

# Package ‘JMI’

May 7, 2026

**Type** Package

**Title** Jackknife Mutual Information

**Version** 0.1.0

**Author** Zeng Xianli <a0123862@u.nus.edu>, Hang Weiqiang <e0010758@u.nus.edu>

**Maintainer** Zeng Xianli <a0123862@u.nus.edu>

**Description** Computes the Jackknife Mutual Information (JMI) between two random vectors and provides the p-value for dependence tests. See Zeng, X., Xia, Y. and Tong, H. (2018) <[doi:10.1073/pnas.1715593115](https://doi.org/10.1073/pnas.1715593115)>.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**Imports** Rcpp

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 6.0.1

**NeedsCompilation** yes

**Repository** CRAN

**Date/Publication** 2018-10-19 15:10:12 UTC

## Contents

JMI .....	2
<b>Index</b>	<b>3</b>

---

JMI

*Jackknife Mutual Information*

---

### Description

This function provides method for dependence test. It uses permutation test to determine the rejection region.

### Usage

```
JMI(x, y, BN = 1000)
```

### Arguments

x	n by p sample matrix.
y	n by q sample matrix.
BN	Number of permutations, the default value is 1000.

### Value

the output is a list which contains:

- mi: the value of Jackknife Mutual information
- pvalue: the p-value of independence test that based on the permutation of JMI, the value is not provided if BN=0.

### References

Zeng, X., Xia, Y., & Tong, H. (2018). Jackknife approach to the estimation of mutual information[J]. Proceedings of the National Academy of Sciences, 201715593.

### Examples

```
x <- matrix(rnorm(50*3),50,3)
y <- matrix(rnorm(50*2),50,2)
#calculate the Jackknife Mutual information between x and y.
JMI(x,y,0)$mi
#calculate the p-value of independent test between x and y that based on 500 permutations.
JMI(x,y,500)$pvalue
```

# Index

JMI, [2](#)