# R/qtl2

## high-dimensional data and multi-parent populations

Karl Broman

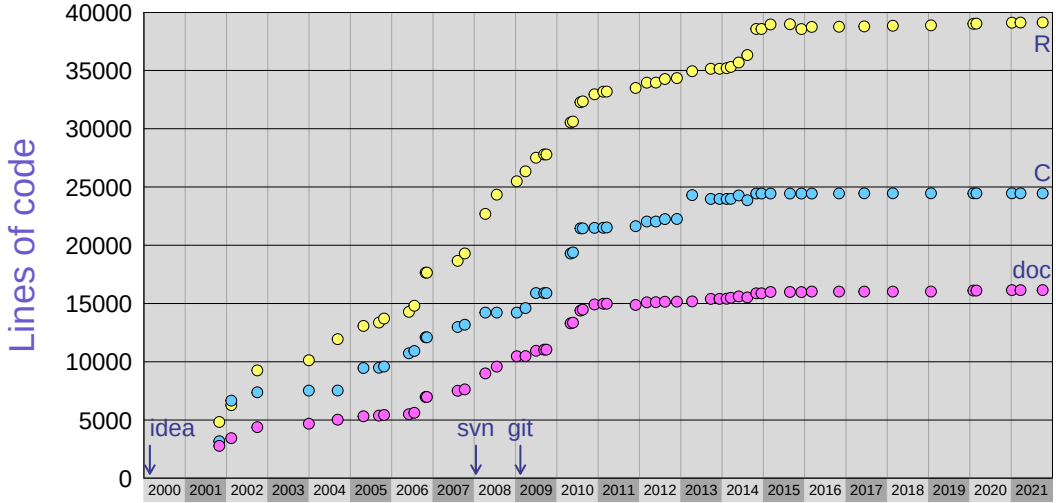
Biostatistics & Medical Informatics, UW–Madison

kbroman.org
github.com/kbroman
@kwbroman

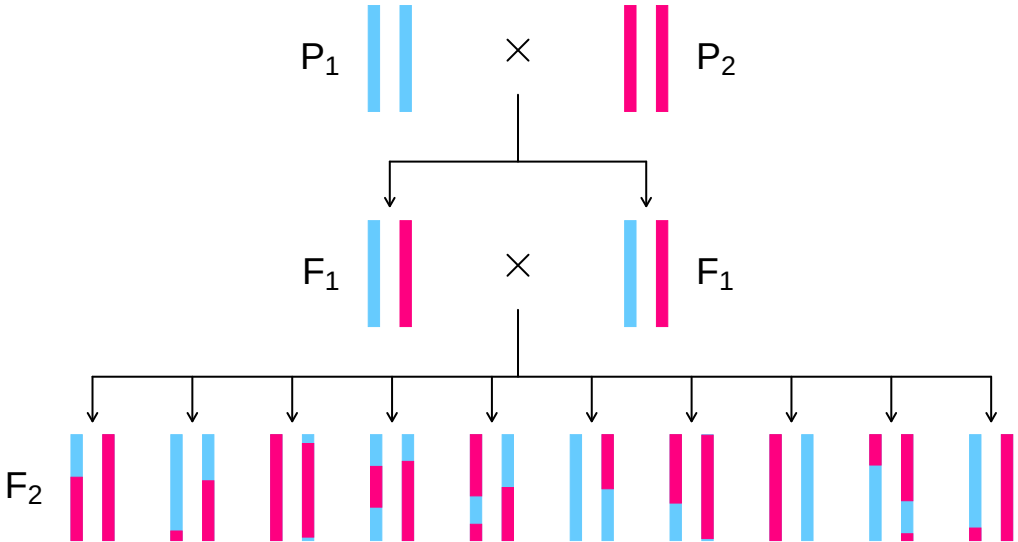
Slides: kbroman.org/Talk_DOWorkshop2021

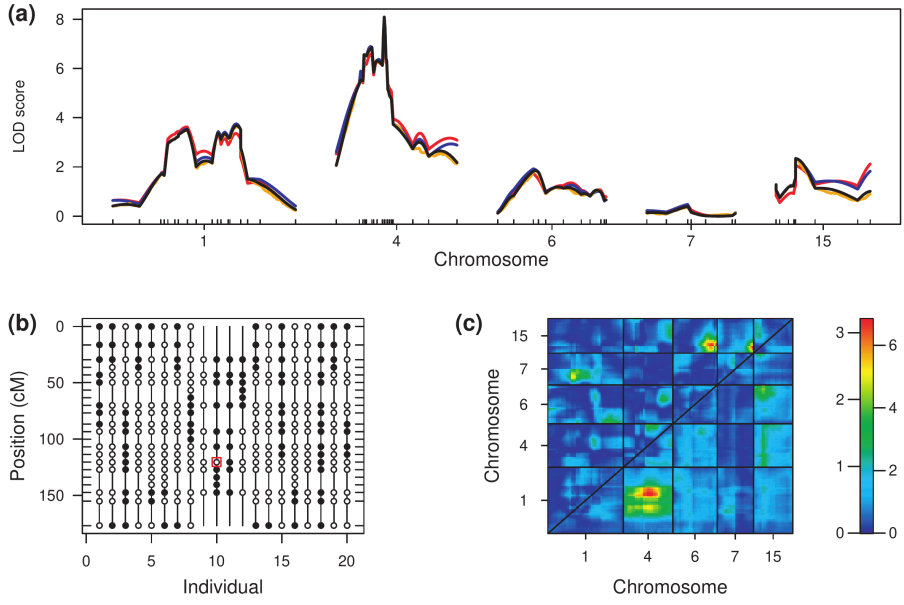
PUBLIC DOMAIN

# 21 years of R/qtl



# Intercross






Broman et al. (2003) doi.org/bsjrwj

# 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

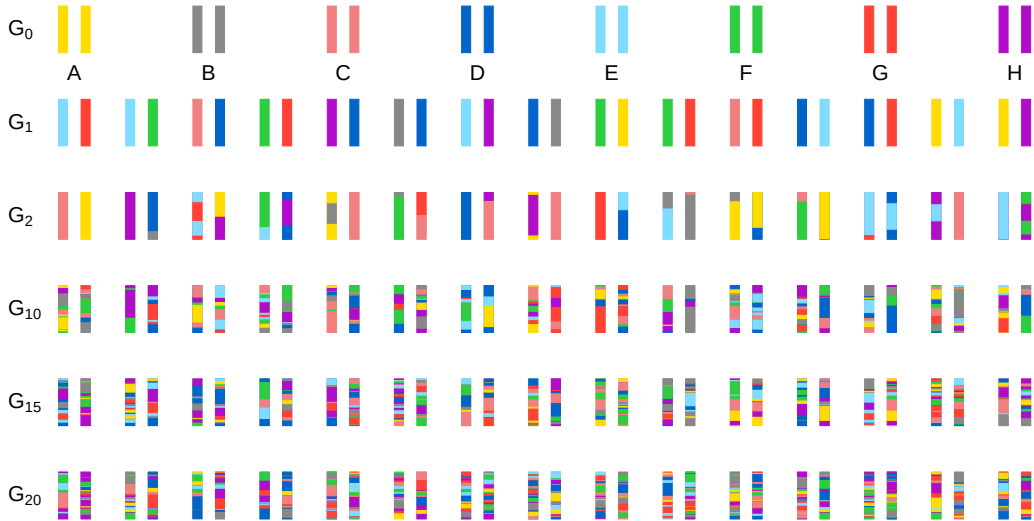
# What's changed in 20 years?

- Genome sequence
- Larger crosses
- Denser SNP genotypes
- Gene expression and other omics data
- Multi-parent populations (MPPs)
- But still hard to find genes underneath QTL

# Improving precision

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

# HS/DO



R/qt12
How in 3D

# R/qtl2

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

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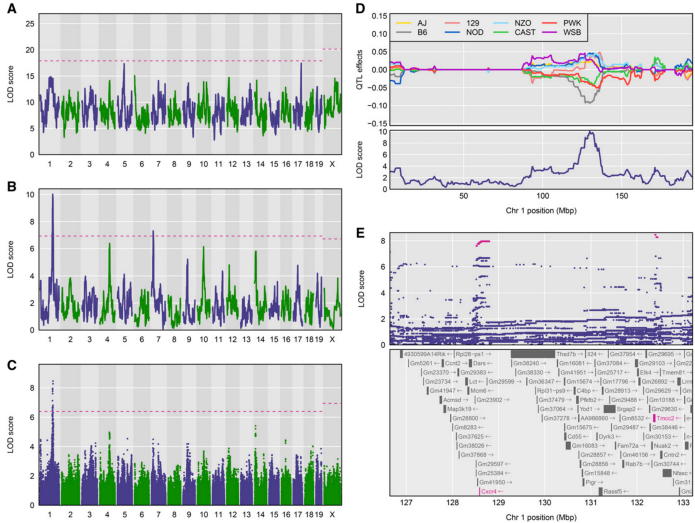
# QTL mapping in MPPs

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

# Genome reconstruction

# QTL mapping in MPPs




Broman et al. (2019) doi.org/gfvknr

# R/qtl2: Let's not make the same mistakes

- C++ and Rcpp
- Roxygen2 for documentation
- Unit tests
- A single "switch" for cross type

# R/qtl2: Let's not make the same mistakes

- C++ and Rcpp
- Roxygen2 for documentation
- Unit tests
- A single "switch" for cross type
- Yet another data input format
- Flatter data structures, but still complex

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@kwbroman