

R/qlt2

high-dimensional data and multi-parent populations

Karl Broman

Biostatistics & Medical Informatics, UW–Madison

`kbroman.org`

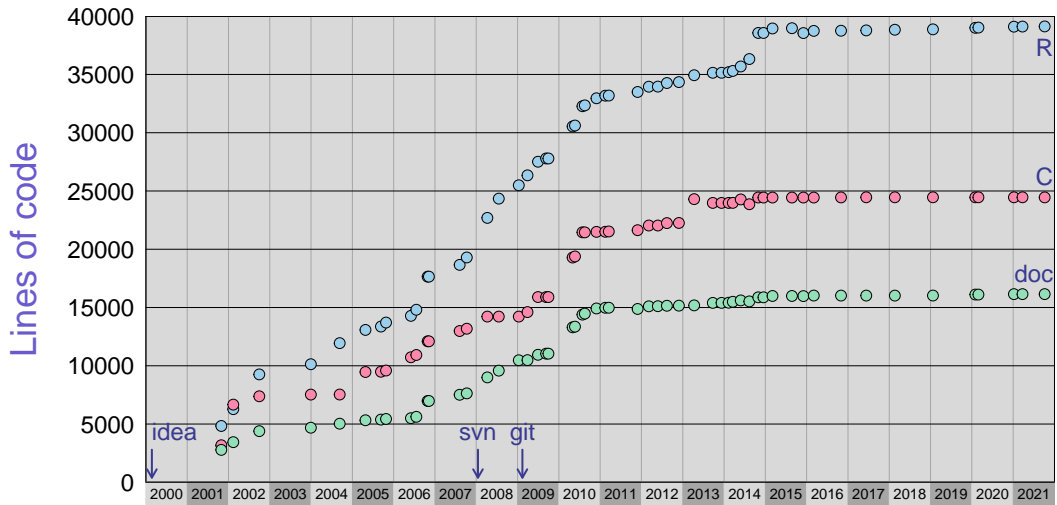
`github.com/kbroman`

`@kwbroman`

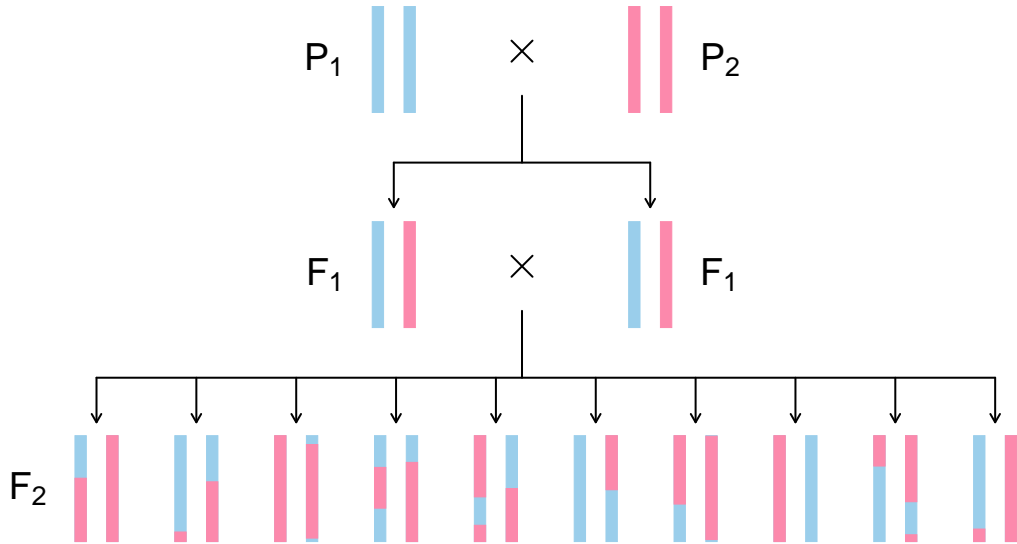
Slides: `kbroman.org/Talk_D0Workshop2021`

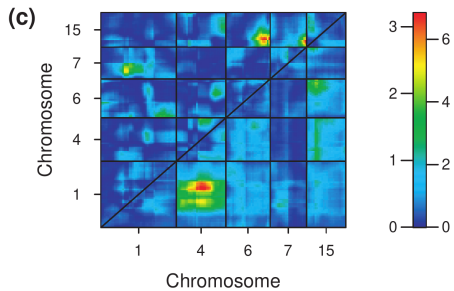
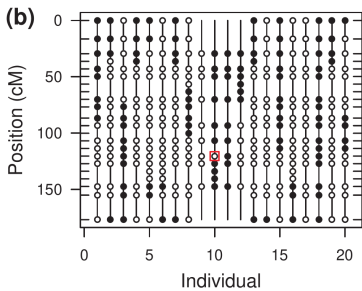
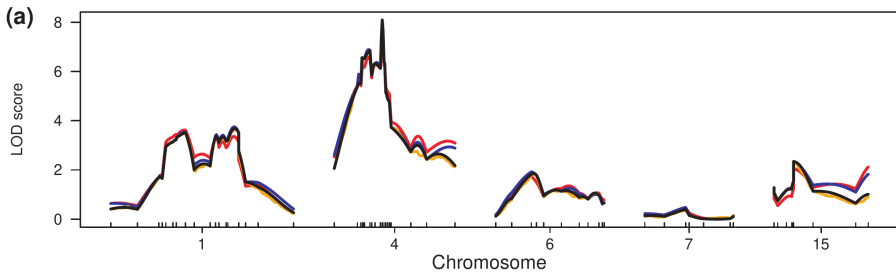


21 years of R/qtl



Intercross





Good things

- ▶ efficient handling of missing genotypes
- ▶ diagnostics and data visualization
- ▶ fit and exploration of multiple-QTL models
- ▶ quite comprehensive
- ▶ quite flexible

Why work on software?

- ▶ to be useful
- ▶ makes our own analyses easier
- ▶ platform for implementing new methods
- ▶ has led to many collaborations

Bad things

- ▶ some really bloated code
- ▶ hard to maintain
- ▶ many inconsistencies in the user interface
- ▶ largely restricted to two-parent crosses

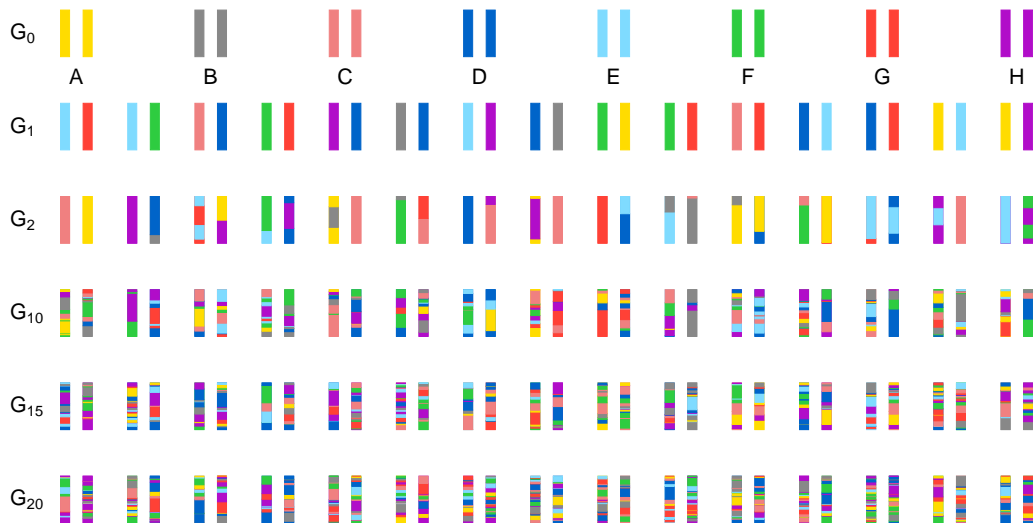
What's changed in 20 years?

- ▶ Genome sequence
- ▶ Large crosses
- ▶ Dense SNP genotypes
- ▶ Gene expression and other -omics data
- ▶ Multi-parent populations (MPPs)

Improving precision

- ▶ more recombinations
- ▶ more individuals
- ▶ more precise phenotype
- ▶ lower-level phenotypes
 - transcripts, proteins, metabolites

HS/DO



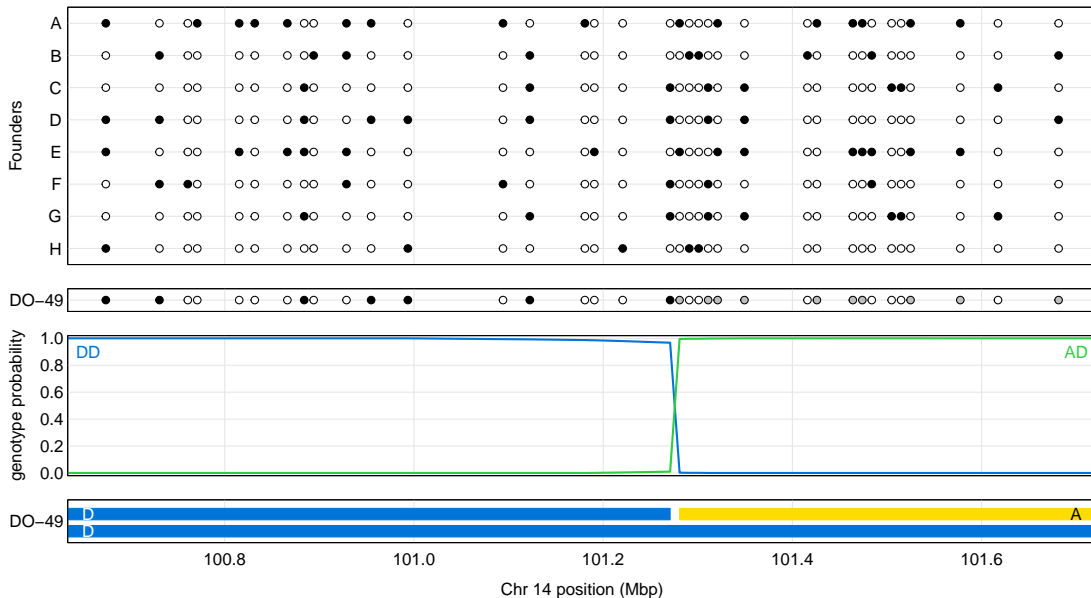


- ▶ High-density genotypes
- ▶ High-dimensional phenotypes
- ▶ Multi-parent populations
- ▶ Linear mixed models

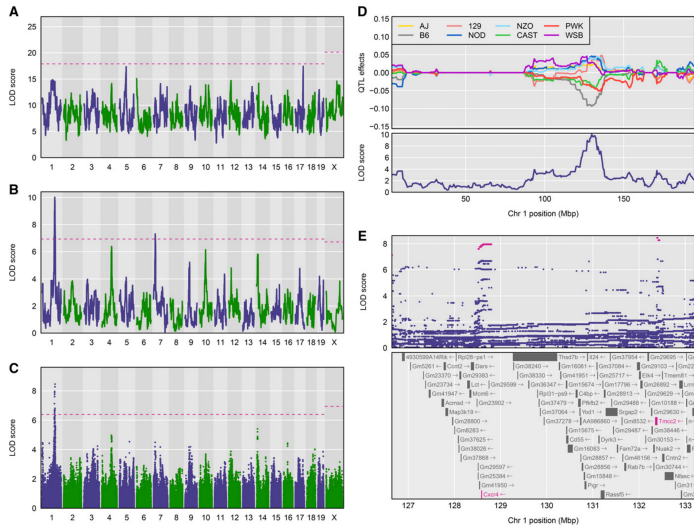
QTL mapping in MPPs

- ▶ Data diagnostics/cleaning
- ▶ Genome reconstruction
- ▶ QTL analysis
- ▶ Visualization/exploration of results

Genome reconstruction



QTL mapping in MPPs



R/qtl2 plans

- ▶ Handling of GBS-based genotypes
- ▶ QTL×QTL and QTL×covariate interactions
- ▶ Multiple causal SNPs within a region

GWAS vs linkage

- ▶ Study design?

Natural population vs experimental cross

- ▶ Organism?

Human vs mouse

- ▶ Analysis method?

SNP alleles vs founder haplotypes

Fine-mapping a QTL

- ▶ Is there a SNP that accounts for the effect?
- ▶ Or some set of SNPs?
- ▶ Nature of genes; nature of SNPs within genes?
- ▶ Gene expression pattern that matches QTL effect?
- ▶ Gene expression that mediates the QTL effect?
- ▶ External information: QTL in human or rat?

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