

QTL mapping in MAGIC populations with R/qtl2

Part 2

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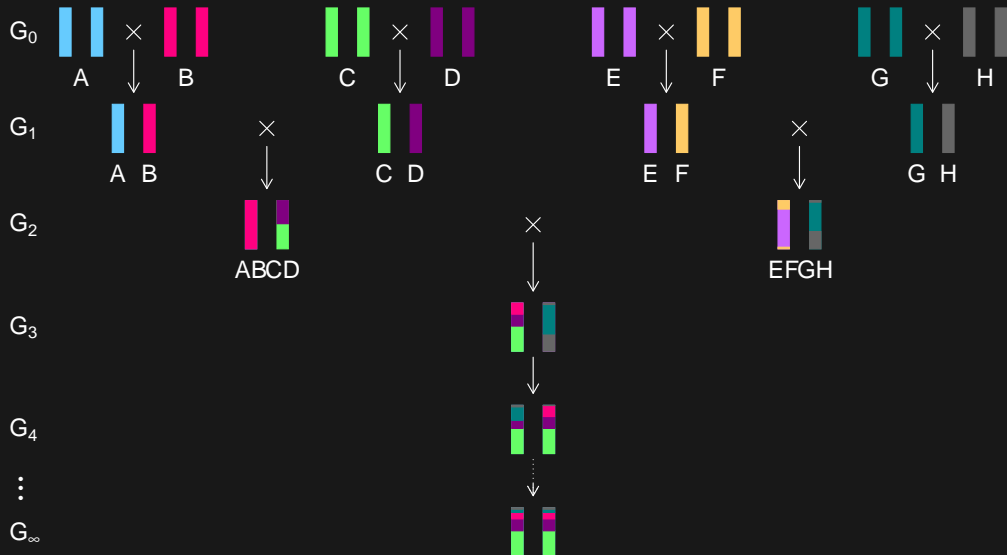
`github.com/kbroman`

`@kwbroman`

Slides: `kbroman.org/Talk_MAGIC2021`



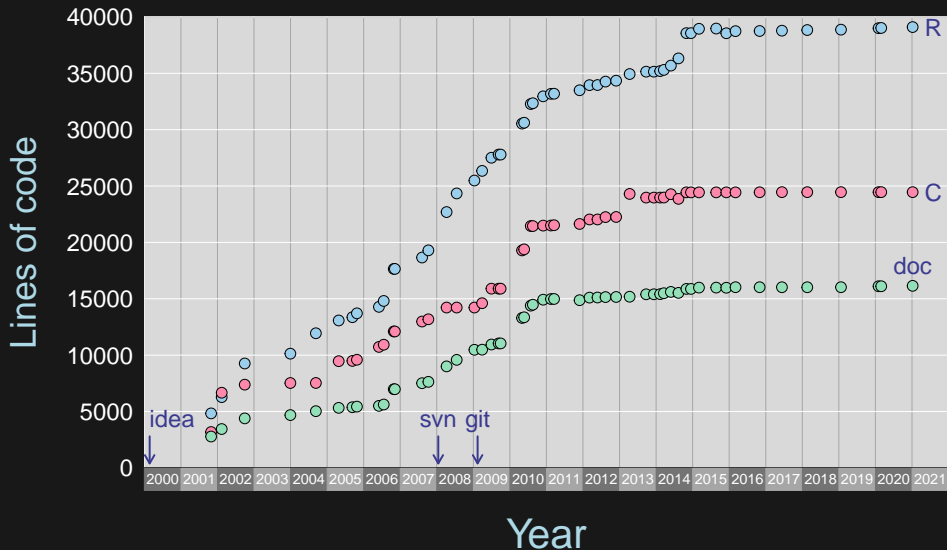
MAGIC



MAGIC is magic

- ▶ Genetic diversity
- ▶ High-precision mapping
- ▶ Predictable linkage disequilibrium
- ▶ Phenotype replicates to reduce individual variation
- ▶ Pool phenotypes from multiple labs, environments, treatments
- ▶ Genotype once
- ▶ Cool name

21 years of R/qtI



R/qtl cross types

- ▶ backcross, doubled haploids, haploid
- ▶ intercross
- ▶ 2-way RIL by selfing or sibling mating
- ▶ phase-known 4-way cross



R/qtI2 cross types

- ▶ backcross, doubled haploids, haploid
- ▶ intercross
- ▶ 2-, 4-, 8-, 16-way RIL by selfing
- ▶ 2-, 4-, 8-way RIL by sibling mating
- ▶ 2-, 3-, 8-way advanced intercross
- ▶ 6- and 19-way MAGIC
- ▶ Diversity Outbred (DO) mice
- ▶ F_1 of DO \times inbred
- ▶ general RIL or AIL

Data files

	A	B	C	D	E	F	G
1	id	bolting_days	seed_weight	seed_area	ttl_seedspruit	branches	height
2	MAGIC.1	15.33	17.15	0.64	45.11	10.5	NA
3	MAGIC.2	22	22.71	0.75	49.11	4.33	42.33
4	MAGIC.3	23	21.03	0.68	57	4.67	50
5	MAGIC.4	18.67	22.45	0.74	54.33	6.33	NA
6	MAGIC.5	18.67	25.36	0.82	38.33	5.67	42.25
7	MAGIC.6	25	21.53	0.71	52	4.33	NA
8	MAGIC.7	15.33	20.92	0.71	39	4	37.35
9	MAGIC.8	14.33	24.2	0.79	50.56	7.33	43.23
10	MAGIC.9	16.33	18.86	0.63	75.78	5.33	42.4
11	MAGIC.10	30	30.46	0.91	56.33	3	48.5
12	MAGIC.11	14	20.58	0.66	41.56	5.67	36.25
13	MAGIC.12	21.33	19.05	0.67	52.33	4.67	49.35
14	MAGIC.14	18.67	21.14	0.72	49.78	6	48.5
15	MAGIC.15	15	21.71	0.73	49	6.33	41.9
16	MAGIC.16	18.33	21.37	0.71	66.67	3.33	18.17

Data files

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1	id	bolting_days	seed_weight	seed_area	ttl_seedspruit	branches	height	
2		A	B	C	D	E	F	G
3	1	marker	MAGIC.1	MAGIC.10	MAGIC.100	MAGIC.101	MAGIC.102	MAGIC.103
4	2	MN1_29291	A	A	A	B	B	A
5	3	MN1_29716	A	A	A	B	B	A
6	4	MN1_112907	A	A	A	B	B	A
7	5	MASC03771	A	B	A	A	B	A
8	6	MN1_197787	A	B	A	B	B	A
9	7	MN1_340810	A	B	A	A	A	A
10	8	MN1_395107	A	A	A	A	B	A
11	9	MN1_444820	A	A	–	A	A	A
12	10	MN1_494205	A	A	A	A	A	A
13	11	MN1_592863	A	B	A	A	A	A
14	12	MN1_592760	A	A	A	A	A	A
15	13	BKN118	A	A	A	A	A	A
16	14	MN1_1042427	A	B	B	A	B	B
	15	CRY2_1021	A	A	A	A	A	A
	16	CRY2_429	A	A	A	A	B	A

Data files

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1	id	bolting_days	seed_weight	seed_area	tll_seedspruit	branches	height															
2		A	B	C	D	E	F	G														
3	1	marker	MAGIC.1	MAGIC.10	MAGIC.100	MAGIC.101	MAGIC.102	MAGIC.103														
4	2		A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
5	3	1	marker	Bur	Can	Col	Ct	Edi	Hi	Kn	Ler	Mt	No	Oy	Po	Rsch	Sf	Tsu	Wil	Ws	Wu	Zu
6	4	2	MN1_29291	B	A	A	B	A	A	B	A	A	A	B	B	A	B	A	A	A	A	A
7	5	3	MN1_29716	B	A	A	B	A	A	B	A	A	A	B	B	A	B	A	A	A	A	A
8	6	4	MN1_112907	B	A	A	A	B	B	B	B	A	A	B	B	A	B	B	A	A	A	A
9	7	5	MASC03771	A	B	A	A	B	A	B	A	A	A	A	A	A	A	A	A	A	A	A
10	8	6	MN1_197787	B	B	A	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B
11	9	7	MN1_340810	B	B	A	B	A	B	A	A	A	A	A	A	A	A	A	A	B	B	A
12	10	8	MN1_395107	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A	A	A
13	11	9	MN1_444820	B	A	A	B	B	A	A	A	A	A	A	A	A	A	B	A	B	B	A
14	12	10	MN1_494205	B	A	A	A	B	A	A	A	A	A	A	A	A	A	A	A	B	A	A
15	13	11	MN1_592863	A	B	A	B	A	A	A	B	A	A	A	A	A	A	B	A	B	A	A
16	14	12	MN1_592760	B	A	A	A	B	A	A	A	A	A	A	A	A	A	A	A	A	A	A
	15	13	BKN118	B	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
	16	14	MN1_1042427	A	B	A	B	A	B	B	A	B	A	A	A	B	A	A	B	A	B	A
		15	CRY2_1021	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A	A	A	A	A
		16	CRY2_429	A	A	A	A	A	B	B	B	A	B	A	A	A	A	A	A	B	A	A
		17	MASC07014	A	A	B	A	A	A	A	A	A	A	A	A	B	A	A	B	A	A	A
		18	MASC03609	A	A	A	A	A	A	B	B	A	B	B	B	A	A	A	A	B	A	A
		19	MN1_1296068	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	B	B	A
		20	MN1_1399466	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	-	B	A	A
		21	AXR1_381	A	B	A	A	A	B	A	A	A	B	A	A	A	A	A	A	B	A	B
		22	MASC07424	A	B	B	A	A	A	A	A	A	A	A	A	A	B	-	A	A	A	A

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4	2		A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	
5	3	1	marker	Bur	Can	Col	Ct	Edi	Hi	Kn	Ler	Mt	No	Ov	Po	Rsch	Sf	Tsu	Wil	Ws	Wu	Zu	
6	4	2	MN1_292				A				B				C	B	A	B	A	A	A	A	
7	5	3	MN1_297	1				marker				chr				pos	B	A	B	A	A	A	A
8	6	4	MN1_112	2				MN1_29291				1				0.029291	B	A	B	B	A	A	A
9	7	5	MASC037	3				MN1_29716				1				0.029757	A	A	A	A	A	A	A
10	8	6	MN1_197	4				MN1_112907				1				0.112907	A	A	B	A	A	B	B
11	9	7	MN1_340	5				MASC03771				1				0.174605	A	A	A	A	A	B	A
12	10	8	MN1_444	6				MN1_197787				1				0.197787	A	A	A	B	A	B	A
13	11	9	MN1_494	7				MN1_340810				1				0.34081	A	A	A	A	A	A	A
14	12	10	MN1_592	8				MN1_395107				1				0.395107	A	A	A	B	A	B	A
15	13	11	MN1_592	9				MN1_444820				1				0.444764	A	A	A	A	A	A	A
16	14	12	BKN118	10				MN1_494205				1				0.494205	A	A	A	A	A	A	A
	15	13	MN1_1042	11				MN1_592863				1				0.592867	A	B	A	A	A	B	A
	16	14	CRY2_1021	12				MN1_592760				1				0.592984	A	A	A	A	A	A	A
		15	CRY2_429	13				BKN118				1				0.761584	A	A	A	A	A	B	A
		16	MN1_1296	14				MN1_1042427				1				1.042428	A	A	A	A	-	B	A
			MN1_1395	15				CRY2_1021				1				1.187841	A	A	A	A	A	B	A
			AXR1_3	16				CRY2_429				1				1.188433	A	A	A	A	A	A	A
			MASC07014	17				MASC07014				1				1.189374							
			MASC03609	18				MASC03609				1				1.22655							

Control file (json or yaml)

```
{
  "description": "Arabidopsis MAGIC data, Gnan et al (2014)",
  "crosstype": "magic19",
  "sep": ",",
  "na.strings": ["-", "NA"],
  "comment.char": "#",
  "geno": "arabmagic_geno.csv",
  "founder_geno": "arabmagic_foundergeno.csv",
  "gmap": "arabmagic_pmap_tair9.csv",
  "pmap": "arabmagic_pmap_tair9.csv",
  "pheno": "arabmagic_pheno.csv",
  "genotypes":
    "A": 1
    "H": 2
    "B": 3
},
  "geno_transposed": true,
  "founder_geno_transposed": true
}
```

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},
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}
```


Reading data into R

```
library(qtl2)  
arab <- read_cross2("arab_magic.json")
```

Reading data into R

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```

19-way Arabidopsis MAGIC

Kover et al. (2009) PLoS Genet

Gnan et al. (2014) Genetics

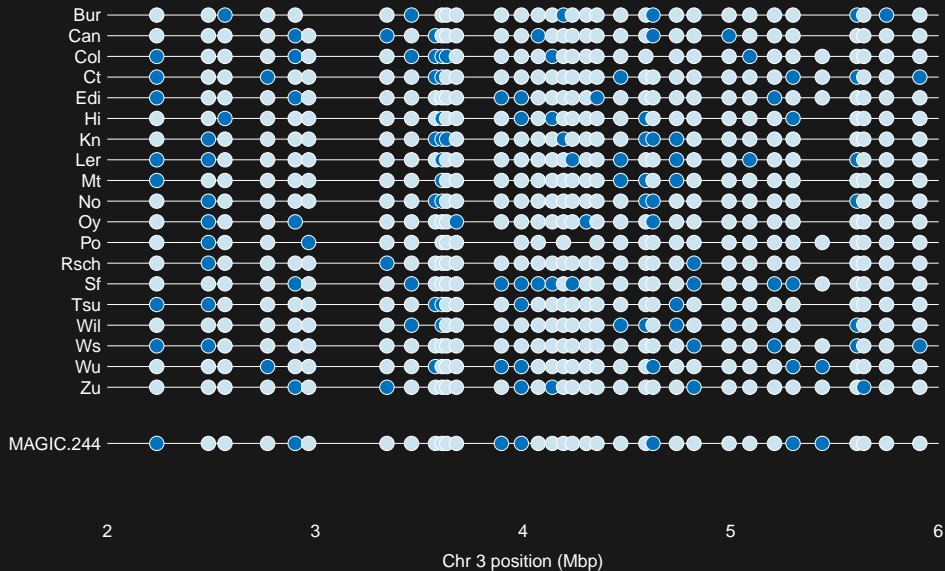
github.com/rqtl/qtl2data

Data diagnostics

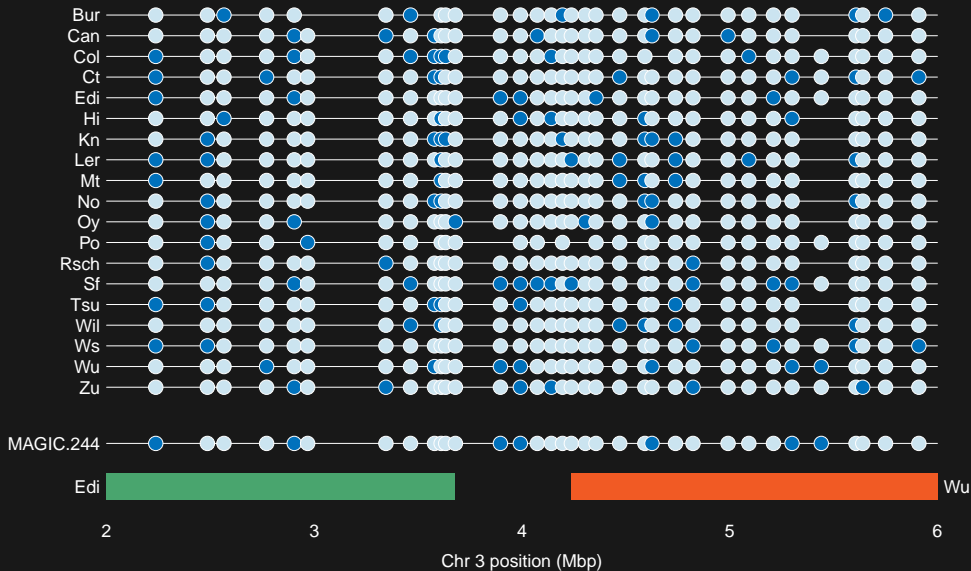
See Broman et al. (2019) Cleaning genotype data from
Diversity Outbred mice. G3 9:1571–1579

doi: [10.1534/g3.119.400165](https://doi.org/10.1534/g3.119.400165)

Genotype reconstruction



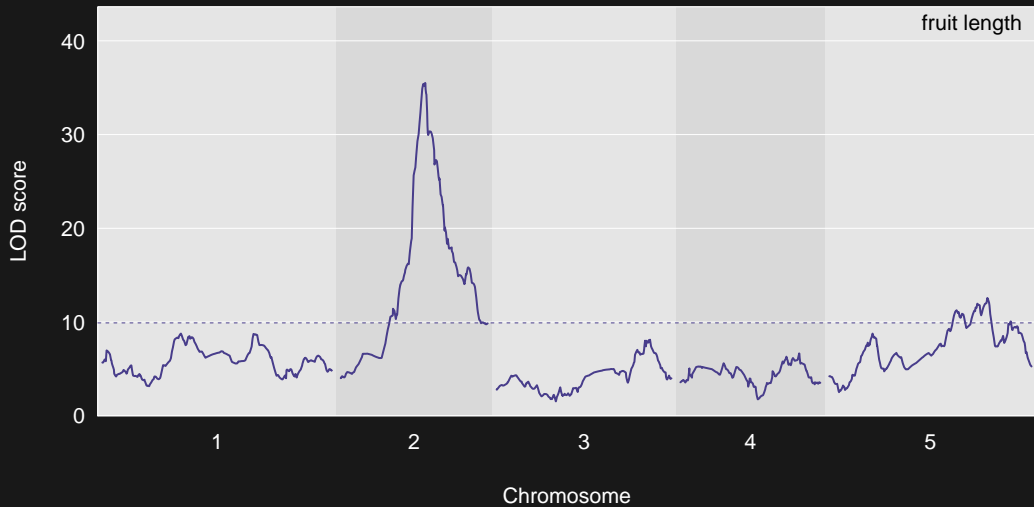
Genotype reconstruction



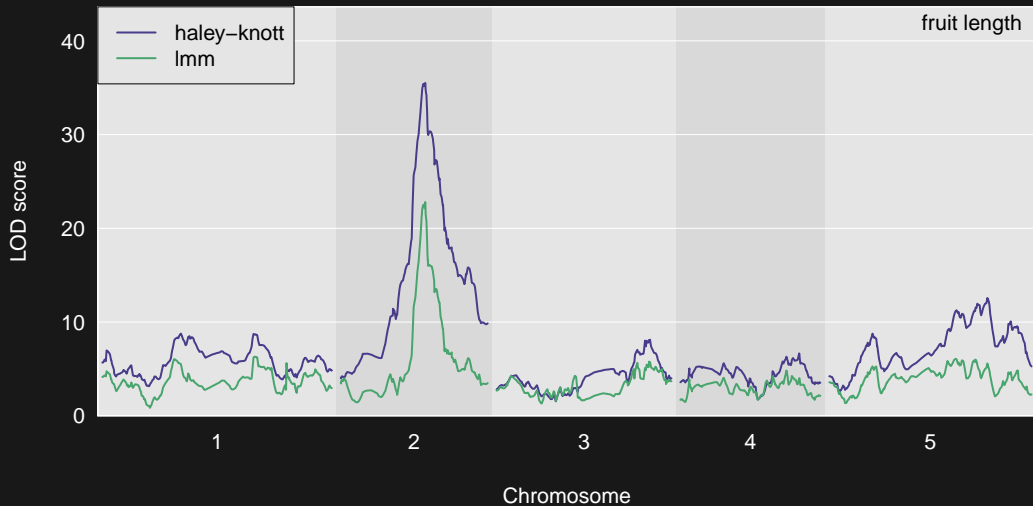
Genotype reconstruction

```
gmap <- insert_pseudomarkers(arab$gmap, step=0.2, stepwidth="max")  
pmap <- interp_map(gmap, arab$gmap, arab$pmap)  
  
pr <- calc_genoprob(arab, gmap, error_prob=0.002, cores=24)
```

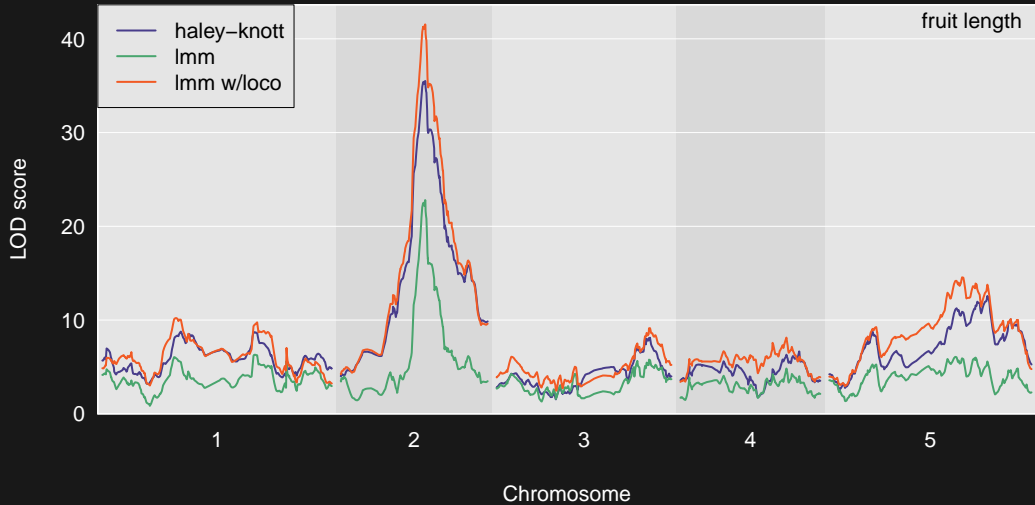
Genome scan



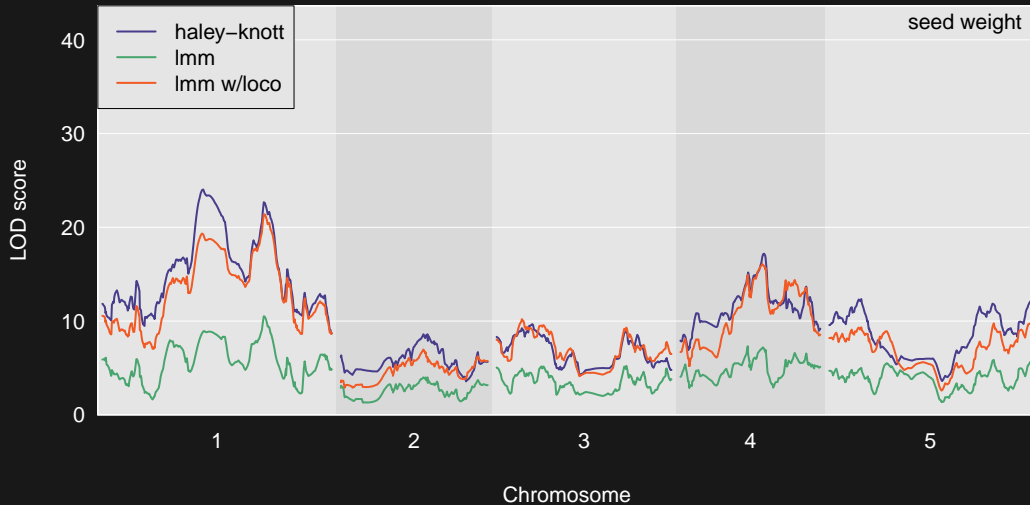
Genome scan



Genome scan



Genome scan



Genome scan

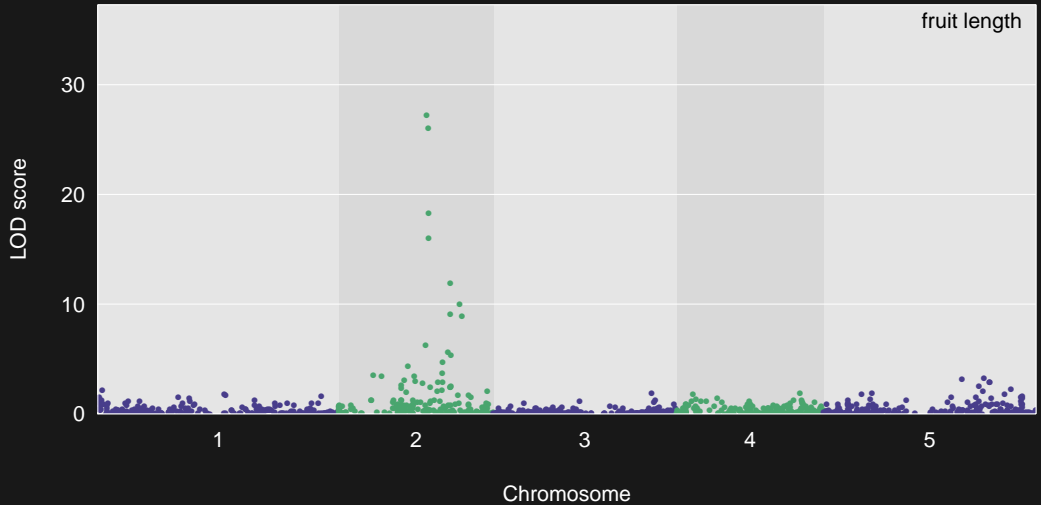
```
out_hk <- scan1(pr, arab$pheno, cores=24)

operm_hk <- scan1perm(pr, arab$pheno, n_perm=1000, cores=24)

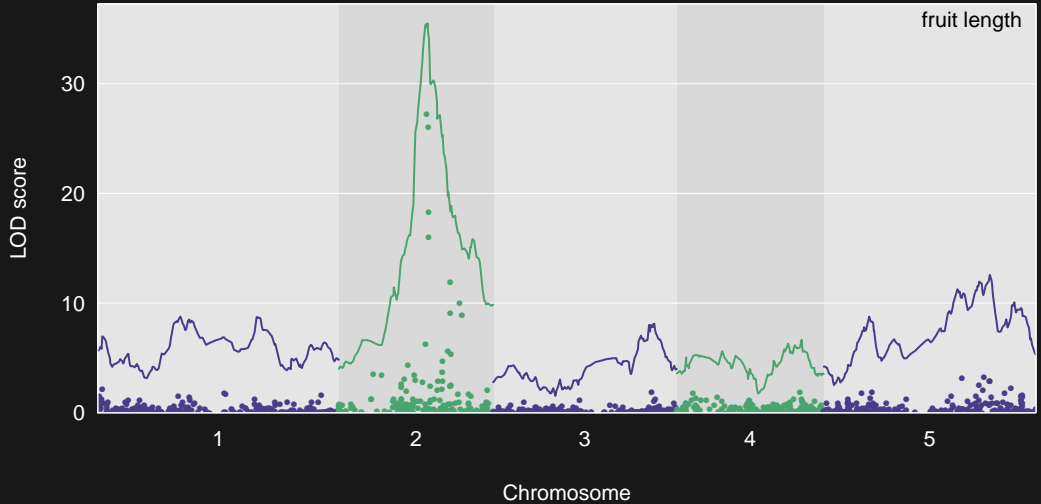
k <- calc_kinship(pr, cores=24)
out_lmm <- scan1(pr, arab$pheno, k, cores=24)

k_loco <- calc_kinship(pr, "loco", cores=24)
out_loco <- scan1(pr, arab$pheno, k_loco, cores=24)
```

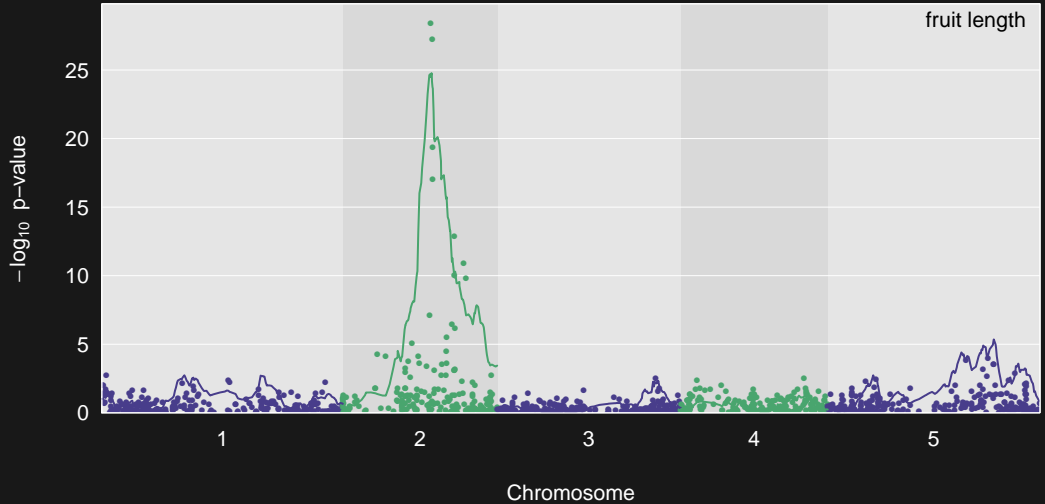
SNP association scan



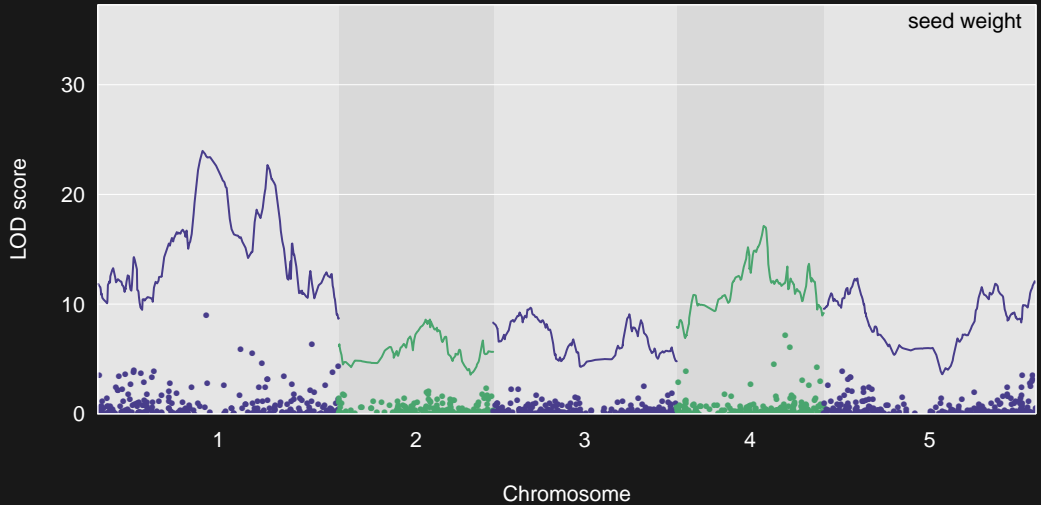
SNP association scan



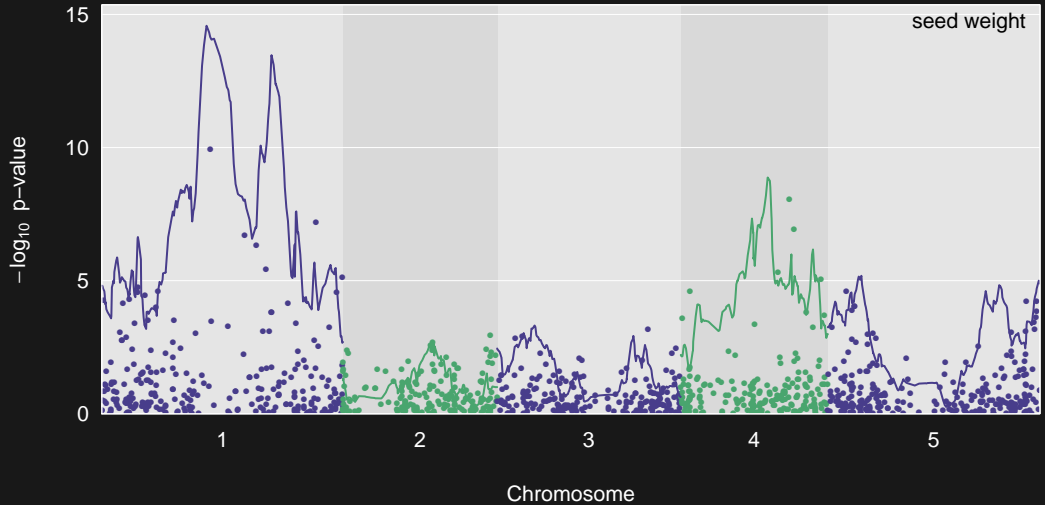
SNP association scan



SNP association scan



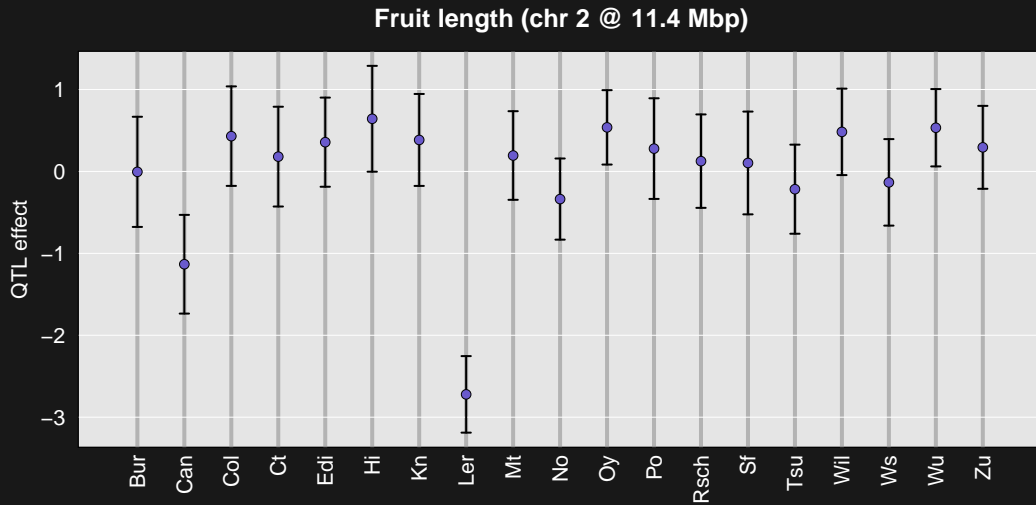
SNP association scan



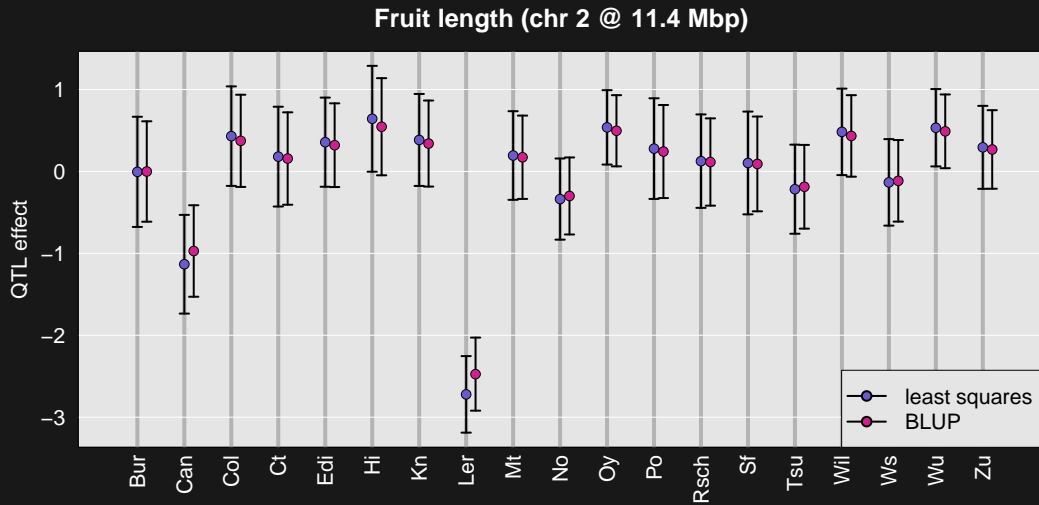
SNP association scan

```
snp_pr <- genoprob_to_snpprob(pr, arab)  
out_snps <- scan1(snp_pr, arab$fruit, cores=24)
```

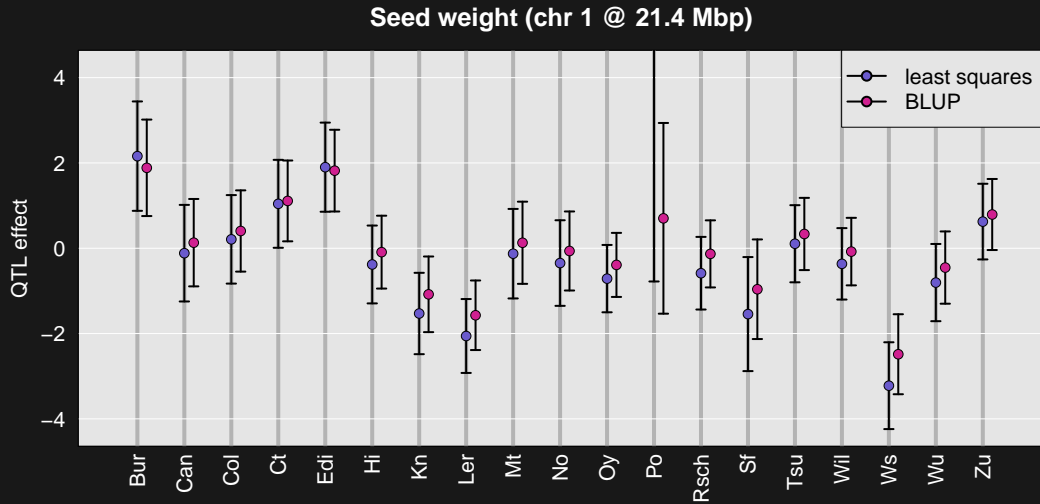
QTL effects



QTL effects



QTL effects



QTL effects

```
fl_peak <- max(out_hk, pmap, lodcolumn="fruit_length")
fl_pr <- pull_genoprobpos(pr, pmap, fl_peak$chr, fl_peak$pos)

fl_fit1 <- fit1(fl_pr, arab$pheno[, "fruit_length"])
fl_blup <- fit1(fl_pr, arab$pheno[, "fruit_length"], blup=TRUE)
```

Goals

- ▶ Genotype reconstructions from external software
- ▶ General models for RIL and AIL
- ▶ Sequencing-based genotype data
- ▶ Multiple-QTL models
- ▶ QTL \times environment interactions
- ▶ Interactive data visualization

Slides: kbroman.org/Talk_MAGIC2021



kbroman.org

kbroman.org/qt12

github.com/kbroman

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