Package ‘MKinfer’

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Details

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library(MKinfer)

Author(s)

Matthias Kohl https://www.stamats.de
Maintainer: Matthias Kohl <matthias.kohl@stamats.de>
Description

This function can be used to compute confidence intervals for binomial proportions.

Usage

```r
binomCI(x, n, conf.level = 0.95, method = "wilson", rand = 123,
        R = 9999, bootci.type = "all",
        alternative = c("two.sided", "less", "greater"), ...)
```

Arguments

- `x`: number of successes
- `n`: number of trials
- `conf.level`: confidence level
- `method`: character string specifying which method to use; see details.
- `rand`: seed for random number generator; see details.
- `R`: number of bootstrap replicates.
- `bootci.type`: type of bootstrap interval; see `boot.ci`.
- `alternative`: a character string specifying one- or two-sided confidence intervals. Must be one of "two.sided" (default), "greater" or "less" (one-sided intervals). You can specify just the initial letter.
- `...`: further arguments passed to function `boot`, e.g. for parallel computing.

Details

The Wald interval is obtained by inverting the acceptance region of the Wald large-sample normal test. There is also a Wald interval with continuity correction ("wald-cc").

The Wilson interval, which is the default, was introduced by Wilson (1927) and is the inversion of the CLT approximation to the family of equal tail tests of $p = p_0$. The Wilson interval is recommended by Agresti and Coull (1998) as well as by Brown et al (2001).

The Agresti-Coull interval was proposed by Agresti and Coull (1998) and is a slight modification of the Wilson interval. The Agresti-Coull intervals are never shorter than the Wilson intervals; cf. Brown et al (2001).

The Jeffreys interval is an implementation of the equal-tailed Jeffreys prior interval as given in Brown et al (2001).

The modified Wilson interval is a modification of the Wilson interval for $x$ close to 0 or $n$ as proposed by Brown et al (2001).

The modified Jeffreys interval is a modification of the Jeffreys interval for $x = 0$ | $x = 1$ and $x = n-1$ | $x = n$ as proposed by Brown et al (2001).
The Clopper-Pearson interval is based on quantiles of corresponding beta distributions. This is sometimes also called exact interval.

The arcsine interval is based on the variance stabilizing distribution for the binomial distribution.

The logit interval is obtained by inverting the Wald type interval for the log odds.


The bootstrap interval is calculated by using function `boot.ci`.


Value

A list with class "confint" containing the following components:

- `estimate` the estimated probability of success.
- `conf.int` a confidence interval for the probability of success.

Note

A first version of this function appeared in R package SLmisc.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

`binom.test`

Examples

```r
binomCI(x = 42, n = 43, method = "wald")
binomCI(x = 42, n = 43, method = "wald-cc")
binomCI(x = 42, n = 43, method = "wilson")
binomCI(x = 42, n = 43, method = "agresti-coull")
binomCI(x = 42, n = 43, method = "jeffreys")
binomCI(x = 42, n = 43, method = "modified wilson")
binomCI(x = 42, n = 43, method = "modified jeffreys")
binomCI(x = 42, n = 43, method = "clopper-pearson")
binomCI(x = 42, n = 43, method = "arcsine")
```
binomDiffCI

binomCI(x = 42, n = 43, method = "logit")
binomCI(x = 42, n = 43, method = "witting")
## bootstrap intervals (R = 999 to reduce computation time for R checks)
binomCI(x = 42, n = 43, method = "boot", R = 999) # may generate values > 1!

## the confidence interval computed by binom.test
## corresponds to the Clopper-Pearson interval
binomCI(x = 42, n = 43, method = "clopper-pearson")$conf.int
binom.test(x = 42, n = 43)$conf.int

## one-sided intervals
binomCI(x = 10, n = 43, alternative = "less")
binomCI(x = 10, n = 43, alternative = "less", method = "boot",
        bootci.type = "bca", R = 999)
binomCI(x = 10, n = 43, alternative = "greater", method = "boot",
        bootci.type = "perc", R = 999)

## parallel computing for bootstrap
binomCI(x = 10, n = 43, method = "boot", R = 9999,
        parallel = "multicore", ncpus = 2)

---

binomDiffCI

Confidence Intervals for Difference of Two Binomial Proportions

Description

This function can be used to compute confidence intervals for the difference of two binomial proportions. It includes methods for the independent and the paired case.

Usage

binomDiffCI(a, b, c, d, conf.level = 0.95, paired = FALSE,
           method = ifelse(paired, "wilson-cc", "wilson"),
           R = 9999, bootci.type = "all",
           alternative = c("two.sided", "less", "greater"), ...)

Arguments

a independent: number of successes of group 1; paired: number of cases with success in group 1 and 2.
b independent: number of successes of group 2; paired: number of cases with success in group 1 and failure in group 2.
c independent: number of failures of group 1; paired: number of cases with failure in group 1 and success in group 2.
d independent: number of failures of group 2; paired: number of cases with failure in group 1 and 2.
conf.level: confidence level
paired: a logical value indicating whether the two groups are paired.
method: character string specifying which method to use; see details.
R: number of bootstrap replicates.
boot.ci.type: type of bootstrap interval; see boot.ci.
alternative: a character string specifying one- or two-sided confidence intervals. Must be one of "two.sided" (default), "greater" or "less" (one-sided intervals). You can specify just the initial letter.
... further arguments passed to function boot, e.g. for parallel computing.

Details

The Wald intervals (independent and paired) are obtained by applying the normal approximation. There are also Wald intervals with continuity correction.

The Wilson intervals are recommended by Newcombe and Altman (2000); see Chapter 6 of Altman et al. (2000). In the paired case, the continuity corrected version of the interval is recommended. The intervals are proposed in Newcombe (1998a) and Newcombe (1998b).

The bootstrap interval is calculated by using function boot.ci.

Value

A list with class "confint" containing the following components:

estimate: the estimated probability of success.
conf.int: a confidence interval for the probability of success.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

prop.test, boot.ci
Examples

## Example 1: Altman et al. (2000, p. 49)
## the confidence interval computed by prop.test
prop.test(c(63, 38), c(93, 92))$conf.int
## wald / simple asymptotic interval
binomDiffCI(a = 63, b = 38, c = 30, d = 54, method = "wald")
## wald / simple asymptotic interval with continuity correction
binomDiffCI(a = 63, b = 38, c = 30, d = 54, method = "wald-cc")
## wilson
binomDiffCI(a = 63, b = 38, c = 30, d = 54)
## bootstrap intervals (R = 999 to reduce computation time for R checks)
binomDiffCI(a = 63, b = 38, c = 30, d = 54, method = "boot", R = 999)
## one-sided
binomDiffCI(a = 63, b = 38, c = 30, d = 54, alternative = "greater")
## bootstrap intervals (R = 999 to reduce computation time for R checks)
binomDiffCI(a = 63, b = 38, c = 30, d = 54, method = "boot", R = 999,
    bootci.type = "bca", alternative = "greater")

## Example 2: Altman et al. (2000, p. 50)
## the confidence interval computed by prop.test
prop.test(c(5, 0), c(56, 29))$conf.int
## wald / simple asymptotic interval
binomDiffCI(a = 5, b = 0, c = 51, d = 29, method = "wald")
## wald / simple asymptotic interval with continuity correction
binomDiffCI(a = 5, b = 0, c = 51, d = 29, method = "wald-cc")
## wilson
binomDiffCI(a = 5, b = 0, c = 51, d = 29)
## bootstrap intervals (R = 999 to reduce computation time for R checks)
binomDiffCI(a = 5, b = 0, c = 51, d = 29, method = "boot", R = 999)
## one-sided
binomDiffCI(a = 5, b = 0, c = 51, d = 29, alternative = "less")
## bootstrap intervals (R = 999 to reduce computation time for R checks)
binomDiffCI(a = 5, b = 0, c = 51, d = 29, method = "boot", R = 999,
    bootci.type = "perc", alternative = "less")

## Example 3: Altman et al. (2000, p. 51)
## wald / simple asymptotic interval
binomDiffCI(a = 14, b = 5, c = 0, d = 22, paired = TRUE, method = "wald")
## wald / simple asymptotic interval with continuity correction
binomDiffCI(a = 14, b = 5, c = 0, d = 22, paired = TRUE, method = "wald-cc")
## wilson
binomDiffCI(a = 14, b = 5, c = 0, d = 22, paired = TRUE, method = "wilson")
## wilson with continuity correction
binomDiffCI(a = 14, b = 5, c = 0, d = 22, paired = TRUE)
## bootstrap intervals (R = 999 to reduce computation time for R checks)
binomDiffCI(a = 14, b = 5, c = 0, d = 22, paired = TRUE, method = "boot", R = 999)

## Example 4: Altman et al. (2000, p. 51)
## wald / simple asymptotic interval
binomDiffCI(a = 212, b = 144, c = 256, d = 707, paired = TRUE, method = "wald")
# wald / simple asymptotic interval with continuity correction
binomDiffCI(a = 212, b = 144, c = 256, d = 707, paired = TRUE, method = "wald-cc")

# wilson
binomDiffCI(a = 212, b = 144, c = 256, d = 707, paired = TRUE, method = "wilson")

# wilson with continuity correction
binomDiffCI(a = 212, b = 144, c = 256, d = 707, paired = TRUE)

# bootstrap intervals (R = 999 to reduce computation time for R checks)
binomDiffCI(a = 212, b = 144, c = 256, d = 707, paired = TRUE, method = "boot",
            bootci.type = c("norm", "basic", "stud", "perc"), R = 999) ## type = "bca" gives error

binomDiffCI(a = 63, b = 38, c = 30, d = 54, method = "boot", R = 9999,
            parallel = "multicore", ncpus = 2)

---

**boot.t.test**

### Bootstrap t-Test

**Description**

Performs one and two sample bootstrap t-tests on vectors of data.

**Usage**

```r
boot.t.test(x, y = NULL, 
            alternative = c("two.sided", "less", "greater"),
            mu = 0, paired = FALSE, var.equal = FALSE,
            conf.level = 0.95, R = 9999, symmetric = FALSE, ...)
```

**Arguments**

- `x`: a (non-empty) numeric vector of data values.
- `y`: an optional (non-empty) numeric vector of data values.
- `alternative`: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
- `mu`: a number indicating the true value of the mean (or difference in means if you are performing a two sample test).
- `paired`: a logical indicating whether you want a paired t-test.
- `var.equal`: a logical variable indicating whether to treat the two variances as being equal. If TRUE then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.
conf.level  confidence level of the interval.
R         number of bootstrap replicates.
symmetric  a logical variable indicating whether to assume symmetry in the two-sided test. If TRUE then the symmetric bootstrap p value otherwise the equal-tail bootstrap p value is computed.
formula   a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs a factor with two levels giving the corresponding groups.
data      an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset   an optional vector specifying a subset of observations to be used.
na.action a function which indicates what should happen when the data contain NAs. Defaults togetOption("na.action").
...       further arguments to be passed to or from methods.

Details

The implemented test corresponds to the proposal of Chapter 16 of Efron and Tibshirani (1993). The function returns bootstrapped p values and confidence intervals as well as the results of the t-test without bootstrap.

The formula interface is only applicable for the 2-sample tests.
alternative = "greater" is the alternative that x has a larger mean than y.
If paired is TRUE then both x and y must be specified and they must be the same length. Missing values are silently removed (in pairs if paired is TRUE). If var.equal is TRUE then the pooled estimate of the variance is used. By default, if var.equal is FALSE then the variance is estimated separately for both groups and the Welch modification to the degrees of freedom is used.
If the input data are effectively constant (compared to the larger of the two means) an error is generated.

Value

A list with class "boot.htest" (derived from class htest) containing the following components:

statistic  the value of the t-statistic.
parameter  the degrees of freedom for the t-statistic.
p.value    the p-value for the test.
boot.p.value the bootstrapped p-value for the test.
conf.int   a confidence interval for the mean appropriate to the specified alternative hypothesis.
boot.conf.int a bootstrap percentile confidence interval for the mean appropriate to the specified alternative hypothesis.
estimate   the estimated mean or difference in means depending on whether it was a one-sample test or a two-sample test.
boot.estimate  bootstrapped estimate.
null.value     the specified hypothesized value of the mean or mean difference depending on
               whether it was a one-sample test or a two-sample test.
stderr         the standard error of the mean (difference), used as denominator in the t-statistic
               formula.
boot.stderr    bootstrapped standard error.
alternative   a character string describing the alternative hypothesis.
method         a character string indicating what type of t-test was performed.
data.name       a character string giving the name(s) of the data.

Note

Code and documentation are for large parts identical to function t.test.

References


See Also

t.test, meanCI, meanDiffCI, perm.t.test

Examples

require(graphics)
t.test(1:10, y = c(7:20))   # P = .00001855
boot.t.test(1:10, y = c(7:20))

t.test(1:10, y = c(7:20, 200)) # P = .1245 -- NOT significant anymore
boot.t.test(1:10, y = c(7:20, 200))

## Classical example: Student's sleep data
plot(extra ~ group, data = sleep)
## Traditional interface
with(sleep, t.test(extra[group == 1], extra[group == 2]))
with(sleep, boot.t.test(extra[group == 1], extra[group == 2]))
## Formula interface
  t.test(extra ~ group, data = sleep)
  boot.t.test(extra ~ group, data = sleep)
Confidence Intervals for Coefficient of Variation

Description

This function can be used to compute confidence intervals for the (classical) coefficient of variation.

Usage

```r
cvCI(x, conf.level = 0.95, method = "miller", R = 9999,
    bootci.type = c("norm", "basic", "perc", "bca"), na.rm = FALSE,
    alternative = c("two.sided", "less", "greater"), ...)
```

Arguments

- `x`: numeric vector with positive numbers.
- `conf.level`: confidence level
- `method`: character string specifying which method to use; see details.
- `R`: number of bootstrap replicates; see details.
- `bootci.type`: type of bootstrap interval; see `boot.ci`. Type "student" does not work.
- `na.rm`: logical. Should missing values be removed?
- `alternative`: a character string specifying one- or two-sided confidence intervals. Must be one of "two.sided" (default), "greater" or "less" (one-sided intervals). You can specify just the initial letter.
- `...`: further arguments passed to function `boot`, e.g. for parallel computing.

Details

For details about the confidence intervals we refer to Gulhar et al (2012) and Arachchige et al (2019).

In case of bootstrap intervals type "student" does not work, since no standard error of CV is provided.

Value

A list with class "confint" containing the following components:

- `estimate`: the estimated coefficient of variation.
- `conf.int`: a confidence interval for the coefficient of variation.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>
References


See Also

CV, boot.ci

Examples

```r
x <- rnorm(100, mean = 10, sd = 2) # CV = 0.2
cvCI(x, method = "miller")
cvCI(x, method = "sharma")
cvCI(x, method = "curto")
cvCI(x, method = "mckay")
cvCI(x, method = "vangel")
cvCI(x, method = "panichkitkosolkul")
cvCI(x, method = "medmiller")
cvCI(x, method = "medmckay")
cvCI(x, method = "medvangel")
cvCI(x, method = "medcurto")
cvCI(x, method = "gulhar")
cvCI(x, method = "boot", R = 999) # R = 999 to reduce computation time for R checks

## one-sided

cvCI(x, alternative = "less")
cvCI(x, alternative = "greater")
cvCI(x, method = "boot", bootci.type = "bca", alternative = "less", R = 999)

## parallel computing for bootstrap

cvCI(x, method = "boot", R = 9999, parallel = "multicore", ncpus = 2)
```

### hsu.t.test

**Hsu Two-Sample t-Test**

**Description**

Performs Hsu two sample t-tests on vectors of data.

**Usage**

```r
hsu.t.test(x, ...)

## Default S3 method:
```
hsu.t.test(x, y,
  alternative = c("two.sided", "less", "greater"),
  mu = 0, conf.level = 0.95, ...)

## S3 method for class 'formula'
hsu.t.test(formula, data, subset, na.action, ...)

Arguments

- **x**: a (non-empty) numeric vector of data values.
- **y**: a (non-empty) numeric vector of data values.
- **alternative**: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
- **mu**: a number indicating the true value of the mean (or difference in means if you are performing a two sample test).
- **conf.level**: confidence level of the interval.
- **formula**: a formula of the form `lhs ~ rhs` where `lhs` is a numeric variable giving the data values and `rhs` a factor with two levels giving the corresponding groups.
- **data**: an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
- **subset**: an optional vector specifying a subset of observations to be used.
- **na.action**: a function which indicates what should happen when the data contain NA's. Defaults to `getOption("na.action")`.
- **...**: further arguments to be passed to or from methods.

Details

The function and its documentation was adapted from `t.test`.

alternative = "greater" is the alternative that `x` has a larger mean than `y`.

If the input data are effectively constant (compared to the larger of the two means) an error is generated.

One should at least have six observations per group to apply the test; see Section 6.8.3 and 7.4.4.2 of Hedderich and Sachs (2018).

Value

A list with class "htest" containing the following components:

- **statistic**: the value of the t-statistic.
- **parameter**: the degrees of freedom for the t-statistic.
- **p.value**: the p-value for the test.
- **conf.int**: a confidence interval for the mean appropriate to the specified alternative hypothesis.
- **estimate**: the estimated means and standard deviations.
null.value the specified hypothesized value of the mean or mean difference depending on whether it was a one-sample test or a two-sample test.

stderr the standard error of the difference in means, used as denominator in the t-statistic formula.

alternative a character string describing the alternative hypothesis.

method a character string indicating what type of t-test was performed.

data.name a character string giving the name(s) of the data.

References


See Also

t.test

Examples

```r
## Examples taken and adapted from function t.test
t.test(1:10, y = c(7:20))  # P = .00001855
t.test(1:10, y = c(7:20, 200)) # P = .1245  -- NOT significant anymore
hsu.t.test(1:10, y = c(7:20))
hsu.t.test(1:10, y = c(7:20, 200))

## Traditional interface
with(sleep, t.test(extra[group == 1], extra[group == 2]))
with(sleep, hsu.t.test(extra[group == 1], extra[group == 2]))

## Formula interface
t.test(extra ~ group, data = sleep)
hsu.t.test(extra ~ group, data = sleep)
```

---

**imputeSD**

**Impute Standard Deviations for Changes from Baseline**

**Description**

The function imputes standard deviations for changes from baseline adopting the approach describe in the Cochrane handbook, Section 16.1.3.2.

**Usage**

```r
imputeSD(SD1, SD2, SDchange, corr)
```
Arguments

SD1 numeric vector, baseline SD.
SD2 numeric vector, follow-up SD.
SDchange numeric vector, SD for changes from baseline.
corr optional numeric vector of correlations; see details below.

Details

The function imputes standard deviations for changes from baseline adopting the approach describe in the Cochrane handbook (2019), Section 6.5.2.8.

1) Missing SD1 are replaced by correspondig values of SD2 and vice versa.
2) Correlations for complete data (rows) are computed. Alternatively, correlations can be provided via argument corr. This option may particularly be useful, if no complete data is available.
3) Minimum, mean and maximum correlation (over rows) are computed.
4) Missing values of SDchange are computed by the formula provided in the handbook. The minimum, mean and maximum correlation are used leading to maximal, mean and minimal SD values that may be used for imputation as well as a sensitivity analysis.

Value
data.frame with possibly imputed SD1 and SD2 values as well as the given SDchange values are returned. Moreover, the computed correlations as well as possible values for the imputation of SDchange are returned.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References


Examples

SD1 <- c(0.149, 0.022, 0.036, 0.085, 0.125, NA, 0.139, 0.124, 0.038)
SD2 <- c(NA, 0.039, 0.038, 0.087, 0.125, NA, 0.135, 0.126, 0.038)
SDchange <- c(NA, NA, NA, 0.026, 0.058, NA, NA, NA, NA)
imputeSD(SD1, SD2, SDchange)
SDchange2 <- rep(NA, 9)
imputeSD(SD1, SD2, SDchange2, corr = c(0.85, 0.9, 0.95))
mi.t.test

Multiple Imputation Student’s t-Test

Description
Performs one and two sample t-tests on multiple imputed datasets.

Usage
mi.t.test(miData, ...)

## Default S3 method:
mi.t.test(miData, x, y = NULL,
    alternative = c("two.sided", "less", "greater"), mu = 0,
    paired = FALSE, var.equal = FALSE, conf.level = 0.95,
    subset = NULL, ...)

Arguments
- miData: list of multiple imputed datasets.
- x: name of a variable that shall be tested.
- y: an optional name of a variable that shall be tested (paired test) or a variable that shall be used to split into groups (unpaired test).
- alternative: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
- mu: a number indicating the true value of the mean (or difference in means if you are performing a two sample test).
- paired: a logical indicating whether you want a paired t-test.
- var.equal: a logical variable indicating whether to treat the two variances as being equal. If TRUE then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.
- conf.level: confidence level of the interval.
- subset: an optional vector specifying a subset of observations to be used.
- ...: further arguments to be passed to or from methods.

Details
alternative = "greater" is the alternative that x has a larger mean than y.

If paired is TRUE then both x and y must be specified and they must be the same length. Missing values are not allowed as they should have been imputed. If var.equal is TRUE then the pooled estimate of the variance is used. By default, if var.equal is FALSE then the variance is estimated separately for both groups and the Welch modification to the degrees of freedom is used.

We use the approach of Rubin (1987) in combination with the adjustment of Barnard and Rubin (1999).
Value

A list with class "htest" containing the following components:

- **statistic**: the value of the t-statistic.
- **parameter**: the degrees of freedom for the t-statistic.
- **p.value**: the p-value for the test.
- **conf.int**: a confidence interval for the mean appropriate to the specified alternative hypothesis.
- **estimate**: the estimated mean (one-sample test), difference in means (paired test), or estimated means (two-sample test) as well as the respective standard deviations.
- **null.value**: the specified hypothesized value of the mean or mean difference depending on whether it was a one-sample test or a two-sample test.
- **alternative**: a character string describing the alternative hypothesis.
- **method**: a character string indicating what type of t-test was performed.
- **data.name**: a character string giving the name(s) of the data.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

t.test

Examples

```r
## Generate some data
set.seed(123)
x <- rnorm(25, mean = 1)
x[sample(1:25, 5)] <- NA
y <- rnorm(20, mean = -1)
y[sample(1:20, 4)] <- NA
pair <- c(rnorm(25, mean = 1), rnorm(20, mean = -1))
g <- factor(c(rep("yes", 25), rep("no", 20)))
D <- data.frame(ID = 1:45, variable = c(x, y), pair = pair, group = g)

## Use Amelia to impute missing values
library(Amelia)
res <- amelia(D, m = 10, p2s = 0, idvars = "ID", noms = "group")

## Per protocol analysis (Welch two-sample t-test)
```
normCI

Confidence Intervals for Mean and Standard Deviation

Description

This function can be used to compute confidence intervals for mean and standard deviation of a normal distribution.

Usage

\[
\text{normCI}(x, \text{mean} = \text{NULL}, \text{sd} = \text{NULL}, \text{conf.level} = 0.95, \\
\text{boot} = \text{FALSE}, R = 9999, \text{bootci.type} = \text{"all"}, \text{na.rm} = \text{TRUE}, \\
\text{alternative} = \text{c("two.sided", \text{\"less\"}, \text{\"greater\"})}, \ldots)
\]

\[
\text{meanCI}(x, \text{conf.level} = 0.95, \text{boot} = \text{FALSE}, R = 9999, \text{bootci.type} = \text{"all"}, \\
\text{na.rm} = \text{TRUE}, \text{alternative} = \text{c("two.sided", \text{\"less\"}, \text{\"greater\"})}, \ldots)
\]

\[
\text{sdCI}(x, \text{conf.level} = 0.95, \text{boot} = \text{FALSE}, R = 9999, \text{bootci.type} = \text{\"all"}, \\
\text{na.rm} = \text{TRUE}, \text{alternative} = \text{c("two.sided", \text{\"less\"}, \text{\"greater\"})}, \ldots)
\]

Arguments

- **x**: vector of observations.
- **mean**: mean if known otherwise NULL.
- **sd**: standard deviation if known otherwise NULL.
The standard confidence intervals for mean and standard deviation are computed that can be found in many textbooks, e.g. Chapter 4 in Altman et al. (2000).

In addition, bootstrap confidence intervals for mean and/or SD can be computed, where function `boot.ci` is applied.

**Value**

A list with class "confint" containing the following components:

- **estimate**: the estimated mean and sd.
- **conf.int**: confidence interval(s) for mean and/or sd.
- **Infos**: additional information.

**Author(s)**

Matthias Kohl <Matthias.Kohl@stamats.de>

**References**


**Examples**

```r
x <- rnorm(50)
## mean and sd unknown
normCI(x)
meanCI(x)
sdCI(x)

## one-sided
normCI(x, alternative = "less")
meanCI(x, alternative = "greater")
sdCI(x, alternative = "greater")
```
normDiffCI

Confidence Intervals for Difference of Means

Description

This function can be used to compute confidence intervals for difference of means assuming normal distributions.

Usage

```r
normDiffCI(x, y, conf.level = 0.95, paired = FALSE, method = "welch", boot = FALSE, R = 9999, bootci.type = "all", na.rm = TRUE, alternative = c("two.sided", "less", "greater"), ...)
meanDiffCI(x, y, conf.level = 0.95, paired = FALSE, method = "welch", boot = FALSE, R = 9999, bootci.type = "all", na.rm = TRUE, alternative = c("two.sided", "less", "greater"), ...)
```

Arguments

- `x`: numeric vector of data values of group 1.
- `y`: numeric vector of data values of group 2.
- `conf.level`: confidence level.
normDiffCI

paired  a logical value indicating whether the two groups are paired.
method  a character string specifying which method to use in the unpaired case; see details.
boot    a logical value indicating whether bootstrapped confidence intervals shall be computed.
R       number of bootstrap replicates.
bootci.type type of bootstrap interval; see boot.ci.
na.rm   a logical value indicating whether NA values should be stripped before the computation proceeds.
alternative a character string specifying one- or two-sided confidence intervals. Must be one of "two.sided" (default), "greater" or "less" (one-sided intervals). You can specify just the initial letter.
...     further arguments passed to function boot, e.g. for parallel computing.

Details

The standard confidence intervals for the difference of means are computed that can be found in many textbooks, e.g. Chapter 4 in Altman et al. (2000).

The method "classical" assumes equal variances whereas methods "welch" and "hsu" allow for unequal variances. The latter two methods use different formulas for computing the degrees of freedom of the respective t-distribution providing the quantiles in the confidence interval. Instead of the Welch-Satterhwaite equation the method of Hsu uses the minimum of the group sample sizes minus 1; see Section 6.8.3 of Hedderich and Sachs (2018).

Value

A list with class "confint" containing the following components:

estimate  point estimate (mean of differences or difference in means).
conf.int  confidence interval.
Infos     additional information.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References


Examples

```r
x <- rnorm(100)
y <- rnorm(100, sd = 2)
## paired
normDiffCI(x, y, paired = TRUE)
## (R = 999 to reduce computation time for R checks)
normDiffCI(x, y, paired = TRUE, boot = TRUE, R = 999)
## compare
normCI(x-y)
## (R = 999 to reduce computation time for R checks)
normCI(x-y, boot = TRUE, R = 999)

## unpaired
y <- rnorm(90, mean = 1, sd = 2)
## classical
normDiffCI(x, y, method = "classical")
## (R = 999 to reduce computation time for R checks)
normDiffCI(x, y, method = "classical", boot = TRUE, R = 999)
## Welch (default as in case of function t.test)
normDiffCI(x, y, method = "welch")
## (R = 999 to reduce computation time for R checks)
normDiffCI(x, y, method = "welch", boot = TRUE, R = 999)
## Hsu
normDiffCI(x, y, method = "hsu")
## In case of bootstrap there is no difference between welch and hsu
## (R = 999 to reduce computation time for R checks)
normDiffCI(x, y, method = "hsu", boot = TRUE, R = 999)

## one-sided
normDiffCI(x, y, alternative = "less")
normDiffCI(x, y, boot = TRUE, R = 999, alternative = "greater")

## parallel computing for bootstrap
normDiffCI(x, y, method = "welch", boot = TRUE, R = 9999,
           parallel = "multicore", ncpus = 2)
```

```r
## Monte-Carlo simulation: coverage probability
M <- 100 # increase for more stable/realistic results!
CIhsu <- CIwelch <- CIclass <- matrix(NA, nrow = M, ncol = 2)
for(i in 1:M){
  x <- rnorm(10)
y <- rnorm(30, sd = 0.1)
  CIclass[i,] <- normDiffCI(x, y, method = "classical")$conf.int
  CIwelch[i,] <- normDiffCI(x, y, method = "welch")$conf.int
  CIhsu[i,] <- normDiffCI(x, y, method = "hsu")$conf.int
}
## coverage probabilities
## classical
sum(CIclass[,1] < 0 & 0 < CIclass[,2])/M
```
p2ses

## Welch
sum(CIwelch[,1] < 0 & 0 < CIwelch[,2])/M

## Hsu
sum(CIhsu[,1] < 0 & 0 < CIhsu[,2])/M

---

### p2ses

#### Compute SES from p value.

---

**Description**

The function computes the SES (standardized effect size) from the p value for permutation/randomisation tests as proposed by Botta-Dukat (2018).

**Usage**

```r
p2ses(p, alternative = c("two.sided", "less", "greater"))
```

**Arguments**

- `p`: numeric vector of p values.
- `alternative`: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.

**Details**

The function uses the probit transformation (qnorm) to compute an alternative SES based on p values from a permutation/randomization test as proposed by Botta-Dukat (2018) for skewed distributions.

**Value**

SES

**Author(s)**

Matthias Kohl <Matthias.Kohl@stamats.de>

**References**

Examples

```r
## symmetric case
x <- rnorm(100)
res <- perm.t.test(x)
p2ses(res$p.value)
abs(res$statistic)

## skewed case
x <- rgamma(100, shape = 5)
res <- perm.t.test(x, mu = 5)
p2ses(res$p.value)
abs(res$statistic)
```

pairwise.ext.t.test  Compute Pairwise t Tests

Description

The function computes pairwise t tests using functions `t.test`, `hsu.t.test`, `boot.t.test` or `perm.t.test`.

Usage

```r
pairwise.ext.t.test(x, g, method = "t.test", p.adjust.method = "holm",
                   paired = FALSE, ...)
```

Arguments

- `x` numeric vector.
- `g` grouping vector or factor
- `method` character giving the name of the function to be applied; that is, "t.test", "hsu.t.test", "boot.t.test" or "perm.t.test".
- `paired` a logical indicating whether you want a paired test.
- `...` additional arguments to `fun`.

Details

The function computes pairwise t tests using function `t.test`, `hsu.t.test`, `boot.t.test` or `perm.t.test`. The implementation is in certain aspects analogously to `pairwise.t.test`. However, a more detailed output is generated.
pairwise.fun

Value

Object of class "pw.htest" containing the following components:

- data.name: a character string giving the names of the data.
- method: the type of test applied.
- null.value: the location parameter mu.
- alternative: a character string describing the alternative hypothesis.
- conf.level: confidence level of the confidence interval.
- results: a data.frame containing the results of function `t.test`, `boot.t.test` or `perm.t.test`.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

See Also

t.test, pairwise.t.test

Examples

```r
set.seed(13)
x <- rnorm(100)
g <- factor(sample(1:4, 100, replace = TRUE))
levels(g) <- c("a", "b", "c", "d")
pairwise.ext.t.test(x, g)
## in contrast to
pairwise.t.test(x, g, pool.sd = FALSE)
## moreover
pairwise.ext.t.test(x, g, method = "hsu.t.test")
pairwise.ext.t.test(x, g, method = "boot.t.test")
pairwise.ext.t.test(x, g, method = "perm.t.test")
```

---

**pairwise.fun**

*Compute pairwise values for a given function*

**Description**

The function computes pairwise values for a given function.

**Usage**

```
pairwise.fun(x, g, fun, ...)
```


**pairwise.wilcox.exact**

**Arguments**

- `x` numeric vector.
- `g` grouping vector or factor
- `fun` some function where the first two arguments have to be numeric vectors for which the function computes some quantity; see example section below.
- `...` additional arguments to `fun`.

**Details**

The function computes pairwise values for a given function.

The implementation is in certain aspects analogously to `pairwise.t.test`.

**Value**

Vector with pairwise function values.

**Author(s)**

Matthias Kohl <Matthias.Kohl@stamats.de>

**See Also**

`pairwise.t.test`

**Examples**

```r
set.seed(13)
x <- rnorm(100)
g <- factor(sample(1:4, 100, replace = TRUE))
levels(g) <- c("a", "b", "c", "d")
pairwise.fun(x, g, fun = function(x, y) t.test(x, y)$p.value)
## in contrast to
pairwise.t.test(x, g, p.adjust.method = "none", pool.sd = FALSE)
```

---

**pairwise.wilcox.exact** *Compute Pairwise Wilcoxon Tests*

**Description**

The function computes pairwise Wilcoxon rank sum and signed rank tests using function `wilcox.exact` of package `exactRankTests`.

**Usage**

```r
pairwise.wilcox.exact(x, g, p.adjust.method = "holm", paired = FALSE, ...)
```
Arguments

- **x**: numeric vector.
- **g**: grouping vector or factor
- **p.adjust.method**: method for adjusting p values (see `p.adjust`). Can be abbreviated.
- **paired**: a logical indicating whether you want a paired test.
- **...**: additional arguments to `fun`.

Details

The function computes pairwise Wilcoxon rank sum and signed rank tests.

The implementation is in certain aspects analogously to `pairwise.wilcox.test`. However, a more detailed output is generated.

Value

Object of class "pw.htest" containing the following components:

- **data.name**: a character string giving the names of the data.
- **method**: the type of test applied.
- **null.value**: the location parameter mu.
- **alternative**: a character string describing the alternative hypothesis.
- **conf.level**: confidence level of the confidence interval.
- **results**: a data.frame containing the results of function `wilcox.exact`

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

See Also

`wilcox.exact`, `pairwise.wilcox.test`

Examples

```r
set.seed(13)
x <- rnorm(100)
g <- factor(sample(1:4, 100, replace = TRUE))
levels(g) <- c("a", "b", "c", "d")
pairwise.wilcox.exact(x, g)
## in contrast to
pairwise.wilcox.test(x, g)
```
Description

Performs one and two sample permutation t-tests on vectors of data.

Usage

perm.t.test(x, ...)

## Default S3 method:
perm.t.test(x, y = NULL,
alternative = c("two.sided", "less", "greater"),
mu = 0, paired = FALSE, var.equal = FALSE,
conf.level = 0.95, R = 9999, symmetric = TRUE, ...)

## S3 method for class 'formula'
perm.t.test(formula, data, subset, na.action, ...)

Arguments

x a (non-empty) numeric vector of data values.
y an optional (non-empty) numeric vector of data values.
alternative a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
mu a number indicating the true value of the mean (or difference in means if you are performing a two sample test).
paired a logical indicating whether you want a paired t-test.
var.equal a logical variable indicating whether to treat the two variances as being equal. If TRUE then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.
conf.level confidence level of the interval.
R number of (Monte-Carlo) permutations.
symmetric a logical variable indicating whether to assume symmetry in the two-sided test. If TRUE then the symmetric permutation p value otherwise the equal-tail permutation p value is computed.
formula a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs a factor with two levels giving the corresponding groups.
data an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset an optional vector specifying a subset of observations to be used.
perm.t.test

na.action a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
...

Details

The implemented test corresponds to the proposal of Chapter 15 of Efron and Tibshirani (1993) for equal variances as well as Janssen (1997) respectively Chung and Romano (2013) for unequal variances.

The function returns permutation p values and confidence intervals as well as the results of the t-test without permutations.

The formula interface is only applicable for the 2-sample tests.

alternative = "greater" is the alternative that x has a larger mean than y.

If paired is TRUE then both x and y must be specified and they must be the same length. Missing values are silently removed (in pairs if paired is TRUE). If var.equal is TRUE then the pooled estimate of the variance is used. By default, if var.equal is FALSE then the variance is estimated separately for both groups and the Welch modification to the degrees of freedom is used.

If the input data are effectively constant (compared to the larger of the two means) an error is generated.

Value

A list with class "perm.htest" (derived from class htest) containing the following components:

- statistic the value of the t-statistic.
- parameter the degrees of freedom for the t-statistic.
- p.value the p-value for the test.
- perm.p.value the (Monte-Carlo) permutation p-value for the test.
- conf.int a confidence interval for the mean appropriate to the specified alternative hypothesis.
- perm.conf.int a (Monte-Carlo) permutation percentile confidence interval for the mean appropriate to the specified alternative hypothesis.
- estimate the estimated mean or difference in means depending on whether it was a one-sample test or a two-sample test.
- perm.estimate (Monte-Carlo) permutation estimate.
- null.value the specified hypothesized value of the mean or mean difference depending on whether it was a one-sample test or a two-sample test.
- stderr the standard error of the mean (difference), used as denominator in the t-statistic formula.
- perm.stderr (Monte-Carlo) permutation standard error.
- alternative a character string describing the alternative hypothesis.
- method a character string indicating what type of t-test was performed.
- data.name a character string giving the name(s) of the data.
Note
Code and documentation are for large parts identical to function \texttt{t.test}.

References

See Also
\texttt{t.test}, \texttt{meanCI}, \texttt{meanDiffCI}, \texttt{boot.t.test}

Examples
```r
require(graphics)
t.test(1:10, y = c(7:20))  # P = .0001855
perm.t.test(1:10, y = c(7:20))

t.test(1:10, y = c(7:20, 200))  # P = .1245  -- NOT significant anymore
perm.t.test(1:10, y = c(7:20, 200))  # perm.conf.int affected by outlier!

## Classical example: Student's sleep data
plot(extra ~ group, data = sleep)
## Traditional interface
with(sleep, t.test(extra[group == 1], extra[group == 2]))
with(sleep, perm.t.test(extra[group == 1], extra[group == 2]))
## Formula interface
t.test(extra ~ group, data = sleep)
perm.t.test(extra ~ group, data = sleep)
```

quantileCI

\textit{Confidence Intervals for Quantiles}

Description
These functions can be used to compute confidence intervals for quantiles (including median).

Usage
```r
quantileCI(x, prob = 0.5, conf.level = 0.95, method = "exact",
          R = 9999, bootci.type = c("norm", "basic", "perc", "bca"),
          na.rm = FALSE, alternative = c("two.sided", "less", "greater"), ...)
medianCI(x, conf.level = 0.95, method = "exact",
```
quantileCI

R = 9999, bootci.type = c("norm", "basic", "perc", "bca"),
na.rm = FALSE, alternative = c("two.sided", "less", "greater"), ...)
madCI(x, conf.level = 0.95, method = "exact",
R = 9999, bootci.type = c("norm", "basic", "perc", "bca"),
na.rm = FALSE, constant = 1.4826,
alternative = c("two.sided", "less", "greater"), ...)

Arguments

x numeric data vector
prob quantile
conf.level confidence level
method character string specifying which method to use; see details.
R number of bootstrap replicates.
bootci.type type of bootstrap interval; see boot.ci.
na.rm logical, remove NA values.
constant scale factor (see mad).
alternative a character string specifying one- or two-sided confidence intervals. Must be one of "two.sided" (default), "greater" or "less" (one-sided intervals). You can specify just the initial letter.
... further arguments passed to function boot, e.g. for parallel computing.

Details

The exact confidence interval (method = "exact") is computed using binomial probabilities; see Section 6.8.1 in Sachs and Hedderich (2009). If the result is not unique, i.e. there is more than one interval with coverage probability closest to conf.level, then a matrix of confidence intervals is returned.

The asymptotic confidence interval (method = "asymptotic") is based on the normal approximation of the binomial distribution; see Section 6.8.1 in Sachs and Hedderich (2009).

In case of discrete data, there are alternative bootstrap approaches that might give better results; see Jentsch and Leucht (2016).

Value

A list with components

estimate the sample quantile.
CI a confidence interval for the sample quantile.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>
References


See Also

quantile

Examples

``` r
## To get a non-trivial exact confidence interval for the median
## one needs at least 6 observations
set.seed(123)
x <- rnorm(8)
## exact confidence interval not unique
medianCI(x)
madCI(x)

## asymptotic confidence interval
medianCI(x, method = "asymptotic")
madCI(x, method = "asymptotic")

## bootstrap confidence interval
x <- rnorm(50)
medianCI(x)
medianCI(x, method = "asymptotic")
## (R = 999 to reduce computation time for R checks)
medianCI(x, method = "boot", R = 999)

madCI(x)
madCI(x, method = "asymptotic")
## (R = 999 to reduce computation time for R checks)
madCI(x, method = "boot", R = 999)

## confidence interval for quantiles
quantileCI(x, prob = 0.25)
quantileCI(x, prob = 0.25, method = "asymptotic")

quantileCI(x, prob = 0.75)
## (R = 999 to reduce computation time for R checks)
quantileCI(x, prob = 0.75, method = "boot", R = 999)

## one-sided
quantileCI(x, prob = 0.75, alternative = "greater")
medianCI(x, alternative = "less", method = "asymptotic")
madCI(x, alternative = "greater", method = "boot", R = 999)

## parallel computing for bootstrap
medianCI(x, method = "boot", R = 9999, parallel = "multicore")
```
Description

Test whether two or more samples have the same locations in a repeated measures setting.

Usage

```r
rm.oneway.test(x, g, id, method = "aov")
```

Arguments

- `x`: numeric, response (outcome, dependent) variable.
- `g`: factor, grouping (independent) variable.
- `id`: factor, subject id (blocking variable).
- `method`: name of method, possible methods are "aov", "lme", "friedman", "quade"

Details

The function wraps the functions `aov`, `lme`, `friedman.test` and `quade.test` into one function for a repeated measures one-way layout.

Value

A list with class "htest" containing the following components:

- `statistic`: the value of the test statistic.
- `parameter`: the degrees of freedom of the exact or approximate F distribution of the test statistic.
- `p.value`: the p-value of the test.
- `method`: a character string indicating the test performed.
- `data.name`: a character string giving the names of the data.

References


**See Also**

`aov, lme, friedman.test, quade.test`

**Examples**

```r
set.seed(123)
outcome <- c(rnorm(10), rnorm(10, mean = 1.5), rnorm(10, mean = 1))
timepoints <- factor(rep(1:3, each = 10))
patients <- factor(rep(1:10, times = 3))
rm.oneway.test(outcome, timepoints, patients)
rm.oneway.test(outcome, timepoints, patients, method = "lme")
rm.oneway.test(outcome, timepoints, patients, method = "friedman")
rm.oneway.test(outcome, timepoints, patients, method = "quade")
```

---

### Volcano Plots

#### Description

Produce volcano plot(s) of the given effect size and p values.

#### Usage

```r
volcano(x, ...)  
```

#### Arguments

- `x` in case of default method: measure of effect size.
- `pval` numeric, (adjusted) p values.
- `effect0` single numeric, value for no effect.
- `sig.level` single numeric, significance level.
- `effect.low` NULL or single numeric, boundary for low effect sizes.
- `effect.high` NULL or single numeric, boundary for low effect sizes.
color.low  color used if effect size smaller than effect.low and (adjusted) p value smaller than sig.level.
color.high  color used if effect size larger than effect.high and (adjusted) p value smaller than sig.level.
xlab  label of x-axis.
ylab  label of y-axis.
title  title of plot.
alpha  bleeding factor (default: no blending.
shape  point shape used.
na.rm  logical, remove NA values before plotting.
...  further arguments that may be passed through).

Details

The plot generates a ggplot2 object that is shown.

Missing values are handled by the ggplot2 functions.

Value

Object of class gg and ggplot.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References


Examples

## Generate some data
x <- matrix(rnorm(1000, mean = 10), nrow = 10)
g1 <- rep("control", 10)
y1 <- matrix(rnorm(500, mean = 11.75), nrow = 10)
y2 <- matrix(rnorm(500, mean = 9.75, sd = 3), nrow = 10)
g2 <- rep("treatment", 10)
group <- factor(c(g1, g2))
Data <- rbind(x, cbind(y1, y2))
pvals <- apply(Data, 2, function(x, group) hsu.t.test(x ~ group)$p.value,
                   group = group)
## compute log-fold change
logfc <- function(x, group){
  res <- tapply(x, group, mean)
  log2(res[1]/res[2])
}
lfcs <- apply(Data, 2, logfc, group = group)
volcano(lfcs, pvals, xlab = "log-fold change")
volcano(lfcs, pvals, effect.low = -0.25, effect.high = 0.25,
  xlab = "log-fold change")
volcano(lfcs, p.adjust(pvals, method = "fdr"),
  effect.low = -0.25, effect.high = 0.25,
  xlab = "log-fold change", ylab = "-log10(adj. p value)"
volcano(2^lfcs, pvals, effect0 = 1, effect.low = 1/2*0.25, effect.high = 2*0.25,
  xlab = "mean difference")
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