

Purpose:

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,

References:

Captivate: Quantitative Genetic Models Theory

Bernardo-Chapter 3

Population 1: Consider the population consisting of RILs in the file named “Quantitative Genetic Models ds6.csv”. 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. 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. Imagine that we now allow this population to random mate.

1. What will be the average effect of each of the alleles at each of the loci in each of the random mated populations?
2. What is the average effect of an allele substitution at each of the loci in the random mated populations?
3. What are the breeding values of the expected genotypes at each of the loci in each of the random mated populations?