

# Package ‘LearnNonparam’

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**Title** 'R6'-Based Flexible Framework for Permutation Tests

**Version** 1.2.4

**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/qddy/LearnNonparam/issues>

**URL** <https://github.com/qddy/LearnNonparam>,  
<https://qddy.github.io/LearnNonparam/>

**License** GPL (>= 2)

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## 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", "asyp"),  
  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()
```

**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(conf_level = 0.95)
```

*Arguments:*

`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	<i>Chi-Square Test on Contingency Table</i>
-----------	---

---

**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", "asyp"), 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 <- "asyp"
t
```

---

ContingencyTableTest	<i>ContingencyTableTest Class</i>
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---

**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", "asyp"),
  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 <- "asyp"
```

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

t$type <- "asypm"
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", "asyp"), 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 <- "asyp"
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", "asyp"),  
  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 <- "asyp"  
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", "asyp"),
  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 = "asyp"
)$test(Table3.2.2)$print()

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

t$type <- "asyp"
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	<i>One-Way Test for Equal Means</i>
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---

## 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", "asyp"), 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 <- "asyp"
t
```

**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", "asyp"),  
  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)  
  
t$type <- "asyp"  
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", "asyp"),
  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 <- "asypm"
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.

*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()` or `ggplot2::stat_bin()`.

*Returns:* The object itself (invisibly).

## 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 <code>pmts()</code> 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 <code>c("none", "rank", "vw", "expon")</code> 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 <code>Rcpp::cppFunction()</code> .

### 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 as const references, and returns a double.

When using Rcpp, the parameters for different `inherit` are listed as follows. Note that the parameter names are for illustration only.

- "twosample": (`Rcpp::NumericVector sample_1`, `Rcpp::NumericVector sample_2`)
- "ksample": (`Rcpp::NumericVector combined_sample`, `Rcpp::IntegerVector one_based_group_index`)

- "paired": (Rcpp::NumericVector sample\_1, Rcpp::NumericVector sample\_2)
- "rcbd": (Rcpp::NumericMatrix block\_as\_column\_data)
- "association": (Rcpp::NumericVector sample\_1, Rcpp::NumericVector sample\_2)
- "table": (Rcpp::IntegerMatrix contingency\_table)

Defining the test statistic using R follows a similar approach. The purpose of this design is to pre-calculate certain constants that remain invariant during permutation.

## 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.

## Examples

```
pmt("twosample.wilcoxon")

pmts("ksample")

x <- rnorm(100)
y <- rnorm(100, 1)

t <- define_pmt(
  inherit = "twosample",
  scoring = base::rank, # equivalent to "rank"
  statistic = function(...) function(x, y) sum(x)
)$test(x, y)$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 = "[[]](NumericVector x, NumericVector y) {
    R_len_t m = x.size();
    R_len_t n = y.size();
    return [=](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("asympt", "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 = "asyp", correct = FALSE
)$test(Table1.1.1)$print()

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

---

RatioMeanDeviance	<i>Ratio Mean Deviance Test</i>
-------------------	---------------------------------

---

**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", "asyp"), 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 <- "asyp"
t
```

RCBDTest

*RCBDTest Class***Description**

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

**Super class**

[LearnNonparam:PermuTest](#) -> RCBDTest

**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", "asyp"),
  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	<i>Two-Sample Sign Test</i>
------	-----------------------------

---

**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", "asyp"),  
  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 <- "asyp"
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", "asyp"),
  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 <- "asyp"
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	<i>Runoff Minutes</i>
------------	-----------------------

---

**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	<i>Hours Until Recharge</i>
------------	-----------------------------

---

**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	<i>Normal Samples</i>
------------	-----------------------

---

**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	<i>Logarithms of Bacteria Counts</i>
------------	--------------------------------------

---

**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	<i>Phosphorus Contents</i>
------------	----------------------------

---

**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	<i>Caloric Intake</i>
------------	-----------------------

---

**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	<i>Cholesterol Reduction</i>
------------	------------------------------

---

**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	<i>Yield Data</i>
------------	-------------------

---

**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	<i>Randomized Complete Block with Ties</i>
------------	--

---

**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	<i>Heterophils and Lymphocytes</i>
------------	------------------------------------

---

**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", "asym"),
  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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