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Proposed tests for location and scale for an umbrella alternative

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Abstract
Three nonparametric tests are proposed for a CRD design with k populations to test for the umbrella alternative with known peak, p, for both location and scale parameters. The tests are combinations of the Mack-Wolfe test (Mack and Wolfe, 1981) and a Moses modified Mack-Wolfe test based on the Moses technique (Moses, 1963). A simulation study was implemented to see if the proposed tests maintained their significant levels. Also, the tests proposed were compared based on estimated powers for different sample sizes, for changes in location parameters only, for changes in scale parameters only, and for changes in both location and scale parameters. Finally, recommendations as to which test is better are given.

Keywords: CRD design, Mack-Wolfe test, umbrella alternative, known turning point, power estimation

Introduction
Nonparametric tests require few assumptions about the underlying populations from which the data are obtained. For many nonparametric tests, it is assumed that the underlying distributions are of the same type, but differ in location or scale only, or possibly both. In some cases, if the k populations parameters could be different, one may be able to assume that they are non-decreasing or non-increasing. One such case could occur when increasing a drug dosage level on groups of experimental units. The researchers may be able to assume that this would cause the parameters to be non-increasing up to a point and non-decreasing after that point, if they are different (umbrella alternative). We could use this additional information to develop tests that have higher powers, to detect if the parameters are different. In the case of treatments being different dosages of a drug, it is possible that the different levels of the drug could affect both the location and scale parameters. In this research, we will propose tests for the umbrella alternative for both location and scale parameters with known turning point, p, in a CRD design. The hypotheses for the umbrella alternative testing for location and scale parameters is given in equation (1):

$$H_0: \mu_1 = \cdots = \mu_k \text{ and } H_0: \sigma_1 = \cdots = \sigma_k$$

$$H_a: \mu_1 \leq \mu_2 \leq \cdots \leq \mu_p \geq \cdots \geq \mu_k \text{ and } H_a: \sigma_1 \leq \sigma_2 \leq \cdots \leq \sigma_p \geq \cdots \geq \sigma_k \tag{1}$$

With at least one strict inequality, where μ_i and σ_i represent the location and scale parameters of the populations. The value, p, is called the turning point or the peak of the umbrella

The Mack-Wolfe test statistic (Mack and Wolfe, 1981) [8] was designed for umbrella alternatives based on a CRD design. Their test is an extension of the Jonckheere and Terpstra test (Jonckheere, 1954) [5] (Terpstra, 1952) [11] which tests for the nondecreasing alternative. The umbrella alternative hypothesis with known, p, is given in equation (1). The test statistic, A_p for the case of known peak p, is the sum of Mann-Whitney (Mann and Whitney, 1947) [7] counts to the left of the peak and the reverse Mann-Whitney counts to the right of the peak and is given in (2).

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$$A_p = \sum_{u=1}^{v-1} \sum_{v=2}^{p} U_{uv} + \sum_{u=p}^{v-1} \sum_{v=p+1}^{k} U_{vu} \qquad (2)$$

Where the Mann-Whitney test statistic U_{vu}, counts the number of times when the observation in sample v is less than observation in the sample u when all sets of paired observations are compared with the first entry coming from the v sample and second entry from the u sample. The test statistic of Mack-Wolfe (A_p) is approximately normally distributed under H_0 as the sample sizes from the k populations increase. Under H_0, the expected value and variance of A_p are given in equation (3).

$$E_0(A_p) = \frac{N_1^2 + N_2^2 - \sum_{i=1}^{k} n_i^2 - n_p^2}{4} \qquad (3)$$

$$var_0(A_p) = \frac{1}{72}\{2(N_1^3 + N_2^3) + 3(N_1^2 + N_2^2) - \sum_{i=1}^{k} n_i^2(n_i + 3) - n_p^2(2n_p + 3)) + 12n_p N_1 N_2 - 12n_p^2 N\}$$

Where, $N_1 = \sum_{i=1}^{p} n_i$, $N_2 = \sum_{i=p}^{k} n_i$, and $N = N_1 + N_2 - n_p$, and n_p= the peak sample size.

Mack and Wolfe (1981) used the standardized test statistic A_p^* of the form

$$A_p^* = \frac{A_p - E(A_p)}{\sqrt{Var(A_p)}} \qquad (4)$$

The null hypothesis is rejected if $A_p^* \geq z_\propto$, where $z_\propto$ is the upper tail value of the standard normal distribution with α probability above this value.

Moses (Moses, 1963) [9] proposed a nonparametric test that was intended to test for the equality of variances in two populations. In order to calculate the test statistic for the Moses test, the first and second samples are divided into m_1 and m_2 subsamples of equal size, q. For each of the first m_1 subsets, the sample mean is calculated; the distance between each observation and the sample mean is found and then squared for each of the subsets. These squared values are then added together. The values of C_1, C_2, …, C_{m1} are used to denote the sum of the squared values for each of the m_1 subsets in the first sample. The values of D_1, D_2, …, D_{m2} denote the sum of the squared values for each of the m_2 subsets in the second sample.

Next, the Mann-Whitney test (Mann and Whitney, 1947) [7] is applied. That means that the m_1 C's and the m_2 D's are combined. Following this step, all observations in the combined set are ranked from smallest to largest. The ranks of the observations from the m_2 D's are then added together. The Moses test statistic (M) is this sum and is given in (5).

$$M = \sum_{i=1}^{m_2} R(D_i) \qquad (5)$$

The standardized version of the Moses test is given by

$$M^* = \frac{M - E_0(M)}{\sqrt{var_0(M)}} \qquad (6)$$

$$E_0(M) = m_2(m_1 + m_2 + 1)/2$$

$$var_0(M) = m_1 m_2(m_1 + m_2 + 1)/12 \qquad (7)$$

The asymptotic null distribution of M^* is the standard normal distribution.

Lepage's test (Lepage, 1971) [6] is a nonparametric test for the two-sample location and scale problem. Lepage's test is to determine if there is a difference for either the location or scale parameters: μ_1 and μ_2, or σ_1 and σ_2. The Lepage's test consists of the Mann-Whitney test (Mann and Whitney, 1947) [7] and the Ansari-Bradley test (Ansari and Bradley, 1960) [1]. The Mann-Whitney test is used to detect location changes while the Ansari-Bradley test is to detect scale changes. The Lepage test has a chi-square distribution with two degrees of freedom under the null hypothesis.

Alsubie and Magel, 2020a [2] proposed two nonparametric tests for differences in location and scale for the simple tree alternative. The simulation study was executed to determine how well the proposed tests preserve their significance levels. Under various conditions for three and four populations, powers were estimated for the proposed tests. The authors used three different kinds of variable parameters vectors which considered, within each vector, a location and a scale parameter. The first type of parameters vectors had different location parameters and equal scale parameters. The second type had different scale parameters and equal location parameters, and the third type had different location and scale parameters.

(Alsubie and Magel, 2020b) [3] proposed three additional nonparametric tests to test for differences in location and scale parameters under the simple tree alternative. Moses technique was used in their tests. Under a variety of conditions for three and four populations, powers were estimated for the proposed tests. The authors considered similar parameter vectors as in Alsubie and Magel (2020a) [2].

Proposed Tests
We proposed three tests for testing the umbrella alternative in (1). These tests involve the Mack-Wolfe (Mack and Wolfe, 1981) [8] and Moses's technique (Moses, 1963) [9] which converts a scale testing problem to a location testing problem.

Moses Mack-Wolfe test
The Moses Mack-Wolfe test statistic for an umbrella alternative based on simple random samples for testing a scale that has a null hypothesis is shown in equation (8).

$$H_0: \sigma_1 = \sigma_2 = \cdots = \sigma_k$$

The alternative hypothesis is as follows:

$$H_a: \sigma_1 \leq \sigma_2 \leq \cdots \leq \sigma_{p-1} \leq \sigma_p \geq \sigma_{p+1} \geq \cdots \geq \sigma_k \qquad (8)$$

Where at least one inequality is strict and $\sigma_1, ..., \sigma_k$ are the scale parameters of the i samples, i=1,2,…,n.

Initial sample sizes of n_1, n_2,....n_k are taken from the k populations. The Moses technique is applied to this data so that a test for scale becomes a test for location by transforming the data. To do so, each treatment sample was randomly divided into m_i subsamples of equal size, q, = 1,2..,k. For the m_i subsets of each treatment $i = 1,2,..,k$, the sample variance was calculated based on the observations in each of the m_i of the subsets for each treatment. The new data set became the m_1 sample variances based on subgroups from the first treatment sample, the m_2 sample variances based on subgroups from the second treatment sample, etc. The Mack-Wolfe test statistic was calculated based on this transformed set of data.

The test statistic, MA_p, for this case with a known peak, p, was the sum of the Mann-Whitney counts to the left of the peak and the reverse of the Mann-Whitney counts to the right

of the peak. Therefore, the test statistic, MA_p, had the following form.

$$MA_p = \sum_{u=1}^{v-1}\sum_{v=2}^{p} U_{uv} + \sum_{u=p}^{v-1}\sum_{v=p+1}^{k} U_{vu} \qquad (9)$$

Under the null hypothesis where all population variances are equal. The expected value, $E_0(MA_p)$, and variance, $var_0(MA_p)$, respectively, are given in equation (10).

$$E_0(MA_p) = \frac{M_1^2 + M_2^2 - \sum_{i=1}^{k} m_i^2 - m_p^2}{4}$$

$$var_0(MA_p) = \frac{1}{72}\{2(M_1^3 + M_2^3) + 3(M_1^2 + N_2^2) - \sum_{i=1}^{k} m_i^2(m_i + 3) - m_p^2(2m_p + 3)) + 12m_p M_1 M_2 - 12m_p^2 M\}$$
$$\qquad (10)$$

Where,
$M_1 = \sum_{i=1}^{p} m_i$, $M_2 = \sum_{i=p}^{k} m_i$, and $M = \sum_{i=1}^{k} m_i = M_1 + M_2 - m_p$; $m_i =$ the number of subsamples; and $m_p =$ the number of subsamples in the peak.

The Moses Mack-Wolfe test statistic utilizes the standardized test statistic, MA_p^*, with the form in (11).

$$MA_p^* = \frac{MA_p - E(MA_p)}{\sqrt{Var(MA_p)}} \qquad (11)$$

The null hypothesis is rejected if $MA_p^* \geq z_\alpha$, where z_α is the critical value for the upper-tail probability of the standard normal distribution. We proposed three test statistics to test for the umbrella alternative on location and scale parameters simultaneously in a CRD which use the Mack-Wolfe test and the Moses Mack-Wolfe test.

Proposed test one
The first proposed test for the hypothesis in (1), is given in equation (12)

$$Z_1 = MA_p^* + A_p^* \qquad (12)$$

Where A_p^* is the standardized Mack-Wolfe test based on the original data given in equation (4), and MA_p^* is the Moses Mack-Wolfe standardized version test of scale as given in equation1 (11). Because MA_p^* and A_p^* have asymptotic standard normal distributions under H_0, the asymptotic distribution of Z_1 is normal with mean zero and variance 2. Therefore, the first proposed standardized version test, T_1, is given below in equation (13):

$$T_1 = \frac{Z_1 - 0}{\sqrt{2}} \qquad (13)$$

Under H_0, T_1 has had an asymptotic standard normal distribution. The null hypothesis is rejected if $T_1 \geq Z_\alpha$, where Z_α is the critical value of the upper tail probability of the standard normal distribution.

Proposed Test Two
The second proposed test, Z_2, for testing the hypotheses in equation (1) for a CRD is given in equation (14)

$$Z_2 = A_P + MA_P \qquad (14)$$

where A_P is the Mack-Wolfe test (CRD) for location as given in equation (2), and MA_P is the Moses Mack-Wolfe test

(CRD) for scale, as shown in equation (9). The mean and variance are given in (15) and (16)

$$E_0(Z_2) = E_0(A_P) + E_0(MA_P) \qquad (15)$$

$$var_0(Z_2) = var_0(A_P) + var_0(MA_P) \qquad (16)$$

The standardized version of the second proposed test is given in equation (17)

$$T_2 = \frac{Z_2 - E_0(Z_2)}{\sqrt{var_0(Z_2)}} \qquad (17)$$

Under H_0, T_2 has an asymptotic standard normal distribution. The null hypothesis is rejected for large values.

Proposed Test Three
The weighted standardized version of the second proposed test is given by

$$TW_2 = \frac{(A_P + 3 * MA_P) - E_0(A_P + 3 * MA_P)}{\sqrt{var_0(A_P + 3 * MA_P)}} \qquad (18)$$

Under H_0, TW_2 has an asymptotic standard normal distribution. The null hypothesis is rejected for large values.
The idea behind proposing this test is that the sample sizes of the Moses Mack-Wolfe test are smaller than the sample sizes of the Mack-Wolfe test and therefore, more weight is applied to the Moses Mack-Wolfe test. In this study, we used subsamples of size 3 in calculating the Moses Mack-Wolfe test and thus, reducing the sample sizes to 1/3 of the sample sizes of the original data. Hence, a weight of 3 was applied to the Moses Mack-Wolfe test.

Simulation Study
A simulation study was conducted to compare the three proposed tests based on estimated power for the CRD design when testing for location and scale parameters. The simulation study was implemented in SAS version 9.4. Powers were estimated when the observations followed three different underlying distributions: normal, exponential and t-distribution with three degrees of freedom. It is assumed that the peak, p, is known and the design used is a CRD design. Powers were estimated for three, four, and five populations. For three populations, the peak was assumed to be 2. For four populations, the peaks considered were at the second and third populations. In the case of five populations, the peaks considered were at the second, third and fourth populations. Equal samples of size 15 were taken from each of the k populations ($n_1 = n_2 = \ldots = n_k = n = 15$). Five subsets of 3 observations each were randomly formed from the 15 observations from each population, the sample variance of each of the subsets was calculated, and the Mack-Wolfe test was then calculated on these sample variances as well as on the original data.
In order to generate data from the above-mentioned distributions, the function RAND was used in SAS and requires the user to state the starting point "seed". This can be done using the Call streaminit function before using the RAND function. The syntax for this function is Call streaminit (seed).
In this paper, seed = 0 is used that instructs RAND to use the system clock. This means each run of the code will produce a different set of data (Bailer, 2010) [4].
The call function for the normal distribution is
F=RAND ('Normal', μ, σ)

X=F *b + a

The function (F) generated a random number from a normal distribution with the mean (μ) and variance (σ^2), respectively, and a and b were the change in location parameters and the change in scale parameters. The mean and variance were 0 and 1, respectively. The values of a and b were initially set to 0 and 1, respectively.
The call function for the exponential distribution is

F=RAND ('Exponential', μ)

X=F * b+a

The function (F) generated a random number from an exponential distribution. The values a and b were used to adjust the location and scale parameters appropriately. Initially, the values of a and b were set to 0 and 1, respectively.
The call function for the t-distribution is

F=RAND ('T', 3)

X=F * b + a

This function generated a random number from a T-distribution with 3 degrees of freedom. Initially, the values of a and b were set to 0 and 1, respectively.
For all simulations, replications of 5,000 samples were used. The three proposed tests were compared in two parts. The first part of the simulation was to get the estimates of the alpha values of the proposed test statistics. The stated alpha values for the proposed test statistics were all 0.05. The alpha values were estimated by counting the number of times the null hypothesis was rejected and then dividing by 5,000. The second part of the simulation study was to compare powers of the test statistics under various conditions. Powers were estimated by counting the number of times the proposed tests were rejected divided by 5,000 for the various conditions.

Power Calculations
In the cases of three, four, and five populations with the peak p assumed to be known, the location and scale parameter configurations (means and variances) considered as the following $(\mu_1, \mu_2, . . , \mu_k)$, $(\sigma_1^2, \sigma_2^2, …, \sigma_k^2)$

Three populations with peak at 2
The powers are estimated in the following case (all treatments have the same scale parameters):
1. The peak is distinct, and there is equal spacing between parameters among location parameters only. For example (0.0, 1.5, 0.0) and (1.0, 1.0, 1.0).
2. The peak is distinct, and there is the unequal spacing between parameters among location parameters only. For example (0.4, 1.8, 0.9) and (1.0, 1.0, 1.0).
3. One additional parameter equals the peak among location parameters only. For example (1.5, 1.5, 0.0) and (0.0, 1.5, 1.5). (1.0, 1.0, 1. 0) and (1.0, 1.0, 1.0).

The powers are estimated in the following case (all treatments have the same location parameters):
1. The peak is distinct and there is equal spacing between parameters among scale parameters. For example (0.0, 0.0, 0.0) and (1.0, 9.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among scale parameters. For example (0.0, 0.0, 0.0) and (2.0, 9.0, 4.0).

3. One additional parameter equals the peak among scale parameters. For example (0.0, 0.0, 0.0) and (0.0, 0.0, 0.0). (9.0, 9.0, 1.0) and (1.0, 9.0, 9.0).

The powers are estimated in the following case (all treatments have the different location and scale parameters)
1. The peak is distinct, and there is equal spacing between parameters among location and scale parameters. For example (0.0, 1.5, 0.0) and (1.0, 9.0, 1.0).
2. The peak is distinct, and there is the unequal spacing between parameters among location and scale parameters. For example (0.4, 1.8, 0.9) and (3.0, 9.0, 5.0).
3. One additional parameter equals the peak among location and scale parameters. For example (1.5, 1.5, 0.0) and (0.0, 1.5, 1.5). (9.0, 9.0, 1.0) and (1.0, 9.0, 9.0).

Four populations with peak at 2
The powers are estimated in the following case (all treatments have the same scale parameters):
1. The peak is distinct, and the location parameters are equal before and after the peak. For example (0.0, 1.5, 0.0, 0.0) and (1.0, 1.0, 1.0, 1.0).
2. The peak is distinct, and there is the unequal spacing between parameters among location parameters only. For example (0.3, 1.8, 0.8, 0.5) and (1.0, 1.0, 1.0, 1.0).
3. One additional parameter equals the peak among location parameters only. For example (1.5, 1.5, 0.0, 0.0) and (0.0, 1.5, 1.5, 0.0). (1.0, 1.0, 1.0, 1.0) and (1.0, 1.0, 1.0, 1.0).

The powers are estimated in the following case (all treatments have the same location parameters)
1. The peak is distinct, and the scale parameters are equal before and after the peak. For example (0.0, 0.0, 0.0, 0.0) and (1.0, 9.0, 1.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among scale parameters. For example (0.0, 0.0, 0.0, 0.0) and (3.0, 9.0, 8.0, 5.0).
3. One additional parameter equals the peak among scale parameters. For example (0.0, 0.0, 0.0, 0.0) and (0.0, 0.0, 0.0, 0.0). (9.0, 9.0, 1.0, 1. 0) and (1.0, 9.0, 9.0, 1.0).

The powers are estimated in the following case (all treatments have the different location and scale parameters)
1. The peak is distinct, and the location and scale parameters are equal before and after the peak. For example (0.0, 1.5, 0.0, 0.0) and (1.0, 9.0, 1.0, 1.0).
2. The peak is distinct, and there is the unequal spacing between parameters among location and scale parameters. For example (0.3, 1.8, 0.8, 0.5) and (3.0, 9.0, 8.0, 5.0).
3. One additional parameter equals the peak among location and scale parameters. For example (1.5, 1.5, 0.0, 0.0) and (0.0, 1.5, 1.5, 0.0). (9.0, 9.0, 1.0, 1. 0) and (1.0, 9.0, 9.0, 1.0).

Four populations with peak at 3
The powers are estimated in the following case (all treatments have the same scale parameters):
1. The peak is distinct, and the location parameters are equal before and after the peak. For example (0.0, 0.0, 1.5, 0.0) and (1.0, 1.0, 1.0, 1.0).
2. The peak is distinct, and there is the unequal spacing between parameters among location parameters only. For example (0.5, 0.8, 1.8, 0.3) and (1.0, 1.0, 1.0, 1.0).

3. One additional parameter equals the peak among location parameters only. For example (0.0, 1.5, 1.5, 0.0) and (0.0, 0.0, 1.5, 1.5). (1.0, 1.0, 1.0, 1. 0) and (1.0, 1.0, 1.0, 1.0).

The powers are estimated in the following case (all treatments have the same location parameters)
1. The peak is distinct, and the scale parameters are equal before and after the peak. For example (0.0, 0.0, 0.0, 0.0) and (1.0, 1.0, 9.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among scale parameters. For example (0.0, 0.0, 0.0, 0.0) and (5.0, 8.0, 9.0, 3.0).
3. One additional parameter equals the peak among scale parameters. For example (0.0, 0.0, 0.0, 0.0) and (0.0, 0.0, 0.0, 0.0). (1.0, 9.0, 9.0, 1. 0) and (1.0, 1.0, 9.0, 9.0).

The powers are estimated in the following case (All treatments have the different location and scale parameters)
1. The peak is distinct, and the location and scale parameters are equal before and after the peak. For example (0.0, 0.0, 1.5, 0.0) and (1.0, 1.0, 9.0, 1.0).
2. The peak is distinct, and there is the unequal spacing between parameters among location and scale parameters. For example (0.5, 0.8, 1.8, 0.3) and (5.0, 8.0, 9.0, 3.0).
3. One additional parameter equals the peak among location and scale parameters. For example (0.0, 1.5, 1.5, 0.0) and (0.0, 0.0, 1.5, 1.5). (1.0, 9.0, 9.0, 1. 0) and (1.0, 1.0, 9.0, 9.0).

Five populations with peak at 2
The powers are estimated in the following case (all treatments have the same scale parameters):
1. The peak is distinct, and the location parameters are equal before and after the peak. For example (0.0, 1.5, 0.0, 0.0, 0.0) and (1.0, 1.0, 1.0, 1.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among location parameters only. For example (0.4, 1.8, 0.8, 0.5, 0.3) and (1.0, 1.0, 1.0, 1.0, 1.0).
3. One additional parameter equals the peak among location parameters only. For example (1.5, 1.5, 0.0, 0.0, 0.0) and (0.0, 1.5, 1.5, 0.0, 0.0). (1.0, 1.0, 1.0, 1.0, 1. 0) and (1.0, 1.0, 1.0, 1.0, 1.0).

The powers are estimated in the following case (All treatments have the same location parameters)
1. The peak is distinct, and the scale parameters are equal before and after the peak. For example (0.0, 0.0, 0.0, 0.0, 0.0) and (1.0, 9.0, 1.0, 1.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among scale parameters. For example (0.0, 0.0, 0.0, 0.0, 0.0) and (4.0, 9.0, 8.0, 5.0, 3.0).
3. One additional parameter equals the peak among scale parameters. For example (0.0, 0.0, 0.0, 0.0, 0.0) and (0.0, 0.0, 0.0, 0.0, 0.0). (9.0, 9.0, 1.0, 1.0, 1. 0) and (1.0, 9.0, 9.0, 1.0, 1.0).

The powers are estimated in the following case (all treatments have the different location and scale parameters)
1. The peak is distinct, and the location and scale parameters are equal before and after the peak. For example (0.0, 1.5, 0.0, 0.0, 0.0) and (1.0, 9.0, 1.0, 1.0, 1.0).

2. The peak is distinct and there is unequal spacing between parameters among location and scale parameters. For example (0.4, 1.8, 0.8, 0.5, 0.3) and (4.0, 9.0, 8.0, 5.0, 3.0).
3. One additional parameter equals the peak among location and scale parameters. For example (1.5, 1.5, 0.0, 0.0, 0.0) and (0.0, 1.5, 1.5, 0.0, 0.0). (9.0, 9.0, 1.0, 1.0, 1. 0) and (1.0, 9.0, 9.0, 1.0, 1.0).

Five populations with peak at 3
The powers are estimated in the following case (all treatments have the same scale parameters):
1. The peak is distinct, and the location parameters are equal before and after the peak. For example (0.0, 0.0, 1.5, 0.0, 0.0) and (1.0, 1.0, 1.0, 1.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among location parameters only. For example (0.3, 0.6, 1.2, 0.8, 0.5) and (1.0, 1.0, 1.0, 1.0, 1.0).
3. One additional parameter equals the peak among location parameters only. For example (0.0, 1.5, 1.5, 0.0, 0.0) and (0.0, 0.0, 1.5, 1.5, 0.0). (1.0, 1.0, 1.0, 1.0, 1. 0) and (1.0, 1.0, 1.0, 1.0, 1.0).

The powers are estimated in the following case (All treatments have the same location parameters)
1. The peak is distinct, and the scale parameters are equal before and after the peak. For example (0.0, 0.0, 0.0, 0.0, 0.0) and (1.0, 1.0, 9.0, 1.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among scale parameters. For example (0.0, 0.0, 0.0, 0.0, 0.0) and (3.0, 5.0, 9.0, 8.0, 4.0).
3. One additional parameter equals the peak among scale parameters. For example (0.0, 0.0, 0.0, 0.0, 0.0) and (0.0, 0.0, 0.0, 0.0, 0.0). (1.0, 9.0, 9.0, 1.0, 1. 0) and (1.0, 1.0, 9.0, 9.0, 1.0).

The powers are estimated in the following case (All treatments have the different location and scale parameters)
1. The peak is distinct, and the location and scale parameters are equal before and after the peak. For example (0.0, 0.0, 1.5, 0.0, 0.0) and (1.0, 1.0, 9.0, 1.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among location and scale parameters. For example (0.3, 0.6, 1.2, 0.8, 0.5) and (3.0, 5.0, 9.0, 8.0, 4.0).
3. One additional parameter equals the peak among location and scale parameters. For example (0.0, 1.5, 1.5, 0.0, 0.0) and (0.0, 0.0, 1.5, 1.5, 0.0). (1.0, 9.0, 9.0, 1.0, 1. 0) and (1.0, 1.0, 9.0, 9.0, 1.0).

Five populations with peak at 4
The powers are estimated in the following case (all treatments have the same scale parameters)
1. The peak is distinct, and the location parameters are equal before and after the peak. For example (0.0, 0.0, 0.0, 1.5, 0.0) and (1.0, 1.0, 1.0, 1.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among location parameters only. For example (0.3, 0.5, 0.8, 1.8, 0.4) and (1.0, 1.0, 1.0, 1.0, 1.0).
3. One additional parameter equals the peak among location parameters only. For example (0.0, 0.0, 1.5, 1.5, 0.0) and (0.0, 0.0, 0.0, 1.5, 1.5). (1.0, 1.0, 1.0, 1.0, 1. 0) and (1.0, 1.0, 1.0, 1.0, 1.0).

The powers are estimated in the following case (All treatments have the same location parameters)
1. The peak is distinct, and the scale parameters are equal before and after the peak. For example (0.0, 0.0, 0.0, 0.0) and (1.0, 1.0, 1.0, 9.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among scale parameters. For example (0.0, 0.0, 0.0, 0.0, 0.0) and (4.0, 5.0, 8.0, 9.0, 3.0).
3. One additional parameter equals the peak among scale parameters. For example (0.0, 0.0, 0.0, 0.0, 0.0) and (0.0, 0.0, 0.0, 0.0, 0.0). (1.0, 1.0, 9.0, 9.0, 1. 0) and (1.0, 1.0, 1.0, 9.0, 9.0).

The powers are estimated in the following case (All treatments have the different location and scale parameters)
1. The peak is distinct, and the location and scale parameters are equal before and after the peak. For example (0.0, 0.0, 0.0, 1.5, 0.0) and (1.0, 1.0, 1.0, 9.0, 1.0).
2. The peak is distinct and there is unequal spacing between parameters among location and scale parameters. For example (0.3, 0.5, 0.8, 1.8, 0.4) and (3.0, 5.0, 8.0, 9.0, 4.0).
3. One additional parameter equals the peak among location and scale parameters. For example (0.0, 0.0, 1.5, 1.5, 0.0) and (0.0, 0.0, 0.0, 1.5, 1.5). (1.0, 1.0, 9.0, 9.0, 1. 0) and (1.0, 1.0, 1.0, 9.0, 9.0).

Results: The results will be separated by the three situations we considered estimating the powers of the tests. The first situation considered is when the location parameters are different, and the scale parameters are equal. The second type considered is when the location parameters are equal, and the scale parameters are different. The third type considered is when the location and scale parameters are both different. Tables 1-3 show the results for 3 different types of populations when the means were different and the variances were equal. Tables 4-6 show estimated powers when the means are the same and the variances are different. Tables 7-9 show estimated powers when both the means and the variances are different.

Table 1: Percentage of Rejection for k=3 Populations p=2; Normal Distribution with different means and equal variances when the common sample size n=15

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
0	1	0	1	0	1	0.0512	0.0496	0.0460
0	1	1.5	1	0	1	0.8984	0.9976	0.9832
0	1	1.5	1	1.5	1	0.3976	0.6404	0.5084
1.5	1	1.5	1	0	1	0.3836	0.6152	0.5122
0.4	1	1.8	1	0.9	1	0.7328	0.9574	0.8896

Table 2: Percentage of Rejection for k=3 Populations p=2; T (3)-Distribution with different means and equal variances when the common sample size n=15

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
0	$1\sigma^2$	0	$1\sigma^2$	0	$1\sigma^2$	0.0534	0.0494	0.0496
0	$1\sigma^2$	1.5	$1\sigma^2$	0	$1\sigma^2$	0.7454	0.9634	0.8950
0	$1\sigma^2$	1.5	$1\sigma^2$	1.5	$1\sigma^2$	0.2896	0.4668	0.3852
1.5	$1\sigma^2$	1.5	$1\sigma^2$	0	$1\sigma^2$	0.2920	0.4742	0.3958
0.4	$1\sigma^2$	1.8	$1\sigma^2$	0.9	$1\sigma^2$	0.5820	0.8408	0.7412

Table 3: Percentage of Rejection for k=3 Populations p=2; Exponential (1)-Distribution with different means and equal variances when the common sample size n=15

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
1	1	0	1	1	1	0.0484	0.0450	0.0430
1	1	1.5	1	1	1	0.6532	0.9190	0.8186
1	1	1.5	1	1.5	1	0.2328	0.3690	0.2996
1.5	1	1.5	1	1	1	0.2488	0.3928	0.3192
1.5	1	1.8	1	1.2	1	0.4366	0.7002	0.5746

Table 4: Percentage of Rejection for k=3 Populations p=2; Normal Distribution with same means and different variances when the sample size n=15

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
0	1	0	1	0	1	0.0518	0.0482	0.0506
0	1	0	9	0	1	0.6882	0.2146	0.4700
0	1	0	9	0	9	0.2626	0.1164	0.1974
0	9	0	9	0	1	0.2580	0.1104	0.1988
0	2	0	9	0	4	0.5348	0.1680	0.2714

Table 5: Percentage of Rejection for k=3 Populations p=2; T (3)-Distribution with same means and different variances when the sample size n=15

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
0	$1\sigma^2$	0	$1\sigma^2$	0	$1\sigma^2$	0.0566	0.0560	0.0550
0	$1\sigma^2$	0	$9\sigma^2$	0	$1\sigma^2$	0.7118	0.1308	0.4208
0	$1\sigma^2$	0	$9\sigma^2$	0	$9\sigma^2$	0.2356	0.0946	0.1696
0	$9\sigma^2$	0	$9\sigma^2$	0	$1\sigma^2$	0.2396	0.0802	0.1636
0	$3\sigma^2$	0	$9\sigma^2$	0	$5\sigma^2$	0.3494	0.0964	0.2256

Table 6: Percentage of Rejection for k=3 Populations p=2; Exponential (1)-Distribution with same means and different variances when the sample size n=1

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
1	1	1	1	1	1	0.0414	0.0454	0.0414
1	1	1	81	1	1	0.7028	0.1372	0.4134
1	1	1	81	1	81	0.2400	0.0842	0.1660
1	81	1	81	1	1	0.2238	0.0840	0.1538
1	9	1	81	1	9	0.2968	0.0880	0.1962

Table 7: Percentage of Rejection for k=3 Populations p=2; Normal Distribution with different means and different variances when the sample size n=15

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
0	1	0	1	0	1	0.0516	0.0548	0.0492
0	1	1.5	9	0	1	0.8584	0.4040	0.6800
0	1	1.5	9	1.5	9	0.3556	0.1764	0.2788
1.5	9	1.5	9	0	1	0.3634	0.1962	0.2872
0.4	5	1.8	9	0.9	3	0.5756	0.2644	0.3936

Table 8: Percentage of Rejection for k=3 Populations p=2; T (3)-Distribution with different means and different variances when the sample size n=15

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
0	$1\,\sigma^2$	0	$1\,\sigma^2$	0	$1\,\sigma^2$	0.0532	0.0504	0.0494
0	$1\,\sigma^2$	1.2	$5\,\sigma^2$	0	$1\,\sigma^2$	0.9968	0.9566	0.9910
0	$1\,\sigma^2$	1.5	$9\,\sigma^2$	1.5	$9\,\sigma^2$	0.7482	0.5946	0.7128
1.5	$9\,\sigma^2$	1.5	$9\,\sigma^2$	0	$1\,\sigma^2$	0.7462	0.5982	0.7132
0.4	$3\,\sigma^2$	1.8	$9\,\sigma^2$	0.9	$5\,\sigma^2$	0.9512	0.9176	0.9528

Table 9: Percentage of Rejection for k=3 Populations p=2; Exponential (1)-Distribution with different means and different variances when the sample size n=15

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	T_1	T_2	TW_2
1	1	1	1	1	1	0.0500	0.0484	0.0482
1	1	3	9	1	1	0.9756	0.9388	0.9726
1	1	3	9	3	9	0.5274	0.4598	0.5250
3	9	3	9	1	1	0.5156	0.4636	0.5220
2	4	4	16	3	9	0.5196	0.4484	0.5092

Discussion and Conclusion

All tests maintained their significance levels. For the three distributions considered with n= 15, and number of populations, and various peaks, T_2 has the largest powers if only the location parameters change. T_1 has the higher powers if only the scale parameters change. T_1 has the highest powers if the location parameters and scale parameters change for the normal and t-distributions. In the case of the exponential distribution, the powers of TW_2 and T_1 are close and both higher than the powers for T_2. Overall, when researchers want to test for differences in either location or scale, T_1 is recommended.

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