BMI 826-001: Statistical methods for QTL mapping (Fall, 2012)
Homework #4: Mapping multiple QTL

Due 15 Nov

We'll consider data on an intercross with 450 mice, from Mrug et al. (2005) J Am Soc Nephrol 16:905-916. We'll focus on just one phenotype, "renal principal component 1." I've omitted a few individuals that were missing the phenotype or were missing most genotypes.

Perform 1- and 2-dimensional QTL scans, exploratory multiple QTL analysis as well as the automated multiple-QTL mapping procedure in `stepwiseQTL` to identify QTL and QTL×QTL interactions with these data.

The main issue concerns the potential for multiple linked QTL on chromosome 4.

Write a short report describing what you did and what you found, including the relative support for different QTL (and, potentially, QTL×QTL interactions).

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

Grab the comma-delimited data file at

```
http://www.biostat.wisc.edu/~kbroman/teaching/qtltopics/hw4_data.csv
```

Or grab the `.RData` file from

```
http://www.biostat.wisc.edu/~kbroman/teaching/qtltopics/hw4_data.RData
```

I've run permutation tests with 1- and 2-dimensional scans and placed the results at the following:

```
http://www.biostat.wisc.edu/~kbroman/teaching/qtltopics/hw4_perms.RData
```