

Package ‘GWASpoly’

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 'GWASpoly.K.R'
 'GWASpoly.R'
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get.QTL	<i>Extract significant QTL</i>
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Description

Output a table with all significant markers

Usage

```
get.QTL(data, traits = NULL, models = NULL)
```

Arguments

data	Output from set.threshold
traits	Vector of trait names (by default, all traits)
models	Vector of model names (by default, all models)

Details

Score = $-\log_{10}(p)$. Effect = marker effect (not available for the general and diplo-general models).

Value

Data frame with results for significant markers

GWASpoly*Compute marker significance scores*

Description

Compute marker significance scores

Usage

```
GWASpoly(data, models, traits = NULL, params = NULL, n.core = 1, quiet = F)
```

Arguments

<code>data</code>	Output from <code>set.K</code>
<code>models</code>	Vector of model names
<code>traits</code>	Vector trait names (by default, all traits)
<code>params</code>	Optional list of params created by <code>set.params</code>
<code>n.core</code>	Number of cores for parallel computing
<code>quiet</code>	TRUE/FALSE whether to suppress output charting progress

Details

The following marker-effect models are available:

- "additive": Indicates the marker effect is proportional to the dosage of the alternate allele
- "X-dom": where X can be any integer between 1 and ploidy/2 and refers to the allele dosage needed for complete dominance (e.g., "1-dom" = simplex dominance, "2-dom" = duplex dominance). The software tries both dominance patterns for a given dosage model, e.g., whether the reference or alternate allele is dominant
- "diplo-general": All heterozygotes have the same effect
- "diplo-additive": All heterozygotes have the same effect, constrained to be halfway between the homozygous effects
- "general": There are no constraints on the effects of the different dosage levels

To specify additional model parameters, such as the inclusion of fixed effects (Q matrix) and the minimum minor allele frequency, use `set.params`

Value

Variable of class `GWASpoly.fitted`

GWASpoly.data-class	<i>S4 class with genotype and phenotype data</i>
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Description

S4 class with genotype and phenotype data

Slots

map data frame with marker,chrom,and position (either bp or cM)
 pheno data frame of phenotypes
 geno matrix (individuals x markers) of allele dosages (0,1,2,...ploidy)
 fixed data frame of fixed effects
 ploidy ploidy

GWASpoly.fitted-class	<i>S4 class with results from genome-wide scan</i>
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Description

S4 class with results from genome-wide scan

Slots

map data frame with marker,chrom,and position (either bp or cM)
 pheno data frame of phenotypes
 geno matrix with allele dosages
 fixed data frame of fixed effects
 ploidy ploidy
 K covariance matrix for polygenic effect
 scores -log10(p) results
 effects estimated marker effects
 params parameters used for the analysis

GWASpoly.K-class	<i>S4 class with genotypes, phenotypes, and polygenic covariance</i>
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Description

S4 class with genotypes, phenotypes, and polygenic covariance

Slots

map data frame with marker,chrom,and position (either bp or cM)

pheno data frame of phenotypes

geno matrix with allele dosages

fixed data frame of fixed effects

ploidy ploidy

K covariance matrix for polygenic effect

GWASpoly.thresh-class	<i>S4 class with results from genome-wide scan and detection threshold</i>
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Description

S4 class with results from genome-wide scan and detection threshold

Slots

map data frame with marker,chrom,and position (either bp or cM)

pheno data frame of phenotypes

geno matrix with allele dosages

fixed data frame of fixed effects

ploidy ploidy

K covariance matrix for polygenic effect

scores $-\log_{10}(p)$ results

effects estimated marker effects

params parameters used for the analysis

threshold thresholds for significance

manhattan.plot	Create Manhattan plot
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Description

Create Manhattan plot

Usage

```
manhattan.plot(data, traits = NULL, models = NULL)
```

Arguments

data	Variable of class GWASpoly.fitted
traits	Vector of trait names (by default, all traits plotted)
models	Vector of model names (by default, all models plotted)

Details

Results for the ref and alt versions of the dominance model are combined

Value

ggplot2 object

qq.plot	Quantile-Quantile (QQ) Plot
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Description

Inspect p-value inflation using a QQ plot

Usage

```
qq.plot(data, traits = NULL, models = NULL)
```

Arguments

data	Variable of class GWASpoly.fitted
traits	Vector of trait names (by default, all traits plotted)
models	Vector of model names (by default, all models plotted)

Value

ggplot2 object

read.GWASpoly

*Read in marker and phenotype data***Description**

Read in marker and phenotype data

Usage

```
read.GWASpoly(ploidy, pheno.file, geno.file, format, n.traits, delim = ",")
```

Arguments

ploidy	Ploidy (e.g., 2 for diploid, 4 for tetraploid)
pheno.file	Name of the phenotype file
geno.file	Name of the genotype file
format	Format for the marker data. See details.
n.traits	Number of traits
delim	Character to indicate the delimiter in the data files (e.g., "," for csv, "\t" for tab-delimited)

Details

The first column of the phenotype file contains the genotype identifier, columns 2 through (n.traits + 1) contain trait values, and subsequent columns contain the levels (for factors) or numeric values (for covariates) of any fixed effects. The first three columns of the genotype file are (1) marker name, (2) chromosome, and (3) position. Subsequent columns contain the marker data for each individual in the population. Marker data can be coded in one of three formats:

- "numeric": markers are coded based on the dosage of the alternate allele, taking on values between 0 and ploidy
- "AB": e.g., AAAB, AB BB for tetraploids
- "ACGT": e.g., AAAT, GGCC for tetraploids

Only bi-allelic markers are allowed. As of version 2.02 of the package, fractional values of dosage are allowed for the "numeric" format, with missing values imputed by the population mean for each marker. The fractional values are only used for the additive genetic model; for the other models, dosages are rounded to the nearest whole number. If the input allele dosages are whole numbers, then missing values are imputed with the population mode (most frequent value) for each marker.

ValueVariable of class `GWASpoly.data`

set.K	<i>Set covariance matrix for polygenic effect</i>
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Description

Set covariance matrix for polygenic effect

Usage

```
set.K(data, K = NULL)
```

Arguments

data	Output from read.GWASpoly
K	Optional: user-supplied matrix

Details

By default, K is computed as $K=MM'$, where M is the centered genotype matrix (lines x markers). For GWAS, the overall scaling of K is irrelevant. At present, K is scaled such that the mean of its diagonal elements is 1. Alternatively, the user can supply any positive semidefinite K (with row.names that match the genotype identifiers).

Value

Variable of class GWASpoly.K

set.params	<i>Set parameters</i>
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Description

Set parameters

Usage

```
set.params(
  fixed = NULL,
  fixed.type = NULL,
  n.PC = 0,
  MAF = 0.05,
  geno.freq = 0.95,
  P3D = T
)
```


Arguments

fixed	Vector of names of fixed effects
fixed.type	Vector of effect types ("numeric" or "factor"), corresponding to the effects listed in "fixed"
n.PC	Number of principal components to include as covariates
MAF	Minimum minor allele frequency
geno.freq	Maximum genotype frequency (after applying dominance relations)
P3D	TRUE/FALSE whether to use the P3D approximation (variance components not re-estimated for every marker)

Details

The list returned by the function should be passed to GWASpoly function.

Value

A list with the following components

fixed	Names of fixed effects
fixed.type	Types of fixed effects
n.PC	Number of principal components to include as covariates
min.MAF	Minimum minor allele frequency
max.geno.freq	Maximum genotype frequency (after applying dominance relations)
P3D	TRUE/FALSE whether to use the P3D approximation

set.threshold	<i>Set the significance threshold</i>
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Description

Set the significance threshold

Usage

```
set.threshold(
  data,
  method = "M.eff",
  level = 0.05,
  n.permute = 1000,
  n.core = 1
)
```

Arguments

data	Variable of class GWASpoly.fitted
method	One of the following: "M.eff", "Bonferroni", "FDR", "permute"
level	Genome-wide false positive or false discovery rate (depending on method).
n.permute	Number of permutations for method "permute"
n.core	Number of cores to use for multicore processing

Details

The default method, "M.eff", is a Bonferroni-type correction but using an effective number of markers that accounts for LD between markers (Moskvina and Schmidt, 2008). The FDR method is based on version 1.30.0 of the qvalue package.

Value

Variable of class GWASpoly.thresh

References

Moskvina V, Schmidt KM (2008) On multiple-testing correction in genome-wide association studies. Genetic Epidemiology 32:567-573. doi:10.1002/gepi.20331

write.GWASpoly	<i>Write results to file</i>
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Description

Write results to file

Usage

```
write.GWASpoly(data, trait, filename, what = "scores", delim = ",")
```

Arguments

data	Variable of class GWASpoly.fitted
trait	Trait name
filename	Filename
what	Either "scores" or "effects"
delim	Delimiter to use in the output file (default is comma)

Details

Score = $-\log_{10}(p)$. Effect = marker effect (not available for the general and diplo-general models).

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