The Concordance Test, an Alternative to Kruskal-Wallis Based on the Kendall-τ Distance: An R Package

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Abstract The Kendall rank correlation coefficient, based on the Kendall-τ distance, is used to measure the ordinal association between two measurements. In this paper, we introduce a new coefficient also based on the Kendall-τ distance, the Concordance coefficient, and a test to measure whether different samples come from the same distribution. This work also presents a new R package, **ConcordanceTest**, with the implementation of the proposed coefficient. We illustrate the use of the Concordance coefficient to measure the ordinal association between quantity and quality measures when two or more samples are considered. In this sense, the Concordance coefficient can be seen as a generalization of the Kendall rank correlation coefficient and an alternative to the non-parametric mean rank-based methods for comparing two or more samples. A comparison of the proposed Concordance coefficient and the classical Kruskal-Wallis statistic is presented through a comparison of the exact distributions of both statistics.

1 Introduction

When we have a sample of observations of a given population it may be difficult to assume that they come from a certain distribution since we may not always have any type of information about the variable under study and when we do, it may not be enough to determine the type of distribution. In these cases, parametric inference is inappropriate. Moreover, this type of technique may be unsuitable should the observations not fulfill any of the basic assumptions on which they are based; normality and a large quantity of data.

Violation of the necessary assumptions in parametric statistics necessitates the use of non-parametric statistics. Non-parametric tests do not depend on the definition of a distribution function or statistical parameters such as mean, variance, etc. The use of non-parametric tests, despite being less powerful, is also adequate when there are not enough observations available, when data are non-normal data or when ordinal data are being analyzed.

Although the first steps in non-parametric statistics began earlier, it was not until the 1930s that a systematic study in this field appeared. Fisher (1935) introduced the permutation test or randomization test as a simple way to compute the sampling distribution for any test statistic under the null hypothesis that does not establish any effect on all possible outcomes. Over the next two decades some of the main non-parametric tests emerged, Friedman (1940); Kendall and Smith (1939); Kendall (1938); Kruskal (1958); Kruskal and Wallis (1952); Mann and Whitney (1947); Pitman (1937); Wilcoxon (1945), among others.

The main advantages of the non-parametric tests are: the data can be nonnumerical observations while they can be classified according to some criterion, they are usually easy to calculate and do not make any hypothesis about the distribution of the population from which the samples are taken. We can also cite two drawbacks: the non-parametric tests are less precise than other statistical models and they are based on the order of the elements in the sample and this order will likely stay the same even if the numerical data change.

There are many non-parametric tests in the literature, which can basically be classified into four categories depending on whether: it is a test to compare two or more than two related samples or a test for comparing related or unrelated samples. Examples of the most used non-parametric tests in the literature for each of these four situations are the following: the *Wilcoxon signed-rank test* (Wilcoxon, 1945) for comparing two related samples, the *Mann-Whitney (Wilcoxon) test* (Mann and Whitney, 1947) for comparing two unrelated samples, the *Friedman test* (Friedman, 1940) for comparing three or more related samples, and the *Kruskal-Wallis test* (Kruskal and Wallis, 1952) for comparing three or more unrelated samples. Several methods that exploit some characteristic of the samples have appeared in the literature in recent years, such as Alhakim and Hooper (2008); Terpstra and Magel (2003).

It is also possible to measure the degree of association of two variables through a non-parametric approach, in that sense we can mention the Kendall rank correlation coefficient (Kendall, 1938) and the Spearman rank correlation coefficient (Spearman, 1904).

In Aparicio et al. (2020), the authors introduce the *Kendall-τ partition ranking*; given a ranking of elements of a set and given a disjoint partition of the same set, the Kendall-τ partition ranking is the

induced linear order of the subsets of the partition which follows from the given ranking of elements of a set. In this work, we propose to use the Kendall-τ distance as a concordance measure between the different samples in an ordered set of observations. In this regard, the proposed measure, which we call *Concordance coefficient*, can be considered as an extension of the Kendall rank correlation coefficient when more than two samples are considered. The main difference between the proposed measure and the previous ones, is the consideration of the Kendall-τ distance instead of ranks, which use classical methods. We also propose a significance test in order to determine when more than two samples come from the same distribution, and present a comparison with the classical Kruskal-Wallis method. We illustrate the use of the proposed coefficient with a new R package, **ConcordanceTest** (Alcaraz et al., 2022), which is freely available from the Comprehensive R Archive Network (CRAN). Actually, R establishes the state of the art in statistical software. There are currently packages for all the non-parametric tests mentioned above, for example: the **Kendall** package (McLeod, 2011), which deals with the Kendall rank correlation coefficient; the **pspearman** package (Savicky, 2014), with the Spearman rank correlation coefficient; or the **stats** package: an R Core Team and contributors' worldwide package that contains many of the non-parametric tests for comparing two or more, related or unrelated, samples. The Kendall-τ distance, on which the proposed coefficient is based, is one of the most used in distance-based models, for which there are also recent alternatives in R. See, for example, the **PerMallows** (Irurozki et al., 2016), **rankdist** (Qian and Yu, 2019) or **BayesMallows** packages (Sorensen et al., 2020).

The remainder of this paper is organized as follows. After a brief review in the next section of the main features of the Kendall rank correlation coefficient and the Kruskal-Wallis statistic, in the following two sections we present the coefficient we propose in this work and illustrate its use with our **ConcordanceTest** package. Specifically, in the third section we introduce the Concordance coefficient while in the fourth section the related statistical test is presented. The fifth section includes a comparison between the Kruskal-Wallis test in the **stats** package and that presented in this work. Some final remarks follow in the last section. Appendix A presents an example of the probability distribution of the Concordance coefficient and the Kruskal-Wallis statistic. Appendix B deals with a comparison between the probability density function of the Concordance coefficient and the Kruskal-Wallis statistic for several experiments. Finally, Appendix C presents some details of how the p-values for the Concordance coefficient have been calculated and shows some critical values and exact p-values.

2 Non-parametric tests

This section presents the Kendall rank correlation coefficient (Kendall, 1938), a coefficient to measure the relationship between two samples ordinally, and the Kruskal-Wallis statistical test (Kruskal and Wallis, 1952), which is a rank-based statistical test to measure whether different samples come from the same distribution, without assuming a given distribution for the population.

Only these two non-parametric tests are presented in detail, since the test proposed in this paper uses the Kendall-τ distance and it can be seen as an extension of the Kendall rank correlation coefficient when more than two samples are considered, and it is presented as an alternative to the Kruskal-Wallis statistical test.

The Kendall rank correlation coefficient is a non-parametric measure of correlation. This measure is based on the Kendall-τ distance between two permutations of n elements. The Kendall-τ distance ($d_{K-\tau}$) is defined as the number or pairwise disagreements between two permutations π_1 and π_2. For instance, if we have three elements, the distance from permutation 123 to permutations 132, 231 and 321 is 1, 2 and 3 respectively. The maximum number of disagreements that may occur between two permutations of n elements is $n(n-1)/2$ and, in this case, all the values of permutation π_1 are in the reverse order of π_2.

The Kendall rank correlation coefficient between permutations π_1 and π_2, denoted by τ, is defined by

$$\tau = 1 - 2\frac{d_{K-\tau(\pi_1,\pi_2)}}{n(n-1)/2}.$$

The Kendall rank correlation coefficient is used as a statistical test to determine whether there is a relationship or dependence between two random variables. The main advantages of this coefficient are: the data can be non-numerical observations if they can be ordered, it is easy to calculate, and the associated statistical test does not assume a known distribution of the population from which the samples are taken.

The Kruskal-Wallis test is a non-parametric statistical method to study whether different samples come from the same population. The test is the extension of the Mann-Whitney Test (Mann and Whitney, 1947) when we have more than two samples or groups. The following example illustrates the Kruskal-Wallis test when comparing three samples.

Example 1 *Let us assume that the effectiveness of three different treatments (A, B, C) has been measured for 6 individuals, two individuals being assigned to each of the treatments, with the effectiveness of each treatment being measured ordinally. We could obtain the result shown in Table 1, where, for example, the effectiveness of treatment A has been rated in first and third place.*

	A	B	A	C	C	B
Rank	1	2	3	4	5	6

Table 1: Result for an experiment with 6 people and 3 treatments.

The Kruskal-Wallis statistic is determined by the difference between the ranks of the individuals in each category with the average rank. In our example, the average rank of the test is $\overline{R} = 3.5$, while the average rank of each of the three treatments are $\overline{R}_A = 2$, $\overline{R}_B = 4$ and $\overline{R}_C = 4.5$. The Kruskal-Wallis statistic, denoted by H, is based on the calculation of the distance of each rank to the average rank, which can be expressed as follows:

$$H = -3(n+1) + \frac{12}{n(n+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_i},$$

where n is the number of observations in the k samples, n_i is the number of observations in the i-th sample and R_i is the sum of the ranks in the i-th sample. In our example, the value of the Kruskal-Wallis statistic is:

$$H = -3(n+1) + \frac{12}{n(n+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_i} = -3(6+1) + \frac{12}{6(6+1)} \left(\frac{4^2}{2} + \frac{8^2}{2} + \frac{9^2}{2} \right) = 2.$$

Table 2 shows the probability distribution of the Kruskal-Wallis statistic for 3 treatments, each with 2 patients. Appendix A presents the Kruskal-Wallis statistic for all possible results in the experiment for 3 treatments with 2 people in each. In Spurrier (2003), the author compares different methods for approximating the null probability points.

H	Prob
0.00	0.06667
0.29	0.13333
0.86	0.13333
1.14	0.13333
2.00	0.13333
2.57	0.06667
3.43	0.13333
3.71	0.13333
4.57	0.06667

Table 2: Probability distribution for the Kruskal-Wallis statistic (H), with sample sizes $N = (2, 2, 2)$.

3 The Concordance coefficient τ_c

In Aparicio et al. (2020), the authors introduce the *Kendall-τ partition ranking*; given a ranking of elements of a set and given a disjoint partition of the same set, the Kendall-τ partition ranking is the induced linear order of the subsets of the partition which follows from the given ranking of elements of a set. The Kendall-τ partition ranking presents an ordinal alternative to the mean-based ranking that uses a pseudo-cardinal scale. Let π be permutation of the elements of set V and let $V_1, V_2, \ldots, V_k$ be a partition of V then, the Kendall-τ distance from permutation π is given by

$$d_{K\text{-}\tau} = \min\{d_{K\text{-}\tau}(\rho, \pi) : \text{ elements in } V_r \text{ are consecutively listed in } \rho, \ \forall r\}.$$

This distance is also called the disorder of permutation π. For the calculation of the disorder of a permutation of elements, in Aparicio et al. (2020), the authors establish that the distance or disorder of a permutation of elements $\pi = (a|a|b|b|a|c|a|b|c|\cdots|c|a|b)$ is given by the solution of the Linear

Ordering Problem (LOP) with the preference matrix M, where the element m_{ab} of matrix M indicates the number of times that an element a of sample A precedes an element b of sample B in the order π. The solution of the Linear Ordering Problem gives us a new order in the elements of π, the closest to π, in which all the elements belonging to the same sample are listed consecutively. The book publication by Martí and Reinelt (2011) provides an exhaustive study of the Linear Ordering Problem.

The authors Aparicio et al. (2020) present the properties of the Kendall-τ partition ranking and compare it with classical mean and median-based rank approaches. Those properties are extracted from social choice theory and are adapted to a partition ranking, see Arrow (1951); Kemeny (1959); Zahid and Swart (2015). Two of these properties are only true for the Kendall-τ partition ranking: the *Condorcet* and *Deletion Independence* properties. The Condorcet property establishes that the most preferred subset must be listed before any other in any ranking; and the Deletion Independence property establishes that if any subset is removed, then the induced order of subsets does not change. In permutation $\pi = (c|c|c|b|a|a|c|c)$ the set C is a condorcet winner, the most preferred set, but B has a lesser mean rank value than set C if set A is not considered in the comparison; therefore, the permutation $\pi = (c|c|c|b|b|a|a|c|c)$ gives an example where ranking subsets from ranks is not very reliable.

From Aparicio et al. (2020), the maximum number of disagreements that may occur in a permutation of n elements (where the elements are classified in k subsets $V_1, V_2, \ldots, V_k$ of sizes $n_1, n_2, \ldots, n_k$ respectively) is $\sum_{r=1}^{k} \sum_{s=r+1}^{k} n_r n_s - (GP_b + \sum_{r=1}^{k} \sum_{s=r+1}^{k} \lfloor \frac{n_r n_s}{2} \rfloor)$, where GP_b is the Generalized Pentagonal Number of b, and b the number of subsets V_k with odd cardinality. The Generalized Pentagonal number GP_b, for $b \in \mathbb{N}$, is

$$GP_b = \begin{cases} \dfrac{\ell(3\ell - 1)}{2} & b = 2\ell \ (b \text{ even}), \\[2ex] \dfrac{\ell(3\ell + 1)}{2} & b = 2\ell + 1 \ (b \text{ odd}). \end{cases}$$

This maximum number of disagreements (the maximum disorder) in a permutation π of elements, allows us to define a relative disorder coefficient of permutation π as

$$relative\,disorder(\pi) = \frac{d_{K\text{-}\tau}(\pi)}{\sum_{r=1}^{k} \sum_{s=r+1}^{k} n_r n_s - (GP_b + \sum_{r=1}^{k} \sum_{s=r+1}^{k} \lfloor \frac{n_r n_s}{2} \rfloor)}.$$

Definition 1 *We define the Concordance coefficient (τ_c) of permutation π as*

$$\tau_c = 1 - relative\,disorder(\pi) = 1 - \frac{d_{K\text{-}\tau}(\pi)}{\sum_{r=1}^{k} \sum_{s=r+1}^{k} n_r n_s - (GP_b + \sum_{r=1}^{k} \sum_{s=r+1}^{k} \lfloor \frac{n_r n_s}{2} \rfloor)}.$$

The Concordance coefficient (τ_c) provides a measure of independence in the k samples, where τ_c is a value between 0 and 1, taking the value of 1 when there is a total order between the samples, and 0 when the disorder is maximum. In this sense, the Concordance coefficient can be seen as a generalization of the Kendall rank correlation coefficient when we have more than two samples. Given that the Concordance coefficient satisfies the properties mentioned above, we consider it is more appropriate for measuring differences between samples than a rank-based method, such as Kruskal-Wallis'.

Example 1 (Cont.) *Continuing with the data in Example 1, the results of the experiment provide the following order or permutation of the treatments $\pi = (a|b|a|c|c|b|)$.*

Given the order of individuals $\pi = (a|b|a|c|c|b|)$, the ordering between individuals that leaves individuals with the same treatment together is ordination ($a\ a\ b\ b\ c\ c$) or ($a\ a\ c\ c\ b\ b$). Both ordinations only need 3 pairwise disagreements from the permutation π. In order to find the permutation of elements (equal elements listed consecutively) closer to a given permutation, it is sufficient to solve the Linear Ordering Problem (LOP) with the preference matrix defined above. In this example, said matrix is:

$$\begin{array}{c c} & \begin{array}{ccc} A & B & C \end{array} \\ \begin{array}{c} A \\ B \\ C \end{array} & \left(\begin{array}{ccc} - & 3 & 4 \\ 1 & - & 2 \\ 0 & 2 & - \end{array} \right) \end{array},$$

where each element of the matrix m_{ij} represents the number of times an individual of a treatment i precedes an individual of the treatment j. The solution of the LOP is the permutation of treatments which maximizes the preferences of order in the experiment, that is, in this example, the permutations of treatments $(A\ B\ C)$ or $(A\ C\ B)$ retain 9 preferences expressed in the order of individuals represented by the permutation π. Therefore, the distance of the permutation π to a total order between treatments is $\sum_{i<j} n_i n_j - 9 = 3$. This distance, which is the number of pairwise disagreements needed in a permutation of elements to reach a permutation that establishes a total order between treatments, is denominated the disorder of a permutation by the authors of the work by Aparicio et al. (2020)[1].

Then, the relative disorder of permutation π can be evaluated as

$$relative\ disorder(\pi) = \frac{d_{K\text{-}\tau}(\pi)}{\sum_{r=1}^{k}\sum_{s=r+1}^{k} n_r n_s - (GP_b + \sum_{r=1}^{k}\sum_{s=r+1}^{k} \lfloor \frac{n_r n_s}{2} \rfloor)} = \frac{3}{12 - (0 + 6)} = \frac{3}{6} = \frac{1}{2},$$

and the Concordance coefficient

$$\tau_c = 1 - relative\ disorder(\pi) = 1 - \frac{1}{2} = \frac{1}{2}.$$

Notice that no set of this example has odd cardinality, therefore the pentagonal number is $GP_0 = 0$.

Table 3 shows the probability distribution of the disorder and the Concordance coefficient for 3 treatments with 2 patients each. Appendix A presents the disorder and the Concordance coefficient for all possible results in the experiment with sample sizes $N = (2, 2, 2)$. Figure 1 compares the probability distribution of the Concordance coefficient and the Kruskal-Wallis statistic, for 3 treatments and 2 people in each treatment. Notice that some Kruskal-Wallis statistic values (H=2.57) are less probable than large ones.

dis	τ_c	Prob
6	0.0000	0.06667
5	0.1667	0.13333
4	0.3333	0.20000
3	0.5000	0.20000
2	0.6667	0.20000
1	0.8333	0.13333
0	1.0000	0.06667

Table 3: Probability distribution of the disorder (*dis*) and the Concordance coefficient (τ_c), with sample sizes $N = (2, 2, 2)$.
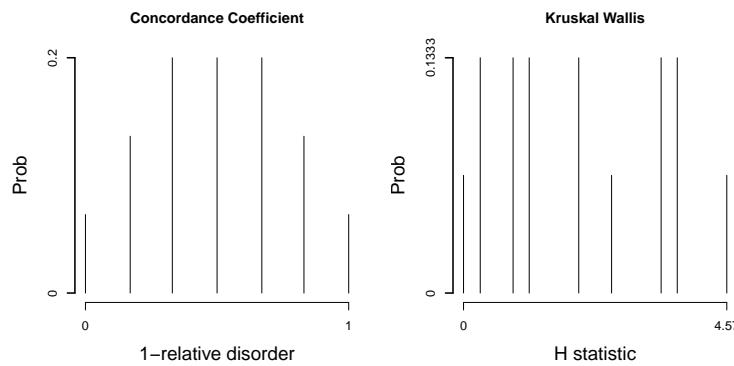
Figure 1: Probability distribution of the Concordance coefficient (τ_c=1-relative disorder) and the Kruskal-Wallis statistic (H), with sample sizes $N = (2, 2, 2)$.

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[1]If the number of samples is small, we can evaluate all the possibilities in order to obtain the solution of the Linear Ordering Problem, for example, if we have 3 samples the number of feasible solutions for the LOP is $3! = 6$.

The Concordance coefficient in ConcordanceTest package

The R package we have developed allows to calculate both the Concordance coefficient and the Kruskal-Wallis statistic in order to facilitate their comparison. Given the high combinatorial degree of the problem of ordering samples of populations, some of the functions implemented in the package can perform the calculations exactly, exploring the entire sample space or possibilities, or they can approximate the sample space or possibilities by simulation.

The **ConcordanceTest** package can be installed from CRAN:

```
install.packages("ConcordanceTest")
library("ConcordanceTest")
```

and its functions can perform the calculations related only to the Concordance coefficient (default option, specified with the parameter H=0) or do them also for the Kruskal-Wallis statistic (H=1), allowing their comparison.

To obtain the probability distribution of the statistics, it is necessary to have the set of all possible permutations that can occur in the result of the experiment that we want to analyze (90=6!/2!2!2! in Example 1). This can be obtained through the function Permutations_With_Repetition(), which has been developed and included in the **ConcordanceTest** package.

The function CT_Distribution() calculates the probability distribution of the Concordance coefficient and the Kruskal-Wallis statistic. The set of possibilities (sample space) grows very quickly with the number of elements and with the number of sets and, in some cases, to calculate the probability distribution in an exact way becomes unaffordable, making it necessary to approximate calculations. Both an exact and an approximate calculation (default option) can be done using the function CT_Distribution(). It is used as follows:

```
CT_Distribution(Sample_Sizes, Num_Sim = 10000, H = 0, verbose = TRUE)
```

where Sample_Sizes is a numeric vector $(n_1, \ldots, n_k)$ containing the number of repetitions of each element, i.e., the size of each sample in the experiment. Num_Sim is the number of simulations to be performed in order to obtain the probability distribution of the statistics (10,000 by default). If Num_Sim is set to 0, the probability distribution tables are obtained exactly using the function Permutations_With_Repetition(). H is the parameter specifying whether the calculations must also be performed for the Kruskal-Wallis statistic, and verbose is a logical parameter that indicates whether some progress report of the simulations should be given.

Example 1 (Cont.) *Using the function* CT_Distribution() *with* Num_Sim *equal to 0, we could obtain the probability distribution of the Kruskal-Wallis statistic and the Concordance coefficient in Example 1 (Tables 2 and 3, respectively) in an exact way. As shown in this example, we can also approximate the probability distributions of Example 1 by simulating, for example, 25,000 permutations of 3 treatments with 2 patients each. Note that, for reproducibility, we always initialize the generator for pseudo-random numbers when the results rely on simulation.*

```
set.seed(12)
Sample_Sizes <- c(2,2,2)
CT_Distribution(Sample_Sizes, Num_Sim = 25000, H = 1)
```

```
$C_freq
     disorder  Concordance coefficient Frequency Probability
[1,]        6                     0.00         6      0.0667
[2,]        5                     0.17        12      0.1333
[3,]        4                     0.33        18      0.2000
[4,]        3                     0.50        18      0.2000
[5,]        2                     0.67        18      0.2000
[6,]        1                     0.83        12      0.1333
[7,]        0                     1.00         6      0.0667


$H_freq
     H Statistic Frequency Probability
[1,]        0.00         6      0.0667
[2,]        0.29        12      0.1333
[3,]        0.86        12      0.1333
[4,]        1.14        12      0.1333
[5,]        2.00        12      0.1333
[6,]        2.57         6      0.0667
```

```
[7,]      3.43      12      0.1333
[8,]      3.71      12      0.1333
[9,]      4.57       6      0.0667
```

The function `CT_Distribution()` returns two elements. `C_freq` is a matrix with the probability distribution of the Concordance coefficient. Each row in the matrix contains the disorder, the value of the Concordance coefficient τ_c, the frequency and its probability. `H_freq` (only returned if `H = 1`) is a matrix with the probability distribution of the Kruskal-Wallis statistic. Each row in the matrix contains the value of the statistic H, the frequency and its probability. The results obtained by the function `CT_Distribution()` are the same as those previously shown in Table 3 and Table 2 of Example 1.

4   Concordance test

In this section, we present the Concordance test in order to evaluate when different samples come from the same population distribution. The randomization test introduced by Fisher (1935) establishes a framework for the statistical test based on permutations, see also Box (1980); Stern (1990); Welch (1990).

If all the samples come from the same distribution, then all possible ways to rank n observations divided into k samples have the same probability of occurring. If a result of the experiment provides an order of the observations with a high disorder, it will support the idea that all observations come from the same population. On the contrary, a result with a small disorder will go against the claim that the observations come from the same population. In this way, we propose to consider samples that come from the same distribution as null hypothesis, while the alternative hypothesis is that some of the samples come from a different distribution.

H_0: There is no difference among the k populations.

H_a: At least one of the populations differs from the other populations.

The decision rule is to reject the null hypothesis if the disorder in the permutation of observations is small, equivalently if the Concordance coefficient τ_c is close to one. We reject the null hypothesis H_0 at the significance level α if τ_c is greater than the percentile $(1 - \alpha)\%$ of the probability distribution of τ_c.

The following example illustrates the use of the Concordance test proposed in this work and compares it with the classical Kruskal-Wallis non-parametric test. The comparison will be made first considering that there are no ties and then modifying the data in the example so that ties appear.

Example 2 *Suppose we have applied three treatments to 18 patients, measuring the number of hours it takes these patients to recover. The results are shown in Table 4.*

	Hours									
Treatment A	12	13	15	20	23	28	30	32	40	48
Treatment B	29	31	49	52	54					
Treatment C	24	26	44							

Table 4: Result for an experiment with 18 patients and 3 treatments.

Concordance test:

The experiment ranks the patients in the following ranking

$$(a\ a\ a\ a\ a\ c\ c\ a\ b\ a\ b\ a\ a\ c\ a\ b\ b\ b).$$

If we perform the contrast using the disorder statistic or the Concordance coefficient τ_c, we must calculate the permutation of treatments that maximizes the order between patients obtained in the experiment. The matrix of preferences between treatments observed is as follows:

$$\begin{array}{c} A \\ B \\ C \end{array} \begin{pmatrix} - & 43 & 19 \\ 7 & - & 2 \\ 11 & 13 & - \end{pmatrix}$$

The order between treatments that maximizes the order between patients corresponds to the order $(A\ C\ B)$, satisfying 75 of the 95 preferences contained in the matrix, where the value 75 is the solution of the Linear Ordering Problem (LOP)[2]. Therefore, exactly 20 = 95-75 is the number of pairwise disagreements necessary to order the samples and obtain the order (ACB), that is, the disorder is 20. The greatest disorder that an order of elements can have with samples of 10, 5 and 3 elements is given by: $\sum_{r=1}^{3}\sum_{s=r+1}^{3} n_r\, n_s - (GP_b + \sum_{r=1}^{3}\sum_{s=r+1}^{3}\lfloor\frac{n_r n_s}{2}\rfloor)) = 95 - (1+47) = 47$, therefore the Concordance coefficient is $\tau_c = 1 - 20/47 = 0.574$. The p-value of the disorder 20 or, equivalently, of the Concordance coefficient $\tau_c = 0.574$ is 0.049272[3], therefore, at a level of significance less than 5% we can reject the null hypothesis of equality in treatments.

Kruskal-Wallis test:

The treatments A, B and C have average ranks of 7.3, 14.2 and 9, respectively, and the sum of ranks are $R_A = 73$, $R_B = 71$ and $R_C = 27$.

The Kruskal-Wallis statistic is given by:

$$H = -3(n+1) + \frac{12}{n(n+1)}\sum\frac{R_i^2}{n_i} = -3(18+1) + \frac{12}{18(18+1)}\left(\frac{73^2}{10} + \frac{71^2}{5} + \frac{27^2}{3}\right) = 5.6$$

In Meyer and Seaman (2015), exact values for the Kruskal-Wallis contrast at different levels of significance are found. We can conclude by looking at the tables that the p-value of the H statistic is greater than 0.05, therefore, we cannot reject the null hypothesis that the treatments are equally effective.

Comparing both methods, the Concordance and Kruskal-Wallis tests provide similar results about the statistic but the conclusion differs.

Example 3 *Suppose we have the same experiment as in Example 2 but with ties. The results are shown in Table 5. Ties are in bold.*

	Hours									
Treatment A	12	13	15	20	**24**	**29**	30	32	40	**49**
Treatment B	**29**	31	**49**	52	54					
Treatment C	**24**	26	44							

Table 5: Result for an experiment with 18 patients and 3 treatments. Example with ties.

Concordance test with ties:

The results of the experiment order the individuals according to the sequence:

$$(a\ a\ a\ a\ (a\ c)\ c\ (a\ b)\ a\ b\ a\ a\ c\ (a\ b)\ b\ b)$$

where the elements grouped in the order indicates that they tie. There are 8 different possibilities in order to undo ties in the ranking of elements. If the same probability is assumed for all of them, the expected preference matrix between treatments is given distributing the preference in the comparison of repeated observations with the same weight, that is, assigning the value 0.5 to each of the treatments when two tied units are compared. The preference matrix for this example would be as follows:

$$\begin{array}{c c} & \begin{array}{ccc} A & B & C \end{array} \\ \begin{array}{c} A \\ B \\ C \end{array} & \left(\begin{array}{ccc} - & 42 & 18.5 \\ 8 & - & 2 \\ 11.5 & 13 & - \end{array}\right) \end{array}$$

Note that the previous matrix represents the matrix of expected preferences if all permutations of items with ties in which they are undone are considered, with the same probability of tie between elements.

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[2]The solution of LOP for this example is the permutation of sets that maximizes the preferences in the preference matrix. It is sufficient to compare the 6 possibilities, $(A\ B\ C) = 64$, $(A\ C\ B) = 75$, $(B\ A\ C) = 28$, $(B\ C\ A) = 20$, $(C\ A\ B) = 67$ and $(C\ B\ A) = 31$.

[3]Tables of p-values for the Concordance coefficient τ_c are in Appendix C.

The order between treatments that maximizes the order between patients, corresponds to the order $(A\ C\ B)$, satisfying 73.5 of the 95 preferences contained in the matrix, where 73.5 is the solution of the Linear Ordering Problem. Therefore, 21.5 = 95-73.5 is the expected number of pairwise disagreements necessary to order the samples and obtain the order $(A\ C\ B)$, that is, the disorder is 21.5 or, equivalently, the Concordance coefficient is $\tau = 1 - 21.5/47 = 0.543$, a value with a significance greater than 0.05, $p - value > 0.05$. In this case, the observed data do not show significant evidence in favor of a difference in the effectiveness of treatments.

Kruskal-Wallis test with ties:

The treatments A, B and C have average ranks of 7.45, 14 and 8.83, respectively, and the sum of ranks are $R_A = 74.5$, $R_B = 70$ and $R_C = 26.5$.

The Kruskal-Wallis statistic is given by:

$$H = -3(n+1) + \frac{12}{n(n+1)}\sum\frac{R_i^2}{n_i} = -3(18+1) + \frac{12}{18(18+1)}\left(\frac{74.5^2}{10} + \frac{70^2}{5} + \frac{26.5^2}{3}\right) = 5.074$$

If we make the adjustment in the statistic for ties, we get:

$$\tilde{H} = \frac{H}{1 - \frac{\sum(t_i^3 - t_i)}{N^3 - N}} = \frac{5.074}{1 - \frac{(2^3 - 2) + (2^3 - 2) + (2^3 - 2)}{18^3 - 18}} = 5.0897$$

where t_i is the number of ties of each value.

In this case, the Kruskal-Wallis test provides the same conclusion as the Concordance test; uncertainty being greater when we have ties.

Concordance test in ConcordanceTest package

The **ConcordanceTest** R-package allows to perform the hypothesis test for testing whether samples originate from the same distribution with the function `CT_Hypothesis_Test()`, which carries out the calculations by simulation. It is used as follows:

```
CT_Hypothesis_Test(Sample_List, Num_Sim = 10000, H = 0, verbose = TRUE)
```

where `Sample_List` is a list of numeric data vectors with the elements of each sample, `Num_Sim` is the number of used simulations (10,000 by default), `H` specifies whether the Kruskal-Wallis test must also be done, and `verbose` is a logical parameter that indicates whether some progress report of the simulations should be given.

Example 2 (Cont.) *We use the* **ConcordanceTest** *package to perform the Concordance and Kruskal-Wallis tests of Example* 2. *We use 25,000 simulations.*

```
set.seed(12)
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_Hypothesis_Test(Sample_List, Num_Sim = 25000, H = 1)

$results
                      Statistic p-value
Concordance coefficient   0.574 0.04928
Kruskal Wallis            5.600 0.05292

$C_p_value
[1] 0.04928

$H_p_value
[1] 0.05292
```

The function `CT_Hypothesis_Test()` provides the value of the statistics together with the p-value associated with each of them. The result of the Kruskal-Wallis test is only returned if H = 1. Note that

the approximated p-values obtained by simulation are close to the exact ones, 0.04927 and 0.05223 for the Concordance coefficient and the Kruskal-Wallis statistic, respectively.

An alternative to the contrast performed with the function `CT_Hypothesis_Test()` is to obtain the critical values of our contrast. This can be done with the **ConcordanceTest** package both in an exact or approximate way, using the function `CT_Critical_Values()`. It is used as follows:

```
CT_Critical_Values(Sample_Sizes, Num_Sim = 10000, H = 0, verbose = TRUE)
```

where `Sample_Sizes` is a numeric vector $(n_1, \ldots, n_k)$ containing the number of repetitions of each element, i.e., the size of each sample in the experiment. `Num_Sim` is the number of simulations carried out in order to obtain the probability distribution of the statistics (10,000 by default). If `Num_Sim` is set to 0, the critical values are obtained in an exact way. Otherwise they are obtained by simulation. `H` is the parameter specifying whether the critical values of the Kruskal-Wallis test must be calculated and returned, and `verbose` is a logical parameter that indicates whether some progress report of the simulations should be given.

The function returns a list with two elements. `C_results` are the critical values and p-values for a desired significance levels of 0.1, .05 and .01 of the Concordance coefficient, and `H_results` are the critical values and p-values of the Kruskal-Wallis statistic (only returned if H = 1).

Example 2 (Cont.) *We show the results of the function* `CT_Critical_Values()` *with sample sizes* $N = (10, 5, 3)$ *and 25,000 simulations. The results allow us to compare the test statistics with different significance levels.*

```
set.seed(12)
Sample_Sizes <- c(10,5,3)
CT_Critical_Values(Sample_Sizes, Num_Sim = 25000, H = 1)

$C_results
            | disorder | Concordance coefficient | p-value
Sig level .10       23                      0.51    0.0954
Sig level .05       20                      0.57    0.0492
Sig level .01       14                      0.70    0.0096

$H_results
            | H Statistic | p-value
Sig level .10        4.55    0.0995
Sig level .05        5.72    0.0497
Sig level .01        7.78    0.0097
```

To obtain the Concordance coefficient and the Kruskal-Wallis statistic from the result of an experiment, the **ConcordanceTest** package has the function `CT_Coefficient()`. This function is useful when we only want to obtain the value of the statistic to check its significance using statistical tables. The function `CT_Coefficient()` is used as follows:

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

where `Sample_List` is a list of numeric data vectors with the elements of each sample, and `H` is defined as usual.

Example 2 (Cont.) *We show the results of the function* `CT_Coefficient()` *for the data in Example 2.*

```
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, H = 1)

$Sample_Sizes
[1] 10  5  3

$order_elements
 [1] 1 1 1 1 1 3 3 1 2 1 2 1 2 1 1 3 1 2 2 2

$disorder
[1] 20
```

```
$Concordance_Coefficient
[1] 0.5744681

$H_Statistic
[1] 5.6
```

The function `CT_Coefficient()` returns a list with the following elements: `Sample_Sizes` is a numeric vector with the sample sizes, `order_elements` is a numeric vector containing the elements order, `disorder` is the disorder of the permutation given by `order_elements`, `Concordance_Coefficient` is the value of the Concordance coefficient τ_c, that is, 1 minus the relative disorder of the permutation given by `order_elements`, and `H_Statistic` is the Kruskal-Wallis statistic (only returned if `H = 1`).

Note that we can also solve problems with ties (as in Example 3) with the **ConcordanceTest** package.

Other functions in the ConcordanceTest package

The graphical visualization of the probability distributions of the Concordance coefficient and the Kruskal-Wallis statistic can be done with the function `CT_Probability_Plot()`. It is used as follows:

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

Using the function `CT_Density_Plot()` of the **ConcordanceTest** package, we can make an approximate representation of the density functions of the statistics, assuming that the probability distributions represent a sample of a continuous variable. It is used as follows:

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

In both functions, `C_freq` is the probability distribution of the Concordance coefficient and `H_freq` is the probability distribution of the Kruskal-Wallis statistic, obtained exactly or approximately with the function `CT_Distribution()`. The function `CT_Probability_Plot()` can represent both probability distributions or only one of them (if it only receives the parameter `C_freq` or `H_freq`). Equivalently, the function `CT_Density_Plot()` can represent both density distributions or only one of them. Appendix B presents the empirical density probability functions for several experiments, where sample sizes vary form $N = (4, 4)$ to $N = (5, 5, 4, 4, 4, 4, 4)$.

Example 2 (Cont.) *Graphical visualization of the probability distributions and the density distributions of Example 2 generated by simulation. The first row of Figure 2 compares the probability distribution of the Concordance coefficient and the Kruskal-Wallis statistic. The second row of Figure 2 shows the probability density function of the Concordance coefficient (continuous line) and the Kruskal-Wallis statistic (dashed line). Note that the H statistic has been normalized between 0 and 1.*

```
set.seed(12)
Sample_Sizes <- c(10,5,3)
ProbDistr <- CT_Distribution(Sample_Sizes, Num_Sim = 25000, H = 1)
layout(matrix(c(1,3,2,3), ncol=2))
CT_Probability_Plot(C_freq = ProbDistr$C_freq, H_freq = ProbDistr$H_freq)
CT_Density_Plot(C_freq = ProbDistr$C_freq, H_freq = ProbDistr$H_freq)
```

As we mentioned in Figure 1, Figure 2 also shows that similar values of the Kruskal-Wallis statistic present very different probabilities, and this leads to a less smooth function than that presented by the Concordance coefficient. We can also see that the Concordance coefficient presents a more symmetrical distribution. This performance is generalized and, therefore, we consider that the Concordance coefficient is more reliable than the Kruskal-Wallis statistic.

The **ConcordanceTest** package also contains the function `LOP()`, which solves the Linear Ordering Problem from a square data matrix. This function allows to calculate the disorder of a permutation of elements from the preference matrix induced by that permutation and, therefore, it is necessary for the calculation of the Concordance coefficient. The function `LOP()` is used by functions `CT_Distribution()`, `CT_Hypothesis_Test()` and `CT_Coefficient()`. It is used as follows:

```
LOP(mat_LOP)
```

where `mat_LOP` is the 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.

The function `LOP()` returns a list with the following elements: `obj_val` is the optimal value of the solution of the Linear Ordering Problem, that is, the sum of the elements above the main diagonal
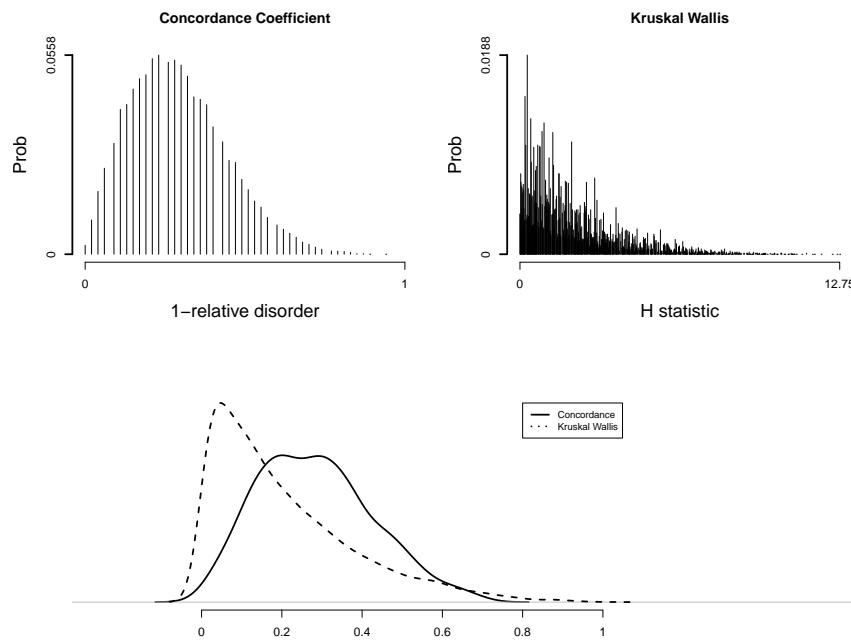
Figure 2: Probability distributions (first row) and density distributions (second row) of the Concordance coefficient (τ_c=1-relative disorder) and the Kruskal-Wallis statistic (H), with sample sizes $N = (10, 5, 3)$.

under the permutation rows/columns solution, `permutation` is the solution of the Linear Ordering Problem, that is, the rows/columns permutation, and `permutation_matrix` is the optimal permutation matrix of the Linear Ordering Problem.

Example 2 (Cont.) *The matrix of preferences between treatments observed in Example 2 was:*

$$
\begin{array}{c}
 \\
A \\
B \\
C
\end{array}
\begin{array}{ccc}
A & B & C \\
\left(\begin{array}{ccc}
- & 43 & 19 \\
7 & - & 2 \\
11 & 13 & -
\end{array}\right)
\end{array}
$$

If we apply the function `LOP()` *on this preference matrix we obtain the following results:*

```
mat_LOP <- matrix(c(0,7,11,43,0,13,19,2,0), nrow=3)
LOP(mat_LOP)

$obj_val
[1] 75

$permutation
[1] 1 3 2

$permutation_matrix
     [,1] [,2] [,3]
[1,]    0    1    1
[2,]    0    0    0
[3,]    0    1    0
```

As we saw previously, the order between treatments that maximizes the order between patients corresponds to the order $(A\ C\ B)$ (permutation = 1 3 2), satisfying obj_val = 75 of the preferences contained in the matrix.

5   Comparison with `kruskal.test()` function from stats package

The well-known **stats** package contains, among many other functions, the function `kruskal.test()` that performs a Kruskal-Wallis rank sum test. In this section, we compare the results obtained with the **ConcordanceTest** package presented in this work and the function `kruskal.test()`, making use of the dataset from Hollander and Wolfe (1973) referenced in the `kruskal.test()` examples.

Example 4 *Comparison of* `kruskal.test()` *(**stats** package) and* `CT_Hypothesis_Test()` *functions with 25,000 simulations (**ConcordanceTest** package) using the dataset from Hollander and Wolfe (1973).*

```
## 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)

kruskal.test(Sample_List)


        Kruskal-Wallis rank sum test

data:  Sample_List
Kruskal-Wallis chi-squared = 0.77143, df = 2, p-value = 0.68

set.seed(12)
CT_Hypothesis_Test(Sample_List, Num_Sim = 25000, H = 1)


results
                      Statistic p-value
Concordance coefficient   0.188 0.78408
Kruskal-Wallis            0.771 0.71080

$C_p_value
[1] 0.78408

$H_p_value
[1] 0.7108
```

As can be observed, the value of the Kruskal-Wallis statistic is the same with both functions (0.771). However, the p-values associated with the statistic differ.

The Kruskal-Wallis statistic follows approximately a χ^2 distribution with degrees of freedom equal to the number of groups minus 1 (Kruskal and Wallis, 1952). For this reason, the function `kruskal.test()` uses a χ^2 distribution to approximate the p-value (using the function `pchisq()`). In the case of the function `CT_Hypothesis_Test()`, it calculates the p-values using the simulations performed (25,000 in this example).

The function `CT_Distribution()` of the **ConcordanceTest** package allows the probability distribution tables of the Concordance coefficient and Kruskal-Wallis statistic to be computed, and they can be obtained exactly or by simulation. We can get the exact probability distribution tables and, consequently, the exact p-values in Example 4 with

```
CT_Distribution(c(5,4,5), Num_Sim = 0, H = 1)
```

In Example 4, the exact p-value for the Kruskal-Wallis statistic is 0.71077. Therefore, the difference between our p-value obtained with 25,000 simulations (0.71080) and the exact one is 0.00003, while the difference between the p-value approximated by the χ^2 distribution (0.68) and the exact one is 0.03077. Regarding the Concordance coefficient, the exact p-value is 0.78468, hence, the difference between our p-value obtained with 25,000 simulations (0.78408) and the exact one is 0.0006.

It is worth noting that the function `kruskal.test()` uses the χ^2 distribution to approximate the p-value regardless of the size of the samples, but Kruskal and Wallis (1952) state that the Kruskal-Wallis statistic is distributed approximately as a χ^2, unless the samples are too small, in which case special

approximations or exact tables should be provided. On the contrary, the **ConcordanceTest** package can always obtain a good approximation of the p-values, regardless of the size of the samples, as long as a high number of simulations is used.

6 Final remarks and future research

A new measure based on the Kendall-τ distance is presented in this work to estimate the *concordance* of different samples. A statistical test to determine when different observations come from the same distribution is also introduced. A comparison with the classical Kruskal-Wallis test is introduced to show that both tests differ. As we have shown, the proposed coefficient is more appropriate and reliable than rank-based methods. This work also describes the R package **ConcordanceTest** (Alcaraz et al., 2022), which contains all the functions needed to work with the proposed Concordance coefficient and allows its comparison with the Kruskal-Wallis statistic.

This work aims to be an introduction of the new concordance measure between samples, but there still remains much to be done. There is a new problem and further challenges for researchers, for example: studying the asymptotic distribution of the Concordance coefficient, exploring the possibility of finding the exact distribution with the help of modern computing, or analyzing the power of the Concordance test presented in this work, among others.

7 Acknowledgments

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1 Appendix A: Results in the experiment with sample sizes $N = (2, 2, 2)$

Table 6 shows the Concordance coefficient (τ_c) and Kruskal-Wallis statistic (H) for all possible results in an experiment with three treatments and two people in each treatment.

	dis	τ_c	H		dis	τ_c	H		dis	τ_c	H
a a b b c c	0	1.0000	4.57	b a a b c c	2	0.6667	3.43	c a a b b c	4	0.3333	1.14
a a b c b c	1	0.8333	3.71	b a a c b c	3	0.5000	2.00	c a a b c b	3	0.5000	2.00
a a b c c b	2	0.6667	3.43	b a a c c b	4	0.3333	1.14	c a a c b b	2	0.6667	3.43
a a c b b c	2	0.6667	3.43	b a b a c c	1	0.8333	3.71	c a b a b c	5	0.1667	0.29
a a c b c b	1	0.8333	3.71	b a b c a c	2	0.6667	2.57	c a b a c b	4	0.3333	0.86
a a c c b b	0	1.0000	4.57	b a b c c a	3	0.5000	2.00	c a b b a c	6	0.0000	0.00
a b a b c c	1	0.8333	3.71	b a c a b c	4	0.3333	0.86	c a b b c a	5	0.1667	0.29
a b a c b c	2	0.6667	2.57	b a c a c b	5	0.1667	0.29	c a b c a b	3	0.5000	1.14
a b a c c b	3	0.5000	2.00	b a c b a c	3	0.5000	1.14	c a b c b a	4	0.3333	0.86
a b b a c c	2	0.6667	3.43	b a c b c a	4	0.3333	0.86	c a c a b b	1	0.8333	3.71
a b b c a c	3	0.5000	2.00	b a c c a b	6	0.0000	0.00	c a c b a b	2	0.6667	2.57
a b b c c a	4	0.3333	1.14	b a c c b a	5	0.1667	0.29	c a c b b a	3	0.5000	2.00
a b c a b c	3	0.5000	1.14	b b a a c c	0	1.0000	4.57	c b a a b c	6	0.0000	0.00
a b c a c b	4	0.3333	0.86	b b a c a c	1	0.8333	3.71	c b a a c b	5	0.1667	0.29
a b c b a c	4	0.3333	0.86	b b a c c a	2	0.6667	3.43	c b a b a c	5	0.1667	0.29
a b c b c a	5	0.1667	0.29	b b c a a c	2	0.6667	3.43	c b a b c a	4	0.3333	0.86
a b c c a b	5	0.1667	0.29	b b c a c a	1	0.8333	3.71	c b a c a b	4	0.3333	0.86
a b c c b a	6	0.0000	0.00	b b c c a a	0	1.0000	4.57	c b a c b a	3	0.5000	1.14
a c a b b c	3	0.5000	2.00	b c a a b c	5	0.1667	0.29	c b b a a c	4	0.3333	1.14
a c a b c b	2	0.6667	2.57	b c a a c b	6	0.0000	0.00	c b b a c a	3	0.5000	2.00
a c a c b b	1	0.8333	3.71	b c a b a c	4	0.3333	0.86	c b b c a a	2	0.6667	3.43
a c b a b c	4	0.3333	0.86	b c a b c a	3	0.5000	1.14	c b c a a b	3	0.5000	2.00
a c b a c b	3	0.5000	1.14	b c a c a b	5	0.1667	0.29	c b c a b a	2	0.6667	2.57
a c b b a c	5	0.1667	0.29	b c a c b a	4	0.3333	0.86	c b c b a a	1	0.8333	3.71
a c b b c a	6	0.0000	0.00	b c b a a c	3	0.5000	2.00	c c a a b b	0	1.0000	4.57
a c b c a b	4	0.3333	0.86	b c b a c a	2	0.6667	2.57	c c a b a b	1	0.8333	3.71
a c b c b a	5	0.1667	0.29	b c b c a a	1	0.8333	3.71	c c a b b a	2	0.6667	3.43
a c c a b b	2	0.6667	3.43	b c c a a b	4	0.3333	1.14	c c b a a b	2	0.6667	3.43
a c c b a b	3	0.5000	2.00	b c c a b a	3	0.5000	2.00	c c b a b a	1	0.8333	3.71
a c c b b a	4	0.3333	1.14	b c c b a a	2	0.6667	3.43	c c b b a a	0	1.0000	4.57

Table 6: Concordance coefficient (τ_c) and Kruskal-Wallis statistic (H) for all possible results in an experiment with sample sizes $N = (2, 2, 2)$.

2 Appendix B: Comparison of distributions

Table 7 shows the probability density function of the Concordance coefficient (continuous lines) and the Kruskal-Wallis statistic (dashed lines) generated by simulation. Number of simulations 100,000. Note that the H statistic has been normalized between 0 and 1.
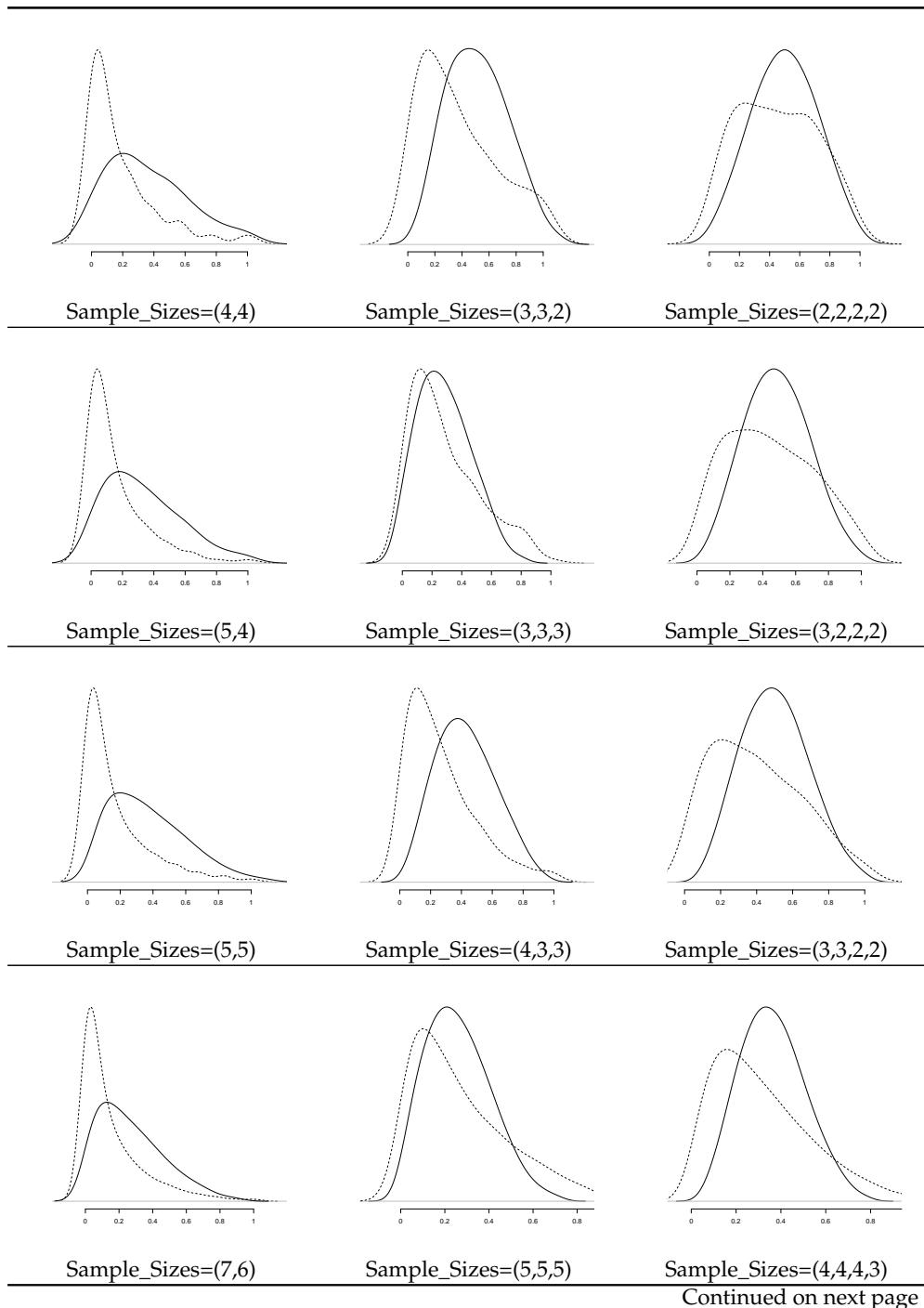
Table 7: Empirical density probability functions for several experiments (Concordance coefficient in continuous lines and Kruskal-Wallis statistic in dashed lines), where sample sizes vary form $N = (4, 4)$ to $N = (5, 5, 4, 4, 4, 4, 4)$.

Table 7 – continued from previous page
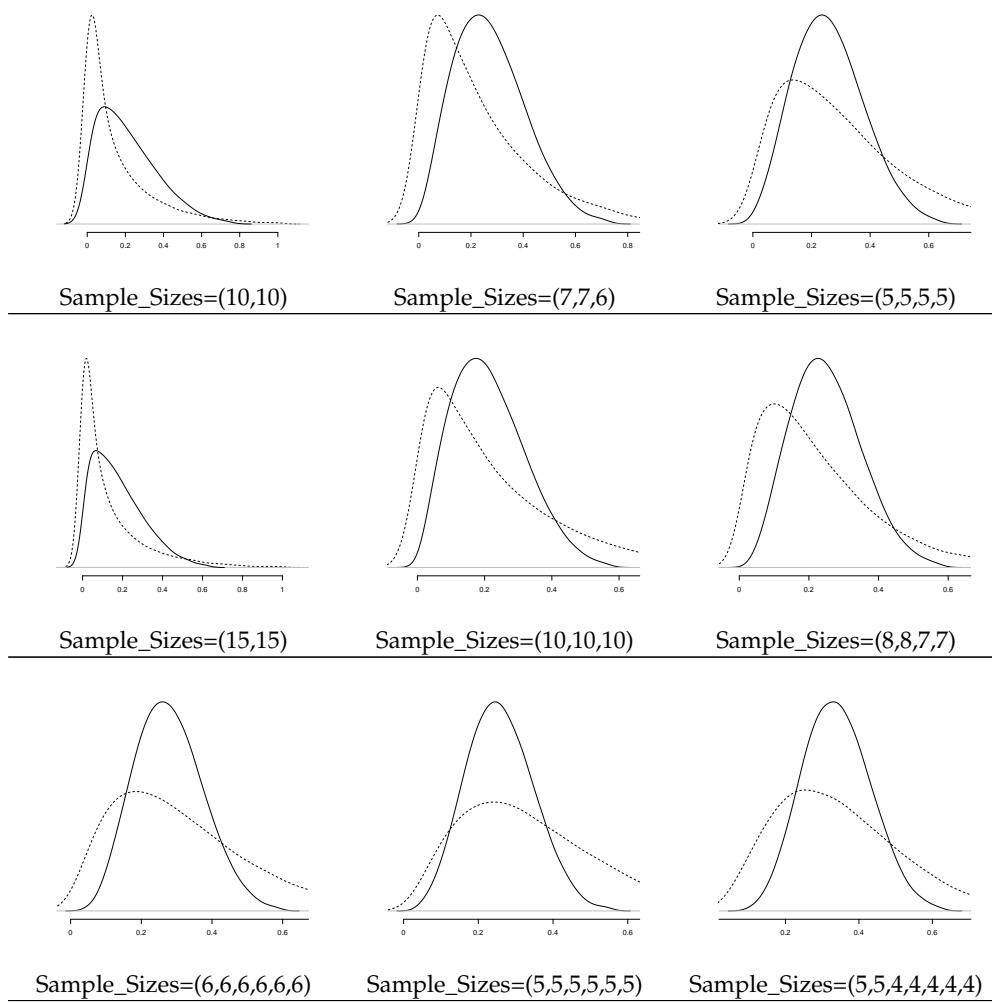
Sample_Sizes=(10,10)   Sample_Sizes=(7,7,6)   Sample_Sizes=(5,5,5,5)

Sample_Sizes=(15,15)   Sample_Sizes=(10,10,10)   Sample_Sizes=(8,8,7,7)

Sample_Sizes=(6,6,6,6,6,6)   Sample_Sizes=(5,5,5,5,5,5)   Sample_Sizes=(5,5,4,4,4,4,4)

Table 7: Empirical density probability functions for several experiments (Concordance coefficient in continuous lines and Kruskal-Wallis statistic in dashed lines), where sample sizes vary form $N = (4, 4)$ to $N = (5, 5, 4, 4, 4, 4, 4)$.

3 Appendix C: Concordance coefficient p-values

In order to compute the probability distribution of the Concordance coefficient, the enumeration of all the permutations of elements from an order is required. Note for example that if we have 4 samples with 6 elements each, $N = (6, 6, 6, 6)$, the number of possible results in the experiment is $24!/6!6!6!6! = 2.15433 \cdot 10^{20}$. The total computational time to compute the Concordance coefficient for all $2.15433 \cdot 10^{20}$ possibilities was more than 60 days in an Intel(R) Xeon (R) processor CPU E5-2650 v3 @ 2.30 GHz, 20 cores and RAM 64 GiB. Algorithm 1 presents the recursive function used to evaluate the Concordance coefficient probability distribution.

Algorithm 1: Algorithm to compute the exact probability distribution function of the Concordance coefficient τ_c

---

 Data:
 p : ordered array of integers with ties.
 n : length of **p**.
 Frequency$[0, max(disorder)]$.

1 **Main (p)**
2 | Permutation(**p**,0,n);
3 | **return**

4 **Permutation (p,s,n):**
5 | Frequency[Disorder(**p**)]++;
6 | int $tmp = 0$;
7 | **if** $s < n$ **then**
8 | | **for** $i = n - 2 : i \geq s; i - -$ **do**
9 | | | **for** $j = i + 1; j < n; j + +$ **do**
10 | | | | **if** $p[i] \neq p[j]$ **then**
11 | | | | | $tmp = p[i]; p[i] = p[j]; p[j] = tmp;$ Permutation(**p**,$i + 1$,n);
12 | | | tmp=p[i];
13 | | | **for** $j = i + 1; j < n; j + +$ **do**
14 | | | | $p[k] = p[k + +];$
15 | | | $p[n - 1] = tmp;$
16 | **return**

17 **Disorder (p)**
 | /* Evaluate the disorder and the Concordance coefficient of permutation **p** */
18 | **return**

Tables 8, 9 and 10 show the critical values and exact p-values of the Concordance coefficient τ_c at desired significance levels of 0.10, 0.05 and 0.01 for *k*=2, *k*=3 and *k*=4 samples, respectively.

Sample Sizes		.10			.05			.01		
		dis	τ_c	p-value	*dis*	τ_c	p-value	*dis*	τ_c	p-value
4	1									
4	2									
4	3	0	1.000000	0.057143						
4	4	1	0.875000	0.057143	0	1.000000	0.028571			
5	1									
5	2	0	1.000000	0.095238						
5	3	1	0.857143	0.071429	0	1.000000	0.035714			
5	4	2	0.800000	0.063492	1	0.900000	0.031746			
5	5	4	0.666667	0.095238	2	0.833333	0.031746	0	1.000000	0.007937
6	1									
6	2	0	1.000000	0.071429						
6	3	2	0.777778	0.095238	1	0.888889	0.047619			
6	4	3	0.750000	0.066667	2	0.833333	0.038095	0	1.000000	0.009524
6	5	5	0.666667	0.082251	3	0.800000	0.030303	1	0.933333	0.008658
6	6	7	0.611111	0.093074	5	0.722222	0.041126	2	0.888889	0.008658
7	1									
7	2	0	1.000000	0.055556						
7	3	2	0.800000	0.066667	1	0.900000	0.033333			
7	4	4	0.714286	0.072727	3	0.785714	0.042424	0	1.000000	0.006061
7	5	6	0.647059	0.073232	5	0.705882	0.047980	1	0.941176	0.005051
7	6	8	0.619048	0.073427	6	0.714286	0.034965	3	0.857143	0.008159
7	7	11	0.541667	0.097319	8	0.666667	0.037879	4	0.833333	0.006993
8	1									
8	2	1	0.875000	0.088889	0	1.000000	0.044444			
8	3	3	0.750000	0.084848	2	0.833333	0.048485			
8	4	5	0.687500	0.072727	4	0.750000	0.048485	1	0.937500	0.008081
8	5	8	0.600000	0.093240	6	0.700000	0.045066	2	0.900000	0.006216
8	6	10	0.583333	0.081252	8	0.666667	0.042624	4	0.833333	0.007992
8	7	13	0.535714	0.093862	10	0.642857	0.040093	6	0.785714	0.009324
8	8	15	0.531250	0.082984	13	0.593750	0.049883	7	0.781250	0.006993
9	1									
9	2	1	0.888889	0.072727	0	1.000000	0.036364			
9	3	3	0.769231	0.063636	2	0.846154	0.036364	0	1.000000	0.009091
9	4	6	0.666667	0.075524	4	0.777778	0.033566	1	0.944444	0.005594
9	5	9	0.590909	0.082917	7	0.681818	0.041958	3	0.863636	0.006993
9	6	12	0.555556	0.087912	10	0.629630	0.049550	5	0.814815	0.007592
9	7	15	0.516129	0.090734	12	0.612903	0.041783	7	0.774194	0.007867
9	8	18	0.500000	0.092719	15	0.583333	0.046401	9	0.750000	0.007898
9	9	21	0.475000	0.093912	17	0.575000	0.039984	11	0.725000	0.007775
10	1									
10	2	1	0.900000	0.060606	0	1.000000	0.030303			
10	3	4	0.733333	0.076923	3	0.800000	0.048951	0	1.000000	0.006993
10	4	7	0.650000	0.075924	5	0.750000	0.035964	2	0.900000	0.007992
10	5	11	0.560000	0.099234	8	0.680000	0.039960	4	0.840000	0.007992
10	6	14	0.533333	0.093407	11	0.633333	0.041958	6	0.800000	0.007493
10	7	17	0.514286	0.087824	14	0.600000	0.043089	9	0.742857	0.009667
10	8	20	0.500000	0.083139	17	0.575000	0.043421	11	0.725000	0.008547
10	9	24	0.466667	0.094720	20	0.555556	0.043474	13	0.711111	0.007621
10	10	27	0.460000	0.089210	23	0.540000	0.043257	16	0.680000	0.008931
11	1									
11	2	1	0.909091	0.051282	0	1.000000	0.025641			
11	3	5	0.687500	0.087912	3	0.812500	0.038462	0	1.000000	0.005495
11	4	8	0.636364	0.077656	6	0.727273	0.039560	2	0.909091	0.005861
11	5	12	0.555556	0.089744	9	0.666667	0.038004	5	0.814815	0.008700
11	6	16	0.515152	0.098255	13	0.606061	0.047673	7	0.787879	0.007111
11	7	19	0.500000	0.085344	16	0.578947	0.044118	10	0.736842	0.008296
11	8	23	0.477273	0.090842	19	0.568182	0.040883	13	0.704545	0.009103
11	9	27	0.448980	0.095177	23	0.530612	0.046452	16	0.673469	0.009693
11	10	31	0.436364	0.098618	26	0.527273	0.042964	18	0.672727	0.007950
11	11	34	0.433333	0.087946	30	0.500000	0.047307	21	0.650000	0.008330
12	1									
12	2	2	0.833333	0.087912	1	0.916667	0.043956			
12	3	5	0.722222	0.070330	4	0.777778	0.048352	1	0.944444	0.008791
12	4	9	0.625000	0.078022	7	0.708333	0.041758	3	0.875000	0.007692
12	5	13	0.566667	0.081771	11	0.633333	0.048481	6	0.800000	0.009373
12	6	17	0.527778	0.083064	14	0.611111	0.041478	9	0.750000	0.009696

Continued on next page

Table 8: Critical values and exact p-values of the Concordance coefficient τ_c for *k*=2 samples.

Table 8 – continued from previous page

Sample Sizes		dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
12	7	21	0.500000	0.083115	18	0.571429	0.044931	12	0.714286	0.009764
12	8	26	0.458333	0.097880	22	0.541667	0.047345	15	0.687500	0.009558
12	9	30	0.444444	0.095451	26	0.518519	0.049073	18	0.666667	0.009288
12	10	34	0.433333	0.093090	29	0.516667	0.042570	21	0.650000	0.008957
12	11	38	0.424242	0.090842	33	0.500000	0.043879	24	0.636364	0.008625
12	12	42	0.416667	0.088734	37	0.486111	0.044902	27	0.625000	0.008293
13	1									
13	2	2	0.846154	0.076190	1	0.923077	0.038095			
13	3	6	0.684211	0.082143	4	0.789474	0.039286	1	0.947368	0.007143
13	4	10	0.615385	0.078992	8	0.692308	0.044538	3	0.884615	0.005882
13	5	15	0.531250	0.094538	12	0.625000	0.045985	7	0.781250	0.009804
13	6	19	0.512820	0.087424	16	0.589744	0.046218	10	0.743590	0.009214
13	7	24	0.466667	0.096801	20	0.555556	0.045562	13	0.711111	0.008462
13	8	28	0.461538	0.089046	24	0.538462	0.044553	17	0.673077	0.009937
13	9	33	0.431035	0.095557	28	0.517241	0.043376	20	0.655172	0.008910
13	10	37	0.430769	0.088294	33	0.492308	0.049329	24	0.630769	0.009888
13	11	42	0.408451	0.093307	37	0.478873	0.047448	27	0.619718	0.008848
13	12	47	0.397436	0.097642	41	0.474359	0.045711	31	0.602564	0.009556
13	13	51	0.392857	0.090847	45	0.464286	0.044117	34	0.595238	0.008601
14	1									
14	2	2	0.857143	0.066667	1	0.928571	0.033333			
14	3	7	0.666667	0.091176	5	0.761905	0.047059	1	0.952381	0.005882
14	4	11	0.607143	0.079085	9	0.678571	0.046405	4	0.857143	0.007843
14	5	16	0.542857	0.087031	13	0.628571	0.043688	7	0.800000	0.007224
14	6	21	0.500000	0.091331	17	0.595238	0.040764	11	0.738095	0.008720
14	7	26	0.469388	0.093774	22	0.551020	0.046096	15	0.693878	0.009684
14	8	31	0.446429	0.095018	26	0.535714	0.042149	18	0.678571	0.008125
14	9	36	0.428571	0.095574	31	0.507936	0.045585	22	0.650794	0.008568
14	10	41	0.414286	0.095643	36	0.485714	0.048404	26	0.628571	0.008851
14	11	46	0.402597	0.095427	40	0.480519	0.044228	30	0.610390	0.009022
14	12	51	0.392857	0.095012	45	0.464286	0.046354	34	0.595238	0.009114
14	13	56	0.384615	0.094479	50	0.450549	0.048173	38	0.582418	0.009150
14	14	61	0.377551	0.093868	55	0.438776	0.049736	42	0.571429	0.009146
15	1									
15	2	3	0.800000	0.088235	1	0.933333	0.029412			
15	3	7	0.681818	0.075980	5	0.772727	0.039216	2	0.909091	0.009804
15	4	12	0.600000	0.079979	10	0.666667	0.048504	5	0.833333	0.009288
15	5	18	0.513514	0.098297	14	0.621622	0.041796	8	0.783784	0.007740
15	6	23	0.488889	0.094833	19	0.577778	0.044855	12	0.733333	0.008367
15	7	28	0.461538	0.091085	24	0.538462	0.046522	16	0.692308	0.008526
15	8	33	0.450000	0.087332	29	0.516667	0.047304	20	0.666667	0.008456
15	9	39	0.417910	0.095507	34	0.492537	0.047584	24	0.641791	0.008255
15	10	44	0.413333	0.090971	39	0.480000	0.047524	29	0.613333	0.009616
15	11	50	0.390244	0.097262	44	0.463415	0.047262	33	0.597561	0.009154
15	12	55	0.388889	0.092610	49	0.455556	0.046866	37	0.588889	0.008710
15	13	61	0.371134	0.097721	54	0.443299	0.046394	42	0.567010	0.009635
15	14	66	0.371429	0.093216	59	0.438095	0.045875	46	0.561905	0.009115
15	15	72	0.357143	0.097526	64	0.428571	0.045334	51	0.544643	0.009875
16	1									
16	2	3	0.812500	0.078431	1	0.937500	0.026144			
16	3	8	0.666667	0.084623	6	0.750000	0.047472	2	0.916667	0.008256
16	4	14	0.562500	0.099484	11	0.656250	0.049948	5	0.843750	0.007430
16	5	19	0.525000	0.091012	15	0.625000	0.040100	9	0.775000	0.008158
16	6	25	0.479167	0.098026	21	0.562500	0.048731	13	0.729167	0.007988
16	7	30	0.464286	0.088694	26	0.535714	0.046876	18	0.678571	0.009578
16	8	36	0.437500	0.092602	31	0.515625	0.044823	22	0.656250	0.008748
16	9	42	0.416667	0.095397	37	0.486111	0.049384	27	0.625000	0.009643
16	10	48	0.400000	0.097414	42	0.475000	0.046707	31	0.612500	0.008685
16	11	54	0.386364	0.098866	47	0.465909	0.044271	36	0.590909	0.009256
16	12	60	0.375000	0.099904	53	0.447917	0.047276	41	0.572917	0.009707
16	13	65	0.375000	0.091611	59	0.432692	0.049924	45	0.567308	0.008738
16	14	71	0.366071	0.092540	64	0.428571	0.047205	50	0.553571	0.009064
16	15	77	0.358333	0.093259	70	0.416667	0.049381	55	0.541667	0.009331
16	16	83	0.351562	0.093812	75	0.414062	0.046815	60	0.531250	0.009551
17	1									
17	2	3	0.823529	0.070175	2	0.882353	0.046784			
17	3	9	0.640000	0.092982	6	0.760000	0.040351	2	0.920000	0.007018

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Table 8: Critical values and exact p-values of the Concordance coefficient τ_c for k=2 samples.

Table 8 – continued from previous page

Sample Sizes		dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
17	4	15	0.558824	0.098580	11	0.676471	0.040434	6	0.823529	0.009023
17	5	20	0.523810	0.084909	17	0.595238	0.047695	10	0.761905	0.008582
17	6	26	0.490196	0.086501	22	0.568627	0.043766	15	0.705882	0.009867
17	7	33	0.440678	0.099490	28	0.525424	0.047171	19	0.677966	0.008518
17	8	39	0.426471	0.097491	34	0.500000	0.049474	24	0.647059	0.009005
17	9	45	0.407895	0.095246	39	0.486842	0.044566	29	0.618421	0.009248
17	10	51	0.400000	0.092922	45	0.470588	0.045937	34	0.600000	0.009341
17	11	57	0.387097	0.090623	51	0.451613	0.046916	39	0.580645	0.009331
17	12	64	0.372549	0.097270	57	0.441176	0.047604	44	0.568627	0.009257
17	13	70	0.363636	0.094466	63	0.427273	0.048075	49	0.554545	0.009141
17	14	77	0.352941	0.099995	69	0.420168	0.048385	54	0.546219	0.008999
17	15	83	0.346457	0.096996	75	0.409449	0.048571	60	0.527559	0.009973
17	16	89	0.345588	0.094235	81	0.404412	0.048664	65	0.522059	0.009731
17	17	96	0.333333	0.098687	87	0.395833	0.048686	70	0.513889	0.009494
18	1									
18	2	4	0.777778	0.094737	2	0.888889	0.042105			
18	3	9	0.666667	0.079699	7	0.740741	0.046617	2	0.925926	0.006015
18	4	16	0.555556	0.098154	12	0.666667	0.042379	6	0.833333	0.007382
18	5	22	0.511111	0.094327	18	0.600000	0.045707	11	0.755556	0.008916
18	6	28	0.481481	0.089527	24	0.555556	0.047193	16	0.703704	0.009421
18	7	35	0.444444	0.096701	30	0.523810	0.047418	21	0.666667	0.009445
18	8	41	0.430556	0.090496	36	0.500000	0.046988	26	0.638889	0.009233
18	9	48	0.407407	0.095074	42	0.481481	0.046198	31	0.617284	0.008893
18	10	55	0.388889	0.098664	48	0.466667	0.045221	37	0.588889	0.009955
18	11	61	0.383838	0.092197	55	0.444444	0.049392	42	0.575758	0.009388
18	12	68	0.370370	0.094866	61	0.435185	0.047865	47	0.564815	0.008851
18	13	75	0.358974	0.097070	67	0.427350	0.046401	53	0.547009	0.009505
18	14	82	0.349206	0.098905	74	0.412698	0.049436	58	0.539683	0.008925
18	15	88	0.348148	0.092994	80	0.407407	0.047795	64	0.525926	0.009432
18	16	95	0.340278	0.094552	86	0.402778	0.046272	70	0.513889	0.009880
18	17	102	0.333333	0.095895	93	0.392157	0.048652	75	0.509804	0.009265
18	18	109	0.327160	0.097059	99	0.388889	0.047085	81	0.500000	0.009631
19	1									
19	2	4	0.789474	0.085714	2	0.894737	0.038095	0	1.000000	0.009524
19	3	10	0.642857	0.087013	7	0.750000	0.040260	3	0.892857	0.009091
19	4	17	0.552632	0.097346	13	0.657895	0.043817	7	0.815789	0.008583
19	5	23	0.510638	0.088368	19	0.595745	0.043902	12	0.744681	0.009270
19	6	30	0.473684	0.092321	25	0.561404	0.042778	17	0.701754	0.009001
19	7	37	0.439394	0.094199	32	0.515152	0.047622	22	0.666667	0.008489
19	8	44	0.421053	0.094915	38	0.500000	0.044792	28	0.631579	0.009436
19	9	51	0.400000	0.094882	45	0.470588	0.047700	33	0.611765	0.008572
19	10	58	0.389474	0.094392	52	0.452632	0.049957	39	0.589474	0.009074
19	11	65	0.375000	0.093614	58	0.442308	0.046502	45	0.567308	0.009429
19	12	72	0.368421	0.092664	65	0.429825	0.048074	51	0.552632	0.009674
19	13	80	0.349594	0.099454	72	0.414634	0.049346	57	0.536585	0.009835
19	14	87	0.345865	0.097861	78	0.413534	0.046065	63	0.526316	0.009935
19	15	94	0.338028	0.096301	85	0.401408	0.047054	69	0.514085	0.009986
19	16	101	0.335526	0.094785	92	0.394737	0.047883	74	0.513158	0.009009
19	17	109	0.322981	0.099827	99	0.385093	0.048578	81	0.496894	0.009991
19	18	116	0.321637	0.098072	106	0.380117	0.049163	87	0.491228	0.009960
19	19	123	0.316667	0.096409	113	0.372222	0.049656	93	0.483333	0.009914
20	1	0	1.000000	0.095238						
20	2	4	0.800000	0.077922	2	0.900000	0.034632	0	1.000000	0.008658
20	3	11	0.633333	0.093732	8	0.733333	0.046302	3	0.900000	0.007905
20	4	18	0.550000	0.096932	14	0.650000	0.045360	8	0.800000	0.009976
20	5	25	0.500000	0.096970	20	0.600000	0.042349	13	0.740000	0.009561
20	6	32	0.466667	0.094905	27	0.550000	0.045858	18	0.700000	0.008652
20	7	39	0.442857	0.091932	34	0.514286	0.047798	24	0.657143	0.009315
20	8	47	0.412500	0.099062	41	0.487500	0.048749	30	0.625000	0.009617
20	9	54	0.400000	0.094682	48	0.466667	0.049091	36	0.600000	0.009687
20	10	62	0.380000	0.099577	55	0.450000	0.049031	42	0.580000	0.009616
20	11	69	0.372727	0.094896	62	0.436364	0.048718	48	0.563636	0.009458
20	12	77	0.358333	0.098543	69	0.425000	0.048240	54	0.550000	0.009249
20	13	84	0.353846	0.093978	76	0.415385	0.047661	60	0.538462	0.009012
20	14	92	0.342857	0.096865	83	0.407143	0.047021	67	0.521429	0.009796
20	15	100	0.333333	0.099377	90	0.400000	0.046348	73	0.513333	0.009462
20	16	107	0.331250	0.094950	98	0.387500	0.049370	79	0.506250	0.009140

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Table 8: Critical values and exact p-values of the Concordance coefficient τ_c for k=2 samples.

Table 8 – continued from previous page

Sample Sizes		dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
20	17	115	0.323529	0.097069	105	0.382353	0.048471	86	0.494118	0.009721
20	18	123	0.316667	0.098957	112	0.377778	0.047600	92	0.488889	0.009363
20	19	130	0.315789	0.094835	119	0.373684	0.046761	99	0.478947	0.009856
20	20	138	0.310000	0.096500	127	0.365000	0.049090	105	0.475000	0.009484

Table 8: Critical values and exact p-values of the Concordance coefficient τ_c for k=2 samples.

Sample Sizes			.10			.05			.01		
			dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
2	1	1									
2	2	1									
2	2	2	0	1.000000	0.066667						
3	1	1									
3	2	1									
3	2	2	1	0.875000	0.085714	0	1.000000	0.028571			
3	3	1	0	1.000000	0.042857	0	1.000000	0.042857			
3	3	2	2	0.800000	0.085714	1	0.900000	0.032143			
3	3	3	3	0.769231	0.064286	2	0.846154	0.028571	0	1.000000	0.003571
4	1	1									
4	2	1	0	1.000000	0.057143						
4	2	2	1	0.900000	0.042857	1	0.900000	0.042857			
4	3	1	1	0.888889	0.064286	0	1.000000	0.021429			
4	3	2	3	0.769231	0.077778	2	0.846154	0.038095	0	1.000000	0.004762
4	3	3	5	0.687500	0.090000	3	0.812500	0.025714	1	0.937500	0.004286
4	4	1	2	0.833333	0.060317	1	0.916667	0.028571	0	1.000000	0.009524
4	4	2	4	0.750000	0.060952	3	0.812500	0.032381	1	0.937500	0.005714
4	4	3	7	0.650000	0.095065	5	0.750000	0.035325	3	0.850000	0.009351
4	4	4	9	0.625000	0.086580	7	0.708333	0.036883	4	0.833333	0.006580
5	1	1									
5	2	1	1	0.875000	0.095238	0	1.000000	0.035714			
5	2	2	2	0.833333	0.058201	1	0.916667	0.023810	0	1.000000	0.007937
5	3	1	2	0.818182	0.075397	1	0.909091	0.035714			
5	3	2	4	0.733333	0.072222	3	0.800000	0.038889	1	0.933333	0.007143
5	3	3	6	0.684211	0.070130	5	0.736842	0.041558	2	0.894737	0.005195
5	4	1	4	0.714286	0.098413	2	0.857143	0.031746	0	1.000000	0.004762
5	4	2	6	0.684211	0.079654	5	0.736842	0.049062	2	0.894737	0.006926
5	4	3	9	0.608696	0.098341	7	0.695652	0.042641	4	0.826087	0.008009
5	4	4	11	0.607143	0.079343	9	0.678571	0.037163	6	0.785714	0.008658
5	5	1	5	0.705882	0.077201	4	0.764706	0.047619	1	0.941176	0.006494
5	5	2	8	0.636364	0.084416	6	0.727273	0.035714	3	0.863636	0.006133
5	5	3	11	0.592593	0.089022	9	0.666667	0.042374	5	0.814815	0.005828
5	5	4	14	0.562500	0.089498	12	0.625000	0.047072	8	0.750000	0.009039
5	5	5	17	0.540541	0.088887	14	0.621622	0.036630	10	0.729730	0.008016
6	1	1									
6	2	1	1	0.900000	0.063492	0	1.000000	0.023810			
6	2	2	3	0.785714	0.066667	2	0.857143	0.034921	0	1.000000	0.004762
6	3	1	3	0.769231	0.083333	2	0.846154	0.045238	0	1.000000	0.007143
6	3	2	5	0.722222	0.067532	4	0.777778	0.039394	1	0.944444	0.003896
6	3	3	8	0.636364	0.087554	6	0.727273	0.035390	3	0.863636	0.005844
6	4	1	5	0.705882	0.089177	3	0.823529	0.032035	1	0.941176	0.007792
6	4	2	8	0.636364	0.096537	6	0.727273	0.041414	3	0.863636	0.007359
6	4	3	11	0.592593	0.099933	9	0.666667	0.048119	5	0.814815	0.006893
6	4	4	14	0.562500	0.099310	11	0.656250	0.036934	7	0.781250	0.006394
6	5	1	7	0.650000	0.094156	5	0.750000	0.040043	2	0.900000	0.007576
6	5	2	10	0.615385	0.087468	8	0.692308	0.041570	4	0.846154	0.005661
6	5	3	13	0.580645	0.081205	11	0.645161	0.041625	7	0.774194	0.007635
6	5	4	17	0.540541	0.097296	14	0.621622	0.040721	10	0.729730	0.009238
6	5	5	20	0.523810	0.087370	17	0.595238	0.039446	12	0.714286	0.007222
6	6	1	9	0.625000	0.095571	7	0.708333	0.046287	3	0.875000	0.006660
6	6	2	12	0.600000	0.080039	10	0.666667	0.041173	6	0.800000	0.007588
6	6	3	16	0.555556	0.089258	13	0.638889	0.036473	9	0.750000	0.008044
6	6	4	20	0.523810	0.094960	17	0.595238	0.043424	12	0.714286	0.008249
6	6	5	24	0.500000	0.098268	21	0.562500	0.049106	15	0.687500	0.008321
6	6	6	27	0.500000	0.082204	24	0.555556	0.042636	18	0.666667	0.008323

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Table 9: Critical values and exact p-values of the Concordance coefficient τ_c for k=3 samples.

Table 9 – continued from previous page

Sample	Sizes		dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
7	1	1	0	1.000000	0.083333						
7	2	1	2	0.818182	0.094444	1	0.909091	0.044444			
7	2	2	4	0.750000	0.076768	3	0.812500	0.042424	1	0.937500	0.009091
7	3	1	4	0.733333	0.092424	2	0.866667	0.028788	0	1.000000	0.004545
7	3	2	7	0.650000	0.098737	5	0.750000	0.039394	2	0.900000	0.006061
7	3	3	9	0.640000	0.071270	8	0.680000	0.047669	4	0.840000	0.006294
7	4	1	6	0.684211	0.083333	4	0.789474	0.033333	1	0.947368	0.004545
7	4	2	9	0.640000	0.078788	7	0.720000	0.035664	4	0.840000	0.007692
7	4	3	12	0.600000	0.074026	10	0.666667	0.036680	6	0.800000	0.006061
7	4	4	16	0.555556	0.090541	13	0.638889	0.036572	9	0.750000	0.007779
7	5	1	8	0.652174	0.077506	6	0.739130	0.035354	3	0.869565	0.007770
7	5	2	12	0.586207	0.089494	10	0.655172	0.046481	6	0.793103	0.008658
7	5	3	16	0.542857	0.098957	13	0.628571	0.040904	9	0.742857	0.009108
7	5	4	19	0.536585	0.081531	17	0.585366	0.048012	12	0.707317	0.009257
7	5	5	23	0.510638	0.085929	20	0.574468	0.041698	15	0.680851	0.009291
7	6	1	11	0.592593	0.096820	8	0.703704	0.035881	5	0.814815	0.009907
7	6	2	15	0.558824	0.097303	12	0.647059	0.040593	8	0.764706	0.009135
7	6	3	19	0.525000	0.096083	16	0.600000	0.043746	11	0.725000	0.008244
7	6	4	23	0.510638	0.092608	20	0.574468	0.045458	14	0.702128	0.007419
7	6	5	27	0.490566	0.088632	24	0.547170	0.046362	18	0.660377	0.009231
7	6	6	31	0.483333	0.084562	28	0.533333	0.046592	21	0.650000	0.008248
7	7	1	13	0.580645	0.088462	11	0.645161	0.049728	6	0.806452	0.007653
7	7	2	17	0.552632	0.081371	15	0.605263	0.048067	10	0.736842	0.009368
7	7	3	22	0.511111	0.093660	19	0.577778	0.045940	13	0.711111	0.007505
7	7	4	26	0.500000	0.083679	23	0.557692	0.043172	17	0.673077	0.008389
7	7	5	31	0.474576	0.090678	27	0.542373	0.040628	21	0.644068	0.009101
7	7	6	36	0.454545	0.095828	32	0.515152	0.046525	25	0.621212	0.009656
7	7	7	40	0.452055	0.085655	36	0.506849	0.043267	28	0.616438	0.007945
8	1	1	0	1.000000	0.066667						
8	2	1	2	0.846154	0.068687	1	0.923077	0.032323			
8	2	2	5	0.722222	0.083502	3	0.833333	0.028283	1	0.944444	0.006061
8	3	1	5	0.705882	0.097980	3	0.823529	0.036364	1	0.941176	0.009091
8	3	2	8	0.652174	0.091064	6	0.739130	0.039627	3	0.869565	0.007615
8	3	3	11	0.607143	0.084582	9	0.678571	0.041026	5	0.821429	0.006394
8	4	1	7	0.681818	0.077389	5	0.772727	0.033877	2	0.909091	0.006216
8	4	2	11	0.607143	0.091553	9	0.678571	0.046309	5	0.821429	0.007681
8	4	3	14	0.588235	0.076546	12	0.647059	0.040884	8	0.764706	0.008560
8	4	4	18	0.550000	0.083417	16	0.600000	0.048629	11	0.725000	0.008991
8	5	1	10	0.615385	0.089355	8	0.692308	0.045732	4	0.846154	0.007881
8	5	2	14	0.575758	0.090768	11	0.666667	0.036408	7	0.787879	0.007489
8	5	3	18	0.538462	0.090415	15	0.615385	0.040041	10	0.743590	0.006990
8	5	4	22	0.521739	0.087620	19	0.586957	0.042130	14	0.695652	0.009212
8	5	5	26	0.500000	0.084260	23	0.557692	0.043404	17	0.673077	0.008280
8	6	1	13	0.580645	0.096881	10	0.677419	0.040004	6	0.806452	0.008614
8	6	2	17	0.552632	0.089066	14	0.631579	0.039832	9	0.763158	0.007065
8	6	3	21	0.533333	0.081197	18	0.600000	0.038672	13	0.711111	0.008335
8	6	4	26	0.500000	0.090348	23	0.557692	0.046990	17	0.673077	0.009265
8	6	5	31	0.474576	0.097034	27	0.542373	0.043907	21	0.644068	0.009983
8	6	6	35	0.469697	0.086285	32	0.515152	0.049960	24	0.636364	0.008137
8	7	1	15	0.571429	0.081138	13	0.628571	0.047786	8	0.771429	0.009091
8	7	2	20	0.534884	0.087307	17	0.604651	0.042356	12	0.720930	0.009450
8	7	3	25	0.500000	0.091071	22	0.560000	0.047473	16	0.680000	0.009437
8	7	4	30	0.482759	0.092169	26	0.551724	0.041134	20	0.655172	0.009202
8	7	5	35	0.461538	0.091936	31	0.523077	0.044101	24	0.630769	0.008929
8	7	6	40	0.452055	0.090824	36	0.506849	0.046234	28	0.616438	0.008639
8	7	7	45	0.437500	0.089477	41	0.487500	0.047863	32	0.600000	0.008348
8	8	1	18	0.550000	0.086668	15	0.625000	0.042022	10	0.750000	0.009297
8	8	2	23	0.520833	0.085381	20	0.583333	0.044213	14	0.708333	0.008570
8	8	3	29	0.482143	0.099335	25	0.553571	0.044954	18	0.678571	0.007749
8	8	4	34	0.468750	0.093356	30	0.531250	0.044695	23	0.640625	0.009074
8	8	5	39	0.458333	0.087277	35	0.513889	0.044004	27	0.625000	0.008054
8	8	6	45	0.437500	0.094509	40	0.500000	0.043013	32	0.600000	0.009033
8	8	7	50	0.431818	0.087903	46	0.477273	0.049055	37	0.579545	0.009894
8	8	8	56	0.416667	0.093322	51	0.468750	0.047287	41	0.572917	0.008809
9	1	1	0	1.000000	0.054545						
9	2	1	3	0.785714	0.093939	1	0.928571	0.024242	0	1.000000	0.009091
9	2	2	6	0.700000	0.090443	4	0.800000	0.035431	1	0.950000	0.004196

Continued on next page

Table 9: Critical values and exact p-values of the Concordance coefficient τ_c for k=3 samples.

Table 9 – continued from previous page

Sample	Sizes		dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
9	3	1	5	0.736842	0.069231	4	0.789474	0.044056	1	0.947368	0.006294
9	3	2	9	0.640000	0.084815	7	0.720000	0.039461	4	0.840000	0.009091
9	3	3	13	0.580645	0.096883	10	0.677419	0.036064	6	0.806452	0.006533
9	4	1	8	0.666667	0.073327	6	0.750000	0.034565	3	0.875000	0.007592
9	4	2	12	0.612903	0.077416	10	0.677419	0.040573	6	0.806452	0.007752
9	4	3	16	0.567568	0.078701	14	0.621622	0.044560	9	0.756757	0.007438
9	4	4	21	0.522727	0.097718	18	0.590909	0.046871	12	0.727273	0.007022
9	5	1	11	0.620690	0.075658	9	0.689655	0.040160	5	0.827586	0.007925
9	5	2	16	0.555556	0.091767	13	0.638889	0.040152	8	0.777778	0.006618
9	5	3	20	0.534884	0.083722	17	0.604651	0.039249	12	0.720930	0.008063
9	5	4	25	0.500000	0.092920	22	0.560000	0.047915	16	0.680000	0.009130
9	5	5	30	0.473684	0.099791	26	0.543860	0.044813	20	0.649123	0.009980
9	6	1	15	0.558824	0.097278	12	0.647059	0.043681	7	0.794118	0.007617
9	6	2	19	0.547619	0.082476	16	0.619048	0.039079	11	0.738095	0.008189
9	6	3	24	0.510204	0.086697	21	0.571429	0.044388	15	0.693878	0.008372
9	6	4	29	0.491228	0.088247	26	0.543860	0.048185	19	0.666667	0.008313
9	6	5	34	0.468750	0.088358	30	0.531250	0.041791	23	0.640625	0.008178
9	6	6	39	0.458333	0.087572	35	0.513889	0.044093	27	0.625000	0.008005
9	7	1	18	0.538462	0.094755	15	0.615385	0.046318	9	0.769231	0.007240
9	7	2	23	0.510638	0.092339	20	0.574468	0.048129	14	0.702128	0.009452
9	7	3	28	0.490909	0.088931	25	0.545455	0.048734	18	0.672727	0.008511
9	7	4	34	0.460317	0.099728	30	0.523810	0.048091	23	0.634921	0.009883
9	7	5	39	0.450704	0.092938	35	0.507042	0.047167	27	0.619718	0.008744
9	7	6	45	0.430380	0.099994	40	0.493671	0.045852	32	0.594937	0.009751
9	7	7	50	0.425287	0.092778	45	0.482759	0.044526	36	0.586207	0.008675
9	8	1	21	0.522727	0.091613	18	0.590909	0.047877	12	0.727273	0.009402
9	8	2	26	0.509434	0.083606	23	0.566038	0.045645	16	0.698113	0.007832
9	8	3	32	0.475410	0.090200	28	0.540984	0.042843	21	0.655738	0.008515
9	8	4	38	0.457143	0.094142	34	0.514286	0.047762	26	0.628571	0.008914
9	8	5	44	0.435897	0.096461	39	0.500000	0.043813	31	0.602564	0.009177
9	8	6	50	0.425287	0.097552	45	0.482759	0.047178	36	0.586207	0.009342
9	8	7	56	0.410526	0.098037	51	0.463158	0.049980	41	0.568421	0.009437
9	8	8	62	0.403846	0.098020	56	0.461538	0.045624	46	0.557692	0.009473
9	9	1	24	0.510204	0.089203	21	0.571429	0.049174	14	0.714286	0.008606
9	9	2	30	0.482759	0.091114	26	0.551724	0.043471	19	0.672414	0.008661
9	9	3	36	0.462687	0.091244	32	0.522388	0.046073	24	0.641791	0.008468
9	9	4	42	0.447368	0.089294	38	0.500000	0.047313	29	0.618421	0.008104
9	9	5	49	0.423529	0.099468	44	0.482353	0.048059	35	0.588235	0.009520
9	9	6	55	0.414894	0.095225	50	0.468085	0.048205	40	0.574468	0.008960
9	9	7	61	0.407767	0.091262	56	0.456311	0.048100	45	0.563107	0.008460
9	9	8	68	0.392857	0.097772	62	0.446429	0.047751	51	0.544643	0.009469
9	9	9	74	0.388430	0.093398	68	0.438017	0.047321	56	0.537190	0.008904
10	1	1	0	1.000000	0.045455	0	1.000000	0.045455			
10	2	1	3	0.812500	0.072261	2	0.875000	0.039627	0	1.000000	0.006993
10	2	2	7	0.681818	0.095238	5	0.772727	0.041292	2	0.909091	0.007326
10	3	1	6	0.714286	0.074925	5	0.761905	0.049950	2	0.904762	0.009491
10	3	2	10	0.642857	0.079853	8	0.714286	0.039361	4	0.857143	0.006061
10	3	3	14	0.588235	0.082105	12	0.647059	0.044843	7	0.794118	0.006581
10	4	1	10	0.629630	0.094439	8	0.703704	0.049817	4	0.851852	0.009058
10	4	2	14	0.588235	0.087796	12	0.647059	0.049534	7	0.794118	0.007709
10	4	3	18	0.560976	0.080364	16	0.609756	0.047764	11	0.731707	0.009629
10	4	4	23	0.520833	0.090451	20	0.583333	0.045339	14	0.708333	0.007948
10	5	1	13	0.593750	0.085331	11	0.656250	0.048701	6	0.812500	0.007992
10	5	2	18	0.550000	0.092437	15	0.625000	0.043398	10	0.750000	0.008731
10	5	3	23	0.510638	0.096662	20	0.574468	0.049272	14	0.702128	0.009033
10	5	4	28	0.490909	0.097473	24	0.563636	0.042664	18	0.672727	0.009027
10	5	5	33	0.467742	0.096851	29	0.532258	0.045909	22	0.645161	0.008935
10	6	1	17	0.552632	0.096918	14	0.631579	0.046615	9	0.763158	0.009887
10	6	2	22	0.521739	0.095008	19	0.586957	0.048928	13	0.717391	0.009192
10	6	3	27	0.500000	0.091298	24	0.555556	0.049602	17	0.685185	0.008356
10	6	4	32	0.483871	0.086315	29	0.532258	0.049122	22	0.645161	0.009852
10	6	5	38	0.457143	0.095262	34	0.514286	0.048127	26	0.628571	0.008761
10	6	6	43	0.448718	0.088541	39	0.500000	0.046806	31	0.602564	0.009842
10	7	1	20	0.534884	0.087281	17	0.604651	0.044752	11	0.744186	0.008261
10	7	2	26	0.500000	0.096557	22	0.576923	0.042974	16	0.692308	0.009396
10	7	3	31	0.483333	0.086789	28	0.533333	0.049625	20	0.666667	0.007738
10	7	4	37	0.463768	0.090962	33	0.521739	0.045577	25	0.637681	0.008213

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Table 9: Critical values and exact p-values of the Concordance coefficient τ_c for k=3 samples.

Table 9 – continued from previous page

Sample Sizes			dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
10	7	5	43	0.441558	0.093529	39	0.493506	0.049803	30	0.610390	0.008552
10	7	6	49	0.430233	0.094802	44	0.488372	0.045397	35	0.593023	0.008781
10	7	7	55	0.414894	0.095476	50	0.468085	0.048288	40	0.574468	0.008936
10	8	1	24	0.510204	0.095314	20	0.591837	0.042629	14	0.714286	0.009362
10	8	2	30	0.482759	0.097293	26	0.551724	0.046727	19	0.672414	0.009415
10	8	3	36	0.462687	0.096898	32	0.522388	0.049214	24	0.641791	0.009154
10	8	4	42	0.447368	0.094647	37	0.513158	0.042505	29	0.618421	0.008738
10	8	5	48	0.435294	0.091545	43	0.494118	0.043502	34	0.600000	0.008310
10	8	6	54	0.425532	0.088149	49	0.478723	0.043991	40	0.574468	0.009585
10	8	7	61	0.407767	0.095600	55	0.466019	0.044145	45	0.563107	0.009021
10	8	8	67	0.401786	0.091405	61	0.455357	0.044080	50	0.553571	0.008511
10	9	1	27	0.500000	0.086557	24	0.555556	0.049882	16	0.703704	0.007882
10	9	2	34	0.468750	0.097666	30	0.531250	0.049878	22	0.656250	0.009353
10	9	3	40	0.452055	0.091779	36	0.506849	0.048772	27	0.630137	0.008369
10	9	4	47	0.433735	0.097637	42	0.493976	0.046800	33	0.602410	0.009150
10	9	5	53	0.423913	0.089682	48	0.478261	0.044758	39	0.576087	0.009781
10	9	6	60	0.411765	0.092986	55	0.460784	0.048988	44	0.568627	0.008606
10	9	7	67	0.396396	0.095498	61	0.450450	0.046335	50	0.549550	0.009061
10	9	8	74	0.388430	0.097309	68	0.438017	0.049566	56	0.537190	0.009435
10	9	9	81	0.376923	0.098701	74	0.430769	0.046792	62	0.523077	0.009745
10	10	1	31	0.483333	0.092777	27	0.550000	0.047070	19	0.683333	0.008615
10	10	2	38	0.457143	0.097689	33	0.528571	0.044350	25	0.642857	0.009229
10	10	3	45	0.437500	0.099986	40	0.500000	0.048153	31	0.612500	0.009472
10	10	4	51	0.433333	0.088023	46	0.488889	0.043698	37	0.588889	0.009472
10	10	5	59	0.410000	0.098994	53	0.470000	0.045715	43	0.570000	0.009375
10	10	6	66	0.400000	0.097217	60	0.454545	0.047170	49	0.554545	0.009231
10	10	7	73	0.391667	0.095144	67	0.441667	0.048198	55	0.541667	0.009064
10	10	8	80	0.384615	0.092953	74	0.430769	0.048911	61	0.530769	0.008881
10	10	9	88	0.371429	0.099700	81	0.421429	0.049390	68	0.514286	0.009996
10	10	10	95	0.366667	0.096934	88	0.413333	0.049695	74	0.506667	0.009709

Table 9: Critical values and exact p-values of the Concordance coefficient τ_c for k=3 samples.

Sample Sizes				.10			.05			.01		
				dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
2	2	1	1									
2	2	2	1	0	1.000000	0.038095	0	1.000000	0.038095			
2	2	2	2	2	0.833333	0.095238	1	0.916667	0.038095	0	1.000000	0.009524
3	1	1	1									
3	2	1	1	0	1.000000	0.057143						
3	2	2	1	1	0.909091	0.050000	0	1.000000	0.014286			
3	2	2	2	3	0.800000	0.077778	2	0.866667	0.036508	0	1.000000	0.003175
3	3	1	1	1	0.888889	0.075000	0	1.000000	0.021429			
3	3	2	1	3	0.785714	0.097619	2	0.857143	0.046429	0	1.000000	0.004762
3	3	2	2	5	0.722222	0.097143	3	0.833333	0.027619	1	0.944444	0.003810
3	3	3	1	4	0.750000	0.069286	3	0.812500	0.034286	1	0.937500	0.005714
3	3	3	2	7	0.681818	0.096883	5	0.772727	0.034805	3	0.863636	0.008442
3	3	3	3	9	0.640000	0.084091	7	0.720000	0.034221	4	0.840000	0.005325
4	1	1	1									
4	2	1	1	1	0.900000	0.085714	0	1.000000	0.028571			
4	2	2	1	2	0.857143	0.055556	1	0.928571	0.022222	0	1.000000	0.006349
4	2	2	2	4	0.777778	0.064444	3	0.833333	0.033016	1	0.944444	0.005079
4	3	1	1	2	0.833333	0.076190	1	0.916667	0.033333	0	1.000000	0.009524
4	3	2	1	4	0.764706	0.077619	3	0.823529	0.041429	1	0.941176	0.007143
4	3	2	2	6	0.727273	0.068312	5	0.772727	0.040173	2	0.909091	0.004329
4	3	3	1	6	0.714286	0.081299	5	0.761905	0.048571	2	0.904762	0.005584
4	3	3	2	9	0.653846	0.092309	7	0.730769	0.038615	4	0.846154	0.006342
4	3	3	3	11	0.645161	0.071618	10	0.677419	0.048871	6	0.806452	0.006678
4	4	1	1	3	0.812500	0.060952	2	0.875000	0.032381	0	1.000000	0.003810
4	4	2	1	6	0.714286	0.089004	4	0.809524	0.031169	2	0.904762	0.007100
4	4	2	2	8	0.692308	0.068283	7	0.730769	0.043579	4	0.846154	0.007734
4	4	3	1	8	0.680000	0.078672	6	0.760000	0.030996	4	0.840000	0.009264
4	4	3	2	11	0.645161	0.078326	9	0.709677	0.035791	6	0.806452	0.007792
4	4	3	3	14	0.611111	0.077325	12	0.666667	0.038965	8	0.777778	0.006591

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Table 10: Critical values and exact p-values of the Concordance coefficient τ_c for k=4 samples.

Table 10 – continued from previous page

Sample Sizes				dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
4	4	4	1	11	0.633333	0.095984	9	0.700000	0.045594	5	0.833333	0.005808
4	4	4	2	14	0.611111	0.084038	12	0.666667	0.043035	8	0.777778	0.007570
4	4	4	3	18	0.571429	0.097366	15	0.642857	0.040186	11	0.738095	0.008775
4	4	4	4	21	0.562500	0.083959	19	0.604167	0.049523	14	0.708333	0.009514
5	1	1	1	0	1.000000	0.071429						
5	2	1	1	1	0.909091	0.047619	1	0.909091	0.047619			
5	2	2	1	3	0.812500	0.058730	2	0.875000	0.028571	0	1.000000	0.003175
5	2	2	2	6	0.714286	0.091631	4	0.809524	0.030592	2	0.904762	0.006638
5	3	1	1	3	0.785714	0.076190	2	0.857143	0.040476	0	1.000000	0.004762
5	3	2	1	5	0.750000	0.065584	4	0.800000	0.037662	2	0.900000	0.008874
5	3	2	2	8	0.680000	0.079221	6	0.760000	0.031025	4	0.840000	0.009235
5	3	3	1	8	0.652174	0.092388	6	0.739130	0.036905	3	0.869565	0.005519
5	3	3	2	11	0.633333	0.089419	9	0.700000	0.041492	6	0.800000	0.009232
5	3	3	3	14	0.588235	0.087484	12	0.647059	0.044634	8	0.764706	0.007746
5	4	1	1	5	0.722222	0.087446	3	0.833333	0.030303	1	0.944444	0.006061
5	4	2	1	8	0.666667	0.099279	6	0.750000	0.041631	3	0.875000	0.006854
5	4	2	2	11	0.633333	0.096947	9	0.700000	0.045865	5	0.833333	0.005972
5	4	3	1	10	0.655172	0.077312	8	0.724138	0.034466	5	0.827586	0.007126
5	4	3	2	14	0.600000	0.093723	12	0.657143	0.048620	8	0.771429	0.008841
5	4	3	3	17	0.585366	0.082249	15	0.634146	0.045133	10	0.756098	0.006435
5	4	4	1	13	0.617647	0.082489	11	0.676471	0.041660	7	0.794118	0.006974
5	4	4	2	17	0.585366	0.088025	15	0.634146	0.048942	10	0.756098	0.007269
5	4	4	3	21	0.553191	0.091439	18	0.617021	0.040930	13	0.723404	0.007254
5	4	4	4	25	0.537037	0.091748	22	0.592593	0.044712	17	0.685185	0.009977
5	5	1	1	7	0.666667	0.098966	5	0.761905	0.041126	2	0.904762	0.006854
5	5	2	1	10	0.642857	0.094933	8	0.714286	0.044483	4	0.857143	0.005606
5	5	2	2	13	0.617647	0.083004	11	0.676471	0.041903	7	0.794118	0.007191
5	5	3	1	13	0.593750	0.093169	11	0.656250	0.047627	7	0.781250	0.008432
5	5	3	2	17	0.575000	0.097342	14	0.650000	0.039675	10	0.750000	0.008422
5	5	3	3	20	0.555556	0.078592	18	0.600000	0.045644	13	0.711111	0.008304
5	5	4	1	16	0.589744	0.086815	14	0.641026	0.047844	9	0.769231	0.006849
5	5	4	2	20	0.565217	0.083163	18	0.608696	0.048813	13	0.717391	0.009174
5	5	4	3	25	0.528302	0.099365	22	0.584906	0.048982	16	0.698113	0.007882
5	5	4	4	29	0.516667	0.091307	26	0.566667	0.047580	20	0.666667	0.009275
5	5	5	1	19	0.558140	0.082239	17	0.604651	0.047987	12	0.720930	0.008799
5	5	5	2	24	0.538462	0.091195	21	0.596154	0.044209	16	0.692308	0.009718
5	5	5	3	29	0.500000	0.098583	25	0.568966	0.040931	19	0.672414	0.007511
5	5	5	4	33	0.507463	0.084597	30	0.552239	0.046171	23	0.656716	0.007853
5	5	5	5	38	0.479452	0.088106	34	0.534247	0.041674	27	0.630137	0.008096
6	1	1	1	0	1.000000	0.047619	0	1.000000	0.047619			
6	2	1	1	2	0.857143	0.066667	1	0.928571	0.028571	0	1.000000	0.009524
6	2	2	1	4	0.789474	0.060462	3	0.842105	0.032468	1	0.947368	0.006061
6	2	2	2	7	0.708333	0.077201	6	0.750000	0.048485	3	0.875000	0.007504
6	3	1	1	4	0.764706	0.075325	3	0.823529	0.042857	1	0.941176	0.009091
6	3	2	1	7	0.695652	0.088095	5	0.782609	0.033983	3	0.869565	0.009848
6	3	2	2	10	0.655172	0.087568	8	0.724138	0.039494	5	0.827586	0.008225
6	3	3	1	10	0.642857	0.099459	8	0.714286	0.045538	4	0.857143	0.005370
6	3	3	2	13	0.617647	0.085707	11	0.676471	0.043064	7	0.794118	0.007064
6	3	3	3	16	0.600000	0.075737	14	0.650000	0.040621	10	0.750000	0.008509
6	4	1	1	6	0.727273	0.073737	5	0.772727	0.046609	2	0.909091	0.007792
6	4	2	1	9	0.678571	0.074026	7	0.750000	0.032534	4	0.857143	0.006460
6	4	2	2	13	0.617647	0.092254	11	0.676471	0.047099	7	0.794118	0.008249
6	4	3	1	12	0.636364	0.074599	10	0.696970	0.036371	7	0.787879	0.009576
6	4	3	2	16	0.600000	0.080891	14	0.650000	0.043967	10	0.750000	0.009549
6	4	3	3	20	0.565217	0.085039	18	0.608696	0.049821	13	0.717391	0.009305
6	4	4	1	16	0.589744	0.094578	13	0.666667	0.037925	9	0.769231	0.007777
6	4	4	2	20	0.565217	0.090522	17	0.630435	0.040149	12	0.739130	0.006927
6	4	4	3	24	0.547170	0.085709	21	0.603774	0.040995	16	0.698113	0.008781
6	4	4	4	29	0.516667	0.097941	25	0.583333	0.040644	19	0.683333	0.007460
6	5	1	1	8	0.680000	0.073704	7	0.720000	0.049728	3	0.880000	0.006494
6	5	2	1	12	0.625000	0.089767	10	0.687500	0.045692	6	0.812500	0.007992
6	5	2	2	16	0.589744	0.095524	13	0.666667	0.038420	9	0.769231	0.008052
6	5	3	1	15	0.605263	0.079615	13	0.657895	0.042893	9	0.763158	0.009229
6	5	3	2	20	0.555556	0.098821	17	0.622222	0.044475	12	0.733333	0.007945
6	5	3	3	24	0.538462	0.093325	21	0.596154	0.045191	16	0.692308	0.009911
6	5	4	1	19	0.568182	0.088703	16	0.636364	0.038969	12	0.727273	0.009856
6	5	4	2	24	0.538462	0.098090	21	0.596154	0.048090	15	0.711538	0.007604

Continued on next page

Table 10: Critical values and exact p-values of the Concordance coefficient τ_c for $k=4$ samples.

Table 10 – continued from previous page

Sample Sizes				dis	τ_c	p-value	dis	τ_c	p-value	dis	τ_c	p-value
6	5	4	3	28	0.525424	0.085898	25	0.576271	0.044131	19	0.677966	0.008293
6	5	4	4	33	0.507463	0.090101	30	0.552239	0.049583	23	0.656716	0.008625
6	5	5	1	23	0.540000	0.096573	20	0.600000	0.047042	14	0.720000	0.007284
6	5	5	2	28	0.517241	0.097004	24	0.586207	0.040080	18	0.689655	0.007270
6	5	5	3	33	0.500000	0.096429	29	0.560606	0.043157	23	0.651515	0.009514
6	5	5	4	38	0.486486	0.093108	34	0.540541	0.044474	27	0.635135	0.008812
6	5	5	5	43	0.475610	0.090015	39	0.524390	0.045390	31	0.621951	0.008195
6	6	1	1	11	0.633333	0.097617	8	0.733333	0.034775	5	0.833333	0.009134
6	6	2	1	14	0.621622	0.076902	12	0.675676	0.041463	8	0.783784	0.008910
6	6	2	2	19	0.568182	0.097046	16	0.636364	0.043344	11	0.750000	0.007713
6	6	3	1	18	0.581395	0.081966	16	0.627907	0.047471	11	0.744186	0.008665
6	6	3	2	23	0.549020	0.091718	20	0.607843	0.044161	15	0.705882	0.009600
6	6	3	3	28	0.517241	0.099031	24	0.586207	0.040890	18	0.689655	0.007417
6	6	4	1	22	0.560000	0.082630	19	0.620000	0.038997	14	0.720000	0.008129
6	6	4	2	27	0.534483	0.084812	24	0.586207	0.043401	18	0.689655	0.008070
6	6	4	3	32	0.515152	0.085020	29	0.560606	0.046268	22	0.666667	0.007791
6	6	4	4	38	0.486486	0.098717	34	0.540541	0.047595	27	0.635135	0.009613
6	6	5	1	26	0.535714	0.082947	23	0.589286	0.042216	17	0.696429	0.007727
6	6	5	2	32	0.507692	0.095002	28	0.569231	0.042368	22	0.661538	0.009272
6	6	5	3	37	0.493151	0.088417	33	0.547945	0.041732	26	0.643836	0.008054
6	6	5	4	43	0.475610	0.094851	39	0.524390	0.048227	31	0.621951	0.008874
6	6	5	5	48	0.466667	0.086446	44	0.511111	0.045656	36	0.600000	0.009533
6	6	6	1	31	0.507936	0.098636	27	0.571429	0.044191	21	0.666667	0.009750
6	6	6	2	36	0.500000	0.087213	32	0.555556	0.041053	25	0.652778	0.007871
6	6	6	3	42	0.481481	0.090321	38	0.530864	0.045479	30	0.629630	0.008168
6	6	6	4	48	0.466667	0.090941	44	0.511111	0.048376	35	0.611111	0.008207
6	6	6	5	54	0.454545	0.090669	49	0.505051	0.043100	40	0.595960	0.008145
6	6	6	6	60	0.444444	0.089781	55	0.490741	0.044896	46	0.574074	0.009741

Table 10: Critical values and exact p-values of the Concordance coefficient τ_c for k=4 samples.

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