1. We will use again the data we generated during the first practical, where we used ms to simulate data from a panmictic population. You may remember we simulated for 500 individuals 20 chromosomes 1 Megabase long.
    a. use function JGTeach::make.traits to simulate a trait with a heritability of 0.8, with 100 causal loci and using all possible SNPs as possible causal loci. Explore the structure of the object generated (you might also want to look at the function help page). Plot a histogram of the distribution of the trait you have generated. Plot the phenotypic value of the trait against its breeding value. **Explain the difference between h2 and h2^**
    b. Create a second trait with the same characteristics but a heritability of 0.3. Plot again breeding value against phenotype and explain the difference from the previous trait (it might be helpful to quantify the spread)
2. Compute heritabilities for trait 1 and 2 using the 3 GRMs and function gaston::lmm.aireml. **Are the heritability estimates from the 3 GRMS similar? The allele sharing and GCTA look similar, but the estimated GRM does not.**
    a. A commonly seen recommendation for the standard GRM is to filter on low MAF. Re-estimate heritabilities using the standard GRM filtered on maf>0.05
    b. **[optional]** using gaston::association.test, perform GWAS using a simple linear model and using a linear mixed model with the fours GRMs estimated before and estimate the genomic inflation factor λ
    c. **[optional]** Evaluate heritabilities for other traits. **Is there a pattern emerging? Different GRMs perform better/worse at different heritability levels.**
3. Simulate one trait with heritability 0.5 and driven by 10 causal loci with MAF>=0.01 using the AMR samples from the 1000 genomes data, and estimate its heritability using the 4 GRMS we used previously (Allele sharing As; c0; standard; and standard filter on maf≥0.05). **Discuss the results and their shortcomings.**
    a. Are estimates of heritability impacted by population structure? Definitely.
    b. **[optional]** Using the function gaston::association.test, perform GWAS on this trait, using either a linear model with no covariate or a linear mixed model with the 4 GRM we discussed; plot the qqplot of the p-values, estimate the genomic correction factor for each and interpret the results.
    c. **[optional]** Using the function gaston::manhattan produce manhattan plots of the p-values along the genome segment, and interpret the results