

Package ‘REBET’

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Title The subREgion-based BurdEn Test (REBET)

Version 1.29.0

Date 2018-08-13

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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Author Bill Wheeler [cre],

Bin Zhu [aut],

Lisa Mirabello [ctb],

Nilanjan Chatterjee [ctb]

Maintainer Bill Wheeler <wheelerb@imsweb.com>

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| data | <i>Data for the example</i> |
|------|-----------------------------|

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 | <i>The REBET package</i> |
|-------|--------------------------|

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.221>

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 <code>paste("Region_", subRegions, sep="")</code> . |
| 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.221>

Examples

```
data(data, package="REBET")
res <- rebet(response, genotypes, subRegions)
h.summary(res)
```

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