

Package ‘ConcordanceTest’

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Title An Alternative to the Kruskal-Wallis Test Based on the Kendall
Tau Ideas

Version 0.1.0

Description The Concordance Test is a non-parametric method for testing whether two or more samples originate from the same distribution. It extends the Kendall Tau correlation coefficient when there are only two groups. For details, see Monge (2019) <arXiv:1912.12880v1>.

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CT_Coefficient	<i>Concordance Coefficient and Kruskal Wallis Statistic</i>
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Description

This function computes the Concordance Coefficient and Kruskal Wallis Statistic.

Usage

```
CT_Coefficient(Sample_List, H = 0)
```

Arguments

Sample_List	List of numeric data vectors with the elements of each sample.
H	0 by default. If set to 1, the Kruskal Wallis Statistic is also calculated and returned.

Value

The function returns a list with the following elements:

1. Sample_Sizes: Numeric vector of sample sizes.
2. order_elements: Numeric vector containing the elements order.
3. disorder: Disorder of the permutation given by order_elements.
4. Concordance_Coefficient: 1-relative disorder of permutation given by order_elements.
5. H_Statistic: Kruskal Wallis Statistic (only if H = 1).

Examples

```
## Example
A <- c(12,13,15,20,23,28,30,32,40,48)
B <- c(29,31,49,52,54)
C <- c(24,26,44)
Sample_List <- list(A, B, C)
CT_Coefficient(Sample_List)
CT_Coefficient(Sample_List, H = 1)

## Example with ties
A <- c(12,13,15,20,24,29,30,32,40,49)
B <- c(29,31,49,52,54)
C <- c(24,26,44)
Sample_List <- list(A, B, C)
CT_Coefficient(Sample_List, H = 1)
```

CT_Critical_Values	<i>Critical Values of Concordance and Kruskal Wallis Tests. Exact Method</i>
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Description

This function computes the critical values of the Concordance and Kruskal Wallis Tests. Exact p-value of desired significance levels of .10, .05 and .01.

Usage

```
CT_Critical_Values(Sample_Sizes, H = 0)
```

Arguments

Sample_Sizes	Numeric vector (n1,...,nk) containing the number of repetitions of each element, i.e., the size of each sample in the experiment.
H	0 by default. If set to 1, the critical values of the Kruskal-Wallis Test are also calculated and returned.

Value

The function returns a list with the following elements:

1. C_results: Concordance Coefficient results. Critical values and exact p-values for a desired significance levels of 0.1, .05 and .01.
2. H_results: Kruskal Wallis results. Critical values and exact p-values for a desired significance levels of 0.1, .05 and .01 (only if H = 1).

Warning

The number of permutations increases rapidly with lenght (Sets). The computational time increases exponetianly with the number of elements and with the number of sets.

Examples

```
Sample_Sizes <- c(4,4,2)
CT_Critical_Values(Sample_Sizes, H = 1)
```

CT_Critical_Values_Sim

Critical Values of Concordance and Kruskal Wallis Tests. Simulation Method

Description

This function computes the critical values of the Concordance and Kruskal Wallis Tests. Simulated p-value of desired significance levels of .10, .05 and .01.

Usage

```
CT_Critical_Values_Sim(Sample_Sizes, Num_Sim = 10000, H = 0)
```

Arguments

Sample_Sizes	Numeric vector (n1,...,nk) containing the number of repetitions of each element, i.e., the size of each sample in the experiment.
Num_Sim	Number of simulations in order to obtain the probability distribution of the statistic. The default is 10000.
H	0 by default. If set to 1, the critical values of the Kruskal-Wallis Test are also calculated and returned.

Value

The function returns a list with the following elements:

1. C_results: Concordance Coefficient results. Critical values and approximate p-values for a desired significance levels of 0.1, .05 and .01.
2. H_results: Kruskal Wallis results. Critical values and approximate p-values for a desired significance levels of 0.1, .05 and .01 (only if H = 1).

Examples

```
Sample_Sizes <- c(4,4,2)
CT_Critical_Values_Sim(Sample_Sizes, Num_Sim = 1000)
CT_Critical_Values_Sim(Sample_Sizes, Num_Sim = 1000, H = 1)
```

CT_Density_Plot	<i>Density Plot from the Concordance Coefficient and Kruskal Wallis Normalized Statistics</i>
-----------------	---

Description

This function performs the graphical visualization of the density distribution of Concordance Coefficient and Kruskal Wallis Statistic.

Usage

```
CT_Density_Plot(C_freq = NULL, H_freq = NULL)
```

Arguments

C_freq	Frequency and probability distribution of Concordance Coefficient obtained from the functions: CT_Distribution , CT_Distribution_Sim .
H_freq	Frequency and probability distribution of Kruskal Wallis statistic obtained from the functions: CT_Distribution , CT_Distribution_Sim .

Examples

```
Sample_Sizes <- c(5,4)
Distributions <- CT_Distribution(Sample_Sizes, H = 1)
C_freq <- Distributions$C_freq
H_freq <- Distributions$H_freq
CT_Density_Plot(C_freq, H_freq)

Sample_Sizes <- c(5,5,5)
Distributions <- CT_Distribution_Sim(Sample_Sizes, Num_Sim = 1000, H = 1)
C_freq <- Distributions$C_freq
H_freq <- Distributions$H_freq
CT_Density_Plot(C_freq, H_freq)
```

CT_Distribution	<i>Probability Distribution of Concordance Coefficient and Kruskal Wallis Statistic</i>
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Description

This function computes the probability distribution tables of Concordance Coefficient and Kruskal Wallis Statistic.

Usage

```
CT_Distribution(Sample_Sizes, H = 0)
```

Arguments

Sample_Sizes	Numeric vector (n1,...,nk) containing the number of repetitions of each element, i.e., the size of each sample in the experiment.
H	0 by default. If set to 1, the probability distribution table of Kruskal-Wallis Statistic is also calculated and returned.

Value

The function returns a list with the following elements:

1. C_freq: Matrix with the probability distribution of Concordance Coefficient. Each row in the matrix contains the disorder, the value of the statistic, the frequency and its probability.
2. H_freq: Matrix with the probability distribution of Kruskal Wallis Statistic. Each row in the matrix contains the value of the statistic, the frequency and its probability (only if H = 1).

Warning

The number of permutations increases rapidly with lenght (Sets). The computational time increases exponetianly with the number of elements and with the number of sets.

Examples

```
Sample_Sizes <- c(5,4)
CT_Distribution(Sample_Sizes)
CT_Distribution(Sample_Sizes, H = 1)

CT_Distribution(c(3,3,3), H = 1)
```

CT_Distribution_Sim	<i>Simulated Probability Distribution of Concordance Coefficient and Kruskal Wallis Statistic</i>
---------------------	---

Description

This function computes by simulation the probability distribution tables of Concordance Coefficient and Kruskal Wallis Statistic.

Usage

```
CT_Distribution_Sim(Sample_Sizes, Num_Sim = 10000, H = 0)
```

Arguments

Sample_Sizes	Numeric vector (n1,...,nk) containing the number of repetitions of each element, i.e., the size of each sample in the experiment.
Num_Sim	Number of simulations in order to obtain the probability distribution of the statistics. The default is 10000.
H	0 by default. If set to 1, the probability distribution table of Kruskal-Wallis Statistic is also calculated and returned.

Value

The function returns a list with the following elements:

1. C_freq: Matrix with the probability distribution of Concordance Coefficient. Each row in the matrix contains the disorder, the value of the statistic, the frequency and its probability.
2. H_freq: Matrix with the probability distribution of Kruskal Wallis Statistic. Each row in the matrix contains the value of the statistic, the frequency and its probability (only if H = 1).

Examples

```
Sample_Sizes <- c(5,4)
CT_Distribution_Sim(Sample_Sizes, Num_Sim = 1000)
CT_Distribution_Sim(Sample_Sizes, Num_Sim = 1000, H = 1)
```

CT_Hyphotesis_Test	<i>Hypothesis test for testing whether samples originate from the same distribution</i>
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Description

This function performs the hypothesis test for testing whether samples originate from the same distribution.

Usage

```
CT_Hyphotesis_Test(Sample_List, Num_Sim = 10000, H = 0)
```

Arguments

Sample_List	List of numeric data vectors with the elements of each sample.
Num_Sim	The number of used simulations. The default is 10000.
H	0 by default. If set to 1, the Kruskal-Wallis Test is also performed.

Value

The function returns a list with the following elements:

1. results: Table with the statistics and the signification levels.
2. C_p-value: Concordance test signification level.
3. H_p-value: Kruskal Wallis test signification level (only if H = 1).

Examples

```
## Hollander & Wolfe (1973), 116.
## Mucociliary efficiency from the rate of removal of dust in normal
## subjects, subjects with obstructive airway disease, and subjects
## with asbestosis.
x <- c(2.9, 3.0, 2.5, 2.6, 3.2) # normal subjects
y <- c(3.8, 2.7, 4.0, 2.4)      # with obstructive airway disease
z <- c(2.8, 3.4, 3.7, 2.2, 2.0) # with asbestosis
Sample_List <- list(x, y, z)
CT_Hyphotesis_Test(Sample_List, Num_Sim = 1000, H = 1)
```

```
## Example
A <- c(12,13,15,20,23,28,30,32,40,48)
B <- c(29,31,49,52,54)
C <- c(24,26,44)
Sample_List <- list(A, B, C)
CT_Hyphotesis_Test(Sample_List, Num_Sim = 1000, H = 1)
```

```
## Example with ties
A <- c(12,13,15,20,24,29,30,32,40,49)
B <- c(29,31,49,52,54)
C <- c(24,26,44)
Sample_List <- list(A, B, C)
CT_Hyphotesis_Test(Sample_List, Num_Sim = 1000, H = 1)
```

CT_Probability_Plot	<i>Probability Plot for Concordance Coefficient and Kruskal Wallis Statistic</i>
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Description

This function performs the graphical visualization of the probability distribution of Concordance Coefficient and Kruskal Wallis Statistic.

Usage

```
CT_Probability_Plot(C_freq = NULL, H_freq = NULL)
```

Arguments

C_freq	Frequency and probability distribution of Concordance Coefficient obtained from the functions: CT_Distribution , CT_Distribution_Sim .
H_freq	Frequency and probability distribution of Kruskal Wallis statistic obtained from the functions: CT_Distribution , CT_Distribution_Sim .

Examples

```
Sample_Sizes <- c(5,4)
Distributions <- CT_Distribution(Sample_Sizes, H = 1)
C_freq <- Distributions$C_freq
H_freq <- Distributions$H_freq
CT_Probability_Plot(C_freq)
CT_Probability_Plot(C_freq, H_freq)

Sample_Sizes <- c(5,5,5)
Distributions <- CT_Distribution_Sim(Sample_Sizes, Num_Sim = 1000, H = 1)
C_freq <- Distributions$C_freq
H_freq <- Distributions$H_freq
CT_Probability_Plot(C_freq, H_freq)
```

LOP	<i>Linear Ordering Problem (LOP)</i>
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Description

This function computes the solution of the Linear Ordering Problem.

Usage

```
LOP(mat_LOP)
```

Arguments

mat_LOP	Preference matrix defining the Linear Ordering Problem. A numeric square matrix for which we want to obtain the permutation of rows/columns that maximizes the sum of the elements above the main diagonal.
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Value

The function returns a list with the following elements:

1. obj_val: Optimal value of the solution of the Linear Ordering Problem, i.e., the sum of the elements above the main diagonal under the permutation rows/cols solution.
2. permutation: Solution of the Linear Ordering Problem, i.e., the rows/cols permutation.
3. permutation_matrix: Optimal permutation matrix of the Linear Ordering Problem.

References

Martí, R. and Reinelt, G. The Linear Ordering Problem: Exact and Heuristic Methods in Combinatorial Optimization. Springer, first edition 2011.

Examples

```
## Square matrix
##
## | 1  2  2 |
## | 2  3  3 |
## | 3  2  2 |
##
## The optimal permutation of rows/cols is (2,3,1),
## and the solution of the Linear Ordering Problem is 8.
## The permutation matrix of the solution is
## | 0  0  0 |
## | 1  0  1 |
## | 1  0  0 |

mat_LOP <- matrix(c(1,2,3,2,3,2,2,3,2), nrow=3)
LOP(mat_LOP)
```

Permutations_With_Repetition

Enumerate the Permutations of the Elements of a Vector When Some of those Elements are Identical

Description

This function enumerates the possible combinations of n elements where the first element is repeated n_1 times, the second element is repeated n_2 times, the third n_3 times, ...

Usage

```
Permutations_With_Repetition(Sample_Sizes)
```

Arguments

Sample_Sizes Numeric vector (n_1, \dots, n_k) that indicates the number of times each element is repeated.

Value

Returns a matrix where each row contains a permutation.

Warning

The number of permutations increases rapidly with length (Sets). The computational time increases exponentially with the number of elements and with the number of sets.

Examples

```
Sample_Sizes <- c(2,2,2)
Permutations_With_Repetition(Sample_Sizes)
```

```
Sample_Sizes <- c(2,3)
Permutations_With_Repetition(Sample_Sizes)
```

```
Permutations_With_Repetition(c(3,2,3))
```

```
Permutations_With_Repetition(c(10,5))
```

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