Applied Statistical Methods - Solution 9

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Problem 1: Milk Dataset

Use the dataset `milk` from package `pedigreemm` and fit a sire model to each of the response variables (`milk`, `fat`, `prot` and `scs`) in the data. The dataset can be loaded using the command `pedigreemm::milk`. The other variables like `lact` and `herd` can be used as fixed effects. The `sire` column is used as a random effect. For this analysis, we assume that sires are unrelated.

Your Tasks

- Analyse the `milk` dataset from package `pedigreemm` using the function `lme4::lmer()` for all given response variables. You can use the same model for each of the responses.
- Compute the estimated heritability for each response variable, using the fact that the heritability h^2 can be computed from the variance σ_s^2 of the sire effects and the phenotypic variance σ_p^2 with the formula

$$h^2 = \frac{4 * \sigma_s^2}{\sigma_p^2}$$

- Compute the summary statistic using the function `summary()` of all the predicted sire breeding values. Solutions for the sire breeding values are obtained using the function `ranef()`

Solution