

# Package ‘fastmit’

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**Type** Package

**Title** Fast Mutual Information Based Independence Test

**Version** 0.1.1

**Description** A mutual information estimator based on k-nearest neighbor method proposed by A. Kraskov, et al. (2004) <[doi:10.1103/PhysRevE.69.066138](https://doi.org/10.1103/PhysRevE.69.066138)> to measure general dependence and the time complexity for our estimator is only squared to the sample size, which is faster than other statistics. Besides, an implementation of mutual information based independence test is provided for analyzing multivariate data in Euclidean space (T B. Berrett, et al. (2019) <[doi:10.1093/biomet/asz024](https://doi.org/10.1093/biomet/asz024)>); furthermore, we extend it to tackle datasets in metric spaces.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**LinkingTo** Rcpp, RcppArmadillo

**Imports** Rcpp, stats

**Suggests** testthat

**NeedsCompilation** yes

**Author** Shiyun Lin [aut, cre],  
Jin Zhu [aut],  
Wenliang Pan [aut],  
Xueqin Wang [aut],  
SC2S2 [cph]

**Maintainer** Shiyun Lin <[linshy27@mail2.sysu.edu.cn](mailto:linshy27@mail2.sysu.edu.cn)>

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mi *kNN Mutual Information Estimators*

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### Description

Estimate mutual information based on the distribution of nearest neighborhood distances. The kNN method is described by Kraskov, et. al (2004).

### Usage

```
mi(x, y, k = 5, distance = FALSE)
```

### Arguments

x	A numeric vector, matrix, data.frame or <code>dist</code> object.
y	A numeric vector, matrix, data.frame or <code>dist</code> object.
k	Order of neighborhood to be used in the kNN method.
distance	Bool flag for considering x and y as distance matrices or not. If distance = TRUE, x and y would be considered as distance matrices, otherwise, these arguments are treated as data and Euclidean distance would be implemented for the samples in x and y. Default: distance = FALSE.

### Details

If two samples are passed to arguments x and y, the sample sizes (i.e. number of rows of the matrix or length of the vector) must agree. Moreover, data being passed to x and y must not contain missing or infinite values.

### Value

mi The estimated mutual information.

### References

Kraskov, A., Stögbauer, H., & Grassberger, P. (2004). Estimating mutual information. Physical review E 69(6): 066138.

### Examples

```
library(fastmit)
set.seed(1)
x <- rnorm(100)
y <- x + rnorm(100)
mi(x, y, k = 5, distance = FALSE)

set.seed(1)
x <- rnorm(100)
```

```
y <- 100 * x + rnorm(100)
distx <- dist(x)
disty <- dist(y)
mi(distx, disty, k = 5, distance = TRUE)
```

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`mi.test`*Mutual Information Test*

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### Description

Mutual Information test of independence. Mutual Information are generic dependence measures in Banach spaces.

### Usage

```
mi.test(x, y, k = 5, distance = FALSE, num.permutations = 99,
        seed = 1)
```

### Arguments

<code>x</code>	A numeric vector, matrix, data.frame or <code>dist</code> object.
<code>y</code>	A numeric vector, matrix, data.frame or <code>dist</code> object.
<code>k</code>	Order of neighborhood to be used in the kNN method.
<code>distance</code>	Bool flag for considering <code>x</code> and <code>y</code> as distance matrices or not. If <code>distance = TRUE</code> , <code>x</code> and <code>y</code> would be considered as distance matrices, otherwise, these arguments are treated as data and Euclidean distance would be implemented for the samples in <code>x</code> and <code>y</code> . Default: <code>distance = FALSE</code> .
<code>num.permutations</code>	The number of permutation replications. If <code>num.permutations = 0</code> , the function just returns the Mutual Information statistic. Default: <code>num.permutations = 99</code> .
<code>seed</code>	The random seed. Default: <code>seed = 1</code> .

### Details

If two samples are passed to arguments `x` and `y`, the sample sizes (i.e. number of rows of the matrix or length of the vector) must agree. Moreover, data being passed to `x` and `y` must not contain missing or infinite values.

`mi.test` utilizes the Mutual Information statistics (see [mi](#)) to measure dependence and derive a  $p$ -value via replicating the random permutation `num.permutations` times.

**Value**

If `num.permutations > 0`, `mi.test` returns a `hstest` class object containing the following components:

<code>statistic</code>	Mutual Information statistic.
<code>p.value</code>	The p-value for the test.
<code>replicates</code>	Permutation replications of the test statistic.
<code>size</code>	Sample size.
<code>alternative</code>	A character string describes the alternative hypothesis.
<code>method</code>	A character string indicates what type of test was performed.
<code>data.name</code>	Description of data.

If `num.permutations = 0`, `mi.test` returns a statistic value.

**Examples**

```
library(fastmit)
set.seed(1)
error <- runif(50, min = -0.3, max = 0.3)
x <- runif(50, 0, 4*pi)
y <- cos(x) + error
# plot(x, y)
res <- mi.test(x, y)
```

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