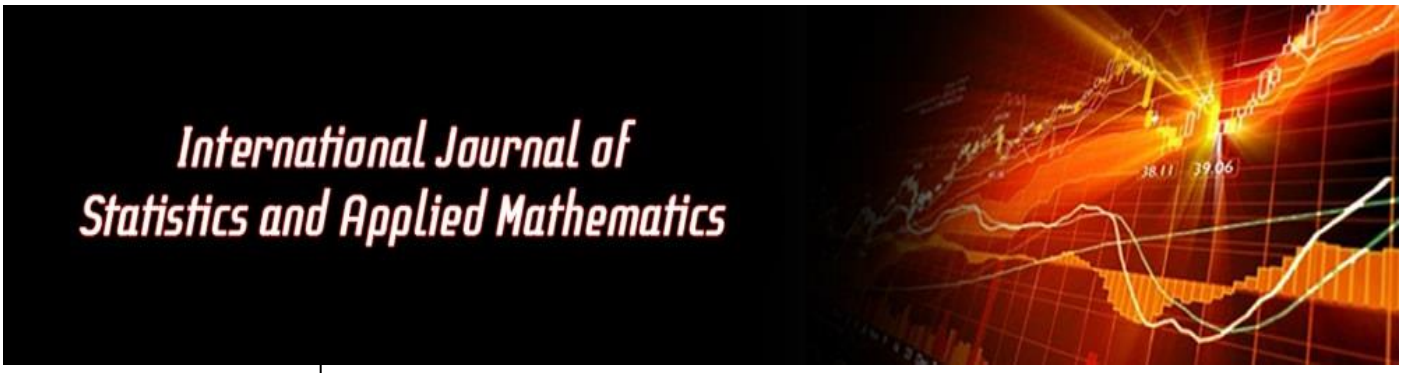

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Proposed nonparametric tests for the simple tree alternative for location and scale testing

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Abstract
Two nonparametric tests are proposed for the simple tree alternative to test for differences in location and/or scale. These tests are combinations of the Fligner-Wolfe test and a modified Ansari-Bradley test. A simulation study is conducted to determine how well the proposed tests maintain their significance levels. Powers are also estimated for the proposed tests under a variety of conditions for three and four populations. Three different types of variable parameters vectors are considered with each vector containing a location and a scale parameter. The first type of parameter vectors considered include different location parameters and equal scale parameters. The second type include different scale parameters and equal location parameters, and the third type include both different location parameters and different scale parameters. Results are given as far as which test does better under certain conditions.

Keywords: Completely randomized design, location-scale problem, power

1. Introduction
Nonparametric methods are used in many fields, including biostatistics, business, pharmaceutical statistics, psychology, and social sciences. Nonparametric tests are often more suitable due to the weaker assumptions they have about the underlying populations and the requirements for the measurement scales (Wang, 2011) [11]. In many cases researchers find themselves in a situation where they want to compare one or more treatments with a standard or control treatment. In these cases, the simple tree hypothesis may be the most appropriate hypothesis (Conroy, 2011) [3]. The simple tree alternative for location is given by:

$$H_0: \mu_1 = \mu_2 = \cdots = \mu_K \quad (1)$$
$$H_\alpha: \mu_1 \leq [\mu_2, \ldots, \mu_k] \text{ (At least one strict inequality)}$$

Where μ_i is the location parameter of population i.
There may be some situations in which a treatment not only may affect the location but also may affect the variance (or scale) of a distribution (Marozzi, 2013) [9]. The treatment may affect one or the other or both simultaneously.
Most of the past works regarding this area, are focused on detecting location changes or scale changes only. There is sometimes a need to test the location and scale parameters at the same time. Researches may want to know if a treatment has any effect at all. The effect of a treatment may include that the treatment increases the mean of the observations or that the treatment increases the variance of the observations.
The most common test for the two-sample location-scale problem is the Lepage test (Lepage, 1971) [7]. This test is based on a combination of the Mann-Whitney test (Mann and Whitney, 1947) [8] and the Ansari-Bradley test (Ansari and Bradley, 1960) [1]. The null hypothesis and alternative hypothesis are given below:

$$H_0: \mu_1 = \mu_2 \text{ and } \sigma_1 = \sigma_2 \quad (2)$$
$$H_\alpha: \mu_1 \neq \mu_2 \text{ and / or } \sigma_1 \neq \sigma_2$$

Where μ_i and σ_i are the location and scale parameters of population i, respectively.

Hollander and Wolfe (1999) [5] mentioned an example where the Lepage test can be applied. The example concerns the effect of maternal steroid therapy on platelet counts of newborn infants. Autoimmune Thrombocytopenic Purpura (ATP) is a disease where the patient produces antibodies to her own platelets. Children of a mother with ATP are frequently born with low platelet counts. The effect of administering corticosteroid prednisone to pregnant women with ATP was studied by (Karpatkin and Porges, 1981) [6] in order to raise the infants' platelet counts to safe levels during their deliveries (Hollander and Wolfe, 1999) [5]. The goal of the study is to determine whether or not predelivery maternal prednisone therapy increases the platelet counts of a newborn baby. The main problem is to detect a possible change in mean platelet counts for the treated population compared to the non-treated population. However, there is also some concern that the variability in newborn baby platelet counts would be increased by the steroid therapy.

This research extends the hypotheses test given in (2) to the hypotheses test given in (3). This research is concerned with testing the hypothesis for the simple tree alternative:

$H_0: \mu_1 = \mu_2 = \cdots = \mu_k,$ (3)

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

$H_\alpha: \mu_1 \leq [\mu_2, \ldots, \mu_k]$ and / or

$H_\alpha: \sigma_1 \leq [\sigma_2, \ldots, \sigma_k]$ (At least one inequality is strict)

Where μ_i is a location parameter (the median or mean) for population i and σ_i is a scale parameter with $i = 1,2, \ldots, k$ and k are the total number of populations. Population one ($i = 1$) is usually referred to the control population, while populations 2 through k are the treatment populations. The treatments may be increasing dosages of a drug.

1.1 Background

1.1.1 Mann-Whitney

The Mann-Whitney test is a standard test statistic for examining the null hypothesis of equal population location parameters (Mann and Whitney, 1947) [8]. The null hypothesis and alternative hypothesis are given below:

$H_0: \mu_1 = \mu_2$ (4)

$H_{\alpha 1}: \mu_1 \neq \mu_2, H_{\alpha 2}: \mu_1 < \mu_2, H_{\alpha 3}: \mu_1 > \mu_2$

In order to compute the test statistic *MW*, it will be assumed that there is a sample of size n_1 from the population 1 and a sample size n_2 of the population 2. The measurements of combined set of n_1 + n_2= *N*, have been arranged in order from smallest to largest. Ranks are then assigned to the ordered measurements and S_j will be the rank of *j*th observation in sample 2, within the set of ranks. The test statistic *MW* is the sum of the ranks of all measurements in the sample 2.

$MW = \sum S_j$ (5)

The standardized version of Mann-Whitney test is given by:

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

$E_0(MW) = \frac{n_2(N+1)}{2}$ (7)

$var_0(MW) = \frac{n_1 n_2 (N+1)}{12}$ (8)

When H_0 is true, the test statistic MW^* has approximately a standard normal distribution. H_0 will be rejected for the two sided alternative when $MW^* \geq Z_{\alpha/2}$ at the α level of significance where $Z_{\alpha/2}$ is the (1- $\alpha/2$) 100% percentile of the standard normal distribution.

1.1.2. Fligner-wolfe test

Often in biological sciences it is necessary to investigate the response of treatments compared to a control. Situations in which this often occurs are clinical trials, pharmacology experiments and agricultural experiments (Olet, 2014). The Fligner-Wolfe test statistic is designed for use in this type of situation (Fligner and Wolfe, 1982) [4].

The Fligner-Wolfe test statistic compares the median of the control group, to the medians of a number of other treatment groups simultaneously (Fligner and Wolfe, 1982) [4]. There are *k* samples with $i = 1$ denoting the control sample and the remaining $2 \leq i \leq k$ indicating treatment samples. It is assumed that the means in the treatment populations are at least as large as the mean of the control population. The null hypothesis and alternative hypothesis are given below:

$H_0: \mu_1 = \mu_2 = \cdots = \mu_k$, versus (9)

$H_\alpha: \mu_1 \leq [\mu_2, \ldots, \mu_k]$ With at least one strict inequality.

In calculating the Fligner-Wolfe test statistic, it is useful to visualize two populations. One population is the control ($i = 1$) and the remaining $k - 1$ populations are the combined treatment population. It will be assumed that there is a sample of size n_1 from the control population and a sample size n_2 of the combined treatment population. In both the control sample and treatment sample, all of the observations will be merged together and subsequently ranked from smallest to largest. Let the rank r_{ij} with $i =$ 1,2 and $j = 1,2,3, \ldots, n_i$ indicate the rank of the j^{th} observation in the i^{th} sample with i equal to 1 for the control sample and i equal to 2 for the combined treatment sample.

$$T_1 = FW = \sum_{\substack{2 \leq i \leq k \\ 1<j<n_i}} r_{ij} \tag{10}$$

k is the number of treatments, n_i the number of observations in treatment i and r_{ij} the rank of the observat e jth group subjected to the ith treatment. The expected value and variance of FW under the null distribution are outlined (10)

$$E(T_1) = E_0(FW) = \frac{n_2(N+1)}{2} \text{ and } var(T_1) = var_0(FW) = \left\{\frac{n_1 n_2 (N+1)}{12}\right\} \tag{11}$$

Where, n_1 is the size of the control population, and n_2 the number of observations in the remaining $k - 1$ treatment populations $n_2 = N - n_1$. The standardized version of Fligner-Wolfe test FW^* is stated below.

$$FW^* = \frac{FW - E_0(FW)}{\sqrt{var_0(FW)}} \tag{12}$$

The null hypothesis is rejected when $FW^* \geq Z_\alpha$ at the α level of significance where Z_α is the (1- α) 100% percentile of the standard normal distribution.

1.1.3. Ansari-bradley test

The Ansari-Bradley test is a nonparametric test designed to test for equality of variances based on independent samples from 2 populations (Ansari and Bradley, 1960) [1]. The null hypothesis and alternative hypothesis are given below:

$$H_0: \sigma_1 = \sigma_2 \tag{13}$$

$$H_{\alpha 1}: \sigma_1 \neq \sigma_2, H_{\alpha 2}: \sigma_1 < \sigma_2, \ H_{\alpha 3}: \sigma_1 > \sigma_2$$

In calculating the Ansari-Bradley test, all the observations from the two samples will be combined together. The combined set of $n_1 + n_2 = N$ observations will be arranged in order from smallest to largest. The ranks will be assigned to the ordered observations as follows:
The smallest observation and the largest observation will each be given a rank of 1
The second smallest observation and the second largest observation will each be given a rank of 2
The ordered observations will continue to be ranked in this manner until all observations have been assigned a rank. At this point R_i will be the rank of i^{th} observation in the first sample in the set of ranks. The test statistic Ansari-Bradley (*AB)* is the sum of the ranks of all observations in the first sample:

$$\text{AB} = \sum R_i \tag{14}$$

The standardized version of Ansari-Bradley test is:

$$AB^* = \frac{AB - E_0(AB)}{\sqrt{var_0(AB)}} \tag{15}$$

If $N = n_1 + n_2$ is an even number :

$$E_0(AB) = \frac{n_1(N+2)}{4} \tag{16}$$

$$var_0(AB) = \left\{\frac{n_1 n_2 (N+2)(N-2)}{48(N-1)}\right\} \tag{17}$$

If $N = n_1 + n_2$ is an odd integer:

$$E_0(AB) = \frac{n_1(N+1)^2}{4N} \tag{18}$$

$$var_0(AB) = \left\{\frac{n_1 n_2 (N+1)(3+N^2)}{48N^2}\right\} \tag{19}$$

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

1.1.4. Lepage's Test

A nonparametric test for the two-sample location-scale problem is the test of Lepage (Lepage, 1971) [7]. The purpose of the Lepage test is to determine whether there are differences (between 2 populations) in either location parameters μ_1 and μ_2 or scale parameters σ_1 and σ_2. The Lepage's test is an amalgamation of the Mann-Whitney test for detecting location changes and the Ansari-Bradley test for detecting scale changes. The null hypothesis and alternative hypothesis are given below:

$H_0: \mu_1 = \mu_2$ and $\sigma_1 = \sigma_2$ (20)

$H_\alpha: \mu_1 \neq \mu_2$ and/ or $\sigma_1 \neq \sigma_2$

The Lepage test statistics is given by:

$$Lepage = \frac{[(MW - E_0(MW)]^2}{var_0(MW)} + \frac{[(AB - E_0(AB)]^2}{var_0(AB)} = (MW^*)^2 + (AB^*)^2 \quad (21)$$

The Lepage test has a chi-square distribution with two degrees of freedom when the null hypothesis is true. H_0 is rejected when Lepage $\geq \chi^2_{2,\alpha}$ where $\chi^2_{2,\alpha}$ is upper a percentile point of the chi-square distribution with two degrees of freedom.

2. Materials and methods

2.1 Proposed tests

2.1.1 Modified ansari-bradley test

Following the work of Lepage (1971) [7], the two-sample location-scale test will be extended to a test to a location-scale test for the simple tree alternative. A modified version of the Ansari-Bradley test will be proposed. A modified version of the Ansari-Bradley test for simple tree alternative as stated below will be proposed.

$H_0: \sigma_1 = \sigma_2 = \cdots = \sigma_k,$ (22)

$H_\alpha: \sigma_1 \leq [\sigma_2, \ldots, \sigma_k]$ Where at least one inequality is strict.

In calculating the modified Ansari-Bradley test, it is helpful to consider a situation with two populations. One population is the control (i=1) and the remaining $k-1$ populations is the combined treatment population. It will be assumed that there is a sample of size n_c from the control population and a sample size n_t of the combined treatment population. The combined set of $n_c + n_t = N$ observations will be arranged in order from smallest to largest. The ranks will be assigned to the ordered observations as follows:

- The smallest observation and the largest observation will each be given a rank of 1
- The second smallest observation and the second largest observation will each be given a rank of 2

The ordered observations will continue to be ranked in this manner until all observations have been assigned a rank. At this point R_i will be the rank of i^{th} observation in the control sample in the combined set of ranks. The test statistic AB is the sum of the ranks of all observations in the control sample,

$T_2: \text{AB} = \sum R_i$ (23)

The standardized version of Ansari-Bradley test is given by:

$$AB^* = \frac{AB - E_0(AB)}{\sqrt{var_0(AB)}} \quad (24)$$

If N= $n_c + n_t$ is an even number :

$$E(T_2): E_0(AB) = \frac{n_c(N+2)}{4} \quad (25)$$

$$var(T_2): var_0(AB) = \left\{\frac{n_c n_t (N+2)(N-2)}{48(N-1)}\right\} \quad (26)$$

If $N = n_c + n_t$ is an odd integer:

$$E(T_2): E_0(AB) = \frac{n_c(N+1)^2}{4N} \quad (27)$$

$$var(T_2): var_0(AB) = \left\{\frac{n_c n_t (N+1)(3+N^2)}{48N^2}\right\} \quad (28)$$

The asymptotic null distribution of AB^* is the standard normal distribution (Ansari and Bradley, 1960) [1].

2.1.2. Proposed test one

The first proposed test L_1 is the sum of standardized test statistics for two tests. The first test being the Fligner-Wolfe test statistic (T_1), obtained using Equation (10) and the second being the modified Ansari-Bradley test statistic (T_2) obtained using Equation (23). The mean and variance for the Fligner-Wolfe test statistic are denoted by $E(T_1)$ and $var\ (T_1)$ and obtained using Equation (11). In this case, T_1 is the sum of the ranks in the combined treatment sample when the observations from the control and treatment samples are combined together.

The standardized Fligner-Wolfe test statistic is given by:

$$Z_1 = \frac{T_1 - E(T_1)}{\sqrt{var(T_1)}} \tag{29}$$

Similarly, the mean and variance for modified Ansari-Bradley test statistic are denoted by $E(T_2)$ and $var(T_2)$, and obtained using Equations (25) and (26). In this case, T_2 is the sum of the ranks of observations in the control sample as described in the Ansari-Bradley test when the control and treatments samples are combined.

The standardized modified Ansari-Bradley test statistic is given by:

$$Z_2 = \frac{T_2 - E(T_2)}{\sqrt{var(T_2)}} \tag{30}$$

Both Z_1 and Z_2 have an asymptotic standard normal distribution under H_0 as given in
(Fligner and Wolfe, 1982) [4] and (Ansari and Bradley, 1960) [1]. When H_0 is true, the asymptotic distribution of $Z_1 + Z_2$ should be normal with a mean of zero (0) and a variance of (2). As a result, the asymptotic distribution of the first proposed test (L_1) under H_0 is a standard normal.

$$L_1 = \frac{Z_1 + Z_2}{\sqrt{2}} \tag{31}$$

H_0 is rejected for a large value which is $L_1 \geq Z_\alpha$ at the α level of significance where Z_α is the (1- α) 100% percentile of the standard normal distribution. If the test is performed at a 5% level of significance then Z_α= 1.645.

2.1.3. Proposed Test Two

The second proposed test is given by:

$$L_2 = \frac{T_1 + T_2 - E(T_1 + T_2)}{\sqrt{var(T_1) + var(T_2)}} \tag{32}$$

Where $E(T_1 + T_2) = E(T_1) + E(T_2)$ and the null standard deviation is $\sqrt{var(T_1) + var(T_2)}$. When the null hypothesis is true, the asymptotic distribution of L_2 is also a standard normal distribution and the null hypothesis will be rejected when L_2 is large.

3. Simulation study

A simulation study is conducted to compare the five proposed tests. The simulation study is implemented in SAS version 9.4. The properties of the proposed test statistics are compared assuming random samples followed normal distribution, t-distribution with 3 degrees of freedom and exponential distribution. In order to generate random samples from a specific distribution, the functions RAND are used in SAS. This 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 research, 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) [2]. The call function for the normal distribution is *RAND ('Normal', μ, σ)* where μ is the mean and σ is the standard deviation.The call function for the t-distribution is *RAND ('T',* 3*)* where T is the name of the distribution and 3 is the degrees of freedom. The call function for the exponential distribution is

RAND ('Exponential'). This function generates a random number from an exponential distribution with a mean and variance of one.

For all simulations, replications of 10,000 samples are used. The proposed tests are compared in two parts. The first part of the simulation is to get the estimates of the alpha values of the proposed test statistics. The stated alpha values for the proposed test statistics are all 0.05. The alpha values are estimated by counting the number of times the null hypothesis was rejected and then dividing by 10,000. This is done when the null hypothesis is true, and all distributions are the same; namely all location parameters are equal, and all scale parameters are equal.

The second part of the simulation study is to compare powers of the test statistics under various conditions. Powers are estimated by counting the number of times the proposed tests are rejected divided by 10,000.

3.1. Simulation outline

The following outline summarizes what is done in the simulations.

1. The alpha values of each test statistic are estimated and compared to the stated alpha values for each simulation conducted. The proposed test statistics are examined in the case of k=2, k=3, and k=4 populations.

2. Powers are estimated for three conditions. Under the first condition, the location parameters are different, while the scale parameters are equal. The second condition assumes that the location parameters are equal, while the scale parameters are different. The final condition assumes, both the location parameters and the scale parameters are different.
3. Equal samples of sizes 9, 18, 30 are used for all populations.
4. A variety of situations where sample of sizes are unequal are considered.
5. Three underlying distributions are considered.

4. Results and Discussion

Tables 1-3 outline the results of simulation study for three treatments under the normal distribution. The results for four treatments are similar. The estimated alpha values are around 0.05 (see first entry in Table 1). The results here are consisted with the results from the t-distribution with 3 degrees of freedom and for all the sample sizes included in the study. When the populations have unequal location parameters and equal scale parameters, L_2 has the highest estimated powers (Table 1). When the populations have equal location parameters and unequal scale parameters, L_1 has the highest estimated powers (Table 2). When the populations have unequal location parameters and unequal scale parameters, L_1 has the higher estimated powers (Table 3).

Table 1: Percentage of Rejection for k=3 Populations; Normal Distribution with different means and equal variances

n_1	n_2	n_3	μ_1	σ_1	μ_2	σ_2	μ_3	σ_3	L_1	L_2
30	30	30	0	1	0	1	0	1	0.0502	0.0492
30	30	30	0	1	0.25	1	0.5	1	0.2787	0.4114
30	30	30	0	1	0.5	1	0.75	1	0.5232	0.7540
30	30	30	0	1	0.75	1	1	1	0.7487	0.9494
30	30	30	0	1	1	1	1.25	1	0.8939	0.9941
30	30	30	0	1	1.25	1	1.5	1	0.9659	0.9996
30	30	30	0	1	1.5	1	1.75	1	0.9924	1

Table 2: Percentage of Rejection for k=3 Populations; Normal Distribution with same means and different variances

n_1	n_2	n_3	μ_1	σ_1	μ_2	σ_2	μ_3	σ_3	L_1	L_2
30	30	30	0	1	0	1.5	0	2	0.5704	0.2948
30	30	30	0	1	0	1.75	0	2.25	0.7362	0.4009
30	30	30	0	1	0	2	0	2.5	0.8293	0.4814
30	30	30	0	1	0	2.25	0	2.75	0.8934	0.5578
30	30	30	0	1	0	2.5	0	3	0.9348	0.6250
30	30	30	0	1	0	2.75	0	3.25	0.9521	0.6618

Table 3: Percentage of Rejection for k=3 Populations; Normal Distribution with different means and different variances

n_1	n_2	n_3	μ_1	σ_1	μ_2	σ_2	μ_3	σ_3	L_1	L_2
30	30	30	0	1	0.25	1.5	0.5	2	0.8472	0.6995
30	30	30	0	1	0.25	1.75	0.5	2.25	0.9207	0.7637
30	30	30	0	1	0.25	2	0.5	2.5	0.9601	0.8131
30	30	30	0	1	0.25	2.25	0.5	2.75	0.9766	0.8402
30	30	30	0	1	0.25	2.5	0.5	3	0.9843	0.8599
30	30	30	0	1	0.25	2.75	0.5	3.25	0.9898	0.8787

Tables 4-6 show the results of simulation study for four treatments under the exponential distribution. The results for 3 treatments were similar. The estimated alpha values are around 0.05 (see first entry in Table 4). The results are consistent across all sample sizes included in the study. When the populations have unequal location parameters and equal scale parameters, L_2 has higher estimated powers than L_1 (Table 4). When the populations have equal location parameters and unequal scale parameters, L_1 has higher estimated powers than L_2 (Table 5). When the populations have unequal location parameters and unequal scale parameters, L_2 has the higher estimated powers (Table 6).

Table 4: Percentage of Rejection for k=4 Populations; Exponential Distribution with different means and equal variances

n_1	n_2	n_3	n_4	μ_1	σ_1	μ_2	σ_2	μ_3	σ_3	μ_4	σ_4	L_1	L_2
18	18	18	18	1	1	1	1	1	1	1	1	0.0461	0.0478
18	18	18	18	1	1	1.25	1	1.5	1	1.75	1	0.0609	0.3698
18	18	18	18	1	1	1.5	1	1.75	1	2	1	0.0657	0.5833
18	18	18	18	1	1	1.75	1	2	1	2.25	1	0.0840	0.7540
18	18	18	18	1	1	2	1	2.25	1	2.5	1	0.0967	0.8640
18	18	18	18	1	1	2.25	1	2.5	1	2.75	1	0.1122	0.9337
18	18	18	18	1	1	2.5	1	2.75	1	3	1	0.1192	0.9681

Table 5: Percentage of Rejection for k=4 Populations; Exponential Distribution with same means and different variances

n_1	n_2	n_3	n_4	μ_1	σ_1	μ_2	σ_2	μ_3	σ_3	μ_4	σ_4	L_1	L_2
18	18	18	18	1	1	1	1.5^2	1	2^2	1	2.5^2	0.3698	0.0726
18	18	18	18	1	1	1	2^2	1	2.5^2	1	3^2	0.4671	0.0850
18	18	18	18	1	1	1	2.5^2	1	3^2	1	3.5^2	0.5325	0.0952
18	18	18	18	1	1	1	3^2	1	3.5^2	1	4^2	0.5663	0.1067
18	18	18	18	1	1	1	3.5^2	1	4^2	1	4.5^2	0.5818	0.1143
18	18	18	18	1	1	1	4^2	1	4.5^2	1	5^2	0.6082	0.1298

Table 6: Percentage of Rejection for k=4 Populations; Exponential Distribution with different means and different variances

n_1	n_2	n_3	n_4	μ_1	σ_1	μ_2	σ_2	μ_3	σ_3	μ_4	σ_4	L_1	L_2
18	18	18	18	1	1	1.25	1.25^2	1.5	1.5^2	1.75	1.75^2	0.2858	0.3431
18	18	18	18	1	1	1.5	1.5^2	1.75	1.75^2	2	2^2	0.4365	0.5461
18	18	18	18	1	1	1.75	1.75^2	2	2^2	2.25	2.25^2	0.5722	0.7088
18	18	18	18	1	1	2	2^2	2.25	2.25^2	2.5	2.5^2	0.6948	0.8365
18	18	18	18	1	1	2.25	2.25^2	2.5	2.5^2	2.75	2.75^2	0.7820	0.9109
18	18	18	18	1	1	2.5	2.5^2	2.75	2.75^2	3	3^2	0.8466	0.9571

5. Conclusion

The overall conclusion is that L_2 has the highest powers when the change is only in location parameters. When the change is only in scale parameters, L_1 has the highest powers. When both the location and scale parameters are different, the test statistic that has higher powers changes depending on the underlying distribution. For both the normal distribution and the t-distribution with 3 degrees of freedom (symmetric distributions), L_1 has higher powers while L_2 has higher powers for the exponential distribution (skewed).

If the distribution that one is sampling from is assumed to be approximately symmetric, L_1 is recommended to test for both an increasing change in the location and/or scale when treatments are applied. L_1 did have lower powers if only the locations (means) were different, but did have higher powers in the other two cases. If one expects the underlying distribution to be relatively skewed, then L_2 is the recommended test statistic to test for both increasing changes in the location and scale when treatments are applied.

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