Package 'rareBF'

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Type Package

Title Bayesian Models for Rare Variant Association Analysis

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Description Bayes factor models for rare variant analysis.

License GPL (>= 2)

Depends R (>= 2.15.2),
stats,
LearnBayes

Encoding latin1

NeedsCompilation no

RoxygenNote 5.0.1

Suggests knitr

VignetteBuilder knitr

R topics documented:

rareBF-package *Methods for rare variant association.*

Description

This packages implements the following methods for rare variant association: reg_eta_miss, mix_eta

BF *Run Bayes factor analysis*

Description

Run Bayes factor analysis

Usage

```
BF(variants, pheno, method = "reg_eta_miss", param, KK = 500, hyper = NA,
  verbose = FALSE)
```

Arguments

pheno	vector Phenotypes (0/1)
method	One of the Bayes Factor methods to use (default reg_eta_miss)
param	Fine tuning of parameter set
KK	Default is 500
hyper	Specify hyper parameters or function returning hyper parameters
verbose	Print additional debugging information
nvariants	matrix Data frame of sites (rows) x individuals (columns)

Details

nvariants contains a matrix of variants per site. Missing data are coded as NA. The following methods are available:

- `reg_eta_miss` : Regular prior, able to handle missing data
- `mix_eta` : Mixed prior
- `mix_both` : Mixed prior both
- `mix_w0` : Mixed prior w0

More information is available at the following link: https://adimitromanolakis.github.io/rareBF/

Value

Bayes Factor (numeric)

See Also

BF

Examples

```
##############################################################################
## Example simulating data from null model
##############################################################################

Nsamples = 20
Nsites = 50
pheno = ( runif(Nsamples) > 0.2 ) ^ 1

v = runif(Nsamples * Nsites) > 0.3
variants = matrix(v, ncol=Nsamples, nrow=Nsites)
BF(variants,pheno,verbose=TRUE)
```

BFvector *BF method for vector data*

Description

BF method for vector data

Usage

```
BFvector(variants, nsites, pheno, method = "reg_eta_miss", param, KK = 500,
  hyper = NA, verbose = FALSE)
```

Arguments

variants	vector Number of sites per individual
nsites	vector Number of (non-missing) sites per individual
pheno	vector Phenotypes (0/1)
method	One of the Bayes Factor methods to use (default reg_eta_miss)
param	Fine tuning of parameter set
KK	Default is 500
hyper	Specify hyper parameters or function returning hyper parameters
verbose	Print additional debugging information

Details

nvariants contains a matrix of variants per site. Missing data are coded as NA. The following methods are available:

- `reg_eta_miss` : Regular prior, able to handle missing data
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Examples

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################################################################################
## Example simulating data from null model
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Nsamples = 20
Nsites = 50
pheno = ( runif(Nsamples) > 0.2 ) ^ 1

v = runif(Nsamples * Nsites) > 0.3
variants = matrix(v, ncol=Nsamples, nrow=Nsites)
BF(variants,pheno,verbose=TRUE)
```

`compute_hyper_parameters` *Return Hyper parameters*

Description

Return Hyper parameters

Usage

```
compute_hyper_parameters(variants_per_individual, non_missing_sites, pheno,
  method, verbose = F)
```

Arguments

variants_per_individual	number of variants per individual (n)
non_missing_sites	numer of non missing sites per individual
pheno	phenotype in 0,1
method	Which method to use

Value

BF

See Also

BF

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example1 *Example 1 for Bayes factor methods*

Description

Example 1 for Bayes factor methods

Usage

```
example1()
```

Value

BF

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run_BF *Wrapper for Bayes factor methods*

Description

Wrapper for Bayes factor methods

Usage

```
run_BF(snps, pheno, method, permuteSamples, KK, hyper, verbose = F)
```

Arguments

snps	Variants

Value

BF

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