

Livestock Breeding and Genomics - Solution 7

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Pedigree

```
nr_animal <- 6
tbl_pedigree <- tibble::tibble(Calf = c(1:nr_animal),
                              Sire = c(NA, NA, NA, 1, 3, 4),
                              Dam = c(NA, NA, NA, 2, 2, 5))

tbl_pedigree

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

Numerator Relationship Matrix

We call the numerator relationship matrix A . The computation of the elements of A are done separately for

1. the diagonal elements $(A)_{ii}$ and
2. the off-diagonal elements $(A)_{ij}$ for $i \neq j$

First all elements of the matrix A are initialized to 0

```
A = matrix(0, nrow = nr_animal, ncol = nr_animal)
A
```

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

Diagonal Elements

Computation: $(A)_{ii} = (1 + F_i)$ and $F_i = 1/2(A)_{sd}$

```
i <- 1
s <- tbl_pedigree$Sire[i]
```

```

d <- tbl_pedigree$Dam[i]

Fi <- ifelse((is.na(s) | is.na(d)), 0, 0.5 * A[s,d])
A[i,i] <- 1+Fi
A
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]  1   0   0   0   0   0
## [2,]  0   0   0   0   0   0
## [3,]  0   0   0   0   0   0
## [4,]  0   0   0   0   0   0
## [5,]  0   0   0   0   0   0
## [6,]  0   0   0   0   0   0

```

Off-diagonal Elements

Off-diagonal $(A)_{ij} = 1/2(A)_{io} + 1/2(A)_{iq}$ where o and q are parents of j

```

for (j in (i+1):6){
  o <- tbl_pedigree$Sire[j]
  q <- tbl_pedigree$Dam[j]
  Aio <- ifelse(is.na(o), 0, A[i,o])
  Aiq <- ifelse(is.na(q), 0, A[i,q])
  A[i,j] <- 0.5 * Aio + 0.5 * Aiq
}
A[(i+1):6,i] <- A[i,(i+1):6]
A

```

```

##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,] 1.00  0   0  0.5  0  0.25
## [2,] 0.00  0   0  0.0  0  0.00
## [3,] 0.00  0   0  0.0  0  0.00
## [4,] 0.50  0   0  0.0  0  0.00
## [5,] 0.00  0   0  0.0  0  0.00
## [6,] 0.25  0   0  0.0  0  0.00

```

Problem 1: Numerator Relationship Matrix

Use the above steps of computation for the complete matrix.

Hint

- Construct a loop with loop-variable i that runs over all the rows of the matrix A .

Solution

Combining both steps for all elements

```

nr_animal <- nrow(tbl_pedigree)

# Init matrix
A <- matrix(0, nrow = nr_animal, ncol = nr_animal)

# loop over all rows
for (i in 1:nr_animal){

```

```

# diagonal element
s <- tbl_pedigree$Sire[i]
d <- tbl_pedigree$Dam[i]
Fi <- ifelse((is.na(s) | is.na(d)), 0, 0.5 * A[s,d])
A[i,i] <- 1+Fi

# off-diagonal element
if (i < nr_animal){
  for (j in (i+1):nr_animal){
    o <- tbl_pedigree$Sire[j]
    q <- tbl_pedigree$Dam[j]
    Aio <- ifelse(is.na(o), 0, A[i,o])
    Aiq <- ifelse(is.na(q), 0, A[i,q])
    A[i,j] <- 0.5 * Aio + 0.5 * Aiq
  }
  A[(i+1):nr_animal,i] <- A[i,(i+1):nr_animal]
}
}
A

```

```

##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,] 1.00  0.0 0.00 0.500 0.000 0.250
## [2,] 0.00  1.0 0.00 0.500 0.500 0.500
## [3,] 0.00  0.0 1.00 0.000 0.500 0.250
## [4,] 0.50  0.5 0.00 1.000 0.250 0.625
## [5,] 0.00  0.5 0.50 0.250 1.000 0.625
## [6,] 0.25  0.5 0.25 0.625 0.625 1.125

```

Check Result

The function `getA()` of the `pedigreemm` package can be used to check the result

```

ped <- pedigreemm::pedigree(sire = tbl_pedigree$Sire,
                           dam = tbl_pedigree$Dam,
                           label = as.character(1:nr_animal))
pedigreemm::getA(ped = ped)

```

```

## 6 x 6 sparse Matrix of class "dsCMatrix"
##      1  2  3  4  5  6
## 1 1.00 .  .  0.500 .  0.250
## 2 .  1.0 .  0.500 0.500 0.500
## 3 .  .  1.00 .  0.500 0.250
## 4 0.50 0.5 .  1.000 0.250 0.625
## 5 .  0.5 0.50 0.250 1.000 0.625
## 6 0.25 0.5 0.25 0.625 0.625 1.125

```