

R/qtl download

Before installing R/qtl, you must first install [R](#), which is available at the [Comprehensive R Archive Network \(CRAN\)](#).

<https://cran.r-project.org>

Once R is installed, and provided that your computer has an internet connection, it is easiest to install R/qtl by first invoking R and then typing the following:
`install.packages("qtl")`

rqtl HP

<http://www.rqtl.org>

A Guide to QTL Mapping with R/qtl: Online complements

<http://www.rqtl.org/book/>

rqtl manual

<http://www.rqtl.org/manual/qtl-manual.pdf>

QTL

read data

```
cross <- read.cross(format = "csvs", genfile = "data/geno_bc.csv", phefile="data/yield.csv")
```

genotype

format = "csvs"

id	Hor5	MWG938	MWG835A	MWG036A	MWG837	Hor1
	1	1	1	1	1	1
	0	0.7	2.1	6.2	11	13.1
1	A	A	A	A	A	A
2	H	H	H	H	H	H
3	A	A	A	A	A	A
4	H	H	H	H	H	H
5	H	H	H	H	H	A
6	A	A	A	A	A	A
7	H	H	H	H	H	H
8	A	A	A	A	A	A

phenotype

id	Env1	Env2	Env3	Env4	Env5
1	4.61	6.829	2.56	3.878	7.232
2	5.159	5.785	2.07	4.554	6.326
3	4.701	6.102	3.18	3.016	6.533
4	5.297	6.022	2.93	2.419	7.469
5	4.883	6.716	3.07	2.952	5.997
6	4.681	5.692	2.65	2.968	6.525
7	4.93	5.544	3.5	3.64	6.564

convert2riself Convert a cross to RIL by selfing

- `cross <- read.cross("csvr", file="test.csv",
estimate.map=FALSE, F.gen = 6)`
- `cross<-convert2riself(cross)`
- <http://www.rqtl.org/manual/qtl-manual.pdf>

QTL - phenotypic variation

How can I get the the percentage of phenotype variance explained by a QTL?

<https://groups.google.com/forum/#!topic/rqtl-disc/wyHxuaBr-gA>

```
$result.full
      df      SS      MS      LOD      %var Pvalue(Chi2)      Pvalue(F)
Model   3 1515.210 505.06993 8.056636 17.08753 4.37793e-08 6.030568e-08
Error 194 7352.131 37.89758      NA      NA      NA      NA
Total 197 8867.341      NA      NA      NA      NA      NA

$result.drop
      df Type III SS      LOD      %var F value Pvalue(Chi2)      Pvalue(F)
2@39.9  1      560.4122 3.158383 6.319958 14.78754 0.0001368593 0.0001631004
6@38.5  1      474.0002 2.686255 5.345460 12.50740 0.0004361334 0.0005070081
8@46.9  1      358.9511 2.049507 4.048013 9.47161 0.0021249709 0.0023887012

%var shows QTL contributions(%).

2@39.9  -> 6.319958
6@38.5  -> 5.345460
8@46.9  -> 4.048013

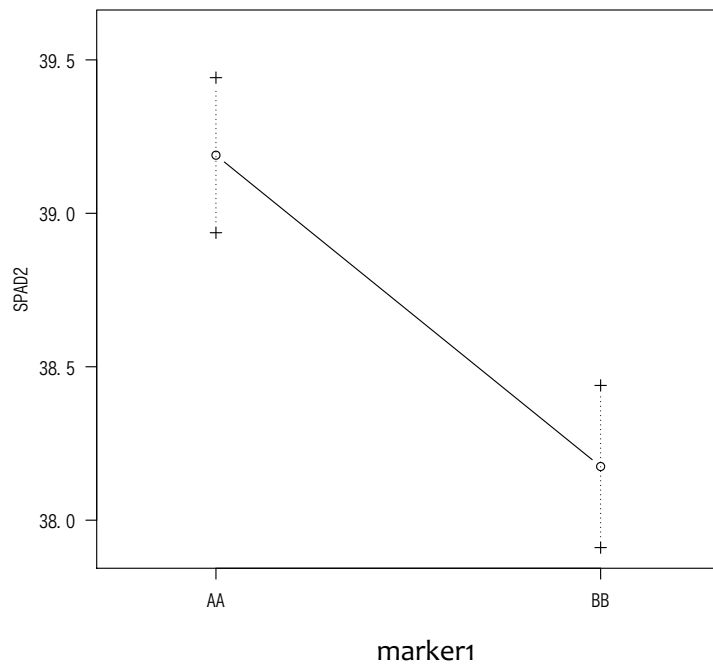
%var = percent of the phenotype variance explained by the QTL.

2@39.9  -> 6.319958 = 560.4122/8867.341
```

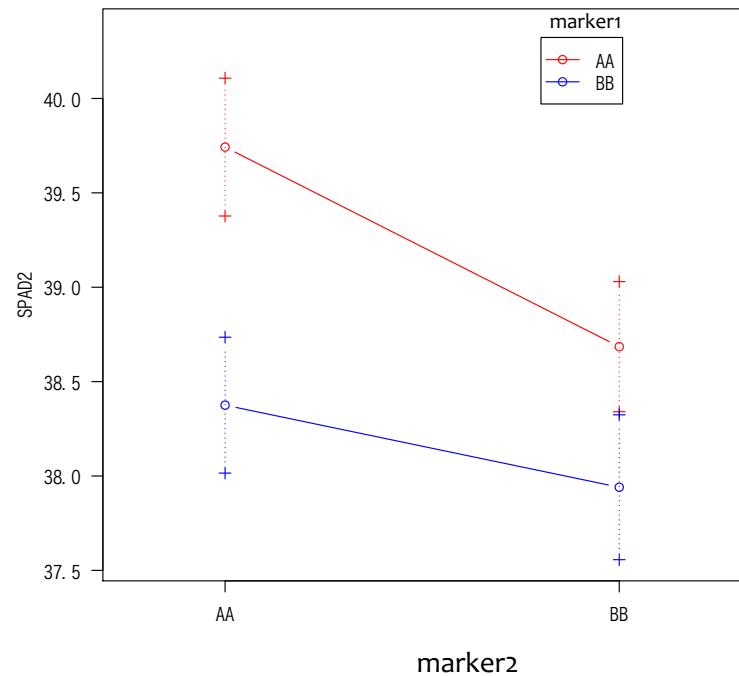
Interaction plot

```
### plot effect  
effectplot(cross,mname1=marker,pheno.col=trait.id)  
effectplot(cross,mname1=marker1,mname2=marker2,pheno.col=trait.id)
```

Effect plot for marker1



Interaction plot for marker1 and marker2



summary.scantwo and plot.scantwo

Full: $y = \mu + \beta_1 q_1 + \beta_2 q_2 + \beta_3 (q_1 \times q_2) + \varrho$

Add: $y = \mu + \beta_1 q_1 + \beta_2 q_2 + \varrho$

One: $y = \mu + \beta_1 q_1 + \varrho$

Null: $y = \mu + \varrho$