

For MRE:

□ Require A^{-1} not A where inverse A^{-1} is defined as the matrix, that satisfies $A \cdot A^{-1} = I$

□ In R: use `pedigreemm::getA()` for A
- For A^{-1} `pedigreemm::getAinv()` for A^{-1}

□ MRE for large data sets ($10^6 - 10^7$ records) are only possible, because A^{-1} can directly be constructed from the pedigree without first computing A

↓
major
selection
response
together with A
before genomic
selection

Decomposing Breeding values

For animal i with parents s and d :