

Revised HW #7 due Thursday, Feb. 28

Download the two files “GenotypesHW7.csv” and “PhenotypesHW7.csv” from Content. The genotypes file is a similar format to last week: different SNPs are on different rows, and unrelated individuals are in the columns 10 to 90. The phenotypes file has different continuous traits in the different rows.

Separately test each trait to see whether or not it depends on any of the SNPs. The R function “aov” will be useful for analysis of variance, and the R function “p.adjust” will be useful for correcting p-values for multiple tests. Next Monday in lecture we will review analysis of variance.

For each trait, report any SNPs that are significant, and make a plot to show whether this dependence is dominant, recessive, or additive. Also, turn in your code.