

# Package: JUMP (via r-universe)

September 6, 2024

**Type** Package

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

**Version** 1.0.1

**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), <<https://www.biorxiv.org/content/10.1101/2023.02.13.528417v2>>].

**License** GPL-3

**Encoding** UTF-8

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

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 7.2.3

**NeedsCompilation** yes

**Author** Pengfei Lyu [aut, ctb], Yan Li [aut, cre, cph], Xiaoquan Wen [aut], Hongyuan Cao [aut, ctb]

**Maintainer** Yan Li <[yanli\\_i@jlu.edu.cn](mailto:yanli_i@jlu.edu.cn)>

**Repository** CRAN

**Date/Publication** 2023-05-24 08:10:08 UTC

## Contents

JUMP . . . . .	2
jump_cutoff . . . . .	3
<b>Index</b>	<b>4</b>

**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 <code>seq(0.01, 0.8, 0.01)</code> .

**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)
```

---

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

---

**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.

# Index

JUMP, [2](#)  
jump\_cutoff, [3](#)