

EBVs combining phenotype and GBV

Use the spreadsheet '*STEBVaccuracy.xls*'.

Consider selection for an additive trait with (total) heritability 0.2 and phenotypic standard deviation equal to 50. For this trait, you have been able to derive genomic breeding values with accuracy (r_{MBV}) equal to 0.5. The following sources of information are available for selection:

- own GBV
- own phenotype
- GBV of the individual's sire
- Phenotype of the individual's sire

Assume the top 20% individuals are selected. The base scenario is having own phenotype and phenotype of the sire only (no genotypes). Evaluate the impact of the following on the accuracy of selection and the genetic superiority of the selected individuals.

- a) Adding genotyping of the individual to the base information of own phenotype and phenotype of the sire.
- b) Adding genotyping of the sire to the information from question a).
- c) Derive the elements of the P matrix and the G vector for question b)
- d) Explain the weight on the GBV of the sire in question b)
- e) Convert this GBV blending problem into a two-trait problem consisting of the original trait and the GBV as a correlated trait with heritability = 1. I.e. derive the genetic and phenotypic correlations between the two traits. Enter the results into MTindex.xls and check that it gives the same answers for question b).