

# Package ‘pecora’

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**Type** Package

**Title** Permutation Conditional Random Tests

**Version** 0.1.2

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**Description** It provides functions to perform permutation conditional random one-sample and two-samples t-tests in a multivariate framework.

**License** GPL ( $\geq 2$ )

**Imports** Rcpp ( $\geq 1.0.3$ ), matrixStats, stats

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**Language** en-US

**NeedsCompilation** yes

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pecora-package

*pecora-package*

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**Description**

The library is devoted to permutation-based inferential methods.

The pecora (permutation conditional random) package provides functions to perform the one-sample and two-samples t-tests using permutations/sign-flipping.

The tests comprised are: the one and two samples t-tests.

**Author(s)**

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**References**

For the general framework of univariate and multivariate permutation tests see: Pesarin, F. (2001) Multivariate Permutation Tests with Applications in Biostatistics. Wiley, New York.

**Examples**

```
X <- matrix(rnorm(100*20), nrow=20)
out <- oneSample(X = X)
pv <- t2p(Test = out, alternative = "two.sided")
```

```
X <- matrix(rnorm(100*20), nrow=20)
rownames(X) <- c(rep(0, 10), rep(1,10))
out<- twoSamples(X = X)
pv <- t2p(Test = out, alternative = "two.sided")
```

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oneSample*Permutatation-based one sample t-test*

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**Description**

Performs sign-flipped one-sample t-tests.

**Usage**

```
oneSample(X, B = 1000, seed = 1234, permReturn = TRUE)
```

**Arguments**

X	data matrix where columns represent the $m$ variables and rows the $n$ observations.
B	numeric value, number of permutations to be performed, including the identity. Default is 1000.
seed	numeric value, specify seed. Default is 1234.
permReturn	logical value, TRUE to return the t-tests permutation distribution. Default is TRUE.

**Value**

Returns an object matrix:

**tv** Matrix with dimensions  $m \times B$  of permuted one-sample t-tests. The first column is the observed one-sample t-tests.

if permReturn = TRUE otherwise returns:

**tv** Vector of  $m$  observed one-sample t-tests

**Author(s)**

Angela Andreella

**Examples**

```
X <- matrix(rnorm(100*20), nrow=20)
out <- oneSample(X = X)
```

---

t2p

*From t-tests to p-values*


---

**Description**

Use permutation distribution of a test statistic to get p-values.

**Usage**

```
t2p(Test, alternative = "two.sided", rankBased = TRUE, permReturn = TRUE, df = Inf)
```

**Arguments**

Test	can be a matrix or a vector. In the first case the columns represent the B permutations and rows the $m$ tests statistic. The observed test statistic is in the first column and the permutation distribution in the remaining columns. In the second case, it is a vector of length $m$ of observed tests statistics. If rankBased = TRUE, you must provide the first option (matrix of permuted statistical tests).
alternative	character string referring to the alternative hypothesis ("greater", "lower", or "two.sided"). is "two.sided".

rankBased	logical value, TRUE to compute p-values by permutation distribution. Default @TRUE.
permReturn	logical value, TRUE to return the t-tests and p-values permutation distribution. Default @TRUE.
df	numerical value. Degrees of freedom ( $> 0$ , maybe non-integer). Default df = Inf

**Value**

Returns an object matrix:

**pv** Matrix with dimensions  $m \times B$  of permuted one-sample p-values. The first column is the p-values for the observed one-sample t-tests.

if permReturn = TRUE otherwise returns:

**pv** Vector of  $m$  p-values for the observed one-sample t-tests

**Author(s)**

Angela Andreella

**Examples**

```
X <- matrix(rnorm(100*20), nrow=20)
out <- oneSample(X = X)
pv <- t2p(Test = out)
```

---

twoSamples

*Permutation-based two sample t-test*

---

**Description**

Performs two-sample t-tests by permutations.

**Usage**

```
twoSamples(X, B = 1000, seed = 1234,
permReturn = TRUE, label = NULL)
```

**Arguments**

X	data matrix where columns represent the $m$ variables and rows the $n$ observations. The columns' name defines the groups' label.
B	numeric value, number of permutations to be performed, including the identity. Default is 1000.
seed	numeric value, specify seed. Default is 1234.

**permReturn** logical value, TRUE to return the t-tests and p-values permutation distribution. Default is TRUE.

**label** by default label = NULL. Labels of the observations, if NULL the rows's name are considered. D

**Value**

Returns a matrix objects:

**Test** Matrix with dimensions  $m \times B$  of permuted two-samples t-tests. The first column is the observed one-sample t-tests.

if permReturn = TRUE otherwise returns:

**Test** Vector of  $m$  observed two-samples t-tests

**Author(s)**

Angela Andreella

**Examples**

```
X <- matrix(rnorm(100*20), nrow=20)
rownames(X) <- c(rep(0, 10), rep(1,10))
out<- twoSamples(X = X)
```

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