Livestock Breeding and Genomics - Solution 10

Peter von Rohr

2023-11-24

Problem 1: Inverse Numerator Relationship Matrix

During the lecture the method of computing the inverse numerator relationship matrix A^{-1} directly was introduced. The computation is based on the LDL-decomposition. As a result, we can write

$$A^{-1} = (L^T)^{-1} \cdot D^{-1} \cdot L^{-1}$$

where $L^{-1} = I - P$, and D^{-1} is a diagonal matrix with $(D^{-1})_{ii} * \sigma_u^{-2} = var(m_i)^{-1}$.

Tasks

- Use the example pedigree given below and compute the matrices L^{-1} and D^{-1} to compute A^{-1}
- Verify your result using the function getAinv() from package pedigreemm.

Pedigree

```
## # A tibble: 6 x 3
##
      Calf Sire
     <int> <dbl> <dbl>
## 1
         1
              NA
                    NA
## 2
         2
              NA
                    NA
## 3
         3
              NA
                    NA
         4
              1
         5
## 5
               3
                     2
## 6
```

Solution

The matrix P comes from the simple decomposition and can be constructed using the pedigree.

```
P = matrix(0, nrow = nr_animal, ncol = nr_animal)
for (i in 1:nr_animal){
    s <- tbl_pedigree$Sire[i]
    d <- tbl_pedigree$Dam[i]
    if (!is.na(s)){
        P[i,s] <- 0.5
    }
    if(!is.na(d)){
        P[i,d] <- 0.5
    }
}</pre>
```

```
##
       [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]
       0.0 0.0 0.0 0.0 0.0
## [2,]
       0.0 0.0 0.0 0.0
                          0.0
                                0
## [3,]
       0.0 0.0 0.0 0.0
                          0.0
                                0
## [4,]
       0.5 0.5 0.0 0.0
                          0.0
                                0
## [5,]
       0.0 0.5 0.5 0.0 0.0
                                0
## [6,]
       0.0 0.0 0.0 0.5 0.5
                                0
```

With that the matrix L^{-1} is

```
I <- diag(1, nrow = nr_animal, ncol = nr_animal)
Linv <- I - P
Linv</pre>
```

```
[,1] [,2] [,3] [,4] [,5] [,6]
## [1,] 1.0 0.0 0.0 0.0 0.0
## [2,]
       0.0 1.0 0.0 0.0
                          0.0
                                 0
## [3,]
       0.0 0.0 1.0 0.0 0.0
                                 0
## [4,] -0.5 -0.5 0.0 1.0 0.0
                                 0
## [5,]
       0.0 -0.5 -0.5 0.0 1.0
                                 0
## [6,]
       0.0 0.0 0.0 -0.5 -0.5
                                 1
```

The matrix D is obtained from the cholesky decomposition of the numerator relationship matrix A and can later be verified by the package <code>pedigreemm</code>. The details on how the matrix D can be obtained from the cholesky decomposition are given in Appendix C of the course notes available at: https://charlottengs.github.io/lbgfs2023/cn/A3_decomp_num_rel_mat.pdf.

```
## [,1] [,2] [,3] [,4] [,5] [,6]
## [1,] 1 0 0 0 0 0
## [2,] 0 1 0 0 0 0
```

```
## [3,]
                     1
                           0
## [4,]
           0
                0
                      0
                           2
                                0
                                      0
## [5,]
                                2
                                      0
## [6,]
                                      2
           0
                0
                      0
                                0
```

The verification via pedigreemm can be done as:

```
D <- pedigreemm::Dmat(ped = ped)
Dinv <- diag(1/D, nrow = nr_animal, ncol = nr_animal)
Dinv</pre>
```

```
##
         [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]
                 0
                            0
                                  0
                                       0
            1
                       0
## [2,]
                                       0
            0
                            0
## [3,]
            0
                 0
                            0
                                  0
                                       0
                       1
## [4,]
           0
                 0
                       0
                            2
                                  0
                                       0
## [5,]
           0
                 0
                       0
                            0
                                  2
                                       0
## [6,]
```

The inverse numerator relationship matrix is

```
Ainv <- t(Linv) %*% Dinv %*% Linv
Ainv
```

```
## [,1] [,2] [,3] [,4] [,5] [,6]

## [1,] 1.5 0.5 0.0 -1.0 0.0 0

## [2,] 0.5 2.0 0.5 -1.0 -1.0 0

## [3,] 0.0 0.5 1.5 0.0 -1.0 0

## [4,] -1.0 -1.0 0.0 2.5 0.5 -1

## [5,] 0.0 -1.0 -1.0 0.5 2.5 -1

## [6,] 0.0 0.0 0.0 -1.0 -1.0 2
```

Verification

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

```
## 6 x 6 Matrix of class "dgeMatrix"

## 1 2 3 4 5 6

## 1 1.5 0.5 0.0 -1.0 0.0 0

## 2 0.5 2.0 0.5 -1.0 -1.0 0

## 3 0.0 0.5 1.5 0.0 -1.0 0

## 4 -1.0 -1.0 0.0 2.5 0.5 -1

## 5 0.0 -1.0 -1.0 0.5 2.5 -1

## 6 0.0 0.0 0.0 -1.0 -1.0 2
```

Problem 2: Rules

The following diagram helps to illustrate the rules for constructing A^{-1}

1	D^{-1}	L^{-1}
	[,1] [,2] [,3] [,4] [,5] [,6] [1,] 1 0 0 0 0 0 [2,] 0 1 0 0 0 0 [3,] 0 0 1 0 0 0 [4,] 0 0 0 2 0 0 [5,] 0 0 0 0 2 0 [6,] 0 0 0 0 2	[,1] [,2] [,3] [,4] [,5] [,6] [1,] 1.0 0.0 0.0 0.0 0.0 0 [2,] 0.0 1.0 0.0 0.0 0.0 0 [3,] 0.0 0.0 1.0 0.0 0.0 0 [4,] -0.5 -0.5 0.0 1.0 0.0 0 [5,] 0.0 -0.5 -0.5 0.0 1.0 0 [6,] 0.0 0.0 0.0 0.0 -0.5 -0.5 1
[,1] [,2] [,3] [,4] [,5] [,6] [1,] 1 0 0 -0.5 0.0 0.0 [2,] 0 1 0 -0.5 -0.5 0.0 [3,] 0 0 1 0.0 -0.5 0.0 [4,] 0 0 0 1.0 0.0 -0.5 [5,] 0 0 0 0.0 1.0 -0.5 [6,] 0 0 0 0.0 1.0 -0.5	[,1] [,2] [,3] [,4] [,5] [,6] [1,] 1 0 0 -1 0 0 [2,] 0 1 0 -1 -1 0 [3,] 0 0 1 0 -1 0 [4,] 0 0 0 2 0 -1 [5,] 0 0 0 0 2 -1 [6,] 0 0 0 0 2	[,1] [,2] [,3] [,4] [,5] [,6] [1,] 1.5 0.5 0.0 -1.0 0.0 0 [2,] 0.5 2.0 0.5 -1.0 -1.0 0 [3,] 0.0 0.5 1.5 0.0 -1.0 0 [4,] -1.0 -1.0 0.0 2.5 0.5 -1 [5,] 0.0 -1.0 -1.0 0.5 2.5 -1 [6,] 0.0 0.0 0.0 -1.0 -1.0 2
$(L^T)^{-1}$	$(L^T)^{-1} \cdot D^{-1}$	A^{-1}

Tasks

- Go through the list of animals in the pedigree and write down the contributions that are made to the different elements of matrix A^{-1}
- Based on the different contributions, try to come up with some general rules

Solution

In what follows, we use the following convention $\delta_i = (D^{-1})_{ii}$.

Animal 1

We start with animal 1.

1	D^{-1}	L^{-1}
	[1,1] [,2] [,3] [,4] [,5] [,6] [1,1]	[1,1] [,2] [,3] [,4] [,5] [,6] [1,1] 1.0 0.0 0.0 0.0 0.0 0 0 0 0 0 0 0 0 0 0
[1,1] [,2] [,3] [,4] [,5] [,6] [1,1] 1 0 0 -0.5 0.0 0.0 [2,1] 0 1 0 -0.5 -0.5 0.0 [3,1] 0 0 1 0.0 -0.5 0.0 [4,1] 0 0 0 1.0 0.0 -0.5 [5,1] 0 0 0 0.0 1.0 -0.5 [6,1] 0 0 0 0.0 0.0 1.0	[1,] [,2] [,3] [,4] [,5] [,6] [1,] 1 0 0 -1 0 0 [2,] 0 1 0 -1 -1 0 [3,] 0 0 1 0 -1 0 [4,] 0 0 0 2 0 -1 [5,] 0 0 0 0 2 -1 [6,] 0 0 0 0 2	[,1] [,2] [,3] [,4] [,5] [,6] [1,1] [1.5] 0.5 0.0 -1.0 0.0 0 [2,] 0.5 2.0 0.5 -1.0 -1.0 0 [3,] 0.0 0.5 1.5 0.0 -1.0 0 [4,] -1.0 -1.0 0.0 2.5 0.5 -1 [5,] 0.0 -1.0 1.0 0.5 2.5 -1 [6,] 0.0 0.0 0.0 -1.0 -1.0 2
$(L^T)^{-1}$	$(L^T)^{-1} \cdot D^{-1}$	A^{-1}

Animal 1 has no parents and therefore the diagonal element $\delta_1 = (D^{-1})_{11}$ of matrix D^{-1} is $\delta_1 = 1$. By looking at the red boxes, we can see that δ_1 is added as a contribution to $(A^{-1})_{11}$. So far we are still missing a contribution of 0.5 to the element $(A^{-1})_{11}$. Again by inspecting the red boxes in the above diagram, we can see that this contribution corresponds to $\delta_4/4$ which comes from offspring 4 of parent 1. Hence diagonal elements of $(A^{-1})_{ss}$ corresponding to parents s of offsprint i receive $\delta_i/4$ as contribution. More details on that is obtained when inspecting the contributions of animal 4. Animals 2 and 3 do not have parents and are therefore analogous to animal 1.

Animal 4

Animal 4 has parents 1 and 2.

$$D^{-1} \qquad \qquad L^{-1}$$

The red boxes in the above diagram show that for animal 4 there is a contribution of δ_4 to the diagonal. Then there are contributions of $\delta_4/4$ for the elements $(A^{-1})_{11}$, $(A^{-1})_{22}$, $(A^{-1})_{12}$ and $(A^{-1})_{21}$. Furthermore there are negative contributions of $\delta_4/2$ to $(A^{-1})_{41}$, $(A^{-1})_{14}$, $(A^{-1})_{24}$ and $(A^{-1})_{42}$.

General Rules

From this the general rules which were first published by Henderson can be deduced as

- Both Parents Known
 - add δ_i to the diagonal-element (i, i)
 - add $-\delta_i/2$ to off-diagonal elements (s,i), (i,s), (d,i) and (i,d)
 - add $\delta_i/4$ to elements (s,s), (d,d), (s,d), (d,s)
- Only One Parent Known
 - add δ_i to diagonal-element (i, i)
 - add $-\delta_i/2$ to off-diagonal elements (s,i), (i,s)
 - add $\delta_i/4$ to element (s,s)
- Both Parents Unknown
 - add δ_i to diagonal-element (i, i)

Problem 3: Program using the Rules

Write a program in R that implements the rules found in the solution of Problem 2. Test your program with the pedigree given in Problem 1. Compare the results that you obtain with the result obtained from the function pedigreemm::getAinv().

Solution

The function takes one input parameter which is the pedigree.

```
get_A_inverse <- function(ptbl_pedigree){</pre>
  # first get values of matrix D
  ped <- pedigreemm::pedigree(sire = ptbl_pedigree$Sire,</pre>
                              dam = ptbl_pedigree$Dam,
                              label = as.character(ptbl pedigree$Calf))
  vec_diag_matD <- pedigreemm::Dmat(ped = ped)</pre>
  vec_delta <- 1/vec_diag_matD</pre>
  # initialize Ainv
  nr_animal <- nrow(ptbl_pedigree)</pre>
  mat_result_ainv <- matrix(data = 0, nrow = nr_animal, ncol = nr_animal)</pre>
  # loop over animals and add contributions to Ainv according to Hendersons rules
  for (idx in 1:nr animal){
    # contribution for animal
    mat_result_ainv[idx,idx] <- mat_result_ainv[idx,idx] + vec_delta[[idx]]</pre>
    n_parent_s <- ptbl_pedigree$Sire[idx]</pre>
    if (!is.na(n_parent_s)){
      mat_result_ainv[idx,n_parent_s] <- mat_result_ainv[idx,n_parent_s] - vec_delta[[idx]]/2</pre>
      mat_result_ainv[n_parent_s,idx] <- mat_result_ainv[n_parent_s,idx] - vec_delta[[idx]]/2</pre>
      mat_result_ainv[n_parent_s,n_parent_s] <- mat_result_ainv[n_parent_s,n_parent_s] +</pre>
        vec_delta[[idx]]/4
    }
    # parent d
    n_parent_d <- ptbl_pedigree$Dam[idx]</pre>
    if (!is.na(n_parent_d)){
      mat_result_ainv[idx,n_parent_d] <- mat_result_ainv[idx,n_parent_d] - vec_delta[[idx]]/2
      mat_result_ainv[n_parent_d,idx] <- mat_result_ainv[n_parent_d,idx] - vec_delta[[idx]]/2</pre>
      mat_result_ainv[n_parent_d,n_parent_d] <- mat_result_ainv[n_parent_d,n_parent_d] +</pre>
        vec_delta[[idx]]/4
    }
    # both parents
    if (!is.na(n_parent_s) && !is.na(n_parent_d)){
     mat_result_ainv[n_parent_d,n_parent_s] <- mat_result_ainv[n_parent_d,n_parent_s] +</pre>
       vec delta[[idx]]/4
     mat_result_ainv[n_parent_s,n_parent_d] <- mat_result_ainv[n_parent_s,n_parent_d] +</pre>
       vec_delta[[idx]]/4
    }
  return(mat_result_ainv)
```

The function $\mathtt{get_A_inverse}()$ is tested with the pedigree from Problem 1.

```
(mat_A_inv <- get_A_inverse(ptbl_pedigree = tbl_pedigree))

##     [,1] [,2] [,3] [,4] [,5] [,6]

## [1,] 1.5 0.5 0.0 -1.0 0.0 0

## [2,] 0.5 2.0 0.5 -1.0 -1.0 0

## [3,] 0.0 0.5 1.5 0.0 -1.0 0

## [4,] -1.0 -1.0 0.0 2.5 0.5 -1

## [5,] 0.0 -1.0 -1.0 0.5 2.5 -1

## [6,] 0.0 0.0 0.0 -1.0 -1.0 2

mat_A_inv - as.matrix(pedigreemm::getAInv(ped = ped))

## 1 2 3 4 5 6

## 1 0 0 0 0 0 0 0

## 2 0 0 0 0 0 0</pre>
```