

18 years of R/qtl

developing, maintaining, and supporting
scientific software

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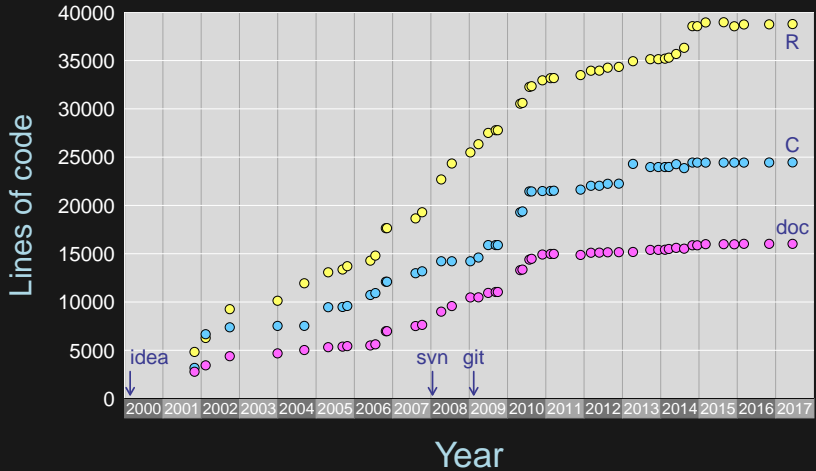
kbroman.org

github.com/kbroman

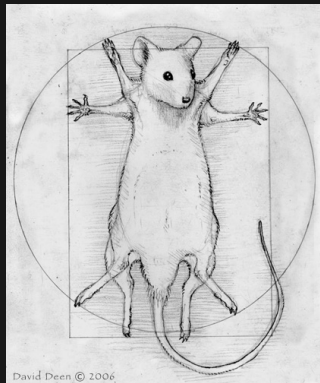
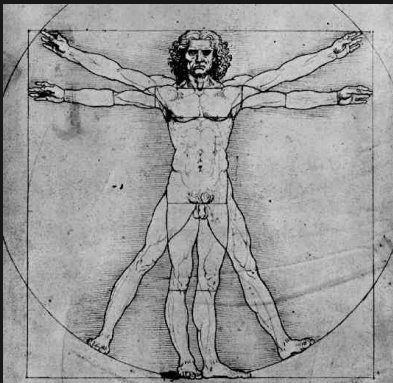
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Slides: bit.ly/UCSF2018

17 years of R/qtI

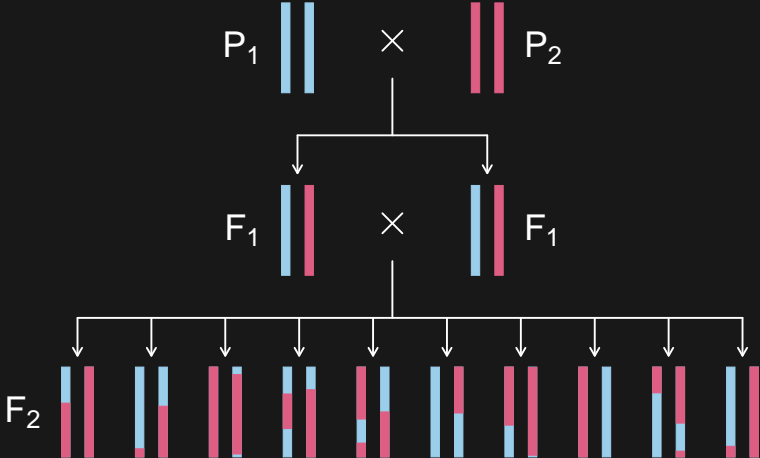




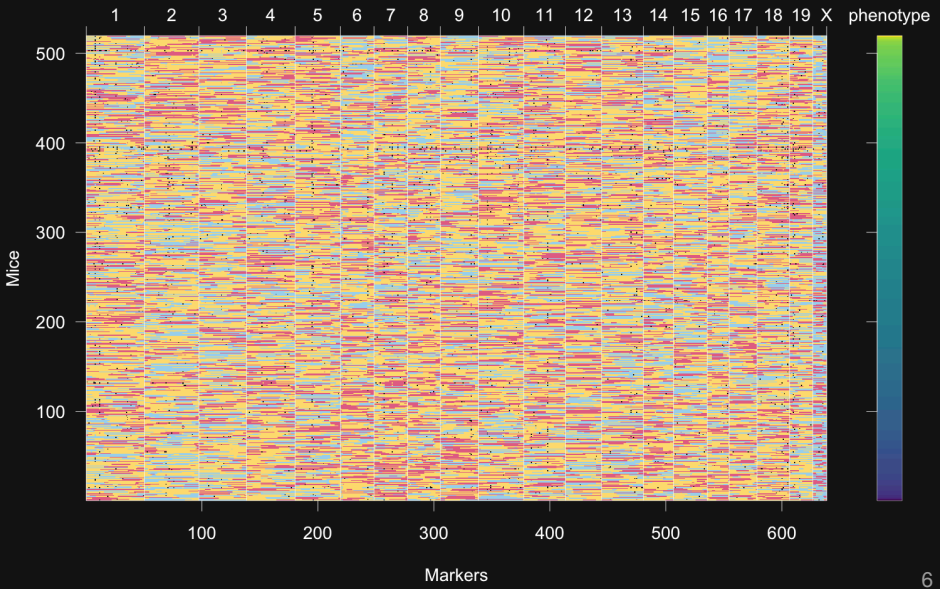


daviddeen.com

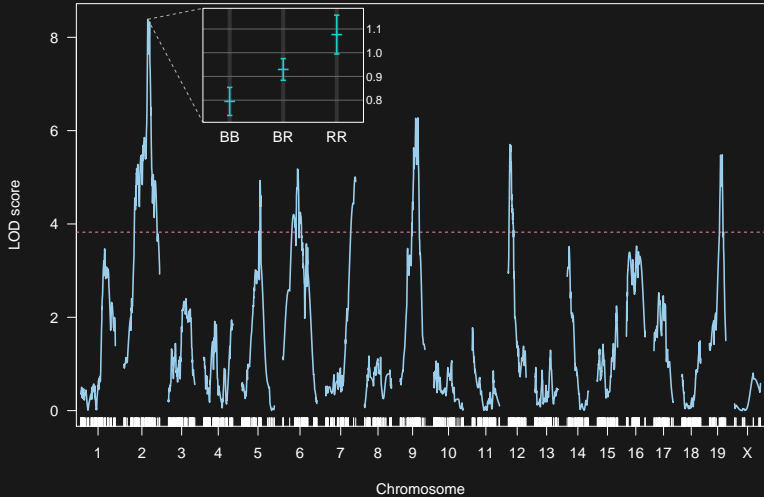
Intercross



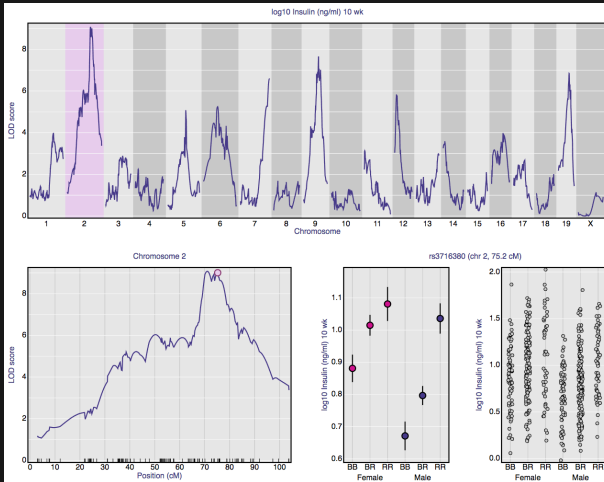
Data



QTL mapping

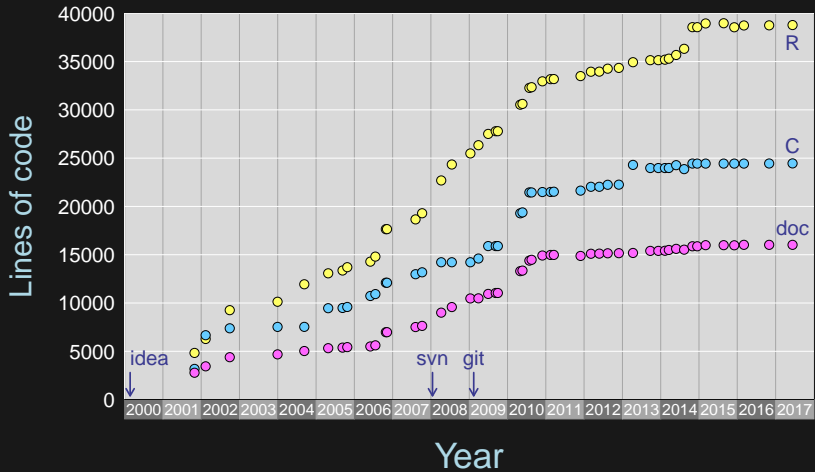


Interactive plot



bit.ly/lod_and_effect

17 years of R/qtI



Good things

Good things

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

Bad things

Input file

	A	B	C	D	E	F	G	H	I
1	liver	spleen	sex	pgm	D1Mit18	D1Mit80	D1Mit17	D2Mit379	D2Mit75
2					1	1	1	2	2
3					27.3	51.4	110.4	38.3	48.1
4	61.92	153.16	m	1	BB	SB	SB	SB	SB
5	88.33	178.58	m	1	-	-	-	BB	BB
6	58	131.91	m	1	BB	SB	SB	SB	SB
7	78.06	126.13	m	1	SB	SB	BB	SS	SS
8	65.31	181.05	m	1	-	-	-	SB	SB
9	59.26	191.54	m	1	-	-	-	SS	SS
10	59.47	154.88	m	1	BB	BB	BB	SB	SB
11	65.63	184.12	m	1	-	-	-	SB	SB
12	38.64	133.05	m	1	SB	BB	SB	SB	SB
13	60.94	275.63	m	1	-	-	-	SB	BB
14	51.48	395.25	m	1	-	-	-	SB	BB
15	47.12	260.45	m	1	BB	SB	SB	BB	BB

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

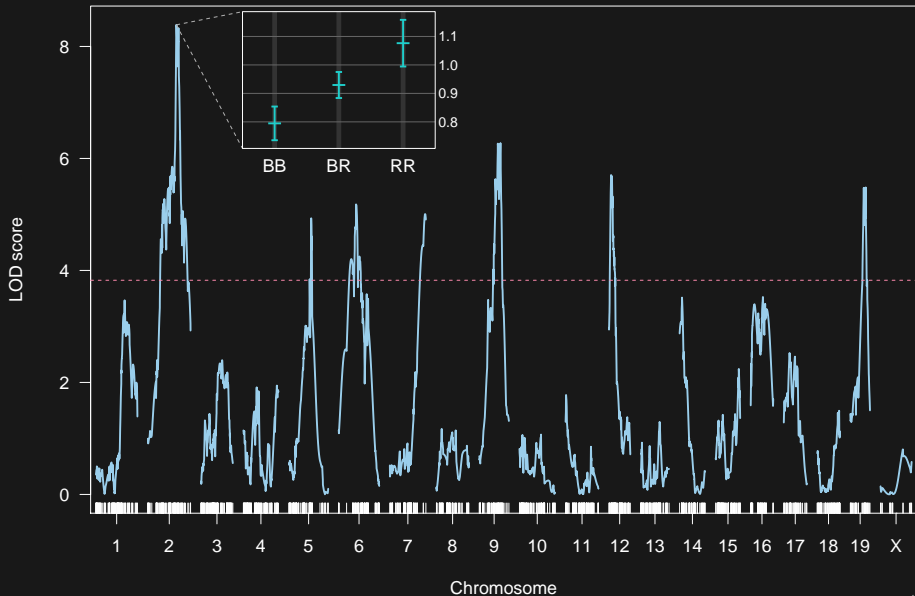
Open source means
everyone can see my stupid mistakes

Version control means
everyone can see every stupid mistake I've ever
made

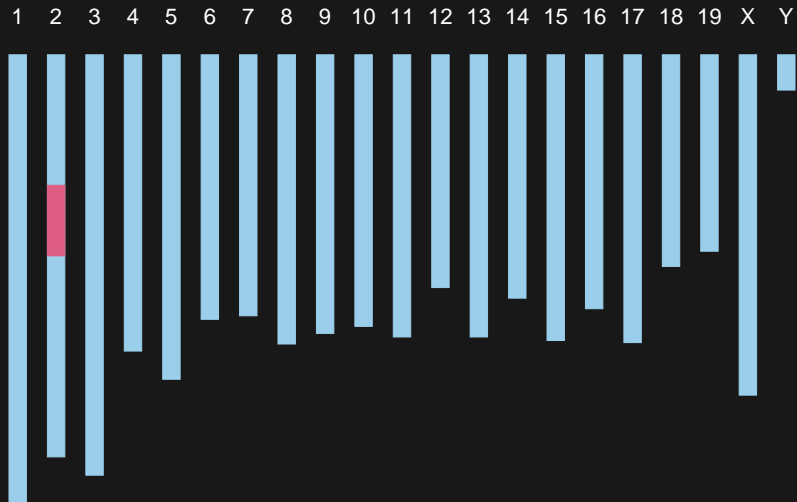
Documentation

Support

QTL mapping



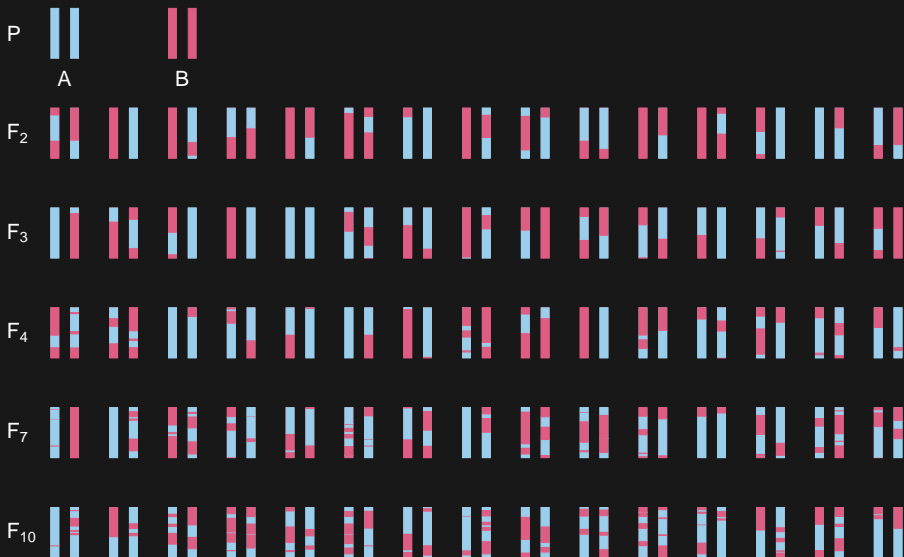
Congenetic line



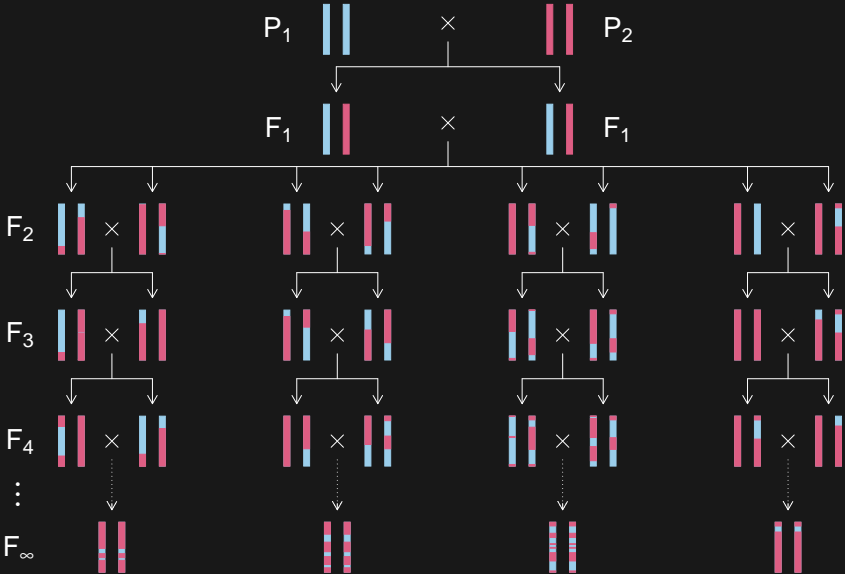
Improving precision

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

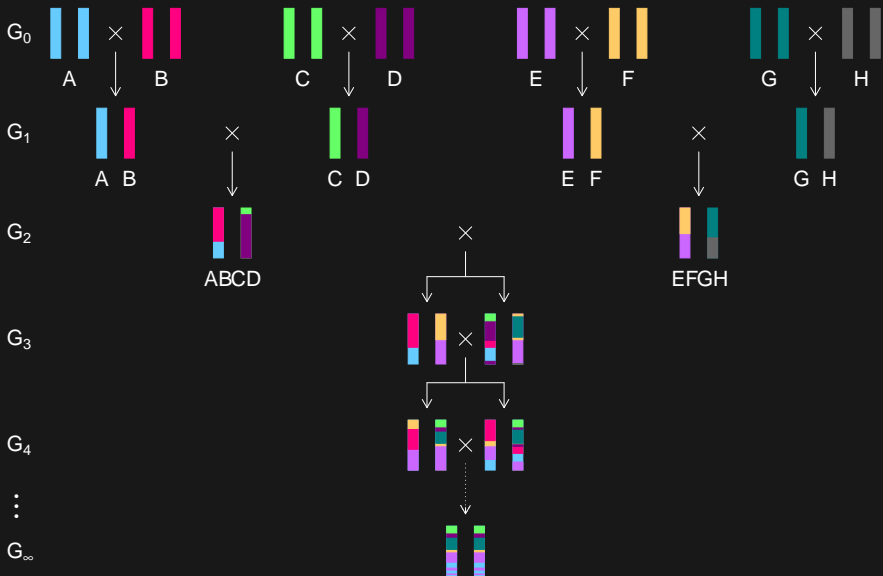
Advanced intercross lines



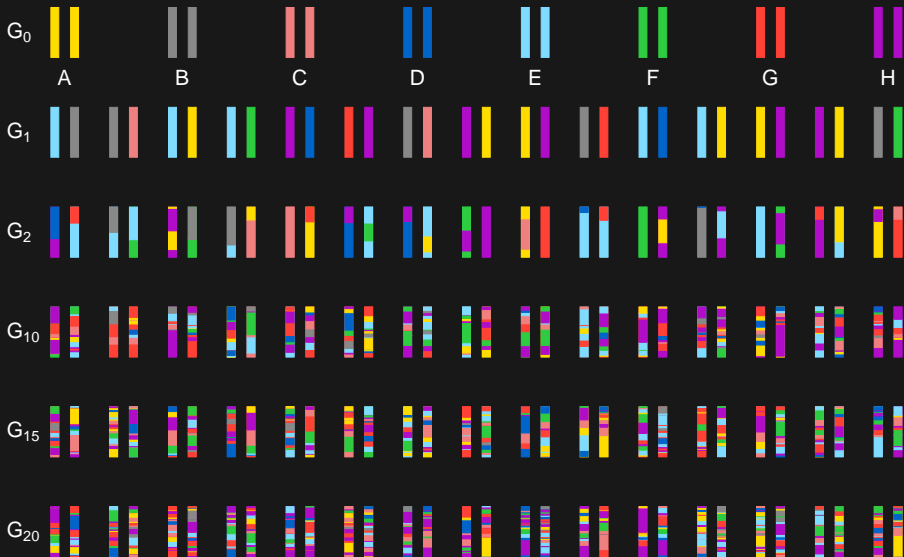
Recombinant inbred lines



Collaborative Cross



Heterogeneous stock

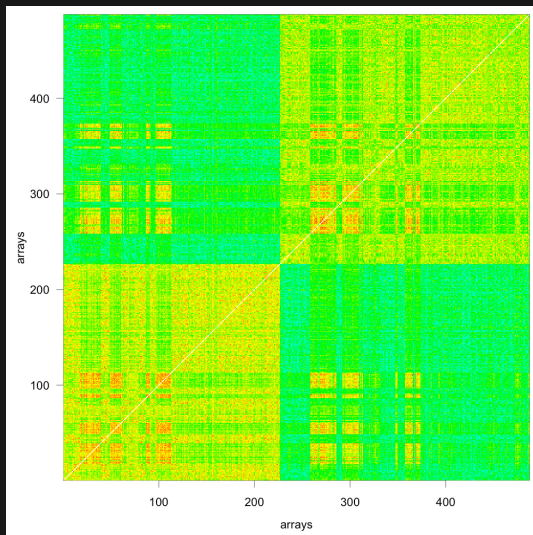


Genome-scale phenotypes

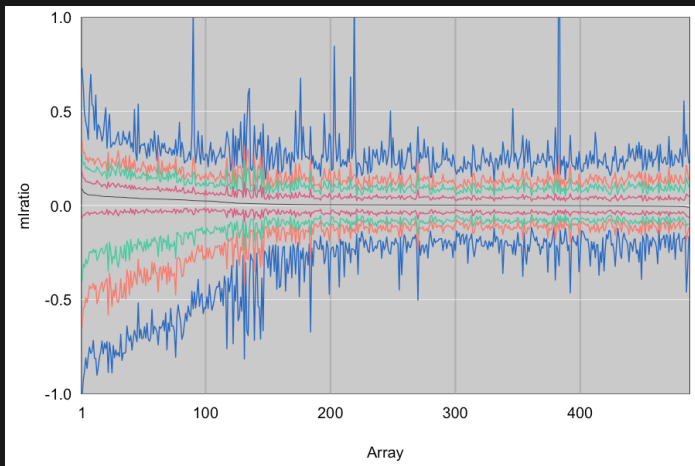


Alan Attie

Challenges: diagnostics



Challenges: diagnostics



bit.ly/many_boxplots

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

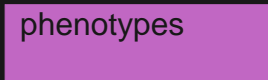
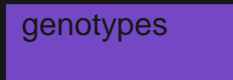
genotypes

phenotypes

Challenges: organizing, automating

genotypes

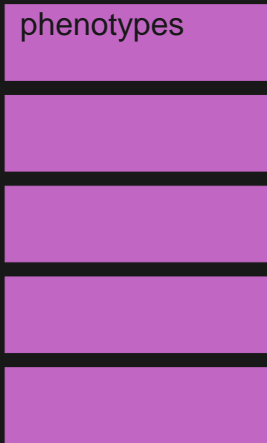
phenotypes



Challenges: organizing, automating

genotypes

phenotypes



Challenges: organizing, automating

genotypes	phenotypes	

Challenges: organizing, automating

genotypes	phenotypes		

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/qt12: Let's not make the same mistakes

- ▶ C++ and Rcpp
- ▶ Roxygen2 for documentation
- ▶ Unit tests
- ▶ A single “switch” for cross type

R/qt12: 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

Danny Arends

Gary Churchill

Nick Furlotte

Dan Gatti

Ritsert Jansen

Pjotr Prins

Śaunak Sen

Petr Simecek

Artem Tarasov

Hao Wu

Brian Yandell

Robert Corty

Timothée Flutre

Lars Ronnegard

Rohan Shah

Laura Shannon

Quoc Tran

Aaron Wolen

NIH/NIGMS

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