17 years of R/qtl
maintaining, supporting, and sustaining scientific software

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github.com/kbroman
@kwbroman
Slides: bit.ly/uchi2017
17 years of R/qtl

Year

Lines of code


idea svn git

R

C
doc
Intercross
QTL mapping
Interactive plot

bit.ly/lod_and_effect
17 years of R/qtl
Good things
Good things

- some of the code
- basics of the user interface
- diagnostics and data visualization
- quite comprehensive
- quite flexible
Bad things
<table>
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Stupidest code ever

n <- ncol(data)
temp <- rep(FALSE,n)
for(i in 1:n) {
  temp[i] <- all(data[2,1:i]=="")
  if(!temp[i]) break
}
if(!any(temp)) stop("...")
n.phe <- max((1:n)[temp])

kbroman.org/blog/2011/08/17/the-stupidest-r-code-ever
Open source means everyone can see my stupid mistakes
Open source means everyone can see my stupid mistakes

Version control means everyone can see every stupid mistake I’ve ever made
Documentation
Support
QTL mapping
Congenic line
Improving precision

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

P
A
B

F₂

F₃

F₄

F₇

F₁₀
Recombinant inbred lines

$P_1 \rightarrow F_1 \rightarrow F_2 \rightarrow F_3 \rightarrow F_4 \rightarrow \cdots \rightarrow F_\infty$

$P_2 \rightarrow F_1 \rightarrow F_2 \rightarrow F_3 \rightarrow F_4 \rightarrow \cdots \rightarrow F_\infty$
Collaborative Cross

$G_0$

$G_1$

$G_2$

$G_3$

$G_4$

$G_\infty$
Heterogeneous stock

G_0
A  B  C  D  E  F  G  H
G_1
G_2
G_10
G_15
G_20
Genome-scale phenotypes
Challenges: diagnostics

kbroman.org/blog/2012/04/25/microarrays-suck
Challenges: diagnostics
Challenges: diagnostics

- What might have gone wrong?
- How might it be revealed?
- Make lots of graphs
- Follow up artifacts
Challenges: scale of results

- genotypes
- phenotypes
Challenges: scale of results

- genotypes
- phenotypes
- results
Challenges: organizing, automating

genotypes

phenotypes
Challenges: organizing, automating

- genotypes
- phenotypes
Challenges: organizing, automating

- genotypes
- phenotypes
Challenges: organizing, automating

genotypes  phenotypes
Challenges: organizing, automating

genotypes

phenotypes
**Challenges:** organizing, automating

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Challenges: organizing, automating

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Challenges: metadata

What the heck is "FAD_NAD SI 8.3_3.3G"?
What was the question again?
R/qtl12
Now in 3D

ropenscilabs.github.io/miner_book
High-density genotypes
High-dimensional phenotypes
Multi-parent populations
Linear mixed models
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
- Split into multiple packages
- Yet another data input format
- Flatter data structures, but still complex
Sustainable academic software
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Laura Shannon
Quoc Tran
Aaron Wolen

NIH/NIGMS
Slides: bit.ly/uchi2017

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