

**Purpose:**

Assess whether students are able to simulate genotypic values, population averages and calculate Breeding Values and Dominance Deviations for single, pairs and multiple loci.

**Keywords:**

Phenotypic and Genotypic Values, Population Mean, Average effect of an allele, Average effect of an allele substitution Breeding Value, Dominance Deviation

**References:**

Captivate: Quant Genet Model Theory  
Bernardo-Chapter 3

Consider

Population 1: Consider the the RILs in ds6. 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. Imagine that we now allow this population to random mate

Population 2: Simulate coded genotypic values of 15 for TT, -15 for CC, and  $d=5$  at locus M1, -5 for AA, 5 for GG, and  $d=5$  at locus M2, and 10 for AA, -10 for GG, and  $d=5$  at locus M3 in DS6. Imagine that we now allow this population to random mate

1. What are the population means for each random mated population?
2. Contrast the population means of the random mated populations with the population means of the RIL populations.
3. What are the dominance deviations of the genotypes at each of the loci in the random mated version of Population 1?
4. What are the dominance deviations of the genotypes at each of the loci in the random mated version of Population 2?