0	0.0	0.0	0.0	-3.0	0.0	-3.0	0.0	0.0	0.0	7.0		7.36
-											-	•	

The solutions are computed as

The solutions are

$\hat{\beta}_1$		[ 18.4889 ]		
$\hat{\beta}_2$		8.1439		
$\hat{a}_1$		-0.0116		
$\hat{a}_2$	=	-0.3593		
$\hat{a}_3$		=		0.3478
$\hat{a}_4$				0.0231
$\hat{a}_5$			-0.5448	
$\hat{a}_6$			0.5159	
$\hat{a}_7$			-0.2377	
$\hat{a}_8$			-0.6113	
$\hat{a}_9$		0.7704		
$\hat{a}_{10}$		0.1190		
L 10 1				