R/qtl2 Workshop

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Why R/qtl2?

- High-dimensional data

  genotypes and phenotypes

- More diverse crosses

  especially multi-parent populations

- Linear mixed models

  especially in DO/HS/AIL

R/qtl → R/qtl2

- See kbroman.org/qtl2/assets/vignettes/rqtl_diff.html

- New data file formats

- New data structures

- Split into multiple packages

  qtl2geno, qtl2scan, qtl2plot, qtl2convert

- New function names

  `read.cross()` → `read_cross2()`

  `calc.genoprob()` → `calc_genoprob()`

  `scanone()` → `scan1()`

- Different treatment of intermediate calculations

- Use of individual IDs for aligning data

- Order of args when subsetting cross objects

  `cross[chr,ind]` → `cross2[ind,chr]`