Package 'JUMP'

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Description Implementing a computationally scalable false discovery rate control procedure for repli cability analysis based on maximum of p-values. Please cite the manuscript corresponding to this package [Lyu, P. et al., (2023), https://www.biorxiv.org/content/10.1101/2023.02.13.528417v2].
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JUMP

JUMP

Replicability Analysis of High-Throughput Experiments

Description

Replicability Analysis of High-Throughput Experiments

Usage

```
JUMP(pvals1, pvals2, alpha = 0.05, lambda = seq(0.01, 0.8, 0.01))
```

Arguments

pvals1	A numeric vector of p-values from study 1.
pvals2	A numeric vector of p-values from study 2.
alpha	The FDR level to control, default is 0.05.
lambda	The values of the tuning parameter to estimate pi_0. Must be in [0,1), default is seq(0.01, 0.8, 0.01).

Value

a list with the following elements:

```
p.max The maximum of p-values across two studies.jump.thr The estimated threshold of p.max to control FDR at level alpha.
```

Examples

```
# Simulate p-values in two studies m = 10000 h = sample(0:3, m, replace = TRUE, prob = c(0.9, 0.025, 0.025, 0.05)) states1 = rep(0, m); states2 = rep(0, m) states1[which(h==2|h==3)] = 1; states2[which(h==1|h==3)] = 1 z1 = rnorm(m, states1*2, 1) z2 = rnorm(m, states2*3, 1) p1 = 1 - pnorm(z1); p2 = 1 - pnorm(z2) # Run JUMP to identify replicable signals res.jump = JUMP(p1, p2, alpha = 0.05) sig.idx = which(res.jump$p.max <= res.jump$jump.thr)
```

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jump_cutoff	Estimate threshold of maximum p-values across two studies to control FDR.

Description

Estimate threshold of maximum p-values across two studies to control FDR.

Usage

```
jump_cutoff(pa_in, pb_in, xi_in, alpha_in)
```

Arguments

pa_in	A numeric vector of p-values from study 1.
pb_in	A numeric vector of p-values from study 2.
xi_in	The estimates of proportions of three null components.
alpha_in	The FDR level to control, default is 0.05.

Value

A list including the maximum of p-values and estimated threshold for FDR control.

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