R/qtl2

high-dimensional data and multi-parent populations

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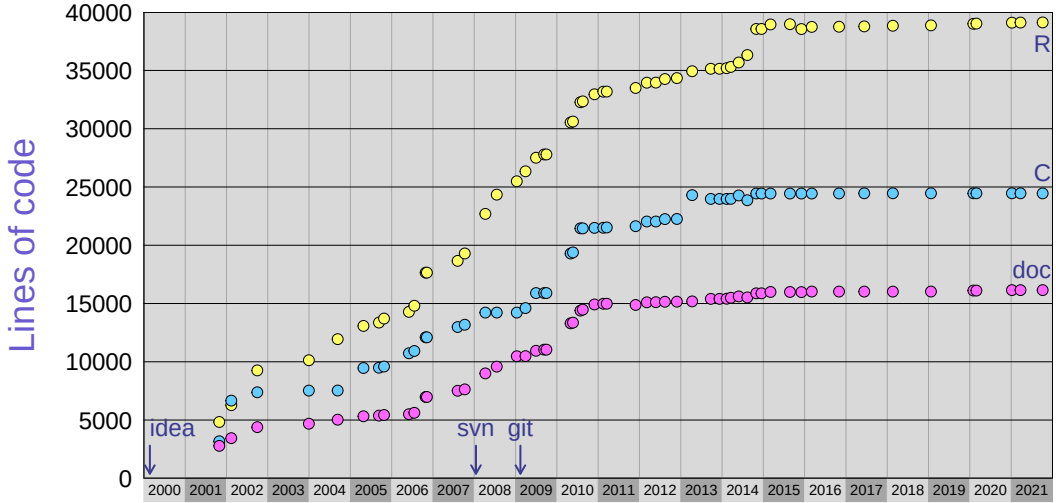
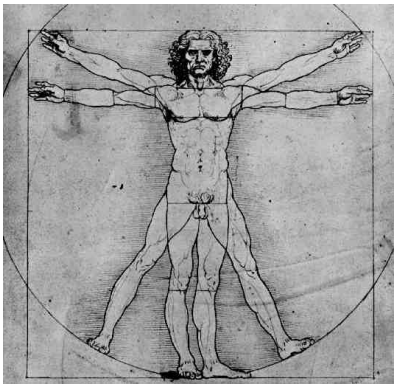
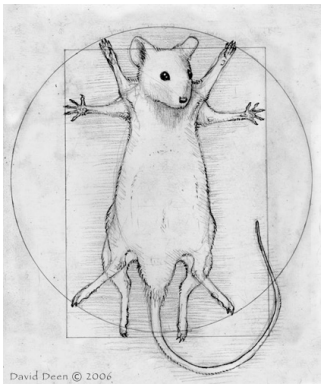
Slides: kbroman.org/Talk_DOWorkshop2021

21 years of R/qtl

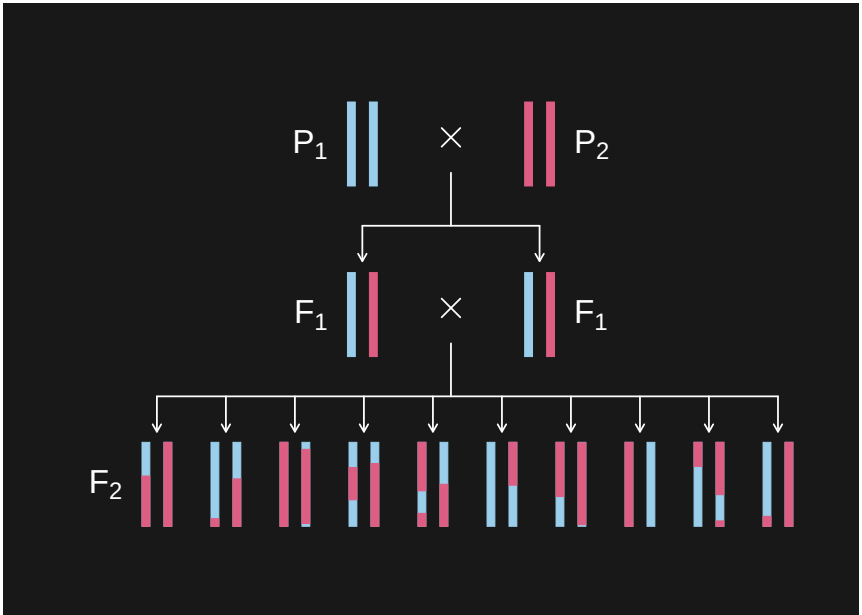




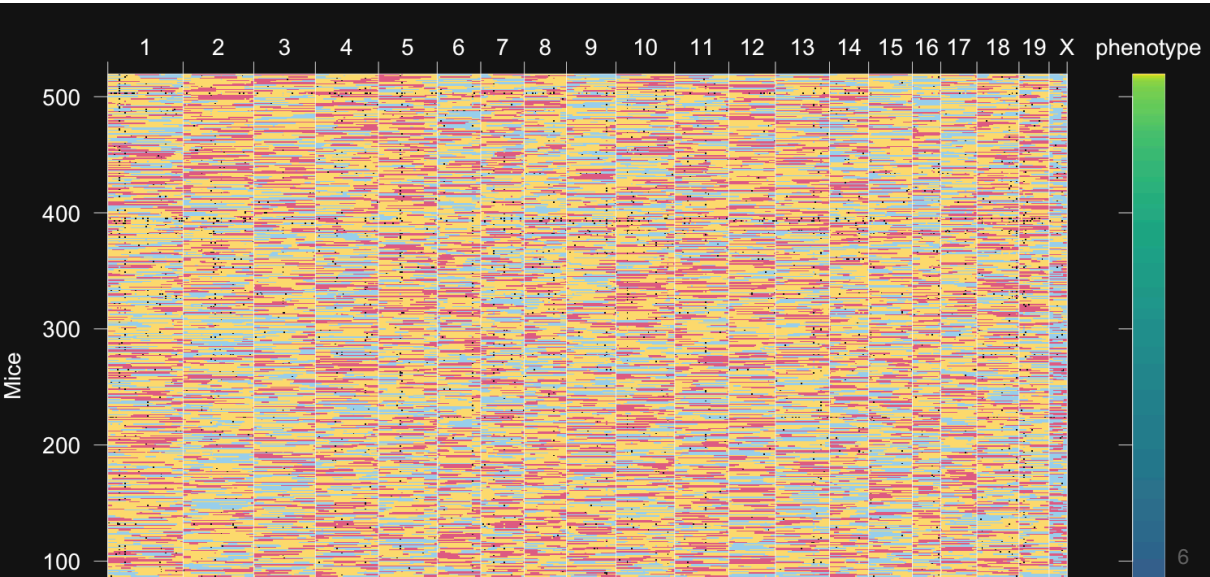


daviddeen.com

Intercross



Data


1
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19
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phenotype
500
400
300
200
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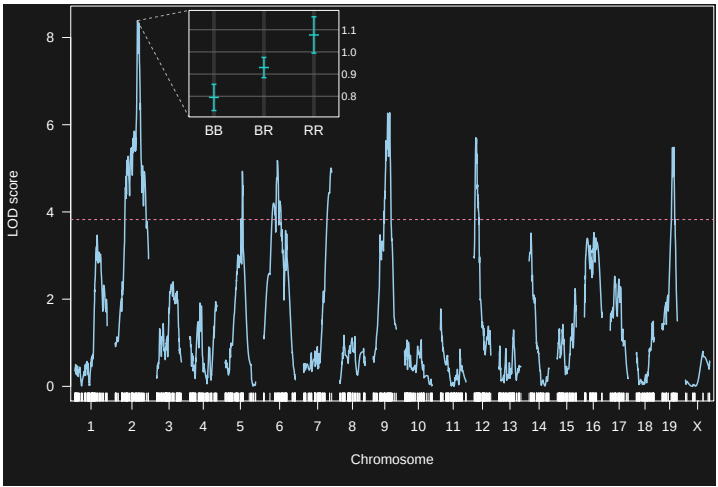
Mice
6

QTL mapping


LOD score
8
6
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1.0
0.9
0.8
BB
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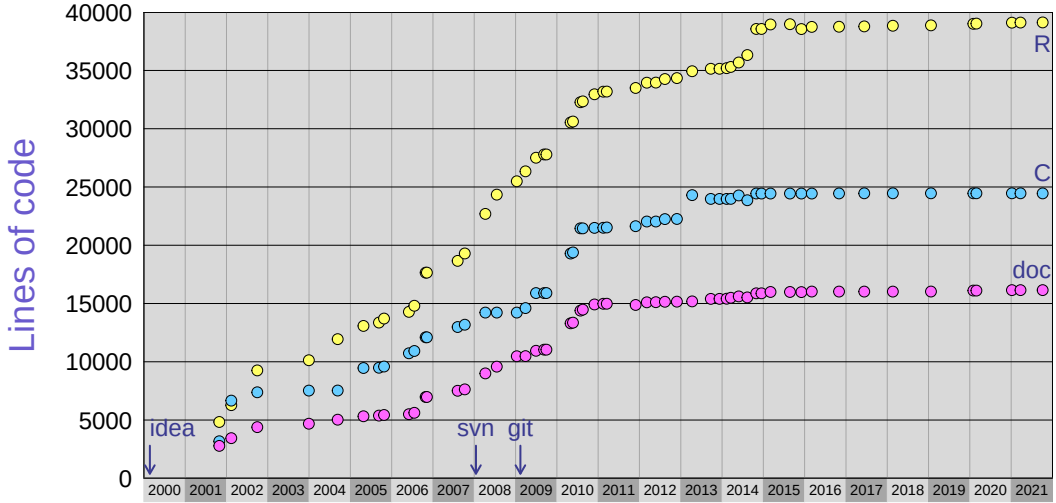
19
X
Chromosome

21 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

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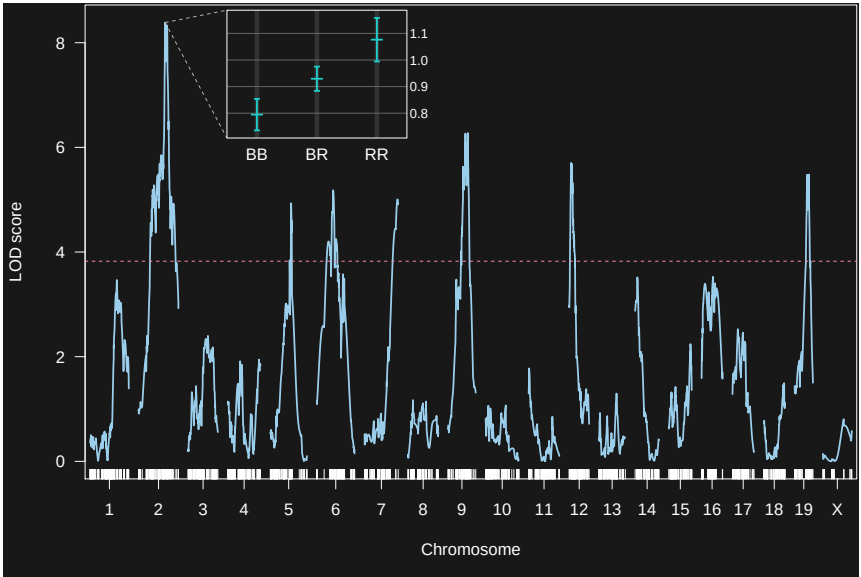
Version control means
everyone can see every stupid mistake I've ever made

Documentation

Support

QTL mapping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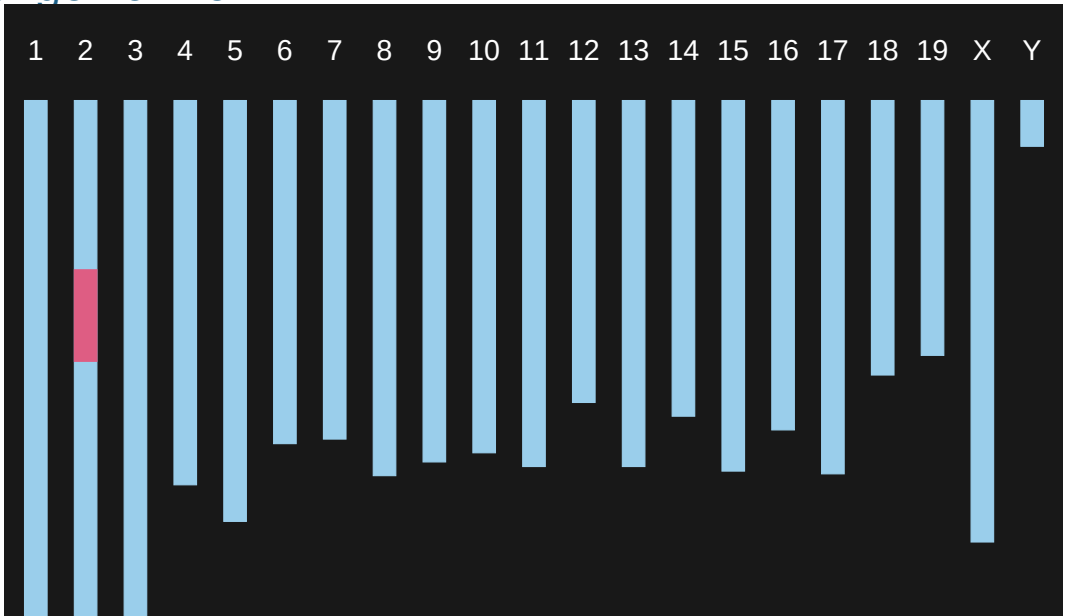
Chromosome

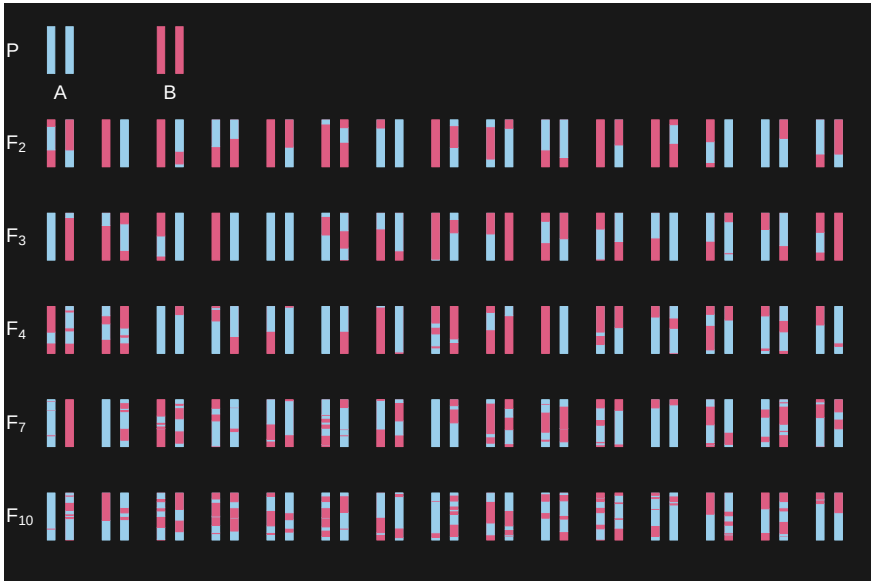
Congenic line



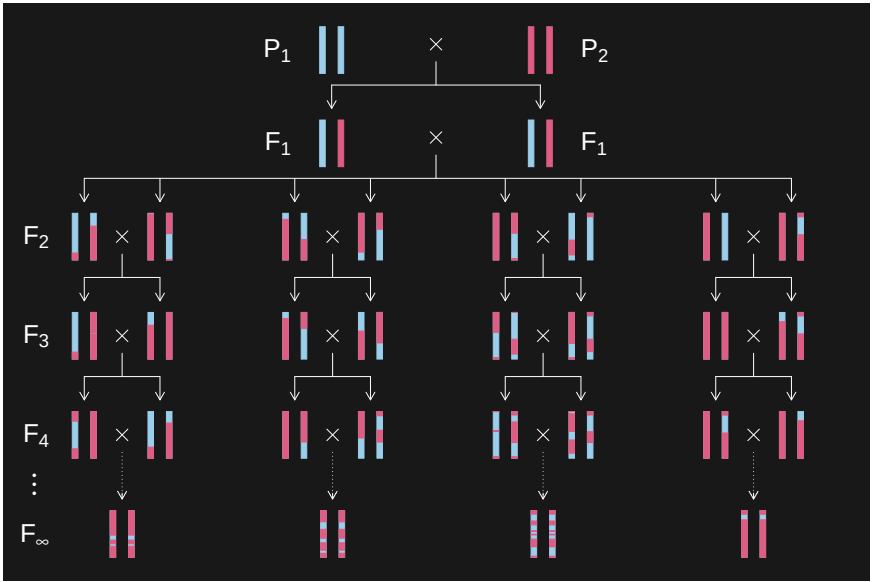
Improving precision

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

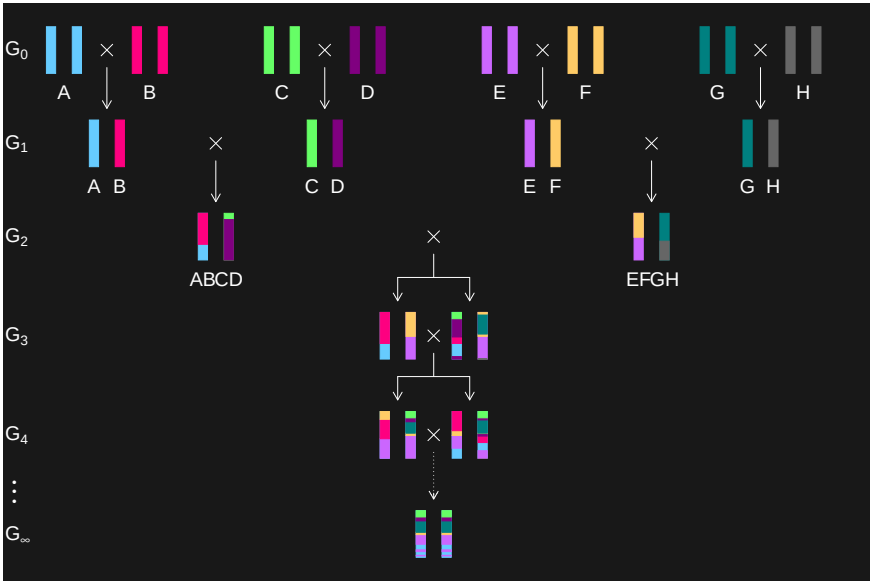
Advanced intercross lines



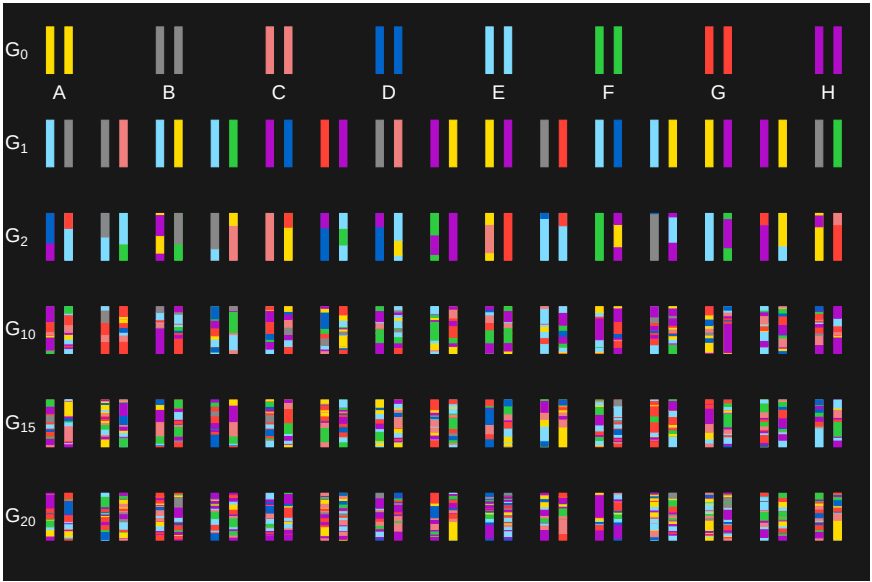
Recombinant inbred lines



Collaborative Cross



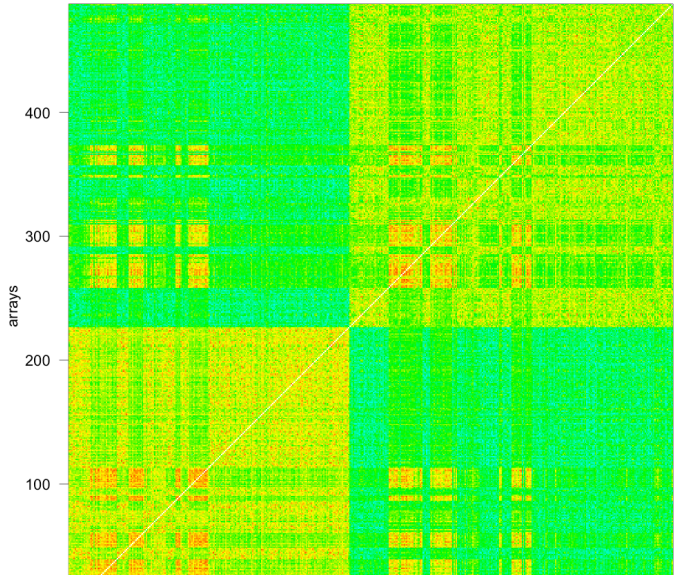
Heterogeneous stock



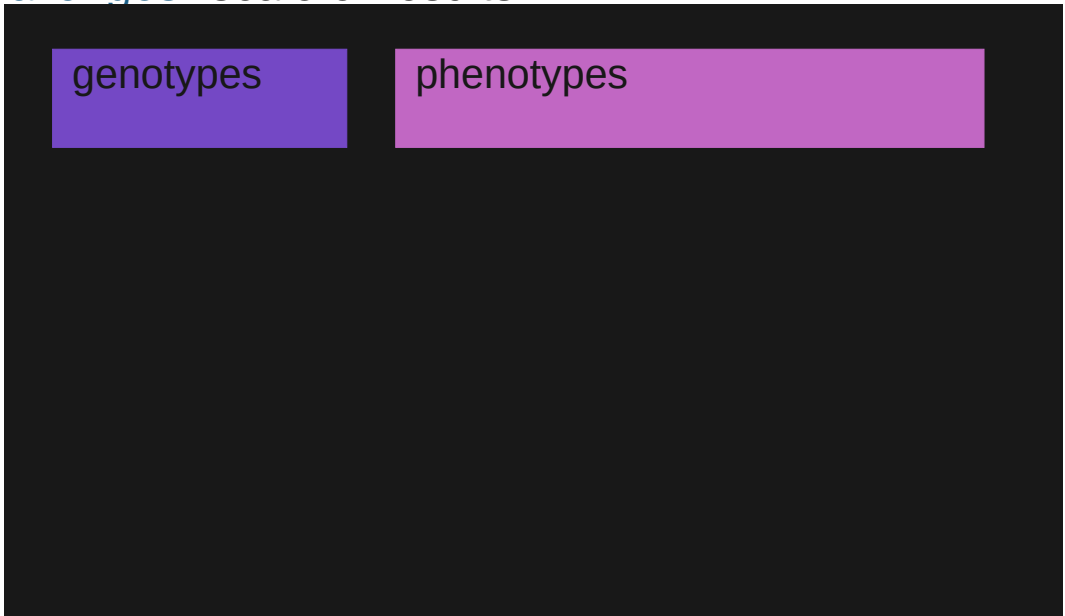
Genome-scale phenotypes

Alan Attie

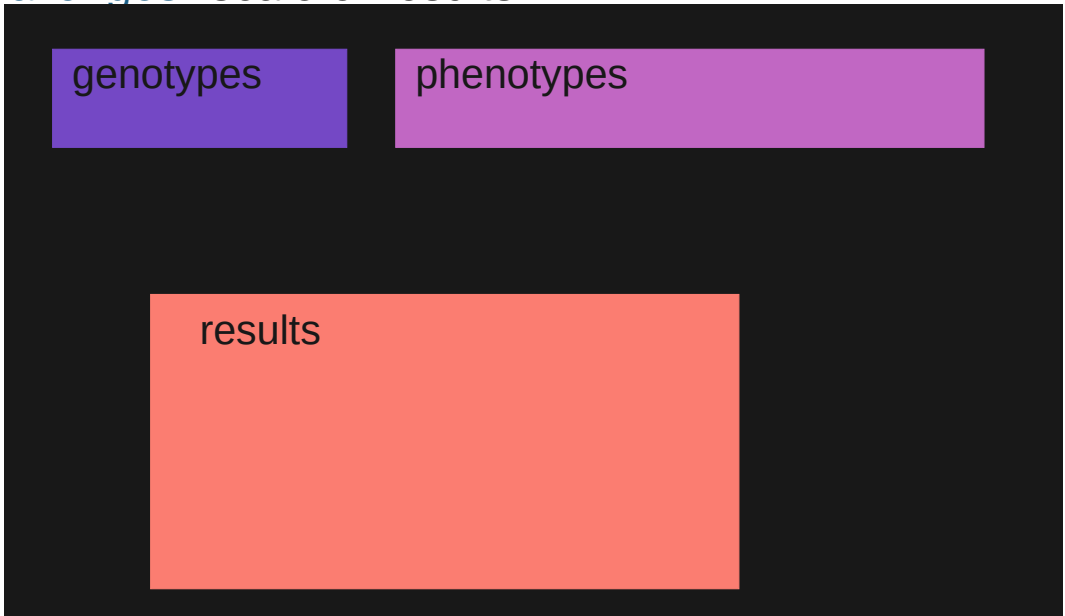
Challenges: diagnostics



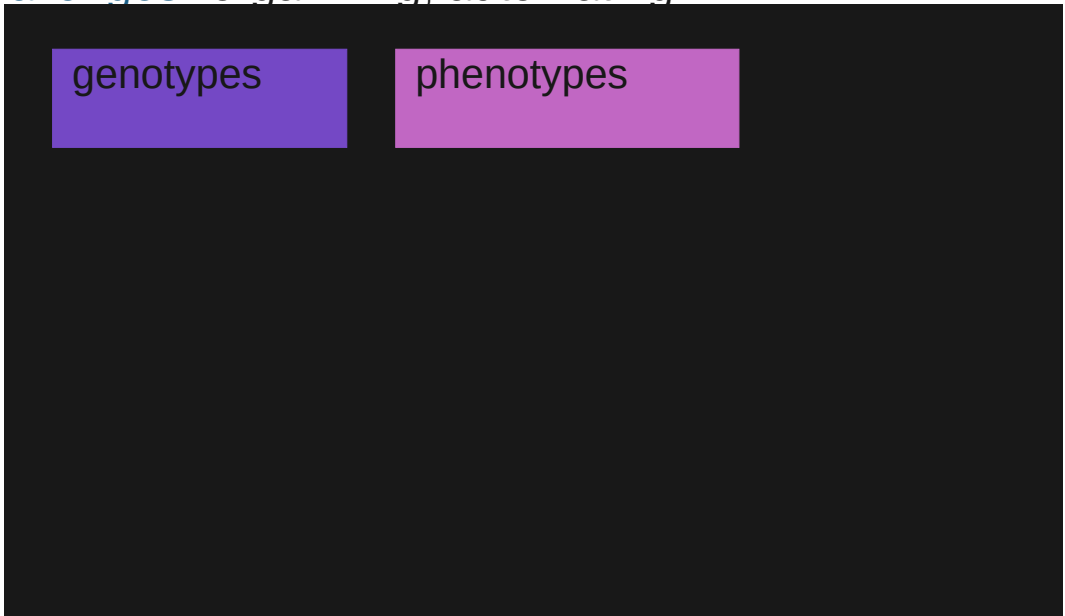
Challenges: scale of results



Challenges: scale of results



Challenges: organizing, automating



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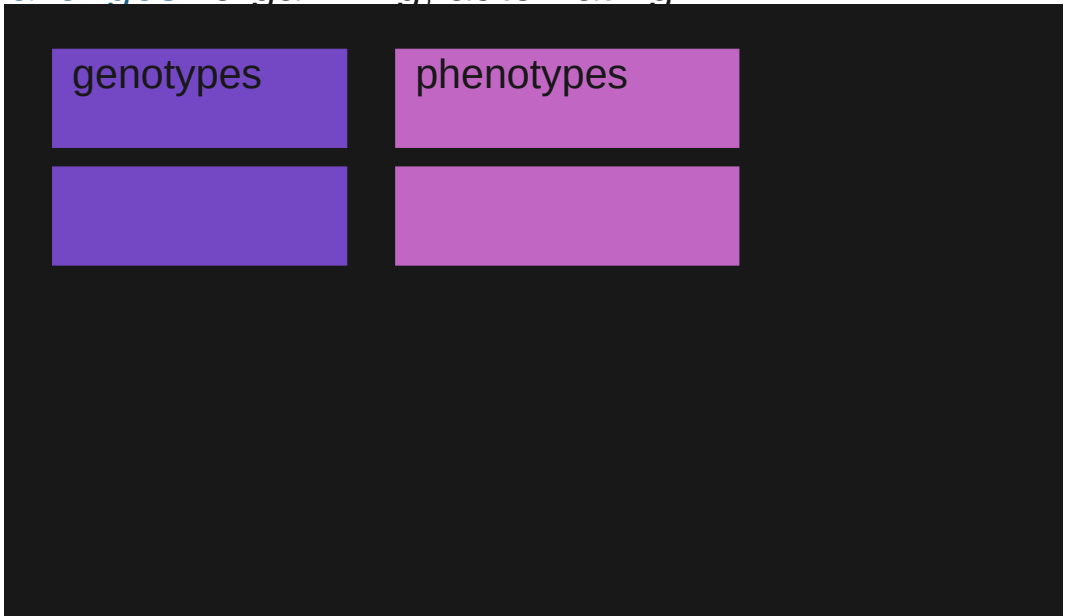

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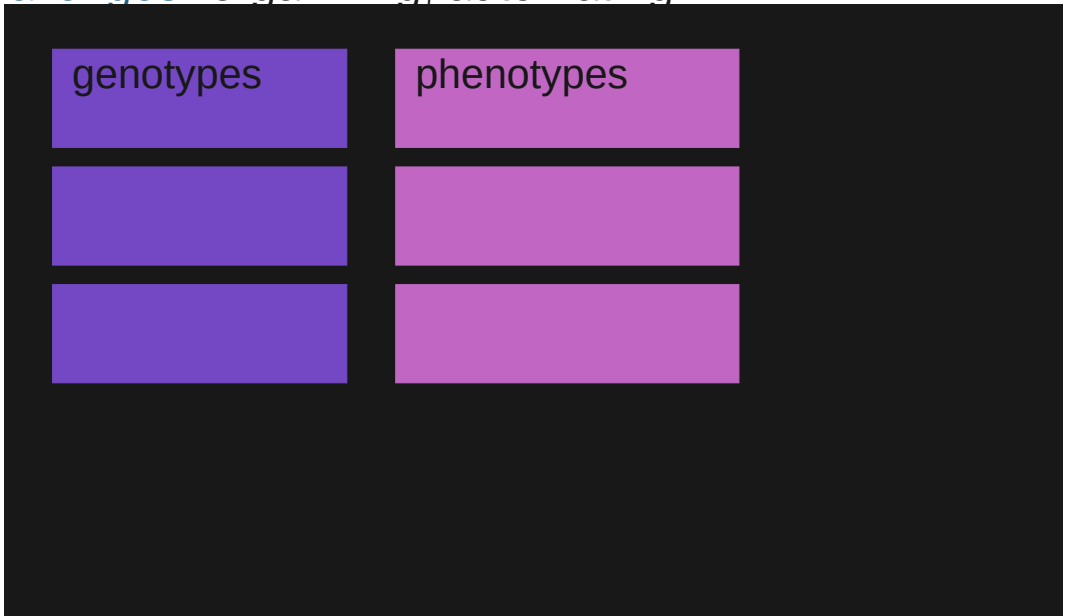

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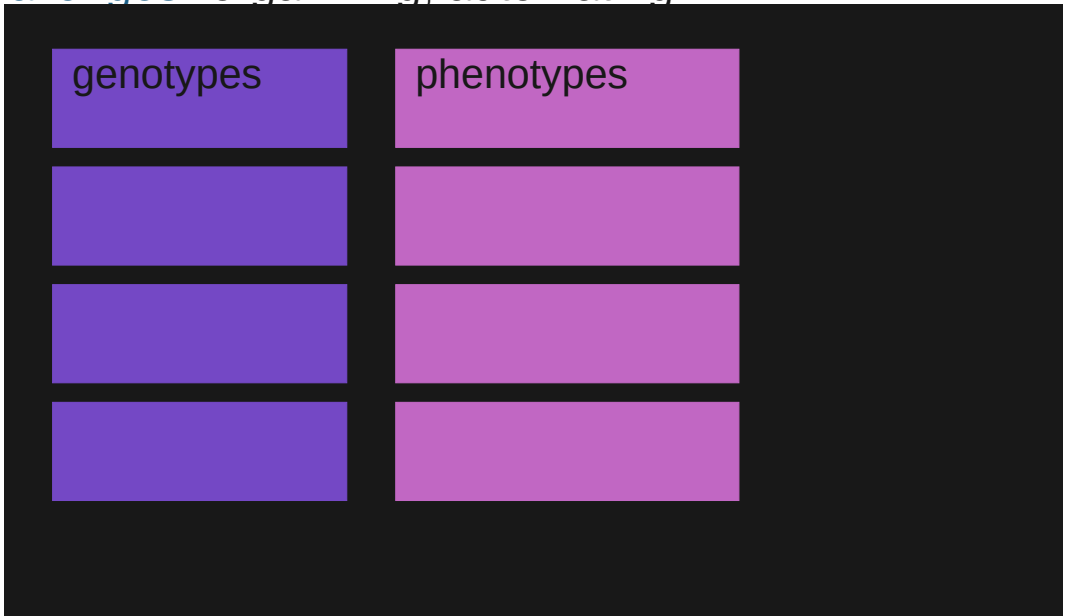

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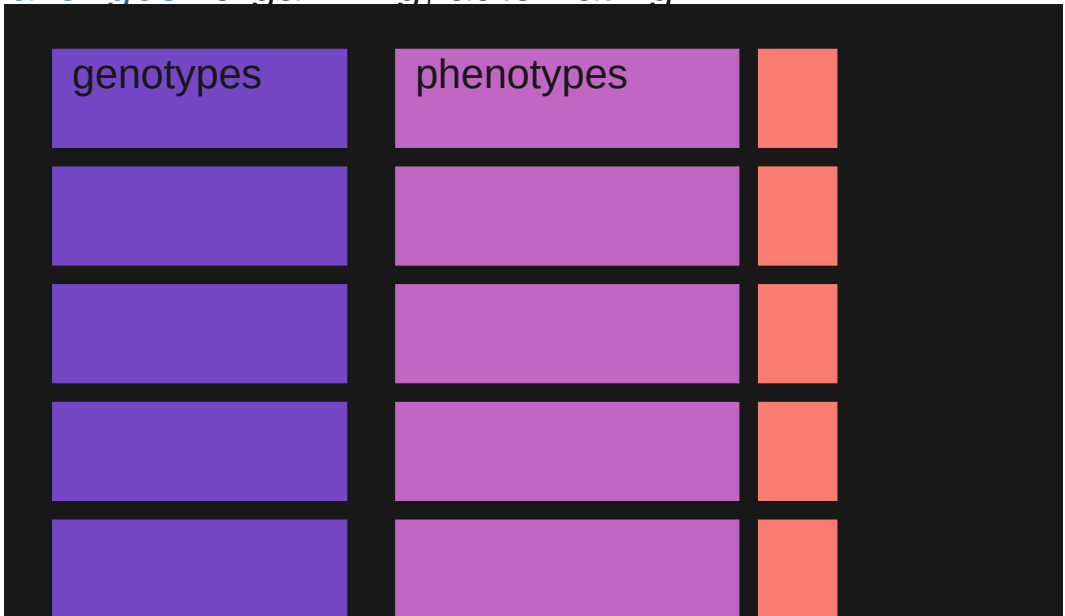

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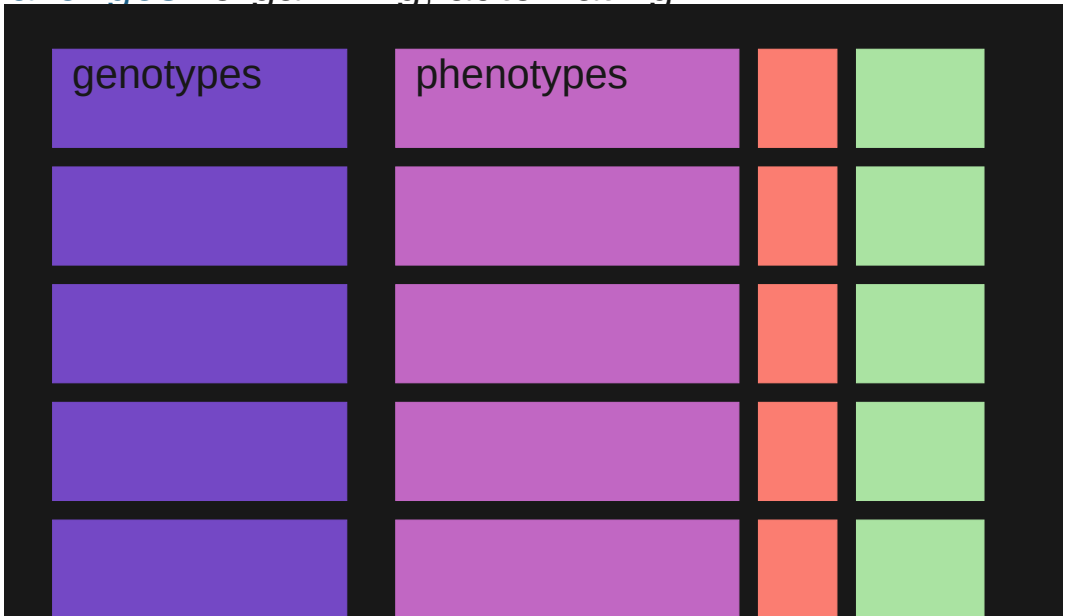

Challenges: metadata

What the heck is `"FAD_NAD SI 8.3_3.3G"`?

What was the question again?


R/qt12
How in 3D

R/qtl2

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

kbroman.org/qtl2

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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Brian Yandell

Robert Corty
Timothée Flutre
Lars Ronnegard
Rohan Shah
Laura Shannon
Quoc Tran
Aaron Wolen

NIH/NIGMS

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