

QTL mapping in MAGIC populations with R/qlt2

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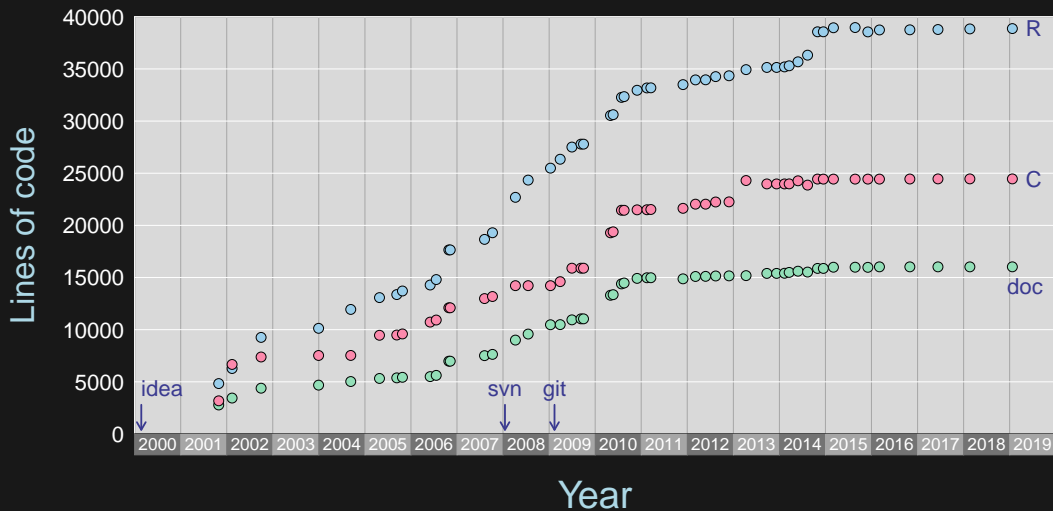
github.com/kbroman

@kwbroman

Slides: bit.ly/MAGIC19



19 years of R/qli



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_seedsfruit	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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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_seedsfruit	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	1	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	
5	3	2	marker	Bur	Can	Col	Ct	Edi	Hi	Kn	Ler	Mt	No	Oy	Po	Rsch	Sf	Tsu	Wil	Ws	Wu	Zu	
6	4	3	MN1_29291	B	A	A	B	A	A	B	A	A	A	B	B	A	B	A	A	A	A	A	
7	5	4	MN1_29716	B	A	A	B	A	A	B	A	A	A	B	B	A	B	B	A	A	A	A	
8	6	5	MN1_112907	B	A	A	A	B	B	B	B	A	A	B	B	A	B	B	A	A	A	A	
9	7	6	MASC03771	A	B	A	A	B	A	B	A	A	A	A	A	A	A	A	A	A	A	A	
10	8	7	MN1_197787	B	B	A	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	
11	9	8	MN1_340810	B	B	A	B	A	B	A	A	A	A	A	A	A	A	A	A	B	B	A	
12	10	9	MN1_395107	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A	A	A	
13	11	10	MN1_444820	B	A	A	B	B	A	A	A	A	A	A	A	A	A	B	A	B	B	A	
14	12	11	MN1_494205	B	A	A	A	B	A	A	A	A	A	A	A	A	A	A	A	A	B	A	
15	13	12	MN1_592863	A	B	A	B	A	A	A	B	A	A	A	A	A	A	B	A	B	A	A	
16	14	13	MN1_592760	B	A	A	A	B	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
	15	14	BKN118	B	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
	16	15	MN1_1042427	A	B	A	B	A	B	B	A	B	A	A	A	B	A	A	B	A	B	A	
		16	CRY2_1021	A	A	A	A	B	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
			CRY2_429	A	A	A	A	A	B	B	B	A	B	A	A	A	A	A	A	B	A	A	
			MASC07014	A	A	B	A	A	A	A	A	A	A	A	A	B	A	A	B	A	A	A	
			MASC03609	A	A	A	A	A	A	B	B	A	B	B	B	A	A	A	A	B	A	A	
			MN1_1296068	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	A	B	B	A	
			MN1_1399466	A	A	A	A	A	A	B	A	A	A	A	A	A	A	A	-	B	A	A	
			AXR1_381	A	B	A	A	A	B	A	A	A	B	A	A	A	A	A	A	B	A	B	
			MASC07424	A	B	B	A	A	A	A	A	A	A	A	A	A	B	-	A	A	A	A	

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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
5	3	1	marker	Bur	Can	Col	Ct	Edi	Hi	Ko	Ler	Mt	No	Ov	Po	Rsch	Sf	Tsu	Wil
6	4	2	MN1_292				A		B				C		B	A	B	A	A
7	5	3	MN1_297	1			marker		chr				pos		B	A	B	B	A
8	6	4	MN1_112	2			MN1_29291		1				0.029291		A	A	A	A	A
9	7	5	MASC037	3			MN1_29716		1				0.029757		A	A	A	A	A
10	8	6	MN1_197	4			MN1_112907		1				0.112907		A	A	A	A	A
11	9	7	MN1_340	5			MASC03771		1				0.174605		A	A	A	A	A
12	10	8	MN1_395	6			MN1_197787		1				0.197787		A	A	A	A	A
13	11	9	MN1_444	7			MN1_340810		1				0.34081		A	A	A	B	A
14	12	10	MN1_494	8			MN1_395107		1				0.395107		A	A	A	A	A
15	13	11	MN1_592	9			MN1_444820		1				0.444764		A	A	A	A	A
16	14	12	MN1_592	10			MN1_494205		1				0.494205		A	A	A	A	A
	15	13	CRY2_10	11			MN1_592863		1				0.592867		A	A	A	A	A
	16	14	CRY2_4	12			MN1_592760		1				0.592984		A	A	A	A	A
	17	15	MASC070	13			BKN118		1				0.761584		B	A	A	A	A
	18	16	MN1_1296	14			MN1_1042427		1				1.042428		A	A	A	A	A
	19	17	MN1_1399	15			CRY2_1021		1				1.187841		A	A	A	A	A
	20	18	AXR1_3	16			CRY2_429		1				1.188433		A	A	B	-	A
	21	19	MASC074	17			MASC07014		1				1.189374						
	22	20		18			MASC03609		1				1.22655						
		21		19			MN1_1296068		1				1.296069						
		22		20			MN1_1399466		1				1.399467						

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": 3
    "H": 3
    "B": 3
},
"geno_transposed": true,
"founder_geno_transposed": true
}
```

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  "pmap": "arabmagic_pmap_tair9.csv",
  "pheno": "arabmagic_pheno.csv",
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    "B": 3
},
"geno_transposed": true,
"founder_geno_transposed": true
}
```

Reading data into R

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

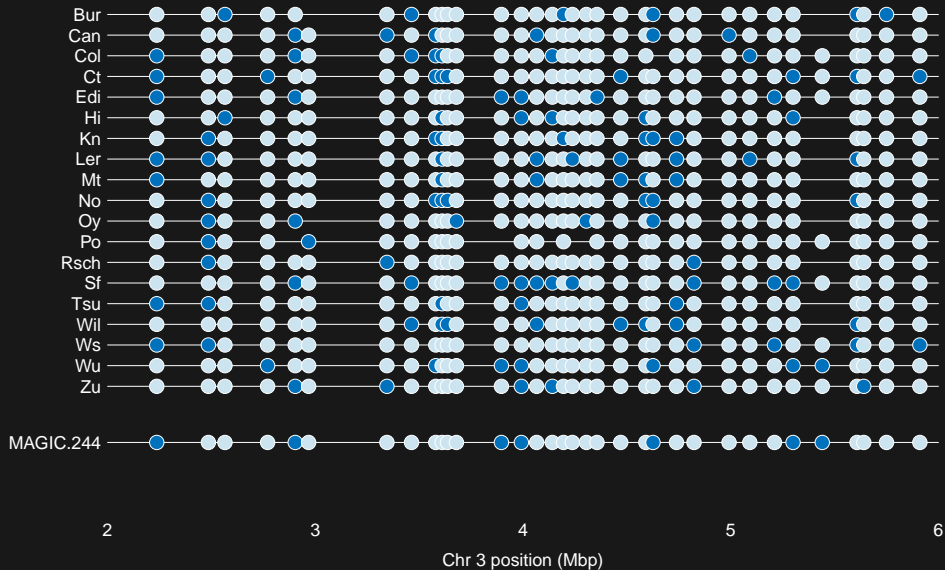
19-way Arabidopsis MAGIC

Kover et al. (2009) PLoS Genet

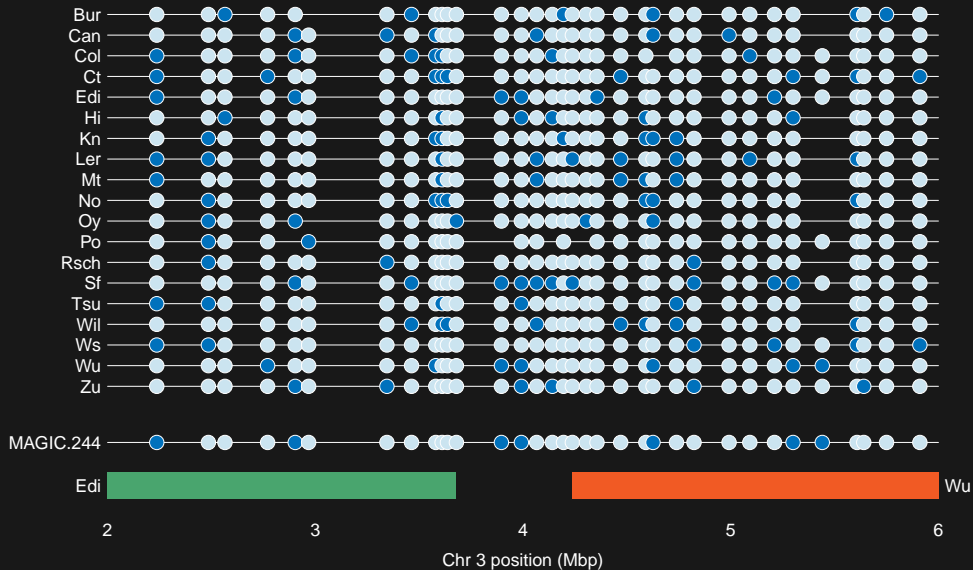
Gnan et al. (2014) Genetics

github.com/rqtl/qtl2data

Genotype reconstruction



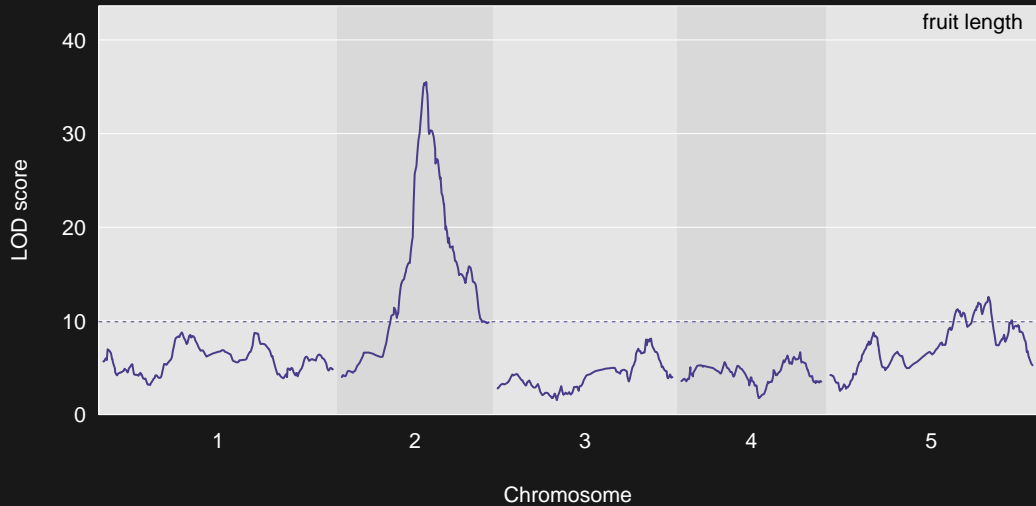
Genotype reconstruction



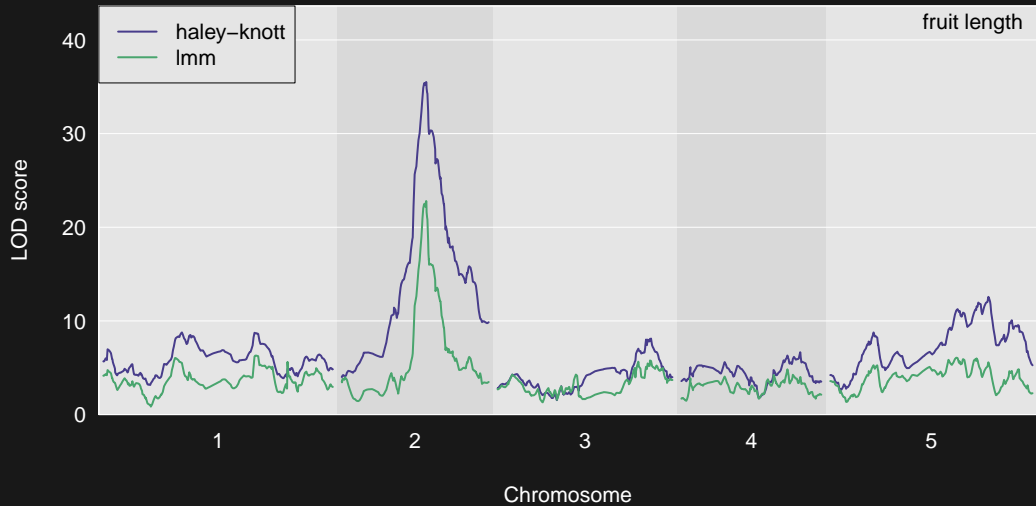
Genotype reconstruction

```
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)
```

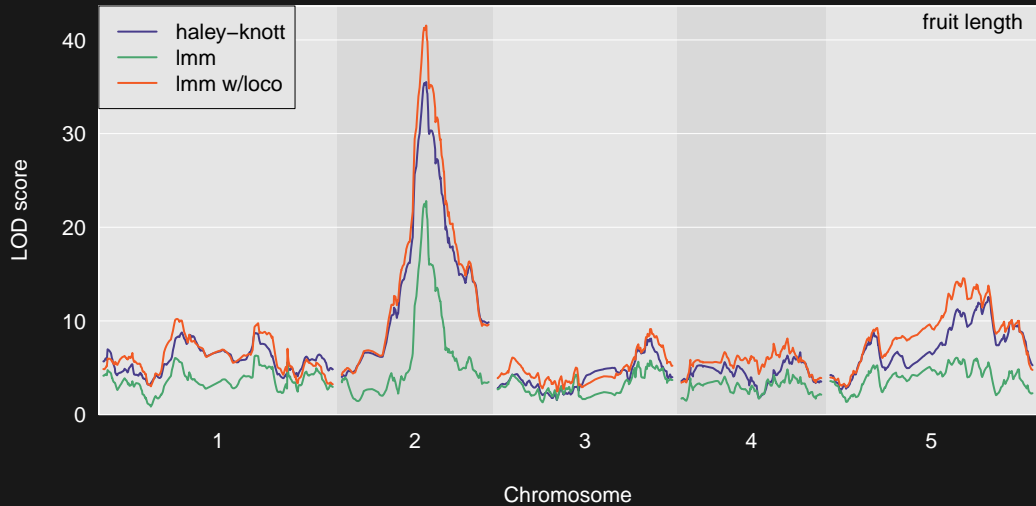
Genome scan



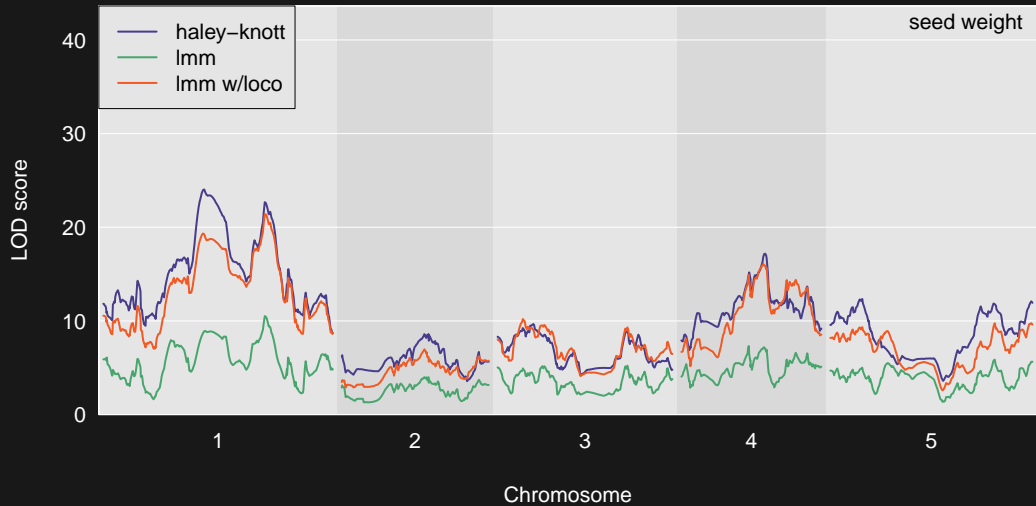
Genome scan



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)
```

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: bit.ly/MAGIC19



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kbroman.org/qt12

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