BMI 826-001: Statistical methods for QTL mapping (Fall, 2012)
Homework #3: Interval mapping with covariates

Due 8 Nov

Grab the comma-delimited data file at

`http://www.biostat.wisc.edu/~kbroman/teaching/qtltopics/hw3.csv`

This is simulated data from a backcross with 400 individuals, with a single quantitative phenotype. There are 200 males (phenotype `sex == 1`) and 200 females (`sex == 0`).

Perform interval mapping with sex as an additive covariate and sex as an interactive covariate, and also with males and females separately.

Which regions of the genome have an effect on the phenotype, and which show QTL × sex interaction?

You can use Haley-Knott regression for all analyses, to save computation time.