Purpose:

Reinforce student's abilities to simulate genotypic values, population averages and calculate Breeding Values and Dominance Deviations for single, pairs and multiple loci.

Use simulated (and real data) for purposes of estimating genetic variance components

Keywords:

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

References:

Captivate: Genetic Variance Components

Bernardo-Chapter 6

ALA:

Consider the R population associated with the marker loci in DS6.

Case 1. 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. The total genotypic variability from these three loci should account for 50% of the total phenotypic variability among the RILs. The remaining phenotypic variability, due to non-genetic sources should account for 40% of the phenotypic variability.

1. Use the resulting phenotypic values, genotypic frequencies, allelic frequencies at each of the three loci to estimate breeding values, dominance deviations and variance components associated with each locus.
2. Evaluate each of the 3 SNP marker loci for associations between segregating genotypes and the phenotypic variability.

Case 2. Let markers M1 and M3 be responsible for all of the genotypic variability. In this case all genotypic variability should be due to epistatic interactions between the two loci. The total genotypic variability should contribute 70% of the total phenotypic variability.

3. Use the resulting phenotypic values, genotypic frequencies, allelic frequencies at each of the three loci to estimate breeding values, dominance deviations and variance components associated with each locus.
4. Evaluate each of the 3 SNP marker loci for associations between segregating genotypes and the phenotypic variability.