

Package ‘wmwm’

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Title Performs Wilcoxon-Mann-Whitney Test with Missing Data

Version 1.0.0

Description Performs Wilcoxon-Mann-Whitney test in the presence of missing data with controlled Type I error regardless of the values of missing data.

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Depends R ($\geq 3.2.1$)

Imports stats ($\geq 3.2.1$)

Suggests spelling, testthat ($\geq 3.0.0$)

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|-----------|---|
| wmwm.test | <i>Wilcoxon-Mann-Whitney Test in the Presence of Arbitrarily Missing Data</i> |
|-----------|---|

Description

Performs the two-sample Wilcoxon-Mann-Whitney test in the presence of missing data, which controls the Type I error regardless of the values of missing data.

Usage

```
wmwm.test(X, Y, alternative = c("two.sided", "less", "greater"),
  ties = NULL, lower.boundary = -Inf, upper.boundary = Inf,
  exact = NULL, correct = TRUE)
```

Arguments

| | |
|----------------|--|
| X, Y | numeric vectors of data values with potential missing data. Inf and -Inf values will be omitted. |
| 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. |
| ties | a logical indicating whether samples could be tied. <ul style="list-style-type: none"> • If observed samples contain tied samples, ties defaults to TRUE. • If observed samples do not contain tied samples, ties defaults to FALSE. |
| lower.boundary | (when ties is TRUE) a number specifying the lower bound of the data set, must be smaller or equal than the minimum of all observed data. |
| upper.boundary | (when ties is TRUE) a number specifying the upper bound of the data set, must be larger or equal than the maximum of all observed data. |
| exact | a logical indicating whether the bounds should be of an exact p-value. |
| correct | a logical indicating whether the bounds should be of a p-value applying continuity correction in the normal approximation. |

Details

`wmwm.test()` performs the two-sample hypothesis test method proposed in (Zeng et al., 2024) for univariate data when not all data are observed. Bounds of the Wilcoxon-Mann-Whitney test statistic and its p-value will be computed in the presence of missing data. The p-value of the test method proposed in (Zeng et al., 2024) is then returned as the maximum possible p-value of the Wilcoxon-Mann-Whitney test.

By default (if `exact` is not specified), this function returns bounds of an exact p-value if the length of X and Y are both smaller than 50, and there are no tied observations. Otherwise, bounds of a p-value calculated using normal approximation with continuity correction will be returned.

Value

p.value the p-value for the test.

bounds.statistic bounds of the value of the Wilcoxon-Mann-Whitney test statistic.

bounds.pvalue bounds of the p-value of the Wilcoxon-Mann-Whitney test.

alternative a character string describing the alternative hypothesis.

ties.method a character string describing whether samples are considered tied.

description.bounds a character string describing the bounds of the p-value.

data.name a character string giving the names of the data.

References

- Zeng Y, Adams NM, Bodenham DA. On two-sample testing for data with arbitrarily missing values. arXiv preprint arXiv:2403.15327. 2024 Mar 22.
- Mann, Henry B., and Donald R. Whitney. "On a test of whether one of two random variables is stochastically larger than the other." The Annals of Mathematical Statistics (1947): 50-60.
- Lehmann, Erich Leo, and Howard J. D'Abrera. Nonparametrics: statistical methods based on ranks. Holden-day, 1975.

See Also

`stats::wilcox.test()` when data are fully observed.

Examples

```
#### Assume all samples are distinct.
X <- c(6.2, 3.5, NA, 7.6, 9.2)
Y <- c(0.2, 1.3, -0.5, -1.7)

## By default, when the sample sizes of both X and Y are smaller than 50,
## exact distribution will be used.
wmwm.test(X, Y, ties = FALSE, alternative = 'two.sided')

## using normality approximation with continuity correction:
wmwm.test(X, Y, ties = FALSE, alternative = 'two.sided', exact = FALSE, correct = TRUE)

#### Assume samples can be tied.
X <- c(6, 9, NA, 7, 9)
Y <- c(0, 1, 0, -1)

## When the samples can be tied, normality approximation will be used.
## By default, lower.boundary = -Inf, upper.boundary = Inf.
wmwm.test(X, Y, ties = TRUE, alternative = 'two.sided')

## specifying lower.boundary and upper.boundary:
wmwm.test(X, Y, ties = TRUE, alternative = 'two.sided', lower.boundary = -1, upper.boundary = 9)
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