

Package ‘nptest’

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Type Package

Title Nonparametric Bootstrap and Permutation Tests

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Depends parallel

Description Robust nonparametric bootstrap and permutation tests for location, correlation, and regression problems, as described in Helwig (2019a) <doi:10.1002/wics.1457> and Helwig (2019b) <doi:10.1016/j.neuroimage.2019.116030>. Univariate and multivariate tests are supported. For each problem, exact tests and Monte Carlo approximations are available. Five different nonparametric bootstrap confidence intervals are implemented. Parallel computing is implemented via the 'parallel' package.

License GPL (>= 2)

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npctest-package

*Nonparametric Bootstrap and Permutation Tests***Description**

Robust nonparametric bootstrap and permutation tests for location, correlation, and regression problems, as described in Helwig (2019a) <doi:10.1002/wics.1457> and Helwig (2019b) <doi:10.1016/j.neuroimage.2019.116030>. Univariate and multivariate tests are supported. For each problem, exact tests and Monte Carlo approximations are available. Five different nonparametric bootstrap confidence intervals are implemented. Parallel computing is implemented via the 'parallel' package.

Details

The DESCRIPTION file:

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Package:      npctest
Type:         Package
Title:        Nonparametric Bootstrap and Permutation Tests
Version:      1.0-2
Date:         2020-10-01
Author:       Nathaniel E. Helwig <helwig@umn.edu>
Maintainer:   Nathaniel E. Helwig <helwig@umn.edu>
Depends:      parallel
Description:  Robust nonparametric bootstrap and permutation tests for location, correlation, and regression problems, as described in Helwig (2019a) and Helwig (2019b).
License:      GPL (>=2)
```

Index of help topics:

flipn	Generate All Sign-Flips of n Elements
mcse	Monte Carlo Standard Errors for Tests
np.boot	Nonparametric Bootstrap Resampling
np.cor.test	Nonparametric Tests of Correlation Coefficients
np.loc.test	Nonparametric Tests of Location Parameters
np.reg.test	Nonparametric Tests of Regression Coefficients
npctest-package	Nonparametric Bootstrap and Permutation Tests
permn	Generate All Permutations of n Elements
plot	Plots Permutation Distribution for Nonparametric Tests

Author(s)

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Examples

```
# See examples for...
# flipn      (generate all sign flip vectors)
# mcse      (Monte Carlo standard errors)
# np.boot    (nonparametric bootstrap resampling)
# np.cor.test (nonparametric correlation tests)
# np.loc.test (nonparametric location tests)
# np.reg.test (nonparametric regression tests)
# permn      (generate all permutation vectors)
```

`flipn`*Generate All Sign-Flips of n Elements*

Description

Generates all 2^n vectors of length n consisting of the elements -1 and 1.

Usage

```
flipn(n)
```

Arguments

`n` Number of elements.

Details

Adapted from the "bincombinations" function in the [e1071](#) R package.

Value

Matrix of dimension n by 2^n where each column contains a unique sign-flip vector.

Warning

For large n this function will consume a lot of memory and may even crash R.

Note

Used for exact tests in [np.loc.test](#) and [np.reg.test](#).

Author(s)

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References

Meyer, D., Dimitriadou, E., Hornik, K., Weingessel, A., & Leisch, F. (2018). e1071: Misc Functions of the Department of Statistics, Probability Theory Group (Formerly: E1071), TU Wien. R package version 1.7-0. <https://CRAN.R-project.org/package=e1071>

Examples

```
flipn(2)
flipn(3)
```

mcse

*Monte Carlo Standard Errors for Tests***Description**

This function calculates Monte Carlo standard errors for (non-exact) nonparametric tests. The MC-SEs can be used to determine (i) the accuracy of a test for a given number of resamples, or (ii) the number of resamples needed to achieve a test with a given accuracy.

Usage

```
mcse(R, delta, conf.level = 0.95, sig.level = 0.05,
      alternative = c("two.sided", "one.sided"))
```

Arguments

R	Number of resamples (positive integer).
delta	Accuracy of the approximation (number between 0 and 1).
conf.level	Confidence level for the approximation (number between 0 and 1).
sig.level	Significance level of the test (number between 0 and 1).
alternative	Alternative hypothesis (two-sided or one-sided).

Details

Note: either R or delta must be provided.

Let $F(x)$ denote the distribution function for the full permutation distribution, and let $G(x)$ denote the approximation obtained from R resamples. The *Monte Carlo standard error* is given by

$$\sigma(x) = \sqrt{F(x)[1 - F(x)]/R}$$

which is the standard deviation of $G(x)$.

A symmetric confidence interval for $F(x)$ can be approximated as

$$G(x) \pm C\sigma(x)$$

where C is some quantile of the standard normal distribution. Note that the critical value C corresponds to the confidence level (`conf.level`) of the approximation.

Let α denote the significance level (`sig.level`) for a one-sided test (α is one-half the significance level for two-sided tests). Define a to be the value of the test statistic such that $F(a) = \alpha$.

The parameter δ (`delta`) quantifies the accuracy of the approximation, such that

$$|G(a) - \alpha| < \alpha\delta$$

with a given confidence, which is controlled by the `conf.level` argument.

Value

mcse	Monte Carlo standard error.
R	Number of resamples.
delta	Accuracy of approximation.
conf.level	Confidence level.
sig.level	Significance level.
alternative	Alternative hypothesis.

Note

This function is only relevant for non-exact tests. For exact tests, $F(x) = G(x)$ so the Monte Carlo standard error is zero.

Author(s)

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References

Helwig, N. E. (2019). Statistical nonparametric mapping: Multivariate permutation tests for location, correlation, and regression problems in neuroimaging. *WIREs Computational Statistics*, 11(2), e1457. doi: 10.1002/wics.1457

See Also

[np.cor.test](#), [np.loc.test](#), [np.reg.test](#)

Examples

```
##### EXAMPLE 1 #####

# get the Monte Carlo standard error and the
# accuracy (i.e., delta) for given R = 10000
# using the default two-sided alternative hypothesis,
# the default confidence level (conf.level = 0.95),
# and the default significance level (sig.level = 0.05)

mcse(R = 10000)

# se = 0.0016
# delta = 0.1224

##### EXAMPLE 2 #####

# get the Monte Carlo standard error and the
# number of resamples (i.e., R) for given delta = 0.01
# using a one-sided alternative hypothesis,
```

```
# the default confidence level (conf.level = 0.95),
# and the default significance level (sig.level = 0.05)

mcse(delta = 0.1, alternative = "one.sided")

# se = 0.0026
# R = 7299
```

np.boot

*Nonparametric Bootstrap Resampling***Description**

Nonparametric bootstrap resampling for univariate and multivariate statistics. Computes bootstrap estimates of the standard error, bias, and covariance. Also computes five different types of bootstrap confidence intervals: normal approximation interval, basic (reverse percentile) interval, percentile interval, studentized (bootstrap-*t*) interval, and bias-corrected and accelerated (BCa) interval.

Usage

```
np.boot(x, statistic, ..., R = 9999, level = c(0.9, 0.95, 0.99),
        method = c("norm", "basic", "perc", "stud", "bca")[-4],
        sdfun = NULL, sdrep = 99, jackknife = NULL,
        parallel = FALSE, cl = NULL, boot.dist = TRUE)
```

Arguments

<code>x</code>	vector of data (for univariate data) or vector of row indices (for multivariate data). See examples for bootstrapping multivariate data.
<code>statistic</code>	function that takes in <code>x</code> (and possibly additional arguments passed using <code>...</code>) and returns a vector containing the statistic(s). See examples.
<code>...</code>	additional named arguments for the <code>statistic</code> function.
<code>R</code>	number of bootstrap replicates
<code>level</code>	desired confidence level(s) for the computed intervals. Default computes 90%, 95%, and 99% confidence intervals.
<code>method</code>	method(s) for computing confidence intervals. Partial matching is allowed. Any subset of allowable methods is permitted (default computes all intervals except studentized). Set <code>method = NULL</code> to produce no confidence intervals.
<code>sdfun</code>	function for computing the standard deviation of <code>statistic</code> . Should produce a vector the same length as the output of <code>statistic</code> . Only applicable if "stud" %in% <code>method</code> . If <code>NULL</code> , an inner bootstrap is used to estimate the standard deviation.
<code>sdrep</code>	number of bootstrap replicates for the inner bootstrap used to estimate the standard deviation of <code>statistic</code> . Only applicable if "stud" %in% <code>method</code> and <code>sdfun = NULL</code> . Larger values produce more accurate estimates (see Note).

jackknife	function that takes in <code>x</code> (and possibly additional arguments passed using <code>...</code>) and returns a vector containing the jackknife statistic(s). Should produce a vector the same length as the output of <code>statistic</code> . Only applicable if <code>"bca"</code> %in% <code>method</code> . If <code>NULL</code> , the jackknife function is defined as the <code>statistic</code> function (default). See the last example for a case when <code>statistic</code> and <code>jackknife</code> are different.
parallel	Logical indicating if the <code>parallel</code> package should be used for parallel computing (of the bootstrap distribution). Defaults to <code>FALSE</code> , which implements sequential computing.
cl	Cluster for parallel computing, which is used when <code>parallel = TRUE</code> . Note that if <code>parallel = TRUE</code> and <code>cl = NULL</code> , then the cluster is defined as <code>makeCluster(detectCores())</code> .
boot.dist	Logical indicating if the bootstrap distribution should be returned (see Note).

Details

The first three intervals (normal, basic, and percentile) are only first-order accurate, whereas the last two intervals (studentized and BCa) are both second-order accurate. Thus, the results from the studentized and BCa intervals tend to provide more accurate coverage rates.

Unless the standard deviation function for the studentized interval is input via the `sdfun` argument, the studentized interval can be quite computationally costly. This is because an inner bootstrap is needed to estimate the standard deviation of the statistic for each (outer) bootstrap replicate—and you may want to increase the default number of inner bootstrap replicates (see Note).

The efficiency of the BCa interval will depend on the sample size n and the computational complexity of the (jackknife) statistic estimate. Assuming that n is not too large and the jackknife statistic is not too difficult to compute, the BCa interval can be computed reasonably quickly—especially in comparison the studentized interval with an inner bootstrap.

Computational details of the various confidence intervals are described in Efron and Tibshirani (1994) and in Davison and Hinkley (1997). For a useful and concise discussion of the various intervals, see Carpenter and Bithell (2000).

Value

<code>t0</code>	Observed statistic, computed using <code>statistic(x, ...)</code>
<code>se</code>	Bootstrap estimate of the standard error.
<code>bias</code>	Bootstrap estimate of the bias.
<code>cov</code>	Bootstrap estimate of the covariance (for multivariate statistics).
<code>normal</code>	Normal approximation confidence interval(s).
<code>basic</code>	Basic (reverse percentile) confidence interval(s).
<code>percent</code>	Percentile confidence interval(s).
<code>student</code>	Studentized (bootstrap- t) confidence interval(s).
<code>bca</code>	Bias-corrected and accelerated (BCa) confidence interval(s).
<code>z0</code>	Bias-correction factor(s). Only provided if <code>bca</code> %in% <code>method</code> .
<code>acc</code>	Acceleration factor(s). Only provided if <code>bca</code> %in% <code>method</code> .
<code>boot.dist</code>	Bootstrap distribution of <code>statistic(s)</code> . Only provided if <code>boot.dist = TRUE</code> .

R	Number of bootstrap replicates (same as input).
level	Confidence level (same as input).
sdfun	Standard deviation function for statistic (same as input).
sdrep	Number of inner bootstrap replicates (same as input).
jackknife	Jackknife function (same as input).

Note

If `boot.dist = TRUE`, the output `boot.dist` will be a matrix of dimension R by `length(statistic(x,...))` if the statistic is multivariate. Otherwise the bootstrap distribution will be a vector of length R.

For the "stud" method, the default of `sdrep = 99` may produce a crude estimate of the standard deviation of the statistic(s). For more accurate estimates, the value of `sdrep` may need to be set substantially larger, e.g., `sdrep = 999`.

Author(s)

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References

- Carpenter, J., & Bithell, J. (2000). Bootstrap confidence intervals: when, which, what? A practical guide for medical statisticians. *Statistics in Medicine*, 19(9), 1141-1164. doi: 10.1002/(SICI)1097-0258(20000515)19:9%3C1141::AID-SIM479%3E3.0.CO;2-F
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Examples

```
##### UNIVARIATE DATA #####

### Example 1: univariate statistic (median)

# generate 100 standard normal observations
set.seed(1)
n <- 100
x <- rnorm(n)

# nonparametric bootstrap
npbs <- np.boot(x = x, statistic = median)
npbs

### Example 2: multivariate statistic (quartiles)

# generate 100 standard normal observations
set.seed(1)
n <- 100
```

```

x <- rnorm(n)

# nonparametric bootstrap
npbs <- np.boot(x = x, statistic = quantile,
               probs = c(0.25, 0.5, 0.75))
npbs

#####**#####  MULTIVARIATE DATA  #####**#####

### Example 1: univariate statistic (correlation)

# correlation matrix square root (with rho = 0.5)
rho <- 0.5
val <- c(sqrt(1 + rho), sqrt(1 - rho))
corsqrt <- matrix(c(val[1], -val[2], val), 2, 2) / sqrt(2)

# generate 100 bivariate observations (with rho = 0.5)
n <- 100
set.seed(1)
data <- cbind(rnorm(n), rnorm(n)) %*% corsqrt

# define statistic function
statfun <- function(x, data) cor(data[x,1], data[x,2])

# nonparametric bootstrap
npbs <- np.boot(x = 1:n, statistic = statfun, data = data)
npbs

### Example 2: multivariate statistic (variances and covariance)

# correlation matrix square root (with rho = 0.5)
rho <- 0.5
val <- c(sqrt(1 + rho), sqrt(1 - rho))
corsqrt <- matrix(c(val[1], -val[2], val), 2, 2) / sqrt(2)

# generate 100 bivariate observations (with rho = 0.5)
n <- 100
set.seed(1)
data <- cbind(rnorm(n), rnorm(n)) %*% corsqrt

# define statistic function
statfun <- function(x, data) {
  cmat <- cov(data[x,])
  ltri <- lower.tri(cmat, diag = TRUE)
  cvec <- cmat[ltri]
  names(cvec) <- c("var(x1)", "cov(x1,x2)", "var(x2)")
  cvec
}

# nonparametric bootstrap

```

```

npbs <- np.boot(x = 1:n, statistic = statfun, data = data)
npbs

## Not run:

#####**##### REGRESSION #####**#####

### Example 1: bootstrap cases

# generate 100 observations
n <- 100
set.seed(1)
x <- seq(0, 1, length.out = n)
y <- 1 + 2 * x + rnorm(n)
data <- data.frame(x = x, y = y)

# define statistic function
statfun <- function(x, data) {
  xmat <- cbind(1, data$x[x])
  xinv <- solve(crossprod(xmat)) %*% t(xmat)
  coef <- as.numeric(xinv %*% data$y[x])
  names(coef) <- c("(Intercept)", "x")
  coef
}

# nonparametric bootstrap
npbs <- np.boot(x = 1:n, statistic = statfun, data = data)
npbs

### Example 2: bootstrap residuals

# generate 100 observations
n <- 100
set.seed(1)
x <- seq(0, 1, length.out = n)
y <- 1 + 2 * x + rnorm(n)

# prepare data
xmat <- cbind(1, x)
xinv <- solve(crossprod(xmat)) %*% t(xmat)
fit <- xmat %*% xinv %*% y
data <- list(fit = fit, resid = y - fit, xinv = xinv, x = x)

# define statistic function
statfun <- function(x, data) {
  ynew <- data$fit + data$resid[x]
  coef <- as.numeric(data$xinv %*% ynew)
  names(coef) <- c("(Intercept)", "x")
  coef
}

```

```

# define jackknife function
jackfun <- function(x, data){
  ynew <- data$fit[x] + data$resid[x]
  xmat <- cbind(1, data$x[x])
  xinv <- solve(crossprod(xmat)) %*% t(xmat)
  coef <- as.numeric(xinv %*% ynew)
  names(coef) <- c("(Intercept)", "x")
  coef
}

# nonparametric bootstrap
npbs <- np.boot(x = 1:n, statistic = statfun, data = data,
               jackknife = jackfun)
npbs

## End(Not run)

```

np.cor.test

*Nonparametric Tests of Correlation Coefficients***Description**

Denoting the Pearson product-moment correlation coefficient as

$$\rho = \text{Cov}(X, Y) / \sqrt{\text{Var}(X)\text{Var}(Y)}$$

this function implements permutation tests of $H_0 : \rho = \rho_0$ where ρ_0 is the user-specified null value. Can also implement tests of partial correlations, semi-partial (or part) correlations, and independence.

Usage

```

np.cor.test(x, y, z = NULL,
            alternative = c("two.sided", "less", "greater"),
            rho = 0, independent = FALSE, partial = TRUE,
            R = 9999, parallel = FALSE, cl = NULL,
            perm.dist = TRUE)

```

Arguments

x	X vector (n by 1).
y	Y vector (n by 1).
z	Optional Z matrix (n by q). If provided, the partial (or semi-partial if partial = FALSE) correlation is calculated between x and y controlling for z.
alternative	Alternative hypothesis. Must be either "two.sided" ($H_1 : \rho \neq \rho_0$), "less" ($H_1 : \rho < \rho_0$), or "greater" ($H_1 : \rho > \rho_0$).

rho	Null hypothesis value ρ_0 . Defaults to zero.
independent	If FALSE (default), the null hypothesis is $H_0 : \rho = \rho_0$. Otherwise, the null hypothesis is that X and Y are independent, i.e., $H_0 : F_{XY}(x, y) = F_X(x)F_Y(y)$.
partial	Only applicable if z is provided. If TRUE (default), the partial correlation between x and y controlling for z is tested. Otherwise the semi-partial correlation is tested. See Details.
R	Number of resamples for the permutation test (positive integer).
parallel	Logical indicating if the parallel package should be used for parallel computing (of the permutation distribution). Defaults to FALSE, which implements sequential computing.
cl	Cluster for parallel computing, which is used when <code>parallel = TRUE</code> . Note that if <code>parallel = TRUE</code> and <code>cl = NULL</code> , then the cluster is defined as <code>makeCluster(detectCores())</code> .
perm.dist	Logical indicating if the permutation distribution should be returned.

Details

Default use of this function tests the Pearson correlation between X and Y using the studentized test statistic proposed by DiCiccio and Romano (2017). If `independent = TRUE`, the classic (unstudentized) test statistic is used to test the null hypothesis of independence.

If Z is provided, the partial or semi-partial correlation between X and Y controlling for Z is tested. For the semi-partial correlation, the effect of Z is partialled out of X .

Value

statistic	Test statistic value.
p.value	p-value for testing $H_0 : \rho = \rho_0$ or $H_0 : F_{XY}(x, y) = F_X(x)F_Y(y)$.
perm.dist	Permutation distribution of statistic.
alternative	Alternative hypothesis.
null.value	Null hypothesis value for ρ .
independent	Independence test?
R	Number of resamples.
exact	Exact permutation test? See Note.
estimate	Sample estimate of correlation coefficient ρ .

Note

The permutation test will be exact when the requested number of resamples R is greater than `factorial(n)` minus one. In this case, the permutation distribution `perm.dist` contains all `factorial(n)` possible values of the test statistic.

If $z = \text{NULL}$, the result will be the same as using [np.reg.test](#) with `method = "perm"`.

If z is supplied and `partial = TRUE`, the result will be the same as using [np.reg.test](#) with `method = "KC"` and `homosced = FALSE`.

Author(s)

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References

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See Also

[plot.np.cor.test](#) S3 plotting method for visualizing the results

Examples

```
# generate data
rho <- 0.5
val <- c(sqrt(1 + rho), sqrt(1 - rho))
corsqrt <- matrix(c(val[1], -val[2], val), 2, 2) / sqrt(2)
set.seed(1)
n <- 10
z <- cbind(rnorm(n), rnorm(n)) %*% corsqrt
x <- z[,1]
y <- z[,2]

# test H0: rho = 0
set.seed(0)
np.cor.test(x, y)

# test H0: X and Y are independent
set.seed(0)
np.cor.test(x, y, independent = TRUE)
```

Description

Performs one and two sample nonparametric (randomization) tests of location parameters, i.e., means and medians. Implements univariate and multivariate tests using eight different test statistics: Student's one-sample t-test, Johnson's modified t-test, Wilcoxon's Signed Rank test, Fisher's Sign test, Student's two-sample t-test, Welch's t-test, Wilcoxon's Rank Sum test (i.e., Mann-Whitney's U test), and a studentized Wilcoxon test for unequal variances.

Usage

```
np.loc.test(x, y = NULL,
            alternative = c("two.sided", "less", "greater"),
            mu = 0, paired = FALSE, var.equal = FALSE,
            median.test = FALSE, symmetric = TRUE,
            R = 9999, parallel = FALSE, cl = NULL,
            perm.dist = TRUE)
```

Arguments

<code>x</code>	Numeric vector (or matrix) of data values.
<code>y</code>	Optional numeric vector (or matrix) of data values.
<code>alternative</code>	Alternative hypothesis. Must be either "two.sided" ($H_1 : \mu \neq \mu_0$), "less" ($H_1 : \mu < \mu_0$), or "greater" ($H_1 : \mu > \mu_0$).
<code>mu</code>	Null hypothesis value μ_0 . Defaults to zero.
<code>paired</code>	Logical indicating whether you want a paired location test.
<code>var.equal</code>	Logical indicating whether to treat the two variances as being equal.
<code>median.test</code>	Logical indicating whether the location test is for the median. Default is FALSE, i.e., μ is the mean.
<code>symmetric</code>	Logical indicating if the distribution of <code>x</code> should be assumed to be symmetric around μ . Only used for one (or paired) sample tests.
<code>R</code>	Number of resamples for the permutation test (positive integer).
<code>parallel</code>	Logical indicating if the parallel package should be used for parallel computing (of the permutation distribution). Defaults to FALSE, which implements sequential computing.
<code>cl</code>	Cluster for parallel computing, which is used when <code>parallel = TRUE</code> . Note that if <code>parallel = TRUE</code> and <code>cl = NULL</code> , then the cluster is defined as <code>makeCluster(detectCores())</code> .
<code>perm.dist</code>	Logical indicating if the permutation distribution should be returned.

Details

One sample	μ is the mean (or median) of X
Paired	μ is the mean (or median) of $X - Y$
Two sample	μ is the mean difference $E(X) - E(Y)$ or the median of the differences $X - Y$

For one (or paired) sample tests, the different test statistics can be obtained using

	median.test = F	median.test = T
symmetric = F	Johnson t test	Fisher sign test
symmetric = T	Student t test	Wilcoxon signed rank test

For two sample tests, the different test statistics can be obtained using

	median.test = F	median.test = T
var.equal = F	Welch t test	Studentized Wilcoxon test
var.equal = T	Student t test	Wilcoxon rank sum test

Value

statistic	Test statistic value.
p.value	p-value for testing $H_0 : \mu = \mu_0$.
perm.dist	Permutation distribution of statistic.
alternative	Alternative hypothesis.
null.value	Null hypothesis value for μ .
var.equal	Assuming equal variances? Only for two sample tests.
median.test	Testing the median?
symmetric	Assuming symmetry? Only for one sample and paired tests.
R	Number of resamples.
exact	Exact permutation test? See Note.
estimate	Estimate of parameter μ .
univariate	Univariate test statistic value for j -th variable (for multivariate input).
adj.p.value	Adjusted p-value for testing significance of j -th variable (for multivariate input).
method	Method used for permutation test. See Details.

Multivariate Tests

If the input x (and possibly y) is a matrix with $m > 1$ columns, the multivariate test statistic is defined as

alternative	statistic
two.sided	$\max(\text{abs}(\text{univariate}))$
less	$\min(\text{univariate})$
greater	$\max(\text{univariate})$

The global null hypothesis (across all m variables) is tested by comparing the observed statistic to the permutation distribution `perm.dist`. This produces the `p.value` for testing the global null

hypothesis.

The local null hypothesis (separately for each variable) is tested by comparing the univariate test statistic to `perm.dist`. This produces the adjusted p-values (`adj.p.values`), which control the familywise Type I error rate across the m tests.

Note

For one sample (or paired) tests, the permutation test will be exact when the requested number of resamples R is greater than 2^n minus one. In this case, the permutation distribution `perm.dist` contains all 2^n possible values of the test statistic.

For two sample tests, the permutation test will be exact when the requested number of resamples R is greater than $\text{choose}(N, n)$ minus one, where $m = \text{length}(x)$, $n = \text{length}(y)$, and $N = m + n$. In this case, the permutation distribution `perm.dist` contains all $\text{choose}(N, n)$ possible values of the test statistic.

Author(s)

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See Also

[plot.np.loc.test](#) S3 plotting method for visualizing the results

Examples

```
##### UNIVARIATE #####

##### ONE SAMPLE #####

# generate data
set.seed(1)
n <- 10
x <- rnorm(n, mean = 0.5)

# one sample t-test
set.seed(0)
np.loc.test(x)

# Johnson t-test
set.seed(0)
np.loc.test(x, symmetric = FALSE)

# Wilcoxon signed rank test
set.seed(0)
np.loc.test(x, median.test = TRUE)

# Fisher sign test
set.seed(0)
np.loc.test(x, median.test = TRUE, symmetric = FALSE)

##### PAIRED SAMPLE #####

# generate data
set.seed(1)
n <- 10
x <- rnorm(n, mean = 0.5)
y <- rnorm(n)

# paired t-test
set.seed(0)
np.loc.test(x, y, paired = TRUE)

# paired Johnson t-test
set.seed(0)
np.loc.test(x, y, paired = TRUE, symmetric = FALSE)

# paired Wilcoxon signed rank test
set.seed(0)
np.loc.test(x, y, paired = TRUE, median.test = TRUE)
```

```
# paired Fisher sign test
set.seed(0)
np.loc.test(x, y, paired = TRUE, median.test = TRUE, symmetric = FALSE)
```

```
##### TWO SAMPLE #####
```

```
# generate data
set.seed(1)
m <- 7
n <- 8
x <- rnorm(m, mean = 0.5)
y <- rnorm(n)
```

```
# Welch t-test
set.seed(0)
np.loc.test(x, y)
```

```
# Student t-test
set.seed(0)
np.loc.test(x, y, var.equal = TRUE)
```

```
# Studentized Wilcoxon test
set.seed(0)
np.loc.test(x, y, median.test = TRUE)
```

```
# Wilcoxon rank sum test
set.seed(0)
np.loc.test(x, y, var.equal = TRUE, median.test = TRUE)
```

```
## Not run:
```

```
##### MULTIVARIATE #####
```

```
##### ONE SAMPLE #####
```

```
# generate data
set.seed(1)
n <- 10
x <- cbind(rnorm(n, mean = 0.5),
           rnorm(n, mean = 1),
           rnorm(n, mean = 1.5))
```

```
# multivariate one sample t-test
set.seed(0)
ptest <- np.loc.test(x)
ptest
ptest$univariate
ptest$adj.p.values
```

```
##### PAIRED SAMPLE #####

# generate data
set.seed(1)
n <- 10
x <- cbind(rnorm(n, mean = 0.5),
           rnorm(n, mean = 1),
           rnorm(n, mean = 1.5))
y <- matrix(rnorm(n * 3), nrow = n, ncol = 3)

# multivariate paired t-test
set.seed(0)
ptest <- np.loc.test(x, y, paired = TRUE)
ptest
ptest$univariate
ptest$adj.p.values

##### TWO SAMPLE #####

# generate data
set.seed(1)
m <- 7
n <- 8
x <- cbind(rnorm(m, mean = 0.5),
           rnorm(m, mean = 1),
           rnorm(m, mean = 1.5))
y <- matrix(rnorm(n * 3), nrow = n, ncol = 3)

# multivariate Welch t-test
set.seed(0)
ptest <- np.loc.test(x, y)
ptest
ptest$univariate
ptest$adj.p.values

## End(Not run)
```

np.reg.test

*Nonparametric Tests of Regression Coefficients***Description**

Assuming a linear model of the form

$$Y = \alpha + X\beta + \epsilon$$

or

$$Y = \alpha + X\beta + Z\gamma + \epsilon$$

this function implements permutation tests of $H_0 : \beta = \beta_0$ where β_0 is the user-specified null vector.

Usage

```
np.reg.test(x, y, z = NULL, method = NULL,
            beta = NULL, homosced = FALSE,
            R = 9999, parallel = FALSE, cl = NULL,
            perm.dist = TRUE)
```

Arguments

x	Matrix of predictor variables (n by p).
y	Response vector or matrix (n by m).
z	Optional matrix of nuisance variables (n by q).
method	Permutation method. See Details.
beta	Null hypothesis value for β (p by m). Defaults to matrix of zeros.
homosced	Are the ϵ terms homoscedastic? If FALSE (default), a robust Wald test statistic is used. Otherwise the classic F test statistic is used.
R	Number of resamples for the permutation test (positive integer).
parallel	Logical indicating if the parallel package should be used for parallel computing (of the permutation distribution). Defaults to FALSE, which implements sequential computing.
cl	Cluster for parallel computing, which is used when parallel = TRUE. Note that if parallel = TRUE and cl = NULL, then the cluster is defined as <code>makeCluster(detectCores())</code> .
perm.dist	Logical indicating if the permutation distribution should be returned.

Details

With no nuisance variables in the model (i.e., $z = \text{NULL}$), there are three possible options for the method argument:

Method	Model
perm	$PY = \alpha + X\beta + \epsilon$
flip	$SY = \alpha + X\beta + \epsilon$
both	$PSY = \alpha + X\beta + \epsilon$

where P is a permutation matrix and S is a sign-flipping matrix.

With nuisance variables in the model, there are eight possible options for the method argument:

Method	Name	Model
HJ	Huh-Jhun	$PQ'R_zY = \alpha + Q'R_zX\beta + \epsilon$
KC	Kennedy-Cade	$PR_zY = \alpha + R_zX\beta + \epsilon$
SW	Still-White	$PR_zY = \alpha + X\beta + \epsilon$
TB	ter Braak	$(PR_m + H_m)Y = \alpha + X\beta + Z\gamma + \epsilon$
FL	Freedman-Lane	$(PR_z + H_z)Y = \alpha + X\beta + Z\gamma + \epsilon$

MA	Manly	$PY = \alpha + X\beta + Z\gamma + \epsilon$
OS	O’Gorman-Smith	$Y = \alpha + PR_zX\beta + Z\gamma + \epsilon$
DS	Draper-Stoneman	$Y = \alpha + PX\beta + Z\gamma + \epsilon$

where P is permutation matrix and Q is defined as $R_z = QQ'$ with $Q'Q = I$.

Note that H_z is the hat matrix for the nuisance variable design matrix, and $R_z = I - H_z$ is the corresponding residual forming matrix. Similarly, H_m and R_m are the hat and residual forming matrices for the full model including the predictor and nuisance variables.

Value

statistic	Test statistic value.
p.value	p-value for testing $H_0 : \beta = \beta_0$.
perm.dist	Permutation distribution of statistic.
method	Permutation method.
null.value	Null hypothesis value for β .
homosced	Homoscedastic errors?
R	Number of resamples.
exact	Exact permutation test? See Note.
coefficients	Least squares estimates of α , β , and γ (if applicable).
univariate	Univariate test statistic value for j -th variable (for multivariate inputs).
adj.p.value	Adjusted p-value for testing significance of j -th variable (for multivariate inputs).

Multivariate Tests

If the input y is a matrix with $m > 1$ columns, the multivariate test statistic is defined as `statistic = max(univariate)` given that the univariate test statistics are non-negative.

The global null hypothesis (across all m variables) is tested by comparing the observed statistic to the permutation distribution `perm.dist`. This produces the `p.value` for testing the global null hypothesis.

The local null hypothesis (separately for each variable) is tested by comparing the univariate test statistic to `perm.dist`. This produces the adjusted p-values (`adj.p.values`), which control the familywise Type I error rate across the m tests.

Note

If `method = "flip"`, the permutation test will be exact when the requested number of resamples R is greater than 2^n minus one. In this case, the permutation distribution `perm.dist` contains all 2^n possible values of the test statistic.

If `method = "both"`, the permutation test will be exact when the requested number of resamples R is greater than $\text{factorial}(n) * (2^n)$ minus one. In this case, the permutation distribution `perm.dist` contains all $\text{factorial}(n) * (2^n)$ possible values of the test statistic.

If method = "HJ", the permutation test will be exact when the requested number of resamples R is greater than $\text{factorial}(n-q-1)$ minus one. In this case, the permutation distribution perm.dist contains all $\text{factorial}(n-q-1)$ possible values of the test statistic.

Otherwise the permutation test will be exact when the requested number of resamples R is greater than $\text{factorial}(n)$ minus one. In this case, the permutation distribution perm.dist contains all $\text{factorial}(n)$ possible values of the test statistic.

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See Also

[plot.np.reg.test](#) S3 plotting method for visualizing the results

Examples

```
##### UNIVARIATE #####

##### TEST ALL COEFFICIENTS #####

# generate data
set.seed(1)
n <- 10
x <- cbind(rnorm(n), rnorm(n))
y <- rnorm(n)

# Wald test (method = "perm")
set.seed(0)
np.reg.test(x, y)

# F test (method = "perm")
set.seed(0)
np.reg.test(x, y, homosced = TRUE)

##### TEST SUBSET OF COEFFICIENTS #####

# generate data
set.seed(1)
n <- 10
x <- rnorm(n)
z <- rnorm(n)
y <- 3 + 2 * z + rnorm(n)

# Wald test (method = "HJ")
set.seed(0)
np.reg.test(x, y, z)

# F test (method = "HJ")
set.seed(0)
np.reg.test(x, y, z, homosced = TRUE)

## Not run:

##### MULTIVARIATE #####

##### TEST ALL COEFFICIENTS #####
```

```

# generate data
set.seed(1)
n <- 10
x <- cbind(rnorm(n), rnorm(n))
y <- matrix(rnorm(n * 3), nrow = n, ncol = 3)

# multivariate Wald test (method = "perm")
set.seed(0)
np.reg.test(x, y)

# multivariate F test (method = "perm")
set.seed(0)
np.reg.test(x, y, homosced = TRUE)

##### TEST SUBSET OF COEFFICIENTS #####

# generate data
set.seed(1)
n <- 10
x <- rnorm(n)
z <- rnorm(n)
y <- cbind(1 + 3 * z + rnorm(n),
           2 + 2 * z + rnorm(n),
           3 + 1 * z + rnorm(n))

# multivariate Wald test (method = "HJ")
set.seed(0)
np.reg.test(x, y, z)

# multivariate F test (method = "HJ")
set.seed(0)
np.reg.test(x, y, z, homosced = TRUE)

## End(Not run)

```

permn

Generate All Permutations of n Elements

Description

Generates all $n!$ vectors of length n consisting of permutations of the integers 1 to n .

Usage

```
permn(n)
```

Arguments

`n` Number of elements.

Details

Adapted from the "permutations" function in the [e1071](#) R package.

Value

Matrix of dimension n by $n!$ where each column contains a unique permutation vector.

Warning

For large n this function will consume a lot of memory and may even crash R.

Note

Used for exact tests in [np.cor.test](#) and [np.reg.test](#).

Author(s)

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References

Meyer, D., Dimitriadou, E., Hornik, K., Weingessel, A., & Leisch, F. (2018). e1071: Misc Functions of the Department of Statistics, Probability Theory Group (Formerly: E1071), TU Wien. R package version 1.7-0. <https://CRAN.R-project.org/package=e1071>

Examples

```
permn(2)
permn(3)
```

plot

Plots Permutation Distribution for Nonparametric Tests

Description

plot methods for object classes "np.cor.test", "np.loc.test", and "np.reg.test"

Usage

```
## S3 method for class 'np.cor.test'
plot(x, alpha = 0.05, col = "grey", col.rr = "red",
     col.stat = "black", lty.stat = 2, lwd.stat = 2,
     xlab = "Test Statistic", main = "Permutation Distribution",
     breaks = "scott", border = NA, box = TRUE, ...)

## S3 method for class 'np.loc.test'
plot(x, alpha = 0.05, col = "grey", col.rr = "red",
     col.stat = "black", lty.stat = 2, lwd.stat = 2,
     xlab = "Test Statistic", main = "Permutation Distribution",
     breaks = "scott", border = NA, box = TRUE, ...)

## S3 method for class 'np.reg.test'
plot(x, alpha = 0.05, col = "grey", col.rr = "red",
     col.stat = "black", lty.stat = 2, lwd.stat = 2,
     xlab = "Test Statistic", main = "Permutation Distribution",
     breaks = "scott", border = NA, box = TRUE, SQR = TRUE, ...)
```

Arguments

<code>x</code>	an object of class "np.cor.test" output by the np.cor.test function, "np.loc.test" output by the np.loc.test function, or "np.reg.test" output by the np.reg.test function
<code>alpha</code>	significance level of the nonparametric test
<code>col</code>	color for plotting the non-rejection region
<code>col.rr</code>	color for plotting the rejection region
<code>col.stat</code>	color for plotting the observed test statistic
<code>lty.stat</code>	line type for plotting the observed test statistic
<code>lwd.stat</code>	line width for plotting the observed test statistic
<code>xlab</code>	x-axis label for the plot
<code>main</code>	title for the plot
<code>breaks</code>	defines the breaks of the histogram (see hist)
<code>border</code>	color of the border around the bars
<code>box</code>	should a box be drawn around the plot?
<code>SQR</code>	for regression tests, should the permutation distribution (and test statistic) be plotted on the square-root scale?
<code>...</code>	additional arguments to be passed to hist

Details

Plots a histogram of the permutation distribution and the observed test statistic. The argument 'alpha' controls the rejection region of the nonparametric test, which is plotted using a separate color (default is red).

Author(s)

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References

Helwig, N. E. (2019). Statistical nonparametric mapping: Multivariate permutation tests for location, correlation, and regression problems in neuroimaging. *WIREs Computational Statistics*, 11(2), e1457. doi: 10.1002/wics.1457

See Also

[np.cor.test](#) for information on nonparametric correlation tests

[np.loc.test](#) for information on nonparametric location tests

[np.reg.test](#) for information on nonparametric regression tests

Examples

```
##### np.cor.test #####

# generate data
rho <- 0.5
val <- c(sqrt(1 + rho), sqrt(1 - rho))
corsqrt <- matrix(c(val[1], -val[2], val), 2, 2) / sqrt(2)
set.seed(1)
n <- 50
z <- cbind(rnorm(n), rnorm(n)) %%% corsqrt
x <- z[,1]
y <- z[,2]

# test H0: rho = 0
set.seed(0)
test <- np.cor.test(x, y)

# plot results
plot(test)

##### np.loc.test #####

# generate data
set.seed(1)
n <- 50
x <- rnorm(n, mean = 0.5)

# one sample t-test
set.seed(0)
test <- np.loc.test(x)

# plot results
plot(test)
```

```
##### np.reg.test #####

# generate data
set.seed(1)
n <- 50
x <- cbind(rnorm(n), rnorm(n))
beta <- c(0.25, 0.5)
y <- x %*% beta + rnorm(n)

# Wald test (method = "perm")
set.seed(0)
test <- np.reg.test(x, y)

# plot results
plot(test)
```

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