Package 'REBET'

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Title The subREgion-based BurdEn Test (REBET)

Version 1.24.0

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Description There is an increasing focus to investigate the association between rare variants and diseases. The REBET package implements the subREgion-based BurdEn Test which is a powerful burden test that simultaneously identifies susceptibility loci and sub-regions.

Imports stats, utils

Depends ASSET

Suggests RUnit, BiocGenerics

License GPL-2

biocViews Software, VariantAnnotation, SNP

RoxygenNote 6.0.1

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Contents

data *Data for the example*

Description

Data for the example.

Details

The data contains a binary phenotype vector `response`, a genotype matrix `genotypes` consisting of 20 rare-variant SNPs, and the sub-region annotation vector `subRegions` for the `rebet` example.

See Also

`rebet`

Examples

```
data(data, package="REBET")

# Display some of the data
table(response)
dim(genotypes)
subRegions
```

REBET *The REBET package*

Description

An R package for the subREgion-based BurdEn Test (REBET).

Details

In rare-variant association studies, aggregating rare and/or low frequency variants, may increase statistical power for detection of the underlying susceptibility gene or region. However, it is unclear which variants, or class of them, in a gene contribute most to the association. This subregion-based burden test (REBET) simultaneously selects susceptibility genes and identifies important underlying sub-regions. The sub-regions are predefined based on shared common biologic characteristics, such as the protein domain or possible functional impact. Based on a subset-based approach considering local correlations between combinations of test statistics of sub-regions, REBET is able to properly control the type I error rate while adjusting for multiple comparisons in a computationally efficient manner. See the reference for the details of this test. The main function in this package is `rebet`, which performs the REBET test.

Author(s)

Bin Zhu <bin.zhu@nih.gov>, Lisa Mirabello and Nilanjan Chatterjee

References

Zhu, B., Mirabello, L., Chatterjee, N. (2018) A Subregion-based Burden Test for Simultaneous Identification of Susceptibility Loci and Sub-regions within Genetic Epidemiology. In press. https://doi.org/10.1002/gepi

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`rebet` *The subREgion-based BurdEn Test (REBET)*

Description

A Subregion-based Burden Test for Simultaneous Identification of Susceptibility Loci and Sub-regions within

Usage

```
rebet(response, genotypes, subRegions, responseType=NULL,
       covariates=NULL, shape1=1, shape2=1, saveMem=FALSE)
```

Arguments

`response`	Numerical vector of phenotypes. A binary phenotype must be coded as 0 and 1.
`genotypes`	Matrix of genotypes with each column as a locus.
`subRegions`	Sub-region annotation vector with length equal to the number of columns of `genotypes`. In the returned object, these regions will appear as `paste("Region_", subRegions, sep="")`.
`responseType`	NULL, "continuous" or "binary". If NULL, then "continuous" or "binary" will be chosen based on `Y`. The default is NULL.
`covariates`	NULL or matrix of covariates. The default is NULL.
`shape1`	The `shape1` parameter in the beta distribution. The default is 1.
`shape2`	The `shape2` parameter in the beta distribution. The default is 1.
`saveMem`	TRUE or FALSE to conserve memory (see details). The default is FALSE.

Details

See the reference for details of this method.

Missing values in any of `response`, `genotypes` or `covariates` will be removed before the analysis. Setting `saveMem` to TRUE will allow for the analysis of a much larger number of subjects, but will take more time to compute. When `saveMem` is FALSE, there needs to be enough memory available to hold two or three NxN matrices, where N is the number of subjects.

This function calls the `h.traits` function in the `ASSET` package.

Value

The object returned from `h.traits` in the `ASSET` package.

Author(s)

Bin Zhu <bin.zhu@nih.gov>, Lisa Mirabello and Nilanjan Chatterjee

References

Zhu, B., Mirabello, L., Chatterjee, N. (2018) A Subregion-based Burden Test for Simultaneous Identification of Susceptibility Loci and Sub-regions within Genetic Epidemiology. In press. https://doi.org/10.1002/gepi

Examples

```
data(data, package="REBET")

res <- rebet(response, genotypes, subRegions)
h.summary(res)
```

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