Package 'LearnNonparam'

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Title 'R6'-Based Flexible Framework for Permutation Tests

Version 1.2.9

Description Implements non-parametric tests from Higgins (2004, ISBN:0534387756), including tests for one sample, two samples, k samples, paired comparisons, blocked designs, trends and association. Built with 'Rcpp' for efficiency and 'R6' for flexible, object-oriented design, the package provides a unified framework for performing or creating custom permutation tests.

BugReports https://github.com/qddyy/LearnNonparam/issues

URL https://github.com/qddyy/LearnNonparam, https://qddyy.github.io/LearnNonparam/

License GPL (>= 2)

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`AnsariBradley` *Ansari-Bradley Test*

Description

Performs Ansari-Bradley test on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `AnsariBradley`

Methods

Public methods:

- `AnsariBradley$new()`

Method `new()`**:** Create a new `AnsariBradley` object.

Usage:

```
AnsariBradley$new(
  type = c("permu", "asymp"),
  alternative = c("two_sided", "less", "greater"),
  n_permu = 10000
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`alternative` a character string specifying the alternative hypothesis.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `AnsariBradley` object.

Examples

```
pmt(
    "twosample.ansari",
    alternative = "greater", n_permu = 0
)$test(Table2.8.1)$print()
```

CDF *Inference on Cumulative Distribution Function*

Description

Performs statistical inference on population cumulative distribution function.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::OneSampleTest` -> `CDF`

Methods

Public methods:

- `CDF$new()`
- `CDF$plot()`

Method `new()`**:** Create a new `CDF` object.

Usage:

```
CDF$new(method = c("binomial", "dkw"), conf_level = 0.95)
```

Arguments:

`method` a character string specifying whether to use a confidence band based on the binomial distribution or the Dvoretzky–Kiefer–Wolfowitz inequality.

`conf_level` a number specifying confidence level of the confidence bounds.

Returns: A `CDF` object.

Method `plot()`**:** Plot the estimate and confidence bounds for population cumulative distribution function.

Usage:

```
CDF$plot(style = c("graphics", "ggplot2"))
```

Arguments:

`style` a character string specifying which package to use.

Returns: The object itself (invisibly).

Examples

```
pmt("onesample.cdf")$test(Table1.2.1)$plot(style = "graphic")
```

ChiSquare *Chi-Square Test on Contingency Table*

Description

Performs chi-square test on contingency tables.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::ContingencyTableTest` -> `ChiSquare`

Methods

Public methods:

- `ChiSquare$new()`

Method `new()`**:** Create a new `ChiSquare` object.

Usage:

```
ChiSquare$new(type = c("permu", "asymp"), n_permu = 10000)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `ChiSquare` object.

Examples

```
t <- pmt(
    "table.chisq", n_permu = 0
)$test(Table5.4.2)$print()

t$type <- "asymp"
t
```

ContingencyTableTest *ContingencyTableTest Class*

Description

Abstract class for tests on contingency tables.

Super class

`LearnNonparam::PermuTest` -> `ContingencyTableTest`

Correlation *Test for Association Between Paired Samples*

Description

Performs correlation coefficient based two-sample association test on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `LearnNonparam::TwoSamplePairedTest` -> `LearnNonparam::TwoSampleAssociationTest` -> `Correlation`

Methods

Public methods:

- `Correlation$new()`

Method `new()`**:** Create a new `Correlation` object.

Usage:

```
Correlation$new(
  type = c("permu", "asymp"),
  method = c("pearson", "kendall", "spearman"),
  alternative = c("two_sided", "less", "greater"),
  n_permu = 10000
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`method` a character string specifying the correlation coefficient to be used.

`alternative` a character string specifying the alternative hypothesis.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `Correlation` object.

Examples

```
pmt(
    "association.corr", method = "pearson",
    alternative = "greater", n_permu = 10000
)$test(Table5.1.2)$print()

t <- pmt(
    "association.corr", method = "spearman",
    alternative = "two_sided", n_permu = 10000
)$test(Table5.1.2)$print()

t$type <- "asymp"
```

```
t

t <- pmt(
    "association.corr", method = "kendall",
    alternative = "greater", n_permu = 0
)$test(Table5.2.2)$print()

t$type <- "asymp"
t
```

`Difference` *Two-Sample Test Based on Mean or Median*

Description

Performs mean/median based two-sample test on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `LearnNonparam::TwoSampleLocationTest` -> `Difference`

Methods

Public methods:

- `Difference$new()`

Method `new()`**:** Create a new `Difference` object.

Usage:

```
Difference$new(
  method = c("mean", "median"),
  alternative = c("two_sided", "less", "greater"),
  null_value = 0,
  n_permu = 10000
)
```

Arguments:

`method` a character string specifying whether to use the mean or the median.

`alternative` a character string specifying the alternative hypothesis.

`null_value` a number indicating the true value of the location shift.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `Difference` object.

Examples

```
pmt(
    "twosample.difference", method = "mean",
    alternative = "greater", n_permu = 0
)$test(Table2.1.1)$print()$plot(
    style = "graphic", breaks = seq(-20, 25, length.out = 9)
)

pmt(
    "twosample.difference", method = "mean",
    alternative = "greater", n_permu = 1000
)$test(Table2.3.1)$print()
```

`Friedman` *Friedman Test*

Description

Performs Friedman test on samples collected in a randomized complete block design.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::RCBDTest` -> `Friedman`

Methods

Public methods:

- `Friedman$new()`

Method `new()`**:** Create a new `Friedman` object.

Usage:

```
Friedman$new(type = c("permu", "asymp"), n_permu = 10000)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `Friedman` object.

Examples

```
t <- pmt(
    "rcbd.friedman", n_permu = 0
)$test(Table4.5.3)$print()

t$type <- "asymp"
t
```

JonckheereTerpstra *Jonckheere-Terpstra Test*

Description

Performs Jonckheere-Terpstra test on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::KSampleTest` -> `JonckheereTerpstra`

Methods

Public methods:

- `JonckheereTerpstra$new()`

Method `new()`**:** Create a new `JonckheereTerpstra` object.

Usage:

```
JonckheereTerpstra$new(
  type = c("permu", "asymp"),
  alternative = c("two_sided", "less", "greater"),
  n_permu = 10000
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`alternative` a character string specifying the alternative hypothesis.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `JonckheereTerpstra` object.

Examples

```
t <- pmt(
    "ksample.jt", alternative = "greater"
)$test(Table3.4.1)$print()

t$type <- "asymp"
t
```

KolmogorovSmirnov *Two-Sample Kolmogorov-Smirnov Test*

Description

Performs two-sample Kolmogorov-Smirnov test on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `KolmogorovSmirnov`

Methods

Public methods:

- `KolmogorovSmirnov$new()`

Method `new()`**:** Create a new `KolmogorovSmirnov` object.

Usage:

```
KolmogorovSmirnov$new(n_permu = 10000)
```

Arguments:

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `KolmogorovSmirnov` object.

Examples

```
pmt(
    "twosample.ks", n_permu = 0
)$test(Table2.8.1)$print()
```

KruskalWallis *Kruskal-Wallis Test*

Description

Performs Kruskal-Wallis test on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::KSampleTest` -> `KruskalWallis`

Methods

Public methods:

- KruskalWallis$new()

Method `new()`**:** Create a new `KruskalWallis` object.

Usage:

```
KruskalWallis$new(
  type = c("permu", "asymp"),
  scoring = c("rank", "vw", "expon"),
  n_permu = 10000
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`scoring` a character string specifying the scoring system.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `KruskalWallis` object.

Examples

```
pmt(
    "ksample.kw", type = "asymp"
)$test(Table3.2.2)$print()

t <- pmt(
    "ksample.kw", type = "permu"
)$test(Table3.2.3)$print()

t$type <- "asymp"
t
```

`KSampleTest` *KSampleTest Class*

Description

Abstract class for k-sample tests.

Super class

`LearnNonparam::PermuTest` -> `KSampleTest`

MultipleComparison *MultipleComparison Class*

Description

Abstract class for multiple comparisons.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::KSampleTest` -> `MultipleComparison`

OneSampleTest *OneSampleTest Class*

Description

Abstract class for one-sample tests.

Super class

`LearnNonparam::PermuTest` -> `OneSampleTest`

Methods

Public methods:

- `OneSampleTest$plot()`

Method `plot()`:

Usage:

```
OneSampleTest$plot(...)
```

Arguments:

`...` ignored.

OneWay *One-Way Test for Equal Means*

Description

Performs F statistic based one-way test on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::KSampleTest` -> `OneWay`

Methods

Public methods:

- `OneWay$new()`

Method `new()`**:** Create a new `OneWay` object.

Usage:

```
OneWay$new(type = c("permu", "asymp"), n_permu = 10000)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `OneWay` object.

Examples

```
t <- pmt(
    "ksample.oneway", n_permu = 0
)$test(Table3.1.2)$print()

t$type <- "asymp"
t
```

Page *Page Test*

Description

Performs Page test on samples collected in a randomized complete block design.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::RCBDTest` -> `Page`

Methods

Public methods:

- `Page$new()`

Method `new()`**:** Create a new `Page` object.

Usage:

```
Page$new(
  type = c("permu", "asymp"),
  alternative = c("two_sided", "less", "greater"),
  n_permu = 10000
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`alternative` a character string specifying the alternative hypothesis.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `Page` object.

Examples

```
t <- pmt(
    "rcbd.page", alternative = "less"
)$test(Table4.4.3)$print()

t$type <- "asymp"
t
```

PairedDifference *Paired Comparison Based on Differences*

Description

Performs differences based paired comparison on samples.

Super classes

LearnNonparam::PermuTest -> LearnNonparam::TwoSampleTest -> LearnNonparam::TwoSamplePairedTest -> PairedDifference

Active bindings

`correct` Whether to apply continuity correction when `scoring` is set to `"rank"`.

Methods

Public methods:

- `PairedDifference$new()`

Method `new()`**:** Create a new `PairedDifference` object.

Usage:

```
PairedDifference$new(
  type = c("permu", "asymp"),
  method = c("with_zeros", "without_zeros"),
  scoring = c("none", "rank", "vw", "expon"),
  alternative = c("two_sided", "less", "greater"),
  null_value = 0,
  n_permu = 10000,
  correct = TRUE
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`method` a character string specifying the method of ranking data in computing adjusted signed scores for tied data, must be one of `"with_zeros"` (default) or `"without_zeros"`.

`scoring` a character string specifying the scoring system.

`alternative` a character string specifying the alternative hypothesis.

`null_value` a number indicating the true value of the location shift.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

`correct` a logical indicating whether to apply continuity correction in the normal approximation for the p-value when `scoring` is set to `"rank"`.

Returns: A `PairedDifference` object.

Examples

```
pmt(
    "paired.difference",
    alternative = "greater", scoring = "none", n_permu = 0
)$test(Table4.1.1)$print()

pmt(
    "paired.difference", n_permu = 0
)$test(Table4.1.3)$print()

t <- pmt(
    "paired.difference", scoring = "rank",
    alternative = "greater", n_permu = 0
)$test(Table4.1.1)$print()

t$type <- "asymp"
t
```

`PermuTest` *PermuTest Class*

Description

Abstract class for permutation tests.

Active bindings

`type` The way to calculate the p-value.

`method` The method used.

`scoring` The scoring system used.

`alternative` The alternative hypothesis.

`null_value` The hypothesized value of the parameter in the null hypothesis.

`conf_level` The confidence level of the interval.

`n_permu` The number of permutations used.

`data` The data.

`statistic` The test statistic.

`p_value` The p-value.

`estimate` The estimated value of the parameter.

`conf_int` The confidence interval of the parameter.

Methods

Public methods:

- `PermuTest$test()`
- `PermuTest$print()`
- `PermuTest$plot()`

Method `test()`**:** Perform test on sample(s).

Usage:

```
PermuTest$test(...)
```

Arguments:

`...` sample(s). Can be numeric vector(s) or a `data.frame` or `list` containing them.

Details: A progress bar is shown by default. Use `options(LearnNonparam.pmt_progress = FALSE)` to disable it.

Returns: The object itself (invisibly).

Method `print()`**:** Print the results of the test.

Usage:

```
PermuTest$print()
```

Returns: The object itself (invisibly).

Method `plot()`**:** Plot histogram(s) of the permutation distribution. Note that this method only works if `type` is set to `"permu"`.

Usage:

```
PermuTest$plot(style = c("graphics", "ggplot2"), ...)
```

Arguments:

`style` a character string specifying which package to use.

`...` passed to `graphics::hist.default()` or `ggplot2::stat_bin()`.

Returns: The object itself (invisibly).

`pmt` *Syntactic Sugar for Object Construction*

Description

Construct test objects in a unified way.

Usage

```
pmt(key, ...)

pmts(
  which = c("all", "onesample", "twosample", "ksample", "multcomp", "paired", "rcbd",
    "association", "table")
)

define_pmt(
  inherit = c("twosample", "ksample", "paired", "rcbd", "association", "table"),
  statistic,
  rejection = c("lr", "l", "r"),
  scoring = "none",
  n_permu = 10000,
  name = "User-Defined Permutation Test",
  alternative = NULL,
  depends = character(),
  plugins = character(),
  includes = character()
)
```

Arguments

key	a character string specifying the test. Check pmts() for valid keys.
...	extra parameters passed to the constructor.
which	a character string specifying the desired tests.
inherit	a character string specifying the type of permutation test.
statistic	definition of the test statistic. See details.
rejection	a character string specifying where the rejection region is.
scoring	one of: - a character string in c("none", "rank", "vw", "expon") specifying the scoring system - a function that takes a numeric vector and returns an equal-length score vector
n_permu	an integer indicating number of permutations for the permutation distribution. If set to 0, all permutations will be used.
name	a character string specifying the name of the test.
alternative	a character string describing the alternative hypothesis.
depends, plugins, includes	passed to Rcpp::cppFunction().

Details

The test statistic can be defined using either R or Rcpp, with the statistic parameter specified as:

- R: a function returning a closure that returns a double.
- Rcpp: a character string defining a captureless lambda (since C++11) returning another lambda that captures by value, accepts parameters of the same type, and returns a double.

The purpose of this design is to pre-calculate certain constants that remain invariant during permutation.

When using Rcpp, the parameters for different `inherit` are listed as follows. Note that the names can be customized, and the types can be replaced with `auto` (thanks to the support for generic lambdas in C++14). See examples.

inherit	Parameter 1	Parameter 2
"twosample"	const NumericVector& sample_1	const NumericVector& sample_2
"ksample"	const NumericVector& combined_sample	const IntegerVector& one_based_group_index
"paired"	const NumericVector& sample_1	const NumericVector& sample_2
"rcbd"	const NumericMatrix& block_as_column_data	
"association"	const NumericVector& sample_1	const NumericVector& sample_2
"table"	const IntegerMatrix& contingency_table	

When using R, the parameters should be the R equivalents of these.

Value

a test object corresponding to the specified key.

a data frame containing keys and corresponding tests implemented in this package.

a test object based on the specified statistic.

Note

- `statistic` should not cause errors or return missing values.
- The data is permuted in-place. Therefore, modifications to the data within `statistic` may lead to incorrect results. Since R has copy-on-modify semantics but C++ does not, it is recommended to pass const references when using Rcpp in `define_pmt`, as shown in the table above.

Examples

```
pmt("twosample.wilcoxon")

pmts("ksample")

x <- rnorm(5)
y <- rnorm(5, 1)

t <- define_pmt(
    inherit = "twosample",
    scoring = base::rank, # equivalent to "rank"
    statistic = function(...) function(x, y) sum(x)
)$test(x, y)$print()

t$scoring <- function(x) qnorm(rank(x) / (length(x) + 1)) # equivalent to "vw"
t$print()
```

```
t$n_permu <- 0
t$print()


r <- define_pmt(
    inherit = "twosample", n_permu = 1e5,
    statistic = function(x, y) {
        m <- length(x)
        n <- length(y)
        function(x, y) sum(x) / m - sum(y) / n
    }
)


rcpp <- define_pmt(
    inherit = "twosample", n_permu = 1e5,
    statistic = "[](const auto& x, const auto& y) {
        auto m = x.length();
        auto n = y.length();
        return [=](const auto& x, const auto& y) {
            return sum(x) / m - sum(y) / n;
        };
    }"
)

# equivalent
# rcpp <- define_pmt(
#     inherit = "twosample", n_permu = 1e5,
#     statistic = "[](const NumericVector& x, const NumericVector& y) {
#         R_xlen_t m = x.length();
#         R_xlen_t n = y.length();
#         return [m, n](const NumericVector& x, const NumericVector& y) -> double {
#             return sum(x) / m - sum(y) / n;
#         };
#     }"
# )

options(LearnNonparam.pmt_progress = FALSE)
system.time(r$test(x, y))
system.time(rcpp$test(x, y))
```

`Quantile` *Quantile Test*

Description

Performs quantile test on a single sample. In addition, an estimation and a confidence interval for the desired quantile will be calculated.

Super classes

LearnNonparam::PermuTest -> LearnNonparam::OneSampleTest -> Quantile

Active bindings

prob The probability associated with the quantile.

correct Whether to apply continuity correction.

Methods

Public methods:

- Quantile$new()

Method new(): Create a new Quantile object.

Usage:

```
Quantile$new(
  type = c("asymp", "exact"),
  alternative = c("two_sided", "less", "greater"),
  null_value = 0,
  conf_level = 0.95,
  prob = 0.5,
  correct = TRUE
)
```

Arguments:

type a character string specifying the way to calculate the p-value.

alternative a character string specifying the alternative hypothesis.

null_value a number indicating the hypothesized value of the quantile.

conf_level a number between zero and one indicating the confidence level to use.

prob a number between zero and one indicating the probability associated with the quantile.

correct a logical indicating whether to apply continuity correction in the normal approximation for the p-value.

Returns: A Quantile object.

Examples

```
pmt(
    "onesample.quantile", prob = 0.5,
    null_value = 75, alternative = "greater",
    type = "asymp", correct = FALSE
)$test(Table1.1.1)$print()

pmt(
    "onesample.quantile",
    prob = 0.25, conf_level = 0.90
)$test(Table1.2.1)$conf_int
```

RatioMeanDeviance *Ratio Mean Deviance Test*

Description

Performs ratio mean deviance test on samples.

Super classes

LearnNonparam::PermuTest -> LearnNonparam::TwoSampleTest -> RatioMeanDeviance

Methods

Public methods:

- RatioMeanDeviance$new()

Method new(): Create a new RatioMeanDeviance object.

Usage:

```
RatioMeanDeviance$new(
  alternative = c("two_sided", "less", "greater"),
  n_permu = 10000
)
```

Arguments:

alternative a character string specifying the alternative hypothesis.

n_permu an integer indicating number of permutations for the permutation distribution. If set to 0, all permutations will be used.

Returns: A RatioMeanDeviance object.

Examples

```
pmt(
    "twosample.rmd",
    alternative = "greater", n_permu = 0
)$test(Table2.8.1)$print()
```

RCBDOneWay *One-Way Test for Equal Means in RCBD*

Description

Performs F statistic based one-way test on samples collected in a randomized complete block design.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::RCBDTest` -> `RCBDOneWay`

Methods

Public methods:

- `RCBDOneWay$new()`

Method `new()`**:** Create a new `RCBDOneWay` object.

Usage:

```
RCBDOneWay$new(type = c("permu", "asymp"), n_permu = 10000)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `RCBDOneWay` object.

Examples

```
t <- pmt(
    "rcbd.oneway", n_permu = 5000
)$test(Table4.4.3)$print()

t$type <- "asymp"
t
```

RCBDTest *RCBDTest Class*

Description

Abstract class for tests on samples collected in randomized complete block designs.

Super class

`LearnNonparam::PermuTest` -> `RCBDTest`

ScoreSum *Two-Sample Test Based on Sum of Scores*

Description

Performs sum of scores based two-sample test on samples. It is almost the same as two-sample wilcoxon rank sum test but uses more scoring systems.

Super classes

LearnNonparam::PermuTest -> LearnNonparam::TwoSampleTest -> LearnNonparam::TwoSampleLocationTest -> ScoreSum

Methods

Public methods:

- ScoreSum$new()

Method `new()`**:** Create a new ScoreSum object.

Usage:

```
ScoreSum$new(
  scoring = c("rank", "vw", "expon"),
  alternative = c("two_sided", "less", "greater"),
  null_value = 0,
  n_permu = 10000
)
```

Arguments:

`scoring` a character string specifying the scoring system.

`alternative` a character string specifying the alternative hypothesis.

`null_value` a number indicating the true value of the location shift.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A ScoreSum object.

Examples

```
pmt(
    "twosample.scoresum", scoring = "expon",
    alternative = "greater", n_permu = 0
)$test(Table2.6.2)$print()
```

SiegelTukey *Siegel-Tukey Test*

Description

Performs Siegel-Tukey test on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `LearnNonparam::TwoSampleLocationTest` -> `LearnNonparam::Wilcoxon` -> `SiegelTukey`

Methods

Public methods:

- `SiegelTukey$new()`

Method `new()`**:** Create a new `SiegelTukey` object.

Usage:

```
SiegelTukey$new(
  type = c("permu", "asymp"),
  alternative = c("two_sided", "less", "greater"),
  n_permu = 10000,
  correct = TRUE
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`alternative` a character string specifying the alternative hypothesis.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

`correct` a logical indicating whether to apply continuity correction in the normal approximation for the p-value.

Returns: A `SiegelTukey` object.

Examples

```
pmt(
    "twosample.siegel",
    alternative = "greater", n_permu = 0
)$test(Table2.8.1)$print()
```

Sign *Two-Sample Sign Test*

Description

Performs two-sample sign test on samples.

Super classes

LearnNonparam::PermuTest -> LearnNonparam::TwoSampleTest -> LearnNonparam::TwoSamplePairedTest -> Sign

Active bindings

`correct` Whether to apply continuity correction.

Methods

Public methods:

- Sign$new()

Method `new()`**:** Create a new Sign object.

Usage:

```
Sign$new(
  type = c("permu", "asymp"),
  alternative = c("two_sided", "less", "greater"),
  n_permu = 10000,
  correct = TRUE
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`alternative` a character string specifying the alternative hypothesis.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

`correct` a logical indicating whether to apply continuity correction in the normal approximation for the p-value.

Returns: A Sign object.

Examples

```
t <- pmt(
    "paired.sign",
    alternative = "greater", n_permu = 0
)$test(
    rep(c(+1, -1), c(12, 5)), rep(0, 17)
)$print()
```

```
t$type <- "asymp"
t
```

`Studentized` *Multiple Comparison Based on Studentized Statistic*

Description

Performs studentized statistic based multiple comparison on samples.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::KSampleTest` -> `LearnNonparam::MultipleComparison` -> `Studentized`

Methods

Public methods:

- `Studentized$new()`

Method `new()`**:** Create a new `Studentized` object.

Usage:

```
Studentized$new(
  type = c("permu", "asymp"),
  method = c("bonferroni", "tukey"),
  scoring = c("none", "rank", "vw", "expon"),
  conf_level = 0.95,
  n_permu = 10000
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`method` a character string specifying whether to use Bonferroni's method or Tukey's HSD method.

`scoring` a character string specifying the scoring system.

`conf_level` a number between zero and one indicating the family-wise confidence level to use.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

Returns: A `Studentized` object.

Examples

```
t <- pmt(
    "multcomp.studentized", method = "bonferroni"
)$test(Table3.3.1)$print()

t$type <- "asymp"
t

t$scoring <- "rank"
t

t$method <- "tukey"
t

t$scoring <- "none"
t

t$type <- "permu"
t
```

`Table1.1.1` *Sodium Contents*

Description

Sodium contents (in mg) of 40 servings of a food product.

Usage

```
Table1.1.1
```

Format

An object of class `numeric` of length 40.

Source

Table 1.1.1

Table1.2.1 *Cycles Until Failure*

Description

The number of cycles (in thousands) that it takes for 20 door latches to fail.

Usage

```
Table1.2.1
```

Format

An object of class `numeric` of length 20.

Source

Table 1.2.1

Table2.1.1 *Test Scores*

Description

Test scores of 7 employees for comparison of methods of instruction.

Usage

```
Table2.1.1
```

Format

An object of class `list` of length 2.

Source

Table 2.1.1

Table2.3.1 *Runoff Minutes*

Description

The numbers of minutes it took to obtain various amounts of runoff on each plot.

Usage

```
Table2.3.1
```

Format

An object of class `data.frame` with 8 rows and 2 columns.

Source

Table 2.3.1

Table2.6.1 *Hours Until Recharge*

Description

The numbers of hours that 2 brands of laptop computers function before battery recharging is necessary.

Usage

```
Table2.6.1
```

Format

An object of class `data.frame` with 4 rows and 2 columns.

Source

Table 2.6.1

Table2.6.2 *Cerium Amounts*

Description

The amounts of cerium measured in samples of granite and basalt.

Usage

```
Table2.6.2
```

Format

An object of class `data.frame` with 6 rows and 2 columns.

Source

Table 2.6.2

Table2.8.1 *Ounces Of Beverage*

Description

The amounts of liquid in randomly selected beverage containers before and after the filling process has been repaired.

Usage

```
Table2.8.1
```

Format

An object of class `data.frame` with 5 rows and 2 columns.

Source

Table 2.8.1

Table3.1.2 *Normal Samples*

Description

Observations randomly sampled from normal populations with means 15, 25 and 30, respectively, and standard deviation 9.

Usage

```
Table3.1.2
```

Format

An object of class `data.frame` with 5 rows and 3 columns.

Source

Table 3.1.2

Table3.2.2 *Logarithms of Bacteria Counts*

Description

Logarithms of counts of bacteria in 4 samples, which respectively were treated with 3 kills and left untreated for the control.

Usage

```
Table3.2.2
```

Format

An object of class `list` of length 4.

Source

Table 3.2.2

Table3.2.3 *Saltiness Scores*

Description

Saltiness scores, on a scale of 1 to 5, assigned by a taste expert to samples of 3 food products that differ in the amounts of soymeal they contain.

Usage

```
Table3.2.3
```

Format

An object of class `list` of length 3.

Source

Table 3.2.3

Table3.3.1 *Percentages of Clay*

Description

The percentages of clay in 6 samples of soil selected from 4 locations.

Usage

```
Table3.3.1
```

Format

An object of class `data.frame` with 6 rows and 4 columns.

Source

Table 3.3.1

Table3.4.1 *Phosphorus Contents*

Description

Phosphorus contents of plants under 4 mowing treatments.

Usage

```
Table3.4.1
```

Format

An object of class `data.frame` with 6 rows and 4 columns.

Source

Table 3.4.1

Table4.1.1 *Caloric Intake*

Description

The estimated daily caloric intake from dietary information provided using 2 methods by a group of college women.

Usage

```
Table4.1.1
```

Format

An object of class `data.frame` with 5 rows and 2 columns.

Source

Table 4.1.1

Table4.1.3 *Cholesterol Reduction*

Description

Reduction in cholesterol after twins were given 2 drugs separately.

Usage

```
Table4.1.3
```

Format

An object of class `data.frame` with 17 rows and 2 columns.

Source

Table 4.1.3

Table4.4.3 *Yield Data*

Description

Yield data for a randomized complete block design in which 4 different types of tractors were used in tilling the soil. The blocking factor is location of the fields.

Usage

```
Table4.4.3
```

Format

An object of class `data.frame` with 4 rows and 6 columns.

Source

Table 4.4.3

Table4.5.3 *Randomized Complete Block with Ties*

Description

A randomized complete block design with 4 treatments and 3 blocks.

Usage

```
Table4.5.3
```

Format

An object of class `data.frame` with 4 rows and 3 columns.

Source

Table 4.5.3

Table5.1.2 *Heterophils and Lymphocytes*

Description

Counts of the heterophils and lymphocytes in blood samples from 18 healthy rabbits.

Usage

```
Table5.1.2
```

Format

An object of class `data.frame` with 18 rows and 2 columns.

Source

Table5.1.2

Table5.2.2 *Scores of Projects*

Description

Scores of 10 projects at a science fair.

Usage

```
Table5.2.2
```

Format

An object of class `data.frame` with 10 rows and 2 columns.

Source

Table5.2.2

Table5.4.2 *Satisfaction with Pain-Relief Treatment*

Description

Patients' responses with 2 methods of relieving postoperative pain.

Usage

```
Table5.4.2
```

Format

An object of class `data.frame` with 2 rows and 3 columns.

Source

Table5.4.2

`TwoSampleAssociationTest` *TwoSampleAssociationTest Class*

Description

Abstract class for two-sample association tests.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `LearnNonparam::TwoSamplePairedTest` -> `TwoSampleAssociationTest`

`TwoSampleLocationTest` *TwoSampleLocationTest Class*

Description

Abstract class for two-sample location tests.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `TwoSampleLocationTest`

`TwoSamplePairedTest` *TwoSamplePairedTest Class*

Description

Abstract class for paired two-sample tests.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `TwoSamplePairedTest`

`TwoSampleTest` *TwoSampleTest Class*

Description

Abstract class for two-sample tests.

Super class

`LearnNonparam::PermuTest` -> `TwoSampleTest`

`Wilcoxon` *Two-Sample Wilcoxon Test*

Description

Performs two-sample wilcoxon test on samples. In addition, an estimation and a confidence interval for the location shift will be calculated.

Super classes

`LearnNonparam::PermuTest` -> `LearnNonparam::TwoSampleTest` -> `LearnNonparam::TwoSampleLocationTest` -> `Wilcoxon`

Active bindings

`correct` Whether to apply continuity correction.

Methods

Public methods:

- `Wilcoxon$new()`

Method `new()`**:** Create a new `Wilcoxon` object.

Usage:

```
Wilcoxon$new(
  type = c("permu", "asymp"),
  alternative = c("two_sided", "less", "greater"),
  null_value = 0,
  conf_level = 0.95,
  n_permu = 10000,
  correct = TRUE
)
```

Arguments:

`type` a character string specifying the way to calculate the p-value.

`alternative` a character string specifying the alternative hypothesis.

`null_value` a number indicating the true value of the location shift.

`conf_level` a number between zero and one indicating the confidence level to use.

`n_permu` an integer indicating number of permutations for the permutation distribution. If set to `0`, all permutations will be used.

`correct` a logical indicating whether to apply continuity correction in the normal approximation for the p-value.

Returns: A `Wilcoxon` object.

Examples

```
pmt(
    "twosample.wilcoxon",
    alternative = "greater", n_permu = 0
)$test(Table2.1.1)$print()

pmt(
    "twosample.wilcoxon",
    alternative = "less", n_permu = 0
)$test(Table2.6.1)$print()

pmt(
    "twosample.wilcoxon", conf_level = 0.90
)$test(Table2.6.2)$conf_int
```

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