Simfit

Tutorials and worked examples for simulation, curve fitting, statistical analysis, and plotting.
https://simfit.org.uk
https://simfit.silverfrost.com

Kendall's coefficient of concordance estimates the extent of agreement between n objects ranked on k different variables in order to test the null hypothesis

$$H_0: \quad \text{There is no agreement between the comparisons.}$$

Open the SimFiT main menu, choose [A/Z], select the SimFiT nonparametric test program **rstest**, then run the Kendall coefficient of concordance option and examine the following default data set of rankings for 10 objects ranked on 3 variables.

1.0	4.5	2.0	4.5	3.0	7.5	6.0	9.0	7.5	10.0
2.5	1.0	2.5	4.5	4.5	8.0	9.0	6.5	10.0	6.5
2.0	1.0	4.4	4.5	4.5	4.5	8.0	8.0	8.0	10.0

The results are as follows, suggesting that H_0 should be rejected.

Kendall coefficient of concordance analysis 1

H_0: no agreement between comparisons		
Data: test file G08DAF.TF1		
Number of columns (objects)	10	
Number of rows (variables)	3	
Kendall coefficient W	0.8277	
$P(\chi^2 \geq W)$	0.0078	Reject H_0 at 1% significance level

The data matrix supplied for analysis can contain observations or ranks as follows.

- Data must have n columns for data/objects/ranks (across), and k rows for comparisons/variables (down).

- The matrix can have original values to be ranked automatically along rows, or else contain pre-calculated ranks instead of values.

- Tied ranks are averaged as usual, so a ranked matrix must have these two properties:

  1. $A(i, j) > 0$ for $i = 1, 2, ..., k$ and $j = 1, 2, ..., n$
  2. Sum of $A(i, j)$ for each i and for $j = 1, 2, ..., n$ must be $n(n + 1)/2$

- Note that, if data values are supplied instead of ranks, then SimFiT will calculate the ranks automatically.

For instance, the data in test file kendall.tf1 contains these measurements for wing length, tail length, and bill length for 12 birds

10.4	10.8	11.1	10.2	10.3	10.2	10.7	10.5	10.8	11.2	10.6	11.4
7.4	7.6	7.9	7.2	7.4	7.1	7.4	7.2	7.8	7.7	7.8	8.3
17.0	17.0	20.0	14.5	15.5	13.0	19.5	16.0	21.0	20.0	18.0	22.0

and then the following ranks, calculated internally by SimFiT before performing the test,

4.0	8.5	10.0	1.5	3.0	1.5	7.0	5.0	8.5	11.0	6.0	12.0
5.0	7.0	11.0	2.5	5.0	1.0	5.0	2.5	9.5	8.0	9.5	12.0
5.5	5.5	9.5	2.0	3.0	1.0	8.0	4.0	11.0	9.5	7.0	12.0

lead to the next table of results.

H_0: no agreement between comparisons		
Data: test file KENDALL.TF1		
Number of columns (objects)	12	
Number of rows (variables)	3	
Kendall coefficient W	0.9241	
$P(\chi^2 \geq W)$	0.0013	Reject H_0 at 1% significance level

As before, the null hypothesis is rejected for this alternative data set.

Calculating the Kendall coefficient of concordance W

Ranks r_{ij} for the the rank of object j in comparison i (with tied values being given averages) are used to calculate the n column rank sums R_j, which would be approximately equal to the average rank sum $k(n+1)/2$ under

$$H_0 : \text{ There is no association among the variables.}$$

For total agreement the R_j would have values from some permutation of $k, 2k, \dots, nk$, and the total squared deviation of these is $k^2 n(n^2 - 1)/12$.

Then the coefficient W is calculated according to

$$W = \frac{\sum_{j=1}^{n} (R_j - k(n+1)/2)^2}{k^2 n(n^2 - 1)/12 - k \sum T}$$

which lies between 0 for complete disagreement and 1 for complete agreement.

Here the denominator correction for ties uses T defined as

$$T = \sum t(t^2 - 1)/12$$

where t is the number of occurrences of each tied rank within a comparison.

For large samples ($n > 7$), $k(n-1)W$ is approximately χ^2_{n-1} distributed, otherwise tables should be used for accurate significance levels.