Package 'cophescan'

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Title Adaptation of the Coloc Method for PheWAS

Version 1.4.1

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Description A Bayesian method for Phenome-wide association studies (PheWAS) that identifies causal associations between genetic variants and traits, while simultaneously addressing confounding due to linkage disequilibrium. For details see Manipur et al (2023) <doi:10.1101/2023.06.29.546856>.

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Encoding UTF-8

LazyData true

VignetteBuilder knitr

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Depends R (>= 3.5.0)

URL https://github.com/ichcha-m/cophescan, https://ichcha-m.github.io/cophescan/

BugReports https://github.com/ichcha-m/cophescan/issues

Imports Rcpp (>= 1.0.7), coloc, data.table, ggplot2, ggrepel, pheatmap, methods, viridis, stats, grDevices, magrittr, utils, matrixStats, dplyr

Suggests knitr, testthat (>= 3.0.0), rmarkdown, RColorBrewer, ggpubr

Collate 'cophescan-package.R' 'singlevar.R' 'multivarsusie.R' 'multitrait.R' 'cophe_hyp_predict.R' 'copheplots.R' 'testdata.R' 'RcppExports.R' 'metrop_hier_priors.R' 'zzz.R'

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Contents

cophescan-package *The 'cophescan' package.*

Description

Coloc adapted Phenome-wide Scans

adjust_priors *adjust_priors*

Description

adjust fixed priors when nsnps in region is high

Usage

```
adjust_priors(
  nsnps,
  pa = 3.82e-05,
  pc = 0.00182,
  p1 = NULL,
  p2 = NULL,
  p12 = NULL
)
```

Arguments

nsnps	number of SNPs
pa	prior probability that a non-query variant is causally associated with the query trait (cophescan prior), default 3.82e-5
pc	prior probability that the query variant is causally associated with the query trait (cophescan prior), default 1.82e-3 (cophescan prior)
p1	prior probability a SNP is associated with trait 1, (coloc prior), pc derived by using $pc = p12/p1 + p12$; use p1, p2, p12 only when pa and pc are unavailable (See vignettes)
p2	prior probability a SNP is associated with trait 2, (coloc prior), pa derived by using $pa = p2$
p12	prior probability a SNP is associated with both traits, (coloc prior), pc derived by using $pc = p12/p1 + p12$

Value

vector of pn, pa and pc adjusted prior probabilities

average_piks *Average of priors: pnk, pak and pck*

Description

Average of priors: pnk, pak and pck

Usage

```
average_piks(params, nsnps, covar_vec, nits, thin, covar = FALSE)
```

Arguments

params	Vector of parameters: α, β and γ
nsnps	number of snps
covar_vec	Vector of the covariate
nits	Number of iterations run in mcmc
thin	thinning
covar	logical: was the covariate inflormation used? default: False

Value

average pik matrix of priors: pnk, pak and pck

average_piks_list *Average of priors: pnk, pak and pck from list (memory intensive)*

Description

Average of priors: pnk, pak and pck from list (memory intensive)

Usage

```
average_piks_list(params, nsnps, covar_vec, nits, thin, covar = FALSE)
```

Arguments

params	Vector of parameters: α, β and γ
nsnps	number of snps
covar_vec	Vector of the covariate
nits	Number of iterations run in mcmc
thin	thinning
covar	logical: was the covariate inflormation used? default: False

Value

average pik matrix of priors: pnk, pak and pck

`average_posterior_prob` *Average of posterior probabilities: Hn, Ha and Hc*

Description

Average of posterior probabilities: Hn, Ha and Hc

Usage

```
average_posterior_prob(
  params,
  lbf_mat,
  nsnps,
  covar_vec,
  nits,
  thin,
  covar = FALSE
)
```

Arguments

`params`	Vector of parameters: α, β and γ
`lbf_mat`	matrix of log bayes factors: lBF.Ha and lBF.Hc
`nsnps`	number of snps
`covar_vec`	Vector of the covariate
`nits`	Number of iterations run in mcmc
`thin`	thinning
`covar`	logical: was the covariate inflormation used? default: False

Value

matrix with average of all the posterior probabilities: Hn, Ha and Hc

---

`average_posterior_prob_list` *Average of posterior probabilities: Hn, Ha and Hc from list (memory intensive)*

Description

Average of posterior probabilities: Hn, Ha and Hc from list (memory intensive)

Usage

```
average_posterior_prob_list(
  params,
  lbf_mat,
  nsnps,
  covar_vec,
  nits,
  thin,
  covar = FALSE
)
```

Arguments

`params`	Vector of parameters: α, β and γ
`lbf_mat`	matrix of log bayes factors: lBF.Ha and lBF.Hc
`nsnps`	number of snps
`covar_vec`	Vector of the covariate
`nits`	Number of iterations run in mcmc
`thin`	thinning
`covar`	logical: was the covariate inflormation used? default: False

Value

matrix with average of all the posterior probabilities: Hn, Ha and Hc

---

`combine.bf` *combine.bf*

Description

Calculate posterior probabilities for all the configurations

Usage

```
combine.bf(lBF_df, pn, pa, pc)
```

Arguments

lBF_df	dataframe with log bayes factors of hypothesis Ha and Hn: column names should be lBF.Ha and lBF.Hc
pn	prior probability that none of the SNPs/variants in the region are associated with the query trait
pa	prior probability that a non-query variant is causally associated with the query trait
pc	prior probability that the query variant is causally associated with the query trait

Value

named numeric vector of posterior probabilities and bayes factors

Author(s)

Ichcha Manipur

---

cophe.hyp.predict *Predict cophescan hypothesis for tested associations*

Description

Predict cophescan hypothesis for tested associations

Usage

```
cophe.hyp.predict(
  cophe.res,
  grouping.vars = c("querysnp", "querytrait"),
  Hc.cutoff = 0.6,
  Hn.cutoff = 0.2
)
```

Arguments

cophe.res	results obtained from cophe.single, cophe.susie or cophe.multitrait or data.frame with the following columns: PP.Hn, PP.Hc, PP.Ha, querysnp, querytrait
grouping.vars	This is important for results from cophe.susie where there are multiple signals. These will be collapsed into one call. If you want to return all signals set this to a single variable eg: grouping.vars = c('querysnp')
Hc.cutoff	threshold for PP.Hc above which the associations are called Hc
Hn.cutoff	threshold for PP.Hn above which the associations are called Hn

Value

returns dataframe with posterior probabilties of Hn, Hc and Ha with the predicted hypothesis based on the provided cut.offs.

See Also

cophe.single, cophe.susie, cophe.multitrait, , multitrait.simplify

---

cophe.multitrait *Run cophescan on multiple traits at once*

Description

Run cophescan on multiple traits at once

Usage

```
cophe.multitrait(
  trait.dat,
  querysnpid,
  querytrait.names,
  LDmat = NULL,
  method = "single",
  simplify = FALSE,
  predict.hyp = TRUE,
  Hn.cutoff = 0.2,
  Hc.cutoff = 0.6,
  est.fdr.based.cutoff = FALSE,
  fdr = 0.05,
  ...
)
```

Arguments

trait.dat	Named(traits) list of coloc structured data for k traits (Total number of traits)
querysnpid	vector of query variant ids = length(trait.dat), if the same variant
querytrait.names	vector of names for the query traits, if the names of the multi.dat list contain the trait names please pass querytrait.names=names(multi.dat)
LDmat	LD matrix
method	either 'single' for cophe.single or 'susie' for cophe.susie
simplify	if TRUE removes intermediate results from output using 'multitrait.simplify'
predict.hyp	if TRUE predicts the hypothesis based on the provided thresholds for pp.Hc and pp.Hn (overrides simplify) using cophe.hyp.predict
Hn.cutoff	threshold for PP.Hc above which the associations are called Hc

`Hc.cutoff`	threshold for PP.Hc above which the associations are called Hn
`est.fdr.based.cutoff`	if True calculates the Hc.cutoff using 1-mean(PP.Hc)|PP.Hc > cutoff
`fdr`	fdr threshold to estimate Hc.cutoff
`...`	additional arguments of priors for `cophe.susie` or `cophe.single`

Value

if simplify is False returns multi-trait list of lists, each with:

- a summary data.frame of the cophescan results
- priors used
- querysnp
- querytrait

if simplify is TRUE only returns dataframe with posterior probabilties of Hn, Hc and Ha with no intermediate results if predict.hyp is TRUE returns a dataframe with output of simplify and the predicted hypotheses for all associations

Author(s)

Ichcha Manipur

`cophe.single` *Bayesian cophescan analysis using Approximate Bayes Factors*

Description

Bayesian cophescan analysis under single causal variant assumption

Usage

```
cophe.single(
  dataset,
  querysnpid,
  querytrait,
  MAF = NULL,
  pa = 3.82e-05,
  pc = 0.00182,
  p1 = NULL,
  p2 = NULL,
  p12 = NULL
)
```

Arguments

dataset	a list with specifically named elements defining the query trait dataset to be analysed.
querysnpid	Id of the query variant, (id in dataset$snp)
querytrait	Query trait name
MAF	Minor allele frequency vector
pa	prior probability that a non-query variant is causally associated with the query trait (cophescan prior), default 3.82e-5
pc	prior probability that the query variant is causally associated with the query trait (cophescan prior), default 1.82e-3 (cophescan prior)
p1	prior probability a SNP is associated with trait 1, (coloc prior), pc derived by using $pc = p12/p1 + p12$; use p1, p2, p12 only when pa and pc are unavailable (See vignettes)
p2	prior probability a SNP is associated with trait 2, (coloc prior), pa derived by using $pa = p2$
p12	prior probability a SNP is associated with both traits, (coloc prior), pc derived by using $pc = p12/p1 + p12$

Details

This function calculates posterior probabilities of different causal variant configurations under the assumption of a single causal variant for each trait.

If regression coefficients and variances are available, it calculates Bayes factors for association at each SNP. If only p values are available, it uses an approximation that depends on the SNP's MAF and ignores any uncertainty in imputation. Regression coefficients should be used if available. Find more input data structure details in the coloc package

Value

a list of two data.frames:

- summary is a vector giving the number of SNPs analysed, and the posterior probabilities of Hn (no shared causal variant), Ha (two distinct causal variants) and Hc (one common causal variant)
- results is an annotated version of the input data containing log Approximate Bayes Factors and intermediate calculations, and the posterior probability SNP.PP.Hc of the SNP being causal for the shared signal *if* Hc is true. This is only relevant if the posterior support for Hc in summary is convincing.

Author(s)

Ichcha Manipur

Examples

```
library(cophescan)
data(cophe_multi_trait_data)
query_trait_1 <- cophe_multi_trait_data$summ_stat[['Trait_1']]
querysnpid <- cophe_multi_trait_data$querysnpid
res.single <- cophe.single(query_trait_1, querysnpid = querysnpid, querytrait='Trait_1')
summary(res.single)
```

`cophe.single.lbf` *cophe.single.lbf*

Description

Calculate log bayes factors for each hypothesis (Single causal variant assumption)

Usage

```
cophe.single.lbf(dataset, querysnpid, querytrait, MAF = NULL)
```

Arguments

`dataset`	a list with specifically named elements defining the query trait dataset to be analysed.
`querysnpid`	Id of the query variant, (id in dataset$snp)
`querytrait`	Query trait name
`MAF`	Minor allele frequency vector

Value

data frame with log bayes factors for Hn and Ha hypotheses

Author(s)

Ichcha Manipur

See Also

`cophe.single`

Examples

```
library(cophescan)
data(cophe_multi_trait_data)
query_trait_1 <- cophe_multi_trait_data$summ_stat[['Trait_1']]
querysnpid <- cophe_multi_trait_data$querysnpid
res.single.lbf <- cophe.single.lbf(query_trait_1, querysnpid = querysnpid, querytrait='Trait_1')
res.single.lbf
```

cophe.susie *run* cophe.susie *using susie to detect separate signals*

Description

Check if a variant causally associated in one trait might be causal in another trait

Usage

```
cophe.susie(
  dataset,
  querysnpid,
  querytrait,
  pa = 3.82e-05,
  pc = 0.00182,
  p1 = NULL,
  p2 = NULL,
  p12 = NULL,
  susie.args = list()
)
```

Arguments

dataset	*either* a list with specifically named elements defining the dataset to be analysed. (see check_dataset)
querysnpid	Id of the query variant
querytrait	Query trait name
pa	prior probability that a non-query variant is causally associated with the query trait (cophescan prior), default 3.82e-5
pc	prior probability that the query variant is causally associated with the query trait (cophescan prior), default 1.82e-3
p1	prior probability a SNP is associated with trait 1, (coloc prior), pc derived by using $pc = p12/p1 + p12$; use p1, p2, p12 only when pa and pc are unavailable (See vignettes)
p2	prior probability a SNP is associated with trait 2, (coloc prior), pa derived by using $pa = p2$
p12	prior probability a SNP is associated with both traits, (coloc prior), pc derived by using $pc = p12/p1 + p12$
susie.args	a named list of additional arguments to be passed to runsusie

Value

a list, containing elements

- summary a data.table of posterior probabilities of each global hypothesis, one row per pairwise comparison of signals from the two traits

- results a data.table of detailed results giving the posterior probability for each snp to be jointly causal for both traits *assuming Hc is true*. Please ignore this column if the corresponding posterior support for H4 is not high.
- priors a vector of the priors used for the analysis

Author(s)

Ichcha Manipur

Examples

```
library(cophescan)
data(cophe_multi_trait_data)
query_trait_1 <- cophe_multi_trait_data$summ_stat[['Trait_1']]
querysnpid <- cophe_multi_trait_data$querysnpid
query_trait_1$LD <- cophe_multi_trait_data$LD
res.susie <- cophe.susie(query_trait_1, querysnpid = querysnpid, querytrait='Trait_1')
summary(res.susie)
```

---

cophe.susie.lbf *cophe.susie.lbf*

Description

Calculate log bayes factors for each hypothesis (SuSIE - multiple causal variant assumption)

Usage

```
cophe.susie.lbf(
  dataset,
  querysnpid,
  querytrait,
  switch = TRUE,
  susie.args = list(),
  MAF = NULL
)
```

Arguments

dataset	a list with specifically named elements defining the query trait dataset to be analysed.
querysnpid	Id of the query variant, (id in dataset$snp)
querytrait	Query trait name
switch	Set switch=TRUE to obtain single BF when credible sets not found with SuSIE
susie.args	a named list of additional arguments to be passed to runsusie
MAF	Minor allele frequency vector

Value

data frame with log bayes factors for Hn and Ha hypotheses

Author(s)

Ichcha Manipur

See Also

cophe.susie

Examples

```
library(cophescan)
data(cophe_multi_trait_data)
query_trait_1 <- cophe_multi_trait_data$summ_stat[['Trait_1']]
query_trait_1$LD <- cophe_multi_trait_data$LD
querysnpid <- cophe_multi_trait_data$querysnpid
res.susie.lbf <- cophe.susie.lbf(query_trait_1, querysnpid = querysnpid,
                                 querytrait='Trait_1', switch=T)
res.susie.lbf
```

---

cophe_heatmap *Heatmap of multi-trait cophescan results*

Description

Heatmap of multi-trait cophescan results

Usage

```
cophe_heatmap(
  multi.dat,
  querysnpid,
  query_trait_names,
  thresh_Hc = 0.5,
  thresh_Ha = 0.5,
  ...
)
```

Arguments

multi.dat	multi trait cophescan results returned from cophe.multitrait or formatted in the same way with multitrait.simplify
querysnpid	query variant
query_trait_names	names of phenotypes corresponding to the multi.dat results

thresh_Hc	Hc threshold to be displayed
thresh_Ha	Ha threshold to be displayed
...	additional arguments to be passed to pheatmap

Value

heatmap of posterior probabilities of the phentypes above the set threshold

---

cophe_multi_trait_data

Simulated multi-trait data

Description

Simulated multi-trait data

Usage

```
data(cophe_multi_trait_data)
```

Format

list of coloc structred datasets for 24 traits (cophe_multi_trait_data$summ_stat), LD matrix (cophe_multi_trait_data$LD) and the id of the query snp (cophe_multi_trait_data$querysnpid). #' The trait dataset are simulated summary statistics (1000 SNPs) for 10 Hn, 10 Ha and 10 Hc.

---

cophe_plot

cophe_plots showing the Ha and Hc of all traits and labelled above the specified threshold

---

Description

cophe_plots showing the Ha and Hc of all traits and labelled above the specified threshold

Usage

```
cophe_plot(
  multi.dat,
  querysnpid,
  query_trait_names,
  thresh_Hc = 0.5,
  thresh_Ha = 0.5,
  beta_p = NULL,
  traits.dat = NULL,
  group_pheno = NULL
)
```

Arguments

multi.dat	multi trait cophescan results returned from cophe.multitrait or multitrait.simplify
querysnpid	query variant (only a single variant for PheWAS plots)
query_trait_names	list of phenotype names
thresh_Hc	Hc threshold to be displayed
thresh_Ha	Ha threshold to be displayed
beta_p	data.frame (from the get.beta function) with four columns : 1. "beta_plot": indicating beta direction (p or n) 2. "beta_plot": -log10(pval) of the queried variant 3. "querysnp" 4. "querytrait".
traits.dat	list of multi-trait coloc structured datasets
group_pheno	Vector with additional grouping of phenotypes

Value

cophescan plots of Ha and Hc

See Also

cophe.single, cophe.susie, cophe.multitrait, , multitrait.simplify

---

get_beta *Extract beta and p-values of queried variant*

Description

Extract beta and p-values of queried variant

Usage

```
get_beta(traits.dat, querysnpid, querytrait)
```

Arguments

traits.dat	list of coloc structured dataset
querysnpid	vector of querysnpid
querytrait	vector of querytrait names

Value

data.frame with one column named beta_plot: indicating beta direction (n/p) and another column named pval_plot with -log10(pval) of the queried variant

get_posterior_prob *Calculation of the posterior prob of Hn, Ha and Hc*

Description

Calculation of the posterior prob of Hn, Ha and Hc

Usage

```
get_posterior_prob(params, lbf_mat, nsnps, covar_vec, covar = FALSE)
```

Arguments

params	Vector of parameters: α, β and γ
lbf_mat	matrix of log bayes factors: lBF.Ha and lBF.Hc
nsnps	number of snps
covar_vec	Vector of the covariate
covar	logical: should the covariate inflormation be used? default: False

Value

posterior prob of Hn, Ha and Hc

Hc.cutoff.fdr *Estimate the Hc.cutoff for the required FDR*

Description

Estimate the Hc.cutoff for the required FDR

Usage

```
Hc.cutoff.fdr(ppHc, fdr = 0.05, return_plot = TRUE)
```

Arguments

ppHc	a vector containing the PP.Hc (the posterior probability of causal association) of all tests
fdr	FDR default: 0.05
return_plot	default: TRUE, plot the fdr estimated at the different Hc.cutoff

Value

the Hc.cutoff value for the specified FDR, if return_plot is True returns a plot showing the FDR calculated at different Hc thresholds

hypothesis.priors *hypothesis.priors*

Description

Estimate priors for each hypothesis

Usage

```
hypothesis.priors(nsnps, pn, pa, pc)
```

Arguments

nsnps	number of SNPs
pn	prior probability that none of the SNPs/variants in the region are associated with the query trait
pa	prior probability that a non-query variant is causally associated with the query trait
pc	prior probability that the query variant is causally associated with the query trait

Value

hypotheses priors

Author(s)

Ichcha Manipur

logd_alpha *dnorm for alpha*

Description

dnorm for alpha

Usage

```
logd_alpha(a, alpha_mean = -10, alpha_sd = 0.5)
```

Arguments

a	current alpha
alpha_mean	prior for the mean of alpha
alpha_sd	prior for the standard deviation of alpha

Value

log dnorm

---

logd_beta *dgamma for beta*

Description

dgamma for beta

Usage

```
logd_beta(b, beta_shape = 2, beta_scale = 2)
```

Arguments

b	current beta
beta_shape	prior for the shape (gamma distibution) of beta
beta_scale	prior for the scale of beta

Value

log dgamma

---

logd_gamma *dgamma for gamma*

Description

dgamma for gamma

Usage

```
logd_gamma(g, gamma_shape = 2, gamma_scale = 2)
```

Arguments

g	current gamma
gamma_shape	prior for the shape (gamma distibution) of gamma
gamma_scale	prior for the scale of gamma

Value

log dgamma

loglik *Log likelihood calculation*

Description

Log likelihood calculation

Usage

```
loglik(params, lbf_mat, nsnps, covar_vec, covar = FALSE)
```

Arguments

params	Vector of parameters: α, β and γ
lbf_mat	matrix of log bayes factors: lBF.Ha and lBF.Hc
nsnps	number of snps
covar_vec	Vector of the covariate
covar	logical: should the covariate inflormation be used? default: False

Value

logpost flog of the posteriors

logpost *Log posterior calculation*

Description

Log posterior calculation

Usage

```
logpost(params, lbf_mat, nsnps, covar_vec, covar = FALSE)
```

Arguments

params	Vector of parameters: α, β and γ
lbf_mat	matrix of log bayes factors: lBF.Ha and lBF.Hc
nsnps	number of snps
covar_vec	Vector of the covariate
covar	logical: should the covariate inflormation be used? default: False

Value

logpost flog of the posteriors

`logpriors` *Calculate log priors*

Description

Calculate log priors

Usage

```
logpriors(
  params,
  covar = FALSE,
  alpha_mean = -10,
  alpha_sd = 0.5,
  beta_shape = 2,
  beta_scale = 2,
  gamma_shape = 2,
  gamma_scale = 2
)
```

Arguments

`params`	Vector of parameters: α, β and γ
`covar`	logical: Should the covariate inflormation be used? default: False
`alpha_mean`	prior for the mean of alpha
`alpha_sd`	prior for the standard deviation of alpha
`beta_shape`	prior for the shape (gamma distibution) of beta
`beta_scale`	prior for the scale of beta
`gamma_shape`	prior for the shape (gamma distibution) of gamma
`gamma_scale`	prior for the scale of gamma

Value

log priors

logsum *logsum*

Description

Internal function, logsum Function directly taken from coloc This function calculates the log of the sum of the exponentiated logs taking out the max, i.e. insuring that the sum is not Inf

Usage

```
logsum(x)
```

Arguments

x	numeric vector

Value

max(x) + log(sum(exp(x - max(x))))

logsumexp *Log sum*

Description

Log sum

Usage

```
logsumexp(x)
```

Arguments

x	vector of log scale values to be added

Value

log sum of input

`metrop_run` *Run the hierarchical mcmc model to infer priors*

Description

Run the hierarchical mcmc model to infer priors

Usage

```
metrop_run(
  lbf_mat,
  nsnps,
  covar_vec,
  covar = FALSE,
  nits = 10000L,
  thin = 1L,
  alpha_mean = -10,
  alpha_sd = 0.5,
  beta_shape = 2,
  beta_scale = 2,
  gamma_shape = 2,
  gamma_scale = 2
)
```

Arguments

`lbf_mat`	matrix of log bayes factors: lBF.Ha and lBF.Hc
`nsnps`	number of snps
`covar_vec`	Vector of the covariate
`covar`	logical: Should the covariate inflormation be used? default: False
`nits`	Number of iterations run in mcmc
`thin`	thinning
`alpha_mean`	prior for the mean of alpha
`alpha_sd`	prior for the standard deviation of alpha
`beta_shape`	prior for the shape (gamma distibution) of beta
`beta_scale`	prior for the scale of beta
`gamma_shape`	prior for the shape (gamma distibution) of gamma
`gamma_scale`	prior for the scale of gamma

Value

named list of log likelihood (ll) and parameters: alpha, beta and gamma

multitrait.simplify *Simplifying the output obtained from* cophe.multitrait, cophe.single *or* cophe.susie

Description

Simplifying the output obtained from cophe.multitrait, cophe.single or cophe.susie

Usage

```
multitrait.simplify(multi.dat, only_BF = FALSE)
```

Arguments

multi.dat	output obtained from cophe.multitrait, cophe.single or cophe.susie
only_BF	return only bayes factors and not posterior probabilities (default=FALSE)

Value

dataframe with posterior probabilties of Hn, Hc and Ha

pars2pik *Conversion of parameters alpha, beta and gamma to pnk, pak and pck*

Description

Conversion of parameters alpha, beta and gamma to pnk, pak and pck

Usage

```
pars2pik(params, nsnps, covar_vec, covar = FALSE)
```

Arguments

params	Vector of parameters: α, β and γ
nsnps	number of snps
covar_vec	Vector of the covariate
covar	logical: should the covariate information be used? default: False

Value

pik matrix of priors: pnk, pak and pck

pars_init *Initiate parameters alpha, beta and gamma*

Description

Initiate parameters alpha, beta and gamma

Usage

```
pars_init(
  covar = FALSE,
  alpha_mean = -10,
  alpha_sd = 0.5,
  beta_shape = 2,
  beta_scale = 2,
  gamma_shape = 2,
  gamma_scale = 2
)
```

Arguments

covar	logical: Should the covariate inflormation be used? default: False
alpha_mean	prior for the mean of alpha
alpha_sd	prior for the standard deviation of alpha
beta_shape	prior for the shape (gamma distibution) of beta
beta_scale	prior for the scale of beta
gamma_shape	prior for the shape (gamma distibution) of gamma
gamma_scale	prior for the scale of gamma

Value

params α, β and γ

per.snp.priors *per.snp.priors*

Description

Estimate per snp priors

Usage

```
per.snp.priors(
  nsnps,
  pa = 3.82e-05,
  pc = 0.00182,
  p1 = NULL,
  p2 = NULL,
  p12 = NULL
)
```

Arguments

nsnps	number of SNPs
pa	prior probability that a non-query variant is causally associated with the query trait (cophescan prior), default 3.82e-5
pc	prior probability that the query variant is causally associated with the query trait (cophescan prior), default 1.82e-3 (cophescan prior)
p1	prior probability a SNP is associated with trait 1, (coloc prior), pc derived by using $pc = p12/p1 + p12$; use p1, p2, p12 only when pa and pc are unavailable (See vignettes)
p2	prior probability a SNP is associated with trait 2, (coloc prior), pa derived by using $pa = p2$
p12	prior probability a SNP is associated with both traits, (coloc prior), pc derived by using $pc = p12/p1 + p12$

Value

priors at the query variant

Author(s)

Ichcha Manipur

---

piks *List of priors: pn, pa and pc over all iterations*

Description

List of priors: pn, pa and pc over all iterations

Usage

```
piks(params, nsnps, covar_vec, covar = FALSE)
```

Arguments

params	Vector of parameters: α, β and γ
nsnps	number of snps
covar_vec	Vector of the covariate
covar	logical: was the covariate inflormation used? default: False

Value

List of priors (len: iterations): pnk, pak and pck

---

plot_trait_manhat *Plot region Manhattan for a trait highlighting the queried variant*

Description

Plot region Manhattan for a trait highlighting the queried variant

Usage

```
plot_trait_manhat(trait.dat, querysnpid, alt.snpid = NULL)
```

Arguments

trait.dat	dataset used as input for running cophescan
querysnpid	the id of the causal variant as present in trait.dat$snp, plotted in red
alt.snpid	the id of the other variants as a vector to be plotted, plotted in blue

Value

regional manhattan plot

---

posterior_prob *List of posterior probabilities: Hn, Ha and Hc over all iterations*

Description

List of posterior probabilities: Hn, Ha and Hc over all iterations

Usage

```
posterior_prob(params, lbf_mat, nsnps, covar_vec, covar = FALSE)
```

Arguments

params	Vector of parameters: α, β and γ
lbf_mat	matrix of log bayes factors: lBF.Ha and lBF.Hc
nsnps	number of snps
covar_vec	Vector of the covariate
covar	logical: was the covariate inflormation used? default: False

Value

List of posterior probabilties (len: iterations): Hn, Ha and Hc

---

prepare_plot_data *Prepare data for plotting*

Description

Prepare data for plotting

Usage

```
prepare_plot_data(
  multi.dat,
  querysnpid,
  query_trait_names,
  thresh_Ha = 0.5,
  thresh_Hc = 0.5,
  hmp = FALSE,
  cophe.plot = TRUE
)
```

Arguments

multi.dat	multi trait cophescan results returned from cophe.multitrait or multitrait.simplify
querysnpid	query variant
query_trait_names	vector of names of the query traits
thresh_Ha	Ha threshold to be displayed
thresh_Hc	Hc threshold to be displayed
hmp	return for heatmap
cophe.plot	default: TRUE, return for cophe_plot

Value

plot list

See Also

cophe_plot, cophe.susie, cophe.multitrait, multitrait.simplify default NULL

`propose` *Proposal distribution*

Description

Proposal distribution

Usage

```
propose(params, propsd = 0.5)
```

Arguments

`params`	Vector of parameters: α, β and γ
`propsd`	Standard deviation for the proposal

Value

vector : proposal

`run_metrop_priors` *Run the hierarchical Metropolis Hastings model to infer priors*

Description

Run the hierarchical Metropolis Hastings model to infer priors

Usage

```
run_metrop_priors(
  multi.dat,
  covar = FALSE,
  covar_vec = NULL,
  is_covar_categorical = FALSE,
  nits = 10000,
  thin = 1,
  posterior = FALSE,
  avg_pik = TRUE,
  avg_posterior = TRUE,
  pik = FALSE,
  alpha_mean = -10,
  alpha_sd = 0.5,
```

```
  beta_shape = 2,
  beta_scale = 2,
  gamma_shape = 2,
  gamma_scale = 2
)
```

Arguments

multi.dat	matrix of bf values, rows=traits, named columns=("lBF.Ha","lBF.Hc","nsnps")
covar	whether to include covariates
covar_vec	vector of covariates
is_covar_categorical	only two categories supported (default=FALSE) - Experimental
nits	number of iterations
thin	burnin
posterior	default: FALSE, estimate posterior probabilities of the hypotheses
avg_pik	default: FALSE, estimate the average of the pik
avg_posterior	default: FALSE, estimate the average of the posterior probabilities of the hypotheses
pik	default: FALSE, inferred prior probabilities
alpha_mean	prior for the mean of alpha
alpha_sd	prior for the standard deviation of alpha
beta_shape	prior for the shape (gamma distibution) of beta
beta_scale	prior for the scale of beta
gamma_shape	prior for the shape (gamma distibution) of gamma
gamma_scale	prior for the scale of gamma

Value

List containing the posterior distribution of the parameters alpha, beta, gamma (if covariate included) and the loglikelihood

if avg_posterior=TRUE matrix with average of all the posterior probabilities of Hn, Ha and Hc

if avg_pik=TRUE matrix with average of all the priors: pn, pa and pc

data, nits and thin contain the input data, number of iterations and burnin respectively specified for the hierarchical model

`sample_alpha` *sample alpha*

Description

sample alpha

Usage

```
sample_alpha(alpha_mean = -10, alpha_sd = 0.5)
```

Arguments

`alpha_mean`	prior for the mean of alpha
`alpha_sd`	prior for the standard deviation of alpha

Value

sample from rnorm for α

`sample_beta` *sample beta*

Description

sample beta

Usage

```
sample_beta(beta_shape = 2, beta_scale = 2)
```

Arguments

`beta_shape`	prior for the shape (gamma distibution) of beta
`beta_scale`	prior for the scale of beta

Value

sample from rgamma for β

sample_gamma *sample gamma*

Description

sample gamma

Usage

```
sample_gamma(gamma_shape = 2, gamma_scale = 2)
```

Arguments

gamma_shape	prior for the shape (gamma distibution) of gamma
gamma_scale	prior for the scale of gamma

Value

sample from rgamma for γ

summary.cophe *print the summary of results from cophescan single or susie*

Description

print the summary of results from cophescan single or susie

Usage

```
## S3 method for class 'cophe'
summary(object, ...)
```

Arguments

object	Result from either cophe.susie or cophe.single
...	additional arguments affecting the summary produced.

Value

log bayes and posterior probabilities

See Also

cophe.single, cophe.susie

`target` *Target distribution*

Description

Target distribution

Usage

```
target(params, lbf_mat, nsnps, covar_vec, covar = FALSE)
```

Arguments

`params`	Vector of parameters: α, β and γ
`lbf_mat`	matrix of log bayes factors: lBF.Ha and lBF.Hc
`nsnps`	number of snps
`covar_vec`	Vector of the covariate
`covar`	logical: Should the covariate inflormation be used? default: False

Value

target

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