R/qtl: An extensible QTL mapping environment

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`http://www.biostat.jhsph.edu/~kbroman/qtl`

Why R/qtl?

- Iteractive QTL mapping environment.
- Allow user to focus on modeling rather than computing.
- Embedded within general data analysis environment, R.
- Access to a variety of QTL mapping approaches, including sophisticated multiple QTL methods.
- Includes functions for estimating genetic maps, identifying genotyping errors, and visualizing data.
- Easy extensibility for use with specialized crosses or specially-tailored models.
- Available for Unix, Windows, and MacOS.

About R

- Open-source implementation of the S language. (Like S-PLUS, and sort of like Matlab, but free.)
- Language and environment for statistical computing and graphics.
- Provides a wide variety of statistical and graphical techniques (including linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering).
- Available for UNIX, Windows and MacOS.

Functionality

Currently

- Analysis of intercross, backcross and 4-way cross.
- One- and two-dimensional scans by interval mapping, imputation and Haley-Knott regression, with covariates.
- Permutation tests.
- Re-estimation of linkage map.
- “Ripple” marker order.
- Calculation of Lincoln & Lander error LOD scores.
- Visualization of genotype data.

Soon

- AILs, RIs, and more complex types of crosses.
- Analysis of multiple QTL models (by MIM or imputation).
- Sophisticated model search techniques.
- Advanced phenotype models, such as generalized linear models or Cox models
- Analysis of (and under) crossover interference.
- Graphical user interface (GUI)