Package ‘DYNATE’

October 14, 2022

Title Dynamic Aggregation Testing
Version 0.1
Description A multiple testing procedure aims to find the rare-variant association regions. When vari-
ants are rare, the single variant association test approach suffers from low power. To im-
prove testing power, the procedure dynamically and hierarchically aggre-
gates smaller genome regions to larger ones and performs multiple testing for disease associa-
tions with a controlled node-level false discovery rate. This method are members of the fam-
ily of ancillary information assisted recursive testing intro-
License GPL-3
Encoding UTF-8
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Imports data.table, tidyverse, Matrix, reshape2, stats, methods,
tibble, dplyr
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VignetteBuilder knitr
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DYNATE Function to conduct hierarchical multiple testing based on the leaf p-values

Description

DYNATE Function to conduct hierarchical multiple testing based on the leaf p-values

Usage

DYNATE(struct_map, L = 5, alpha = 0.05)

Arguments

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<td>a data frame with both leaf information and P-value information.</td>
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<tr>
<td>L</td>
<td>maximum number of layers</td>
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<td>alpha</td>
<td>desired FDR</td>
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Value

a data frame with testing results.

References


Examples

```r
data("p_leaf")

# Set tuning parameters
L <- 3 # layer number
alpha <- 0.05 # desired FDR

# conduct dynamic and hierarchical testing based on the leaf level p values.
out <- DYNATE(struct_map=p_leaf,L=L,alpha=alpha)
summary(out)
```
**p_leaf**

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A data frame with 16281 rows and 5 variables. Each row links to a SNP that belongs to a leaf with testing p-value < 1.

**snp_dat**

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A data frame with 210454 rows and 6 variables.

**Test_Leaf**

*Test_Leaf* The function is used to generate Leaf P-values for case-control study. Users can input the leaf information through argument *struct_map*. If there is no leaf information e.g. *struct_map=NULL*, *Test_Leaf* will automatically construct leaf. Argument *thresh_val* specifies the leaf size constructed from the function. When the argument *Gmat_case* and *Gmat_ctrl* is null, *Test_Leaf* will automatically generate those matrices.
Description

Test_Leaf The function is used to generate Leaf P-values for case-control study. Users can input the leaf information through argument struct_map. If there is not leaf information e.g. struct_map=NULL, Test_Leaf will automatically construct leaf. Argument thresh_val specifies the leaf size constructed from the function. When the argument Gmat_case and Gmat_ctrl is null, Test_Leaf will automatically generate those matrices.

Usage

Test_Leaf(snp_dat = NULL, thresh_val = 10, covars = NULL, teststat = "FET")

Arguments

- **snp_dat**: an optional data frame containing patients mutation information. If snp_dat=NULL, the mutation information should be taken from Gmat_case, Gmat_ctrl and glm_input. See vignettes for detail.
- **thresh_val**: a positive integer for leaf size.
- **covars**: an optional vector about the name of covariates to be considered in the fitting process. Should be NULL (default) or a character vector.
- **teststat**: the statistic used to derive p-value. Must be one of "FET" (default) or "score".

Value

a dataframe of rejected leaves with snp information.

Examples

data("snp_dat")

# Set leaf size M
M <- 5

#Construct leaves and generate leaf p-value.
p.leaf <- Test_Leaf(snp_dat=snp_dat,thresh_val=M)
summary(p.leaf)
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