

Package ‘Clipper’

August 31, 2020

Title What the Package Does (One Line, Title Case)

Version 0.0.0.9000

Description What the package does (one paragraph).

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

Clipper 1

Index 3

Clipper	<i>use Clipper to find discoveries from two vectors or tables of measurements (rows = features, columns = replicates) from two conditions</i>
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Description

use Clipper to find discoveries from two vectors or tables of measurements (rows = features, columns = replicates) from two conditions

Usage

```
Clipper(  
  score.exp,  
  score.back,  
  FDR = 0.05,  
  alternative = "two.sided",  
  contrast.score = "max",
```

```

procedure = "GZ",
use.permutation = NULL,
n.permutation = NULL,
seed = 12345
)

```

Arguments

<code>score.exp</code>	a numeric vector or matrix of measurements under experimental condition. If it is a matrix, its rows are the features and its columns are the replicates.
<code>score.back</code>	a numeric vector or matrix of measurements under background condition. If it is a matrix, its rows are the features and its columns are the replicates.
<code>FDR</code>	a number indicating target FDR threshold or a numeric vector indicating multiple target FDR thresholds
<code>alternative</code>	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less".
<code>contrast.score</code>	a character string specifying the contrast score, can be 'max' (default) or 'diff'.
<code>procedure</code>	a character string specifying the FDR control procedure, can be 'GZ' (default) 'BC' or 'aBH'.
<code>use.permutation</code>	a logical value, whether to use permutations.
<code>n.permutation</code>	the number of permutations.
<code>seed</code>	random seed, used in permutations.

Value

Clipper returns a list containing the following components:

count: a count matrix with rows representing genes and columns representing cells;

genesUp: a character vector giving the names of up-regulated genes from state g-1 to g;

genesDown: a character vector giving the names of down-regulated genes from state g-1 to g.

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Index

Clipper, [1](#)