

Package: colocPropTest (via r-universe)

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Title Proportional Testing for Colocalisation Analysis

Version 0.9.3

Description Colocalisation analysis tests whether two traits share a causal genetic variant in a specified genomic region. Proportional testing for colocalisation has been previously proposed [Wallace (2013) <[doi:10.1002/gepi.21765](https://doi.org/10.1002/gepi.21765)>], but is reimplemented here to overcome barriers to its adoption. Its use is complementary to the fine-mapping based colocalisation method in the 'coloc' package, and may be used in particular to identify false "H3" conclusions in 'coloc'.

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Encoding UTF-8

RoxygenNote 7.3.2

VignetteBuilder knitr

Depends magrittr, data.table

Imports car, coloc, graphics, stats, utils

Suggests knitr, plotrix, testthat (>= 3.0.0)

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NeedsCompilation no

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adjust_LD	<i>adjust LD for variable sample size</i>
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Description

adjust LD for variable sample size

Usage

```
adjust_LD(S, LD)
```

Arguments

S	coloc style dataset, with additional entries n0 and n1 which are *vectors* giving the number of cases and controls genotyped at each SNP
LD	matrix of LD, with dimnames given by snps in S\$snp

Value

adjusted LD matrix

Examples

```
library(coloc)

data(coloc_test_data)
attach(coloc_test_data)
LD=D1$LD
dimnames(LD)=list(D1$snp,D1$snp)
D1$type="cc"
D1$s=.5
D1$n1=D1$N * sample(c(0.25,.5),length(D1$snp), replace=TRUE)
D1$n0=rep(0.5*D1$N,length(D1$snp))
```

```
aLD=colocPropTest::adjust_LD(D1,LD)
LD[1:6,1:6]
aLD[1:6,1:6]
detach(coloc_test_data)
```

estprop	<i>Proportional colocalisation testing supplying only a pair of regression coefficients.</i>
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Description

Proportional colocalisation testing supplying only a pair of regression coefficients.

Usage

```
estprop(b1, b2, V1, V2)
```

Arguments

b1	regression coefficients for trait 1, expect length(b1)=2
b2	regression coefficients for trait 2, expect length(b2)=2
V1	2x2 variance-covariance matrix for trait 1
V2	2x2 variance-covariance matrix for trait 2

Value

a list, containing * result: the test statistic * plot.data: dataset for plotting the input data * plot.eta: dataset for plotting chisq as a function of theta or eta

Author(s)

Chris Wallace

estprop_slow	<i>Proportional colocalisation testing</i>
--------------	--

Description

This should return the same as estprop for a pair of snps, but is slower. Left here for checking. Also accomodates more than two snps.

Usage

```
estprop_slow(b1, b2, V1, V2)
```

Arguments

b1	regression coefficients for trait 1
b2	regression coefficients for trait 2
V1	variance-covariance matrix for trait 1
V2	variance-covariance matrix for trait 2

Value

a list, containing the test statistic and two datasets for plotting the input data or eta

Author(s)

Chris Wallace

keep_from_S	<i>keep snp subset of coloc dataset</i>
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Description

keep snp subset of coloc dataset

Usage

```
keep_from_S(S, keep)
```

Arguments

S	coloc dataset
keep	snps to keep

Value

subset of coloc dataset

lp	<i>logp</i>
----	-------------

Description

uses logs in calculation to avoid numerical issues with very small std errors / p values

Usage

lp(beta, se)

Arguments

beta	coefficient
se	std error of coefficient

Value

-log₁₀ p

marg_with_V	<i>create variance-covariance matrix for pair of marginal beta + vbeta, given estimate of r between snps</i>
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Description

create variance-covariance matrix for pair of marginal beta + vbeta, given estimate of r between snps

Usage

marg_with_V(beta, vbeta, rho)

Arguments

beta	vector of two coefficients at two snps
vbeta	vector of two variance of coefficients at the same two snps
rho	LD (r) between the two snps

Value

list of coefficient & variance-covariance matrix

nform	<i>Helper function to adjust LD parameter r for differential sample size between snps</i>
-------	---

Description

Estimate the r between effect estimates at snps which were genotyped on different sets of cases and controls. The adjusted r will be $nform(\dots) * r$ (where r is the population correlation between snps).

Usage

```
nform(n0a, n1a, n0b, n1b, n0ab = pmin(n0a, n0b), n1ab = pmin(n1a, n1b))
```

Arguments

n0a	number of controls with data at snp a
n1a	number of cases with data at snp a
n0b	number of controls with data at snp b
n1b	number of cases with data at snp b
n0ab	number of controls with data at both snps a and b
n1ab	number of cases with data at both snps a and b

Value

proportionality constant that depends on sample size.

plot_ellipses	<i>draw two ellipses</i>
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Description

draw two ellipses

Usage

```
plot_ellipses(
  b1,
  vb1,
  b2,
  vb2,
  legend = c("inferred", "observed"),
  include_origin = FALSE,
  ...
)
```

Arguments

b1 ellipse 1 centre (2d)
 vb1 ellipse 1 vcov matrix
 b2 ellipse 2 centre (2d)
 vb2 ellipse 2 vcov matrix
 legend character vector length 2 naming ellipse 1 and 2
 include_origin if TRUE, ensure plot includes (0,0)
 ... arguments passed to plot()

Value

draw ellipses on current graphics device

Author(s)

Chris Wallace

Examples

```

plot_ellipses(b1=c(5,5), vb1=diag(2),
              b2=c(2,2), vb2=matrix( c(1,0.5,0.5,1), 2, 2 ),
              legend=c("circle", "ellipse"),
              include.origin=TRUE)

```

run_proptests	<i>run proportional tests on extreme subset of snp pairs from two coloc style datasets. Of all functions in this package, this is the main one that should be used.</i>
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Description

run proportional tests on extreme subset of snp pairs from two coloc style datasets. Of all functions in this package, this is the main one that should be used.

Usage

```

run_proptests(
  S1,
  S2,
  LD,
  topsnps = "auto",
  r2.thr = 0.95,
  maxtests = 10000,
  nauto = 200,
  nsnps = NULL,
  adjust_n = FALSE
)

```

Arguments

S1	coloc dataset 1
S2	coloc dataset 2
LD	LD matrix - rownames, colnames capture the snps and S1\$snp[j] must be represented
topsnp	list of topsnps to be considered for testing or, if "auto", will be automatically selected
r2.thr	r2 threshold for initial tagging step - includes only one of any set of snps in mutually high LD with $r^2 > r2.thr$
maxtests	maximum number of test pairs to consider. if more than maxtests pairs available, will select a random sample.
nauto	number of snps to use when automatically defining topsnps. only has an effect if topsnps=="auto"
nsnps	if you are supplying data for only a subset of the snps in a region, then use nsnps to supply the total number of snps in the region. This is used to define the FDR correction. If NULL (default), will use the number of snps in common between S1 and S2.
adjust_n	TRUE if you want to adjust for variable sample size between snps. This is only set up for case control data at the moment (ask if you need quantitative) and requires that you supply separately the number of cases and controls at each snp in each dataset, as vector elements of the lists S1 and S2, called n1 (cases) and n0 (controls)

Value

data.table containing the tests run

Author(s)

Chris Wallace

Examples

```
library(colocPropTest)
library(coloc)
data(coloc_test_data)
attach(coloc_test_data)
LD=D1$LD
dimnames(LD)=list(D1$snp,D1$snp)
results=run_proptests(D1,D2,LD=LD,topsnps=D1$snp,maxtests=100)
min(results$fd)
```

tag	<i>Derive tag SNPs using heirarchical clustering</i>
-----	--

Description

Uses complete linkage and the `hclust` function to define clusters, then cuts the tree at `1-tag.threshold`

Usage

```
tag(r2, r2_threshold = 0.95, quiet = FALSE, method = "complete")
```

Arguments

<code>r2</code>	matrix of rsquared values
<code>r2_threshold</code>	only 1 of a set of snps with <code>r2 > r2_threshold</code> will be kept
<code>quiet</code>	if FALSE (default), show progress messages
<code>method</code>	method used for heirarchical clustering. See <code>hclust</code> for options.

Value

character vector, names are snps, values are the tag for each SNP

Author(s)

Chris Wallace

tester_marg	<i>run proportional test directly on marginal test stats from coloc datasets</i>
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Description

run proportional test directly on marginal test stats from coloc datasets

Usage

```
tester_marg(j, S1, S2, LD1, LD2 = LD1)
```

Arguments

<code>j</code>	indices of thw two snps
<code>S1</code>	coloc dataset 1
<code>S2</code>	coloc dataset 2
<code>LD1</code>	LD matrix for dataset 1 - rownames, colnames capture the snps and <code>S1\$snps[j]</code> must be represented
<code>LD2</code>	LD matrix for dataset 2 - rownames, colnames capture the snps and <code>S2\$snps[j]</code> must be represented. if not supplied, defaults to LD1

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tester_marg

Value

result from estprop

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