BMI 826-001: Statistical methods for QTL mapping (Fall, 2012)
Homework #2: Interval mapping

Due 18 Oct

Grab the comma-delimited data file at

`http://www.biostat.wisc.edu/~kbroman/teaching/qtltopics/hw2.csv`

This is simulated data from a backcross with 300 individuals, with a single quantitative phenotype. A selective genotyping strategy was used.

1. Use each of standard interval mapping and Haley-Knott regression to map QTL in this cross. Also, use a permutation test to establish significance of identified QTL, and calculate 1.5-LOD support intervals for the locations of inferred QTL.

   Do two versions of the permutation test: the usual kind plus a stratified permutation test (with individuals stratified by the amount of genotyping).

   To perform the stratified permutation test, do something like this:

   ```
   nmis <- nmissing(mycross)
   strat <- as.numeric(nmis > mean(unique(nmis)))
   operm <- scanone(mycross, method="hk", n.perm=1000, perm.strat=strat)
   ```

2. How do the results change if you omit the individuals that were not genotyped?

   To drop the non-genotyped, individuals, use code like

   ```
   subcross <- subset(mycross, ind=(ntyped(mycross) > 0))
   ```

3. How do the results change if you consider only the genotyped individuals and define a binary trait (high/low phenotype)?

   To define the binary trait, use code like

   ```
   phe <- subcross$pheno[,1]
   phe <- as.numeric(phe > mean(phe))
   subcross$pheno[,1] <- phe
   ```