Pedigree BLUP - Sire Model

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Independence Assumption

So far

- random residuals: $var(e) = I * \sigma_e^2$ and
- random sire effects: $var(s) = I * \sigma_s^2$

In real livestock datasets, this is not realistic, because sires are related

Example Dataset

Animal	Sire	Sex	WWG
4	1	M	4.5
5	3	F	2.9
6	1	F	3.9
7	4	M	3.5
8	3	M	5.0

Relationship

- For son i and sire k of i

$$cov(s_i, s_k) = 1/2 * \sigma_s^2$$

Sire Relationship Matrix

```
library(pedigreemm)
ped_sire <- pedigree(sire = c(rep(NA,2), 1),
                     dam = rep(NA,3),
                     label = as.character(c(1,3,4)))
mat_A <- getA(ped = ped_sire)
```

$$A = \begin{bmatrix} 1 & 0 & 0.5 \\ 0 & 1 & 0 \\ 0.5 & 0 & 1 \end{bmatrix}$$

Sire Model

- pedigreemm

```
lmem_sire <- pedigreemm(
  formula = WWG ~ Sex + (1 | Sire),
  data = tbl_sire_model,
  pedigree = list(Sire = ped_sire)
)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(lmem_sire)
```

```
## Linear mixed model fit by REML ['lmerpedigreemm']
## Formula: WWG ~ Sex + (1 | Sire)
##    Data: tbl_sire_model
##
## REML criterion at convergence: 8.5
##
## Scaled residuals:
##      Min         1Q  Median           3Q      Max
```

Mixed model equations

$$\left[\begin{array}{cc} X^T X & X^T Z \\ Z^T X & Z^T Z + \lambda A_s^{-1} \end{array}\right] \left[\begin{array}{c} \hat{b} \\ \hat{s} \end{array}\right] = \left[\begin{array}{c} X^T y \\ Z^T y \end{array}\right]$$