Proposed Nonparametric Tests for the Umbrella Alternative in a Mixed Design for Location and Scale

ABSTRACT

Aims: To develop and compare tests for a mixed design of an RCBD with a CRD with k populations in testing for the umbrella alternative with known peak, p, for both location and scale parameters. These tests were combinations of the Mack-Wolfe test, the Kim-Kim test, and both the Mack-Wolfe test, and the Kim-Kim test using the Moses technique.
Study design: Monte Carlo Simulation Study
Place and Duration of Study: North Dakota State University, Department of Statistics, August 2020-December 2021.
Methodology: A simulation study was implemented to see how well the proposed tests maintained their significant levels. Powers were estimated for different ratios of sample size in the CRD to the number of blocks in the RCBD; we assumed equal variance ratios between the CRD and the RCBD. Different parameter changes were considered to see if they would impact which test statistics had greater power. In all cases, it was assumed three observations per treatment, per block in the RCBD portion.
Conclusion: All proposed tests maintained their significance levels. An overall test is recommended if both location and scale parameters change.

Keywords: CRD design; RCBD design; known turning point; Mixed design for location and scale

1. INTRODUCTION

The nonparametric approach is often preferred by researchers since it requires few assumptions about the underlying populations from which the data are obtained and the measurement scale that is needed is often weaker. There are times when researchers may want to test whether there is a difference in either location or scale parameters or both. In some of these cases, the researcher is able to assume that there is an umbrella effect among the parameters if they are different. Namely, the parameters may be nondecreasing up to a point, and then nonincreasing after that point, where at least two are different. It is possible that a researcher may be able to assume this effect when increasing the dosages of a drug. The drug effect on the experimental unit may, at first, be increasing (or nondecreasing), but after a certain level, the drug effect on the experimental unit might start to decrease with increasing dosage of the drug. The umbrella alternative is then the most appropriate hypothesis. The test of hypotheses for the umbrella alternative testing for location and scale parameters is given in equation (1):

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

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

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. On one side of the peak, the parameters are nondecreasing and on the other side of the peak, the parameters are nonincreasing. In this research, we developed tests for location and scale parameters for the umbrella alternative in a mixed design consisting of a completely randomized portion (CRD) and a randomized complete block portion (RCBD). We defined the SB Ratio as the sample size in CRD to the number of blocks in the RCBD. In this research we considered SB ratios of 1/2, 1, and 2, and different underlying distributions. We also estimated the powers of the tests that were developed when just the location parameters differed, when just the scale parameters differed, and then when both the location and scale parameters differed.

In this section we present different proposed nonparametric test statistics related to mixed design that can be used for analyzing data from independent samples when testing for location and scale parameters.

1.1 Mack-Wolfe

The Mack-Wolfe test statistic [1] was designed for umbrella alternatives based on a CRD design. This test is an extension of the Jonckheere and Terpstra test [2,3] 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 [4] counts to the left of the peak and the reverse Mann-Whitney counts to the right of the peak and is given in (2).

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

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):

$$\mathrm{E}_0(\mathrm{A_p}) = \frac{\mathrm{N_1^2+N_2^2-\sum_{i=1}^{k} n_i^2 - n_p^2}}{4} \qquad (3)$$

$$var_0(A_p) = \frac{1}{72}\left\{2(N_1^3 + N_2^3) + 3(N_1^2 + N_2^2) - \sum_{i=1}^{k} n_i^2(2n_i + 3) - n_p^2(2n_p + 3)) + 12n_pN_1N_2 - 12n_p^2N\right\}$$

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-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.

1.2 Kim-Kim

The Kim-Kim statistic [5] was proposed to test for the umbrella alternative in the RCBD layout with known peaks. This statistic is an extension of the Mack-Wolfe test to the RCBD design. The Kim-Kim test statistic (A) considers an RCBD with b as blocks and k as treatments without interaction and is considered to be the sum of the Mack-Wolfe test statistics in each block, and it is given by

$$A = \sum_{j=1}^{b} A_{jp} \tag{5}$$

where, A_{jp} is the Mack-Wolfe test statistics for the j^{th} block. The b is the number of blocks in the RCBD. The p and k are the known treatment peak level and the number of treatments, respectively. A_{ip} can be calculated using equation (2) for each block with i= 1, 2, ..., b.

The mean and variance of the Kim-Kim test statistic are given by

$$E_0(A) = \sum_{j=1}^{b}\left\{\frac{\left\{N_{j1}^2 + N_{j2}^2 - \sum_{i=1}^{k} n_{ji}^2 - n_{jp}^2\right\}}{4}\right\}$$

$$var_0(A) = \frac{1}{72}\sum_{j=1}^{b}\left\{2\left(N_{j1}^3 + N_{j2}^3\right) + 3\left(N_{j1}^2 + N_{j2}^2\right) - \sum_{i=1}^{k} n_{ji}^2\left(2n_{ji} + 3\right) - n_{jp}^2\left(2n_{jp} + 3\right) + 12n_{jp}N_{j1}N_{j2} - 12n_{jp}^2N_j\right\} \tag{6}$$

where, n_{ji} = samples size for i^{th} treatment in j^{th}block, n_{jp} = samples size for p^{th} treatment in j^{th}block, $N_{j1} = \sum_{i=1}^{p} n_{ji}$, $N_{j2} = \sum_{i=p}^{k} n_{ji}$, $N_j = N_{j1} + N_{j2} - n_{jp}$, b = the number of blocks, k = The number of treatments, and p = the known peak. In this research, we considered the case when n_{ji}= 1 (after applying the Moses technique when testing for variances) reduced the expected value and variance of A when n_{ji}= 1 (there is one observation per treatment for each block) to the form given below

$$E_0(A) = \frac{b\left(p^2+(k-p+1)^2-k-1\right)}{4}$$

and

$$var_0(A) = \frac{b}{72}\left[\begin{matrix}2(p^3 + (k-p+1)^3) + 3(p^2 + (k-p+1)^2) - 5k \\ -5 + 12p(k-p+1) - 12k\end{matrix}\right] \tag{7}$$

When H_0 is true, the standardized version of the Kim-Kim test has an asymptotic standard normal distribution and is given by

$$A^* = \frac{A-E_0(A)}{\sqrt{var_0(A)}} \tag{8}$$

The null hypothesis is rejected when $A^* \geq Z_\alpha$, where Z_α is upper tail value in standard normal distribution with α probability above it.

1.3 Alotaibi and Magel's Test

Alotaibi and Magel [6] extended the work of [7] who proposed two tests to test for the umbrella alternative with respect to location parameters in a mixed design consisting of an RCBD and a CRD. The test statistics were combinations of the Mack-Wolfe test statistic for the CRD [1] and the Kim-Kim test statistic for the RCBD [5]. Alotaibi and Magel [6] examined the performance of the tests proposed by Magel et al. [7] by examining what happened when the error variance for the CRD was larger than the error variance for the

RCBD. They considered cases when the ratio of CRD error variance to the RCBD error variance, referred to as CR ratio, was two, four, and nine. Powers were estimated for both tests when the sample size ratio in the CRD portion compared to the number of blocks in the RCBD portion, referred to as SB Ratio, was 1/8, 1/4, 1/3, 1/2, 1, 2, 3, 4, and 8. In all cases in the RCBD portion, it was assumed that there was one observation per treatment per block. They also assumed equal sample sizes for all treatments in the CRD portion.

Alotaibi and Magel [8] proposed three nonparametric tests for an umbrella alternative in a completely randomized design (CRD) with peak known to test differences in location and scale parameters. These tests were combinations of the Mack-Wolfe test for the location parameters and a Moses Mack-Wolfe test for the scale parameters. When calculating the Moses Mack-Wolfe test, the technique used in the Moses test [9]was applied before performing the Mack-Wolfe procedure. To do so, each treatment sample was 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 within the m_i of the subsets. The new observation set became the m_1 sample variances for the first sample treatment, the m_2 sample variances for the second sample set, and so on. The Mack-Wolfe test statistic was applied to this new set of observations. By applying the Moses technique, a test for scale parameters is transformed into a test for location parameters.

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:

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

The expected value, $E_0(MA_p)$, and variance, $var_0(MA_p)$, respectively, are given in (10).

$$E_0(MA_p) = \frac{M_1^2 + M_2^2 - \sum_{i=1}^{k} m_i^2 - m_p^2}{4} \tag{10}$$

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

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 following form.:

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

The null hypothesis is rejected if $MA_p^* \geq z_\propto$, where $z_\propto$ is the critical value for the upper-tail probability of the standard normal distribution.

Their first proposed test, Z_1 is as shown in equation (12):

$$Z_1 = A_p^* + MA_p^* \tag{12}$$

where the Mack-Wolfe standardized version test of location for CRD is A_p^* as given in equation (4), and MA_p^* is the Moses Mack-Wolfe standardized version test of scale for CRD as given in equation (10). Because MA_p^* and A_p^* have asymptotic standard normal distributions under H_0, the asymptotic distribution of Z_1 should be normal with a mean of zero and a variance of 2. Their first proposed standardized version test, T_1, is given below in equation (13):

$$T_1 = \frac{Z_1 - 0}{\sqrt{2}} \tag{13}$$

Under H_0, T_1 has an asymptotic standard normal distribution. Therefore, the null hypothesis is rejected if $T_1 \geq z_\propto$, where $z_\propto$ is the critical value of the upper tail probability of the standard normal distribution.

Their second proposed test, Z_2 , for testing the hypotheses in equation (1) for a CRD is given in equation (14):

$$Z_2 = A_P + MA_P \tag{14}$$

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 by:

$$E_0(Z_2) = E_0(A_P) + E_0(MA_P) \tag{15}$$

$$var_0(Z_2) = var_0(A_P) + var_0(MA_P) \tag{16}$$

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

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

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

The weighted standardized version of their second proposed test is given by:

$$TW_2 = \frac{(A_P + 3 * MA_P) - E_0(A_P + 3 * MA_P)}{\sqrt{var_0(A_P + 9 * MA_P)}} \tag{18}$$

Under H_0, TW_2 has an asymptotic standard normal distribution. The null hypothesis is rejected for large values.

1.4 Lepage Test

Lepage's test [10] is a nonparametric test that tests for the two-sample location and scale problem. Lepage's aim 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 [4] and the Ansari-Bradley test [11]. The Mann-Whitney test is used to detect location changes while the Ansari-Bradley test is utilized to detect scale changes. The Lepage test has a chi-square distribution with two degrees of freedom under the null hypothesis.

1.5 Alsubie and Magel's Test

Alsubie, A., & Magel, R [12] proposed two nonparametric tests for differences in location and scale for the simple tree alternative. The executed a simulation study 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, A., & Magel, R. [13] proposed three additional nonparametric tests to test for differences in location and scale parameters under the simple tree alternative. Moses technique [9] 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 [12].

2 EXPERIMENTAL DETAILS / METHODOLOGY

We proposed three tests for testing the hypothesis given in (1) under a mixed design. The three tests are based on various combinations of the Mack-Wolfe [1]; Kim-Kim [5]; Moses Mack-Wolfe [8]; and Moses Kim-Kim using Moses's techniques (discussed in 2.1).

2.1 Moses Kim-Kim test

The Moses Kim-Kim test statistic will be for testing for the umbrella alternative for scale parameters in an RCBD.

Initial sample sizes of $n_1, \ldots\ldots, n_k$ are taken from the k populations. The Moses technique is applied to this data so that test for scale becomes a test location by transforming the data. To do so, each sample in the treatment was divided into m_i subsamples of equal size, q=3, i= 1, 2, …, k. For each m_i subset of each treatment i= 1, 2, …, k, the sample variance was calculated on the observations in each of the m_i subsets for each treatment. The new data set became the m_1 sample variances based on the subgroups from the first treatment sample, the m_2 sample variances based on the subgroups from the second treatment sample, etc. The Kim-Kim test statistic was calculated based on this transformed set data. The Moses Kim-Kim test statistic, MA, 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, had the following form:

$$MA = \sum_{j=1}^{b} MA_{jp} \tag{19}$$

where b is the number of blocks in the RCBD and p is the known treatment peak.

MA_{jp} denotes the Moses Mack-Wolfe test statistics for the j^{th} blocks as follows:

$$MA_{jp} = \left\{ \sum_{u=1}^{v-1} \sum_{v=2}^{p} U_{juv} + \sum_{u=p}^{v-1} \sum_{v=p+1}^{k} U_{jvu} \right\}$$

Here, b is the number of blocks in the RCBD, and p and k are the known treatment peak level and the number of treatments, respectively. Also, M_{jp} denotes the Moses Mack-Wolfe test statistic of the j^{th} block. The U_{juv} and U_{jvu} are the U statistics associated with the j^{th} block. In proposing this test statistic, we assume no interaction between blocks and treatments

The Moses Kim-Kim test statistic follows an asymptotic normal distribution when H_0 is true, with the mean and variance given by:

$$E_0(MA) = \sum_{j=1}^{b} \left\{ \frac{\{M_1^2 + M_2^2 - \sum_{i=1}^{k} m_i^2 - m_p^2\}}{4} \right\}$$

$$var_0(MA) = \frac{1}{72} \sum_{j=1}^{b} \Bigg\{ 2(M_{j1}^3 + M_{j2}^3) + 3(M_{j1}^2 + M_{j2}^2) - \sum_{i=1}^{k} m_{ij}^2(2m_{ij} + 3) - m_{jp}^2(2m_{jp} + 3) + 12 m_{jp} M_{j1} M_{j2} - 12 m_{jp}^2 M_j \Bigg\}$$

where M $= M_1 + M_2 - m_p$, $M_1 = \sum_{i=1}^{p} m_i$, $M_2 = \sum_{i=p}^{k} m_i$, b = the number of blocks, k = the number of treatments, p = the known peak, m_i = the number of subsamples, and m_p= the number of subsamples in the peak. When m_i = 1, the expected value and the variance are reduced to the form given by:

$$E_0(MA) = \frac{b(p^2 + (k-p+1)^2 - k - 1)}{4} \qquad (20)$$

and

$$var_0(MA) = \frac{b}{72}[2(p^3 + (k-p+1)^3) + 3(p^2 + (k-p+1)^2) - 5k - 5 + 12p(k-p+1) - 12k]$$

When H_0 is true, the standardized version of the Moses Kim-Kim test has an asymptotic standard normal distribution and is given by:

$$MA^* = \frac{MA - E_0(MA)}{\sqrt{var_0(MA)}} \qquad (21)$$

The null hypothesis is rejected when $MA^* \geq z_\propto$, where $z_\propto$ is the critical value for the upper-tail probability of the standard normal distribution. We proposed three test statistics to test the umbrella alternative for location and scale parameters simultaneously in a mixed design (RCBD and CRD) that used the Mack-Wolfe test, the Moses Mack-Wolfe test, the Kim-Kim test, and the Moses Mack-Wolfe.

2.2 Proposed test one

The first test statistic for the hypothesis in (1) is given in equation (22)

$$TK_1 = A_p^* + MA_p^* + A^* + MA^* \qquad (22)$$

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 equation (10). Also, $A^*$is the standardized Kim-Kim test based on the original data for RCBD given in equation (7), and MA^* is the Moses Kim-Kim standardized version test of scale for

RCBD as given in equation (19). Therefore, the first proposed standardized version test, L_1, is given below in equation (23):

$$L_1 = \frac{TK_1 - 0}{\sqrt{4}} \tag{23}$$

Under H_0, L_1 has an asymptotic standard normal distribution. The null hypothesis is rejected if $L_1 \geq z_\propto$, where $z_\propto$ is the critical value for the upper-tail probability of the standard normal distribution. If the test is performed at a 5% level of significance, then $z_\propto$ = 1.645.

2.3 Proposed Test Two

The second test statistic, TK_2, for testing the hypotheses in equation (1) is given in equation (24)

$$TK_2 = A_p + MA_p + A + MA \tag{24}$$

where, A_P is the Mack-Wolfe test (CRD) for location parameters, as shown in equation (2), and MA_P is the Moses Mack-Wolfe test (CRD) for scale as given in equation (9). Also, A is the Kim-Kim test statistic (RCBD) for location parameters, as shown in equation (5), and MA is the Moses Kim-Kim test statistic (RCBD) for scale as given in equation (19). The expected value and variance of TK_2 are the sum of the means and variances for the Mack-Wolfe tests for location, the Moses Mack-Wolfe test for scale, and the Kim-Kim tests for location, and the Moses Kim-Kim test for scale. The mean and variance are given in equations (25) and (26)

$$E_0(TK_2) = E_0(A_P) + E_0(MA_P) + E_0(A) + E_0(MA) \tag{25}$$

and

$$var_0(TK_2) = var_0(A_P) + var_0(MA_P) + var_0(A) + var_0(MA) \tag{26}$$

The standardized version of the second proposed test is given in equation (27)

$$L_2 = \frac{TK_2 - E_0(TK_2)}{\sqrt{var_0(TK_3)}} \tag{27}$$

Under H_0, L_2 has an asymptotic standard normal distribution. The null hypothesis is rejected for large values, $Z_\propto$.

2.4 Proposed Test Three

The weighted standardized version of the second proposed test is the third proposed test and is given in equation (28):

$$LW_2 = \frac{((A_p + 3*MA_p) + (A + 3*MA)) - E_0((A_p + 3*MA_p)) + (A + 3*MA))}{\sqrt{var_0(A_p + 9*MA_p) + var_0(A + 9*MA)}} \tag{28}$$

Under H_0, LW_2 has an asymptotic standard normal distribution. The null hypothesis is rejected for large values, $z_\propto$.

The idea behind proposing this test is that the sample size of the Moses Kim-Kim test is smaller than the sample size of the Kim-Kim test and therefore, more weight is applied to the Moses Kim-Kim test. In order to find Moses Kim-Kim test, the original sample must be divided into subsamples and the sum of the squared deviations found within each subsample. Since subsamples of size 3 were used in this study, the sample size used for the Moses Kim-Kim test was only 1/3 the sample size used for the Kim-Kim test. Hence, a weight of 3 was applied to the Moses Kim-Kim test.

2.5 Simulation Study

A simulation study was conducted to compare the three proposed tests based on estimated power for the mixed design of a CRD and RCBD when testing for location and scale parameters. The simulation study was implemented in SAS version 9.4 [14]. Powers were estimated when the observations followed three underlying distributions: normal, exponential, and t-distribution with three degrees of freedom. It was assumed that the peak, p, was known and the design used was a mixed CRD and RCBD 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 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 12 were taken from each of the k populations ($n_1=n_2=\ldots=n_k=n=12$). Four subsets of 3 observations each were randomly formed from the 12 observations from each population, the sample variance of each of the subsets was calculated, and the Mack-Wolfe test and the Kim-Kim test were 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 that 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 was used that instructs RAND to use the system clock. This means each run of the code produced a different set of data.

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 the standard deviation (σ), respectively, and a and b were the change in location parameters and the change in scale parameters. The mean and standard deviation 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 +a

The function (*F*) generated a random number from an exponential distribution. The value a was used to adjust the location parameter appropriately. Initially, the value of a was set to 0. The location and scale parameters changed with different values of µ.
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 estimated 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 that number by 5,000. The second part of the simulation study compared powers of the test statistics under various conditions. Powers were estimated by counting the number of times the proposed tests were rejected and then dividing that number by 5,000 for the various conditions.

2.6 Power Calculations

In the cases of three, four, and five populations with the peak p assumed to be known, the locations and scale parameter configurations were considered as the following $(\mu_1, \mu_2, .., \mu_k)$, $(\sigma_1, \sigma_2, \ldots, \sigma_k)$.

2.6.1 Three populations with peak at 2:

The powers were estimated in the following for the case (all treatments have the same scale parameters):

1. The peak was distinct, and there was equal spacing between parameters among location parameters only, for example (0.0, 1.5, 0.0), (1.0, 1.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location parameters only, for example (1.5, 2.0, 1.8), (1.0, 1.0, 1.0).
3. One additional parameter equaled 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 were estimated in the following for the case (all treatments have the same location parameters):

1. The peak was distinct and there was equal spacing between parameters among scale parameters, for example (0.0, 0.0, 0.0), (1.0, 5.0, 1.0).
2. The peak was distinct and there was unequal spacing between parameters among scale parameters, for example (0.0, 0.0, 0.0), (5.0, 9.0, 8.0).
3. One additional parameter equaled the peak among scale parameters, for example (0.0, 0.0, 0.0) and (0.0, 0.0, 0.0). (5.0, 5.0, 1.0), (1.0, 5.0, 5.0).

The powers were estimated in the following for the case (all treatments have the different location-Scale parameters):

1. The peak was distinct, and there was equal spacing between parameters among location and/or scale parameters, for example (0.0, 1.5, 0.0), (1.0, 5.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location and/or scale parameters, for example (1.5, 2.0,1.8), (5.0, 9.0, 8.0).
3. One additional parameter equaled the peak among location and/or scale parameters, for example (1.5, 1.5, 0.0) and (0.0, 1.5, 1.5). (5.0, 5.0, 1.0), (0.0, 5.0, 5.0).

2.6.2 Four populations with peak at 2

The powers were estimated in the following for the case (all treatments have the same scale parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among location parameters only, for example (0.0, 1.5, 0.0, 0.0), (1.0, 1.0, 1.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location parameters only, for example (1.2, 2.0, 1.8, 1.5), (1.0, 1.0, 1.0, 1.0).

3. One additional parameter equaled 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 were estimated in the following for the case (all treatments have the same location parameters):

1. The peak was distinct and there was equal spacing between parameters among scale parameters around the peak, for example (0.0, 0.0, 0.0, 0.0), (1.0, 5.0, 1.0, 1.0).
2. The peak was distinct and there was unequal spacing between parameters among scale parameters, for example (0.0, 0.0, 0.0, 0.0), (2.0, 9.0, 8.0, 5.0).
3. One additional parameter equaled the peak among scale parameters, for example (0.0, 0.0, 0.0, 0.0) and (0.0, 0.0, 0.0, 0.0). (5.0, 5.0, 1.0, 1.0), (1.0, 5.0, 5.0, 1.0).

The powers were estimated in the following for the case (all treatments have the different location-Scale parameters):

1. The peak was distinct and there was equal spacing between parameters among location and/or scale parameters around the peak, for example (0.0,1.5, 0.0, 0.0), (1.0, 5.0, 1.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location and/or scale parameters, for example (1.2, 2.0, 1.8, 1.5), (2.0, 9.0, 8.0, 5.0).
3. One additional parameter equaled the peak among location and/or scale parameters, for example (1.5, 1.5, 0.0, 0.0) and (0.0, 1.5, 1.5, 0.0). (5.0, 5.0, 1.0, 1.0), (1.0, 5.0, 5.0, 1.0).

2.6.3 Four populations with peak at 3:

The powers were estimated in the following for the case (all treatments have the same scale parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among location parameters only, for example (0.0, 0.0, 1.5, 0.0), (1.0, 1.0, 1.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location parameters only, for example (1.5, 1.8, 2.0, 1.2), (1.0, 1.0, 1.0, 1.0).
3. One additional parameter equaled 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 were estimated in the following for the case (all treatments have the same location parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among scale parameters, for example (0.0, 0.0, 0.0, 0.0), (1.0, 1.0, 5.0, 1.0).
2. The peak was distinct and there was unequal spacing between parameters among scale parameters, for example (0.0, 0.0, 0.0, 0.0), (5.0, 8.0, 9.0, 2.0).
3. One additional parameter equaled 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, 5.0, 5.0, 1.0), (1.0, 1.0, 5.0, 5.0).

The powers were estimated in the following for the case (all treatments have the different location-Scale parameters):

1. The peak was distinct and there was equal spacing between parameters among location and/or scale parameters around the peak, for example (0.0, 0.0, 1.5, 0.0), (1.0, 1.0, 5.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location and/or scale parameters, for example (1.5, 1.8, 2.0, 1.2), (5.0, 8.0, 9.0, 2.0).
3. One additional parameter equaled the peak among location and/or scale parameters, for example (0.0, 1.5, 1.5, 0.0) and (0.0, 0.0, 1.5, 1.5). (1.0, 5.0, 5.0, 1.0), (1.0, 1.0, 5.0, 5.0).

2.6.4 Five populations with peak at 2:

The powers were estimated in the following for the case (all treatments have the same scale parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among location parameters only, for example (0.0, 1.5, 0.0, 0.0, 0.0), (1.0, 1.0, 1.0, 1.0, 1.0).
2. The peak was distinct and there was unequal spacing between parameters around the peak among location parameters only, for example (1.4, 2.0, 1.8, 1.5, 1.2), (1.0, 1.0, 1.0, 1.0, 1.0).
3. One additional parameter equaled 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 were estimated in the following for the case (all treatments have the same location parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among scale parameters, for example (0.0, 0.0, 0.0, 0.0, 0.0), (1.0, 5.0, 1.0, 1.0, 1.0).
2. The peak was distinct and there was unequal spacing between parameters among scale parameters, for example (0.0, 0.0, 0.0, 0.0, 0.0), (4.0, 9.0, 8.0, 5.0, 2.0).
3. One additional parameter equaled 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). (5.0, 5.0, 1.0, 1.0, 1.0), (1.0, 5.0, 5.0, 1.0, 1.0).

The powers were estimated in the following for the case (all treatments have the different location-Scale parameters):

1. The peak was distinct and there was equal spacing between parameters among location and/or scale parameters around the peak, for example (0.0, 1.5, 0.0, 0.0, 0.0), (1.0, 5.0, 1.0, 1.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location and/or scale parameters, for example (1.4, 2.0, 1.8, 1.5, 1.2), (4.0, 9.0, 8.0, 5.0, 2.0).
3. One additional parameter equaled the peak among location and/or 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). (5.0, 5.0, 1.0, 1.0, 1.0), (1.0, 5.0, 5.0, 1.0, 1.0).

2.6.5 Five populations with peak at 3:

The powers were estimated in the following for the case (all treatments have the same scale parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among location parameters only, for example (0.0, 0.0, 1.5, 0.0, 0.0), (1.0, 1.0, 1.0, 1.0, 1.0).
2. The peak was distinct and there was unequal spacing between parameters among location parameters only, for example (1.2, 1.5, 2.0, 1.8, 1.4), (1.0, 1.0, 1.0, 1.0, 1.0).
3. One additional parameter equaled 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 were estimated in the following for the case (all treatments have the same location parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among scale parameters, for example (0.0, 0.0, 0.0, 0.0, 0.0), (1.0, 1.0, 5.0, 1.0, 1.0).
2. The peak was distinct and there was unequal spacing between parameters among scale parameters, for example (0.0, 0.0, 0.0, 0.0, 0.0), (2.0, 5.0, 9.0, 8.0, 5.0).

3. One additional parameter equaled 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, 5.0, 5.0, 1.0, 1.0), (1.0, 1.0, 5.0, 5.0, 1.0).

The powers were estimated in the following for the case (all treatments have the different location-Scale parameters):

1. The peak was distinct and there was equal spacing between parameters among location and/or scale parameters around the peak, for example (0.0, 0.0, 1.5, 0.0, 0.0), (1.0, 1.0, 5.0, 1.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location and/or scale parameters, for example (1.2, 1.5, 2.0, 1.8, 1.4), (2.0, 5.0, 9.0, 8.0, 5.0).
3. One additional parameter equaled the peak among location and/or 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, 5.0, 5.0, 1.0, 1.0), (1.0, 1.0, 5.0, 5.0, 1.0).

<u>2.6.6 Five populations with peak at 4</u>:

The powers were estimated in the following for the case (all treatments have the same scale parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among location parameters only, for example (0.0, 0.0, 0.0, 1.5, 0.0), (1.0, 1.0, 1.0, 1.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location parameters only, for example (1.2, 1.5, 0.8, 1.8, 1.4), (1.0, 1.0, 1.0, 1.0, 1.0).
3. One additional parameter equaled 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 were estimated in the following for the case (all treatments have the same location parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among scale parameters, for example (0.0, 0.0, 0.0, 0.0), (1.0, 1.0, 1.0, 5.0, 1.0).
2. The peak was distinct and there was unequal spacing between parameters among scale parameters, for example (0.0, 0.0, 0.0, 0.0, 0.0), (2.0, 5.0, 8.0, 9.0, 4.0).
3. One additional parameter equaled 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, 5.0, 5.0, 1.0), (1.0, 1.0, 1.0, 5.0, 5.0).

The powers were estimated in the following for the case (all treatments have the different location-Scale parameters):

1. The peak was distinct and there was equal spacing between parameters around the peak among location and/or scale parameters, for example (0.0, 0.0, 0.0, 1.5, 0.0), (1.0, 1.0, 1.0, 5.0, 1.0).
2. The peak was distinct, and there was the unequal spacing between parameters among location and/or scale parameters, for example (1.2, 1.5, 0.8, 1.8, 1.4), (2.0, 5.0, 8.0, 9.0, 4.0).
3. One additional parameter equaled the peak among location and/or 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, 5.0, 5.0, 1.0), (1.0, 1.0, 1.0, 5.0, 5.0).

3. RESULTS AND DISCUSSION

Selected results are given in Tables 1-7. The tables give results using various SB ratios and various underlying distributions. The SB Ratio was that the number of blocks in the RCBD portion divided by the sample size in the CRD portion. SB ratios were ½, 1, and 2 in this study Three situations of power estimates were considered in this study based on the parameter changes. The first situation considered was when at least some of the location parameters were different, and the scale parameters were equal. The second situation considered was when the location parameters were equal, and at least some of the scale parameters were different. The third situation considered was when at least some of the location and some of the scale parameters were both different. Tables 1-3 show the results for 3 different types of populations when the locations (means) were different, and the scales (variances) were equal. Tables 4-6 show estimated powers when the locations (means) were the same and the scales (variances) were different. Tables 7-9 show estimated powers when both the locations (means) and the scales (variances) were different.

Table 1: Percentage of Rejection for k=3 Populations p=2; Normal Distributions with different means and equal variances when number of blocks half the sample size under mixed design. (n=12, Blk=6)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	L_1	L_2	LW_2
0	1	0	1	0	1	0.0518	0.0474	0.0534
0	1	1.5	1	0	1	0.9096	0.9922	0.9656
0	1	1.5	1	1.5	1	0.3978	0.5596	0.4600
1.5	1	1.5	1	0	1	0.3956	0.5672	0.4528
1.5	1	2	1	1.8	1	0.1816	0.2382	0.2048

Table 2: Percentage of Rejection for k=3 Populations p=2; T (3)-Distributions with different means and equal variances when number of blocks half the sample size under mixed design. (n= 12, Blk=6)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	L_1	L_2	LW_2
0	1 σ^2	0	1 σ^2	0	1 σ^2	0.0534	0.0496	0.0506
0	1 σ^2	1.5	1 σ^2	0	1 σ^2	0.7686	0.9256	0.8414
0	1 σ^2	1.5	1 σ^2	1.5	1 σ^2	0.3066	0.4268	0.3518
1.5	1 σ^2	1.5	1 σ^2	0	1 σ^2	0.3056	0.4238	0.3386
1.5	1 σ^2	2	1 σ^2	1.8	1 σ^2	0.1534	0.1948	0.1648

Table 3: Percentage of Rejection for k=3 Populations p=2; Exponential (1)-Distributions with different means and equal variance when number of blocks half the sample size under mixed design. (n= 12, Blk=6)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	$L1$	L_2	LW_2
1	1	1	1	1	1	0.0526	0.0472	0.0450
1	1	1.5	1	1	1	0.8682	0.9758	0.9254
1	1	1.5	1	1.5	1	0.3824	0.5092	0.4304
1.5	1	1.5	1	1	1	0.3854	0.5246	0.4400
1.5	1	2	1	1.8	1	0.6412	0.8152	0.7090

Table 4: Percentage of Rejection for k=3 Populations p=2; Normal Distribution with equal means and different variance when number of blocks equal the sample size under mixed design. (n=12, Blk=12)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	L_1	L_2	LW_2
0	1	0	1	0	1	0.0486	0.0546	0.0552
0	1	0	5	0	1	0.7914	0.2152	0.4980
0	1	0	5	0	5	0.3058	0.1056	0.1948
0	5	0	5	0	1	0.3140	0.1116	0.2062
0	5	0	9	0	8	0.2140	0.0868	0.1474

Table 5: Percentage of Rejection for k=3 Populations p=2; T (3)-Distribution with equal means and different variance when number of blocks equal the sample size under mixed design. (n= 12, Blk=12)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	L_1	L_2	LW_2
0	$1\ \sigma^2$	0	$1\ \sigma^2$	0	$1\ \sigma^2$	0.0476	0.0476	0.0480
0	$1\ \sigma^2$	0	$5\ \sigma^2$	0	$1\ \sigma^2$	0.7852	0.1414	0.1904
0	$1\ \sigma^2$	0	$5\ \sigma^2$	0	$5\ \sigma^2$	0.2792	0.0790	0.0952
0	$5\ \sigma^2$	0	$5\ \sigma^2$	0	$1\ \sigma^2$	0.2852	0.0834	0.1050
0	$5\ \sigma^2$	0	$9\ \sigma^2$	0	$5\ \sigma^2$	0.3066	0.0924	0.1110

Table 6: Percentage of Rejection for k=3 Populations p=2; Exponential (1)-Distribution with equal means and different variance when number of blocks equal the sample size under mixed design. (n= 12, Blk=12)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	L_1	L_2	LW_2
1	1^2	1	1^2	1	1^2	0.0486	0.0432	0.0444
1	1^2	1	5^2	1	1^2	0.9966	0.2052	0.7248
1	1^2	1	5^2	1	5^2	0.6078	0.1054	0.2788
1	5^2	1	5^2	1	1^2	0.6178	0.1098	0.2856
1	5^2	1	9^2	1	8^2	0.2820	0.0718	0.1444

Table 7: Percentage of Rejection for k=3 Populations p=2; Normal Distribution with different means and different variance when number of blocks twice the sample size under mixed design. (n=12, Blk=24)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	L_1	L_2	LW_2
0	1	0	1	0	1	0.0486	0.0478	0.0496
0	1	1.5	5	0	1	0.9960	0.6264	0.8836
0	1	1.5	5	1.5	5	0.6844	0.2804	0.4458
1.5	5	1.5	5	0	1	0.6910	0.2824	0.4436
1.5	5	2	9	1.8	8	0.3124	0.1222	0.2038

Table 8: Percentage of Rejection for k=3 Populations p=2; T (3)-Distribution with different means and different variance when number of blocks twice the sample size under mixed design. (n= 12, Blk=24)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	L_1	L_2	LW_2
0	1 σ^2	0	1 σ^2	0	1 σ^2	0.0550	0.0536	0.0584
0	1 σ^2	1.5	5 σ^2	0	1 σ^2	1.0000	0.9962	0.9998
0	1 σ^2	1.5	5 σ^2	1.5	5 σ^2	0.9468	0.6494	0.8234
1.5	5 σ^2	1.5	5 σ^2	0	1 σ^2	0.9492	0.6496	0.8170
1.5	5 σ^2	2	9 σ^2	1.5	8 σ^2	0.5254	0.2884	0.3918

Table 9: Percentage of Rejection for k=3 Populations p=2; Exponential (1)-Distribution with different means and different variance when number of blocks twice the sample size under mixed design. (n= 12, Blk=24)

μ_1	σ_1^2	μ_2	σ_2^2	μ_3	σ_3^2	L_1	L_2	LW_2
1	1^2	1	1^2	1	1^2	0.0452	0.0478	0.0484
1	1^2	2	2^2	1	1^2	1.0000	0.9576	0.9868
1	1^2	2	2^2	2	2^2	0.8870	0.5314	0.6186
2	2^2	2	2^2	1	1^2	0.8858	0.5362	0.6342
2	2^2	4	4^2	3	3^2	0.9926	0.7914	0.8814

4. Conclusion

All of the tests maintained their significance levels of 0.05. The results as to which test statistic had greater powers were the same for all the SB ratios considered and all distributions considered depending upon which set of parameters changed. For the three distributions considered with n= 12 and four subsets of 3 observations in each, number of populations, and various peaks, the L_2 test had the largest powers if only the location parameters change. The L_1 test had the higher powers if only the scale parameters change. The L_1 test had the highest powers if the location parameters and scale parameters change for all distributions. Overall, when researchers want to test for differences in either both location and scale or scale, L_1 test is recommended.

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