INTRODUCTION

The Jonckheere test is a popular distribution-free test for the null hypothesis of equal treatment effects in a one-way layout. This test differs from the one-way analysis-of-variance and the distribution-free Kruskal-Wallis test by having the alternative hypothesis of ordered treatment effects. Jonckheere's test is not available by name among SAS statistical procedures and as a consequence a SAS program has been written using a number of data steps, SAS procedures, and the macro language (Huang and Robles 1988). In this article we present a simple method for performing Jonckheere's test using the KENDALL option of the CORR procedure.

A correspondence between Jonckheere's test for ordered alternatives and Kendall's test for correlation has long been known (Jonckheere 1954; Kendall 1975, p. 165). Indeed, the test usually attributed to Jonckheere was proposed two years earlier by Terpstra (1952) in a paper whose title refers to Kendall's test. Evidently, though, the relationship between these two tests has not been widely exploited for computational purposes. We first present the relationship between Jonckheere's statistic \( J \) and Kendall's correlation coefficient \( T \), and then show how to obtain \( J \) and the associated small sample and large sample significance tests from \( T \).

RELATIONSHIP BETWEEN JONCKHEERE'S J AND KENDALL'S \( T \)

The data for Jonckheere's test consist of \( N = \sum_{i=1}^{k} n_i \) observations from \( k \) treatments with \( n_i \) observations from treatment \( i, i = 1, 2, \ldots, k \).

| Treatment | \( 1 \) | \( 2 \) | \( 3 \) | \( \ldots \) | \( k \) |
|-----------|------|------|------|----------|
| \( y_{11} \) | \( y_{12} \) | \( y_{13} \) | \( \ldots \) | \( y_{1k} \) |
| \( y_{21} \) | \( y_{22} \) | \( y_{23} \) | \( \ldots \) | \( y_{2k} \) |
| \( \vdots \) | \( \vdots \) | \( \vdots \) | \( \ddots \) | \( \vdots \) |
| \( y_{n_11} \) | \( \ldots \) | \( \ldots \) | \( \ldots \) | \( y_{n_1k} \) |
| \( \ldots \) | \( \vdots \) | \( \vdots \) | \( \ddots \) | \( \vdots \) |
| \( y_{n_{11}} \) | \( \ldots \) | \( \ldots \) | \( \ldots \) | \( y_{n_{1k}} \) |

Assume that the treatment columns have been arranged in order from smallest to largest hypothesized effect. To compute Jonckheere's statistic, consider a pair of observations, \( y_{ij} \) and \( y_{ik} \), from two different treatments \( i < k \). Associate a score with this pair of observations: 1 if \( y_{ij} < y_{ik} \), 1/2 if \( y_{ij} = y_{ik} \), and 0 if \( y_{ij} > y_{ik} \). The Jonckheere statistic \( J \) is the sum of scores over all pairs of observations from all pairs of treatments. Specifically, let \( C \) be the number of pairs for which \( y_{ij} < y_{ik} \); these pairs are termed "concordant" because they appear in the hypothesized treatment order. Let \( D \) be the number of pairs for which \( y_{ij} > y_{ik} \); these pairs are termed "discordant" because they are ordered contrary to the hypothesized treatment order. Let \( S \) be the number of "ties", that is, the number of pairs for which \( y_{ij} = y_{ik} \). Jonckheere's statistic is then the sum of scores

\[ J = C + \frac{S}{2}. \]

Now consider the same data rearranged in two columns with single subscripts on the \( y \)'s corresponding to observation number.

| Treatment | \( 1 \) | \( 2 \) | \( \ldots \) | \( k \) |
|-----------|------|------|----------|
| \( y_{11} \) | \( \ldots \) | \( \ldots \) | \( \ldots \) | \( y_{1k} \) |
| \( y_{21} \) | \( \ldots \) | \( \ldots \) | \( \ldots \) | \( y_{2k} \) |
| \( \vdots \) | \( \vdots \) | \( \ddots \) | \( \vdots \) | \( \vdots \) |
| \( y_{n_{11}} \) | \( \ldots \) | \( \ldots \) | \( \ldots \) | \( y_{n_{1k}} \) |

To compute Kendall's statistic for correlation between treatment \( x \)'s and response \( y \)'s, consider a pair of bivariate observations, \( (x_i, y_i) \) and \( (x_j, y_j) \), \( i < j \). Associate a score with this pair of observations: 1 if \( x_i < x_j \) and \( y_i < y_j \), 0 if either \( x_i = x_j \) or \( y_i = y_j \), and -1 if \( x_i < x_j \) and \( y_i > y_j \). (Note that in this particular application, \( x_i \leq x_j \).) The Kendall statistic \( K \) is the sum of scores over all pairs of bivariate observations. Since the number of 1's assigned is \( C \), and the number of -1's assigned is \( D \), \( K \) can be written as \( K = C - D \), the number of concordant pairs minus the number of discordant pairs.

To establish the relationship between Jonckheere's \( J \) and Kendall's \( K \), let \( T \) be the number of 0's assigned in the Kendall statistic. \( T \) can be written as the number of ties among the \( x \)'s plus the number of additional ties among the \( y \)'s.

\[ T = \left( \frac{n_1}{2} \right) + \left( \frac{n_2}{2} \right) + \cdots + \left( \frac{n_k}{2} \right) + S, \]

where \( S \) is the number of times \( y_i = y_j \) when \( x_i \neq x_j \). Since

\[ N = 2C + D + T, \]

we have

\[ D = \left( \frac{N}{2} \right) - C - \left( \frac{n_1}{2} \right) - \left( \frac{n_2}{2} \right) - \cdots - \left( \frac{n_k}{2} \right) - S. \]

Substituting this expression for \( D \) into the definition of \( K \) yields

\[ K = 2C + S + \left( \frac{n_1}{2} \right) + \left( \frac{n_2}{2} \right) + \cdots + \left( \frac{n_k}{2} \right) - \left( \frac{N}{2} \right) \]

\[ = 2J - \sum_{i=1}^{k} n_i, \]

where \( t_i \) is the size of the \( i \)th tied group of \( X \) values and \( u_i \) is defined similarly for the \( Y \)'s (Kendall 1975, correcting a missprint on page 869 of the SAS User's Guide: Basics (SAS Institute Inc. 1985)). In this particular application of
Kendall's test, $t_i = \mu_i$ for all $i$. Substituting for $K$, rearranging, and simplifying gives Jonckheere's $J$ as a function of Kendall's $r_i$:

$$J = \left( r_i \sqrt{N^2 - \sum \mu_i^2} \right) \frac{N(N - 1) - \sum \mu_i (\mu_i - 1)}{N^2 - \sum \mu_i^2} + \frac{N^2 - \sum \mu_i^2}{4}.$$  

(2)

**HYPOTHESIS TESTS**

1. Small Sample Test

For samples of limited size, one can obtain exact p-values by referring Jonckheere's $J$ to tabulated values like those found in Hollander and Wolfe (1973, pp. 311-327). Computing $J$ using equation (2) requires the sums $N = \sum \mu_i$, $\sum \mu_i^2$, and $\sum \mu_i (\mu_i - 1)$, which can be obtained from the original data. An example of SAS code which accomplishes this is provided in the Appendix.

2. Large Sample Test

The KENDALL option of PROC CORR provides a large sample test of the hypothesis that $r_i = 0$ against the two-tailed alternative that $r_i \neq 0$ by referring $K/\sqrt{\text{Var}(K)}$ to the standard normal distribution. Substituting expression (1) for $K$ into $K/\sqrt{\text{Var}(K)}$ yields

$$\frac{K}{\text{Var}(K)} = \frac{J - \frac{1}{4} \sum \mu_i^2}{\sqrt{\text{Var}(J)}}.$$  

This expression is the large sample test statistic for Jonckheere's test, since

$$\text{Exp}(J) = \frac{N^2 - \frac{1}{4} \sum \mu_i^2}{4}$$

(Lehmann 1975, page 223). Note that the variance of $J$, given by Lehmann (1975, page 235), is exactly $1/4$ the variance of $K$, given on page 876 of the SAS User's Guide: Basics (SAS Institute Inc. 1985). Therefore, in contrast to the small sample test, $J$ need not be calculated in order to obtain a p-value for the large sample Jonckheere test.

The p-value reported by PROC CORR for Kendall's $r_i$ is the same as the p-value of a two-tailed, large sample Jonckheere's test. Ordinarily we wish to perform a one-tailed Jonckheere test. Because the normal distribution is symmetric, a one-tailed test can be obtained by dividing the p-value given by PROC CORR in half.

**DISCUSSION**

A note of caution is in order concerning one-tailed Jonckheere tests computed using PROC CORR. Throughout our discussion we have assumed, as will usually be the case, that the alternative hypothesis of interest is one-tailed. In defining Jonckheere's $J$, treatments were ordered from smallest to greatest hypothesized effect and indexed by integers 1 through $k$. These treatment indices are then used to compute Kendall's $r_i$ using the CORR procedure, as illustrated in the Appendix. We reject the null hypothesis if $r_i > 0$ is sufficiently large. The large sample p-value for a one-tailed test is one half the value reported by PROC CORR. The small sample p-value is obtained from tabulated values of the upper tail of the distribution of $J$.

On the other hand, if treatments are naturally indexed by a numeric variable (like dose in the Appendix) and the response variable is hypothesized to decrease with increasing treatment values, it is not necessary to invert the order of treatment indices to perform a one-tailed Jonckheere test. We reject the null hypothesis in favor of this alternative hypothesis if $r_i < 0$ is sufficiently small. Because of the symmetry of $r_i$ around 0, the large sample p-value is, as before, half the p-value reported by PROC CORR. Care must be taken to note that $r_i$ is less than 0, since a large positive value of $r_i$ is contrary to the alternative hypothesis under consideration and should not lead to rejection of the null hypothesis. For the small sample test, computation of $J$ from $r_i$ when treatment and response variables are inversely related will result in small values of $J$ from the lower tail of the distribution. These values of $J$ are not usually tabulated; therefore, the corresponding upper tail $J$ value must be found by either subtracting the observed $J$ from its maximum possible value of $(N^2 - \sum \mu_i^2)/2$ or by computing $J$ using the absolute value of $r_i$. Both of these solutions depend upon the symmetry of the null distributions of $J$ and $r_i$.

There are several advantages to using the CORR procedure to perform Jonckheere's test. First, this method is simple because it exploits an existing SAS procedure that is available on all operating systems. This simplifies the maintenance of SAS code in programs for routine analyses and places the burden of programming efficiency and quality assurance on SAS Institute. Second, this approach is flexible because any number of treatments may be included without modifying the code. Also, by-group processing, as shown in the Appendix, is available. Third, the method is applicable to data sets with many ties among the responses because the variance formula for $K$ used by PROC CORR is properly corrected for ties. The correction for ties does not appear in all textbook treatments of Jonckheere's test (e.g., Hollander and Wolfe 1973) and may be overlooked by users.

**APPENDIX**

- *********************************************;
  * The data represent mouse body weights at the *;
  * conclusion of a 13 week subchronic bioassay for *;
  * toxicity carried out by the National Toxicology *;
  * Program. Both male and female weights are given *;
  * to illustrate by-group processing. *;
  *********************************************;

**DATA BODY WT**;
  INPUT SEX $ DOSE @;
  DO I=1 TO 6;
  END;
  DROP I;
  OUTPUT;

END;

1338
Order doses from smallest to largest hypothesized body weight.

```sas
DATA BODY_WT;
SET BODY_WT;
BY SEX DOSE;
IF FIRST.SEX THEN TREATMNT=6;
IF FIRST.DOSE THEN TREATMNT+(1);
DROP DOSE;
```

Compute the P-value for a large sample Jonckheere test.

```sas
PROC CORR DATA=BODY_WT NOSIMPLE
OUTK=TAU_B;
BY SEX;
```

Remaining code is for small sample test.

```sas
PROC FREQ DATA=BODY_WT;
BY SEX;
TABLES TREATMNT/NOPRINT OUT=DOSES;
TABLES WEIGHT/NOPRINT OUT=WEIGHTS;
```

Collect sums of tied group sizes and compute J.

```sas
DATA JONCK_J;
SET WEIGHTS(IN=WT)
DOSES(IN=DOS)
TAU_B(IN=TAU);
BY SEX;
IF FIRST.SEX THEN DO;
SUM_U=0; SUM_N=0; SUM_NSQR=0;
END;
IF WT THEN SUM_U+(COUNT*(COUNT+1));
IF DOS THEN SUM N+COUNT;
SUM_NSQR+COUNT**2;
END;
IF TAU & _NAME_='TREATMNT' THEN DO;
J=(WEIGHT*SQRT((SUM_N**2-SUM_NSQR)*
((SUM_N**2-SUM_N)-SUM_U))
+SUM_N**2-SUM_NSQR)/4;
OUTPUT;
END;
KEEP SEX J;
PROC PRINT DATA=JONCK_J;
```

REFERENCES


