

Example Pedigree

Definition of pedigree in package pedigreeemm

```
ped <- pedigreeemm::pedigree(sire = c(NA,NA,NA,1,3,4),
                             dam  = c(NA,NA,NA,2,2,5),
                             label = as.character(1:6))

ped
```

```
##   sire dam
## 1 <NA> <NA>
## 2 <NA> <NA>
## 3 <NA> <NA>
## 4    1    2
## 5    3    2
## 6    4    5
```

The numerator relationship matrix A

```
(sparse_A = pedigreeemm::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
```

The cholesky decomposition of A

```
A <- as.matrix(sparse_A)
(R <- t(chol(A)))
```

```
##      1  2  3  4  5  6
## 1 1.00 0.0 0.00 0.0000000 0.0000000 0.0000000
## 2 0.00 1.0 0.00 0.0000000 0.0000000 0.0000000
## 3 0.00 0.0 1.00 0.0000000 0.0000000 0.0000000
## 4 0.50 0.5 0.00 0.7071068 0.0000000 0.0000000
## 5 0.00 0.5 0.50 0.0000000 0.7071068 0.0000000
## 6 0.25 0.5 0.25 0.3535534 0.3535534 0.7071068
```

To get to the matrix L , we have to use the definition of $R = L*S$ and S is the diagonal matrix with elements corresponding to the square root of matrix D . Matrix D can be obtained as

```
(D <- diag(pedigreeemm::Dmat(ped = ped), nrow = 6))
```

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

```
## [5,] 0 0 0 0.0 0.5 0.0
## [6,] 0 0 0 0.0 0.0 0.5
```

Matrix S is obtained from matrix D

```
(S <- sqrt(D))
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,] 1 0 0 0.0000000 0.0000000 0.0000000
## [2,] 0 1 0 0.0000000 0.0000000 0.0000000
## [3,] 0 0 1 0.0000000 0.0000000 0.0000000
## [4,] 0 0 0 0.7071068 0.0000000 0.0000000
## [5,] 0 0 0 0.0000000 0.7071068 0.0000000
## [6,] 0 0 0 0.0000000 0.0000000 0.7071068
```

The matrix L is obtained from the definition of matrix $R = L * S$, therefore the matrix $L = R * S^{-1}$

```
(L <- R %*% solve(S))
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6]
## 1 1.00 0.0 0.00 0.0 0.0 0
## 2 0.00 1.0 0.00 0.0 0.0 0
## 3 0.00 0.0 1.00 0.0 0.0 0
## 4 0.50 0.5 0.00 1.0 0.0 0
## 5 0.00 0.5 0.50 0.0 1.0 0
## 6 0.25 0.5 0.25 0.5 0.5 1
```

The matrix P that we used in the simple decomposition, is computed from the relationship $L^{-1} = I - P$ and from that we get $P = I - L^{-1}$

```
(P <- round(diag(1,nrow = 6) - solve(L), digits = 2))
```

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

The inbreeding coefficients F_i for all animals in the pedigree, can also be obtained with pedigreeemm

```
pedigreeemm::inbreeding(ped = ped)
```

```
## [1] 0.000 0.000 0.000 0.000 0.000 0.125
```