

Package ‘diaQTL’

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Title QTL Analysis in Diallel Populations

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Author Jeffrey B. Endelman and Rodrigo R. Amadeu

Maintainer Jeffrey Endelman <endelman@wisc.edu>

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

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License GPL-3

LazyData true

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Imports BGLR, ggplot2, methods, coda, Matrix, scam, parallel, arrangements, tidyr, ggfittext, ggden-
dro, labeling

Suggests knitr, rmarkdown

VignetteBuilder knitr

R topics documented:

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BayesCI	<i>Bayesian Credible Interval for QTL position</i>
---------	--

Description

Bayesian Credible Interval for QTL position

Usage

```
BayesCI(scan1_data, data, chrom, CI.prob = 0.9)
```

Arguments

scan1_data	data frame output from scan1
data	variable of class <code>diallel_geno_pheno</code>
chrom	chromosome
CI.prob	probability for the credible interval

Details

Parameter `CI.prob` sets the probability for the Bayesian credible interval (e.g., 0.90, 0.95) using the likelihood (10^{LOD}) distribution.

Value

subset of `scan1_data` with markers in the CI

Examples

```
## Not run:
BayesCI(scan1_example, data, chrom="10", CI.prob=0.9)

## End(Not run)
```

diallel_geno-class *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).

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

diallel_geno_pheno_G-class

S4 class with genotype and phenotype data and the additive relationship matrix

Description

S4 class with genotype and phenotype data and the additive relationship matrix

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

G1 additive relationship matrix computed by [IBDmat](#)

diplo_freq

Diplotype frequencies

Description

Plot the frequency of individuals with diplotype dosage above a threshold

Usage

```
diplo_freq(data, diplotypes, dosage, position, chrom = NULL)
```

Arguments

data	Variable inheriting from class diallel_geno
diplotypes	Names of diplotypes
dosage	Dosage threshold
position	Either "cM" or "bp" for plotting
chrom	Names of chromosomes (default is all)

Details

Useful for visualizing selection in selfed populations.

F1codes	<i>Genotype codes for F1 populations</i>
---------	--

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	<i>Fit a single QTL model</i>
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Description

Fit a single QTL model

Usage

```
fitQTL(
  data,
  trait,
  marker,
  params,
  dominance = 1,
  CI.prob = 0.9,
  polygenic = TRUE,
  cofactor = NULL
)
```

Arguments

data	Variable of class diallel_geno_pheno
trait	Name of trait
marker	Name of marker to fit as QTL
params	List containing the number of burn-in (burnIn) and total iterations (nIter)
dominance	Dominance degree
CI.prob	Probability for Bayesian credible interval
polygenic	TRUE/FALSE whether to include polygenic background effect
cofactor	Name of marker to fit as cofactor (optional)

Details

For quantitative traits, R2 is the percent of variation explained by the regression (MSS/TSS). For binary traits, R2 is the squared phi correlation (as a percentage). LOD score is the difference between the log10-likelihood for the QTL model vs. no QTL model; higher values are better. deltaDIC is the difference between the Deviance Information Criterion for the QTL model vs. no QTL model; lower values are better. Parameter dominance controls the genetic model: 1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance. MCMC params can be estimated using `set_params`. Parameter CI.prob sets the probability (e.g., 0.90, 0.95) for the Bayesian credible interval for the estimated effects. The returned list `effects` contains the additive (and when included) digenic dominance effects. The proportion of variance for each effect is returned in `var`. The returned object `plots$dom` shows the digenic dominance effects above the diagonal, and below the diagonal is the sum of the additive and digenic dominance effects. The polygenic background effect has covariance equal to the additive relationship computed by `IBDmat`, leaving out the chromosome with the QTL. For faster execution with the polygenic model, use `Gprep` first.

Value

List containing

R2 Coefficient of determination

deltaDIC Deviance Information Criterion relative to null model

resid Residuals

var Matrix with proportion of variance for the effects

effects List of matrices containing the additive and higher order effects

plots List of ggplot objects for the effects

Examples

```
## Not run:
## additive effects
params1 <- set_params( diallel_example, trait = "tuber_shape" ,q=0.05,r=0.05)

fit1 <- fitQTL( data = diallel_example,
               trait = "tuber_shape",
               params = params1,
               marker = "solcap_snp_c2_25522",
               CI.prob = 0.9)

## additive + dominance effects
params2 <- set_params( diallel_example, trait = "tuber_shape", dominance=2,q=0.05,r=0.05)

fit2 <- fitQTL( data = diallel_example,
               trait = "tuber_shape",
               params = params2,
               marker = "solcap_snp_c2_25522",
               dominance = 2,
               CI.prob=0.9)

## End(Not run)
```

Gprep

Compute realized relationship matrix for fitQTL

Description

Compute realized relationship matrix for fitQTL

Usage

```
Gprep(data, marker)
```

Arguments

data	variable inheriting from class <code>diallel_geno_pheno</code>
marker	marker that will be used for <code>fitQTL</code>

Details

Computes the additive realized relationship matrix with `IBDmat` so that `fitQTL` does not need to and can run more quickly. The chromosome containing marker is excluded from the relationship calculation.

Value

variable inheriting from class `diallel_geno_pheno_G`

Examples

```
## Not run:
diallel_example <- Gprep(data = diallel_example, marker = "solcap_snp_c2_25522")

## End(Not run)
```

haplo_cluster

Cluster parental haplotypes

Description

Cluster parental haplotypes

Usage

```
haplo_cluster(filename, marker, haplotypes = NULL)
```

Arguments

filename	Name of CSV input file
marker	Either target marker or marker interval (see Details).
haplotypes	Vector of haplotype names (default is all)

Details

The input file (diaQTL_parents.csv) should be generated by [read_polyancestry](#). The argument marker can be either a single marker or vector of two markers. If a single marker, the function finds the smallest interval containing that marker such that the phased SNP haplotypes are all unique. If two markers are provided, that interval is used. Clustering utilizes hclust(method="average"). See also [phased_parents](#) for an additional visualization tool.

Value

- List containing
 - haplo** Data frame of haplotypes
 - dendro** Dendrogram

haplo_freq	<i>Haplotype frequencies</i>
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Description

Plots the frequency of individuals with haplotype dosage above a threshold

Usage

```
haplo_freq(  
  data,  
  haplotypes,  
  dosage,  
  id = NULL,  
  position = "cM",  
  chrom = NULL,  
  markers = NULL  
)
```

Arguments

- data Variable inheriting from class [diallel_geno](#)
- haplotypes Names of haplotypes
- dosage Dosage threshold
- id Vector of id names (default is entire population)
- position Either "cM" (default) or "bp" for plotting
- chrom Names of chromosomes (default is all)
- markers Optional, markers to indicate with dashed line. Only available when plotting a single chromosome.

Details

Useful for visualizing selection in selfed populations. For multiple chromosomes, each haplotype is shown in its own panel using facet_wrap. For one chromosome, the haplotypes are shown on the same set of axes.

haplo_plot	<i>Plot parental haplotype dosage</i>
------------	---------------------------------------

Description

Plot parental haplotype dosages across the chromosome for one individual

Usage

```
haplo_plot(data, id, chrom, position = "cM", markers = NULL)
```

Arguments

data	Variable inheriting from class <code>diallel_geno</code>
id	Name of individual
chrom	Name of chromosome
position	Either "cM" (default) or "bp"
markers	Optional, markers 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

IBDmat	<i>Realized IBD relationship</i>
--------	----------------------------------

Description

Calculates realized relationship matrices (additive and dominance) from founder genotype probabilities

Usage

```
IBDmat(data, dominance = 1, chrom = NULL)
```

Arguments

data	Variable inheriting from class <code>diallel_geno</code>
dominance	One of 1,2,3,4
chrom	Optional, vector of chromosome names to include

Details

Parameter dominance refers to 1 = additive, 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

Relationship matrix

References

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

Examples

```
## Not run:
  IBD_example = IBDmat(data = diallel_example, dominance=1) #additive
  IBD_example = IBDmat(data = diallel_example, dominance=2) #digenic dominance

## End(Not run)
```

LODthresh	<i>LOD thresholds for scan1</i>
-----------	---------------------------------

Description

LOD thresholds for scan1

Usage

```
LODthresh(genome.size, num.parents, ploidy, dominance = 1)
```

Arguments

genome.size	Genome size in Morgans (not centiMorgans)
num.parents	Number of parents
ploidy	2 or 4
dominance	1 (additive) or 2 (digenic dominance)

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

phased_parents	<i>Visualize phased SNPs of parents</i>
----------------	---

Description

Visualize phased SNPs of parents

Usage

```
phased_parents(filename, interval, markers, parents)
```

Arguments

filename	Name of CSV input file
interval	Vector of length 2 with the first and last marker names
markers	Vector of marker names to plot
parents	Vector of parent names to plot

Details

The input file can be generated by [read_polyancestry](#). The solid circles in the figure represent the allele counted by dosage.

Value

ggplot2 object

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

Description

Reads genotype, pedigree, and phenotype data files

Usage

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

Arguments

genofile	File with map and genotype probabilities
ploidy	Either 2 or 4
pedfile	File with pedigree data (id,parent1,parent2)
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	Maximum value of dominance that will be used for analysis (1-4). See Details.
n.core	Number of cores for parallel execution (only available for UNIX/Linux/MacOS command line)

Details

Genotype and pedigree input files can be created from PolyOrigin output using [read_polyancestry](#). The first 3 columns of the genotype file should be the genetic map (labeled marker, chrom, cM), and a fourth column for a reference genome position (labeled bp) can also be included. The map is followed by the members of the population. The genotype data 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. Missing data in the phenotype file should be coded as NA. The parameter dominance specifies the maximum value of dominance that can be used in subsequent analysis: 1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance. For maximum flexibility, use dominance = 4, but more memory is required. This will allow you to use any value of dominance (from 1 to 4) in functions such as [scan1](#) and [fitQTL](#). Output files from the BGLR package are stored in a folder named 'tmp' in the current directory.

Value

Variable of class [diallel_genos](#) if phenofile is NULL, otherwise [diallel_genos_pheno](#)

Examples

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

read_polyancestry	<i>Create diaQTL input files from polyancestry file</i>
-------------------	---

Description

Create diaQTL input files from polyancestry file

Usage

```
read_polyancestry(filename, mapfile = NULL, remove.outliers = TRUE)
```

Arguments

filename	Name of polyancestry file
mapfile	Optional name of CSV file containing the physical map (marker, chrom, bp)
remove.outliers	Should offspring flagged as outliers be removed (default is TRUE)

Details

Creates the pedigree (diaQTL_pedfile.csv) and genotype (diaQTL_genofile.csv) input files needed for [read_data](#) from the polyancestry output file generated by the PolyOrigin software. PolyOrigin outputs a genetic map in cM. To add a physical map in bp, use the option mapfile. The input file needed for [phased_parents](#) (diaQTL_parents.csv) is also created.

S1codes	<i>Genotype codes for S1 populations</i>
---------	--

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 diallel_geno_pheno
trait	Name of trait
params	List containing burnIn and nIter
dominance	Dominance degree (1-4)
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 quantitative traits, R2 is the percent of variation explained by the regression (MSS/TSS). For binary traits, R2 is the squared phi correlation (as a percentage). LOD score is the difference between the log10-likelihood for the QTL model vs. no QTL model; higher values are better. deltaDIC is the difference between the Deviance Information Criterion for the QTL model vs. no QTL model; lower values are better. Parameter dominance controls the genetic model: 1 = additive, 2 = digenic dominance, 3 = trigenic dominance, 4 = quadrigenic dominance. MCMC 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>
---------------	-----------------------------------

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 diallel_geno_pheno
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>
---------------	--------------------------------

Description

Summary of scan1 result

Usage

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

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

*Determine burn-in and total number of iterations***Description**

Determine burn-in and total number of iterations

Usage

```
set_params(
  data,
  trait,
  dominance = 1,
  marker = NULL,
  q = 0.5,
  r = 0.1,
  nIter = 2000
)
```

Arguments

data	variable of class <code>diallel_geno_pheno</code>
trait	name of trait
dominance	dominance degree
marker	name of marker (optional)
q	quantile to estimate
r	tolerance for quantile
nIter	number of iterations

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 estimate for quantile q of the additive effects is within the interval $(q-r, q+r)$. The 90th percentile for burn-in and total iterations across the additive effects is returned. 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 must be parameter must still be specified when calling functions such as `scan1` or `fitQTL`. Suggested values for `scan1` are $q=0.5$ and $r=0.1$. For `fitQTL`, the values depend on the desired Bayesian credible interval. For a 90% CI, suggested values are $q=0.05$ and $r=0.025$. If `marker=NULL` (default), the first marker of every chromosome is analyzed to generate parameters suitable for `scan1`. Parameter `nIter` sets the number of iterations used to apply the Raftery and Lewis diagnostic; the default value is 2000, and if a larger number is needed, an error will be generated with this information.

Value

List containing

burnIn Number of burn-in iterations

nIter Total number of iterations

Examples

```
## Not run:
# Parameters for scan1
par1 <- set_params(data = diallel_example,
                   trait = "tuber_shape", q=0.5, r=0.1)

# Parameters for fitQTL
par2 <- set_params(data = diallel_example,
                   trait = "tuber_shape", q=0.05, r=0.05, marker="solcap_c2_25522")

## End(Not run)
```

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