Package ‘rFDP’

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Type Package

Title Resampling-Based False Discovery Proportion Control

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Description Methods for Resampling-based False Discovery Proportion control.
A function is provided that provides simultaneous, multi-resolution
False Discovery Exceedance (FDX) control as described in
Hemerik (2025) <doi:10.48550/arXiv.2509.02376>.

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Imports methods

NeedsCompilation no

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Contents

`mr.FDX` *Multi-resolution FDX control based on resampling*

Description

Provides a threshold that guarantees multi-resolution FDX control, given a matrix of resampled test statistics

Usage

```
mr.FDX(teststats,alpha,gamma,sequential=FALSE,ncombs=25)
```

Arguments

`teststats`	A matrix of resampled test statistics. The first row corrresponds to the original data.
`alpha`	The desired FDX rate
`gamma`	The target (maximal) FDP
`sequential`	Set to TRUE if the (slower) sequential method should be used
`ncombs`	The nr. of random combinations that the sequential method checks.

Value

The rejection threshold that guarantees multi-resolution FDX control.

Examples

```
set.seed(123)

n=10   #samle size per group
m=100  #nr. of hypotheses
w=50   #nr of random permutations

X <- matrix(rnorm((2*n)*m), 2*n, m) #make data matrix (m columns, i.e., m hypotheses)
y <- c(numeric(n)+1,numeric(n)-1)   #group labels

Y <- t(replicate(w, sample(y, size=2*n, replace=FALSE)))  #make matrix with permuted group labels
Y[1,] <- y

#Add some signal to the first 50 columns, so that 50 hypotheses are false:
X[1:n,1:50] <- X[1:n,1:50] + 1.5


#Make matrix with test statistics for permuted versions of the data:
tstats <- matrix(nr=w,nc=m) #Matrix with resampled test statistics
for(j in 1:w){
  for(i in 1:m){
    # Compute t-statistic for j-th permutation for i-th hypothesis:
    avg1 <- (sum(X[Y[j,]==1,i]))/n; avg2 <- (sum(X[Y[j,]==-1,i]))/n
   s <- sqrt( (sum( (X[Y[j,]==1,i]-avg1)^2 ) + sum( (X[Y[j,]==-1,i]-avg2)^2 )  )/(2*n-2) )
    tstats[j,i] <- abs( (avg1-avg2)/ ( sqrt(2/n) * s  ))
  }
}


q = mr.FDX(teststats=tstats,alpha=0.1,gamma=0.1,sequential=FALSE)

#Check which hypotheses are rejected (for the maximum threshold that provides FDX control):
which( tstats[1,] > q )
```

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