# Livestock Breeding and Genomics - Exercise 7

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## Problem 1: Predict Breeding Values Using Selection Index

The data set from exercise 6 was extended by an own performance record for our selection candidate $i$. The new data set is shown in the table below. Predict the breeding value $a_i$ for animal $i$ using all available information using the selection index.

We assume that our selection candidate $i$ has animals 1 and 2 as parents and the observation for our selection candidate is shown last in the above table as `Measurement` 10. The heritability is assumed to be $h^2 = 0.36$ and the phenotypic standard deviation corresponds to $\sigma_y = 31.8$. The population mean $\mu$ is assumed to be 250.4.

Table 1: Phenotypic Measurements for Full-Sibs, Half-Sibs and an Own Performance Record

| Animal | Sire | Dam | Weight |
|---:|---:|---:|---:|
| 4 | 1 | 2 | 270.10 |
| 5 | 1 | 2 | 263.52 |
| 6 | 1 | 3 | 221.49 |
| 7 | 1 | 3 | 280.41 |
| 8 | 1 | 3 | 215.75 |
| 9 | 1 | 3 | 292.45 |
| 10 | 1 | 2 | 187.56 |

Figrure 1 shows the structure of the data shown in Table 1.

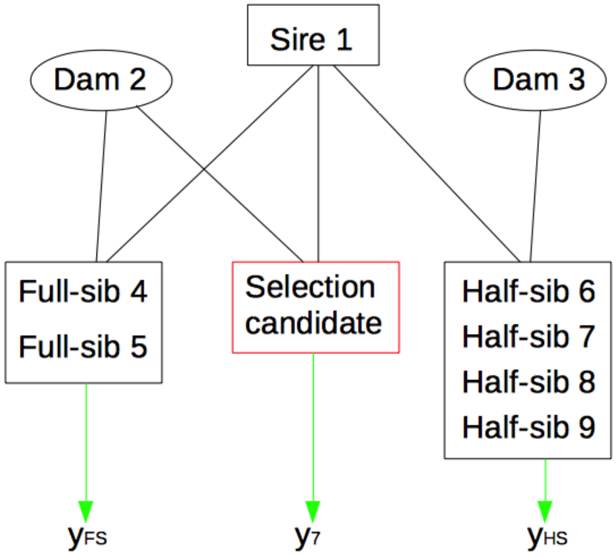

Figure 1: Information Sources To Predict Breeding Values

## Problem 2: Sire Model

We are using the following dataset shown in Table 2 to predict breeding values using a sire model.

Table 2: Example Data Set for Weaning Weight in Beef Cattle

| Animal | Sire | Dam | Herd | Weaning Weight |
|---|---|---|---|---|
| 12 | 1 | 4 | 1 | 2.61 |
| 13 | 1 | 4 | 1 | 2.31 |
| 14 | 1 | 5 | 1 | 2.44 |
| 15 | 1 | 5 | 1 | 2.41 |
| 16 | 1 | 6 | 2 | 2.51 |
| 17 | 1 | 6 | 2 | 2.55 |
| 18 | 1 | 7 | 2 | 2.14 |
| 19 | 1 | 7 | 2 | 2.61 |
| 20 | 2 | 8 | 1 | 2.34 |
| 21 | 2 | 8 | 1 | 1.99 |
| 22 | 2 | 9 | 1 | 3.10 |
| 23 | 2 | 9 | 1 | 2.81 |
| 24 | 2 | 10 | 2 | 2.14 |
| 25 | 2 | 10 | 2 | 2.41 |
| 26 | 3 | 11 | 2 | 2.54 |
| 27 | 3 | 11 | 2 | 3.16 |

### Your Tasks

- Specify the sire model for the dataset given in Table 2.
- Besides the model indicate also the expected values and the variances for all the random components in the model.
- Set up the mixed model equations for the sire model and compute the estimates for the fixed effects (Herd) and the predicted breeding values for the sires.

### Assumptions

We assume that the sires are unrelated and that the genetic additive variance $\sigma_a^2 = 0.0254$. Hence the variance-covariance matrix $G$ of all sire effects corresponds to

$$var(s) = G = I * \sigma_s^2 = I * \frac{\sigma_a^2}{4}$$

Furthermore, the residuals $e$ are not correlated which means that the variance-covariance matrix $R$ is

$$var(e) = R = I * \sigma_e^2$$

with $\sigma_e^2 = 0.076$.