18 years of R/qtl
developing, maintaining, and supporting scientific software

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Slides: bit.ly/UCSF2018
17 years of R/qtl
Intercross

P_1 \times P_2 \rightarrow F_1 \times F_1 \rightarrow F_2
QTL mapping
Interactive plot

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

▶ some of the code
▶ basics of the user interface
▶ diagnostics and data visualization
▶ quite comprehensive
▶ quite flexible
Good things

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

```r
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
Recombinant inbred lines
Collaborative Cross

G₀
A  B
C  D
E  F
G  H
A  B  C  D  E  F  G  H

G₁
A  B
C  D
E  F
G  H
A  B  C  D  E  F  G  H

G₂
A  B  C  D
E  F
G  H
A  B  C  D  E  F  G  H

G₃
A  B  C  D
E  F
G  H
A  B  C  D  E  F  G  H

G₄
A  B  C  D
E  F
G  H
A  B  C  D  E  F  G  H

...
Heterogeneous stock
Genome-scale phenotypes

Alan Attie
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
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/qtl2

- 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
- Yet another data input format
- Flatter data structures, but still complex
Sustainable academic software
Acknowledgments

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Quoc Tran
Aaron Wolen

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