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:

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rareBF-package   *Methods for rare variant association.*

Description

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

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adaptivePermutation   *Adaptive truncated permuatation methods*

Description

Adaptive truncated permuatation methods

Usage

```
adaptivePermutation(f, maxPerm = 3e+06, parapply = lapply)
```

BF   *Run Bayes factor analysis*

Description

Run Bayes factor analysis

Usage

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

Arguments

variants	vector (required) Number of sites per individual
nsites	vector (required) Number of (non-missing) sites per individual
pheno	vector (required) Phenotypes (0/1)
method	One of the Bayes Factor methods to use (default reg_eta_miss)
KK	Default is 500
hyper	Specify hyper parameters or function returning hyper parameters
permutations	(integer) Perform a permutation test to obtain p-values
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
- 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) or permutation info (list of 4 elements)

See Also

[BF](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)
```

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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

example2	*Example 2 for Bayes factor methods: Using reg_eta and vector input data*

Description

Example 2 for Bayes factor methods: Using reg_eta and vector input data

Usage

```
example2()
```

Value

BF

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run_BF	*Wrapper for Bayes factor methods*

Description

Wrapper for Bayes factor methods

Usage

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

Arguments

```
variants_per_individual
                 vector
non_missing_sites
                 vector
pheno            vector
```

Value

BF

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