

# Package ‘JUMP’

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**Type** Package

**Title** Replicability Analysis of High-Throughput Experiments

**Version** 1.0.2

**Description** Implementing a computationally scalable false discovery rate control procedure for replicability analysis based on maximum of p-values. Please cite the manuscript corresponding to this package [Lyu, P. et al., (2023), <[doi:10.1093/bioinformatics/btad366](https://doi.org/10.1093/bioinformatics/btad366)>].

**License** GPL-3

**Encoding** UTF-8

**Depends** R (>= 4.1.2), Rcpp, splines, stats

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 7.2.3

**NeedsCompilation** yes

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**Repository** CRAN

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**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 | <i>Estimate threshold of maximum p-values across two studies to control FDR.</i> |
|-------------|----------------------------------------------------------------------------------|

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**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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