

Excerpt from Chapter 5 of:

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5.3 Rank correlations

Textbooks of nonparametric statistics propose a few methods only for the analysis of bi- or multivariate semiquantitative data. Section 5.1 has shown that there actually exist many numerical approaches for analysing multidimensional data, corresponding to all levels of precision (Table 5.1). These methods, which include most of those described in this book, belong to *nonparametric statistics* in a general sense, because they do not focus on the parameters of the data distributions. Within the specific realm of *ranking tests*, however, the only statistical techniques available for

Table 5.3 Numerical example. Perfect rank correlation between descriptors y_1 and y_2 .

Objects (observation units)	Ranks of objects on the two descriptors	
	y_1	y_2
x_1	5	5
x_2	1	1
x_3	4	4
x_4	2	2
x_5	3	3

multidimensional semiquantitative data are two *rank correlation coefficients* (Spearman r and Kendall τ), which both quantify the relationship between two descriptors, and the *coefficient of concordance* (Kendall W), which assesses the relationship among several descriptors. These are described in some detail in the present section.

Spearman
corr. coeff.

The Spearman r statistic, also called ρ (rho), is based on the idea that two descriptors y_1 and y_2 carry the same information if the largest object on y_1 also has the highest rank on y_2 , and so on for all other objects. Two descriptors are said to be in perfect correlation when the ranks of all object are the same on both descriptors, as in the numerical example of Table 5.3. If, however, object x_1 which has rank 5 on y_1 had rank 2 on y_2 , it would be natural to use the difference between these ranks $d_1 = (y_{11} - y_{12}) = (5 - 2) = 3$ as a measure of the difference between the two descriptors, for this object. For the whole set of objects, differences d_i are squared before summing them, in order to prevent differences with opposite signs from cancelling each other out.

The expression for the Spearman r may be derived from the general formula of correlation coefficients (Kendall, 1948):

$$r_{jk} = \frac{\sum_{i=1}^n (y_{ij} - \bar{y}_j)(y_{ik} - \bar{y}_k)}{\sqrt{\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 \sum_{i=1}^n (y_{ik} - \bar{y}_k)^2}} \quad (5.1)$$

For ranked data, the average ranks \bar{y}_j and \bar{y}_k are equal, so that $(y_{ij} - \bar{y}_j) - (y_{ik} - \bar{y}_k) = (y_{ij} - y_{ik})$. One can write the difference between the ranks of object i on the two descriptors as $d_i = (y_{ij} - y_{ik}) = (y_{ij} - \bar{y}_j) - (y_{ik} - \bar{y}_k)$, which leads to:

$$\sum_{i=1}^n d_i^2 = \sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 + \sum_{i=1}^n (y_{ik} - \bar{y}_k)^2 - 2 \sum_{i=1}^n (y_{ij} - \bar{y}_j)(y_{ik} - \bar{y}_k)$$

Isolating the right-hand sum gives:

$$\sum_{i=1}^n (y_{ij} - \bar{y}_j)(y_{ik} - \bar{y}_k) = \frac{1}{2} \left[\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 + \sum_{i=1}^n (y_{ik} - \bar{y}_k)^2 - \sum_{i=1}^n d_i^2 \right]$$

Using this result, eq. 5.1 is rewritten as:

$$r_{jk} = \frac{\frac{1}{2} \left[\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 + \sum_{i=1}^n (y_{ik} - \bar{y}_k)^2 - \sum_{i=1}^n d_i^2 \right]}{\sqrt{\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 \sum_{i=1}^n (y_{ik} - \bar{y}_k)^2}} \quad (5.2)$$

The sum of ranks for each descriptor, which is the sum of the first n integers, is equal to $n(n+1)/2$ and the sum of their squares is $\sum_{i=1}^n y_{ij}^2 = n(n+1)(2n+1)/6$. Since the sum of deviations from the mean rank is

$$\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 = \sum_{i=1}^n y_{ij}^2 - \frac{1}{n} \left(\sum_{i=1}^n y_{ij} \right)^2$$

one can write:

$$\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 = \frac{n(n+1)(2n+1)}{6} - \frac{1}{n} \left[\frac{n^2(n+1)^2}{4} \right] = \frac{n^3 - n}{12}$$

It follows that, when using ranks, the numerator of eq. 5.2 becomes:

$$\frac{1}{2} \left[\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 + \sum_{i=1}^n (y_{ik} - \bar{y}_k)^2 - \sum_{i=1}^n d_i^2 \right] = \frac{1}{2} \left[\frac{n^3 - n}{12} + \frac{n^3 - n}{12} - \sum_{i=1}^n d_i^2 \right]$$

while its denominator reduces to:

$$\sqrt{\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 \sum_{i=1}^n (y_{ik} - \bar{y}_k)^2} = \sqrt{\left(\frac{n^3 - n}{12} \right) \left(\frac{n^3 - n}{12} \right)} = \frac{n^3 - n}{12}$$

Table 5.4 Numerical example. Ranks of four objects on two descriptors, y_1 and y_2 .

Objects (observation units)	Ranks of objects on the two descriptors	
	y_1	y_2
x_1	3	3
x_2	4	1
x_3	2	4
x_4	1	2

The final formula is obtained by replacing the above two expressions in eq. 5.2. This development shows that, when using ranks, eq. 5.1 simplifies to the following formula for Spearman's r :

$$r_{jk} = \frac{\frac{1}{2} \left[\frac{n^3 - n}{12} + \frac{n^3 - n}{12} - \sum_{i=1}^n d_i^2 \right]}{\frac{n^3 - n}{12}} = 1 - \frac{6 \sum_{i=1}^n d_i^2}{n^3 - n} \quad (5.3)$$

Alternatively, the Spearman rank correlation coefficient may be obtained in two steps: (1) replace all observations by ranks (columnwise) and (2) compute the Pearson correlation coefficient (eq. 4.7) between the ranked variables. The result is the same as obtained from eq. 5.3.

The Spearman r coefficient varies between +1 and -1, just like the Pearson r . Descriptors that are perfectly matched, in terms of ranks, exhibit values $r = +1$ (direct relationship) or $r = -1$ (inverse relationship), whereas $r = 0$ indicates the absence of a monotonic relationship between the two descriptors. (Relationships that are not monotonic, e.g. Fig. 4.4d, can be quantified using polynomial or nonlinear regression, or else contingency coefficients; see Sections 6.2 and 10.3.)

Numerical example. A small example (ranked data, Table 5.4) illustrates the equivalence between eq. 5.1 computed on ranks and eq. 5.3. Using eq. 5.1 gives:

$$r_{12} = \frac{-2}{\sqrt{5 \times 5}} = \frac{-2}{5} = -0.4$$

The same result is obtained from eq. 5.3:

$$r_{12} = 1 - \frac{6 \times 14}{4^3 - 4} = 1 - \frac{84}{60} = 1 - 1.4 = -0.4$$

Two or more objects may have the same rank on a given descriptor. This is often the case with descriptors used in ecology, which may have a small number of states or ordered classes. Such observations are said to be *tied*. Each of them is assigned the average of the ranks which would have been assigned had no ties occurred. If the proportion of tied observations is large, correction factors must be introduced into the sums of squared deviations of eq. 5.2, which become:

$$\sum_{i=1}^n (y_{ij} - \bar{y}_j)^2 = \frac{1}{12} \left[(n^3 - n) - \sum_{r=1}^q (t_{rj}^3 - t_{rj}) \right]$$

and

$$\sum_{i=1}^n (y_{ik} - \bar{y}_k)^2 = \frac{1}{12} \left[(n^3 - n) - \sum_{r=1}^s (t_{rk}^3 - t_{rk}) \right]$$

where t_{rj} and t_{rk} are the numbers of observations in descriptors \mathbf{y}_j and \mathbf{y}_k which are tied at ranks r , these values being summed over the q sets of tied observations in descriptor j and the s sets in descriptor k .

Significance of the Spearman r is usually tested against the null hypothesis $H_0: r = 0$. When $n \geq 10$, the test statistic is the same as for Pearson's r (eq. 4.13):

$$t = \sqrt{v} \frac{r_{ki}}{\sqrt{1 - r_{ki}^2}} \quad (5.4)$$

H_0 is tested by comparing statistic t to the value found in a table of critical values of t , with $v = n - 2$ degrees of freedom. H_0 is rejected when the probability corresponding to t is smaller than a predetermined level of significance (α , for a two-tailed test). The rules for one-tailed and two-tailed tests are the same as for the Pearson r (Section 4.2). When $n < 10$, which is not often the case in ecology, one must refer to a special table of critical values of the Spearman rank correlation coefficient, found in textbooks of nonparametric statistics.

Kendall
corr. coeff.

Kendall's τ (tau) is another rank correlation coefficient, which can be used for the same types of descriptors as Spearman's r . One major advantage of τ over Spearman's r is that the former can be generalized to a partial correlation coefficient (below), which is not the case for the latter. While Spearman's r was based on the differences between the ranks of objects on the two descriptors being compared, Kendall's τ refers to a somewhat different concept, which is best explained using an example.

Numerical example. Kendall's τ is calculated on the example of Table 5.4, already used for computing Spearman's r . In Table 5.5, the order of the objects was rearranged so as to obtain increasing ranks on one of the two descriptors (here \mathbf{y}_1). The Table is used to determine the degree of dependence between the two descriptors. Since the ranks are now in increasing order

Table 5.5 Numerical example. The order of the four objects from Table 5.4 has been rearranged in such a way that the ranks on y_1 are now in increasing order

Objects (observation units)	Ranks of objects on the two descriptors	
	y_1	y_2
x_4	1	2
x_3	2	4
x_1	3	3
x_2	4	1

on y_1 , it is sufficient to determine how many *pairs of ranks* are also in increasing order on y_2 to obtain a measure of the association between the two descriptors. Considering the object in first rank (i.e. x_4), at the top of the right-hand column, the first pair of ranks (2 and 4, belonging to objects x_4 and x_3) is in increasing order; a score of +1 is assigned to it. The same goes for the second pair (2 and 3, belonging to objects x_4 and x_1). The third pair of ranks (2 and 1, belonging to objects x_4 and x_2) is in decreasing order, however, so that it earns a negative score -1. The same operation is repeated for every object in successive ranks along y_1 , i.e. for the object in second rank (x_3): first pair of ranks (4 and 3, belonging to objects x_3 and x_1), etc. The sum S of scores assigned to each of the $n(n-1)/2$ different pairs of ranks is then computed.

Kendall's rank correlation coefficient is defined as follows:

$$\tau_a = \frac{S}{n(n-1)/2} = \frac{2S}{n(n-1)} \quad (5.5)$$

where S stands for "sum of scores". Kendall's τ_a is thus the sum of scores for pairs in increasing and decreasing order, divided by the total number of pairs $(n(n-1)/2)$. For the example of Tables 5.4 and 5.5, τ_a is:

$$\tau_a = \frac{2(1+1-1-1-1-1)}{4 \times 3} = \frac{2(-2)}{12} = -0.33$$

Clearly, in the case of perfect agreement between two descriptors, all pairs receive a positive score, so that $S = n(n-1)/2$ and thus $\tau_a = +1$. When there is complete disagreement, $S = -n(n-1)/2$ and thus $\tau_a = -1$. When the descriptors are totally unrelated, the positive and negative scores cancel out, so that S as well as τ_a are near 0.

Equation 5.5 cannot be used for computing τ when there are tied observations. This is often the case with ecological *semiquantitative* descriptors, which may have a small number of states. The Kendall rank correlation is then computed on a contingency table (see Chapter 6) crossing two semiquantitative descriptors.

Table 5.6 Numerical example. Contingency table giving the distribution of 80 objects among the states of two semiquantitative descriptors, **a** and **b**. Numbers in the table are frequencies (f).

	b_1	b_2	b_3	b_4	t_j
a_1	20	10	10	0	40
a_2	0	10	0	10	20
a_3	0	0	10	0	10
a_4	0	0	0	10	10
t_k	20	20	20	20	80

Table 5.6 is a contingency table crossing two ordered descriptors. For example, descriptor **a** could represent the relative abundances of arthropods in soil enumerated on a semiquantitative scale (e.g. absent, present, abundant and very abundant), while descriptor **b** could be the concentration of organic matter in the soil, divided into 4 classes. For simplicity, descriptors are called **a** and **b** here, as in Chapter 6. The states of **a** vary from 1 to r (number of rows) while the states of **b** go from 1 to c (number of columns).

To compute τ with tied observations, S is calculated as the difference between the numbers of positive (P) and negative (Q) scores, $S = P - Q$. P is the sum of all frequencies f in the contingency table, each one multiplied by the sum of all frequencies located *lower* and on its *right*:

$$P = \sum_{j=1}^r \sum_{k=1}^c \left[f_{jk} \times \sum_{l=j+1}^r \sum_{m=k+1}^c f_{lm} \right]$$

Likewise, Q is the sum of all frequencies f in the table, each one multiplied by the sum of all frequencies *lower* and on its *left*:

$$Q = \sum_{j=1}^r \sum_{k=1}^c \left[f_{jk} \times \sum_{l=j+1}^r \sum_{m=1}^{k-1} f_{lm} \right]$$

Numerical example. For Table 5.6:

$$P = (20 \times 40) + (10 \times 30) + (10 \times 20) + (10 \times 20) + (10 \times 10) = 1600$$

$$Q = (10 \times 10) + (10 \times 10) = 200$$

$$S = P - Q = 1600 - 200 = 1400$$

Using this value S , there are two approaches for calculating τ , depending on the numbers of states in the two descriptors. When \mathbf{a} and \mathbf{b} have the same numbers of states ($r = c$), τ_b is computed using a formula that includes the total number of pairs $n(n-1)/2$, as in the case of τ_a (eq. 5.5). The difference with eq. 5.5 is that τ_b includes corrections for the number of pairs L_1 tied in \mathbf{a} and the number of pairs L_2 tied in \mathbf{b} , where

$$L_1 = \sum_{j=1}^r \frac{1}{2} t_j (t_j - 1) \text{ in which } t_j \text{ is the marginal total for row } j$$

$$L_2 = \sum_{k=1}^c \frac{1}{2} t_k (t_k - 1) \text{ in which } t_k \text{ is the marginal total for column } k.$$

The formula for τ_b is:

$$\tau_b = \frac{S}{\sqrt{\frac{1}{2} n (n - 1) - L_1} \sqrt{\frac{1}{2} n (n - 1) - L_2}} \quad (5.6)$$

When there are no tied observations, $L_1 = L_2 = 0$ and eq. 5.6 becomes identical to eq. 5.5.

Numerical example. For Table 5.6:

$$L_1 = \frac{40 \times 39}{2} + \frac{20 \times 19}{2} + \frac{10 \times 9}{2} + \frac{10 \times 9}{2} = 1060$$

$$L_2 = \frac{20 \times 19}{2} + \frac{20 \times 19}{2} + \frac{20 \times 19}{2} + \frac{20 \times 19}{2} = 760$$

$$\tau_b = \frac{1400}{\sqrt{\frac{1}{2} (80 \times 79) - 1060} \sqrt{\frac{1}{2} (80 \times 79) - 760}} = 0.62$$

Without correction for ties, the calculated value (eq. 5.5) would have been

$$\tau_a = (2 \times 1400) / (80 \times 79) = 0.44$$

The second approach for calculating τ with tied observations should be used when \mathbf{a} and \mathbf{b} do not have the same number of states ($r \neq c$). The formula for τ_c uses the minimum number of states in either \mathbf{a} or \mathbf{b} , $\min(r, c)$:

$$\tau_c = \frac{S}{\frac{1}{2} n^2 \left(\frac{\min - 1}{\min} \right)} \quad (5.7)$$

The significance of Kendall's τ is tested by reference to the null hypothesis $H_0: r=0$ (i.e. independence of the two descriptors). A test statistic is obtained by transforming τ into z (or t_{α}) using the following formula (Kendall, 1948):

$$z = \left[|\tau| \sqrt{\frac{9n(n-1)}{2(2n+5)}} \right] - \sqrt{\frac{18}{n(n-1)(2n+5)}} \quad (5.8)$$

When $n \geq 30$, the second term of eq. 5.8 becomes negligible (at $n=30$, the value of this term is only 0.0178). For $n \geq 10$, the sampling distribution of τ is almost the same as the normal distribution, so that H_0 is tested using a table of z . Since z tables are one-tailed, the z statistic of eq. 5.8 may be used directly for one-tailed tests by comparing it to the value z_{α} read in the table. For two-tailed tests, the statistic is compared to the value $z_{\alpha/2}$ from the z table. When $n < 10$, which is seldom the case in ecology, one should refer to Table B, at the end of this book. Table B gives the critical values of τ_{α} for $4 \leq n \leq 50$ (one-tailed and two-tailed tests).

Spearman's r provides a better approximation of Pearson's r when the data are almost quantitative and there are but a few tied observations, whereas Kendall's τ does better when there are many ties. Computing both Spearman's r and Kendall's τ_a on the same numerical example, above, produced different numerical values (i.e. $r = -0.40$ versus $\tau_a = -0.33$). This is because the two coefficients have different underlying scales, so that their numerical values cannot be directly compared. However, given their different sampling distributions, they both reject H_0 at the same level of significance. If applied to quantitative data that are meeting all the requirements of Pearson's r , both Spearman's r and Kendall's τ have power nearly as high (about 91%; Hotelling & Pabst, 1936) as their parametric equivalent. In all other cases, they are more powerful than Pearson's r . This refers to the notion of *power* of statistical tests: a test is more powerful than another if it is more likely to detect small deviations from H_0 (i.e. smaller type II error), for constant type I error.

Power

The chief advantage of Kendall's τ over Spearman's r , as already mentioned, is that it can be generalized to a partial correlation coefficient, which cannot be done with Spearman's (Siegel, 1956: 214). The formula for a partial τ is:

$$\tau_{12.3} = \frac{\tau_{12} - \tau_{13}\tau_{23}}{\sqrt{1 - \tau_{13}^2} \sqrt{1 - \tau_{23}^2}} \quad (5.9)$$

This formula is algebraically the same as that of first-order partial Pearson r (eq. 4.36) although, according to Kendall (1948: 103), this would be merely coincidental because the two formulae are derived using entirely different approaches. The three τ coefficients on the right-hand side of eq. 5.9 may themselves be partial τ 's, thus allowing one to control for more than one descriptor (i.e. high order partial correlation coefficients). Siegel & Castellan (1988) give tables for testing the significance of the Kendall partial correlation coefficient.

Rank correlation coefficients should not be used in the Q mode, i.e. for comparing objects instead of descriptors. This is also the case for the Pearson r (Section 7.5). The reasons for this are the following:

- While physical dimensions disappear when computing correlation coefficients between variables expressed in different units, the same coefficients computed between objects have complex and non-interpretable physical dimensions.
- Physical descriptors are usually expressed in somewhat arbitrary units (e.g. mm, cm, m, or km are all equally correct, in principle). Any arbitrary change in units could dramatically change the values of correlations computed between objects.
- Descriptors may be standardized first to alleviate these problems but standardization of quantitative descriptors, before rank-ordering the data within objects, changes the values along object vectors in a nonmonotonic way. The correlation between two objects is a function of the values of all the other objects in the data set.
- Consider species abundance data. At most sampling sites, several species are represented by a small number of individuals, this number being subject to stochastic variability. It follows that their ranks, in a given observation unit, may not strictly correspond to their quantitative importance in the ecosystem. A rank correlation coefficient computed between observation units would thus have high variance since it would be computed on many uncertain ranks, giving a preponderant importance to the many poorly sampled species.
- While the central limit theorem insures that means, variances, covariances, and correlations converge towards their population values when the number of objects increases, computing these same parameters in the Q mode is likely to have the opposite effect since the addition of new variables into the calculations is likely to change the values of these parameters in a non-trivial way.
- Correlation coefficients can be tested by the method of permutations, as described in Subsection 1.2.3. In the R mode, permuting the values of a variable within a column makes physical sense: under H_0 , that value could be found at any one site. In the Q mode, however, permuting values within a row of the data matrix does not make sense because, in the real world, these values could not belong to different variables. As an illustration, it would not make sense to move a salinity of 35 psu to the pH column.

Kendall
coeff. of
concordance

The rank correlation coefficients described above measure the correlation for pairs of descriptors, based on n objects. In contrast, Kendall's coefficient of concordance W measures the relationship among *several* rank-ordered variables for n objects. In Table 5.1, Kendall's W is listed as equivalent to the coefficient of multiple linear correlation R , but the approach is actually quite different.

The analysis is conducted on a table which contains, in each column, the ranks of the n objects on one of the p descriptors, e.g. Table 5.7. Friedman (1937) has shown

that, when the number of rows and/or columns is large enough, the following statistic is approximately distributed as χ^2 with $\nu = n - 1$ degrees of freedom:

$$X^2 = \left[\frac{12}{pn(n+1)} \sum_{i=1}^n R_i^2 \right] - 3p(n+1) \quad (5.10)$$

where R_i is the sum of the ranks for row i . This is Friedman's statistic for two-way analysis of variance by ranks. Kendall's coefficient of concordance (Kendall, 1948) can be obtained by transforming the Friedman's X^2 statistic as follows:

$$W = \frac{X^2}{p(n-1)} \quad (5.11)$$

It can be shown that the following expression is equivalent to eq. 5.11:

$$W = \frac{12 \sum_{i=1}^n (R_i - \bar{R})^2}{p^2 (n^3 - n)} \quad (5.12)$$

Kendall's W statistic is simply the variance of the row sums of ranks R_i divided by the maximum possible value that this variance can take; this occurs when all variables are in total agreement. Hence $0 \leq W \leq 1$. Two properties are used to demonstrate the equivalence of eqs. 5.11 and 5.12. The first one is that

$$\sum_{i=1}^n (R_i - \bar{R})^2 = \sum_{i=1}^n R_i^2 - \frac{1}{n} \left(\sum_{i=1}^n R_i \right)^2$$

and the second is that the sum of the all R_i values in the table is $pn(n+1)/2$.

In the presence of tied values, the formula is modified as follows:

*** develop from the Kendall paper***

When there are no ties, W can be computed from the mean, r , of the Spearman correlations among all variables (Siegel & Castellan 1988):

$$W = \frac{(p-1)r + 1}{p} \quad (5.13)$$

Table 5.7 Numerical example. Ranks of six objects on three descriptors, y_1 , y_2 , and y_3 .

Objects (observation units)	Ranks of objects on the three descriptors			Row sums
	y_1	y_2	y_3	R_i
x_1	1	1	6	8
x_2	6	5	3	14
x_3	3	6	2	11
x_4	2	4	5	11
x_5	5	2	4	11
x_6	4	3	1	8

Coefficient W varies between 0 (no concordance) and 1 (maximum concordance). Its significance is tested either using eq. 5.11 directly, or after transforming W into the associated X^2 statistic:

$$X^2 = p(n-1)W$$

The null hypothesis (H_0) subjected to testing is that the row sums R_i are equal or, in other words, that the p sets of ranks (or the p semiquantitative descriptors) are independent of one another. The X^2 statistic is compared to a χ^2_{α} value read in a table of critical values of χ^2 , for $\nu = (n-1)$. When X^2 is smaller than the critical value χ^2_{α} (i.e. probability larger than α), the null hypothesis that the row sums R_i are equal cannot be rejected; this leads to the conclusion that the p descriptors are independent and differ in the way they rank the n objects. On the contrary, $X^2 \geq \chi^2_{\alpha}$ (i.e. probability smaller than or equal to α) indicates good agreement among the descriptors in the way they rank the objects. Textbooks of nonparametric statistics provide modified formulae for X^2 , for data sets with tied observations.

Numerical example. Calculation of Kendall's coefficient of concordance is illustrated using the numerical example of Table 5.7. Data could be semiquantitative rank scores, or quantitative descriptors coded into ranks. It is important to note that the $n = 6$ objects are ranked on each descriptor (column) separately. The last column gives, for each object i , the sum R_i of its ranks on the $p = 3$ descriptors. The sum of squared deviations from the mean, $\sum (R_i - \bar{R})^2$, is equal to 25.5 for this example. The Friedman statistic is calculated with eq. 5.10:

$$X^2 = \left[\frac{12}{3 \times 6(6+1)} (64 + 196 + 121 + 121 + 121 + 64) \right] - [3 \times 3(6+1)] = 2.429$$

Using eq. 5.11, the X^2 statistic is transformed into Kendall's W :

$$W = \frac{2.429}{3(6-1)} = 0.162$$

Alternatively, W could have been computed using eq. 5.12:

$$W = \frac{12 \times 25.5}{9(216-6)} = 0.162$$

A table of critical values of χ^2 indicates that $X^2 = 2.43$, for $\nu = 6 - 1 = 5$, corresponds to a probability of ca. 0.80; the probability associated with this X^2 statistic is actually 0.787. The hypothesis (H_0) that the row sums R_i are equal cannot be rejected. One concludes that the three descriptors differ in the way they rank the 6 objects.

Permutation
test

The Kendall coefficient of concordance can also be tested by permutation. The Kendall concordance method with permutation testing has been used for the search for species association (Legendre 2005), which is one of the classical problems of community ecology. It is implemented in the functions 'kendall.global' (global test of the concordance among all members of an association) and 'kendall.post' (*a posteriori* test of the contribution of individual species to the overall concordance of their group) of the R-language library 'vegan' (Oksanen et al. 2009).

The concordance among distance matrices (CADM) can be tested using a test of significance proposed by Legendre & Lapointe (2004, 2005). The distance matrices under comparison are strung out like the descriptors in Table 5.7. The coefficient of concordance is computed and tested using the same permutation procedure as in the Mantel test (Subsection 10.5.1). This test is actually a generalization of the Mantel test of matrix correspondence to any number of distance matrices. This method is available in the functions 'CADM.global' and 'CADM.post' of the R-language library 'ape' (Paradis et al. 2009).

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