

# Package ‘diaQTL’

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**Title** QTL Analysis in Diallel Populations

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**Description** QTL analysis of diploid and autotetraploid diallel populations. Phenotypes are regressed on genotype probabilities, and the regression coefficients are random effects.

**Depends** R (>= 3.5.0)

**License** GPL-3

**LazyData** true

**RoxygenNote** 7.1.0

**Roxygen** list(markdown = TRUE)

**Encoding** UTF-8

**Imports** BGLR, ggplot2, methods, coda, Matrix, scam, parallel, arrangements

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

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---

Amat

*A matrix*


---

### Description

Calculates the additive (A) relationship matrix from founder genotype probabilities

### Usage

```
Amat(data, chrom = NULL)
```

### Arguments

data	Variable inheriting from class <code>diallel_genoclass</code>
chrom	Optional, vector of chromosome names to include

### Details

Additive relationships are calculated from kinship coefficients of order 2 (Gallais 2003). Can specify to use only a subset of the chromosomes (by default, all chromosomes are used). Calculated based on the marker bins.

### Value

A matrix

### References

Gallais, A. 2003. Quantitative Genetics and Breeding Methods in Autopolyploid Plants. Institut National de la Recherche Agronomique, Paris.

### Examples

```
## Not run:
Amat_example = Amat(data = diallel_example)
Amat_example = Amat(data = diallel_example, chrom=c(1:11)) #leave chromosome 12 out

## End(Not run)
```

---

diallel\_genoclass

*S4 class with genotype data*


---

### Description

S4 class with genotype data

**Slots**

ploidy Either 2 or 4  
 dominance Integer 1-4 indicating 1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance.  
 X.GCA Incidence matrix for GCA effects  
 map data frame with marker,chrom, position (cM and/or bp) and bin  
 geno list of length equal to the number of marker bins. Each element is a list of length dominance. The elements in the nested list are sparse matrices with dimensions (id x effects).

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diallel geno pheno-class

*S4 class with genotype and phenotype data*


---

**Description**

S4 class with genotype and phenotype data

**Slots**

ploidy Either 2 or 4  
 dominance Integer 1-4 indicating 1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance.  
 X.GCA Incidence matrix for GCA effects  
 map data frame with marker,chrom, position (cM and/or bp) and bin  
 geno list of length equal to the number of marker bins. Each element is a list of length ploidy corresponding to additive, digenic, trigenic, and quadrigenic effects. The elements in the nested list are sparse matrices with dimensions (id x effects).  
 pheno data frame of phenotypes  
 X incidence matrix for fixed effects  
 Z incidence matrix for individuals

---

Dmat

*Dominance matrix*


---

**Description**

Calculates the dominance (D) relationship matrix from founder genotype probabilities

**Usage**

```
Dmat(data, chrom = NULL, dominance = 2)
```

**Arguments**

data	Variable inheriting from class <code>diallel geno</code>
chrom	Optional, vector of chromosome names to include
dominance	Either 2, 3, or 4

**Details**

Parameter dominance refers to 2 = digenic, 3 = trigenic, 4 = quadrigenic (Gallais 2003). Can specify to use only a subset of the chromosomes (by default, all chromosomes are used). Calculated based on the marker bins.

**Value**

Dominance relationship matrix

**References**

Gallais, A. 2003. Quantitative Genetics and Breeding Methods in Autopolyploid Plants. Institut National de la Recherche Agronomique, Paris.

**Examples**

```
## Not run:
Dmat_example = Dmat(data = diallel_example, dominance=2) #digenic dominance
Dmat_example = Dmat(data = diallel_example, dominance=3) #trigenic dominance

## End(Not run)
```

---

F1codes

*Genotype codes for F1 populations*


---

**Description**

Character vector with the 100 possible tetraploid genotypes for a F1 population. Maternal haplotypes are denoted 1,2,3,4 and paternal haplotypes 5,6,7,8.

**Usage**

```
data(F1codes)
```

**Format**

character vector

fitQTL

*Fit a single QTL model***Description**

Fit a single QTL model

**Usage**

```
fitQTL(data, params, dominance = 1, trait, marker, cofactor = NULL)
```

**Arguments**

<code>data</code>	Variable of class <code>diallel_geno_pheno</code>
<code>params</code>	List containing the number of burn-in ( <code>burnIn</code> ) and total iterations ( <code>nIter</code> )
<code>dominance</code>	Dominance degree (1-4). See Details.
<code>trait</code>	Name of trait
<code>marker</code>	Name of marker to fit as QTL
<code>cofactor</code>	Name of marker to fit as cofactor

**Details**

Standard errors of the posterior mean estimates are calculated by dividing the SD of the Markov Chain by the square root of the effective number of iterations, which is calculated by function `effectiveSize` in R package `coda`. The error bars on the plot of additive effects correspond to  $\pm 1.96 \cdot \text{SE}$  (95 percent confidence interval). For binary traits,  $R^2$  = the squared phi correlation. The additive and dominance variances are reported as a proportion of the total variance:  $h^2 = V_a / (V_a + V_d + V_{\text{resid}})$  and  $d^2 = V_d / (V_a + V_d + V_{\text{resid}})$ . Parameter `dominance` controls the genetic model: 1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance.

**Value**

List containing

**R2** Coefficient of determination**deltaDIC** Deviance Information Criterion relative to null model**h2** Mean and SE for proportion of variance due to additive effects**effectsA** Mean and SE of the additive effects for parental haplotypes**plotA** ggplot object for additive effectsIf `dominance > 1`, the list also contains**d2** Mean and SE for proportion of variance due to dominance (all orders)**effectsD** Mean and SE of the digenic dominance effects**plotD** ggplot object for digenic dominance effects

## Examples

```
## Not run:
## additive effects
params1 <- set_params( diallel_example, trait = "tuber_shape" )

fit1 <- fitQTL( data = diallel_example,
               trait = "tuber_shape",
               params = params1,
               marker = "solcap_snp_c2_25522")

## additive + dominance effects
params2 <- set_params( diallel_example, trait = "tuber_shape", dominance = TRUE )

fit2 <- fitQTL( data = diallel_example,
               trait = "tuber_shape",
               params = params2,
               marker = "solcap_snp_c2_25522",
               dominance = 2)

## End(Not run)
```

---

haplotypes

*Dosage of parental haplotypes*


---

## Description

Dosage of parental haplotypes

## Usage

```
haplotypes(data, marker = NULL, id = NULL)
```

## Arguments

data	Variable inheriting from class <code>diallel_geno</code>
marker	Name of marker
id	Name of individual

## Details

Function can be used to get parental haplotype dosage estimates at a single marker for all individuals (in which case `id` should be `NULL`) or for a single individual for all markers (in which case `marker` should be `NULL`)

## Value

Matrix of (id or markers) x parental haplotypes

**Examples**

```
## Not run:
haplo_example = haplotypes(data = diallel_example,
                           marker = "solcap_snp_c2_25522")
haplo_example = haplotypes(data = diallel_example,
                           id = "W15263-8R")

## End(Not run)
```

---

haplo_plot	<i>Plot parental haplotype dosage</i>
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**Description**

Plot parental haplotype dosages across the chromosome for one individual

**Usage**

```
haplo_plot(data, id, chrom, position, marker = NULL)
```

**Arguments**

data	Variable inheriting from class <code>diallel_geno</code>
id	Name of individual
chrom	Name of chromosome
position	Either "cM" or "bp"
marker	Optional, marker to indicate with dashed line

**Details**

For "cM" plotting, only one marker per bin is displayed. For "bp" plotting, all markers are included.

**Value**

ggplot object

**Examples**

```
## Not run:
haplo_plot(data = diallel_example,
           id = "W15263-8R",
           chrom = 10)

haplo_plot(data = diallel_example,
           id = "W15263-8R",
           chrom = 10,
           marker = "solcap_snp_c2_25522")

## End(Not run)
```

---

haplo_switch	<i>Find haplotype switches</i>
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### Description

Find haplotype switches

### Usage

```
haplo_switch(data, marker, haplotype, position, jump = 0.8)
```

### Arguments

data	Variable inheriting from class <code>diallel_geno</code>
marker	Name of focal marker
haplotype	Name of parental haplotype
position	Either "cM" or "bp"
jump	Change in dosage to designate haplotype switch

### Details

Designed to help with fine mapping of QTL. Function returns the location of the nearest haplotype switch on both sides (left, right) of a marker and haplotype of interest that represent the presumed location of a QTL allele.

### Value

Data frame with the locations of the nearest haplotype switch on the left and right side of the focal marker for all individuals with a haplotype switch

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LODthresh	<i>LOD thresholds for scan1</i>
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### Description

LOD thresholds for scan1

### Usage

```
LODthresh(genome.size, num.parents, ploidy)
```

### Arguments

genome.size	Genome size in Morgans (not centiMorgans)
num.parents	Number of parents
ploidy	2 or 4



## Details

LOD thresholds to control the genome-wide false positive rate at 0.05 were determined via simulation for up to 20 parents and genome sizes up to 12 Morgans. A monotone increasing concave curve was fit to these results using R package *scam* and is used for prediction. (The LOD threshold does not depend on population size.)

## Value

LOD threshold

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read_data	<i>Read data files</i>
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---

## Description

Reads genotype, pedigree, and phenotype data files

## Usage

```
read_data(
  genofile,
  ploidy = 4,
  pedfile,
  phenofile = NULL,
  fixed = NULL,
  bin.markers = T,
  dominance = 2,
  n.core = 1
)
```

## Arguments

genofile	File with map and genotype probabilities
ploidy	Either 2 or 4
pedfile	File with pedigree information (id,mother,father)
phenofile	File with phenotype data (optional)
fixed	If there are fixed effects, this is a character vector of "factor" or "numeric"
bin.markers	TRUE/FALSE whether to bin markers with the same cM position
dominance	Dominance degree (1-4). See Details.
n.core	Number of cores for parallel execution (only available from Linux or Mac command line)

## Details

The first 3 or 4 columns of the genotype file are the map (marker, chrom, bp and/or cM), followed by the members of the population. The genotype information for each marker x individual combination is a string with the format "statestatestate...=>problproblprob...", where "state" refers to the genotype state and "prob" is the genotype probability in decimal format. Only states with nonzero probabilities need to be listed. The encoding for the states in tetraploids is described in the documentation for the F1codes and S1codes datasets that come with the package. For diploids, there are 4 F1 genotype codes, 1,2,3,4, which correspond to haplotype combinations 1-3,1-4,2-3,2-4, respectively; the S1 genotype codes 1,2,3 correspond to 1-1,1-2,2-2, respectively. For the phenotype file, first column is id, followed by traits, and then any fixed effects. Pass a character vector for the function argument "fixed" to specify whether each effect is a factor or numeric covariate. The number of traits is deduced based on the number of columns. Binary traits must be coded N/Y and are converted to 0/1 internally for analysis by probit regression. Parameter dominance controls the genetic model: 1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance.

## Value

Variable of class `diallel_geno` if phenofile is NULL, otherwise `diallel_geno_pheno`

## Examples

```
## Not run:
## Get the location of raw csv files examples
genocsv = system.file( "tutorial", "potato_geno.csv", package = "diaQTL" )
pedcsv = system.file( "tutorial", "potato_ped.csv", package = "diaQTL" )
phenocsv = system.file( "tutorial", "potato_pheno.csv", package = "diaQTL" )

## Check their location in the system
print(genocsv)
print(pedcsv)
print(phenocsv)

## Load them in R
diallel_example <- read_data(genofile = genocsv,
                             ploidy = 4,
                             pedfile = pedcsv,
                             phenofile = phenocsv)

## End(Not run)
```

---

S1codes

*Genotype codes for S1 populations*

---

## Description

Character vector with the 35 possible tetraploid genotypes for a S1 population. Haplotypes are denoted 1,2,3,4.

## Usage

```
data(S1codes)
```

**Format**

character vector

---

scan1	<i>Single QTL scan</i>
-------	------------------------

---

**Description**

Performs a linear regression for each position in the map.

**Usage**

```
scan1(  
  data,  
  trait,  
  params,  
  dominance = 1,  
  chrom = NULL,  
  cofactor = NULL,  
  n.core = 1  
)
```

**Arguments**

data	Variable of class <a href="#">diallel_geno_pheno</a>
trait	Name of trait
params	List containing burnIn and nIter
dominance	Dominance degree (1-4). See Details.
chrom	Names of chromosomes to scan (default is all)
cofactor	Optional name of marker to include as cofactor in the scan
n.core	Number of cores for parallel execution (only available from Linux or Mac command line)

**Details**

For non-binary traits, R2 is the proportion of variance explained by the regression. For binary traits, R2 is the squared phi correlation. LOD score is the difference between the log-likelihood of the model with QTL and the null model (no QTL); higher values are better. deltaDIC is the difference between the DIC of the model with QTL minus the DIC of the null model; lower values are better. Parameter dominance controls the genetic model: 1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance. Parameter params can be estimated using [set\\_params](#).

**Value**

Data frame containing the map, LOD, R2 and deltaDIC results.

## Examples

```
## Not run:
par1 <- set_params(data = diallel_example,
                   trait = "tuber_shape")

scan1_example <- scan1(data = diallel_example,
                      chrom = 10,
                      trait = "tuber_shape",
                      params = par1)

## End(Not run)
```

---

scan1_permute	<i>Permutation test for scan1</i>
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---

## Description

Permutation test for scan1

## Usage

```
scan1_permute(
  data,
  trait,
  params,
  n.permute = 1000,
  chrom = NULL,
  dominance = 1,
  cofactor = NULL,
  n.core = 1
)
```

## Arguments

data	Variable of class <a href="#">diallel_geno_pheno</a>
trait	Name of trait
params	List containing burnIn and nIter
n.permute	Number of permutations
chrom	Names of chromosomes to scan (default is all)
dominance	Dominance degree (1-4)
cofactor	Optional name of marker to include as cofactor in the scan
n.core	Number of cores for parallel execution (only available from Linux or Mac command line)

## Value

Data frame with maximum LOD and minimum deltaDIC for each iteration

**Examples**

```
## Not run:
par1 <- set_params(data = diallel_example,
                   trait = "tuber_shape")

ans1_permut <- scan1_permute(data = diallel_example,
                             chrom = 10,
                             trait = "tuber_shape",
                             params = par1,
                             n.permute = 100)

## End(Not run)
```

---

scan1_summary	<i>Summary of scan1 result</i>
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---

**Description**

Summary of scan1 result

**Usage**

```
scan1_summary(scan1_data, thresh = NULL, chrom = NULL, position)
```

**Arguments**

scan1_data	output from scan1
thresh	optional, LOD threshold for plotting
chrom	optional, subset of chromosomes to plot
position	Either "cM" or "bp"

**Value**

List containing

**peaks** Data frame of the markers with the highest LOD score per chromosome

**plot** ggplot object

**Examples**

```
## Not run:
scan1_summary( scan1_example )
scan1_summary( scan1_example, chrom = "10" )
scan1_summary( scan1_example, chrom = c( "10", "12" ) )

## End(Not run)
```

---

set_params	<i>Determine parameters for scan1</i>
------------	---------------------------------------

---

## Description

Determine parameters for scan1

## Usage

```
set_params(data, trait, dominance = 1, tol = 0.1, burnIn = 50, nIter = 1000)
```

## Arguments

data	Variable of class <a href="#">diallel_geno_pheno</a>
trait	Name of trait
dominance	Dominance degree (1-4). See Details.
tol	tolerance for estimating the median
burnIn	initial value for burnIn parameter
nIter	initial value for nIter parameter

## Details

Determines the burn-in and total number of iterations using the Raftery and Lewis diagnostic from R package coda, based on a 95% probability that the estimated median of the additive effects is between the quantiles (0.5-tol) to (0.5+tol). For greater precision, decrease the tol parameter. Parameter dominance specifies which genetic model (1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance) to use when determining the number of iterations, but this information is not returned and must be independently specified when calling functions such as [scan1](#) or [fitQTL](#).

## Value

List containing

**burnIn** Number of burn-in iterations

**nIter** Total number of iterations

## Examples

```
## Not run:
par1 <- set_params(data = diallel_example,
                   trait = "tuber_shape")

## End(Not run)
```

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