

Purpose:

Simulate genotypic values and population averages for single, pairs and multiple loci.

Keywords:

Phenotypic and Genotypic Values, Population Mean

References:

Captivate: Quantitative Genetic Models Theory
Bernardo-Chapter 3

Consider Simulate coded genotypic values of 5 for TT, -5 for CC, and $d=0$ at locus M1, -5 for AA, 5 for GG, and $d=0$ at locus M2, and 5 for AA, -5 for GG, and $d=0$ at locus M3 in DS6.

1. Create 3 tables similar to those found in the Quant Genet Model Theory moduls for all pairs of loci and calculate the population mean for each pair of loci.
2. Extend the table to include all 3 loci and generate a population mean based on all 3 loci.
3. Are the means the same? Is this expected? Why?