Maintaining, supporting, and sustaining scientific software

Biostatistics & Medical Informatics, UW–Madison

kbroman.org
github.com/kbroman
@kwbroman
Course web: kbroman.org/AdvData
20 years of R/qtl
Why?
Good things
Good things

- some of the code
- basics of the user interface
- diagnostics and data visualization
- quite comprehensive
- quite flexible
Bad things
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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
More typically bad code

The `scantwo()` function is **1446 lines** long.

The related C code is 20% of the C code in R/qtl.
Baroque data structures

attr(mycross$geno[["X"]]+$probs, "map")
Documentation
User support
“I tried X and it didn’t work.”
“Could you look at the attached 25-page Word document containing code and output and tell me if I’m doing something wrong?”
Incorporating others’ code
Version control
Tests
QTL mapping
Heterogeneous stock

G₀

A

B

C

D

E

F

G

H

G₁

G₂

G₁₀

G₁₅

G₂₀
Challenge: scale of results

genotypes

phenotypes
Challenge: scale of results

- genotypes
- phenotypes
- results
Challenge: organizing, automating

genotypes
phenotypes
Challenge: organizing, automating

- genotypes
- phenotypes
Challenge: organizing, automating

genotypes

phenotypes
Challenge: organizing, automating

genotypes
phenotypes
Challenge: organizing, automating

genotypes

phenotypes
Challenge: organizing, automating

- genotypes
- phenotypes
**Challenge:** organizing, automating

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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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Rohan Shah
Laura Shannon
Quoc Tran
Aaron Wolen

NIH/NIGMS