

Package: rFDP (via r-universe)

May 7, 2026

Type Package

Title Resampling-Based False Discovery Proportion Control

Version 0.1.1

Date 2025-09-03

Maintainer Jesse Hemerik <hemerik@ese.eur.nl>

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](https://doi.org/10.48550/arXiv.2509.02376)>.

License GNU General Public License

Imports methods

NeedsCompilation no

Author Jesse Hemerik [aut, cre]

Repository <https://cran.r-universe.dev>

Date/Publication 2025-09-09 13:00:02 UTC

RemoteUrl <https://github.com/cran/rFDP>

RemoteRef HEAD

RemoteSha 49ff8a45d076fe8be426d3f5247db5923f0b82d5

Contents

mr.FDX	2
Index	4

 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 corresponds 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 )
```

Index

mr . FDX, [2](#)