

# Package: qtlpoly (via r-universe)

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**Type** Package

**Title** Random-Effect Multiple QTL Mapping in Autopolyploids

**Version** 0.2.4

**Maintainer** Gabriel de Siqueira Gesteira <gdesiqu@ncsu.edu>

**Description** Performs random-effect multiple interval mapping (REMIM) in full-sib families of autopolyploid species based on restricted maximum likelihood (REML) estimation and score statistics, as described in Pereira et al. (2020) <[doi:10.1534/genetics.120.303080](https://doi.org/10.1534/genetics.120.303080)>.

**License** GPL-3

**URL** <https://gabrielgesteira.github.io/QTLpoly/>

**BugReports** <https://github.com/gabrielgesteira/QTLpoly/issues>

**Encoding** UTF-8

**LazyData** TRUE

**LazyDataCompression** xz

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**LinkingTo** Rcpp, RcppArmadillo, RcppProgress

**Suggests** rmarkdown, devtools, knitr

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**NeedsCompilation** yes

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code for variance component tests using score statistics in  
 R/varComp.R), Giovanni Covarrubias-Pazaran [ctb] (C code for  
 fitting mixed models with REML estimation in src/MNR.cpp)

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## Contents

B2721 . . . . .	2
breeding_values . . . . .	3
feim . . . . .	5
fit_model . . . . .	7
fit_model2 . . . . .	8
hexafake . . . . .	10
maps4x . . . . .	11
maps6x . . . . .	12
modify_qtl . . . . .	13
null_model . . . . .	14
null_model2 . . . . .	16
optimize_qtl . . . . .	17
permutations . . . . .	19
pheno4x . . . . .	21
pheno6x . . . . .	22
plot_profile . . . . .	23
plot_qtl . . . . .	24
plot_sint . . . . .	26
profile_qtl . . . . .	27
qtl_effects . . . . .	29
read_data . . . . .	31
read_data2 . . . . .	33
remim . . . . .	35
remim2 . . . . .	37
search_qtl . . . . .	39
simulate_qtl . . . . .	41
<b>Index</b>	<b>44</b>

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B2721

*Autotetraploid potato dataset*

---

## Description

A dataset of the B2721 population which derived from a cross between two tetraploid potato varieties: Atlantic × B1829-5.

**Usage**

```
B2721
```

**Format**

An object of class `mappoly.data` from the package **mappoly**.

**Author(s)**

Marcelo Mollinari, <mmollin@ncsu.edu>

**References**

Mollinari M, Garcia AAF (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, *G3: Genes|Genomes|Genetics* 9 (10): 3297-3314. doi:10.1534/g3.119.400378

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Pereira GS, Mollinari M, Schumann MJ, Clough ME, Zeng ZB, Yencho C (2021) The recombination landscape and multiple QTL mapping in a *Solanum tuberosum* cv. 'Atlantic'-derived F<sub>1</sub> population. *Heredity*. doi:10.1038/s4143702100416x.

**Examples**

```
library(mappoly)
print(B2721)
```

---

breeding_values	<i>Prediction of QTL-based breeding values from REMIM model</i>
-----------------	---

---

**Description**

Computes breeding values for each genotyped individual based on multiple QTL models

**Usage**

```
breeding_values(data, fitted)

## S3 method for class 'qtlpoly.bvalues'
plot(x, pheno.col = NULL, ...)
```

**Arguments**

data	an object of class <code>qtlpoly.data</code> .
fitted	an object of class <code>qtlpoly.fitted</code> .
x	an object of class <code>qtlpoly.bvalues</code> to be plotted.
pheno.col	a numeric vector with the phenotype column numbers to be plotted; if NULL, all phenotypes from 'data' will be included.
...	currently ignored

**Value**

An object of class `qtlpoly.bvalues` which is a list of results for each trait containing the following components:

pheno.col	a phenotype column number.
y.hat	a column matrix of breeding value for each individual.

A **ggplot2** histogram with the distribution of breeding values.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

**See Also**

[read\\_data](#), [fit\\_model](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob) #5,7
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)

# Fit model
fitted.mod = fit_model(data = data, model = remim.mod, probs = "joint", polygenes = "none")

# Predict genotypic values
```

```
y.hat = breeding_values(data = data, fitted = fitted.mod)
plot(y.hat)
```

feim

*Fixed-effect interval mapping (FEIM)***Description**

Performs interval mapping using the single-QTL, fixed-effect model proposed by Hackett et al. (2001).

**Usage**

```
feim(
  data = data,
  pheno.col = NULL,
  w.size = 15,
  sig.lod = 7,
  d.sint = 1.5,
  plot = NULL,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.feim'
print(x, pheno.col = NULL, sint = NULL, ...)
```

**Arguments**

data	an object of class <code>qtlpoly.data</code> .
pheno.col	a numeric vector with the phenotype columns to be analyzed; if <code>NULL</code> (default), all phenotypes from 'data' will be included.
w.size	a number representing the window size (in centiMorgans) to be avoided on either side of QTL already in the model when looking for a new QTL, e.g. 15 (default).
sig.lod	the vector of desired significance LOD thresholds (usually permutation-based) for declaring a QTL for each trait, e.g. 5 (default); if a single value is provided, the same LOD threshold will be applied to all traits.
d.sint	a $d$ value to subtract from logarithm of the odds ( $LOD - d$ ) for support interval calculation, e.g. $d = 1.5$ (default) represents approximate 95% support interval.
plot	a suffix for the file's name containing plots of every algorithm step, e.g. "remim" (default); if <code>NULL</code> , no file is produced.
verbose	if <code>TRUE</code> (default), current progress is shown; if <code>FALSE</code> , no output is produced.
x	an object of class <code>qtlpoly.feim</code> to be printed.
sint	whether "upper" or "lower" support intervals should be printed; if <code>NULL</code> (default), QTL peak information will be printed.
...	currently ignored

**Value**

An object of class `qtlpoly.feim` which contains a list of results for each trait with the following components:

<code>pheno.col</code>	a phenotype column number.
<code>LRT</code>	a vector containing LRT values.
<code>LOD</code>	a vector containing LOD scores.
<code>AdjR2</code>	a vector containing adjusted $R^2$ .
<code>qtls</code>	a data frame with information from the mapped QTL.
<code>lower</code>	a data frame with information from the lower support interval of mapped QTL.
<code>upper</code>	a data frame with information from the upper support interval of mapped QTL.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Hackett CA, Bradshaw JE, McNicol JW (2001) Interval mapping of quantitative trait loci in autotetraploid species, *Genetics* 159: 1819-1832.

**See Also**

[permutations](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 5)

# Perform remim
feim.mod = feim(data = data, sig.lod = 7)
```

---

fit_model	<i>Fits multiple QTL models</i>
-----------	---------------------------------

---

### Description

Fits alternative multiple QTL models by performing variance component estimation using REML.

### Usage

```
fit_model(
  data,
  model,
  probs = "joint",
  polygenes = "none",
  keep = TRUE,
  verbose = TRUE,
  pheno.col = NULL
)

## S3 method for class 'qtlpoly.fitted'
summary(object, pheno.col = NULL, ...)
```

### Arguments

data	an object of class <code>qtlpoly.data</code> .
model	an object of class <code>qtlpoly.profile</code> or <code>qtlpoly.remim</code> .
probs	a character string indicating if either "joint" (genotypes) or "marginal" (parental gametes) conditional probabilities should be used.
polygenes	a character string indicating if either "none", "most" or "all" QTL should be used as polygenes.
keep	if TRUE (default), stores all matrices and estimates from fitted model; if FALSE, nothing is stored.
verbose	if TRUE (default), current progress is shown; if FALSE, no output is produced.
pheno.col	a numeric vector with the phenotype column numbers to be summarized; if NULL (default), all phenotypes from 'data' will be included.
object	an object of class <code>qtlpoly.fitted</code> to be summarized.
...	currently ignored

### Value

An object of class `qtlpoly.fitted` which contains a list of results for each trait with the following components:

pheno.col	a phenotype column number.
fitted	a <b>sommer</b> object of class <code>mmer</code> .
qtls	a data frame with information from the mapped QTL.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Covarrubias-Pazarán G (2016) Genome-assisted prediction of quantitative traits using the R package sommer. *PLoS ONE* 11 (6): 1–15. doi:10.1371/journal.pone.0156744.

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

**See Also**

[read\\_data](#), [remim](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)

# Fit model
fitted.mod = fit_model(data=data, model=remim.mod, probs="joint", polygenes="none")
```

---

fit\_model2

*Fits multiple QTL models*

---

**Description**

Fits alternative multiple QTL models by performing variance component estimation using REML.

**Usage**

```
fit_model2(
  data,
  model,
  probs = "joint",
  polygenes = "none",
  keep = TRUE,
```



```

    verbose = TRUE,
    pheno.col = NULL
  )

```

### Arguments

data	an object of class <code>qtlpoly.data</code> .
model	an object of class <code>qtlpoly.profile</code> or <code>qtlpoly.remim</code> .
probs	a character string indicating if either "joint" (genotypes) or "marginal" (parental gametes) conditional probabilities should be used.
polygenes	a character string indicating if either "none", "most" or "all" QTL should be used as polygenes.
keep	if TRUE (default), stores all matrices and estimates from fitted model; if FALSE, nothing is stored.
verbose	if TRUE (default), current progress is shown; if FALSE, no output is produced.
pheno.col	a numeric vector with the phenotype column numbers to be summarized; if NULL (default), all phenotypes from 'data' will be included.

### Value

An object of class `qtlpoly.fitted` which contains a list of results for each trait with the following components:

pheno.col	a phenotype column number.
fitted	a <b>sommer</b> object of class <code>mmer</code> .
qtls	a data frame with information from the mapped QTL.

### Author(s)

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

### References

Covarrubias-Pazarán G (2016) Genome-assisted prediction of quantitative traits using the R package `sommer`. *PLoS ONE* 11 (6): 1–15. doi:10.1371/journal.pone.0156744.

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

### See Also

[read\\_data](#), [remim](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)

# Fit model
fitted.mod = fit_model(data=data, model=remim.mod, probs="joint", polygenes="none")
```

---

hexafake

*Simulated autohexaploid dataset.*


---

**Description**

A dataset of a hypothetical autohexaploid full-sib population containing three homology groups

**Usage**

hexafake

**Format**

An object of class `mappoly.data` which contains a list with the following components:

**plody** ploidy level = 6

**n.ind** number individuals = 300

**n.mrk** total number of markers = 1500

**ind.names** the names of the individuals

**mrk.names** the names of the markers

**dosage.p1** a vector containing the dosage in parent P for all `n.mrk` markers

**dosage.p2** a vector containing the dosage in parent Q for all `n.mrk` markers

**chrom** a vector indicating the chromosome each marker belongs. Zero indicates that the marker was not assigned to any chromosome

**genome.pos** Physical position of the markers into the sequence

**geno.dose** a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by `plody_level + 1 = 7`

**n.phen** There are no phenotypes in this simulation

**phen** There are no phenotypes in this simulation

**chisq.pval** vector containing p-values for all markers associated to the chi-square test for the expected segregation patterns under Mendelian segregation

**Author(s)**

Marcelo Mollinari, <mmollin@ncsu.edu>

**References**

Mollinari M, Garcia AAF (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, *G3: Genes|Genomes|Genetics* 9 (10): 3297-3314. doi:10.1534/g3.119.400378

**Examples**

```
library(mappoly)
plot(hexafake)
```

---

maps4x

*Autotetraploid potato map*

---

**Description**

A real autotetraploid potato map containing 12 homology groups from a tetraploid potato full-sib family (Atlantic x B1829-5).

**Usage**

```
maps4x
```

**Format**

An object of class "mappoly.map" from the package **mappoly**, which is a list of 12 linkage groups (LGs)

**Author(s)**

Marcelo Mollinari, <mmollin@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2019) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Mollinari M, Garcia AAF (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, *G3: Genes|Genomes|Genetics* 9 (10): 3297-3314. doi:10.1534/g3.119.400378

Pereira GS, Mollinari M, Schumann MJ, Clough ME, Zeng ZB, Yencho C (2021) The recombination landscape and multiple QTL mapping in a *Solanum tuberosum* cv. 'Atlantic'-derived F<sub>1</sub> population. *Heredity*. doi:10.1038/s4143702100416x.

**See Also**

[hexafake](#), [pheno6x](#)

**Examples**

```
library(mappoly)
plot_map_list(maps4x)
```

---

maps6x

*Simulated autohexaploid map*

---

**Description**

A simulated map containing three homology groups of a hypothetical cross between two auto-hexaploid individuals.

**Usage**

```
maps6x
```

**Format**

An object of class "mappoly.map" from the package **mappoly**, which is a list of three linkage groups (LGs):

**LG 1** 538 markers distributed along 112.2 cM

**LG 2** 329 markers distributed along 54.6 cM

**LG 3** 443 markers distributed along 98.2 cM

**Author(s)**

Marcelo Mollinari, <mmollin@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2019) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Mollinari M, Garcia AAF (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, *G3: Genes|Genomes|Genetics* 9 (10): 3297-3314. doi:10.1534/g3.119.400378

**See Also**

[hexafake](#), [pheno6x](#)

**Examples**

```
library(mappoly)
plot_map_list(maps6x)
```

---

modify_qtl	<i>Modify QTL model</i>
------------	-------------------------

---

**Description**

Adds or removes QTL manually from a given model.

**Usage**

```
modify_qtl(
  model,
  pheno.col = NULL,
  add.qtl = NULL,
  drop.qtl = NULL,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.modify'
print(x, pheno.col = NULL, ...)
```

**Arguments**

model	an object of class <code>qtlpoly.model</code> containing the QTL to be modified.
pheno.col	a phenotype column number whose model will be modified or printed.
add.qtl	a marker position number to be added.
drop.qtl	a marker position number to be removed.
verbose	if TRUE (default), current progress is shown; if FALSE, no output is produced.
x	an object of class <code>qtlpoly.modify</code> to be printed.
...	currently ignored

**Value**

An object of class `qtlpoly.modify` which contains a list of results for each trait with the following components:

pheno.col	a phenotype column number.
stat	a vector containing values from score statistics.
pval	a vector containing $p$ -values from score statistics.
qtls	a data frame with information from the mapped QTL.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

**See Also**

[read\\_data](#), [remim](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)

# Modify model
modified.mod = modify_qtl(model = remim.mod, pheno.col = 1, drop.qtl = 18)
```

---

null\_model

*Null model*

---

**Description**

Creates a null model (with no QTL) for each trait.

**Usage**

```
null_model(
  data,
  offset.data = NULL,
  pheno.col = NULL,
  n.clusters = NULL,
  plot = NULL,
  verbose = TRUE
)
```

```
## S3 method for class 'qtlpoly.null'
print(x, pheno.col = NULL, ...)
```

```
## S3 method for class 'qtlpoly.null'
print(x, pheno.col = NULL, ...)
```

### Arguments

data	an object of class <code>qtlpoly.data</code> .
offset.data	a data frame with the same dimensions of <code>data\$pheno</code> containing offset variables; if <code>NULL</code> (default), no offset variables are considered.
pheno.col	a numeric vector with the phenotype columns to be analyzed; if <code>NULL</code> , all phenotypes from 'data' will be included.
n.clusters	number of parallel processes to spawn.
plot	a suffix for the file's name containing simple plots of every QTL search round, e.g. "null" (default); if <code>NULL</code> , no file is produced.
verbose	if <code>TRUE</code> (default), current progress is shown; if <code>FALSE</code> , no output is produced.
x	an object of class <code>qtlpoly.null</code> to be printed.
...	currently ignored

### Value

An object of class `qtlpoly.null` which contains a list of results for each trait with the following components:

pheno.col	a phenotype column number.
stat	a vector containing values from score statistics.
pval	a vector containing <i>p</i> -values from score statistics.
qtls	a data frame with information from the mapped QTL ( <code>NULL</code> at this point).

### Author(s)

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

### References

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Qu L, Guennel T, Marshall SL (2013) Linear score tests for variance components in linear mixed models and applications to genetic association studies. *Biometrics* 69 (4): 883-92.

### See Also

[read\\_data](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Build null models
null.mod = null_model2(data = data, pheno.col = 1, n.clusters = 1)
```

---

null\_model2

*Null model*


---

**Description**

Creates a null model (with no QTL) for each trait.

**Usage**

```
null_model2(
  data,
  offset.data = NULL,
  pheno.col = NULL,
  n.clusters = NULL,
  plot = NULL,
  verbose = TRUE
)
```

**Arguments**

data	an object of class <code>qtlpoly.data</code> .
offset.data	a data frame with the same dimensions of <code>data\$pheno</code> containing offset variables; if <code>NULL</code> (default), no offset variables are considered.
pheno.col	a numeric vector with the phenotype columns to be analyzed; if <code>NULL</code> , all phenotypes from 'data' will be included.
n.clusters	number of parallel processes to spawn.
plot	a suffix for the file's name containing simple plots of every QTL search round, e.g. "null" (default); if <code>NULL</code> , no file is produced.
verbose	if <code>TRUE</code> (default), current progress is shown; if <code>FALSE</code> , no output is produced.



**Value**

An object of class `qtlpoly.null` which contains a list of results for each trait with the following components:

<code>pheno.col</code>	a phenotype column number.
<code>stat</code>	a vector containing values from score statistics.
<code>pval</code>	a vector containing <i>p</i> -values from score statistics.
<code>qtls</code>	a data frame with information from the mapped QTL (NULL at this point).

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>, Gabriel de Siqueira Gesteira, <gdesiqu@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Qu L, Guennel T, Marshall SL (2013) Linear score tests for variance components in linear mixed models and applications to genetic association studies. *Biometrics* 69 (4): 883–92.

**See Also**

[read\\_data](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Build null models
null.mod = null_model(data = data, pheno.col = 1, n.clusters = 1)
```

---

optimize\_qtl

*Model optimization*

---

**Description**

Tests each QTL at a time and updates its position (if it changes) or drops the QTL (if non-significant).

**Usage**

```
optimize_qtl(
  data,
  offset.data = NULL,
  model,
  sig.bwd = 0.05,
  score.null = NULL,
  polygenes = FALSE,
  n.clusters = NULL,
  plot = NULL,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.optimize'
print(x, pheno.col = NULL, ...)
```

**Arguments**

<code>data</code>	an object of class <code>qtlpoly.data</code> .
<code>offset.data</code>	a data frame with the same dimensions of <code>data\$pheno</code> containing offset variables; if <code>NULL</code> (default), no offset variables are considered.
<code>model</code>	an object of class <code>qtlpoly.model</code> containing the QTL to be optimized.
<code>sig.bwd</code>	the desired score-based $p$ -value threshold for backward elimination, e.g. 0.0001 (default).
<code>score.null</code>	an object of class <code>qtlpoly.null</code> with results of score statistics from resampling.
<code>polygenes</code>	if <code>TRUE</code> all QTL but the one being tested are treated as a single polygenic effect, if <code>FALSE</code> (default) all QTL effect variances have to be estimated.
<code>n.clusters</code>	number of parallel processes to spawn.
<code>plot</code>	a suffix for the file's name containing plots of every QTL optimization round, e.g. "optimize" (default); if <code>NULL</code> , no file is produced.
<code>verbose</code>	if <code>TRUE</code> (default), current progress is shown; if <code>FALSE</code> , no output is produced.
<code>x</code>	an object of class <code>qtlpoly.optimize</code> to be printed.
<code>pheno.col</code>	a numeric vector with the phenotype columns to be printed; if <code>NULL</code> , all phenotypes from 'data' will be included.
<code>...</code>	currently ignored

**Value**

An object of class `qtlpoly.optimize` which contains a list of results for each trait with the following components:

<code>pheno.col</code>	a phenotype column number.
<code>stat</code>	a vector containing values from score statistics.
<code>pval</code>	a vector containing $p$ -values from score statistics.
<code>qtls</code>	a data frame with information from the mapped QTL.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Qu L, Guennel T, Marshall SL (2013) Linear score tests for variance components in linear mixed models and applications to genetic association studies. *Biometrics* 69 (4): 883–92.

Zou F, Fine JP, Hu J, Lin DY (2004) An efficient resampling method for assessing genome-wide statistical significance in mapping quantitative trait loci. *Genetics* 168 (4): 2307-16. doi:10.1534/genetics.104.031427

**See Also**

[read\\_data](#), [null\\_model](#), [search\\_qtl](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Build null model
null.mod = null_model(data = data, pheno.col = 1, n.clusters = 1)

# Perform forward search
search.mod = search_qtl(data = data, model = null.mod,
w.size = 15, sig.fwd = 0.01, n.clusters = 1)

# Optimize model
optimize.mod = optimize_qtl(data = data, model = search.mod, sig.bwd = 0.0001, n.clusters = 1)
```

---

permutations

*Fixed-effect interval mapping (FEIM) model permutations*


---

**Description**

Stores maximum LOD scores for a number of permutations of given phenotypes.

**Usage**

```

permutations(
  data,
  offset.data = NULL,
  pheno.col = NULL,
  n.sim = 1000,
  probs = c(0.9, 0.95),
  n.clusters = NULL,
  seed = 123,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.perm'
print(x, pheno.col = NULL, probs = c(0.9, 0.95), ...)

## S3 method for class 'qtlpoly.perm'
plot(x, pheno.col = NULL, probs = c(0.9, 0.95), ...)

```

**Arguments**

<code>data</code>	an object of class <code>qtlpoly.data</code> .
<code>offset.data</code>	a subset of the data object to be used in permutation calculations.
<code>pheno.col</code>	a numeric vector with the phenotype columns to be analyzed; if <code>NULL</code> (default), all phenotypes from 'data' will be included.
<code>n.sim</code>	a number of simulations, e.g. 1000 (default).
<code>probs</code>	a vector of probability values in [0, 1] representing the quantiles, e.g. <code>c(0.90, 0.95)</code> for the 90% and 95% quantiles.
<code>n.clusters</code>	a number of parallel processes to spawn.
<code>seed</code>	an integer for the <code>set.seed()</code> function; if <code>NULL</code> , no reproducible seeds are set.
<code>verbose</code>	if <code>TRUE</code> (default), current progress is shown; if <code>FALSE</code> , no output is produced.
<code>x</code>	an object of class <code>qtlpoly.perm</code> to be printed or plotted.
<code>...</code>	currently ignored

**Value**

An object of class `qtlpoly.perm` which contains a list of results for each trait with the maximum LOD score per permutation.

LOD score thresholds for given quantiles for each trait.

A **ggplot2** histogram with the distribution of ordered maximum LOD scores and thresholds for given quantiles for each trait.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

## References

Churchill GA, Doerge RW (1994) Empirical threshold values for quantitative trait mapping, *Genetics* 138: 963-971.

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

## See Also

[feim](#)

## Examples

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Perform permutations
perm = permutations(data = data, pheno.col = 1, n.sim = 10, n.clusters = 1)
```

---

pheno4x

*Autotetraploid potato phenotypes*

---

## Description

A subset of phenotypes from a tetraploid potato full-sib family (Atlantic x B1829-5).

## Usage

```
pheno4x
```

## Format

A data frame of phenotypes with 156 named individuals in rows and three named phenotypes in columns, which are:

**FM07** Foliage maturity evaluated in 2007.

**FM08** Foliage maturity evaluated in 2008.

**FM14** Foliage maturity evaluated in 2014.

## Author(s)

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

## References

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Pereira GS, Mollinari M, Schumann MJ, Clough ME, Zeng ZB, Yencho C (2021) The recombination landscape and multiple QTL mapping in a *Solanum tuberosum* cv. 'Atlantic'-derived F<sub>1</sub> population. *Heredity*. doi:10.1038/s4143702100416x.

## Examples

```
head(pheno4x)
```

---

pheno6x	<i>Simulated phenotypes</i>
---------	-----------------------------

---

## Description

A simulated data set of phenotypes for a hipotetical autohexaploid species map.

## Usage

```
pheno6x
```

## Format

A data frame of phenotypes with 300 named individuals in rows and three named phenotypes in columns, which are:

**T32** 3 QTLs, with heritabilities of 0.20 (LG 1 at 32.03 cM), 0.15 (LG 1 at 95.02 cM) and 0.30 (LG 2 at 40.01 cM).

**T17** 1 QTL, with heritability of 0.15 (LG 3 at 34.51 cM).

**T45** no QTLs.

## Author(s)

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

## References

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2019) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

**See Also**

[simulate\\_qtl](#), [pheno4x](#)

**Examples**

```
head(pheno6x)
```

---

 plot\_profile

*Logarithm of P-value (LOP) profile plots*


---

**Description**

Plots profiled logarithm of score-based  $P$ -values (LOP) from individual or combined traits.

**Usage**

```
plot_profile(
  data = data,
  model = model,
  pheno.col = NULL,
  sup.int = FALSE,
  main = NULL,
  legend = "bottom",
  ylim = NULL,
  grid = FALSE
)
```

**Arguments**

data	an object of class <code>qtlpoly.data</code> .
model	an object of class <code>qtlpoly.profile</code> or <code>qtlpoly.remim</code> .
pheno.col	a numeric vector with the phenotype column numbers to be plotted; if <code>NULL</code> , all phenotypes from 'data' will be included.
sup.int	if <code>TRUE</code> , support interval are shown as shaded areas; if <code>FALSE</code> (default), no support interval is show.
main	a character string with the main title; if <code>NULL</code> , no title is shown.
legend	legend position (either "bottom", "top", "left" or "right"); if <code>NULL</code> , no legend is shown.
ylim	a numeric value pair supplying the limits of y-axis, e.g. <code>c(0,10)</code> ; if <code>NULL</code> (default), limits will be provided automatically.
grid	if <code>TRUE</code> , profiles will be organized in rows (one per trait); if <code>FALSE</code> (default), profiles will appear superimposed. Only effective when plotting profiles from more than one trait.

**Value**

A **ggplot2** with the LOP profiles for each trait.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

**See Also**

[profile\\_qtl](#), [remim](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)

# Plot profile
plot_profile(data = data, model = remim.mod, grid = FALSE)
```

---

plot\_qtl

*QTL heritability and significance plot*

---

**Description**

Creates a plot where dot sizes and colors represent the QTLs heritabilities and their *p*-values, respectively.



**Usage**

```
plot_qtl(  
  data = data,  
  model = model,  
  fitted = fitted,  
  pheno.col = NULL,  
  main = NULL,  
  drop.pheno = TRUE,  
  drop.lgs = TRUE  
)
```

**Arguments**

data	an object of class <code>qtlpoly.data</code> .
model	an object of class <code>qtlpoly.profile</code> or <code>qtlpoly.remim</code> .
fitted	an object of class <code>qtlpoly.fitted</code> .
pheno.col	the desired phenotype column numbers to be plotted. The order here specifies the order of plotting (from top to bottom.)
main	plot title; if NULL (the default), no title is shown.
drop.pheno	if FALSE, shows the names of all traits from <code>pheno.col</code> , even of those with no QTLs; if TRUE (the default), shows only the traits with QTL(s).
drop.lgs	if FALSE, shows all linkage groups, even those with no QTL; if TRUE (the default), shows only the linkage groups with QTL(s).

**Value**

A **ggplot2** with dots representing the QTLs.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

**See Also**

[read\\_data](#), [remim](#), [fit\\_model](#)

**Examples**

```

# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)

# Fit model
fitted.mod = fit_model(data, remim.mod, probs="joint", polygenes="none")

# Plot QTL
plot_qtl(data, remim.mod, fitted.mod)

```

---

plot\_sint

*QTLs with respective support interval plots*


---

**Description**

Creates a plot where colored bars represent the support intervals for QTL peaks (black dots).

**Usage**

```
plot_sint(data, model, pheno.col = NULL, main = NULL, drop = FALSE)
```

**Arguments**

data	an object of class <code>qtlpoly.data</code> .
model	an object of class <code>qtlpoly.profile</code> or <code>qtlpoly.remim</code> .
pheno.col	a numeric vector with the phenotype column numbers to be plotted; if <code>NULL</code> , all phenotypes from 'data' will be included.
main	a character string with the main title; if <code>NULL</code> , no title will be shown.
drop	if <code>TRUE</code> , phenotypes with no QTL will be dropped; if <code>FALSE</code> (default), all phenotypes will be shown.

**Value**

A **ggplot2** with QTL bars for each linkage group.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

## References

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

## See Also

[read\\_data](#), [remim](#), [profile\\_qtl](#)

## Examples

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)

# Plot support intervals
plot_sint(data = data, model = remim.mod)
```

---

profile\_qtl

*QTL profiling*

---

## Description

Generates the score-based genome-wide profile conditional to the selected QTL.

## Usage

```
profile_qtl(
  data,
  model,
  d.sint = 1.5,
  polygenes = FALSE,
  n.clusters = NULL,
  plot = NULL,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.profile'
print(x, pheno.col = NULL, sint = NULL, ...)
```

**Arguments**

data	an object of class <code>qtlpoly.data</code> .
model	an object of class <code>qtlpoly.model</code> containing the QTL to be profiled.
d.sint	a $d$ value to subtract from logarithm of $p$ -value ( $LOP - d$ ) for support interval calculation, e.g. $d = 1.5$ (default) represents approximate 95% support interval.
polygenes	if TRUE all QTL but the one being tested are treated as a single polygenic effect, if FALSE (default) all QTL effect variances have to estimated.
n.clusters	number of parallel processes to spawn.
plot	a suffix for the file's name containing plots of every QTL profiling round, e.g. "profile" (default); if NULL, no file is produced.
verbose	if TRUE (default), current progress is shown; if FALSE, no output is produced.
x	an object of class <code>qtlpoly.profile</code> to be printed.
pheno.col	a numeric vector with the phenotype column numbers to be plotted; if NULL, all phenotypes from 'data' will be included.
sint	whether "upper" or "lower" support intervals should be printed; if NULL (default), only QTL peak information will be printed.
...	currently ignored

**Value**

An object of class `qtlpoly.profile` which contains a list of results for each trait with the following components:

pheno.col	a phenotype column number.
stat	a vector containing values from score statistics.
pval	a vector containing $p$ -values from score statistics.
qtls	a data frame with information from the mapped QTL.
lower	a data frame with information from the lower support interval of mapped QTL.
upper	a data frame with information from the upper support interval of mapped QTL.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Qu L, Guennel T, Marshall SL (2013) Linear score tests for variance components in linear mixed models and applications to genetic association studies. *Biometrics* 69 (4): 883-92.

**Examples**

```

# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Build null model
null.mod = null_model(data, pheno.col = 1, n.clusters = 1)

# Perform forward search
search.mod = search_qtl(data = data, model = null.mod,
w.size = 15, sig.fwd = 0.01, n.clusters = 1)

# Optimize model
optimize.mod = optimize_qtl(data = data, model = search.mod, sig.bwd = 0.0001, n.clusters = 1)

# Profile model
profile.mod = profile_qtl(data = data, model = optimize.mod, d.sint = 1.5, n.clusters = 1)

```

---

qtl\_effects

*QTL allele effect estimation*


---

**Description**

Computes allele specific and allele combination (within-parent) heritable effects from multiple QTL models.

**Usage**

```

qtl_effects(ploidy = 6, fitted, pheno.col = NULL, verbose = TRUE)

## S3 method for class 'qtlpoly.effects'
plot(x, pheno.col = NULL, p1 = "P1", p2 = "P2", ...)

```

**Arguments**

ploidy	a numeric value of ploidy level of the cross (currently, only 2, 4 or 6).
fitted	a fitted multiple QTL model of class <code>qtlpoly.fitted</code> .
pheno.col	a numeric vector with the phenotype column numbers to be plotted; if <code>NULL</code> , all phenotypes from 'fitted' will be included.
verbose	if <code>TRUE</code> (default), current progress is shown; if <code>FALSE</code> , no output is produced.
x	an object of class <code>qtlpoly.effects</code> to be plotted.
p1	a character string with the first parent name, e.g. "P1" (default).
p2	a character string with the second parent name, e.g. "P2" (default).
...	currently ignored

**Value**

An object of class `qtlpoly.effects` which is a list of results for each containing the following components:

`pheno.col`      a phenotype column number.  
`y.hat`            a vector with the predicted values.

A **ggplot2** barplot with parental allele and allele combination effects.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>, with modifications by Gabriel Gesteira, <gdesiqu@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

Kempthorne O (1955) The correlation between relatives in a simple autotetraploid population, *Genetics* 40: 168-174.

**See Also**

[read\\_data](#), [remim](#), [fit\\_model](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)

# Fit model
fitted.mod = fit_model(data, model=remim.mod, probs="joint", polygenes="none")

# Estimate effects
est.effects = qtl_effects(ploidy = 4, fitted = fitted.mod, pheno.col = 1)

# Plot results
plot(est.effects)
```

---

read_data	<i>Read genotypic and phenotypic data</i>
-----------	---

---

### Description

Reads files in specific formats and creates a `qtlpoly.data` object to be used in subsequent analyses.

### Usage

```
read_data(
  ploidy = 6,
  geno.prob,
  geno.dose = NULL,
  double.reduction = FALSE,
  pheno,
  weights = NULL,
  step = 1,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.data'
print(x, detailed = FALSE, ...)
```

### Arguments

<code>ploidy</code>	a numeric value of ploidy level of the cross.
<code>geno.prob</code>	an object of class <code>mappoly.genoprob</code> from <b>mappoly</b> .
<code>geno.dose</code>	an object of class <code>mappoly.data</code> from <b>mappoly</b> .
<code>double.reduction</code>	if TRUE, double reduction genotypes are taken into account; if FALSE, no double reduction genotypes are considered.
<code>pheno</code>	a data frame of phenotypes (columns) with individual names (rows) identical to individual names in <code>geno.prob</code> and/or <code>geno.dose</code> object.
<code>weights</code>	a data frame of phenotype weights (columns) with individual names (rows) identical to individual names in <code>pheno</code> object.
<code>step</code>	a numeric value of step size (in centiMorgans) where tests will be performed, e.g. 1 (default); if NULL, tests will be performed at every marker.
<code>verbose</code>	if TRUE (default), current progress is shown; if FALSE, no output is produced.
<code>x</code>	an object of class <code>qtlpoly.data</code> to be printed.
<code>detailed</code>	if TRUE, detailed information on linkage groups and phenotypes is shown; if FALSE, no details are printed.
<code>...</code>	currently ignored

**Value**

An object of class `qtlpoly.data` which is a list containing the following components:

<code>ploidy</code>	a scalar with ploidy level.
<code>nlg</code>	a scalar with the number of linkage groups.
<code>nind</code>	a scalar with the number of individuals.
<code>nmrk</code>	a scalar with the number of marker positions.
<code>nphe</code>	a scalar with the number of phenotypes.
<code>lgs.size</code>	a vector with linkage group sizes.
<code>cum.size</code>	a vector with cumulative linkage group sizes.
<code>lgs.nmrk</code>	a vector with number of marker positions per linkage group.
<code>cum.nmrk</code>	a vector with cumulative number of marker positions per linkage group.
<code>lgs</code>	a list with selected marker positions per linkage group.
<code>lgs.all</code>	a list with all marker positions per linkage group.
<code>step</code>	a scalar with the step size.
<code>pheno</code>	a data frame with phenotypes.
<code>G</code>	a list of relationship matrices for each marker position.
<code>Z</code>	a list of conditional probability matrices for each marker position for genotypes.
<code>X</code>	a list of conditional probability matrices for each marker position for alleles.
<code>Pi</code>	a matrix of identical-by-descent shared alleles among genotypes.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>, with minor updates by Gabriel de Siqueira Gesteira, <gdesiqu@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yenchu GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

**See Also**

[maps6x](#), [pheno6x](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)
```



---

read_data2	<i>Read genotypic and phenotypic data</i>
------------	---

---

### Description

Reads files in specific formats and creates a `qtlpoly.data` object to be used in subsequent analyses.

### Usage

```
read_data2(
  ploidy = 6,
  geno.prob,
  geno.dose = NULL,
  double.reduction = FALSE,
  pheno,
  weights = NULL,
  step = 1,
  verbose = TRUE
)
```

### Arguments

<code>ploidy</code>	a numeric value of ploidy level of the cross.
<code>geno.prob</code>	an object of class <code>mappoly.genoprob</code> from <b>mappoly</b> .
<code>geno.dose</code>	an object of class <code>mappoly.data</code> from <b>mappoly</b> .
<code>double.reduction</code>	if TRUE, double reduction genotypes are taken into account; if FALSE, no double reduction genotypes are considered.
<code>pheno</code>	a data frame of phenotypes (columns) with individual names (rows) identical to individual names in <code>geno.prob</code> and/or <code>geno.dose</code> object.
<code>weights</code>	a data frame of phenotype weights (columns) with individual names (rows) identical to individual names in <code>pheno</code> object.
<code>step</code>	a numeric value of step size (in centiMorgans) where tests will be performed, e.g. 1 (default); if NULL, tests will be performed at every marker.
<code>verbose</code>	if TRUE (default), current progress is shown; if FALSE, no output is produced.

### Value

An object of class `qtlpoly.data` which is a list containing the following components:

<code>ploidy</code>	a scalar with ploidy level.
<code>nlg</code>	a scalar with the number of linkage groups.
<code>nind</code>	a scalar with the number of individuals.
<code>nmrk</code>	a scalar with the number of marker positions.

nphe	a scalar with the number of phenotypes.
lgs.size	a vector with linkage group sizes.
cum.size	a vector with cumulative linkage group sizes.
lgs.nmrk	a vector with number of marker positions per linkage group.
cum.nmrk	a vector with cumulative number of marker positions per linkage group.
lgs	a list with selected marker positions per linkage group.
lgs.all	a list with all marker positions per linkage group.
step	a scalar with the step size.
pheno	a data frame with phenotypes.
G	a list of relationship matrices for each marker position.
Z	a list of conditional probability matrices for each marker position for genotypes.
X	a list of conditional probability matrices for each marker position for alleles.
Pi	a matrix of identical-by-descent shared alleles among genotypes.

### Author(s)

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>, Gabriel de Siqueira Gesteira, <gdesiqu@ncsu.edu>

### References

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

### See Also

[maps6x](#), [pheno6x](#)

### Examples

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)
```

---

remim	<i>Random-effect multiple interval mapping (REMIM)</i>
-------	--

---

### Description

Automatic function that performs REMIM algorithm using score statistics.

### Usage

```
remim(
  data,
  pheno.col = NULL,
  w.size = 15,
  sig.fwd = 0.01,
  sig.bwd = 1e-04,
  score.null = NULL,
  d.sint = 1.5,
  polygenes = FALSE,
  n.clusters = NULL,
  n.rounds = Inf,
  plot = NULL,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.remim'
print(x, pheno.col = NULL, sint = NULL, ...)
```

### Arguments

<code>data</code>	an object of class <code>qtlpoly.data</code> .
<code>pheno.col</code>	a numeric vector with the phenotype columns to be analyzed or printed; if <code>NULL</code> (default), all phenotypes from 'data' will be included.
<code>w.size</code>	the window size (in centiMorgans) to avoid on either side of QTL already in the model when looking for a new QTL, e.g. 15 (default).
<code>sig.fwd</code>	the desired score-based significance level for forward search, e.g. 0.01 (default).
<code>sig.bwd</code>	the desired score-based significance level for backward elimination, e.g. 0.001 (default).
<code>score.null</code>	an object of class <code>qtlpoly.null</code> with results of score statistics from resampling.
<code>d.sint</code>	a $d$ value to subtract from logarithm of $p$ -value ( $LOP - d$ ) for support interval calculation, e.g. $d = 1.5$ (default) represents approximate 95% support interval.
<code>polygenes</code>	if <code>TRUE</code> all QTL already in the model are treated as a single polygenic effect; if <code>FALSE</code> (default) all QTL effect variances have to be estimated.
<code>n.clusters</code>	number of parallel processes to spawn.
<code>n.rounds</code>	number of search rounds; if <code>Inf</code> (default) forward search will stop when no more significant positions can be found.

plot	a suffix for the file's name containing plots of every algorithm step, e.g. "remim"; if NULL (default), no file is produced.
verbose	if TRUE (default), current progress is shown; if FALSE, no output is produced.
x	an object of class <code>qt1poly.remim</code> to be printed.
sint	whether "upper" or "lower" support intervals should be printed; if NULL (default), only QTL peak information will be printed.
...	currently ignored

### Value

An object of class `qt1poly.remim` which contains a list of results for each trait with the following components:

pheno.col	a phenotype column number.
stat	a vector containing values from score statistics.
pval	a vector containing $p$ -values from score statistics.
qtls	a data frame with information from the mapped QTL.
lower	a data frame with information from the lower support interval of mapped QTL.
upper	a data frame with information from the upper support interval of mapped QTL.

### Author(s)

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

### References

- Kao CH, Zeng ZB, Teasdale RD (1999) Multiple interval mapping for quantitative trait loci. *Genetics* 152 (3): 1203–16.
- Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.
- Qu L, Guennel T, Marshall SL (2013) Linear score tests for variance components in linear mixed models and applications to genetic association studies. *Biometrics* 69 (4): 883–92.
- Zou F, Fine JP, Hu J, Lin DY (2004) An efficient resampling method for assessing genome-wide statistical significance in mapping quantitative trait loci. *Genetics* 168 (4): 2307-16. doi:10.1534/genetics.104.031427

### See Also

[read\\_data](#)

## Examples

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)
```

---

remim2

*Random-effect multiple interval mapping (REMIM)*


---

## Description

Automatic function that performs REMIM algorithm using score statistics.

## Usage

```
remim2(
  data,
  pheno.col = NULL,
  w.size = 15,
  sig.fwd = 0.01,
  sig.bwd = 1e-04,
  score.null = NULL,
  d.sint = 1.5,
  polygenes = FALSE,
  n.clusters = NULL,
  n.rounds = Inf,
  plot = NULL,
  verbose = TRUE
)
```

## Arguments

<code>data</code>	an object of class <code>qtlpoly.data</code> .
<code>pheno.col</code>	a numeric vector with the phenotype columns to be analyzed or printed; if <code>NULL</code> (default), all phenotypes from 'data' will be included.
<code>w.size</code>	the window size (in centiMorgans) to avoid on either side of QTL already in the model when looking for a new QTL, e.g. 15 (default).
<code>sig.fwd</code>	the desired score-based significance level for forward search, e.g. 0.01 (default).
<code>sig.bwd</code>	the desired score-based significance level for backward elimination, e.g. 0.001 (default).

score.null	an object of class <code>qtlpoly.null</code> with results of score statistics from resampling.
d.sint	a $d$ value to subtract from logarithm of $p$ -value ( $LOP - d$ ) for support interval calculation, e.g. $d = 1.5$ (default) represents approximate 95% support interval.
polygenes	if TRUE all QTL already in the model are treated as a single polygenic effect; if FALSE (default) all QTL effect variances have to be estimated.
n.clusters	number of parallel processes to spawn.
n.rounds	number of search rounds; if Inf (default) forward search will stop when no more significant positions can be found.
plot	a suffix for the file's name containing plots of every algorithm step, e.g. "remim"; if NULL (default), no file is produced.
verbose	if TRUE (default), current progress is shown; if FALSE, no output is produced.
sint	whether "upper" or "lower" support intervals should be printed; if NULL (default), only QTL peak information will be printed.

### Value

An object of class `qtlpoly.remim` which contains a list of results for each trait with the following components:

pheno.col	a phenotype column number.
stat	a vector containing values from score statistics.
pval	a vector containing $p$ -values from score statistics.
qtls	a data frame with information from the mapped QTL.
lower	a data frame with information from the lower support interval of mapped QTL.
upper	a data frame with information from the upper support interval of mapped QTL.

### Author(s)

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>, Getúlio Caixeta Ferreira, <getulio.caifer@gmail.com>

### References

- Kao CH, Zeng ZB, Teasdale RD (1999) Multiple interval mapping for quantitative trait loci. *Genetics* 152 (3): 1203–16.
- Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yenchu GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.
- Qu L, Guennel T, Marshall SL (2013) Linear score tests for variance components in linear mixed models and applications to genetic association studies. *Biometrics* 69 (4): 883–92.
- Zou F, Fine JP, Hu J, Lin DY (2004) An efficient resampling method for assessing genome-wide statistical significance in mapping quantitative trait loci. *Genetics* 168 (4): 2307-16. doi:10.1534/genetics.104.031427

**See Also**[read\\_data](#)**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Search for QTL
remim.mod = remim2(data = data, pheno.col = 1, w.size = 15, sig.fwd = 0.0011493379,
sig.bwd = 0.0002284465, d.sint = 1.5, n.clusters = 1)
```

---

`search_qtl`*QTL forward search*

---

**Description**

Searches for QTL and adds them one at a time to a multiple random-effect QTL model based on score statistics.

**Usage**

```
search_qtl(
  data,
  offset.data = NULL,
  model,
  w.size = 15,
  sig.fwd = 0.2,
  score.null = NULL,
  polygenes = FALSE,
  n.rounds = Inf,
  n.clusters = NULL,
  plot = NULL,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.search'
print(x, pheno.col = NULL, ...)
```

**Arguments**

data	an object of class <code>qtlpoly.data</code> .
offset.data	a data frame with the same dimensions of <code>data\$pheno</code> containing offset variables; if <code>NULL</code> (default), no offset variables are considered.
model	an object of class <code>qtlpoly.model</code> from which a forward search will start.
w.size	the window size (in cM) to avoid on either side of QTL already in the model when looking for a new QTL.
sig.fwd	the desired score-based $p$ -value threshold for forward search, e.g. 0.01 (default).
score.null	an object of class <code>qtlpoly.null</code> with results of score statistics from resampling.
polygenes	if <code>TRUE</code> all QTL but the one being tested are treated as a single polygenic effect; if <code>FALSE</code> (default) all QTL effect variances have to be estimated.
n.rounds	number of search rounds; if <code>Inf</code> (default) forward search will stop when no more significant positions can be found.
n.clusters	number of parallel processes to spawn.
plot	a suffix for the file's name containing plots of every QTL search round, e.g. "search" (default); if <code>NULL</code> , no file is produced.
verbose	if <code>TRUE</code> (default), current progress is shown; if <code>FALSE</code> , no output is produced.
x	an object of class <code>qtlpoly.search</code> to be printed.
pheno.col	a numeric vector with the phenotype column numbers to be printed; if <code>NULL</code> , all phenotypes from 'data' will be included.
...	currently ignored

**Value**

An object of class `qtlpoly.search` which contains a list of results for each trait with the following components:

pheno.col	a phenotype column number.
stat	a vector containing values from score statistics.
pval	a vector containing $p$ -values from score statistics.
qtls	a data frame with information from the mapped QTL.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

- Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yenchu GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.
- Qu L, Guennel T, Marshall SL (2013) Linear score tests for variance components in linear mixed models and applications to genetic association studies. *Biometrics* 69 (4): 883-92.



Zou F, Fine JP, Hu J, Lin DY (2004) An efficient resampling method for assessing genome-wide statistical significance in mapping quantitative trait loci. *Genetics* 168 (4): 2307-16. doi:10.1534/genetics.104.031427

### See Also

[read\\_data](#), [null\\_model](#)

### Examples

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Build null model
null.mod = null_model(data, pheno.col = 1, n.clusters = 1)

# Perform forward search
search.mod = search_qtl(data, model = null.mod, w.size = 15, sig.fwd = 0.01, n.clusters = 1)
```

---

simulate\_qtl

*Simulations of multiple QTL*

---

### Description

Simulate new phenotypes with a given number of QTL and creates new object with the same structure of class `qtlpoly.data` from an existing genetic map.

### Usage

```
simulate_qtl(
  data,
  mu = 0,
  h2.qtl = c(0.3, 0.2, 0.1),
  var.error = 1,
  linked = FALSE,
  n.sim = 1000,
  missing = TRUE,
  w.size = 20,
  seed = 123,
  verbose = TRUE
)

## S3 method for class 'qtlpoly.simul'
print(x, detailed = FALSE, ...)
```

**Arguments**

<code>data</code>	an object of class <code>qtlpoly.data</code> .
<code>mu</code>	simulated phenotype mean, e.g. 0 (default).
<code>h2.qtl</code>	vector with QTL heritabilities, e.g. <code>c(0.3, 0.2, 0.1)</code> for three QTL (default); if NULL, only error is simulated.
<code>var.error</code>	simulated error variance, e.g. 1 (default).
<code>linked</code>	if TRUE (default), at least two QTL will be linked; if FALSE, QTL will be randomly assigned along the genetic map. Linkage is defined by a genetic distance smaller than the selected <code>w.size</code> .
<code>n.sim</code>	number of simulations, e.g. 1000 (default).
<code>missing</code>	if TRUE (default), phenotypes are simulated with the same number of missing data observed in <code>data\$pheno</code> .
<code>w.size</code>	the window size (in centiMorgans) between two (linked) QTL, e.g. 20 (default).
<code>seed</code>	integer for the <code>set.seed()</code> function.
<code>verbose</code>	if TRUE (default), current progress is shown; if FALSE, no output is produced.
<code>x</code>	an object of class <code>qtlpoly.sim</code> to be printed.
<code>detailed</code>	if TRUE, detailed information on linkage groups and phenotypes is shown; if FALSE, no details are printed.
<code>...</code>	currently ignored

**Value**

An object of class `qtlpoly.sim` which contains a list of results with the same structure of class `qtlpoly.data`.

**Author(s)**

Guilherme da Silva Pereira, <gdasilv@ncsu.edu>

**References**

Pereira GS, Gemenet DC, Mollinari M, Olukolu BA, Wood JC, Mosquera V, Gruneberg WJ, Khan A, Buell CR, Yencho GC, Zeng ZB (2020) Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population, *Genetics* 215 (3): 579-595. doi:10.1534/genetics.120.303080.

**See Also**

[read\\_data](#)

**Examples**

```
# Estimate conditional probabilities using mappoly package
library(mappoly)
library(qtlpoly)
genoprob4x = lapply(maps4x[c(5)], calc_genoprob)
data = read_data(ploidy = 4, geno.prob = genoprob4x, pheno = pheno4x, step = 1)

# Simulate new phenotypes
sim.dat = simulate_ql(data = data, n.sim = 1)
sim.dat
```

# Index

- \* **datasets**
  - B2721, [2](#)
  - hexafake, [10](#)
  - maps4x, [11](#)
  - maps6x, [12](#)
  - pheno4x, [21](#)
  - pheno6x, [22](#)
  
- B2721, [2](#)
- breeding\_values, [3](#)
  
- feim, [5](#), [21](#)
- fit\_model, [4](#), [7](#), [25](#), [30](#)
- fit\_model2, [8](#)
  
- hexafake, [10](#), [12](#)
  
- maps4x, [11](#)
- maps6x, [12](#), [32](#), [34](#)
- modify\_qtl, [13](#)
  
- null\_model, [14](#), [19](#), [41](#)
- null\_model2, [16](#)
  
- optimize\_qtl, [17](#)
  
- permutations, [6](#), [19](#)
- pheno4x, [21](#), [23](#)
- pheno6x, [12](#), [22](#), [32](#), [34](#)
- plot.qtlpoly.bvalues (breeding\_values), [3](#)
- plot.qtlpoly.effects (qtl\_effects), [29](#)
- plot.qtlpoly.perm (permutations), [19](#)
- plot\_profile, [23](#)
- plot\_qtl, [24](#)
- plot\_sint, [26](#)
- print.qtlpoly.data (read\_data), [31](#)
- print.qtlpoly.feim (feim), [5](#)
- print.qtlpoly.modify (modify\_qtl), [13](#)
- print.qtlpoly.null (null\_model), [14](#)
- print.qtlpoly.optimize (optimize\_qtl), [17](#)
- print.qtlpoly.perm (permutations), [19](#)
- print.qtlpoly.profile (profile\_qtl), [27](#)
- print.qtlpoly.remim (remim), [35](#)
- print.qtlpoly.search (search\_qtl), [39](#)
- print.qtlpoly.simul (simulate\_qtl), [41](#)
- profile\_qtl, [24](#), [27](#), [27](#)
  
- qtl\_effects, [29](#)
  
- read\_data, [4](#), [8](#), [9](#), [14](#), [15](#), [17](#), [19](#), [25](#), [27](#), [30](#), [31](#), [36](#), [39](#), [41](#), [42](#)
- read\_data2, [33](#)
- remim, [8](#), [9](#), [14](#), [24](#), [25](#), [27](#), [30](#), [35](#)
- remim2, [37](#)
  
- search\_qtl, [19](#), [39](#)
- simulate\_qtl, [23](#), [41](#)
- summary.qtlpoly.fitted (fit\_model), [7](#)