Purpose:

- Demonstrate that simulated phenotypic distributions are indistinguishable from experimental phenotypic distributions.
- Simulate genotypic values, population averages and estimate variance components among and within families for the simulated data set

Keywords:

Phenotypic and Genotypic Values, Genetic Variance Components

References:

Captivate: Genetic Variance Components

Bernardo-Chapter 6

ALA:

We have a maize stiff-stalk breeding population consisting of 7 elite lines, referred to as P1, P2, P3, P4, P5, P6 and P7. We are going to generate doubled haploid lines for testcross evaluation with a single non-stiff-stalk tester in multiple environments. There are 21 DH families that have been produced, each with a minimum of 100 DH lines that have enough seed to evaluate in two replicates at a single environment. For purposes of this ALA we will simulate 3 of the DH families.

1. Simulate phenotypes for 100 DH progeny crossed to a single tester for 3 families. The average phenotypic value needs to be 220 bu/ac. The distribution of the genotypic values should be +5% of the mean for the first family, = to the mean for the second family and -5% of the mean for the third family. The genetic contribution of DH testcrossed progeny within families should be sampled from a Normal distributions and contribute 50% of the total phenotypic variability. Phenotypic data should be simulated for a RCBD field trial with two replicates for each entry in the test. Use the simulated phenotypic variability to evaluate the contributions of replicates, families, lines and residual variability to the total phenotypic variability.
2. Is it possible to determine the additive, dominance and epistatic sources of phenotypic variability from these data?