Package 'PSCAN'

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Type Package

Title Protein-structure-guided scan method for detecting gene-level associations and signal variants

Version 1.1

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Description Protein-structure-guided scan (PSCAN) method for testing the gene-level association with complex traits and detecting signal clusters in protein space.

License GPL (>=2)

Depends R (>= 3.1.1), MASS, SKAT, igraph, rgl

NeedsCompilation no

R topics documented:

PSCAN–package	*Protein-structure-guided scan tests for detecting gene-level associations and signal variants*

Description

PSCAN package has the main PSCAN function that implements protein-structure-guided scan (PSCAN) methods for detecting gene-level associations and signal variants.

Details

Package:	PSCAN
Type:	Package
Version:	1.1
Date:	2020-07-30
License:	GPL (>=2)

PSCAN

Author(s)

Zheng-Zheng Tang

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References

Tang ZZ, Sliwoski GR, Chen G, Jin B, Bush WS, Li B, and Capra JA. (2020). Spatial scan tests guided by protein structures improve complex disease gene discovery and signal variant detection. Genome Biology.

Examples

```
data(one.gene)
U = one.gene$U
V = one.gene$V
MAC = one.gene$MAC
weight = one.gene$weight
# perform PSCAN mean-based test and signal region detection
PSCAN(type="mean", U=U, V=V, MAC=MAC, weight=weight, N.MC=1000, FWER=0.05, plot3D=TRUE)
```

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one.gene	*Score statistics, covariance matrix, and SNP weights for a gene*

Description

The data are derived from the genetic association study for a gene.

Usage

```
data("one.gene")
```

Format

one.gene contains the following objects:

- U: a vector of score statistics
- V: a covariance matrix
- weight: a vector of SNP weights

Examples

```
data(one.gene)
```

PSCAN	*Protein-structure-guided scan tests for detecting gene-level associations and signal variants*

Description

This function allows users to (a) perform PSCAN gene-level association tests; (b) run PSCAN procedures to identify trait-associated variants.

Usage

```
PSCAN(type="mean", p.comb="Cauchy", U, V, MAC, weight=NULL, N.MC = 1000, FWER = 0.05,
f=0, details=FALSE, plot3D = FALSE)
```

Arguments

type	type="mean" is the scan test for testing the mean of the effects and type="variance" is the scan test for testing the variance
p.comb	p.comb="Cauchy" or "minP" is to use Cauchy method or minimum p-value method to obtain the gene-level p-value
U	a vector of score statistics with names as SNP ID in chr:position format
V	a covariance matrix for the score statistics
MAC	a vector of minor allele count
weight	a vector contains the weights for SNPs (default = NULL, flat weight)
N.MC	the number of Monte Carlo simulations for minP gene-level test and signal region detection.
FWER	family wise error rate for the PSCAN signal region detection
f	overlap fraction cutoff in the signal detection algorithm (0<=f<=1). When f = 0, algorithm identifies nonoverlapping signal regions. When f = 1, algorithm essentially keeps every region passing the significance threshold as the detected signal regions.
details	whether output additional information, including p-values for individual signal regions, the type of protein sturcture used in the algorithm (experimentally determined protein structure ("PDB") or computationally predicted structure ("Modbase")), and the 3D coordinates of variants in the protein space.
plot3D	whether generate interactive 3D plot for signal regions in protein space. In the plot, the purple spheres represent signal variants and grey spheres represent non-signal variants. The plot will not be generated if no signal region is detected

Value

pscan.pval	a p-value of PSCAN mean-based or variance-based test
signal	a list of vector with each vector contains SNP IDs in a signal region
signal.pval	a vector of p-values with each p-value corresponds to the mean-based or variance-based test p-value for a signal region

Author(s)

Zheng-Zheng Tang

References

Tang ZZ, Sliwoski GR, Chen G, Jin B, Bush WS, Li B, and Capra JA. (2020). Spatial scan tests guided by protein structures improve complex disease gene discovery and signal variant detection. Genome Biology.

Examples

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