NONPARAMETRIC TEST FOR THE UMBRELLA ALTERNATIVE IN A RANDOMIZED COMPLETE BLOCK AND BALANCED INCOMPLETE BLOCK MIXED DESIGN

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ABSTRACT

Nonparametric tests have served as robust alternatives to traditional statistical tests with rigid underlying assumptions. If a researcher expects the treatment effects to follow an umbrella alternative, then the test developed in this research will be applicable in the Balanced Incomplete Block Design (Hemmer's test). It is hypothesized that Hemmer's test will prove to be more powerful than the Durbin test when the umbrella alternative is true. A mixed design consisting of a Balanced Incomplete Block Design and a Randomized Complete Block Design will also be considered, where two additional test statistics are developed for the umbrella alternative. Monte Carlo simulation studies were conducted using SAS to estimate powers. Various underlying distributions were used with 3, 4, and 5 treatments, and a variety of peaks and mean paramater values. For the mixed design, different ratios of complete to incomplete blocks were considered. Recommendations are given.

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CHAPTER 1. INTRODUCTION

There are two significant branches of hypothesis testing: parametric and nonparametric. While parametric tests are more well-known and recognizable throughout the world of research, there are a multitude of assumptions that these tests require before they can be performed. The most prevalent assumption accompanying parametric tests is that the underlying distributions of the populations must be known before the procedure can be used. There are many situations where this is unknown to the researcher or could prove difficult to verify. If this assumption, in addition to others, is not met, any conclusions reached through a parametric hypothesis test are invalid. Nonparametric hypothesis testing provides a way to conduct tests on populations when an assumption from a parametric test cannot be verified.

There are several significant advantages to using nonparametric statistical procedures. The assumptions associated with parametric testing are rigid and detailed, whereas in nonparametric methods, these assumptions are much broader and therefore met more easily. This in turn leads to more nonparametric tests being applied properly and making the conclusions of the test applicable. Nonparametric procedures typically require only simple calculations, so they may be appealing to more researchers, particularly those without a strong background in statistics. Nonparametric tests can also be applied when the data are measured on a weak measurement scale, like when only count or rank data are available (Daniel, 1990).

The most typical motivation behind conducting a hypothesis test is to study the effect of a treatment, or multiple treatments against one another. It is possible that the effects of these treatments can be confounded by nuisance factors, if they are present during the experiment. For example, a researcher collects a sample of people and gives half of the subjects a migraine-relief drug and the other half a placebo. If the drug is suspected to have a weaker effect on older people, and the average age of the subjects who received the drug was significantly greater than that of the placebo-group, then age is a factor that will affect and ultimately detract from the goals of the experiment. To counteract this interference, a researcher can obtain multiple samples from various levels of the nuisance factor and apply the t treatments to each sample, where t is the number of total treatments in the experiment. These samples at different levels of the nuisance factor are called *blocks*. By analyzing the treatment effect within each block, a researcher can ensure that they are studying the effect of the desired treatment without a confounding effect. When every treatment level is applied to every block level, this experimental design is called a *Randomized Complete Block Design* (RCBD).

Circumstances may arise when it is not desirable to conduct an experiment using a full RCBD. The cost or time associated with obtaining enough subjects from every block so that all t treatment levels can be applied may be too great or even realistically impossible. So instead, a researcher can obtain $t - a$ subjects for each block, where a is a number between 1 and $t - 1$. It follows that only $t - a$ treatment levels can be applied within each block. If the experiment is designed so that each of the t treatments are applied the same number of times, and each possible pair of treatments are applied the same number of times, the design is known as a *Balanced Incomplete Block Design* (BIBD).

There are a variety of different hypotheses to consider when conducting a formal statistical procedure. When considering multiple treatments, the most basic scenario is testing the null hypothesis that the effects of the different treatments are all equivalent, with an alternative hypothesis that a significant difference exists between at least two treatment effects (the treatment effects are not all equal). Another set of hypotheses for researchers to utilize is the non-decreasing ordered alternative, which employs the same null hypothesis mentioned above with an alternative stating that the magnitude of treatment effects is ordered in a non-decreasing manner. A third set of hypotheses has an alternative known as the umbrella alternative. This set of hypotheses consist of the same null hypothesis as previously mentioned, with the alternative that the magnitude of treatment effects is non-decreasing until a specific treatment, known as the peak, and is non-increasing for all treatments afterwards. Some of the nonparametric tests available to test these three sets of hypotheses, depending on which experimental design is employed, are the Kruskal-Wallis test (1953), the Friedman test (Friedman (1937), Friedman (1940)), the Jonckheere-Terpstra test (Jonckheere (1954), Terpstra (1952)), Page's test (1963), the Durbin test (1951), the Mack-Wolfe test (1981) and the Kim-Kim test (1992).

While an experiment is being implemented, it is realistic to expect that some of the conditions around the research may change. For example, a researcher may initially conduct their experiment intending to employ a full RCBD, but issues may arise while the data are being collected. Perhaps the cost of obtaining subjects was higher than projected or the number of subjects responding to the experiment's questionnaire was lower than expected for certain blocks. Due to real-life circumstances such as these, it may prove impractical to continue using the RCBD, which entails applying each treatment to all observations within each block. The researcher could continue conducting the remainder of the experiment, but by implementing the BIBD, so that every treatment does not need to be applied to all observations within each block. Once all of the data are collected, they will be organized in what is known as a mixture of the RCBD and BIBD designs.

There are nonparametric procedures to test for a variety of differences between treatment effects, under either the RCBD or BIBD design types. However, utilizing nonparametric statistical tests within a mixture of these two designs is a field that has remained relatively unexplored. In a more specific case, the researcher could assume that if there is a difference between the treatment effects, that difference should follow an umbrella-like fashion, where the peak is known. The Kim-Kim test has already been established to test the equality of treatment effects with an umbrella alternative in an RCBD. There has been no statistical procedure proposed to test these same hypotheses in a BIBD, nor in a RCBD-BIBD mixture.

This research will aim to accomplish two tasks. First, a new nonparametric test will be proposed that will test for a difference in treatment effects with an umbrella alternative in a BIBD. Second, this newly-introduced test and the Kim-Kim test will be used to develop a test for the umbrella alternative in a mixture design of an RCBD and a BIBD.

The next chapter details existing statistical procedures and their applications, in an RCBD, BIBD and mixture designs. Chapter 3 proposes a new test for testing the umbrella alternative in the BIBD and also proposes two new statistics when combining cases of an RCBD and a BIBD. Chapter 4 describes a simulation study conducted to test the effectiveness of the statistical tests discussed in Chapter 3. Chapter 5 compares the powers estimated from the simulation study to existing nonparametric procedures to evaluate the effectiveness of the proposed tests. Chapter 6 states the conclusions made from the simulation study.

CHAPTER 2. SURVEY OF LITERATURE

In this chapter, the only scenarios that will be considered are *t*-sample nonparametric tests for a variety of experimental designs and alternative hypotheses. The first design type to consider is the Completely Randomized Design (CRD).

Kruskal and Wallis (1953) developed a test to detect a difference in treatment medians. The Kruskal-Wallis test assumes that if the treatment populations do differ, it is only with respect to location. Jonckheere (1954) and Terpstra (1952) developed a test that would also detect a difference in medians, but the alternative hypothesis of the Jonckheere-Terpstra test states that the magnitude of the treatment medians differs in a nondecreasing pattern. Mack and Wolfe (1981) developed a test for a difference in medians, with the umbrella alternative when the peak, *p*, is known and unknown. When *p* is known, the set of hypotheses can be written as, where at least one inequality in the alternative hypothesis is strict:

$$Ho: M_1 = M_2 = \cdots = M_{p-1} = M_p = M_{p+1} = \cdots = M_t$$

$$H_1: M_1 \leq M_2 \leq \cdots \leq M_{p-1} \leq M_p \geq M_{p+1} \geq \cdots \geq M_t$$

The Mann-Whitney test (1947) tests for a difference in medians between two independent populations. The Mack-Wolfe test statistic for peak p (A_p) calculates the Mann-Whitney test statistic (U) multiple times. Every time U is calculated, the researcher is only considering two treatment effects, specifically the treatment levels corresponding to the test statistic subscript. The Mack-Wolfe test statistic is the sum of Mann-Whitney test statistics and is calculated as follows:

$$A_p = \sum_{u=1}^{v-1} \sum_{v=2}^{p} U_{uv} + \sum_{u=p}^{v-1} \sum_{v=p+1}^{t} U_{vu}$$

The next design to consider is the Randomized Complete Block Design (RCBD). The Friedman test (Friedman 1937, 1940) was developed to test for any difference in treatment medians. Friedman's test ranked the observations within each block, but not between blocks. This process ensures that the different blocks, which represent various levels of a nuisance factor, will not have an effect on the analysis of the treatment effects. If observations within a block are of an equal value, their average rank is used. Page's test (1963) tests for the nondecreasing alternative in a RCBD. Page used the same ranking scheme as performed in Friedman's test, ranking within blocks but not between.

Kim and Kim (1992) developed a test for the umbrella alternative in a RCBD with a known peak. The same ranking scheme was applied as in Page's test and Friedman's test. The set of hypotheses used in the Kim-Kim test are as follows, where at least one inequality in the alternative hypothesis is strict:

$$Ho: M_1 = M_2 = \cdots = M_{p-1} = M_p = M_{p+1} = \cdots = M_t$$

$$H_1: M_1 \leq M_2 \leq \cdots \leq M_{p-1} \leq M_p \geq M_{p+1} \geq \cdots \geq M_t$$

The Kim-Kim test initially requires the Mack-Wolfe test statistic to be calculated within each block. Kim-Kim's proposed test statistic is the sum of these Mack-Wolfe statistics across all blocks.

$$KK = \sum_{j=1}^{b} A_{jp}$$

where

b = the number of blocks in the RCBD

p = known treatment level peak.

Note that this statistic assumes that there is no interaction between blocks and treatments. When assuming *Ho* is true, the Kim-Kim test statistic follows an asymptotic normal distribution with an expected value and variance given by:

$$E(KK;Ho) = {\sum_{j=1}^{b}\left\{{N_{j1}}^{2} + N_{j2}^{2} - \sum_{i=1}^{t}\left(n_i^2 - n_p^2\right)\right\}}\Big/_{4}$$

$$V(KK;Ho\,) = \sum_{j=1}^{b}\left\{2*\left({N_{j1}}^{3} + N_{j2}^{3}\right) + 3*\left({N_{j1}}^{2} + N_{j2}^{2}\right)\right.$$

$$\left. - \sum_{i=1}^{t} n_{ij}^{2} * \left(2n_{ij} + 3\right) - n_{jp}^{2} * \left(2n_{jp} + 3\right) + 12 * n_{jp}N_{j1}N_{j2} - 12n_{jp}^{2}N_j\right\}/72$$

where

b = the number of blocks

t = the number of treatments

p = the known peak treatment level.

The standardized Kim-Kim test statistic can be calculated and then compared to the standard normal distribution to make the test’s decision.

When considering a Balanced Incomplete Block Design (BIBD), the Durbin test (1951) can be used to detect any type of significant difference between treatment effects. When conducting the Durbin test, it is assumed that any difference that is detected is only in regards to the location of the populations of the treatments. The set of hypotheses for the Durbin test is as follows:

$$Ho: \ M_1 = M_2 = \cdots = M_t$$

$$H_1: \ At\ least\ one\ M_i\ is\ different.$$

The ranking scheme used in the Durbin test is similar to that used in Friedman's test, with the additional condition that missing observations receive a rank of 0. The Durbin test statistic is as follows:

$$T = \frac{12(t-1)}{rt(k-1)(k+1)} \sum_{i=1}^{t} R_i^2 - \frac{3r(t-1)(k+1)}{k-1}$$

where

t = the number of treatments

k = the number of subjects per block

r = the number of times each treatment occurs

Rj = the sum of the ranks for treatment *i*.

T follows an asymptotic chi-square distribution with $t - 1$ degrees of freedom. *Ho* is rejected if $T > \chi^2_{\alpha,t-1}$.

Cao (2010) conducted a study to compare the powers of Durbin's test to the powers of the Wilcoxon-Signed-Rank test (1945) in a BIBD with two observations per incomplete block for the nondecreasing alternative. Cao concluded that the Wilcoxon-Signed-Rank test was a superior test when the treatment effects were nondecreasing.

Ndungu (2011) developed a test for the nondecreasing alternative in a BIBD. Ndungu's test statistic is similar to Page's, in that it sums the ranked observations within blocks but not between.

Magel, Terpstra and Wen (2009) developed tests for the nondecreasing ordered alternative in a CRD/RCBD mixed design. The two tests were combinations of Page's test and the Jonckheere-Terpstra test. One test proposed initially standardizing the test statistics from Page's and the Jonckheere-Terpstra test separately, adding them together and restandardizing. A second test added unstandardized test statistics from the two tests and then standardized the sum. Their work concluded that there are circumstances when the first test is superior to the second test, and vice versa.

Magel, Terpstra, Canonizado and Park (2010) constructed tests for the umbrella alternative in a CRD/RCBD mixed design. Two tests that combined the Mack-Wolfe and Kim-Kim tests were created. The tests were developed in a similar fashion to the work done by Magel, Terpstra and Wen (2009). One test added standardized versions of Mack-Wolfe and Kim-Kim, then restandardized. The second test added unstandarized versions of the test statistics and then standardized the sum. The test that initially standardized the separate test statistics resulted in higher powers and was therefore found to be a superior test.

Mathisen (2011) developed tests for the nondecreasing alternative in a RCBD/BIBD mixed design. Mathisen specifically created two test statistics that combined the Page's test and Ndungu's test. The two tests were developed in a similar manner as Magel, Terpstra and Wen (2009) and Magel, Terpstra, Canonizado and Park (2010). One test proposed adding the standardized test statistics from Page's and Ndungu's tests and then restandardizing. The second test added unstandardized statistics from the separate tests and then the sum was standardized. Mathisen concluded that there were some scenarios when the first method was a better test than the second method, and vice versa.

CHAPTER 3. HEMMER'S TEST STATISTIC & NEW RCBD/BIBD MIXED DESIGN TEST STATISTICS

In this chapter, we will propose a test for the BIBD and two tests for a mixed design consisting of an RCBD and a BIBD. The first test can be applied in a BIBD with an umbrella alternative when the peak is known, and will be referred to as Hemmer's test. The two other tests are applicable for the same alternative in a mixed design consisting of an RCBD and a BIBD, and will be referred to as Method 1 and Method 2.

As stated before, Hemmer's test can be applied for the umbrella alternative with a known peak, *p*, in the BIBD. The null and alternative hypotheses of the test are as follows, where at least one inequality in the alternative hypothesis is strict:

$$Ho\colon\ M_1 = M_2 = \cdots = M_t$$

$$H_1\colon\ \ M_1 \le M_2 \le \cdots \le M_{p-1} \le M_p \ge M_{p+1} \ge \cdots \ge M_{t-1} \ge M_t$$

In Chapter 2, it was stated that the Durbin test for a BIBD tests for the general alternative. Hemmer's test is proposed specifically for the umbrella alternative, with a known peak, in a BIBD. The test statistic for Hemmer's test is defined as follows:

$$T = \sum_{j=1}^{b}\left\{\sum_{i=1}^{t}(t-1-|p-i|)*R_i\right\} \qquad (\mathbf{1})$$

where

t = the number of treatments

b = the number of blocks

p = known peak treatment level

R_i = sum of the ranks of the observations receiving treatment i.

It is noted that observations are ranked only within blocks. It is assumed that k treatments appear in each block, where $k < t$. Observations within each block are ranked from 1 to k.

It is also worth noting that T follows an asymptotically normal distribution, since it is a rank statistic. Therefore, if the expected values and variances of T are obtained, Hemmer's test statistic can be standardized, Z_T. Z_T will have an asymptotic standard normal distribution, assuming the null hypothesis, H_0 , is true. H_0 is rejected if $Z_T > Z_\alpha$, where Z_α denotes the value of the standard normal distribution where there is α area above it.

Since there are t treatments with k treatments appearing within each incomplete block, a BIBD can be constructed by taking $b = \binom{t}{k}$ blocks and assigning a different combination of treatments to each block. Note that b is the minimum number of blocks required to complete one repetition of a symmetric BIBD. The following table provides the calculated expected values and variances of Hemmer's test statistic, when considering only one repetition of the BIBD, for 3, 4, and 5 treatments. See Appendix I for a demonstration on these calculations.

There may be a set of circumstances when a researcher begins an experiment with an RCBD and realizes after an initial period that not every treatment can be applied within each of the remaining blocks. The researcher can change the design to a BIBD partially through the experiment and will then be using a design that is a mixture of an RCBD and a BIBD. Two tests are proposed for this type of design. The tests are linear combinations of the Kim-Kim test and Hemmer's test and will be referred to as Method 1, M_1, and Method 2, M_2.

3.1 Method 1 Test for a Mixed Design consisting of an RCBD and a BIBD

In Chapter 2, the standardized test statistic of the Kim-Kim test was defined as follows.

Table 1 – Expected Values and Variances of Hemmer's test statistic, T, for 3, 4, and 5 Treatments

b	***k***	***p***	**E(T)**	**Var(T)**		***b***	***k***	***p***	**E(T)**	**Var(T)**
3	2	Trt II	12	0.5		5	4	Trt III	90	18.26087
4	3	Trt II	48	16/3		5	3	Trt III	108	14
4	2	Trt II	36	2		5	2	Trt III	54	3.5
4	3	Trt III	48	16/3		5	4	Trt IV	130	32.5
4	2	Trt III	36	2		5	3	Trt IV	156	26
5	4	Trt II	130	32.5		5	2	Trt IV	78	6.5
5	3	Trt II	156	26						
5	2	Trt II	78	6.5						

b = number of blocks, k = number of treatments appearing per incomplete block, p = known peak treatment level.

$$Z_{KK} = \frac{KK - E(KK)}{\sqrt{Var(KK)}}$$

where

$KK = \sum_{i=1}^{b} A_{ip}$,

$$E(KK) = \sum_{i=1}^{b}\left\{{N_{i1}}^2 + N_{i2}^2 - \sum_{j=1}^{t}\left(n_j^2 - n_p^2\right)\right\} \Big/ 4,$$

$$Var(KK) = \sum_{i=1}^{b}\left\{2*\left({N_{i1}}^3 + N_{i2}^3\right) + 3*\left({N_{i1}}^2 + N_{i2}^2\right) - \sum_{j=1}^{t} n_{ij}^2 * \left(2n_{ij} + 3\right) - n_{ip}^2 * \left(2n_{ip} + 3\right) + 12 * n_{ip} N_{i1} N_{i2} - 12 n_{ip}^2 N_i\right\} /72,$$

b = the number of blocks

p = known peak treatment level

t = the number of treatments.

Method 1 proposes to separately standardize the test statistics from the Kim-Kim and Hemmer's tests, add the two standardized statistics and restandardize the sum. The test statistic for Method 1 is given by

$$M_1{}^* = \frac{Z_{KK} + Z_T}{\sqrt{2}}$$

Since the asymptotic null distributions of both Z_{KK} and Z_T are the standard normal, it follows that the asymptotic null distribution of $M_1{}^*$ is also the standard normal. The null hypothesis is rejected when $M_1{}^* \geq Z_\alpha$.

3.2 Method 2 Test for a Mixed Design consisting of an RCBD and a BIBD

The second proposed test statistic first adds the unstandardized test statistics from the Kim-Kim test for the RCBD and Hemmer's test for the BIBD. This second proposed test statistic is given by

$$M_2 = KK + T = \sum_{k=1}^{c} A_{kp} + \sum_{j=1}^{d} \left\{ \sum_{i=1}^{t} (t - 1 - |p - i|) * R_i \right\}$$

where

c = the number of complete blocks

d = the number of incomplete blocks

t = the number of treatments

p = known peak treatment level.

M_2 as provided above is an unstandardized statistic. After obtaining the expected value and variance, we can standardize the Method 2 test statistic as follows

$$M_2{}^{*} = {\{M2 - (E(KK) + E(T)\ )\}}\Big/{\sqrt{Var(KK) + Var(T)}}$$

The asymptotic null distribution of $M_2{}^{*}$ is a standard normal distribution. The null hypothesis is rejected when $M_2{}^{*} \geq Z_\alpha$.

CHAPTER 4. A DESCRIPTION OF THE SIMULATION STUDY

To determine the effectiveness of the tests defined in the previous chapter, we will use Monte Carlo simulation to generate random data under various conditions. Using these data, we can calculate estimated powers of the proposed tests and make the proper comparisons to determine the better statistical test. The estimated power was calculated by counting the number of times the null hypothesis of equal treatment means was rejected divided by the number of simulations, which was always 10,000 for this thesis. This procedure was performed for different underlying distributions, treatment means for the data, as well as different peak treatments. Several of these different circumstances were used to calculate each of the following test statistics. Hemmer's and Durbin's test statistics were calculated for various BIBD scenarios and their powers were compared. When considering a mixed design of an RCBD and a BIBD, the estimated powers of the Method 1 and Method 2 test statistics were calculated and were compared to one another. The estimated powers of Method 1 and Method 2 were also compared to those of the Hemmer and Kim-Kim tests, which were conducted separately on the mixed design data. 95% confidence intervals were calculated for each estimated power measurement. A test statistic was considered to be significantly best if it had the highest power and if the estimated power's confidence interval did not overlap with the confidence interval of any other statistic's power. SAS statistical software was utilized to conduct the simulations.

The underlying distributions considered for the simulations were the normal, exponential and Student's t distribution with three degrees of freedom. These three distributions were utilized because the shapes of the distributions are each distinctly different from one another. The normal distribution and the Student's t distribution with 3 degrees of freedom are both shaped symmetrically, but the normal has a more pronounced mound-shape while the Student's t with 3 degrees of freedom has a greater variance. The exponential distribution is a non-symmetrical distribution, which is a significant deviation from the other two distributions. The SAS function RANNOR was used to generate random samples from the normal distribution, with a mean and variance specified by the user as input for the SAS macro. The RANEXP function was used to generate data from the standard exponential distribution and then the mean for each treatment was added to simulate exponentially distributed data with the desired mean. To simulate from the Student's t distribution, the RANUNI function was used to generate a random value between 0 and 1 from the Uniform distribution. That value was then used as input for the TINV function, which interpreted the RANUNI output as the cumulative area for the Student's t distribution with three degrees of freedom, and the proper Student's t distribution value was then calculated.

The first part of the simulation study focused on the BIBD case and compared Hemmer's and Durbin's test when considering three, four and five total treatments. For the three treatment scenario, each block contained only two treatments and each treatment contained only two blocks. When evaluating four treatments, each block contained three treatments and for five treatments, only four treatments appeared within each block.

The second part of the simulation study tested the two tests proposed for the mixed design of the RCBD and BIBD. Three, four and five treatments were considered in this part of the study as well. When considering the three treatment scenario, the complete blocks making up the RCBD case contained all three treatments. Meanwhile, the incomplete blocks consisted of two treatments per block, which was the same set up for the BIBD environment used in the first part of the simulation study. For the four treatment scenario, each complete block contained observations from all four treatments while the incomplete blocks contained three treatments each, again matching the BIBD used earlier. For the five treatment scenario, complete blocks consisted of observations from all five treatments while incomplete blocks had data from four treatments.

The ratio of complete blocks to incomplete blocks within the mixture design was considered in this part of the study. Simulations were conducted when there were an even number of complete and incomplete blocks, as well as scenarios with more complete blocks and more incomplete blocks. Specifically when three treatments were considered, 10 complete and 10 incomplete blocks were considered for a simulation of the even case. For the scenario with more complete blocks, 15 complete and 5 incomplete blocks were considered. Likewise, there were 5 complete and 15 incomplete blocks when the case of more incomplete blocks was used. For the even case, more complete case and more incomplete case, the ratios of complete to incomplete blocks remained 50% / 50%, 75% / 25% and 25% / 75% for the four and five treatment scenarios.

There were four different scenarios of population mean parameters that were considered in the simulation study. To verify the level of α was equal to 0.05, each treatment had a mean of 0 and the number of times the test statistic rejected was counted and divided by the number of simulations, 10,000. Next, a situation where the treatment means followed a true umbrella alternative was considered. For example, in the case of five treatments with a known peak at the 4^{th} treatment, the underlying treatment means were assigned values of (0.1, 0.2, 0.3, 0.4, 0.3). Additionally, scenarios where the treatment mean of the known peak was equal to one or both of its adjacent treatment means were considered. Again, considering the case of five treatments with a peak at the 4th treatment, the treatment means were distributed as (0, 0, 0, 0.3, 0.3) or (0, 0, 0.3, 0.3, 0) or (0, 0, 0.3, 0.3, 0.3). Finally, the circumstances were considered where the largest treatment mean was different than where the peak is assumed to be. The umbrella alternative is not true in these cases, so the researcher does not want to be rejected. A better test will have lower estimated powers in these scenarios. For the five treatment case where the peak is assumed to be at the 4th treatment, the treatment means could be distributed in a random fashion, as long as the largest treatment mean does not occur at the peak, such as (0.05, 0.2, 0.05, 0.25, 0.3).

Results from the simulation study are provided in Chapter 5 and the corresponding conclusions are in Chapter 6.

CHAPTER 5. RESULTS OF SIMULATION STUDY

5.1. Balanced Incomplete Block Design Case

5.1.1. Results for 3 treatments with 2 treatments per incomplete block and peak at treatment II

The first section of results comes from the BIBD case, where the estimated powers of Hemmer's test will be compared to those of Durbin's test under various scenarios. All tables specify the total number of treatments (t) and the number of treatments per incomplete block (k).

Table 2 gives the estimated powers and confidence intervals for the powers for the normal distribution. The underlying mean distributions follow the pattern as described in Chapter 4. When the peak treatment mean is distinct, Hemmer's test is significantly more powerful than Durbin's. When the peak treatment mean is equivalent to an adjacent treatment mean, Durbin's test has more power than Hemmer's test. For the random treatment mean assortments, Durbin's test is also significantly more powerful than Hemmer's.

Table 3 gives the estimated powers and corresponding confidence intervals for the same scenario under the exponential distribution. The results are similar to those from the normal distribution. When there is a distinct peak, Hemmer's test is significantly more powerful than Durbin's test. Otherwise, Durbin's test yields higher levels of power than Hemmer's.

Table 4 gives the estimated powers and confidence intervals for the powers for the Student's t distribution, with 3 degrees of freedom. The results are similar to when the normal and exponential distributions are used; Hemmer's test proves to be more powerful when there is a more pronounced distinct peak and Durbin's test is more powerful in the other scenario.

Table 2 - Power Comparison with 95% Confidence Intervals; t = 3, k = 2, *peak* = *II*, Normal Distribution

Mu1	**Mu2**	**Mu3**	**Hemmer's**	**Durbin's**
0	0	0	4.02 (3.64, 4.40)	5.05 (4.62, 5.48)
0.1	0.75	0.5	43.64 (42.67, 44.61)	41.13 (40.17, 42.09)
0.6	0.75	0.3	24.24 (23.40, 25.08)	20.78 (19.98, 21.58)
0	0.5	0	50.83 (49.85, 51.81)	32.54 (31.62, 33.46)
0	0.5	0.5	18.84 (18.07, 19.61)	33.14 (32.22, 34.06)
0.05	0.4	0.5	9.50 (8.93, 10.07)	22.50 (21.68, 23.32)
0.30	0	0.15	0.60 (0.45, 0.75)	11.23 (10.61, 11.85)

Table 3 – Power Comparison with 95% Confidence Intervals; t = 3, k = 2, *peak* = *II*, Exponential Distribution

Mu1	**Mu2**	**Mu3**	**Hemmer's**	**Durbin's**
0	0	0	4.04 (3.65, 4.43)	5.09 (4.66, 5.52)
0.1	0.75	0.5	69.37 (68.47, 70.27)	71.90 (71.02, 72.78)
0.6	0.75	0.3	44.89 (43.92, 45.86)	45.71 (44.73, 46.69)
0	0.5	0	79.90 (79.11, 80.69)	61.73 (60.78, 62.68)
0	0.5	0.5	30.05 (29.15, 30.95)	60.67 (59.71, 61.63)
0.05	0.4	0.5	12.46 (11.81, 13.11)	46.77 (45.79, 47.75)
0.30	0	0.15	0.10 (0.04, 0.16)	22.82 (22.00, 23.64)

Table 4 – Power Comparison with 95% Confidence Intervals; *t* = 3, *k* = 2, *peak* = *II*, Student's t Distribution (3 d.f.)

Mu1	Mu2	Mu3	Hemmer's	Durbin's
0	0	0	4.13 (3.74, 4.52)	5.06 (4.63, 5.49)
0.1	0.75	0.5	31.77 (30.86, 32.68)	27.84 (26.96, 28.72)
0.6	0.75	0.3	18.79 (18.02, 19.56)	15.05 (14.35, 15.75)
0	0.5	0	37.99 (37.04, 38.94)	22.57 (21.75, 23.39)
0	0.5	0.5	15.31 (14.60, 16.02)	22.38 (21.56, 23.20)
0.05	0.4	0.5	8.19 (7.65, 8.73)	16.15 (15.43, 16.87)
0.30	0	0.15	0.70 (0.54, 0.86)	9.49 (8.92, 10.06)

5.1.2. Results for 4 treatments with 3 treatments per incomplete block and peak at treatment II

Tables 5, 6, and 7 give the estimated powers and the confidence intervals for the powers with an underlying normal distribution, exponential distribution and Student's t distribution, with 3 degrees of freedom, respectively. When the distinct peak is true, Hemmer's test shows to be significantly more powerful than Durbin's test, regardless of underlying distribution. When the peak treatment and an adjacent treatment are equal, there are some scenarios when Durbin's test proves to be more powerful than Hemmer's and vice versa. When the treatment means are distributed in a random fashion for all distributions, Durbin's test has greater power.

Table 5 – Power Comparison with 95% Confidence Intervals; *t* = 4, *k* = 3, *peak* = *II*, Normal Distribution

μ1	**μ2**	**μ3**	**μ4**	**Hemmer's**	**Durbin's**
0	0	0	0	4.70 (4.29, 5.11)	4.76 (4.34, 5.18)
0.3	0.5	0.3	0.1	37.48 (36.53, 38.43)	17.14 (16.40, 17.88)
0.2	0.5	0.4	0	49.87 (48.89, 50.85)	30.13 (29.23, 31.03)
0.1	0.5	0.1	0.05	42.60 (41.63, 43.57)	26.49 (25.63, 27.35)
0	0.5	0	0	49.77 (48.79, 50.75)	36.50 (35.56, 37.44)
0	0.5	0.5	0	49.79 (48.81, 50.77)	48.67 (47.69, 49.65)
0.5	0.5	0.5	0	48.71 (47.73, 49.69)	35.62 (34.68, 36.56)
0.05	0.2	0.05	0.25	3.23 (2.88, 3.58)	9.25 (8.68, 9.82)
0.75	0.45	0.5	0.6	1.47 (1.23, 1.71)	12.03 (11.39, 12.67)

Table 6 – Power Comparison with 95% Confidence Intervals; *t* = 4, *k* = 3, *peak* = *II*, Exponential Distribution

μ1	**μ2**	**μ3**	**μ4**	**Hemmer's**	**Durbin's**
0	0	0	0	4.34 (3.94, 4.74)	4.99 (4.56, 5.42)
0.3	0.5	0.3	0.1	65.37 (66.44, 66.30)	38.32 (37.37, 39.27)
0.2	0.5	0.4	0	80.23 (79.45, 81.01)	62.03 (61.08, 62.98)
0.1	0.5	0.1	0.05	71.45 (70.56, 72.34)	55.28 (54.31, 56.25)
0	0.5	0	0	76.93 (76.10, 77.76)	70.41 (69.52, 71.30)
0	0.5	0.5	0	76.83 (76.00, 77.66)	82.68 (81.94, 83.42)
0.5	0.5	0.5	0	75.51 (74.67, 76.35)	67.25 (66.33, 68.17)
0.05	0.2	0.05	0.25	2.08 (1.80, 2.36)	18.66 (17.90, 19.42)
0.75	0.45	0.5	0.6	0.85 (0.67, 1.03)	26.68 (25.81, 27.55)

Table 7 – Power Comparison with 95% Confidence Intervals; t = 4, k = 3, *peak* = *II*, Student's t Distribution (3 d.f.)

μ1	**μ2**	**μ3**	**μ4**	**Hemmer's**	**Durbin's**
0	0	0	0	4.60 (4.19, 5.01)	4.98 (4.55, 5.41)
0.3	0.5	0.3	0.1	27.59 (26.71, 28.47)	12.60 (11.95, 13.25)
0.2	0.5	0.4	0	37.40 (36.45, 38.35)	20.37 (19.58, 21.16)
0.1	0.5	0.1	0.05	32.73 (31.81, 33.65)	19.07 (18.30, 19.84)
0	0.5	0	0	36.37 (35.43, 37.31)	24.44 (23.60, 25.28)
0	0.5	0.5	0	37.00 (36.05, 37.95)	32.27 (31.35, 33.19)
0.5	0.5	0.5	0	36.75 (35.81, 37.69)	24.92 (24.07, 25.77)
0.05	0.2	0.05	0.25	3.28 (2.93, 3.63)	7.66 (7.14, 8.18)
0.75	0.45	0.5	0.6	1.70 (1.45, 1.95)	9.67 (9.09, 10.25)

5.1.3. Results for 4 treatments with 3 treatments per incomplete block and peak at treatment III

Tables 8, 9, and 10 provide the powers and confidence intervals for the normal distribution, exponential distribution and Student's t distribution with 3 degrees of freedom, respectively. Hemmer's test is significantly more powerful than Durbin's for all scenarios when the peak occurs at Treatment 3, as well as the scenario when both of the adjacent treatments (2 and 4) are equal to Treatment 3. However, when only one adjacent treatment mean is equal to the peak, Durbin's test is at least as powerful as Hemmer's test. Durbin's test is more powerful when there is a random assortment of treatment means.

Table 8 – Power Comparison with 95% Confidence Intervals; *t* = 4, *k* = 3, *peak* = *III*, Normal Distribution

µ1	**µ2**	**µ3**	**µ4**	**Hemmer's**	**Durbin's**
0	0	0	0	4.49 (4.08, 4.90)	4.87 (4.45, 5.29)
0.1	0.3	0.5	0.3	36.80 (35.85, 37.75)	17.39 (16.65, 18.13)
0	0.4	0.5	0.2	48.82 (47.84, 49.80)	29.73 (28.83, 30.63)
0.05	0.1	0.5	0.1	43.06 (42.09, 44.03)	26.82 (25.95, 27.69)
0	0	0.5	0	49.19 (48.21, 50.17)	36.66 (35.72, 37.60)
0	0	0.5	0.5	48.84 (47.87, 49.83)	48.09 (47.11, 49.07)
0	0.5	0.5	0.5	49.01 (48.03, 49.99)	36.88 (35.93, 37.83)
0.05	0.2	0.05	0.25	4.31 (3.91, 4.71)	9.44 (8.87, 10.01)
0.75	0.45	0.5	0.6	0.48 (0.34, 0.62)	12.84 (26.00, 27.74)

Table 9 – Power Comparison with 95% Confidence Intervals; *t* = 4, *k* = 3, *peak* = *III*, Exponential Distribution

µ1	**µ2**	**µ3**	**µ4**	**Hemmer's**	**Durbin's**
0	0	0	0	4.47 (4.06, 4.88)	4.83 (4.41, 5.25)
0.1	0.3	0.5	0.3	66.71 (65.79, 67.63)	38.83 (37.87, 39.79)
0	0.4	0.5	0.2	80.03 (79.25, 80.81)	61.47 (60.52, 62.42)
0.05	0.1	0.5	0.1	71.89 (71.01, 72.77)	55.73 (54.76, 56.70)
0	0	0.5	0	77.22 (76.40, 78.04)	70.28 (69.38, 71.18)
0	0	0.5	0.5	77.30 (76.48, 78.12)	83.08 (82.35, 83.81)
0	0.5	0.5	0.5	75.97 (75.13, 76.81)	67.42 (66.50, 68.34)
0.05	0.2	0.05	0.25	4.95 (4.52, 5.38)	18.73 (17.97, 19.49)
0.75	0.45	0.5	0.6	0.08 (0.02, 0.14)	26.87 (26.00, 27.74)

Table 10 – Power Comparison with 95% Confidence Intervals; *t* = 4, *k* = 3, *peak = III*, Student's t Distribution (3 d.f.)

µ1	**µ2**	**µ3**	**µ4**	**Hemmer's**	**Durbin's**
0	0	0	0	4.58 (4.17, 4.99)	4.88 (4.46, 5.30)
0.1	0.3	0.5	0.3	27.89 (27.01, 28.77)	13.07 (12.41, 13.73)
0	0.4	0.5	0.2	37.22 (36.27, 38.17)	20.01 (19.23, 20.79)
0.05	0.1	0.5	0.1	31.68 (30.77, 32.59)	17.76 (17.01, 18.51)
0	0	0.5	0	37.46 (36.51, 38.41)	24.94 (24.09, 25.79)
0	0	0.5	0.5	43.80 (42.83, 44.77)	42.24 (41.27, 43.21)
0	0.5	0.5	0.5	37.17 (36.22, 38.12)	24.74 (23.89, 25.59)
0.05	0.2	0.05	0.25	4.95 (4.52, 5.38)	7.53 (7.01, 8.05)
0.75	0.45	0.5	0.6	0.81 (0.63, 0.99)	10.61 (10.01, 11.21)

5.1.4. Results for 5 treatments with 4 treatments per incomplete block and peak at treatment II

Tables 11, 12, and 13 give the powers and confidence intervals for the powers for the normal distribution, exponential distribution and Student's t Distribution with 3 degrees of freedom, respectively. The following results were consistent across all three distributions. Whenever there was a distinct peak and when one or both adjacent treatment means were equal to the peak, Hemmer's test was more powerful than Durbin's. When a random assortment of means was considered, Durbin's test had higher estimated power.

Table 11 – Power Comparison with 95% Confidence Intervals; *t* = 5, *k* = 4, *peak* = *II*, Normal Distribution

μ1	μ2	μ3	μ4	μ5	Hemmer's	Durbin's
0	0	0	0	0	5.00 (4.57, 5.43)	4.73 (4.31, 5.15)
0.3	0.4	0.3	0.2	0.1	38.12 (37.17, 39.07)	15.91 (15.19, 16.63)
0.3	0.4	0.25	0.15	0	55.35 (54.38, 56.32)	25.03 (24.18, 25.88)
0.1	0.4	0.1	0.05	0	46.89 (45.91, 47.87)	26.56 (25.69, 27.43)
0	0.3	0	0	0	27.95 (27.07, 28.83)	19.67 (18.89, 20.45)
0	0.3	0.3	0	0	39.90 (38.94, 40.86)	28.79 (27.90, 29.68)
0.3	0.3	0.3	0	0	51.59 (50.61, 52.57)	29.04 (28.15, 29.93)
0.05	0.2	0.05	0.25	0.3	0.53 (0.39, 0.67)	15.41 (14.70, 16.12)
0.75	0	0.3	0.6	0.1	2.16 (1.88, 2.44)	85.70 (85.01, 86.39)

Table 12 – Power Comparison with 95% Confidence Intervals; *t* = 5, *k* = 4, *peak* = *II*, Exponential Distribution

μ1	μ2	μ3	μ4	μ5	Hemmer's	Durbin's
0	0	0	0	0	4.95 (4.52, 5.38)	4.99 (4.56, 5.42)
0.3	0.4	0.3	0.2	0.1	69.57 (68.67, 70.47)	36.52 (35.58, 37.46)
0.3	0.4	0.25	0.15	0	86.52 (85.85, 87.19)	57.86 (56.89, 58.83)
0.1	0.4	0.1	0.05	0	78.15 (77.34, 78.96)	59.91 (58.95, 60.87)
0	0.3	0	0	0	50.63 (49.65, 51.61)	46.03 (45.05, 47.01)
0	0.3	0.3	0	0	68.71 (67.80, 69.62)	64.78 (63.84, 65.72)
0.3	0.3	0.3	0	0	83.74 (83.02, 84.46)	64.43 (63.49, 65.37)
0.05	0.2	0.05	0.25	0.3	0.16 (0.08, 0.24)	37.17 (36.22, 38.12)
0.75	0	0.3	0.6	0.1	2.15 (1.87, 2.43)	99.56 (99.43, 99.69)

Table 13 – Power Comparison with 95% Confidence Intervals; t = 5, k = 4, *peak* = *II*, Student's t Distribution (3 d.f.)

μ1	**μ2**	**μ3**	**μ4**	**μ5**	**Hemmer's**	**Durbin's**
0	0	0	0	0	5.19 (4.76, 5.62)	4.98 (4.55, 5.41)
0.3	0.4	0.3	0.2	0.1	29.24 (28.35, 30.13)	11.28 (10.66, 11.90)
0.3	0.4	0.25	0.15	0	42.39 (41.42, 43.36)	17.67 (16.92, 18.42)
0.1	0.4	0.1	0.05	0	35.06 (34.12, 36.00)	17.64 (16.89, 18.39)
0	0.3	0	0	0	21.58 (20.77, 22.39)	14.14 (13.46, 14.82)
0	0.3	0.3	0	0	29.89 (28.99, 30.79)	19.47 (18.69, 20.25)
0.3	0.3	0.3	0	0	38.66 (37.71, 39.61)	19.59 (18.81, 20.37)
0.05	0.2	0.05	0.25	0.3	1.20 (0.99, 1.41)	12.05 (11.41, 12.69)
0.75	0	0.3	0.6	0.1	3.28 (2.93, 3.63)	65.76 (64.83, 66.69)

5.1.5. Results for 5 treatments with 4 treatments per incomplete block and peak at treatment III

Tables 14, 15, and 16 contain the powers and the confidence intervals for the powers when the normal distribution, exponential distribution and Student's t Distribution, with 3 degrees of freedom, are used as the underlying distribution for generating data. The findings are similar to those from the previous scenario 5A.4, when there were 5 Treatments with 4 Treatments per Incomplete Block and Peak at Treatment II. Hemmer's test was more powerful when there was a distinct peak, including when an adjacent treatment mean was equal to the peak treatment mean, and Durbin's test was only more powerful when the random assortment of means was considered.

Table 14 – Power Comparison with 95% Confidence Intervals; t = 5, k = 4, *peak = III*, Normal Distribution

μ1	μ2	μ3	μ4	μ5	Hemmer's	Durbin's
0	0	0	0	0	4.78 (4.36, 5.20)	4.81 (4.39, 5.23)
0.1	0.2	0.3	0.2	0.1	24.02 (23.18, 24.86)	10.12 (9.53, 10.71)
0.05	0.25	0.3	0.2	0.15	25.12 (24.27, 25.97)	12.26 (11.62, 12.90)
0	0.05	0.3	0.05	0	28.12 (27.24, 29.00)	12.62 (11.97, 13.27)
0	0	0.3	0	0	33.15 (32.23, 34.07)	20.17 (19.38, 20.96)
0	0	0.3	0.3	0	41.52 (40.55, 42.49)	29.31 (28.42, 30.20)
0	0.3	0.3	0.3	0	49.30 (48.32, 50.28)	28.91 (28.02, 29.80)
0.05	0.2	0.05	0.25	0.3	1.60 (1.35, 1.85)	15.61 (14.90, 16.32)
0.75	0	0.3	0.6	0.1	0.76 (0.59, 0.93)	85.44 (84.75, 86.13)

Table 15 – Power Comparison with 95% Confidence Intervals; t = 5, k = 4, *peak = III*, Exponential Distribution

μ1	μ2	μ3	μ4	μ5	Hemmer's	Durbin's
0	0	0	0	0	4.78 (4.36, 5.20)	4.95 (4.52, 5.38)
0.1	0.2	0.3	0.2	0.1	46.85 (45.87, 47.83)	21.21 (20.41, 22.01)
0.05	0.25	0.3	0.2	0.15	48.69 (47.71, 49.67)	26.58 (25.71, 27.45)
0	0.05	0.3	0.05	0	54.43 (53.45, 55.41)	29.40 (28.51, 30.29)
0	0	0.3	0	0	59.82 (58.86, 60.78)	45.28 (44.30, 46.26)
0	0	0.3	0.3	0	72.56 (71.69, 73.43)	65.06 (64.13, 65.99)
0	0.3	0.3	0.3	0	81.48 (80.72, 82.24)	64.41 (63.47, 65.35)
0.05	0.2	0.05	0.25	0.3	0.88 (0.70, 1.06)	35.67 (34.73, 36.61)
0.75	0	0.3	0.6	0.1	0.21 (0.12, 0.30)	99.55 (99.42, 99.68)

Table 16 – Power Comparison with 95% Confidence Intervals; t = 5, k = 4, *peak* = *III*, Student's t Distribution (3 d.f.)

μ1	**μ2**	**μ3**	**μ4**	**μ5**	**Hemmer's**	**Durbin's**
0	0	0	0	0	4.85 (4.43, 5.27)	4.82 (4.40, 5.24)
0.1	0.2	0.3	0.2	0.1	19.31 (18.54, 20.08)	8.50 (7.95, 9.05)
0.05	0.25	0.3	0.2	0.15	18.51 (17.75, 19.27)	9.34 (8.77, 9.91)
0	0.05	0.3	0.05	0	21.33 (20.53, 22.13)	9.53 (8.95, 10.11)
0	0	0.3	0	0	25.00 (24.15, 25.85)	13.79 (13.11, 14.47)
0	0	0.3	0.3	0	30.98 (30.07, 31.89)	19.74 (18.96, 20.52)
0	0.3	0.3	0.3	0	37.13 (36.18, 38.08)	19.81 (19.03, 20.59)
0.05	0.2	0.05	0.25	0.3	1.85 (1.59, 2.11)	11.83 (11.20, 12.46)
0.75	0	0.3	0.6	0.1	0.96 (0.77, 1.15)	64.85 (63.91, 65.79)

5.1.6. Results for 5 treatments with 4 treatments per incomplete block and peak at treatment IV

Tables 17, 18, and 19 give the estimated powers and confidence intervals for the powers for the normal distribution, exponential distribution and Student's t Distribution with 3 degrees of freedom, respectively. The results for this section are similar to the results from the previous section. When there is a distinct peak or when any treatments adjacent to the peak are equivalent, Hemmer's test shows to have more power than Durbin's test across all data-generating distributions. Otherwise, when the treatment means are assorted randomly, Durbin's test has greater power than Hemmer's.

Table 17 – Power Comparison with 95% Confidence Intervals; t = 5, k = 4, *peak = IV*, Normal Distribution

µ1	**µ2**	**µ3**	**µ4**	**µ5**	**Hemmer's**	**Durbin's**
0	0	0	0	0	4.89 (4.47, 5.31)	4.64 (4.23, 5.05)
0.1	0.2	0.3	0.4	0.3	38.33 (37.38, 39.28)	14.89 (14.19, 15.59)
0	0.15	0.25	0.4	0.3	53.95 (52.97, 54.93)	25.25 (24.40, 26.10)
0	0.05	0.1	0.4	0.1	45.96 (44.98, 46.94)	26.29 (25.43, 27.15)
0	0	0	0.3	0	28.29 (27.41, 29.17)	19.53 (18.75, 20.31)
0	0	0	0.3	0.3	39.21 (38.25, 40.17)	29.69 (28.79, 30.59)
0	0	0.3	0.3	0.3	51.92 (50.94, 52.90)	29.53 (28.64, 30.42)
0.05	0.2	0.05	0.25	0.3	17.64 (16.89, 18.39)	15.59 (14.88, 16.30)
0.75	0	0.3	0.6	0.1	1.59 (1.34, 1.84)	85.13 (84.43, 85.83)

Table 18 – Power Comparison with 95% Confidence Intervals; t = 5, k = 4, *peak = IV*, Exponential Distribution

µ1	**µ2**	**µ3**	**µ4**	**µ5**	**Hemmer's**	**Durbin's**
0	0	0	0	0	5.17 (4.74, 5.60)	4.82 (4.40, 5.24)
0.1	0.2	0.3	0.4	0.3	68.77 (67.86, 69.68)	35.05 (34.11, 35.99)
0	0.15	0.25	0.4	0.3	86.85 (86.19, 87.51)	58.30 (57.33, 59.27)
0	0.05	0.1	0.4	0.1	77.93 (77.12, 78.74)	59.82 (58.86, 60.78)
0	0	0	0.3	0	50.21 (49.23, 51.19)	46.07 (45.09, 47.05)
0	0	0	0.3	0.3	69.42 (68.52, 70.32)	65.92 (64.99, 66.85)
0	0	0.3	0.3	0.3	83.08 (82.35, 83.81)	64.16 (63.22, 65.10)
0.05	0.2	0.05	0.25	0.3	32.88 (31.96, 33.80)	36.92 (35.97, 37.87)
0.75	0	0.3	0.6	0.1	0.18 (0.10, 0.26)	99.60 (99.48, 99.72)

Table 19 – Power Comparison with 95% Confidence Intervals; *t* = 5, *k* = 4, *peak* = *IV*, Student's t Distribution (3 d.f.)

μ1	μ2	μ3	μ4	μ5	Hemmer's	Durbin's
0	0	0	0	0	4.77 (4.35, 5.19)	4.97 (4.54, 5.40)
0.1	0.2	0.3	0.4	0.3	29.48 (28.59, 30.37)	11.36 (10.74, 11.98)
0	0.15	0.25	0.4	0.3	41.69 (40.72, 42.66)	17.91 (17.16, 18.66)
0	0.05	0.1	0.4	0.1	35.36 (34.42, 36.30)	17.98 (17.23, 18.73)
0	0	0	0.3	0	21.49 (20.68, 22.30)	13.87 (13.19, 14.55)
0	0	0	0.3	0.3	29.83 (28.93, 30.73)	19.15 (18.38, 19.92)
0	0	0.3	0.3	0.3	39.24 (38.28, 40.20)	19.88 (19.10, 20.66)
0.05	0.2	0.05	0.25	0.3	14.95 (14.25, 15.65)	11.15 (10.53, 11.77)
0.75	0	0.3	0.6	0.1	1.83 (1.57, 2.09)	65.68 (64.75, 66.61)

5.2 Mixed Design

5.2.1. Results for 3 treatments with 2 treatments per incomplete block and peak at treatment II

Table 20 gives the estimated powers and confidence intervals for the powers when the normal distribution was used to generate data for the mixed design consisting of an RCBD and a BIBD. When the same number of complete and incomplete blocks are used in the mixed design (Completeness: 'Even'), there was no significant difference between Method 1 and Method 2. When more complete blocks are used in the mixed design, relative to incomplete blocks (Completeness: 'More Complete'), Method 2 is significantly more powerful than Method 1. Finally, in the case when more incomplete blocks are present in the mixture design than complete blocks (Completeness: 'Less Complete'), Method 2 is significantly more powerful than Method 1. For all cases of completeness, Method 1 and Method 2 each had significantly higher power than Hemmer's test or the Kim-Kim test, except when more complete blocks were used and there was a large distinct peak in the treatment means. In this scenario, there was no significant difference between the powers of the Kim-Kim test or Method 1.

Tables 21 and 22 give the estimated powers and corresponding confidence intervals for the exponential distribution and for the Student's t distribution, with 3 degrees of freedom, respectively. The results were similar to those found when using the normal distribution to generate data. Method 1 was significantly more powerful than Method 2 when an even number of complete and incomplete blocks were used, and when more incomplete blocks were used. When more complete blocks were used, Method 2 was significantly more powerful than Method 1. Method 1 and Method 2 were each significantly more powerful than Hemmer's test or the

Kim-Kim test, except in the case when more complete blocks were used and a large distinct peak was present in the treatment means. In this case, the power of Method 1 was not significantly different than the power of the Kim-Kim test.

Table 20 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 3, k = 2, *peak* = *II*, Normal Distribution

Completeness	Mu1	Mu2	Mu3	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	5.81 (5.35, 6.27)	4.40 (4.00, 4.80)	4.67 (4.26, 5.08)	4.24 (3.85, 4.63)
	0.1	0.75	0.5	31.40 (30.49, 32.31)	50.91 (49.93, 51.89)	62.94 (61.99, 63.89)	62.22 (61.27, 63.17)
	0.6	0.75	0.3	20.44 (19.65, 21.23)	28.99 (28.10, 29.88)	37.26 (36.31, 38.21)	36.17 (35.23, 37.11)
	0	0.5	0	36.68 (35.74, 37.62)	57.13 (56.16, 58.10)	70.24 (69.34, 71.14)	69.83 (68.93, 70.73)
	0	0.5	0.5	16.51 (15.78, 17.24)	22.98 (22.16, 23.80)	27.85 (26.97, 28.73)	27.45 (26.58, 28.32)
	0.05	0.4	0.5	9.96 (9.37, 10.55)	11.11 (10.49, 11.73)	12.71 (12.06, 13.36)	12.29 (11.65, 12.93)
	0.30	0.1	0.15	3.00 (2.67, 3.33)	1.52 (1.28, 1.76)	1.35 (1.12, 1.58)	1.07 (0.87, 1.27)
More Complete	0	0	0	5.68 (5.23, 6.13)	4.11 (3.72, 4.50)	5.08 (4.65, 5.51)	4.63 (4.22, 5.04)
	0.1	0.75	0.5	20.75 (19.96, 21.54)	62.95 (62.00, 63.90)	64.84 (63.90, 65.78)	70.44 (69.55, 71.33)
	0.6	0.75	0.3	14.45 (13.76, 15.14)	35.79 (34.85, 36.73)	39.37 (38.41, 40.33)	42.32 (41.35, 43.29)
	0	0.5	0	23.78 (22.95, 24.61)	71.62 (70.74, 72.50)	73.17 (72.30, 74.04)	79.09 (78.29, 79.89)
	0	0.5	0.5	11.96 (11.32, 12.60)	27.66 (26.78, 28.54)	29.45 (28.56, 30.34)	32.61 (31.69, 33.53)
	0.05	0.4	0.5	8.14 (7.60, 8.68)	12.19 (11.55, 12.83)	13.95 (13.27, 14.63)	14.56 (13.87, 15.25)
	0.30	0.1	0.15	3.10 (2.76, 3.44)	0.98 (0.79, 1.17)	1.52 (1.28, 1.76)	1.13 (0.92, 1.34)
Less Complete	0	0	0	4.88 (4.46, 5.30)	4.04 (3.65, 4.43)	5.15 (4.72, 5.58)	6.06 (5.59, 6.53)
	0.1	0.75	0.5	38.74 (37.79, 39.69)	28.43 (27.55, 29.31)	56.19 (55.22, 57.16)	59.11 (58.15, 60.07)
	0.6	0.75	0.3	22.16 (21.35, 22.97)	16.99 (16.25, 17.73)	32.85 (31.93, 33.77)	35.88 (34.94, 36.82)
	0	0.5	0	45.46 (44.48, 46.44)	32.58 (31.66, 33.50)	64.50 (63.56, 65.44)	67.24 (66.32, 68.16)
	0	0.5	0.5	18.42 (17.66, 19.18)	13.35 (12.68, 14.02)	25.66 (24.80, 26.52)	28.20 (27.32, 29.08)
	0.05	0.4	0.5	10.12 (9.53, 10.71)	7.34 (6.83, 7.85)	12.36 (11.71, 13.01)	14.11 (13.43, 14.79)
	0.30	0.1	0.15	1.89 (1.62, 2.16)	1.73 (1.47, 1.99)	1.51 (1.27, 1.75)	1.88 (1.61, 2.15)

Table 21 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 3, k = 2, *peak* = *II*, Exponential Distribution

Completeness	Mu1	Mu2	Mu3	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	6.22 (5.75, 6.69)	4.53 (4.12, 4.94)	4.83 (4.41, 5.25)	4.45 (4.05, 4.85)
	0.1	0.75	0.5	50.95 (49.97, 51.93)	78.10 (77.29, 78.91)	88.85 (88.23, 89.47)	89.07 (88.46, 89.68)
	0.6	0.75	0.3	32.40 (31.48, 33.32)	49.59 (48.61, 50.57)	62.74 (61.79, 63.69)	62.44 (61.49, 63.39)
	0	0.5	0	59.47 (58.51, 60.43)	88.00 (87.36, 88.64)	94.48 (94.03, 94.93)	95.01 (94.58, 95.44)
	0	0.5	0.5	24.20 (23.36, 25.04)	35.41 (34.47, 36.35)	47.23 (46.25, 48.21)	45.72 (44.74, 46.70)
	0.05	0.4	0.5	12.15 (11.51, 12.79)	15.01 (14.31, 15.71)	18.34 (17.58, 19.10)	17.60 (16.85, 18.35)
	0.30	0.1	0.15	1.84 (1.58, 2.10)	0.87 (0.69, 1.05)	0.54 (0.40, 0.68)	0.50 (0.36, 0.64)
More Complete	0	0	0	5.46 (5.01, 5.91)	4.29 (3.89, 4.69)	5.48 (5.03, 5.93)	4.99 (4.56, 5.42)
	0.1	0.75	0.5	32.09 (31.18, 33.00)	90.63 (90.06, 91.20)	90.49 (89.92, 91.06)	94.44 (93.99, 94.89)
	0.6	0.75	0.3	21.20 (20.40, 22.00)	64.49 (63.55, 65.43)	66.26 (65.33, 67.19)	73.00 (72.13, 73.87)
	0	0.5	0	37.28 (36.33, 38.23)	96.00 (95.62, 96.38)	95.27 (94.85, 95.69)	97.80 (97.51, 98.09)
	0	0.5	0.5	15.85 (15.13, 16.57)	45.29 (44.31, 46.27)	47.45 (46.47, 48.43)	52.73 (51.75, 53.71)
	0.05	0.4	0.5	9.46 (8.89, 10.03)	17.39 (16.65, 18.13)	19.43 (18.65, 20.21)	21.12 (20.32, 21.92)
	0.30	0.1	0.15	2.58 (2.27, 2.89)	0.41 (0.28, 0.54)	0.53 (0.39, 0.67)	0.52 (0.38, 0.66)
Less Complete	0	0	0	4.65 (4.24, 5.06)	4.03 (3.64, 4.42)	4.94 (4.52, 5.36)	6.00 (5.53, 6.47)
	0.1	0.75	0.5	62.98 (62.03, 63.93)	47.62 (46.64, 48.60)	83.90 (83.18, 84.62)	85.83 (85.15, 86.51)
	0.6	0.75	0.3	40.33 (39.37, 41.29)	27.70 (26.82, 28.58)	58.10 (57.13, 59.07)	60.86 (59.90, 61.82)
	0	0.5	0	71.56 (70.68, 72.44)	57.23 (56.26, 58.20)	90.86 (90.30, 91.42)	92.19 (91.66, 92.72)
	0	0.5	0.5	28.13 (27.25, 29.01)	19.23 (18.46, 20.00)	41.31 (40.34, 42.28)	44.30 (43.33, 45.27)
	0.05	0.4	0.5	12.67 (12.02, 13.32)	9.11 (8.55, 9.67)	16.75 (16.02, 17.48)	18.99 (18.22, 19.76)
	0.30	0.1	0.15	1.14 (0.93, 1.35)	1.28 (1.06, 1.50)	0.85 (0.67, 1.03)	1.08 (0.88, 1.28)

Table 22 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 3, k = 2, *peak* = *II*, Student's t Distribution (3 d.f.)

Completeness	Mu1	Mu2	Mu3	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	5.60 (5.15, 6.05)	4.75 (4.33, 5.17)	4.93 (4.51, 5.35)	4.51 (4.10, 4.92)
	0.1	0.75	0.5	25.31 (24.46, 26.16)	37.29 (36.34, 38.24)	47.52 (46.54, 48.50)	46.21 (45.23, 47.19)
	0.6	0.75	0.3	17.28 (16.54, 18.02)	22.04 (21.23, 22.85)	27.84 (26.96, 28.72)	27.10 (26.23, 27.97)
	0	0.5	0	29.49 (28.60, 30.38)	44.33 (43.36, 45.30)	55.99 (55.02, 56.96)	55.54 (54.57, 56.51)
	0	0.5	0.5	13.59 (12.92, 14.26)	17.47 (16.73, 18.21)	21.49 (20.68, 22.30)	20.97 (20.17, 21.77)
	0.05	0.4	0.5	9.45 (8.88, 10.02)	9.79 (9.21, 10.37)	11.42 (10.80, 12.04)	10.44 (9.84, 11.04)
	0.30	0.1	0.15	3.63 (3.26, 4.00)	1.94 (1.67, 2.21)	1.63 (1.38, 1.88)	1.45 (1.22, 1.68)
More Complete	0	0	0	5.54 (5.09, 5.99)	4.43 (4.03, 4.83)	5.25 (4.81, 5.69)	4.79 (4.37, 5.21)
	0.1	0.75	0.5	17.11 (16.37, 17.85)	47.05 (46.07, 48.03)	49.40 (48.42, 50.38)	54.01 (53.03, 54.99)
	0.6	0.75	0.3	12.02 (11.38, 12.66)	26.72 (25.85, 27.59)	28.75 (27.86, 29.64)	31.64 (30.73, 32.55)
	0	0.5	0	18.67 (17.91, 19.43)	55.07 (54.10, 56.04)	56.62 (55.65, 57.59)	62.87 (61.92, 63.82)
	0	0.5	0.5	10.42 (9.82, 11.02)	20.93 (20.13, 21.73)	23.24 (22.41, 24.07)	24.90 (24.05, 25.75)
	0.05	0.4	0.5	7.65 (7.13, 8.17)	10.23 (9.64, 10.82)	12.11 (11.47, 12.75)	12.18 (11.54, 12.82)
	0.30	0.1	0.15	3.74 (3.37, 4.11)	1.27 (1.05, 1.49)	1.76 (1.50, 2.02)	1.35 (1.12, 1.58)
Less Complete	0	0	0	4.98 (4.55, 5.41)	4.08 (3.69, 4.47)	4.86 (4.44, 5.28)	5.82 (5.36, 6.28)
	0.1	0.75	0.5	29.16 (28.27, 30.05)	20.95 (20.15, 21.75)	42.81 (41.84, 43.78)	45.94 (44.96, 46.92)
	0.6	0.75	0.3	17.98 (17.23, 18.73)	13.23 (12.57, 13.89)	25.30 (24.45, 26.15)	28.05 (27.17, 28.93)
	0	0.5	0	34.37 (33.44, 35.30)	25.42 (24.57, 26.27)	50.29 (49.31, 51.27)	53.61 (52.63, 54.59)
	0	0.5	0.5	14.78 (14.08, 15.48)	11.44 (10.82, 12.06)	20.00 (19.22, 20.78)	22.41 (21.59, 23.23)
	0.05	0.4	0.5	8.31 (7.77, 8.85)	6.79 (6.30, 7.28)	10.29 (9.69, 10.89)	11.94 (11.30, 12.58)
	0.30	0.1	0.15	2.31 (2.02, 2.60)	2.07 (1.79, 2.35)	2.15 (1.87, 2.43)	2.57 (2.26, 2.88)

5.2.2. Results for 4 treatments with 3 treatments per incomplete block and peak at treatment II

Table 23 gives the estimated powers and corresponding confidence intervals when using the normal distribution to generate data. When there was an even ratio of complete and incomplete blocks, there was no significant difference between Method 1 and Method 2. When more complete blocks were used, Method 2 was more powerful than Method 1. When more incomplete blocks were present in the mixed design, there was no significant difference between Method 1 and Method 2.

Tables 24 and 25 give the powers and corresponding confidence intervals for the exponential distribution and the Student's t distribution, with 3 degrees of freedom, respectively. The findings are similar to those when the normal distribution was used to generate data.

For all three distributions, Method 1 and Method 2 were significantly more powerful than Hemmer's test or the Kim-Kim test. The only exception to this result was when more complete blocks were used and a large distinct peak was present in the treatment means. In this scenario, the power of the Kim-Kim test was not significantly different than the power of Method 1.

Table 23 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 4, k = 3, *peak* = *II*, Normal Distribution

Completeness	**μ1**	**μ2**	**μ3**	**μ4**	**Hemmer's**	**Kim-Kim**	**Method 1**	**Method 2**
Even	0	0	0	0	4.38 (3.98, 4.78)	5.70 (5.25, 6.15)	4.93 (4.51, 5.35)	4.96 (4.53, 5.39)
	0.3	0.5	0.3	0.1	23.56 (22.73, 24.39)	32.76 (31.84, 33.68)	43.68 (42.71, 44.65)	43.87 (42.90, 44.84)
	0.2	0.5	0.4	0	30.38 (29.48, 31.28)	44.91 (43.94, 45.88)	58.87 (57.91, 59.83)	59.13 (58.17, 60.09)
	0.1	0.5	0.1	0.05	27.09 (26.22, 27.96)	44.69 (43.72, 45.66)	55.84 (54.87, 56.81)	56.09 (55.12, 57.06)
	0	0.5	0	0	30.40 (29.50, 31.30)	53.07 (52.09, 54.05)	64.68 (63.74, 65.62)	65.13 (64.20, 66.06)
	0	0.5	0.5	0	29.92 (29.02, 30.82)	52.30 (51.32, 53.28)	64.21 (63.27, 65.15)	64.59 (63.65, 65.53)
	0.5	0.5	0.5	0	30.13 (29.23, 31.03)	31.80 (30.89, 32.71)	49.10 (48.12, 50.08)	49.20 (48.22, 50.18)
	0.05	0.2	0.05	0.25	3.56 (3.20, 3.92)	6.32 (5.84, 6.80)	4.64 (4.23, 5.05)	4.70 (4.29, 5.11)
	0.75	0.45	0.5	0.6	1.97 (1.70, 2.24)	1.23 (1.01, 1.45)	1.00 (0.80, 1.20)	0.99 (0.80, 1.18)
More Complete	0	0	0	0	5.05 (4.62, 5.48)	4.61 (4.20, 5.02)	4.86 (4.44, 5.28)	5.30 (4.86, 5.74)
	0.3	0.5	0.3	0.1	17.05 (16.31, 17.79)	37.03 (36.08, 37.98)	42.04 (41.07, 43.01)	46.74 (45.76, 47.72)
	0.2	0.5	0.4	0	21.74 (20.93, 22.55)	53.58 (52.60, 54.56)	58.79 (57.83, 59.75)	65.03 (64.10, 65.96)
	0.1	0.5	0.1	0.05	19.34 (18.57, 20.11)	53.37 (52.39, 54.35)	55.42 (54.45, 56.39)	62.07 (61.12, 63.02)
	0	0.5	0	0	21.57 (20.76, 22.38)	62.77 (61.82, 63.72)	65.45 (64.52, 66.38)	71.84 (70.96, 72.72)
	0	0.5	0.5	0	21.07 (20.27, 21.87)	64.35 (63.41, 65.29)	66.13 (65.20, 67.06)	72.99 (72.12, 73.86)
	0.5	0.5	0.5	0	21.32 (20.52, 22.12)	36.34 (35.40, 37.28)	45.97 (44.99, 46.95)	49.20 (48.22, 50.18)
	0.05	0.2	0.05	0.25	4.78 (4.36, 5.20)	4.90 (4.48, 5.32)	4.79 (4.37, 5.21)	5.12 (4.69, 5.55)
	0.75	0.45	0.5	0.6	2.89 (2.56, 3.22)	0.53 (0.39, 0.67)	0.77 (0.60, 0.94)	0.69 (0.53, 0.85)
Less Complete	0	0	0	0	4.98 (4.55, 5.41)	6.45 (5.97, 6.93)	5.04 (4.61, 5.47)	4.92 (4.50, 5.34)
	0.3	0.5	0.3	0.1	30.52 (29.62, 31.42)	22.75 (21.93, 23.57)	39.49 (38.53, 40.45)	39.50 (38.54, 40.46)
	0.2	0.5	0.4	0	41.74 (40.77, 42.71)	30.65 (29.75, 31.55)	54.31 (53.33, 55.29)	54.52 (53.54, 55.50)
	0.1	0.5	0.1	0.05	35.93 (34.99, 36.87)	30.48 (29.58, 31.38)	50.44 (49.46, 51.42)	49.41 (48.43, 50.39)
	0	0.5	0	0	41.60 (40.63, 42.57)	36.67 (35.73, 37.61)	58.98 (58.02, 59.94)	57.57 (56.60, 58.54)
	0	0.5	0.5	0	41.32 (40.35, 42.29)	35.77 (34.83, 36.71)	57.99 (57.02, 58.96)	57.05 (56.08, 58.02)
	0.5	0.5	0.5	0	40.96 (40.00, 41.92)	22.31 (21.49, 23.13)	46.59 (45.61, 47.57)	48.43 (47.45, 49.41)
	0.05	0.2	0.05	0.25	3.63 (3.26, 4.00)	6.90 (6.40, 7.40)	4.00 (3.62, 4.38)	3.61 (3.24, 3.98)
	0.75	0.45	0.5	0.6	1.84 (1.58, 2.10)	2.21 (1.92, 2.50)	1.09 (0.89, 1.29)	1.10 (0.90, 1.30)

Table 24 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 4, k = 3, *peak* = *II*, Exponential Distribution

Completeness	μ1	μ2	μ3	μ4	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	4.59 (4.18, 5.00)	5.58 (5.13, 6.03)	5.23 (4.79, 5.67)	5.31 (4.87, 5.75)
	0.3	0.5	0.3	0.1	42.26 (41.29, 43.23)	57.27 (56.30, 58.24)	75.04 (74.19, 75.89)	75.27 (74.42, 76.12)
	0.2	0.5	0.4	0	54.87 (53.89, 55.85)	72.95 (72.08, 73.82)	88.53 (87.91, 89.15)	88.66 (88.04, 89.28)
	0.1	0.5	0.1	0.05	45.55 (44.57, 46.53)	73.86 (73.00, 74.72)	86.17 (85.49, 86.85)	86.40 (85.73, 87.07)
	0	0.5	0	0	51.12 (50.14, 52.10)	82.00 (81.25, 82.75)	91.80 (91.26, 92.34)	92.00 (91.47, 92.53)
	0	0.5	0.5	0	50.33 (49.35, 51.31)	79.94 (79.16, 80.72)	89.58 (88.98, 90.18)	89.84 (89.25, 90.43)
	0.5	0.5	0.5	0	51.06 (50.08, 52.04)	49.30 (48.32, 50.28)	74.76 (73.91, 75.61)	74.79 (73.94, 75.64)
	0.05	0.2	0.05	0.25	2.68 (2.36, 3.00)	5.40 (4.96, 5.84)	3.52 (3.16, 3.88)	3.54 (3.18, 3.90)
	0.75	0.45	0.5	0.6	0.98 (0.79, 1.17)	0.33 (0.22, 0.44)	0.20 (0.11, 0.29)	0.20 (0.11, 0.29)
More Complete	0	0	0	0	5.30 (4.86, 5.74)	4.51 (4.10, 4.92)	4.92 (4.50, 5.34)	5.29 (4.85, 5.73)
	0.3	0.5	0.3	0.1	27.70 (26.82, 28.58)	67.11 (66.19, 68.03)	73.13 (72.26, 74.00)	78.44 (77.63, 79.25)
	0.2	0.5	0.4	0	35.02 (34.09, 35.95)	83.54 (82.81, 84.27)	86.81 (86.15, 87.47)	90.85 (90.28, 91.42)
	0.1	0.5	0.1	0.05	30.36 (29.46, 31.26)	84.59 (83.88, 85.30)	86.22 (85.54, 86.90)	91.26 (90.71, 91.81)
	0	0.5	0	0	32.65 (31.73, 33.57)	92.16 (91.63, 92.69)	92.08 (91.55, 92.61)	95.75 (95.35, 96.15)
	0	0.5	0.5	0	32.51 (31.59, 33.43)	89.84 (89.25, 90.43)	90.58 (90.01, 91.15)	94.37 (93.92, 94.82)
	0.5	0.5	0.5	0	33.56 (32.63, 34.49)	59.83 (58.87, 60.79)	71.55 (70.67, 72.43)	74.73 (73.88, 75.58)
	0.05	0.2	0.05	0.25	3.18 (2.84, 3.52)	4.64 (4.23, 5.05)	4.23 (3.84, 4.62)	4.65 (4.24, 5.06)
	0.75	0.45	0.5	0.6	2.09 (1.81, 2.37)	0.24 (0.14, 0.34)	0.30 (0.19, 0.41)	0.17 (0.09, 0.25)
Less Complete	0	0	0	0	5.15 (4.72, 5.58)	6.05 (5.58, 6.52)	5.25 (4.81, 5.69)	5.05 (4.62, 5.48)
	0.3	0.5	0.3	0.1	56.53 (55.56, 57.50)	38.28 (37.33, 39.23)	70.40 (69.51, 71.29)	70.99 (70.10, 71.88)
	0.2	0.5	0.4	0	70.10 (69.20, 71.00)	50.52 (49.54, 51.50)	84.33 (83.62, 85.04)	84.31 (83.60, 85.02)
	0.1	0.5	0.1	0.05	62.01 (61.06, 62.96)	49.92 (48.94, 50.90)	80.69 (79.92, 81.46)	79.75 (78.96, 80.54)
	0	0.5	0	0	67.15 (66.23, 68.07)	57.14 (56.17, 58.11)	87.10 (86.44, 87.76)	85.36 (84.67, 86.05)
	0	0.5	0.5	0	65.85 (64.92, 66.78)	55.55 (54.58, 56.52)	84.83 (84.13, 85.53)	84.06 (83.34, 84.78)
	0.5	0.5	0.5	0	65.55 (64.62, 66.48)	34.07 (33.14, 35.00)	73.42 (72.55, 74.29)	75.71 (74.87, 76.55)
	0.05	0.2	0.05	0.25	2.45 (2.15, 2.75)	5.93 (5.47, 6.39)	3.14 (2.80, 3.48)	2.73 (2.41, 3.05)
	0.75	0.45	0.5	0.6	0.81 (0.63, 0.99)	1.15 (0.94, 1.36)	0.43 (0.30, 0.56)	0.43 (0.30, 0.56)

Table 25 - Power Comparison with 95% Confidence Intervals; Mixed Design, t = 4, k = 3, *peak* = *II*, Student's t Distribution (3 d.f.)

Completeness	μ1	μ2	μ3	μ4	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	4.75 (4.33, 5.17)	5.75 (5.29, 6.21)	5.06 (4.63, 5.49)	5.09 (4.66, 5.52)
	0.3	0.5	0.3	0.1	18.17 (17.41, 18.93)	25.34 (24.49, 26.19)	33.18 (32.26, 34.10)	33.46 (32.54, 34.38)
	0.2	0.5	0.4	0	23.74 (22.91, 24.57)	34.67 (33.74, 35.60)	45.54 (44.56, 46.52)	45.72 (44.74, 46.70)
	0.1	0.5	0.1	0.05	20.51 (19.72, 21.30)	34.70 (33.77, 35.63)	42.77 (41.80, 43.74)	43.06 (42.09, 44.03)
	0	0.5	0	0	23.19 (22.36, 24.02)	40.66 (39.70, 41.62)	49.99 (49.01, 50.97)	50.37 (49.39, 51.35)
	0	0.5	0.5	0	22.78 (21.96, 23.60)	41.01 (40.05, 41.97)	49.32 (48.34, 50.30)	49.51 (48.53, 50.49)
	0.5	0.5	0.5	0	22.91 (22.09, 23.73)	24.07 (23.23, 24.91)	36.90 (35.95, 37.85)	36.96 (36.01, 37.91)
	0.05	0.2	0.05	0.25	3.61 (3.24, 3.98)	5.76 (5.30, 6.22)	4.27 (3.87, 4.67)	4.31 (3.91, 4.71)
	0.75	0.45	0.5	0.6	2.44 (2.14, 2.74)	1.77 (1.51, 2.03)	1.35 (1.12, 1.58)	1.35 (1.12, 1.58)
More Complete	0	0	0	0	5.27 (4.83, 5.71)	4.78 (4.36, 5.20)	5.15 (4.72, 5.58)	5.70 (5.25, 6.15)
	0.3	0.5	0.3	0.1	13.59 (12.92, 14.26)	26.79 (25.92, 27.66)	31.96 (31.05, 32.87)	35.12 (34.18, 36.06)
	0.2	0.5	0.4	0	16.51 (15.78, 17.24)	39.72 (38.76, 40.68)	44.58 (43.61, 45.55)	49.25 (48.27, 50.23)
	0.1	0.5	0.1	0.05	15.55 (14.84, 16.26)	39.94 (38.98, 40.90)	42.64 (41.67, 43.61)	48.06 (47.08, 49.04)
	0	0.5	0	0	16.85 (16.12, 17.58)	49.54 (48.56, 50.52)	50.52 (49.54, 51.50)	57.40 (56.43, 58.37)
	0	0.5	0.5	0	17.64 (16.89, 18.39)	48.22 (47.24, 49.20)	50.79 (49.81, 51.77)	56.93 (55.96, 57.90)
	0.5	0.5	0.5	0	17.22 (16.48, 17.96)	27.14 (26.27, 28.01)	34.94 (34.01, 35.87)	37.28 (36.33, 38.23)
	0.05	0.2	0.05	0.25	4.37 (3.97, 4.77)	4.78 (4.36, 5.20)	4.75 (4.33, 5.17)	5.27 (4.83, 5.71)
	0.75	0.45	0.5	0.6	3.40 (3.04, 3.76)	0.88 (0.70, 1.06)	1.31 (1.09, 1.53)	1.18 (0.97, 1.39)
Less Complete	0	0	0	0	4.77 (4.35, 5.19)	6.48 (6.00, 6.96)	5.12 (4.69, 5.55)	4.83 (4.41, 5.25)
	0.3	0.5	0.3	0.1	23.55 (22.72, 24.38)	18.93 (18.16, 19.70)	30.31 (29.41, 31.21)	30.24 (29.34, 31.14)
	0.2	0.5	0.4	0	31.55 (30.64, 32.46)	24.36 (23.52, 25.20)	41.95 (40.98, 42.92)	41.76 (40.79, 42.73)
	0.1	0.5	0.1	0.05	27.16 (26.29, 28.03)	24.39 (23.55, 25.53)	38.38 (37.43, 39.33)	37.55 (36.60, 38.50)
	0	0.5	0	0	31.14 (30.23, 32.05)	28.59 (27.70, 29.48)	44.36 (43.39, 45.33)	43.32 (42.35, 44.29)
	0	0.5	0.5	0	30.89 (29.98, 31.80)	27.43 (26.56, 28.30)	44.00 (43.03, 44.97)	42.94 (41.97, 43.91)
	0.5	0.5	0.5	0	31.92 (31.01, 32.83)	17.74 (16.99, 18.49)	35.23 (34.29, 36.17)	36.88 (35.93, 37.83)
	0.05	0.2	0.05	0.25	4.11 (3.72, 4.50)	6.54 (6.06, 7.02)	4.67 (4.26, 5.08)	4.37 (3.97, 4.77)
	0.75	0.45	0.5	0.6	2.11 (1.83, 2.39)	2.50 (2.19, 2.81)	1.52 (1.28, 1.76)	1.52 (1.28, 1.76)

5.2.3. Results for 4 treatments with 3 treatments per incomplete block and peak at treatment III

Tables 26, 27, and 28 provide the estimated powers and confidence intervals for those powers when respectively using the normal distribution, exponential distribution and Student's t distribution with 3 degrees of freedom. The following results were consistent across all underlying distributions. When an even number of complete and incomplete blocks was used, there was no significant difference between Method 1 and Method 2. When more complete blocks were used, Method 2 was significantly more powerful than Method 1. When more incomplete blocks were present, there was no significant difference between Method 1 and Method 2.

For all three distributions, Method 1 and Method 2 were significantly more powerful than Hemmer's test or the Kim-Kim test. There was one exception when more complete blocks were used in the mixed design and there was a large distinct peak in the treatment means. In this scenario, the power of the Kim-Kim test was not significantly different than the power of Method 1.

Table 26 – Power Comparison with 95% Confidence Intervals; Mixed Design, $t = 4$, $k = 3$, *peak* = *III*, Normal Distribution

Completeness	**μ1**	**μ2**	**μ3**	**μ4**	**Hemmer's**	**Kim-Kim**	**Method 1**	**Method 2**
Even	0	0	0	0	4.40 (4.00, 4.80)	5.77 (5.31, 6.23)	5.01 (4.58, 5.44)	5.06 (4.63, 5.49)
	0.1	0.3	0.5	0.3	23.40 (22.57, 24.23)	31.99 (31.08, 32.90)	43.47 (42.50, 44.44)	43.63 (42.66, 44.60)
	0	0.4	0.5	0.2	30.37 (29.47, 31.27)	45.45 (44.47, 46.43)	58.77 (57.81, 59.73)	59.11 (58.15, 60.07)
	0.05	0.1	0.5	0.1	26.89 (26.02, 27.76)	44.23 (43.26, 45.20)	55.82 (54.85, 56.79)	56.08 (55.11, 57.05)
	0	0	0.5	0	29.56 (28.67, 30.45)	52.58 (51.60, 53.56)	64.44 (63.50, 65.38)	64.72 (63.78, 65.66)
	0	0	0.5	0.5	30.66 (29.76, 31.56)	31.42 (30.51, 32.33)	48.41 (47.43, 49.39)	48.51 (47.53, 49.49)
	0	0.5	0.5	0.5	30.74 (29.84, 31.64)	32.07 (31.16, 32.98)	49.44 (48.46, 50.42)	49.50 (48.52, 50.48)
	0.05	0.2	0.05	0.25	4.78 (4.36, 5.20)	3.07 (2.73, 3.41)	3.35 (3.00, 3.70)	3.38 (3.03, 3.73)
	0.75	0.45	0.5	0.6	1.29 (1.07, 1.51)	1.25 (1.03, 1.47)	0.63 (0.47, 0.79)	0.65 (0.49, 0.81)
More Complete	0	0	0	0	4.93 (4.51, 5.35)	4.65 (4.24, 5.06)	4.91 (4.49, 5.33)	5.43 (4.99, 5.87)
	0.1	0.3	0.5	0.3	16.11 (15.39, 16.83)	37.59 (36.64, 38.54)	42.65 (41.68, 43.62)	46.62 (45.64, 47.60)
	0	0.4	0.5	0.2	21.82 (21.01, 22.63)	53.57 (52.59, 54.55)	58.78 (57.82, 59.74)	64.35 (63.41, 65.29)
	0.05	0.1	0.5	0.1	19.16 (18.39, 19.93)	53.94 (52.96, 54.92)	56.01 (55.04, 56.98)	62.33 (61.38, 63.28)
	0	0	0.5	0	20.78 (19.98, 21.58)	63.49 (62.55, 64.43)	65.34 (64.41, 66.27)	72.00 (71.12, 72.88)
	0	0	0.5	0.5	20.89 (20.09, 21.69)	37.11 (36.16, 38.06)	46.73 (45.75, 47.71)	49.56 (48.58, 50.54)
	0	0.5	0.5	0.5	20.90 (20.10, 21.70)	36.37 (35.43, 37.31)	46.51 (45.53, 47.49)	49.31 (48.33, 50.29)
	0.05	0.2	0.05	0.25	5.23 (4.79, 5.67)	2.51 (2.20, 2.82)	3.22 (2.87, 3.57)	3.23 (2.88, 3.58)
	0.75	0.45	0.5	0.6	1.90 (1.63, 2.17)	0.55 (0.41, 0.69)	0.59 (0.44, 0.74)	0.47 (0.34, 0.60)
Less Complete	0	0	0	0	4.68 (4.27, 5.09)	6.26 (5.79, 6.73)	4.95 (4.52, 5.38)	4.71 (4.29, 5.13)
	0.1	0.3	0.5	0.3	31.12 (30.21, 32.03)	22.96 (22.14, 23.78)	39.89 (38.93, 40.85)	40.04 (39.08, 41.00)
	0	0.4	0.5	0.2	41.78 (40.81, 42.75)	30.58 (29.68, 31.48)	54.46 (53.48, 55.44)	54.36 (53.38, 55.34)
	0.05	0.1	0.5	0.1	35.39 (34.45, 36.33)	30.89 (29.98, 31.80)	50.41 (49.43, 51.39)	49.33 (48.35, 50.31)
	0	0	0.5	0	42.39 (41.42, 43.36)	36.11 (35.17, 37.05)	59.03 (58.07, 59.99)	57.82 (56.85, 58.79)
	0	0	0.5	0.5	40.86 (39.90, 41.82)	21.60 (20.79, 22.41)	46.16 (45.18, 47.14)	48.43 (47.45, 49.41)
	0	0.5	0.5	0.5	41.67 (40.70, 42.64)	22.60 (21.78, 23.42)	47.92 (46.94, 48.90)	49.41 (48.43, 50.39)
	0.05	0.2	0.05	0.25	4.84 (4.42, 5.26)	4.61 (4.20, 5.02)	4.10 (3.71, 4.49)	4.05 (3.66, 4.44)
	0.75	0.45	0.5	0.6	0.76 (0.59, 0.93)	2.26 (1.97, 2.55)	0.51 (0.37, 0.65)	0.43 (0.30, 0.56)

Table 27 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 4, k = 3, *peak* = *III*, Exponential Distribution

Completeness	μ1	μ2	μ3	μ4	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	4.69 (4.28, 5.10)	6.11 (5.64, 6.58)	5.36 (4.92, 5.80)	5.38 (4.94, 5.82)
	0.1	0.3	0.5	0.3	41.23 (40.27, 42.19)	57.54 (56.57, 58.51)	74.20 (73.34, 75.06)	74.49 (73.64, 75.34)
	0	0.4	0.5	0.2	54.81 (53.83, 55.79)	73.68 (72.82, 74.54)	88.66 (88.04, 89.28)	88.78 (88.16, 89.40)
	0.05	0.1	0.5	0.1	46.80 (45.82, 47.78)	74.36 (73.50, 75.22)	87.09 (86.43, 87.75)	87.33 (86.68, 87.98)
	0	0	0.5	0	50.41 (49.43, 51.39)	82.54 (81.80, 83.28)	91.45 (90.90, 92.00)	91.65 (91.11, 92.19)
	0	0	0.5	0.5	50.41 (49.43, 51.39)	49.98 (49.00, 50.96)	76.64 (75.81, 77.47)	76.71 (75.88, 77.54)
	0	0.5	0.5	0.5	50.09 (49.11, 51.07)	49.61 (48.63, 50.59)	74.63 (73.78, 75.48)	74.74 (73.89, 75.59)
	0.05	0.2	0.05	0.25	4.96 (4.53, 5.39)	3.29 (2.94, 3.64)	3.20 (2.86, 3.54)	3.22 (2.87, 3.57)
	0.75	0.45	0.5	0.6	0.36 (0.24, 0.48)	0.41 (0.28, 0.54)	0.19 (0.10, 0.28)	0.19 (0.10, 0.28)
More Complete	0	0	0	0	5.14 (4.71, 5.57)	4.41 (4.01, 4.81)	5.07 (4.64, 5.50)	5.53 (5.08, 5.98)
	0.1	0.3	0.5	0.3	27.23 (26.36, 28.10)	68.82 (67.91, 69.73)	73.83 (72.97, 74.69)	79.40 (78.61, 80.19)
	0	0.4	0.5	0.2	35.52 (34.58, 36.46)	84.49 (83.78, 85.20)	88.28 (87.65, 88.91)	92.11 (91.58, 92.64)
	0.05	0.1	0.5	0.1	30.45 (29.55, 31.35)	86.05 (85.37, 86.73)	86.56 (85.89, 87.23)	91.82 (91.28, 92.36)
	0	0	0.5	0	32.32 (31.40, 33.24)	91.82 (91.28, 92.36)	92.13 (91.60, 92.66)	95.62 (95.22, 96.02)
	0	0	0.5	0.5	32.43 (31.51, 33.35)	59.68 (58.72, 60.64)	72.93 (72.06, 73.80)	76.65 (75.82, 77.48)
	0	0.5	0.5	0.5	33.05 (32.13, 33.97)	59.86 (58.90, 60.82)	71.76 (70.88, 72.64)	74.89 (74.04, 75.74)
	0.05	0.2	0.05	0.25	5.52 (5.07, 5.97)	2.13 (1.85, 2.41)	2.97 (2.64, 3.30)	2.66 (2.34, 2.98)
	0.75	0.45	0.5	0.6	1.00 (0.80, 1.20)	0.11 (0.05, 0.17)	0.09 (0.03, 0.15)	0.11 (0.05, 0.17)
Less Complete	0	0	0	0	4.55 (4.14, 4.96)	6.09 (5.62, 6.56)	4.90 (4.48, 5.32)	4.50 (4.09, 4.91)
	0.1	0.3	0.5	0.3	56.15 (55.18, 57.12)	38.06 (37.11, 39.01)	70.22 (69.32, 71.12)	71.10 (70.21, 71.99)
	0	0.4	0.5	0.2	69.82 (68.92, 70.72)	51.07 (50.09, 52.05)	84.24 (83.53, 84.95)	84.42 (83.71, 85.13)
	0.05	0.1	0.5	0.1	61.60 (60.65, 62.55)	50.33 (49.35, 51.31)	81.20 (80.43, 81.97)	80.46 (79.86, 81.24)
	0	0	0.5	0	66.65 (65.73, 67.57)	56.68 (55.71, 57.65)	87.32 (86.67, 87.97)	86.04 (85.36, 86.72)
	0	0	0.5	0.5	66.58 (65.66, 67.50)	31.88 (30.97, 32.79)	73.67 (72.81, 74.53)	76.40 (75.57, 77.23)
	0	0.5	0.5	0.5	65.86 (64.93, 66.79)	33.75 (32.82, 34.68)	73.02 (72.15, 73.89)	75.41 (74.57, 76.25)
	0.05	0.2	0.05	0.25	5.59 (5.14, 6.04)	4.49 (4.08, 4.90)	4.14 (3.75, 4.53)	4.40 (4.00, 4.80)
	0.75	0.45	0.5	0.6	0.26 (0.16, 0.36)	1.04 (0.84, 1.24)	0.10 (0.04, 0.16)	0.08 (0.02, 0.14)

Table 28 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 4, k = 3, *peak* = *III*, Student's t Distribution (3 d.f.)

Completeness	μ1	μ2	μ3	μ4	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	4.32 (3.92, 4.72)	5.48 (5.03, 5.93)	5.13 (4.70, 5.56)	5.13 (4.70, 5.56)
	0.1	0.3	0.5	0.3	18.38 (17.62, 19.14)	24.73 (23.88, 25.58)	31.86 (30.95, 32.77)	32.08 (31.17, 32.99)
	0	0.4	0.5	0.2	23.61 (22.78, 24.44)	33.89 (32.96, 34.82)	44.86 (43.89, 45.83)	45.03 (44.05, 46.01)
	0.05	0.1	0.5	0.1	20.92 (20.12, 21.72)	35.20 (34.26, 36.14)	43.56 (42.59, 44.53)	43.77 (42.80, 44.74)
	0	0	0.5	0	23.74 (22.91, 24.57)	41.06 (40.10, 42.02)	50.64 (49.66, 51.62)	50.98 (50.00, 51.96)
	0	0	0.5	0.5	23.01 (22.19, 23.83)	24.77 (23.92, 25.62)	37.09 (36.14, 38.04)	37.15 (36.20, 38.10)
	0	0.5	0.5	0.5	22.91 (22.09, 23.73)	24.40 (23.56, 25.24)	36.43 (35.49, 37.37)	36.67 (35.73, 37.61)
	0.05	0.2	0.05	0.25	4.60 (4.19, 5.01)	4.03 (3.64, 4.42)	4.07 (3.68, 4.46)	4.11 (3.72, 4.50)
	0.75	0.45	0.5	0.6	1.43 (1.20, 1.66)	1.48 (1.24, 1.72)	0.71 (0.55, 0.87)	0.72 (0.55, 0.89)
More Complete	0	0	0	0	5.23 (4.79, 5.67)	4.80 (4.38, 5.22)	5.34 (4.90, 5.78)	5.61 (5.16, 6.06)
	0.1	0.3	0.5	0.3	14.12 (13.44, 14.80)	29.04 (28.15, 29.93)	32.53 (31.61, 33.45)	36.02 (35.08, 36.96)
	0	0.4	0.5	0.2	17.53 (16.78, 18.28)	39.49 (38.53, 40.45)	44.97 (43.99, 45.95)	49.38 (48.40, 50.36)
	0.05	0.1	0.5	0.1	15.33 (14.62, 16.04)	40.56 (39.60, 41.52)	42.40 (41.43, 43.37)	48.32 (47.34, 49.30)
	0	0	0.5	0	16.96 (16.22, 17.70)	48.68 (47.70, 49.66)	51.29 (50.31, 52.27)	57.40 (56.43, 58.37)
	0	0	0.5	0.5	17.35 (16.61, 18.09)	28.46 (27.58, 29.34)	36.09 (35.15, 37.03)	38.44 (37.49, 39.39)
	0	0.5	0.5	0.5	16.88 (16.15, 17.61)	28.48 (27.60, 29.36)	35.11 (34.17, 36.05)	38.15 (37.20, 39.10)
	0.05	0.2	0.05	0.25	5.08 (4.65, 5.51)	2.90 (2.57, 3.23)	3.30 (2.95, 3.65)	3.37 (3.02, 3.72)
	0.75	0.45	0.5	0.6	2.24 (1.95, 2.53)	0.84 (0.66, 1.02)	0.76 (0.59, 0.93)	0.80 (0.63, 0.97)
Less Complete	0	0	0	0	4.74 (4.32, 5.16)	5.98 (5.52, 6.44)	5.22 (4.78, 5.66)	4.81 (4.39, 5.23)
	0.1	0.3	0.5	0.3	23.51 (22.68, 24.34)	18.82 (18.05, 19.59)	30.44 (29.54, 31.34)	30.44 (29.54, 31.34)
	0	0.4	0.5	0.2	31.05 (30.14, 31.96)	23.98 (23.14, 24.82)	41.26 (40.30, 42.22)	41.09 (40.13, 42.05)
	0.05	0.1	0.5	0.1	27.50 (26.62, 28.38)	24.03 (23.19, 24.87)	38.06 (37.11, 39.01)	37.87 (36.92, 38.82)
	0	0	0.5	0	31.60 (30.69, 32.51)	28.65 (27.76, 29.54)	44.95 (43.98, 45.92)	43.84 (42.87, 44.81)
	0	0	0.5	0.5	31.50 (30.59, 32.41)	18.41 (17.65, 19.17)	36.02 (35.08, 36.96)	37.42 (36.47, 38.37)
	0	0.5	0.5	0.5	30.86 (29.95, 31.77)	18.14 (17.38, 18.90)	34.90 (33.97, 35.83)	36.55 (35.61, 37.49)
	0.05	0.2	0.05	0.25	4.57 (4.16, 4.98)	5.16 (4.73, 5.59)	4.14 (3.75, 4.53)	4.10 (3.71, 4.49)
	0.75	0.45	0.5	0.6	1.36 (1.13, 1.59)	2.89 (2.56, 3.22)	1.14 (0.93, 1.35)	0.94 (0.75, 1.13)

5.2.4. Results for 5 treatments with 4 treatments per incomplete block and peak at treatment II

Table 29 provides the calculated powers and confidence intervals for the powers when using the normal distribution. When there was an even number of complete and incomplete blocks, Method 1 was significantly more powerful than Method 2 when the treatment means followed a large distinct peak. Otherwise, Method 2 was at least as powerful as Method 1, meaning Method 2 was not significantly different than Method 1 or Method 2 had higher power. When there were more complete blocks in the mixed design, Method 2 had higher power than Method 1, but the difference was not significant. When there were more incomplete blocks present, Method 1 was significantly more powerful than Method 2 when there was a large distinct peak in the treatment means. Otherwise, Method 2 was at least as powerful as Method 1.

Table 30 gives the powers and confidence intervals for the powers using the exponential distribution. The results we find from Table 30 are similar to the findings from Table 29, while using the normal distribution. The exception is that in the case with more complete blocks, Method 2 is significantly more powerful than Method 1 when there is a large distinct peak.

Table 31 gives the powers and confidence intervals for the powers using the Student's t distribution, with 3 degrees of freedom. The results again resemble those in the normal distribution, except no differences between Method 1 and Method 2 were significant.

For all three distributions, Method 1 and Method 2 were significantly more powerful than Hemmer's test or the Kim-Kim test. The one exception is when more complete blocks were used in the mixed design and there was a large distinct peak in the treatment means. In this scenario, the power of the Kim-Kim test was not significantly different than that of Method 1.

Table 29 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 5, k = 4, *peak* = *II*, Normal Distribution

Completeness	**µ1**	**µ2**	**µ3**	**µ4**	**µ5**	**Hemmer's**	**Kim-Kim**	**Method 1**	**Method 2**
Even	0	0	0	0	0	5.28 (4.84, 5.72)	5.18 (4.75, 5.61)	4.92 (4.50, 5.34)	5.07 (4.64, 5.50)
	0.3	0.4	0.3	0.2	0.1	25.69 (24.83, 26.55)	25.22 (24.37, 26.07)	39.29 (38.33, 40.25)	38.70 (37.75, 39.65)
	0.3	0.4	0.25	0.15	0	35.45 (34.51, 36.39)	34.83 (33.90, 35.76)	54.44 (53.46, 55.42)	53.64 (52.66, 54.62)
	0.1	0.4	0.1	0.05	0	30.61 (29.71, 31.51)	40.11 (39.15, 41.07)	54.48 (53.50, 55.46)	51.90 (50.92, 52.88)
	0	0.3	0	0	0	19.31 (18.54, 20.08)	27.19 (26.32, 28.06)	36.28 (35.34, 37.22)	34.38 (33.45, 35.31)
	0	0.3	0.3	0	0	26.00 (25.14, 26.86)	38.13 (37.18, 39.08)	49.77 (48.79, 50.75)	47.01 (46.03, 47.99)
	0.3	0.3	0.3	0	0	34.22 (33.29, 35.15)	28.18 (27.30, 29.06)	48.09 (47.11, 49.07)	48.26 (47.28, 49.24)
	0.05	0.2	0.05	0.25	0.3	1.47 (1.23, 1.71)	2.34 (2.04, 2.64)	1.20 (0.99, 1.41)	1.22 (1.00, 1.44)
	0.75	0	0.3	0.6	0.1	3.22 (2.87, 3.57)	0.15 (0.07, 0.23)	0.27 (0.17, 0.37)	0.49 (0.35, 0.63)
More Complete	0	0	0	0	0	4.88 (4.46, 5.30)	4.62 (4.21, 5.03)	4.68 (4.27, 5.09)	4.64 (4.23, 5.05)
	0.3	0.4	0.3	0.2	0.1	15.04 (14.34, 15.74)	32.61 (31.69, 33.53)	37.28 (36.33, 38.23)	37.94 (36.99, 38.89)
	0.3	0.4	0.25	0.15	0	21.51 (20.70, 22.32)	45.88 (44.90, 46.86)	53.77 (52.79, 54.75)	54.66 (53.68, 55.64)
	0.1	0.4	0.1	0.05	0	18.59 (17.83, 19.35)	51.17 (50.19, 52.15)	54.46 (53.48, 55.44)	55.75 (54.78, 56.72)
	0	0.3	0	0	0	12.99 (12.33, 13.65)	36.81 (35.86, 37.76)	37.07 (36.12, 38.02)	38.38 (37.43, 39.33)
	0	0.3	0.3	0	0	15.89 (15.17, 16.61)	50.26 (49.28, 51.24)	51.15 (50.17, 52.13)	52.56 (51.58, 53.54)
	0.3	0.3	0.3	0	0	19.35 (18.58, 20.12)	36.87 (35.92, 37.82)	45.34 (44.36, 46.32)	46.00 (45.02, 46.98)
	0.05	0.2	0.05	0.25	0.3	1.73 (1.47, 1.99)	1.84 (1.58, 2.10)	1.20 (0.99, 1.41)	1.21 (1.00, 1.42)
	0.75	0	0.3	0.6	0.1	3.06 (2.72, 3.40)	0.08 (0.02, 0.14)	0.20 (0.11, 0.29)	0.16 (0.08, 0.24)
Less Complete	0	0	0	0	0	4.45 (4.05, 4.85)	4.68 (4.27, 5.09)	4.89 (4.47, 5.31)	4.83 (4.41, 5.25)
	0.3	0.4	0.3	0.2	0.1	29.94 (29.04, 30.84)	17.00 (16.26, 17.74)	37.64 (36.69, 38.59)	38.03 (37.08, 38.98)
	0.3	0.4	0.25	0.15	0	44.20 (43.23, 45.17)	21.62 (20.81, 22.43)	52.79 (51.81, 53.77)	54.78 (53.80, 55.76)
	0.1	0.4	0.1	0.05	0	37.26 (36.31, 38.21)	24.50 (23.66, 25.34)	49.57 (48.59, 50.55)	48.73 (47.75, 49.71)
	0	0.3	0	0	0	22.86 (22.04, 23.68)	17.33 (16.59, 18.07)	32.14 (31.22, 33.06)	30.13 (29.23, 31.03)
	0	0.3	0.3	0	0	30.59 (29.69, 31.49)	24.06 (23.22, 24.90)	44.16 (43.19, 45.13)	42.21 (41.24, 43.18)
	0.3	0.3	0.3	0	0	40.75 (39.79, 41.71)	18.41 (17.65, 19.17)	46.25 (45.27, 47.23)	48.89 (47.91, 49.87)
	0.05	0.2	0.05	0.25	0.3	0.85 (0.67, 1.03)	3.13 (2.79, 3.47)	1.22 (1.00, 1.44)	0.88 (0.70, 1.06)
	0.75	0	0.3	0.6	0.1	2.42 (2.12, 2.72)	0.42 (0.29, 0.55)	0.64 (0.48, 0.80)	1.29 (1.07, 1.51)

Table 30 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 5, k = 4, *peak* = *II*, Exponential Distribution

Completeness	μ1	μ2	μ3	μ4	μ5	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	0	5.37 (4.93, 5.81)	4.77 (4.35, 5.19)	4.95 (4.52, 5.38)	5.05 (4.62, 5.48)
	0.3	0.4	0.3	0.2	0.1	47.03 (46.05, 48.01)	48.48 (47.50, 49.46)	72.07 (71.19, 72.95)	70.30 (69.40, 71.20)
	0.3	0.4	0.25	0.15	0	63.07 (62.12, 64.02)	64.57 (63.63, 65.51)	87.56 (86.91, 88.21)	86.25 (85.58, 86.92)
	0.1	0.4	0.1	0.05	0	52.84 (51.86, 53.82)	70.70 (69.81, 71.59)	86.74 (86.08, 87.40)	84.31 (83.60, 85.02)
	0	0.3	0	0	0	31.36 (30.45, 32.27)	50.51 (49.53, 51.49)	64.16 (63.22, 65.10)	60.37 (59.41, 61.33)
	0	0.3	0.3	0	0	46.15 (45.17, 47.13)	67.33 (66.41, 68.25)	82.25 (81.50, 83.00)	78.21 (77.40, 79.02)
	0.3	0.3	0.3	0	0	58.18 (57.21, 59.15)	50.00 (49.02, 50.98)	79.57 (78.78, 80.36)	79.20 (78.40, 80.00)
	0.05	0.2	0.05	0.25	0.3	0.48 (0.34, 0.62)	1.13 (0.92, 1.34)	0.25 (0.15, 0.35)	0.23 (0.14, 0.32)
	0.75	0	0.3	0.6	0.1	3.23 (2.88, 3.58)	0.07 (0.02, 0.12)	0.15 (0.07, 0.23)	0.27 (0.17, 0.37)
More Complete	0	0	0	0	0	4.73 (4.31, 5.15)	4.92 (4.50, 5.34)	4.96 (4.53, 5.39)	4.87 (4.45, 5.29)
	0.3	0.4	0.3	0.2	0.1	27.91 (27.03, 28.79)	63.43 (62.49, 64.37)	70.80 (69.91, 71.69)	72.01 (71.13, 72.89)
	0.3	0.4	0.25	0.15	0	37.73 (36.79, 38.69)	79.53 (78.74, 80.32)	85.23 (84.53, 85.93)	86.25 (85.58, 86.92)
	0.1	0.4	0.1	0.05	0	30.88 (29.97, 31.79)	85.56 (84.87, 86.25)	86.74 (86.08, 87.40)	88.19 (87.56, 88.82)
	0	0.3	0	0	0	19.02 (18.25, 19.79)	65.63 (64.70, 66.56)	65.87 (64.94, 66.80)	67.75 (66.83, 68.67)
	0	0.3	0.3	0	0	26.43 (25.57, 27.29)	82.55 (81.81, 83.29)	82.57 (81.83, 83.31)	84.03 (83.31, 94.75)
	0.3	0.3	0.3	0	0	36.14 (35.20, 37.08)	64.95 (64.01, 65.89)	76.95 (76.12, 77.78)	77.69 (76.87, 78.51)
	0.05	0.2	0.05	0.25	0.3	0.93 (0.74, 1.12)	0.84 (0.66, 1.02)	0.51 (0.37, 0.65)	0.50 (0.36, 0.64)
	0.75	0	0.3	0.6	0.1	3.21 (2.86, 3.56)	0.03 (0, 0.06)	0.07 (0.02, 0.12)	0.06 (0.01, 0.11)
Less Complete	0	0	0	0	0	4.81 (4.39, 5.23)	4.76 (4.34, 5.18)	4.94 (4.52, 5.36)	4.86 (4.44, 5.28)
	0.3	0.4	0.3	0.2	0.1	56.82 (55.85, 57.79)	30.20 (29.30, 31.10)	68.28 (67.37, 69.19)	69.04 (68.13, 69.95)
	0.3	0.4	0.25	0.15	0	77.38 (76.56, 78.20)	39.85 (38.89, 40.81)	85.74 (85.05, 86.43)	87.32 (86.67, 87.97)
	0.1	0.4	0.1	0.05	0	67.07 (66.15, 67.99)	44.28 (43.31, 45.25)	83.53 (82.80, 84.26)	81.92 (81.17, 82.67)
	0	0.3	0	0	0	40.64 (39.68, 41.60)	28.97 (28.08, 29.86)	58.25 (57.28, 59.22)	55.55 (54.58, 56.52)
	0	0.3	0.3	0	0	57.40 (56.43, 58.37)	42.77 (41.80, 43.74)	76.69 (75.86, 77.52)	73.09 (72.22, 73.96)
	0.3	0.3	0.3	0	0	72.51 (71.63, 73.39)	32.28 (31.36, 33.20)	79.13 (78.33, 79.93)	82.17 (81.42, 82.92)
	0.05	0.2	0.05	0.25	0.3	0.18 (0.10, 0.26)	1.83 (1.57, 2.09)	0.27 (0.17, 0.37)	0.20 (0.11, 0.29)
	0.75	0	0.3	0.6	0.1	2.43 (21.3, 2.73)	0.36 (0.24, 0.48)	0.28 (0.18, 0.38)	0.99 (0.80, 1.18)

Table 31 – Power Comparison with 95% Confidence Intervals; Mixed Design, *t* = 5, *k* = 4, *peak* = *II*, Student's t Distribution (3 d.f.)

Completeness	μ_1	μ_2	μ_3	μ_4	μ_5	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	0	5.43 (4.99, 5.87)	4.70 (4.29, 5.11)	4.79 (4.37, 5.21)	5.05 (4.62, 5.48)
	0.3	0.4	0.3	0.2	0.1	19.29 (18.52, 20.06)	19.87 (19.09, 20.65)	28.69 (27.80, 29.58)	28.36 (27.48, 29.24)
	0.3	0.4	0.25	0.15	0	26.57 (25.70, 27.44)	25.91 (25.05, 26.77)	41.70 (40.73, 42.67)	41.15 (40.19, 42.11)
	0.1	0.4	0.1	0.05	0	23.39 (22.56, 24.22)	30.29 (29.39, 31.19)	41.60 (40.63, 42.57)	39.82 (38.86, 40.78)
	0	0.3	0	0	0	15.93 (15.21, 16.65)	21.94 (21.13, 22.75)	27.30 (26.43, 28.17)	26.25 (25.39, 27.11)
	0	0.3	0.3	0	0	21.66 (20.85, 22.47)	28.69 (27.80, 29.58)	38.27 (37.32, 39.22)	36.08 (35.14, 37.02)
	0.3	0.3	0.3	0	0	26.85 (25.98, 27.72)	21.63 (20.82, 22.44)	37.30 (36.35, 38.25)	37.56 (36.61, 38.51)
	0.05	0.2	0.05	0.25	0.3	1.78 (1.52, 2.04)	2.58 (2.27, 2.89)	1.48 (1.24, 1.72)	1.36 (1.13, 1.59)
	0.75	0	0.3	0.6	0.1	3.69 (3.32, 4.06)	0.32 (0.21, 0.43)	0.70 (0.54, 0.86)	1.04 (0.84, 1.24)
More Complete	0	0	0	0	0	5.01 (4.58, 5.44)	4.57 (4.16, 4.98)	5.04 (4.61, 5.47)	4.87 (4.45, 5.29)
	0.3	0.4	0.3	0.2	0.1	13.39 (12.72, 14.06)	24.87 (24.02, 25.72)	28.39 (27.51, 29.27)	28.85 (27.96, 29.74)
	0.3	0.4	0.25	0.15	0	16.99 (16.25, 17.73)	34.17 (33.24, 35.10)	39.85 (38.89, 40.81)	40.41 (39.45, 41.37)
	0.1	0.4	0.1	0.05	0	14.58 (13.89, 15.27)	40.46 (39.50, 41.42)	41.86 (40.89, 42.83)	43.00 (42.03, 43.97)
	0	0.3	0	0	0	10.81 (10.20, 11.42)	27.66 (26.78, 28.54)	28.00 (27.12, 28.88)	28.85 (27.96, 29.74)
	0	0.3	0.3	0	0	13.07 (12.41, 13.73)	37.84 (36.89, 38.79)	39.25 (38.29, 40.21)	40.47 (39.51, 41.43)
	0.3	0.3	0.3	0	0	16.37 (15.64, 17.10)	27.94 (27.06, 28.82)	34.71 (33.78, 35.64)	35.07 (34.13, 36.01)
	0.05	0.2	0.05	0.25	0.3	2.41 (2.11, 2.71)	2.68 (2.36, 3.00)	2.01 (1.73, 2.29)	1.96 (1.69, 2.23)
	0.75	0	0.3	0.6	0.1	3.51 (3.15, 3.87)	0.16 (0.08, 0.24)	0.44 (0.31, 0.57)	0.41 (0.28, 0.54)
Less Complete	0	0	0	0	0	4.82 (4.40, 5.24)	4.33 (3.93, 4.73)	4.71 (4.29, 5.13)	4.97 (4.54, 5.40)
	0.3	0.4	0.3	0.2	0.1	23.27 (22.44, 24.10)	13.16 (12.50, 13.82)	28.07 (27.19, 28.95)	28.86 (27.97, 29.75)
	0.3	0.4	0.25	0.15	0	33.34 (32.42, 34.26)	17.61 (16.86, 19.36)	40.20 (39.24, 41.16)	41.68 (40.71, 42.65)
	0.1	0.4	0.1	0.05	0	27.90 (27.02, 28.78)	19.59 (18.81, 20.37)	37.88 (36.93, 38.83)	36.95 (36.00, 37.90)
	0	0.3	0	0	0	18.17 (17.41, 18.93)	14.90 (14.20, 15.60)	25.04 (24.19, 25.89)	23.82 (22.99, 24.65)
	0	0.3	0.3	0	0	24.01 (23.17, 24.85)	19.31 (18.54, 20.08)	34.94 (34.01, 35.87)	33.28 (32.36, 34.20)
	0.3	0.3	0.3	0	0	32.61 (31.69, 33.53)	14.83 (14.13, 15.53)	36.39 (35.45, 37.33)	38.59 (37.64, 39.54)
	0.05	0.2	0.05	0.25	0.3	1.22 (1.00, 1.44)	3.47 (3.11, 3.83)	1.45 (1.22, 1.68)	1.30 (1.08, 1.52)
	0.75	0	0.3	0.6	0.1	2.76 (2.44, 3.08)	0.71 (0.55, 0.87)	0.99 (0.80, 1.18)	1.76 (1.50, 2.02)

5.2.5. Results for 5 treatments with 4 treatments per incomplete block and peak at treatment III

Tables 32, 33, and 34 provide the calculated powers and confidence intervals for the powers when respectively using the normal distribution, exponential distribution and Student's t distribution with 3 degrees of freedom.

Table 32 provides the powers and confidence intervals for the powers for the normal distribution. When considering the even ratio of complete to incomplete blocks, Method 1 has higher power than Method 2 when there is a large distinct peak, but the difference is not significant. When more complete blocks are being considered, Method 2 is significantly more powerful than Method 1 when there is a large distinct peak present in the treatment means. When more incomplete blocks are used, Method 1 has higher powers than Method 2 when there is a large peak, but the differences are not significant.

Table 33 gives the powers and confidence intervals for the powers for the exponential distribution. For the even ratio of complete to incomplete blocks, Method 1 is significantly more powerful than Method 2 when the treatment means follow a distinct peak. Otherwise, there is no significant difference between Method 1 and Method 2. When more complete blocks are present in the mixed design, Method 2 is significantly more powerful than Method 1 when there is a distinct peak in the treatment means. In the other scenarios, there is no significant difference. When more incomplete blocks are used, Method 1 has a significantly greater power than Method 2 when a large distinct peak is present. There is no significant difference between Method 1 and Method 2 in the other scenarios.

Table 34 gives the powers and confidence intervals for the powers for the Student's t distribution with 3 degrees of freedom. When an even number of complete and incomplete blocks are used, Method 1 is more powerful than Method 2 but the difference is not significant. When more complete blocks are used, Method 2 has higher power than Method 1, but the difference is also not significant. When more incomplete blocks are used, Method 1 is more powerful than Method 2 when a distinct peak is present, but the difference is insignificant.

For all underlying distributions, Method 1 and Method 2 were significantly more powerful than Hemmer's test or the Kim-Kim test. The only exception is when more complete blocks were used in the mixed design and the treatment means formed a distinct peak. In that scenario, the power of the Kim-Kim test was not significantly different from the power of Method 1.

Table 32 – Power Comparison with 95% Confidence Intervals; Mixed Design, *t* = 5, *k* = 4, *peak* = *III*, Normal Distribution

Completeness	**µ1**	**µ2**	**µ3**	**µ4**	**µ5**	**Hemmer's**	**Kim-Kim**	**Method 1**	**Method 2**
Even	0	0	0	0	0	4.40 (4.00, 4.80)	4.56 (4.15, 4.97)	5.26 (4.82, 5.70)	5.10 (4.67, 5.53)
	0.1	0.2	0.3	0.2	0.1	15.44 (14.73, 16.15)	17.67 (16.92, 18.42)	26.23 (25.37, 27.09)	25.53 (24.68, 26.38)
	0.05	0.25	0.3	0.2	0.15	16.02 (15.30, 16.74)	18.43 (17.67, 19.19)	27.10 (26.23, 27.97)	26.55 (25.68, 27.42)
	0	0.05	0.3	0.05	0	22.38 (21.56, 23.20)	30.49 (29.59, 31.39)	43.13 (42.16, 44.10)	42.00 (41.03, 42.97)
	0	0	0.3	0	0	20.05 (19.27, 20.83)	30.03 (29.13, 30.93)	41.30 (40.33, 42.27)	39.93 (38.97, 40.89)
	0	0	0.3	0.3	0	25.18 (24.33, 26.03)	30.45 (29.55, 31.35)	46.16 (45.18, 47.14)	45.41 (44.42, 46.39)
	0.05	0.2	0.05	0.25	0.3	1.83 (1.57, 2.09)	1.44 (1.21, 1.67)	1.28 (1.06, 1.50)	1.24 (1.02, 1.46)
	0.75	0	0.3	0.6	0.1	1.23 (1.01, 1.45)	1.30 (1.08, 1.52)	0.87 (0.69, 1.05)	0.87 (0.69, 1.05)
More Complete	0	0	0	0	0	3.77 (3.40, 4.14)	5.01 (4.58, 5.44)	4.84 (4.42, 5.26)	4.49 (4.08, 4.90)
	0.1	0.2	0.3	0.2	0.1	11.05 (10.44, 11.66)	24.22 (23.38, 25.06)	25.73 (24.87, 26.59)	26.56 (25.69, 27.43)
	0.05	0.25	0.3	0.2	0.15	10.95 (10.34, 11.56)	23.34 (22.51, 24.17)	25.77 (24.91, 26.63)	26.70 (25.83, 27.57)
	0	0.05	0.3	0.05	0	14.36 (13.67, 15.05)	40.96 (40.00, 41.92)	43.09 (42.12, 44.06)	45.33 (44.35, 46.31)
	0	0	0.3	0	0	13.25 (12.59, 13.91)	41.27 (40.31, 42.23)	41.55 (40.58, 42.52)	43.74 (42.77, 44.71)
	0	0	0.3	0.3	0	16.17 (15.45, 16.89)	40.78 (39.82, 41.74)	44.78 (43.81, 45.75)	46.69 (45.71, 47.67)
	0.05	0.2	0.05	0.25	0.3	2.40 (2.10, 2.70)	1.04 (0.84, 1.24)	1.21 (1.00, 1.42)	1.10 (0.90, 1.30)
	0.75	0	0.3	0.6	0.1	1.65 (1.40, 1.90)	0.98 (0.79, 1.17)	0.95 (0.76, 1.14)	0.76 (0.59, 0.93)
Less Complete	0	0	0	0	0	4.12 (3.73, 4.51)	4.53 (4.12, 4.94)	4.91 (4.49, 5.33)	4.38 (3.98, 4.78)
	0.1	0.2	0.3	0.2	0.1	18.95 (18.18, 19.72)	12.37 (11.72, 13.02)	25.41 (24.56, 26.26)	24.89 (24.04, 25.74)
	0.05	0.25	0.3	0.2	0.15	20.19 (19.40, 20.98)	11.95 (11.31, 12.59)	25.70 (24.84, 26.56)	25.74 (24.88, 26.60)
	0	0.05	0.3	0.05	0	28.53 (27.64, 29.42)	18.97 (18.20, 19.74)	39.48 (38.52, 40.44)	38.25 (37.30, 39.20)
	0	0	0.3	0	0	25.69 (24.83, 26.55)	19.14 (18.37, 19.91)	37.29 (36.34, 38.24)	36.17 (35.23, 37.11)
	0	0	0.3	0.3	0	33.87 (32.94, 34.80)	19.07 (18.30, 19.84)	43.59 (42.62, 44.56)	43.59 (42.62, 44.56)
	0.05	0.2	0.05	0.25	0.3	1.75 (1.49, 2.01)	1.97 (1.70, 2.24)	1.45 (1.22, 1.68)	1.58 (1.34, 1.82)
	0.75	0	0.3	0.6	0.1	0.78 (0.61, 0.95)	1.59 (1.34, 1.84)	0.81 (0.63, 0.99)	0.55 (0.41, 0.69)

Table 33 - Power Comparison with 95% Confidence Intervals; Mixed Design, *t* = 5, *k* = 4, *peak* = *III*, Exponential Distribution

Completeness	μ1	μ2	μ3	μ4	μ5	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	0	4.74 (4.32, 5.16)	4.77 (4.35, 5.19)	4.88 (4.46, 5.30)	4.93 (4.51, 5.35)
	0.1	0.2	0.3	0.2	0.1	27.63 (26.75, 28.51)	35.82 (34.88, 36.76)	52.93 (51.95, 53.91)	51.70 (50.72, 52.68)
	0.05	0.25	0.3	0.2	0.15	29.65 (28.75, 30.55)	33.59 (32.66, 34.52)	52.82 (51.84, 53.80)	51.99 (51.01, 52.97)
	0	0.05	0.3	0.05	0	40.56 (39.60, 41.52)	56.26 (55.29, 57.23)	77.02 (76.20, 77.84)	75.30 (74.45, 76.15)
	0	0	0.3	0	0	36.15 (35.21, 37.09)	56.45 (55.48, 57.42)	73.44 (72.57, 74.31)	71.57 (70.69, 72.45)
	0	0	0.3	0.3	0	45.15 (44.17, 46.13)	55.31 (54.34, 56.28)	77.76 (76.94, 78.58)	76.74 (75.91, 77.57)
	0.05	0.2	0.05	0.25	0.3	1.41 (1.18, 1.64)	0.94 (0.75, 1.13)	0.43 (0.30, 0.56)	0.43 (0.30, 0.56)
	0.75	0	0.3	0.6	0.1	0.56 (0.41, 0.71)	0.86 (0.68, 1.04)	0.28 (0.18, 0.38)	0.25 (0.15, 0.35)
More Complete	0	0	0	0	0	3.95 (3.57, 4.33)	4.63 (4.22, 5.04)	4.66 (4.25, 5.07)	4.48 (4.07, 4.89)
	0.1	0.2	0.3	0.2	0.1	16.96 (16.22, 17.70)	47.30 (46.32, 48.28)	51.90 (50.92, 52.88)	53.92 (52.94, 54.90)
	0.05	0.25	0.3	0.2	0.15	18.40 (17.64, 19.16)	46.98 (46.00, 47.96)	52.71 (51.73, 53.69)	54.36 (53.38, 55.34)
	0	0.05	0.3	0.05	0	23.25 (22.42, 24.08)	74.34 (73.48, 75.20)	76.60 (75.77, 77.43)	79.76 (78.97, 80.55)
	0	0	0.3	0	0	21.60 (20.79, 22.41)	73.13 (72.26, 74.00)	73.72 (72.86, 74.58)	77.55 (76.73, 78.37)
	0	0	0.3	0.3	0	26.32 (25.46, 27.18)	72.71 (71.84, 73.58)	77.50 (76.68, 78.32)	80.09 (79.31, 80.87)
	0.05	0.2	0.05	0.25	0.3	1.71 (1.46, 1.96)	0.65 (0.49, 0.81)	0.54 (0.40, 0.68)	0.43 (0.30, 0.56)
	0.75	0	0.3	0.6	0.1	1.05 (0.85, 1.25)	0.57 (0.42, 0.72)	0.42 (0.29, 0.55)	0.33 (0.22, 0.44)
Less Complete	0	0	0	0	0	4.43 (4.03, 4.83)	4.19 (3.80, 4.58)	4.93 (4.51, 5.35)	4.74 (4.32, 5.16)
	0.1	0.2	0.3	0.2	0.1	37.58 (36.63, 38.53)	20.04 (19.26, 20.82)	48.63 (47.65, 49.61)	48.80 (47.82, 49.78)
	0.05	0.25	0.3	0.2	0.15	40.14 (39.18, 41.10)	19.68 (18.90, 20.46)	48.94 (47.96, 49.92)	50.24 (49.26, 51.22)
	0	0.05	0.3	0.05	0	54.36 (53.38, 55.34)	32.69 (31.77, 33.61)	72.01 (71.13, 72.89)	70.86 (69.97, 71.75)
	0	0	0.3	0	0	47.84 (46.86, 48.82)	30.83 (29.92, 31.74)	67.53 (66.61, 68.45)	65.50 (64.57, 66.43)
	0	0	0.3	0.3	0	59.97 (59.01, 60.93)	31.86 (30.95, 32.77)	73.64 (72.78, 74.50)	74.80 (73.95, 75.65)
	0.05	0.2	0.05	0.25	0.3	1.01 (0.81, 1.21)	1.44 (1.21, 1.67)	0.82 (0.64, 1.00)	0.83 (0.65, 1.01)
	0.75	0	0.3	0.6	0.1	0.44 (0.31, 0.57)	1.28 (1.06, 1.50)	0.51 (0.37, 0.65)	0.36 (0.24, 0.48)

Table 34 – Power Comparison with 95% Confidence Intervals; Mixed Design, $t = 5$, $k = 4$, *peak* = *III*, Student's t Distribution (3 d.f.)

Completeness	μ1	μ2	μ3	μ4	μ5	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	0	4.37 (3.97, 4.77)	4.61 (4.20, 5.02)	4.97 (4.54, 5.40)	4.84 (4.42, 5.26)
	0.1	0.2	0.3	0.2	0.1	12.34 (11.70, 12.98)	14.99 (14.29, 15.69)	21.00 (20.20, 21.80)	20.45 (19.66, 21.24)
	0.05	0.25	0.3	0.2	0.15	13.74 (13.07, 14.41)	15.10 (14.40, 15.80)	21.55 (20.74, 22.36)	21.13 (20.33, 21.93)
	0	0.05	0.3	0.05	0	16.83 (16.10, 17.56)	23.46 (22.63, 24.29)	32.58 (31.66, 33.50)	31.68 (30.77, 32.59)
	0	0	0.3	0	0	15.92 (15.20, 16.64)	23.19 (22.36, 24.02)	30.84 (29.93, 31.75)	29.48 (28.59, 30.37)
	0	0	0.3	0.3	0	19.19 (18.42, 19.96)	22.91 (22.09, 23.73)	33.69 (32.76, 34.62)	32.85 (31.93, 33.77)
	0.05	0.2	0.05	0.25	0.3	2.36 (2.06, 2.66)	1.91 (1.64, 2.18)	1.77 (1.51, 2.03)	1.73 (1.47, 1.99)
	0.75	0	0.3	0.6	0.1	1.41 (1.18, 1.64)	1.66 (1.41, 1.91)	0.97 (0.78, 1.16)	0.85 (0.67, 1.03)
More Complete	0	0	0	0	0	4.24 (3.85, 4.63)	5.15 (4.72, 5.58)	4.67 (4.26, 5.08)	4.71 (4.29, 5.13)
	0.1	0.2	0.3	0.2	0.1	8.75 (8.20, 9.30)	19.43 (18.65, 20.21)	20.00 (19.22, 20.78)	20.81 (20.01, 21.61)
	0.05	0.25	0.3	0.2	0.15	9.45 (8.88, 10.02)	18.56 (17.80, 19.32)	19.67 (18.89, 20.45)	20.28 (19.49, 21.07)
	0	0.05	0.3	0.05	0	11.30 (10.68, 11.92)	30.84 (29.93, 31.75)	32.20 (31.28, 33.12)	33.68 (32.75, 34.61)
	0	0	0.3	0	0	11.25 (10.63, 11.87)	31.47 (30.56, 32.38)	32.10 (31.18, 33.02)	33.87 (32.94, 34.80)
	0	0	0.3	0.3	0	12.52 (11.87, 13.17)	30.82 (29.91, 31.73)	33.10 (32.18, 34.02)	34.84 (33.91, 35.77)
	0.05	0.2	0.05	0.25	0.3	2.91 (2.58, 3.24)	1.90 (1.63, 2.17)	1.59 (1.34, 1.84)	1.47 (1.23, 1.71)
	0.75	0	0.3	0.6	0.1	2.02 (1.74, 2.30)	1.34 (1.11, 1.57)	1.26 (1.04, 1.48)	1.15 (0.94, 1.36)
Less Complete	0	0	0	0	0	4.08 (3.69, 4.47)	4.38 (3.98, 4.78)	4.94 (4.52, 5.36)	4.75 (4.33, 5.17)
	0.1	0.2	0.3	0.2	0.1	15.25 (14.55, 15.95)	10.23 (9.64, 10.82)	19.28 (18.51, 20.05)	19.08 (18.31, 19.85)
	0.05	0.25	0.3	0.2	0.15	15.28 (14.57, 15.99)	10.03 (9.44, 10.62)	19.38 (18.61, 20.15)	19.45 (18.67, 20.23)
	0	0.05	0.3	0.05	0	22.01 (21.20, 22.82)	14.74 (14.05, 15.43)	29.98 (29.08, 30.88)	29.84 (28.94, 30.74)
	0	0	0.3	0	0	19.98 (19.20, 20.76)	14.85 (14.15, 15.55)	28.50 (27.62, 29.38)	27.30 (26.43, 28.17)
	0	0	0.3	0.3	0	24.58 (23.74, 25.42)	14.63 (13.94, 15.32)	32.43 (31.51, 33.35)	32.14 (31.22, 33.06)
	0.05	0.2	0.05	0.25	0.3	2.04 (1.76, 2.32)	2.28 (1.99, 2.57)	1.83 (1.57, 2.09)	1.76 (1.50, 2.02)
	0.75	0	0.3	0.6	0.1	1.30 (1.08, 1.52)	2.21 (1.92, 2.50)	1.32 (1.10, 1.54)	1.27 (1.05, 1.49)

5.2.6. Results for 5 treatments with 4 treatments per incomplete block and peak at treatment IV

Tables 35, 36, and 37 provide the calculated powers and confidence intervals for the powers when respectively using the normal distribution, exponential distribution and Student's t distribution with 3 degrees of freedom.

Table 35 provides the calculated powers and confidence intervals for the powers when using the normal distribution. When an even ratio of complete to incomplete blocks was used in the mixed design, Method 1 was significantly more powerful than Method 2 when a large distinct peak was present in the treatment means. When more complete blocks were used, Method 2 had higher powers than Method 1 for all of the treatment mean scenarios but the differences were not significant. When more incomplete blocks were used, Method 1 had higher powers than Method 2 when a distinct peak was present, but the differences were not significant. For the other treatment mean scenarios, Method 2 was at least as powerful as Method 1.

Table 36 gives the powers and confidence intervals for the powers when using the exponential distribution. When an equal number of complete and incomplete blocks were considered, Method 1 was significantly more powerful than Method 2 when there was a large distinct peak in the treatment means. When more complete blocks were used in the mixed design, Method 2 had higher power than Method 1 across the treatment mean scenarios but the differences were not significant. When more incomplete blocks were used, Method 1 was significantly more powerful than Method 2 when a large distinct peak was present, while Method 2 had significantly higher power than Method 1 for the other treatment mean scenarios.

Table 37 gives the powers and confidence intervals for the powers for the Student's t distribution with 3 degrees of freedom. When an even number of complete and incomplete blocks were used, Method 1 had slightly higher powers than Method 2 when a distinct peak was present but the difference was not significant. When more complete blocks were considered, Method 2 had higher power than Method 1 across all treatment mean scenarios but no difference was significant. When more incomplete blocks were used, and when a large distinct peak was present, Method 1 had higher power than Method 2, but the differences were not significant. For the other treatment mean scenarios in the less complete mixed design, Method 2 was significantly more powerful than Method 1.

For all three distributions, Method 1 and Method 2 were significantly more powerful than Hemmer's test or the Kim-Kim test. The only exception is when more complete blocks were present in the mixed design and when a large distinct peak was present in the treatment means. In this scenario, the power of the Kim-Kim test is not significantly different than the power of Method 1.

Table 35 – Power Comparison with 95% Confidence Intervals; Mixed Design, *t* = 5, *k* = 4, *peak* = *IV*, Normal Distribution

Completeness	μ1	μ2	μ3	μ4	μ5	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	0	5.78 (5.32, 6.24)	4.83 (4.41, 5.25)	5.18 (4.75, 5.61)	5.39 (4.95, 5.83)
	0.1	0.2	0.3	0.4	0.3	24.71 (23.86, 25.56)	24.25 (23.41, 25.09)	38.18 (37.23, 39.13)	37.80 (36.85, 38.75)
	0	0.15	0.25	0.4	0.3	34.88 (33.95, 35.81)	34.18 (33.25, 35.11)	53.44 (52.46, 54.42)	52.74 (51.76, 53.72)
	0	0.05	0.1	0.4	0.1	30.72 (29.82, 31.62)	39.08 (38.12, 40.04)	54.00 (53.02, 54.98)	51.51 (50.53, 52.49)
	0	0	0	0.3	0	19.57 (18.79, 20.35)	26.94 (26.07, 27.81)	35.43 (34.49, 36.37)	33.93 (33.00, 34.86)
	0	0	0	0.3	0.3	27.17 (26.30, 28.04)	19.33 (18.56, 20.10)	34.72 (33.79, 35.65)	35.29 (34.35, 36.23)
	0	0	0.3	0.3	0.3	33.75 (32.82, 34.68)	28.19 (27.31, 29.07)	48.50 (47.52, 49.48)	48.96 (47.98, 49.94)
	0.05	0.2	0.05	0.25	0.3	14.00 (13.32, 14.68)	9.53 (8.95, 10.11)	15.03 (14.33, 15.73)	15.97 (15.25, 16.69)
	0.75	0	0.3	0.6	0.1	2.23 (1.94, 2.52)	8.22 (7.68, 8.76)	4.15 (3.76, 4.54)	3.58 (3.22, 3.94)
More Complete	0	0	0	0	0	4.72 (4.30, 5.14)	4.83 (4.41, 5.25)	5.06 (4.63, 5.49)	4.88 (4.46, 5.30)
	0.1	0.2	0.3	0.4	0.3	15.47 (14.76, 16.18)	32.68 (31.76, 33.60)	37.30 (36.35, 38.25)	38.08 (37.13, 39.03)
	0	0.15	0.25	0.4	0.3	21.49 (20.68, 22.30)	45.96 (44.98, 46.94)	52.42 (51.44, 53.40)	53.12 (52.14, 54.10)
	0	0.05	0.1	0.4	0.1	18.60 (17.84, 19.36)	52.09 (51.11, 53.07)	54.02 (53.04, 55.00)	55.73 (54.76, 56.70)
	0	0	0	0.3	0	12.47 (11.82, 13.12)	36.38 (35.44, 37.32)	36.77 (35.82, 37.72)	37.65 (36.70, 38.60)
	0	0	0	0.3	0.3	16.74 (16.01, 17.47)	24.99 (24.14, 25.84)	32.68 (31.76, 33.60)	32.91 (31.99, 33.83)
	0	0	0.3	0.3	0.3	20.91 (20.11, 21.71)	37.12 (36.17, 38.07)	45.51 (44.53, 46.49)	46.01 (45.03, 46.99)
	0.05	0.2	0.05	0.25	0.3	9.78 (9.20, 10.36)	10.91 (10.30, 11.52)	14.10 (13.42, 14.78)	13.87 (13.19, 14.55)
	0.75	0	0.3	0.6	0.1	2.46 (2.16, 2.76)	10.00 (9.41, 10.59)	6.00 (5.53, 6.47)	6.37 (5.89, 6.85)
Less Complete	0	0	0	0	0	4.43 (4.03, 4.83)	5.21 (4.77, 5.65)	4.95 (4.52, 5.38)	5.08 (4.65, 5.51)
	0.1	0.2	0.3	0.4	0.3	30.41 (29.51, 31.31)	16.54 (15.81, 17.27)	37.26 (36.31, 38.21)	38.21 (37.26, 39.16)
	0	0.15	0.25	0.4	0.3	45.38 (44.40, 46.36)	22.36 (21.54, 23.18)	53.46 (52.48, 54.44)	55.21 (54.24, 56.18)
	0	0.05	0.1	0.4	0.1	37.99 (37.04, 38.94)	24.29 (23.45, 25.13)	50.08 (49.10, 51.06)	49.70 (48.72, 50.68)
	0	0	0	0.3	0	22.70 (21.88, 23.52)	18.49 (17.73, 19.25)	32.58 (31.66, 33.50)	30.84 (29.93, 31.75)
	0	0	0	0.3	0.3	21.79 (30.88, 32.70)	13.67 (13.00, 14.34)	34.22 (33.29, 35.15)	37.12 (36.17, 38.07)
	0	0	0.3	0.3	0.3	41.29 (40.32, 42.26)	17.97 (17.22, 18.72)	46.18 (45.20, 47.16)	49.93 (48.95, 50.91)
	0.05	0.2	0.05	0.25	0.3	15.57 (14.86, 16.28)	7.74 (7.22, 8.26)	14.98 (14.28, 15.68)	17.12 (16.38, 17.86)
	0.75	0	0.3	0.6	0.1	1.52 (1.28, 1.76)	6.60 (6.11, 7.09)	3.32 (2.97, 3.67)	2.18 (1.89, 2.47)

Table 36 – Power Comparison with 95% Confidence Intervals; Mixed Design, *t* = 5, *k* = 4, *peak* = *IV*, Exponential Distribution

Completeness	μ1	μ2	μ3	μ4	μ5	Hemmer's	Kim-Kim	Method 1	Method 2
Even	0	0	0	0	0	5.05 (4.62, 5.48)	4.69 (4.28, 5.10)	4.67 (4.26, 5.08)	4.78 (4.36, 5.20)
	0.1	0.2	0.3	0.4	0.3	46.93 (45.95, 47.91)	48.45 (47.47, 49.43)	71.30 (70.41, 72.19)	70.24 (69.34, 71.14)
	0	0.15	0.25	0.4	0.3	63.84 (62.90, 64.78)	64.15 (63.21, 65.09)	87.99 (87.35, 88.63)	87.01 (86.35, 87.67)
	0	0.05	0.1	0.4	0.1	54.02 (53.04, 55.00)	70.37 (69.48, 71.26)	86.52 (85.85, 87.19)	83.74 (83.02, 84.46)
	0	0	0	0.3	0	32.92 (32.00, 33.84)	50.57 (49.59, 51.55)	64.63 (63.69, 65.57)	61.24 (60.29, 62.19)
	0	0	0	0.3	0.3	45.34 (44.36, 46.32)	32.45 (31.53, 33.37)	61.61 (60.66, 62.56)	62.01 (61.06, 62.96)
	0	0	0.3	0.3	0.3	59.89 (58.93, 60.85)	50.76 (49.78, 51.74)	80.12 (79.34, 80.90)	80.00 (79.22, 80.78)
	0.05	0.2	0.05	0.25	0.3	22.15 (21.34, 22.96)	13.76 (13.08, 14.44)	26.60 (25.73, 27.47)	27.33 (26.46, 28.20)
	0.75	0	0.3	0.6	0.1	0.69 (0.53, 0.85)	7.52 (7.00, 8.04)	2.42 (2.12, 2.72)	1.88 (1.61, 2.15)
More Complete	0	0	0	0	0	5.17 (4.74, 5.60)	4.94 (4.52, 5.36)	5.09 (4.66, 5.52)	4.96 (4.53, 5.39)
	0.1	0.2	0.3	0.4	0.3	27.30 (26.43, 28.17)	63.48 (62.54, 64.42)	70.09 (69.19, 70.99)	71.27 (70.38, 72.16)
	0	0.15	0.25	0.4	0.3	39.38 (38.42, 40.34)	79.07 (78.27, 79.87)	85.72 (85.03, 86.41)	86.89 (86.23, 87.55)
	0	0.05	0.1	0.4	0.1	32.19 (31.27, 33.11)	85.23 (84.53, 85.93)	87.11 (86.45, 87.77)	88.35 (87.72, 88.98)
	0	0	0	0.3	0	19.85 (19.07, 20.63)	66.07 (65.14, 67.00)	66.41 (65.48, 67.34)	68.21 (67.30, 69.12)
	0	0	0	0.3	0.3	27.55 (26.67, 28.43)	44.03 (43.06, 45.00)	57.56 (56.59, 58.53)	58.14 (57.17, 59.11)
	0	0	0.3	0.3	0.3	35.49 (34.55, 36.43)	65.38 (64.45, 66.31)	76.36 (75.53, 77.19)	77.21 (76.39, 78.03)
	0.05	0.2	0.05	0.25	0.3	14.71 (14.02, 15.40)	16.74 (16.01, 17.47)	23.68 (22.85, 24.51)	23.51 (22.68, 24.34)
	0.75	0	0.3	0.6	0.1	0.99 (0.80, 1.18)	10.76 (10.15, 11.37)	4.41 (4.01, 4.81)	5.03 (4.60, 5.46)
Less Complete	0	0	0	0	0	4.87 (4.45, 5.29)	5.18 (4.75, 5.61)	5.37 (4.93, 5.81)	5.48 (5.03, 5.93)
	0.1	0.2	0.3	0.4	0.3	57.09 (56.12, 58.06)	29.57 (28.68, 30.46)	68.48 (67.57, 69.39)	68.68 (67.77, 69.59)
	0	0.15	0.25	0.4	0.3	77.05 (76.23, 77.87)	39.87 (38.91, 40.83)	86.04 (85.36, 86.72)	86.93 (86.27, 87.59)
	0	0.05	0.1	0.4	0.1	67.00 (66.08, 67.92)	44.26 (43.29, 45.23)	83.21 (82.48, 83.94)	81.13 (80.36, 81.90)
	0	0	0	0.3	0	40.23 (39.27, 41.19)	30.04 (29.14, 30.94)	58.33 (57.36, 59.30)	55.28 (54.31, 56.25)
	0	0	0	0.3	0.3	57.95 (56.98, 58.92)	19.60 (18.82, 20.38)	61.92 (60.97, 62.87)	66.44 (65.51, 67.37)
	0	0	0.3	0.3	0.3	72.37 (71.49, 73.25)	31.24 (30.33, 32.15)	79.06 (78.26, 79.86)	81.66 (80.90, 82.42)
	0.05	0.2	0.05	0.25	0.3	26.22 (25.36, 27.08)	10.25 (9.66, 10.84)	26.69 (25.82, 27.56)	30.22 (29.32, 31.12)
	0.75	0	0.3	0.6	0.1	0.48 (0.34, 0.62)	5.41 (4.97, 5.85)	1.50 (1.26, 1.74)	0.80 (0.63, 0.97)

Table 37 – Power Comparison with 95% Confidence Intervals; Mixed Design, t = 5, k = 4, *peak* = *IV*, Student's t Distribution (3 d.f.)

Completeness	**μ1**	**μ2**	**μ3**	**μ4**	**μ5**	**Hemmer's**	**Kim-Kim**	**Method 1**	**Method 2**
Even	0	0	0	0	0	5.30 (4.86, 5.74)	4.98 (4.55, 5.41)	5.00 (4.57, 5.43)	5.17 (4.74, 5.60)
	0.1	0.2	0.3	0.4	0.3	19.93 (19.15, 20.71)	19.51 (18.73, 20.29)	29.32 (28.43, 30.21)	29.30 (28.41, 30.19)
	0	0.15	0.25	0.4	0.3	28.07 (27.19, 28.95)	26.49 (25.63, 27.35)	42.28 (41.31, 43.25)	41.58 (40.61, 42.55)
	0	0.05	0.1	0.4	0.1	24.10 (23.26, 24.94)	29.89 (28.99, 30.79)	41.51 (40.54, 42.48)	40.13 (39.17, 41.09)
	0	0	0	0.3	0	16.05 (15.33, 16.77)	22.12 (21.31, 22.93)	28.25 (27.37, 29.13)	26.76 (25.89, 27.63)
	0	0	0	0.3	0.3	20.83 (20.03, 21.63)	15.58 (14.87, 16.29)	26.56 (25.69, 27.43)	27.17 (26.30, 28.04)
	0	0	0.3	0.3	0.3	25.89 (25.02, 26.75)	21.91 (21.10, 22.72)	36.33 (35.39, 37.27)	36.22 (35.28, 37.16)
	0.05	0.2	0.05	0.25	0.3	11.59 (10.96, 12.22)	8.74 (8.19, 9.29)	12.47 (11.82, 13.12)	12.98 (12.32, 13.64)
	0.75	0	0.3	0.6	0.1	2.74 (2.42, 3.06)	7.66 (7.14, 8.18)	4.33 (3.93, 4.73)	3.99 (3.61, 4.37)
More Complete	0	0	0	0	0	4.53 (4.12, 4.94)	4.75 (4.33, 5.17)	4.73 (4.31, 5.15)	4.72 (4.30, 5.14)
	0.1	0.2	0.3	0.4	0.3	12.58 (11.93, 13.23)	25.76 (24.90, 26.62)	29.11 (28.22, 30.00)	29.71 (28.81, 30.61)
	0	0.15	0.25	0.4	0.3	16.99 (16.25, 17.73)	34.07 (33.14, 35.00)	40.31 (39.35, 41.27)	40.81 (39.85, 41.77)
	0	0.05	0.1	0.4	0.1	14.18 (13.50, 14.86)	39.11 (38.15, 40.07)	41.84 (40.87, 42.81)	43.12 (42.15, 44.09)
	0	0	0	0.3	0	10.97 (10.36, 11.58)	28.70 (27.81, 29.59)	28.47 (27.59, 29.35)	29.49 (28.60, 30.38)
	0	0	0	0.3	0.3	12.73 (12.08, 13.38)	19.14 (18.37, 19.91)	24.47 (23.63, 25.31)	24.54 (23.70, 25.38)
	0	0	0.3	0.3	0.3	15.90 (15.18, 16.62)	27.74 (26.86, 28.62)	34.53 (33.60, 35.46)	34.80 (33.87, 35.73)
	0.05	0.2	0.05	0.25	0.3	8.35 (7.81, 8.89)	9.59 (9.01, 10.17)	11.83 (11.20, 12.46)	11.47 (10.85, 12.09)
	0.75	0	0.3	0.6	0.1	2.71 (2.39, 3.03)	8.51 (7.96, 9.06)	5.05 (4.62, 5.48)	5.24 (4.80, 5.68)
Less Complete	0	0	0	0	0	4.93 (4.51, 5.35)	4.43 (4.03, 4.83)	4.98 (4.55, 5.41)	5.03 (4.60, 5.46)
	0.1	0.2	0.3	0.4	0.3	23.42 (22.59, 24.25)	14.13 (13.45, 14.81)	28.08 (27.20, 28.96)	28.90 (28.01, 29.79)
	0	0.15	0.25	0.4	0.3	34.04 (33.11, 34.97)	17.53 (16.78, 18.28)	40.10 (39.14, 41.06)	41.72 (40.75, 42.69)
	0	0.05	0.1	0.4	0.1	27.54 (26.66, 28.42)	19.07 (18.30, 19.84)	38.13 (37.18, 39.08)	36.52 (35.58, 37.46)
	0	0	0	0.3	0	18.28 (17.52, 19.04)	14.67 (13.98, 15.36)	25.18 (24.33, 26.03)	24.15 (23.31, 24.99)
	0	0	0	0.3	0.3	24.57 (23.73, 25.41)	11.83 (11.20, 12.46)	26.99 (26.12, 27.86)	28.98 (28.09, 29.87)
	0	0	0.3	0.3	0.3	31.93 (31.02, 32.84)	14.36 (13.67, 15.05)	35.79 (34.85, 36.73)	37.84 (36.89, 38.79)
	0.05	0.2	0.05	0.25	0.3	12.27 (11.63, 12.91)	7.22 (6.71, 7.73)	12.85 (12.19, 13.51)	13.78 (13.10, 14.46)
	0.75	0	0.3	0.6	0.1	2.10 (1.82, 2.38)	6.70 (6.21, 7.19)	4.00 (3.62, 4.38)	2.88 (2.55, 3.21)

CHAPTER 6. CONCLUSION

After conducting the simulation studies, the underlying distributions have no significant effect on determining whether Hemmer's or Durbin's tests were more powerful in the BIBD case. When the treatment means followed the umbrella alternative, Hemmer's test was more powerful than Durbin's test. When there was an adjacent treatment mean that was equal to the peak treatment mean, Durbin's test had higher estimated power when the experiment consisted of 3 or 4 treatments. When there were 5 treatments, Hemmer's test remained more powerful. This shows that when there are a small number of treatments in the experiment, Hemmer's test is sensitive to equivalent treatment effects near the peak treatment.

Underlying distributions also had no significant impact in the RCBD/BIBD mixed design. When an even ratio of complete to incomplete blocks was used, Method 1 tended to be a better test than Method 2. When there were more complete blocks used in the mixed design, Method 2 was significantly superior in most scenarios. When more incomplete blocks were present, Method 2 tended to be the better test in most scenarios. Overall, it is recommended to use Method 2 to test for the umbrella alternative with a known peak in the RCBD/BIBD mixed design.

When there were more complete blocks used relative to incomplete blocks in the mixed design, the Kim-Kim test had significantly higher power than Hemmer's test, and sometimes comparable with Method 1. When more incomplete blocks were incorporated, Hemmer's test had higher estimated power than the Kim-Kim test, but significantly lower than Method 1 and Method 2. The most likely explanation for this result is that Hemmer's test is calculated from incomplete blocks, which contain less data, which results in lower levels of power.

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APPENDIX I. DERIVING EXPECTED VALUES AND VARIANCES FOR HEMMER'S TEST

Consider the case when there are 4 treatments, with 3 treatments appearing within each incomplete block, and a known peak at Treatment II. We can calculate that $\binom{4}{3}$ blocks will be required to complete one repetition of the Balanced Incomplete Block Design, with the requirement that each treatment must appear in 3 different blocks and each unique pair of treatments appears two different times. The incidence matrix of this BIBD is as follows:

Table A.1 – Incidence Matrix for BIBD; *t*=4, *k*=3, *peak*=II.

		TREATMENTS			
		I	**II**	**III**	**IV**
BLOCKS	**1**	x	x	x	
	2	x	x		x
	3	x		x	x
	4		x	x	x

Referring to formula ***(1)***, we can calculate the test statistic for Hemmer's test for this scenario to be

$$T = \sum_{j=1}^{4} \left\{ \sum_{i=I}^{IV} (4 - 1 - |2 - i|) * R_i \right\}$$

$$= \sum_{j=1}^{4} \{\mathbf{2} * R_I + \mathbf{3} * R_{II} + \mathbf{2} * R_{III} + R_{IV}\}$$

We need to calculate the expected value and variance of *T* at each of the 4 incomplete blocks separately, because each block contains a unique combination of 3 of the 4 possible treatments. The respective sums of these 4 expected values and 4 variances will provide the expected value and variance for Hemmer's test statistic *T* for one repetition of the BIBD case.

First, we must consider all of the possible ways that the 3 observations within each incomplete block can be ranked. Next, we must calculate the values of *T* for each combination of ranks for a specific incomplete block. Consider Block 1, where Treatments I, II, and III are present in the incomplete block. All possible values of *T* for Block 1 are as follows.

Table A.2 – Possible Values for *T* for Block 1; *t*=4, *k*=3, *peak*=II.

Combination	I	II	III	***, Block 1***
1	1	2	3	= **2**(1) + **3**(2) + **2**(3) = 14
2	1	3	2	= **2**(1) + **3**(3) + **2**(2) = 15
3	2	1	3	= **2**(2) + **3**(1) + **2**(3) = 13
4	2	3	1	= **2**(2) + **3**(3) + **2**(1) = 15
5	3	1	2	= **2**(3) + **3**(1) + **2**(2) = 13
6	3	2	1	= **2**(3) + **3**(2) + **2**(1) = 14

With this population of *T* values for Block 1, we can calculate the expected value and the variance of *T*, specifically for Block 1.

$$E(T, Block\ 1) = \sum_{r=1}^{k!} \frac{(T_r, Block\ 1)}{k!}$$

$$V(T, Block\ 1) = \sum_{r=1}^{k!} \frac{\{(T_r, Block\ 1) - E(T, Block\ 1)\}^2}{k!}$$

where

k = the number of treatments per incomplete block

T_r = the value of Hemmer's test statistic for the *r*th combination of ranked values.

Or written generically for any incomplete block,

$$E(T, Block\ i) = \sum_{r=1}^{k!} \frac{T_r, Block\ i}{k!}$$

$$V(T, Block\ i) = \sum_{r=1}^{k!} \frac{\{(T_r, Block\ i) - E(T, Block\ i)\}^2}{k!}$$

The expected values and variances for all 4 incomplete blocks are as follows.

Table A.3 - Expected Values and Variances of *T*, by Block; *t*=4, *k*=3, *peak*=II.

		I	**II**	**III**	**IV**		
BLOCKS	**1**	x	x	x		14	2/3
	2	x	x		x	12	2
	3	x		x	x	10	2/3
	4		x	x	x	12	2

Recall that the sums of the expected values and variances of each complete block will provide the expected value and variance, respectively, of Hemmer's test statistic for one complete repetition of the BIBD. They are given by

. $E(T) = \sum_{j=1}^{b} E(T, Block\ j) = 48$ $\qquad$ $V(T) = \sum_{j=1}^{b} V(T, Block\ j) = 16/3.$

Therefore, in the case where there are 4 treatments, with 3 treatments per incomplete block and a known peak at treatment II, the standardized test statistic of Hemmer's test is as follows

$$Z_T = \frac{T - E(T)}{\sqrt{V(T)}} = \frac{T - 48}{\sqrt{16/3}}.$$

Z_T follows a standard normal distribution and Ho will be rejected when $Z_T > Z_\alpha$.

Another case to consider is when there are 5 treatments, with 2 treatments appearing per incomplete block and a known peak at treatment III. We can calculate that it will take $\binom{5}{2}$ or 10 blocks to complete one repetition of a BIBD, with the requirement that each treatment must appear in 4 different blocks and each unique pair of treatments appears one time.

Table A.4 – Incidence Matrix for BIBD; *t*=5, *k*=2, *peak*=III.

		TREATMENTS				
		I	**II**	**III**	**IV**	**V**
BLOCKS	**1**	x	x			
	2	x		x		
	3	x			x	
	4	x				x
	5		x	x		
	6		x		x	
	7		x			x
	8			x	x	
	9			x		x
	10				x	x

Referring to formula ***(1)***, we can determine the formula for Hemmer's test statistic for this specific BIBD case as

$$T = \sum_{j=1}^{5} \left\{ \sum_{i=I}^{V} (5 - 1 - |3 - i|) * R_i \right\}$$

$$= \sum_{j=1}^{5} \{R_I + \mathbf{2} * R_{II} + \mathbf{3} * R_{III} + \mathbf{2} * R_{IV} + R_V\}.$$

We need to calculate the expected value and variance of *T* at each of the 10 incomplete blocks separately, because each block contains a unique combination of 2 of the 5 possible treatments. The respective sums of these 10 expected values and 10 variances will provide the expected value and variance for Hemmer's test statistic *T* for one repetition of the BIBD.

After considering all possible ways to arrange the ranked values between the two treatments within an incomplete block, the values of *T* will be calculated at each combination. Consider Block 1, where Treatments I and II are present in the incomplete block. All possible values of *T* for Block 1 are as follows.

Table A.5 – Possible Values for *T* for Block 1; *t*=5, *k*=2, *peak*=III.

Combination	I	II	***, Block 1***
1	1	2	= **1**(1) + **2**(2) = 5
2	2	1	= **1**(2) + **2**(1) = 4

The expected value for a single block can be found by

$$E(T, Block\ i) = \sum_{r=1}^{k!} \frac{T_r, Block\ i}{k!},$$

and the variance for a single block is given by

$$V(T, Block\ i) = \sum_{r=1}^{k!} \frac{\{(T_r, Block\ i) - E(T, Block\ i)\}^2}{k!}.$$

The following table provides the expected values and variances for each of the 10 blocks required to complete one repetition of the BIBD.

Table A.6 – Expected Values and Variances of *T*, Block *i*; *t*=5, *k*=4, *peak*=III.

		I	II	III	IV	V		
	1	x	x				4.5	0.25
	2	x		x			6	1
	3	x			x		4.5	0.25
	4	x				x	3	0
BLOCKS	**5**		x	x			7.5	0.25
	6		x		x		6	0
	7		x			x	4.5	0.25
	8			x	x		7.5	0.25
	9			x		x	6	1
	10				x	x	4.5	0.25

Therefore, the expected value and variance of the test statistic in Hemmer's test for one repetition of the BIBD is

$$E(T) = \sum_{j=1}^{b} E(T, Block\ j) = 54 \qquad V(T) = \sum_{j=1}^{b} V(T, Block\ j) = 3.5.$$

Furthermore, in the case where there are 5 treatments, with 2 treatments per incomplete block and a known peak at treatment III, then the standardized test statistic of Hemmer's test is as follows

$$Z_T = \frac{T - E(T)}{\sqrt{V(T)}} = \frac{T-54}{\sqrt{3.5}}.$$

APPENDIX II. SAS CODE FOR BIBD FOR 3 TREATMENTS WITH 2 TREATMENTS PER INCOMPLETE BLOCK

```
*********************************************************************************
The following SAS code generates data from 4 treatments, with 3 treatments appearing within
each incomplete block.  The number of simulations, the number of incomplete block cycles, the
underlying distribution and its associated parameters are passed in as macro parameters.  The
powers of Hemmer's test and Durbin's test and the corresponding confidence intervals were
calculated with a significance level of 5%.
*********************************************************************************;
%macro bibd3(nsim, nrep, dist, mu1, mu2, mu3, sigma);
%let t = 3;
%let k = 2;
%let r = 2;
%let peak = II;
data raw (keep=sim rep block y1-y&t Mu_T Var_T);
	array seed{&t} seed1 - seed&t;
	do i = 1 to &t;
		seed{i} = int(ranuni(0)*1e6);
	end;
		Mu_T = 12*&nrep;	Var_T = 0.5*&nrep;
	put seed1 - seed&t;
	do sim = 1 to &nsim;
	do rep = 1 to &nrep;
	do block = 1 to &t;
	if &dist = 'Normal' then do;
		call rannor(seed1, y1);
			y1 = &mu1 + &sigma*y1;
		call rannor(seed2,y2);
			y2 = &mu2 + &sigma*y2;
		call rannor(seed3,y3);
			y3 = &mu3 + &sigma*y3;
	end;
	else if &dist = 'Exp' then do;
		call ranexp(seed1, y1);
			y1 = &mu1 + y1;
		call ranexp (seed2,y2);
```

```
                    y2 = &mu2 + y2;
          call ranexp (seed3,y3);
                    y3 = &mu3 + y3;
     end;
     else if &dist = 'T' then do;
          call ranuni(seed1, y1);
                    y1 = tinv(y1, 3);
                    y1 = &mu1 + &sigma*y1;
          call ranuni (seed2,y2);
                    y2 = tinv(y2, 3);
                    y2 = &mu2 + &sigma*y2;
          call ranuni (seed3,y3);
                    y3 = tinv(y3, 3);
                    y3 = &mu3 + &sigma*y3;
     end;
          if block = 1 then y1=.;
          else if block = 2 then y2=.;
          else if block = 3 then y3=.;
          output; end; end; end;
run;
data test;
     set raw;
     by sim rep;
     array data{&t} y1 - y&t;
     array trt_value{2} A B;
     array trt_number{2} Ai Bi;
     array rank{&t} rank1 - rank&t;
     array sumrank{&t} sumrank1 - sumrank&t;
     array sumranksq{&t} sumranksq1 - sumranksq&t;
     ctr = 0;
     do i = 1 to &t;
     if data{i} > . then do;
          ctr + 1;
          trt_value{ctr} = data{i};
          trt_number{ctr} = i;
          end;
     end;
if A < B then do; rank{Ai} = 1; rank{Bi} = 2; end;
else if A > B then do; rank{Ai} = 2; rank{Bi} = 1; end;
     do i = 1 to &t;
          if first.sim then sumrank{i} = 0;
          sumrank{i} + rank{i};
          if last.sim then sumranksq{i} = sumrank{i}**2;
```

```
        end;
        if last.sim then do;
                S = sum(sumranksq1, sumranksq2, sumranksq3);
                durbin = (12 * (&t - 1) * S/(&r * &nrep * &t * (&k-1)*(&k+1)) )
        - (3 * &r * &nrep * (&t-1)*(&k+1)) / (&k-1);
                if durbin > 5.99 then power_durbin = 1;
                        else power_durbin = 0;
        output; end;
        do j=1 to (&t-1);
                if trt_number{j}=2 then do; rank2 = rank2*2; end;
        end;
T = sum(rank1, rank2, rank3);
if first.sim then sumT = 0;
sumT+T;
if last.sim then do;
        Z_T = (sumT - Mu_T) / sqrt(Var_T);
        if Z_T > 1.645 then power_Hemmer = 1;
                else power_Hemmer = 0;
        output; end;
run;
proc means data=test noprint;
        var power_Hemmer power_durbin;
        output out=power sum= ;
run;
data power;
        set power;
        pH = sum(power_Hemmer) / &nsim;
                pH_CIupper = round(100 * (pH + 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
                pH_CIlower = round(100 * (pH - 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
        pD = sum(power_durbin) / (2*&nsim);
                pD_CIupper = round(100 * (pD + 1.96*sqrt(pD * (1-pD) / &nsim)), 0.01);
                pD_CIlower = round(100 * (pD - 1.96*sqrt(pD * (1-pD) / &nsim)), 0.01);
run;
proc print data=power;
        var pH pH_CIlower pH_CIupper pD pD_CIlower pD_CIupper;
        title2 "&dist Distribution";
        title3 "Mu1=&mu1     Mu2=&mu2    Mu3=&mu3";
        title4 "Power_Hemmer CI      Power_Durbin CI";
run;
%mend bibd3;

%bibd3(10000, 20, 'Normal', 0,0,0,1);
%bibd3(10000, 20, 'Normal', 0.1, 0.75, 0.5, 1)
```

```
%bibd3(10000, 20, 'Normal', 0.6, 0.75, 0.3, 1)
%bibd3(10000, 20, 'Normal', 0, 0.5, 0, 1)
%bibd3(10000, 20, 'Normal', 0, 0.5, 0.5, 1)
%bibd3(10000, 20, 'Normal', 0.05, 0.4, 0.5, 1)
%bibd3(10000, 20, 'Normal', 0.3, 0, 0.15, 1)

%bibd3(10000, 20, 'Exp', 0,0,0,1);
%bibd3(10000, 20, 'Exp', 0.1, 0.75, 0.5, 1)
%bibd3(10000, 20, 'Exp', 0.6, 0.75, 0.3, 1)
%bibd3(10000, 20, 'Exp', 0, 0.5, 0, 1)
%bibd3(10000, 20, 'Exp', 0, 0.5, 0.5, 1)
%bibd3(10000, 20, 'Exp', 0.05, 0.4, 0.5, 1)
%bibd3(10000, 20, 'Exp', 0.3, 0, 0.15, 1)

%bibd3(10000, 20, 'T', 0,0,0,1);
%bibd3(10000, 20, 'T', 0.1, 0.75, 0.5, 1)
%bibd3(10000, 20, 'T', 0.6, 0.75, 0.3, 1)
%bibd3(10000, 20, 'T', 0, 0.5, 0, 1)
%bibd3(10000, 20, 'T', 0, 0.5, 0.5, 1)
%bibd3(10000, 20, 'T', 0.05, 0.4, 0.5, 1)
%bibd3(10000, 20, 'T', 0.3, 0, 0.15, 1)
```

APPENDIX III. SAS CODE FOR BIBD FOR 4 TREATMENTS WITH 3 TREATMENTS PER INCOMPLETE BLOCK

****
The following SAS code generates data from 4 treatments, with 3 treatments appearing within each incomplete block. The number of simulations, the number of incomplete block cycles, the treatment where the peak is assumed to occur, the underlying distribution and its associated parameters are passed in as macro parameters. The powers of Hemmer's test and Durbin's test and the corresponding confidence intervals were calculated with a significance level of 5%.

```
*********************************************************************************;
%macro bibd4(nsim, nrep, dist, peak, mu1, mu2, mu3, mu4, sigma);
%let t = 4;
%let k = 3;
%let r = 3;
data raw (keep=sim rep block y1-y&t Mu_T Var_T);
        array seed{&t} seed1 - seed&t;
        do i = 1 to &t;
                seed{i} = int(ranuni(0)*1e6);
        end;
        put seed1 - seed&t;
        do sim = 1 to &nsim;
        do rep = 1 to &nrep;
        do block = 1 to &t;
        if &dist = 'Normal' then do;
                call rannor(seed1, y1);
                        y1 = &mu1 + &sigma*y1;
                call rannor(seed2,y2);
                        y2 = &mu2 + &sigma*y2;
                call rannor(seed3,y3);
                        y3 = &mu3 + &sigma*y3;
                call rannor(seed4, y4);
                        y4 = &mu4 + &sigma*y4;
        end;
        else if &dist = 'Exp' then do;
                call ranexp(seed1, y1);
                        y1 = &mu1 + y1;
```

```
                call ranexp (seed2,y2);
                        y2 = &mu2 + y2;
                call ranexp (seed3,y3);
                        y3 = &mu3 + y3;
                call ranexp (seed4, y4);
                        y4 = &mu4 + y4;
        end;
        else if &dist = 'T' then do;
                call ranuni(seed1, y1);
                        y1 = tinv(y1, 3);
                        y1 = &mu1 + &sigma*y1;
                call ranuni (seed2,y2);
                        y2 = tinv(y2, 3);
                        y2 = &mu2 + &sigma*y2;
                call ranuni (seed3,y3);
                        y3 = tinv(y3, 3);
                        y3 = &mu3 + &sigma*y3;
                call ranuni (seed4, y4);
                        y4 = tinv(y4, 3);
                        y4 = &mu4 + &sigma*y4;
        end;
                if block = 1 then y1=.;
                else if block = 2 then y2=.;
                else if block = 3 then y3=.;
                else if block = 4 then y4=.;
                output; end; end; end;
run;
data test;
        set raw;
        by sim rep;
        array data{&t} y1 - y&t;
        array trt_value{3} A B C;
        array trt_number{3} Ai Bi Ci;
        array rank{&t} rank1 - rank&t;
        array sumrank{&t} sumrank1 - sumrank&t;
        array sumranksq{&t} sumranksq1 - sumranksq&t;
        Mu_T = 48*&nrep;    Var_T = (16/3)*&nrep;
        ctr = 0;
        do i = 1 to &t;
        if data{i} > . then do;
                ctr + 1;
                trt_value{ctr} = data{i};
                trt_number{ctr} = i;
```

```
			end;
		end;
	if C > B > A then do; rank{Ai} = 1; rank{Bi} = 2; rank{Ci} = 3; end;
	else if A > B > C then do; rank{Ai} = 3; rank{Bi} = 2; rank{Ci} = 1; end;
	else if B > C > A then do; rank{Ai} = 1; rank{Bi} = 3; rank{Ci} = 2; end;
	else if B > A > C then do; rank{Ai} = 2; rank{Bi} = 3; rank{Ci} = 1; end;
	else if A > C > B then do; rank{Ai} = 3; rank{Bi} = 1; rank{Ci} = 2; end;
	else if C > A > B then do; rank{Ai} = 2; rank{Bi} = 1; rank{Ci} = 3; end;
		do i = 1 to &t;
			if first.sim then sumrank{i} = 0;
			sumrank{i} + rank{i};
			if last.sim then sumranksq{i} = sumrank{i}**2;
		end;
		if last.sim then do;
			S = sum(sumranksq1, sumranksq2, sumranksq3, sumranksq4);
			durbin = (12 * (&t - 1) * S/(&r * &nrep * &t * (&k-1)*(&k+1)) )
		- (3 * &r * &nrep * (&t-1)*(&k+1)) / (&k-1);
			if durbin > 7.81 then power_durbin = 1;
				else power_durbin = 0;
		output; end;
		if &peak = II then do j=1 to (&t-1);
			if trt_number{j}=1 then do; rank1 = rank1*2; end;
			if trt_number{j}=2 then do; rank2 = rank2*3; end;
			if trt_number{j}=3 then do; rank3 = rank3*2; end;
		end;
		else if &peak = III then do j=1 to (&t-1);
			if trt_number{j}=2 then do; rank2 = rank2*2; end;
			if trt_number{j}=3 then do; rank3 = rank3*3; end;
			if trt_number{j}=4 then do; rank4 = rank4*2; end;
		end;
	T = sum(rank1, rank2, rank3, rank4);
	if first.sim then sumT = 0;
	sumT+T;
	if last.sim then do;
		Z_T = (sumT - Mu_T) / sqrt(Var_T);
		if Z_T > 1.645 then power_Hemmer = 1;
			else power_Hemmer = 0;
		output; end;
	run;
	proc means data=test noprint;
		var power_Durbin power_Hemmer;
		output out=power sum= ;
	run;
```

```
data power;
	set power;
	pH = sum(power_Hemmer) / &nsim;
		pH_CIupper = round(100 * (pH + 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
		pH_CIlower = round(100 * (pH - 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
	pD = sum(power_durbin) / (2*&nsim);
		pD_CIupper = round(100 * (pD + 1.96*sqrt(pD * (1-pD) / &nsim)), 0.01);
		pD_CIlower = round(100 * (pD - 1.96*sqrt(pD * (1-pD) / &nsim)), 0.01);
run;
proc print data=power;
	var pH pH_CIlower pH_CIupper pD pD_CIlower pD_CIupper;
	title1 "&t Treatments, Peak at &peak";
	title2 "&dist Distribution";
	title3 "Mu1=&mu1    Mu2=&mu2    Mu3=&mu3    Mu4=&mu4";
	title4 "Power_Hemmer CI     Power_Durbin CI";
run;
%mend bibd4;

***	Peak = II	***;
%bibd4(10000, 12, 'Normal', 2, 0,0,0,0, 1);
%bibd4(10000, 12, 'Normal', 2, 0.3, 0.5, 0.3, 0.1, 1)
%bibd4(10000, 12, 'Normal', 2, 0.2, 0.5, 0.4, 0, 1)
%bibd4(10000, 12, 'Normal', 2, 0.1, 0.5, 0.1, 0.05, 1);
%bibd4(10000, 12, 'Normal', 2, 0, 0.5, 0, 0, 1)
%bibd4(10000, 12, 'Normal', 2, 0, 0.5, 0.5, 0, 1)
%bibd4(10000, 12, 'Normal', 2, 0.5, 0.5, 0.5, 0, 1)
%bibd4(10000, 12, 'Normal', 2, 0.05, 0.2, 0.05, 0.25, 1)
%bibd4(10000, 12, 'Normal', 2, 0.75, 0.45, 0.5, 0.6, 1)

%bibd4(10000, 12, 'Exp', 2, 0,0,0,0, 1);
%bibd4(10000, 12, 'Exp', 2, 0.3, 0.5, 0.3, 0.1, 1)
%bibd4(10000, 12, 'Exp', 2, 0.2, 0.5, 0.4, 0, 1)
%bibd4(10000, 12, 'Exp', 2, 0.1, 0.5, 0.1, 0.05, 1);
%bibd4(10000, 12, 'Exp', 2, 0, 0.5, 0, 0, 1)
%bibd4(10000, 12, 'Exp', 2, 0, 0.5, 0.5, 0, 1)
%bibd4(10000, 12, 'Exp', 2, 0.5, 0.5, 0.5, 0, 1)
%bibd4(10000, 12, 'Exp', 2, 0.05, 0.2, 0.05, 0.25, 1)
%bibd4(10000, 12, 'Exp', 2, 0.75, 0.45, 0.5, 0.6, 1)

%bibd4(10000, 12, 'T', 2, 0,0,0,0, 1);
%bibd4(10000, 12, 'T', 2, 0.3, 0.5, 0.3, 0.1, 1)
%bibd4(10000, 12, 'T', 2, 0.2, 0.5, 0.4, 0, 1)
%bibd4(10000, 12, 'T', 2, 0.1, 0.5, 0.1, 0.05, 1);
```

```
%bibd4(10000, 12, 'T', 2, 0, 0.5, 0, 0, 1)
%bibd4(10000, 12, 'T', 2, 0, 0.5, 0.5, 0, 1)
%bibd4(10000, 12, 'T', 2, 0.5, 0.5, 0.5, 0, 1)
%bibd4(10000, 12, 'T', 2, 0.05, 0.2, 0.05, 0.25, 1)
%bibd4(10000, 12, 'T', 2, 0.75, 0.45, 0.5, 0.6, 1)

***     Peak = III      ***;
%bibd4(10000, 12, 'Normal', 3, 0,0,0,0, 1);
%bibd4(10000, 12, 'Normal', 3, 0.1, 0.3, 0.5, 0.3, 1);
%bibd4(10000, 12, 'Normal', 3, 0, 0.4, 0.5, 0.2, 1);
%bibd4(10000, 12, 'Normal', 3, 0.05, 0.1, 0.5, 0.1, 1);
%bibd4(10000, 12, 'Normal', 3, 0, 0, 0.5, 0, 1);
%bibd4(10000, 12, 'Normal', 3, 0, 0, 0.5, 0.5, 1)
%bibd4(10000, 12, 'Normal', 3, 0, 0.5, 0.5, 0.5, 1)
%bibd4(10000, 12, 'Normal', 3, 0.05, 0.2, 0.05, 0.25, 1)
%bibd4(10000, 12, 'Normal', 3, 0.75, 0.45, 0.5, 0.6, 1)

%bibd4(10000, 12, 'Exp', 3, 0,0,0,0, 1);
%bibd4(10000, 12, 'Exp', 3, 0.1, 0.3, 0.5, 0.3, 1);
%bibd4(10000, 12, 'Exp', 3, 0, 0.4, 0.5, 0.2, 1);
%bibd4(10000, 12, 'Exp', 3, 0.05, 0.1, 0.5, 0.1, 1);
%bibd4(10000, 12, 'Exp', 3, 0, 0, 0.5, 0, 1);
%bibd4(10000, 12, 'Exp', 3, 0, 0, 0.5, 0.5, 1)
%bibd4(10000, 12, 'Exp', 3, 0, 0.5, 0.5, 0.5, 1)
%bibd4(10000, 12, 'Exp', 3, 0.05, 0.2, 0.05, 0.25, 1)
%bibd4(10000, 12, 'Exp', 3, 0.75, 0.45, 0.5, 0.6, 1)

%bibd4(10000, 12, 'T', 3, 0,0,0,0, 1);
%bibd4(10000, 12, 'T', 3, 0.1, 0.3, 0.5, 0.3, 1);
%bibd4(10000, 12, 'T', 3, 0, 0.4, 0.5, 0.2, 1);
%bibd4(10000, 12, 'T', 3, 0.05, 0.1, 0.5, 0.1, 1);
%bibd4(10000, 12, 'T', 3, 0, 0, 0.5, 0, 1);
%bibd4(10000, 12, 'T', 3, 0, 0, 0.5, 0.5, 1)
%bibd4(10000, 12, 'T', 3, 0, 0.5, 0.5, 0.5, 1)
%bibd4(10000, 12, 'T', 3, 0.05, 0.2, 0.05, 0.25, 1)
%bibd4(10000, 12, 'T', 3, 0.75, 0.45, 0.5, 0.6, 1)
```

APPENDIX IV. SAS CODE FOR BIBD FOR 5 TREATMENTS WITH 4 TREATMENTS PER INCOMPLETE BLOCK

```
*********************************************************************************
The following SAS code generates data from 5 treatments, with 4 treatments appearing within
each incomplete block.  The number of simulations, the number of incomplete block cycles, the
treatment where the peak is assumed to occur, the underlying distribution and its associated
parameters are passed in as macro parameters.  The powers of Hemmer's test and Durbin's test
and the confidence intervals for the powers were calculated with a significance level of 5%.
*********************************************************************************;
%macro bibd5(nsim, nrep, dist, peak, mu1, mu2, mu3, mu4, mu5, sigma);
%let t = 5;	%let k = 4;	%let r = 4;
data raw (keep=sim rep block y1-y&t);
	array seed{&t} seed1 - seed&t;
	do i = 1 to &t;
		seed{i} = int(ranuni(0)*1e6);
	end;
	put seed1 - seed&t;
	do sim = 1 to &nsim;
	do rep = 1 to &nrep;
	do block = 1 to &t;
	if &dist = 'Normal' then do;
		call rannor(seed1, y1);
			y1 = &mu1 + &sigma*y1;
		call rannor(seed2,y2);
			y2 = &mu2 + &sigma*y2;
		call rannor(seed3,y3);
			y3 = &mu3 + &sigma*y3;
		call rannor(seed4, y4);
			y4 = &mu4 + &sigma*y4;
		call rannor(seed5, y5);
			y5 = &mu5 + &sigma*y5;
	end;
	else if &dist = 'Exp' then do;
		call ranexp(seed1, y1);
			y1 = &mu1 + y1;
		call ranexp (seed2,y2);
```

```
                y2 = &mu2 + y2;
        call ranexp (seed3,y3);
                y3 = &mu3 + y3;
        call ranexp (seed4, y4);
                y4 = &mu4 + y4;
        call ranexp (seed5, y5);
                y5 = &mu5 + y5;
    end;
    else if &dist = 'T' then do;
        call ranuni(seed1, y1);
                y1 = tinv(y1, 3);
                y1 = &mu1 + &sigma*y1;
        call ranuni (seed2,y2);
                y2 = tinv(y2, 3);
                y2 = &mu2 + &sigma*y2;
        call ranuni (seed3,y3);
                y3 = tinv(y3, 3);
                y3 = &mu3 + &sigma*y3;
        call ranuni (seed4, y4);
                y4 = tinv(y4, 3);
                y4 = &mu4 + &sigma*y4;
        call ranuni (seed5, y5);
                y5 = tinv(y5, 3);
                y5 = &mu5 + &sigma*y5;
    end;
        if block = 1 then y1=.;
        else if block = 2 then y2=.;
        else if block = 3 then y3=.;
        else if block = 4 then y4=.;
        else if block = 5 then y5=.;
        output; end; end; end;
run;
data test;
    set raw;
    by sim rep;
    array data{&t} y1 - y&t;
    array trt_value{4} A B C D;
    array trt_number{4} Ai Bi Ci Di;
    array rank{&t} rank1 - rank&t;
    array sumrank{&t} sumrank1 - sumrank&t;
    array sumranksq{&t} sumranksq1 - sumranksq&t;
    if &peak = III then do;
        Mu_T = 90*&nrep;    Var_T = 18.2609*&nrep;      end;
```

```
        else if then do;
                Mu_T = 130*&nrep;   Var_T = 32.5*&nrep; end;
        ctr = 0;
        do i = 1 to &t;
        if data{i} > . then do;
                ctr + 1;
                trt_value{ctr} = data{i};
                trt_number{ctr} = i;
                end;
        end;
if A > B > C > D then do; rank{Ai} = 4; rank{Bi} = 3; rank{Ci} = 2; rank{Di} = 1; end;
else if A > C > B > D then do; rank{Ai} = 4; rank{Bi} = 2; rank{Ci}=3; rank{Di}=1; end;
else if A > B > D > C then do; rank{Ai} = 4; rank{Bi} = 3; rank{Ci}=1; rank{Di}=2; end;
else if A > C > D > B then do; rank{Ai} = 4; rank{Bi} = 1; rank{Ci}=3; rank{Di}=2; end;
else if A > D > C > B then do; rank{Ai} = 4; rank{Bi} = 1; rank{Ci}=2; rank{Di}=3; end;
else if A > D > B > C then do; rank{Ai} = 4; rank{Bi} = 2; rank{Ci}=1; rank{Di}=3; end;

if B > A > C > D then do; rank{Ai} = 3; rank{Bi} = 4; rank{Ci} = 2; rank{Di} = 1; end;
else if B > C > A > D then do; rank{Ai} = 2; rank{Bi} = 4; rank{Ci}=3; rank{Di}=1; end;
else if B > A > D > C then do; rank{Ai} = 3; rank{Bi} = 4; rank{Ci}=1; rank{Di}=2; end;
else if B > C > D > A then do; rank{Ai} = 1; rank{Bi} = 4; rank{Ci}=3; rank{Di}=2; end;
else if B > D > C > A then do; rank{Ai} = 1; rank{Bi} = 4; rank{Ci}=2; rank{Di}=3; end;
else if B > D > A > C then do; rank{Ai} = 2; rank{Bi} = 4; rank{Ci}=1; rank{Di}=3; end;

if C > A > B > D then do; rank{Ai} = 3; rank{Bi} = 2; rank{Ci} = 4; rank{Di} = 1; end;
else if C > B > A > D then do; rank{Ai} = 2; rank{Bi} = 3; rank{Ci}=4; rank{Di}=1; end;
else if C > A > D > B then do; rank{Ai} = 3; rank{Bi} = 1; rank{Ci}=4; rank{Di}=2; end;
else if C > B > D > A then do; rank{Ai} = 1; rank{Bi} = 3; rank{Ci}=4; rank{Di}=2; end;
else if C > D > B > A then do; rank{Ai} = 1; rank{Bi} = 2; rank{Ci}=4; rank{Di}=3; end;
else if C > D > A > B then do; rank{Ai} = 2; rank{Bi} = 1; rank{Ci}=4; rank{Di}=3; end;

if D > A > B > C then do; rank{Ai} = 3; rank{Bi} = 2; rank{Ci} = 1; rank{Di} = 4; end;
else if D > B > A > C then do; rank{Ai} = 2; rank{Bi} = 3; rank{Ci}=1; rank{Di}=4; end;
else if D > A > C > B then do; rank{Ai} = 3; rank{Bi} = 1; rank{Ci}=2; rank{Di}=4; end;
else if D > B > C > A then do; rank{Ai} = 1; rank{Bi} = 3; rank{Ci}=2; rank{Di}=4; end;
else if D > C > B > A then do; rank{Ai} = 1; rank{Bi} = 2; rank{Ci}=3; rank{Di}=4; end;
else if D > C > A > B then do; rank{Ai} = 2; rank{Bi} = 1; rank{Ci}=3; rank{Di}=4; end;
        do i = 1 to &t;
                if first.sim then sumrank{i} = 0;
                sumrank{i} + rank{i};
                if last.sim then sumranksq{i} = sumrank{i}**2;
        end;
        if last.sim then do;
```

```
            S = sum(sumranksq1, sumranksq2, sumranksq3, sumranksq4, sumranksq5);
            durbin = (12 * (&t - 1) * S/(&r * &nrep * &t * (&k-1)*(&k+1)) )
        - (3 * &r * &nrep * (&t-1)*(&k+1)) / (&k-1);
            if durbin > 9.49 then power_durbin = 1;
                else power_durbin = 0;
        output; end;
        if &peak = II then do j=1 to (&t-1);
            if trt_number{j}=1 then rank1 = rank1*3;
            if trt_number{j}=2 then rank2 = rank2*4;
            if trt_number{j}=3 then rank3 = rank3*3;
            if trt_number{j}=4 then rank4 = rank4*2;
        end;
        else if &peak = III then do j=1 to (&t-1);
            if trt_number{j}=2 then rank2 = rank2*2;
            if trt_number{j}=3 then rank3 = rank3*3;
            if trt_number{j}=4 then rank4 = rank4*2;
        end;
        else if &peak = IV then do j=1 to (&t-1);
            if trt_number{j}=2 then rank2 = rank2*2;
            if trt_number{j}=3 then rank3 = rank3*3;
            if trt_number{j}=4 then rank4 = rank4*4;
            if trt_number{j}=5 then rank5 = rank5*3;
        end;
    T = sum(rank1, rank2, rank3, rank4, rank5);
    if first.sim then sumT = 0;
    sumT+T;
    if last.sim then do;
        Z_T = (sumT - Mu_T) / sqrt(Var_T);
        if Z_T > 1.645 then power_Hemmer = 1;
            else power_Hemmer = 0;
        output; end;
    run;
    proc means data=test noprint;
        var power_Hemmer power_Durbin;
        output out=power sum= ;
    run;
    data power;
        set power;
        pH = sum(power_Hemmer) / &nsim;
            pH_CIupper = round(100 * (pH + 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
            pH_CIlower = round(100 * (pH - 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
        pD = sum(power_durbin) / (2*&nsim);
            pD_CIupper = round(100 * (pD + 1.96*sqrt(pD * (1-pD) / &nsim)), 0.01);
```

```
                    pD_CIlower = round(100 * (pD - 1.96*sqrt(pD * (1-pD) / &nsim)), 0.01);
run;
proc print data=power;
          var pH pH_CIlower pH_CIupper pD pD_CIlower pD_CIupper;
          title1 "&t Treatments, Peak at &peak";
          title2 "&dist Distribution";
          title3 "Mu1=&mu1     Mu2=&mu2    Mu3=&mu3    Mu4=&mu4    Mu5=&mu5";
          title4 "Power_Hemmer CI      Power_Durbin CI";
run;
%mend bibd5;
***                 Peak = II          ***;
%bibd5(10000, 12, 'Normal', 2, 0,0,0,0,0,1);
%bibd5(10000, 12, 'Normal', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%bibd5(10000, 12, 'Normal', 2, 0.3, 0.4, 0.25, 0.15, 0, 1)
%bibd5(10000, 12, 'Normal', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%bibd5(10000, 12, 'Normal', 2, 0, 0.3, 0, 0, 0, 1);
%bibd5(10000, 12, 'Normal', 2, 0, 0.3, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'Normal', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'Normal', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'Normal', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%bibd5(10000, 12, 'Exp', 2, 0,0,0,0,0,1);
%bibd5(10000, 12, 'Exp', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%bibd5(10000, 12, 'Exp', 2, 0.3, 0.4, 0.25, 0.15, 0, 1)
%bibd5(10000, 12, 'Exp', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%bibd5(10000, 12, 'Exp', 2, 0, 0.3, 0, 0, 0, 1);
%bibd5(10000, 12, 'Exp', 2, 0, 0.3, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'Exp', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'Exp', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'Exp', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%bibd5(10000, 12, 'T', 2, 0,0,0,0,0,1);
%bibd5(10000, 12, 'T', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%bibd5(10000, 12, 'T', 2, 0.3, 0.4, 0.25, 0.15, 0, 1)
%bibd5(10000, 12, 'T', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%bibd5(10000, 12, 'T', 2, 0, 0.3, 0, 0, 0, 1);
%bibd5(10000, 12, 'T', 2, 0, 0.3, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'T', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'T', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'T', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

***                 Peak = III         ***;
%bibd5(10000, 12, 'Normal', 3, 0,0,0,0,0,1);
```

```
%bibd5(10000, 12, 'Normal', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%bibd5(10000, 12, 'Normal', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%bibd5(10000, 12, 'Normal', 3, 0.05, 0.1, 0.3, 0.1, 0.05, 1);
%bibd5(10000, 12, 'Normal', 3, 0, 0, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'Normal', 3, 0, 0, 0.3, 0.3, 0, 1);
%bibd5(10000, 12, 'Normal', 3, 0, 0.3, 0.3, 0.3, 0, 1);
%bibd5(10000, 12, 'Normal', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'Normal', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%bibd5(10000, 12, 'Exp', 3, 0,0,0,0,0,1);
%bibd5(10000, 12, 'Exp', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%bibd5(10000, 12, 'Exp', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%bibd5(10000, 12, 'Exp', 3, 0.05, 0.1, 0.3, 0.1, 0.05, 1);
%bibd5(10000, 12, 'Exp', 3, 0, 0, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'Exp', 3, 0, 0, 0.3, 0.3, 0, 1);
%bibd5(10000, 12, 'Exp', 3, 0, 0.3, 0.3, 0.3, 0, 1);
%bibd5(10000, 12, 'Exp', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'Exp', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%bibd5(10000, 12, 'T', 3, 0,0,0,0,0,1);
%bibd5(10000, 12, 'T', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%bibd5(10000, 12, 'T', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%bibd5(10000, 12, 'T', 3, 0.05, 0.1, 0.3, 0.1, 0.05, 1);
%bibd5(10000, 12, 'T', 3, 0, 0, 0.3, 0, 0, 1);
%bibd5(10000, 12, 'T', 3, 0, 0, 0.3, 0.3, 0, 1);
%bibd5(10000, 12, 'T', 3, 0, 0.3, 0.3, 0.3, 0, 1);
%bibd5(10000, 12, 'T', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'T', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

***          Peak = IV     ***;
%bibd5(10000, 12, 'Normal', 4, 0,0,0,0,0,1);
%bibd5(10000, 12, 'Normal', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%bibd5(10000, 12, 'Normal', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%bibd5(10000, 12, 'Normal', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%bibd5(10000, 12, 'Normal', 4, 0, 0, 0, 0.3, 0, 1);
%bibd5(10000, 12, 'Normal', 4, 0, 0, 0, 0.3, 0.3, 1);
%bibd5(10000, 12, 'Normal', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%bibd5(10000, 12, 'Normal', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'Normal', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%bibd5(10000, 12, 'Exp', 4, 0,0,0,0,0,1);
%bibd5(10000, 12, 'Exp', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%bibd5(10000, 12, 'Exp', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
```

```
%bibd5(10000, 12, 'Exp', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%bibd5(10000, 12, 'Exp', 4, 0, 0, 0, 0.3, 0, 1);
%bibd5(10000, 12, 'Exp', 4, 0, 0, 0, 0.3, 0.3, 1);
%bibd5(10000, 12, 'Exp', 4, 0, 0, 0.5, 0.5, 0.5, 1);
%bibd5(10000, 12, 'Exp', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'Exp', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%bibd5(10000, 12, 'T', 4, 0,0,0,0,0,1);
%bibd5(10000, 12, 'T', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%bibd5(10000, 12, 'T', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%bibd5(10000, 12, 'T', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%bibd5(10000, 12, 'T', 4, 0, 0, 0, 0.3, 0, 1);
%bibd5(10000, 12, 'T', 4, 0, 0, 0, 0.3, 0.3, 1);
%bibd5(10000, 12, 'T', 4, 0, 0, 0.5, 0.5, 0.5, 1);
%bibd5(10000, 12, 'T', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%bibd5(10000, 12, 'T', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);
```

APPENDIX V. SAS CODE FOR MIXED DESIGN FOR 3 TREATMENTS WITH 2 TREATMENTS PER INCOMPLETE BLOCK

```
*********************************************************************************
The following SAS code generates data from 3 treatments, with 2 treatments appearing within
each block that is incomplete.  The number of simulations, the number of combined complete
and incomplete block cycles, the ratio of complete to incomplete blocks, the treatment which is
assumed to be the peak, the underlying distribution and its associated parameters were passed in
as macro parameters.  The power of the Kim-Kim test would be calculated for complete blocks
and the power of Hemmer;s Test will be calculated for the incomplete blocks.  The power of the
two proposed tests, Method 1 and Method 2, are calculated for all blocks.  All tests and
confidence intervals were conducted with a significance level of 5%.
********************************************************************************;
%macro mixed3(nsim, nrep, dist, split, peak, mu1, mu2, mu3, sigma);
%let t = 3;
data raw;
	array seed{&t} seed1-seed&t;
	do i = 1 to &t;
		seed{i} = int(ranuni(0)*1e6);
	end;
	if &split = 'Even' then split = 0.5 * &nrep;
		else if &split = 'MoreComplete' then split = 0.75 * &nrep;
		else if &split = 'LessComplete' then split = 0.25 * &nrep;
	put seed1 - seed&t;
	do sim = 1 to &nsim;
	do rep = 1 to &nrep;
	do block = 1 to &t;
	if &dist = 'Normal' then do;
		call rannor(seed1, y1);
			y1 = &mu1 + &sigma*y1;
		call rannor(seed2, y2);
			y2 = &mu2 + &sigma*y2;
		call rannor(seed3, y3);
			y3 = &mu3 + &sigma*y3;
```

```
	end;
	else if &dist = 'Exp' then do;
		call ranexp(seed1, y1);
			y1 = &mu1 + y1;
		call ranexp(seed2, y2);
			y2 = &mu2 + y2;
		call ranexp(seed3, y3);
			y3 = &mu3 + y3;
	end;
	else if &dist = 'T' then do;
		call ranuni(seed1, y1);
			y1 = tinv(y1, 3);
			y1 = &mu1 + &sigma*y1;
		call ranuni(seed2, y2);
			y2 = tinv(y2, 3);
			y2 = &mu2 + &sigma*y2;
		call ranuni(seed3, y3);
			y3 = tinv(y3, 3);
			y3 = &mu3 + &sigma*y3;
	end;
	output; end; end; end;
run;
data raw;
	set raw;
	if rep > split then do;
		if block = 1 then do; y1 = .; end;
		else if block = 2 then do; y2 = .; end;
		else if block = 3 then do; y3 = .; end;
	end;
run;
data new;
	set raw;
	by sim rep;
	array data{&t} y1 - y&t;
	array trt_value{2} A B;
	array trt_number{2} Ai Bi;
	array rank{&t} rank1 - rank&t;
if rep <= split then do;
	ctr = 0;
	if y1 < y2 then do;
		ctr = 1; end;
	if y1 = y2 then do;
		ctr = 0.5; end;
```

```
		if y3 < y2 then do;
			ctr = ctr + 1; end;
		if y3 = y2 then do;
			ctr = ctr + 0.5; end;
		output; end;
	if rep > split then do;
		pl = 0;
		do j = 1 to &t;
		if data{j} > . then do;
			pl + 1;
			trt_value{pl} = data{j};
			trt_number{pl} = j;
			end;	end;
	if A < B then do; rank{Ai} = 1; rank{Bi} = 2; end;
	else if A > B then do; rank{Ai} = 2; rank{Bi} = 1; end;
		do j=1 to (&t-1);
			if trt_number{j}=2 then rank2 = rank2*2;
		end;
		T = sum(rank1, rank2, rank3);
		output; end;
run;
proc sort data=new;
	by sim rep;
run;
proc means data=new sum noprint;
	by sim;
	var ctr T;
	output out = one sum = KK sumT;
run;
data one;
	set one;
	if &split = 'Even' then split = 0.5 * &nrep;
		else if &split = 'MoreComplete' then split = 0.75 * &nrep;
		else if &split = 'LessComplete' then split = 0.25 * &nrep;
	Mu_T = 12*&nrep;	Var_T = 0.5*&nrep;
data final;
	set one;
	Mu_KK = &t * &nrep * (&peak**2 + (&t-&peak+1)**2 - &t - 1) / (4*(&nrep/split) );
	Var_KK = &t * &nrep * (2 * (&peak**3 + (&t-&peak+1)**3) +
3*(&peak**2 + (&t-&peak+1)**2) - 5*&t - 5 + 12*&peak*(&t-&peak+1) - 12*&t) / (72 *
(&nrep/split) );
	Z_KK = (KK - Mu_KK) / sqrt(Var_KK);
		if Z_KK > 1.645 then power_KK = 1;
```

```
        Mu_T1 = Mu_T / (&nrep/(&nrep-split));
        Var_T1 = Var_T / (&nrep/(&nrep-split));
        Z_T = (sumT - Mu_T1) / sqrt(Var_T1);
                if Z_T > 1.645 then power_Hemmer = 1;
        M1 = (Z_T + Z_KK) / sqrt(2);
                if M1 > 1.645 then power_M1 = 1;
        M2 = ((sumT + KK) - (Mu_T1 + Mu_KK)) / sqrt(Var_T1 + Var_KK);
                if M2 > 1.645 then power_M2 = 1;
run;
proc means data=final noprint;
        var power_M1 power_M2 power_KK power_Hemmer;
        output out=power sum= ;
run;
data power;
        set power;
        pH = sum(power_Hemmer) / &nsim;
                pH_CIupper = round(100 * (pH + 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
                pH_CIlower = round(100 * (pH - 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
        pKK = sum(power_KK) / &nsim;
                pKK_CIupper = round(100 * (pKK + 1.96*sqrt(pKK * (1-pKK) / &nsim) ),
0.01);
                pKK_CIlower = round(100 * (pKK - 1.96*sqrt(pKK * (1-pKK) / &nsim) ), 0.01);
        pM1 = sum(power_M1) / &nsim;
                pM1_CIupper = round(100 * (pM1 + 1.96*sqrt(pM1 * (1-pM1) / &nsim) ), 0.01);
                pM1_CIlower = round(100 * (pM1 - 1.96*sqrt(pM1 * (1-pM1) / &nsim) ), 0.01);
        pM2 = sum(power_M2) / &nsim;
                pM2_CIupper = round(100 * (pM2 + 1.96*sqrt(pM2 * (1-pM2) / &nsim) ), 0.01);
                pM2_CIlower = round(100 * (pM2 - 1.96*sqrt(pM2 * (1-pM2) / &nsim) ), 0.01);
run;
proc print data=power;
        var pH pH_CIlower pH_CIupper pKK pKK_CIlower pKK_CIupper;
        title2 "&dist Dist -- &split split -- Peak @ &peak";
        title3 "Mu1=&mu1 , Mu2=&mu2 , Mu3=&mu3";
        title4 "Power Kim-Kim          Power Hemmer's";
run;
proc print data = power;
        var pM1 pM1_CIlower pM1_CIupper pM2 pM2_CIlower pM2_CIupper;
        title2 "&dist Dist -- &split split -- Peak @ &peak";
        title3 "Mu1=&mu1 , Mu2=&mu2 , Mu3=&mu3";
        title4 "Power_Method 1          Power_Method 2";
run;
%mend mixed3;
```

```
%mixed3(10000, 20, 'Normal', 'Even', 2, 0,0,0,1);
%mixed3(10000, 20, 'Normal', 'Even', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'Even', 2, 0.6, 0.75, 0.3, 1)
%mixed3(10000, 20, 'Normal', 'Even', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'Normal', 'Even', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'Even', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'Even', 2, 0.3, 0.1, 0.15, 1)

%mixed3(10000, 20, 'Normal', 'MoreComplete', 2, 0,0,0,1);
%mixed3(10000, 20, 'Normal', 'MoreComplete', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'MoreComplete', 2, 0.6, 0.75, 0.3, 1)
%mixed3(10000, 20, 'Normal', 'MoreComplete', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'Normal', 'MoreComplete', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'MoreComplete', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'MoreComplete', 2, 0.3, 0.1, 0.15, 1)

%mixed3(10000, 20, 'Normal', 'LessComplete', 2, 0,0,0,1);
%mixed3(10000, 20, 'Normal', 'LessComplete', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'LessComplete', 2, 0.6, 0.75, 0.3, 1)
%mixed3(10000, 20, 'Normal', 'LessComplete', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'Normal', 'LessComplete', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'LessComplete', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'Normal', 'LessComplete', 2, 0.3, 0.1, 0.15, 1)

%mixed3(10000, 20, 'Exp', 'Even', 2, 0,0,0,1);
%mixed3(10000, 20, 'Exp', 'Even', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'Even', 2, 0.6, 0.75, 0.3, 1)
%mixed3(10000, 20, 'Exp', 'Even', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'Exp', 'Even', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'Even', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'Even', 2, 0.3, 0.1, 0.15, 1)

%mixed3(10000, 20, 'Exp', 'MoreComplete', 2, 0,0,0,1);
%mixed3(10000, 20, 'Exp', 'MoreComplete', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'MoreComplete', 2, 0.6, 0.75, 0.3, 1)
%mixed3(10000, 20, 'Exp', 'MoreComplete', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'Exp', 'MoreComplete', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'MoreComplete', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'MoreComplete', 2, 0.3, 0.1, 0.15, 1)

%mixed3(10000, 20, 'Exp', 'LessComplete', 2, 0,0,0,1);
%mixed3(10000, 20, 'Exp', 'LessComplete', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'LessComplete', 2, 0.6, 0.75, 0.3, 1)
```

```
%mixed3(10000, 20, 'Exp', 'LessComplete', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'Exp', 'LessComplete', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'LessComplete', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'Exp', 'LessComplete', 2, 0.3, 0.1, 0.15, 1) ;

%mixed3(10000, 20, 'T', 'Even', 2, 0,0,0,1);
%mixed3(10000, 20, 'T', 'Even', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'T', 'Even', 2, 0.6, 0.75, 0.3, 1)
%mixed3(10000, 20, 'T', 'Even', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'T', 'Even', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'T', 'Even', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'T', 'Even', 2, 0.3, 0.1, 0.15, 1)

%mixed3(10000, 20, 'T', 'MoreComplete', 2, 0,0,0,1);
%mixed3(10000, 20, 'T', 'MoreComplete', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'T', 'MoreComplete', 2, 0.6, 0.75, 0.3, 1)
%mixed3(10000, 20, 'T', 'MoreComplete', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'T', 'MoreComplete', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'T', 'MoreComplete', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'T', 'MoreComplete', 2, 0.3, 0.1, 0.15, 1)

%mixed3(10000, 20, 'T', 'LessComplete', 2, 0,0,0,1);
%mixed3(10000, 20, 'T', 'LessComplete', 2, 0.1, 0.75, 0.5, 1)
%mixed3(10000, 20, 'T', 'LessComplete', 2, 0.6, 0.75, 0.3, 1)
%mixed3(10000, 20, 'T', 'LessComplete', 2, 0, 0.5, 0, 1)
%mixed3(10000, 20, 'T', 'LessComplete', 2, 0, 0.5, 0.5, 1)
%mixed3(10000, 20, 'T', 'LessComplete', 2, 0.05, 0.4, 0.5, 1)
%mixed3(10000, 20, 'T', 'LessComplete', 2, 0.3, 0.1, 0.15, 1)
```

APPENDIX VI. SAS CODE FOR MIXED DESIGN FOR 4 TREATMENTS WITH 3 TREATMENTS PER INCOMPLETE BLOCK

****
The following SAS code generates data from 4 treatments, with 3 treatments appearing within each block that is incomplete. The number of simulations, the number of combined complete and incomplete block cycles, the ratio of complete to incomplete blocks, the treatment which is assumed to be the peak, the underlying distribution and its associated parameters were passed in as macro parameters. The power of the Kim-Kim test would be calculated for complete blocks and the power of Hemmer's test will be calculated for the incomplete blocks. The power of the two proposed tests, Method 1 and Method 2, are calculated for all blocks. All tests and confidence intervals were conducted with a significance level of 5%.

```
******************************************************************************;
%macro mixed4(nsim, nrep, dist, split, peak, mu1, mu2, mu3, mu4, sigma);
%let t = 4;
data raw;
	array seed{&t} seed1-seed&t;
	do i = 1 to &t;
		seed{i} = int(ranuni(0)*1e6);
	end;
	if &split = 'Even' then split = 0.5 * &nrep;
		else if &split = 'MoreComplete' then split = 0.75 * &nrep;
		else if &split = 'LessComplete' then split = 0.25 * &nrep;
	put seed1 - seed&t;
	do sim = 1 to &nsim;
	do rep = 1 to &nrep;
	do block = 1 to &t;
	if &dist = 'Normal' then do;
		call rannor(seed1, y1);
			y1 = &mu1 + &sigma*y1;
		call rannor(seed2, y2);
			y2 = &mu2 + &sigma*y2;
		call rannor(seed3, y3);
			y3 = &mu3 + &sigma*y3;
```

```
            call rannor(seed4, y4);
                  y4 = &mu4 + &sigma*y4;
      end;
      else if &dist = 'Exp' then do;
            call ranexp(seed1, y1);
                  y1 = &mu1 + y1;
            call ranexp(seed2, y2);
                  y2 = &mu2 + y2;
            call ranexp(seed3, y3);
                  y3 = &mu3 + y3;
            call ranexp(seed4, y4);
                  y4 = &mu4 + y4;
      end;
      else if &dist = 'T' then do;
            call ranuni(seed1, y1);
                  y1 = tinv(y1, 3);
                  y1 = &mu1 + &sigma*y1;
            call ranuni(seed2, y2);
                  y2 = tinv(y2, 3);
                  y2 = &mu2 + &sigma*y2;
            call ranuni(seed3, y3);
                  y3 = tinv(y3, 3);
                  y3 = &mu3 + &sigma*y3;
            call ranuni(seed4, y4);
                  y4 = tinv(y4, 3);
                  y4 = &mu4 + &sigma*y4;
      end;
      output; end; end; end;
run;
data raw;
      set raw;
      if rep > split then do;
            if block = 1 then do; y1 = .; end;
            else if block = 2 then do; y2 = .; end;
            else if block = 3 then do; y3 = .; end;
            else if block = 4 then do; y4 = .; end;
      end;
run;
data new;
      set raw;
      by sim rep;
      array data{&t} y1 - y&t;
      array trt_value{3} A B C ;
```

```
		array trt_number{3} Ai Bi Ci;
		array rank{&t} rank1 - rank&t;
	if rep <= split then do;
		ctr = 0;
	if &peak = II then do;
		if y1 < y2 then do;
			ctr = 1; end;
		if y1 = y2 then do;
			ctr = 0.5; end;
		if y3 < y2 then do;
			ctr = ctr + 1; end;
		if y3 = y2 then do;
			ctr = ctr + 0.5; end;
		if y4 < y2 then do;
			ctr = ctr + 1; end;
		if y4 = y2 then do;
			ctr = ctr + 0.5; end;
		if y4 < y3 then do;
			ctr = ctr + 1; end;
		if y4 = y3 then do;
			ctr = ctr + 0.5; end;
		output;
	end;
	else if &peak = III then do;
		if y1 < y2 then do;
			ctr = 1; end;
		if y1 = y2 then do;
			ctr = 0.5; end;
		if y1 < y3 then do;
			ctr = ctr + 1; end;
		if y1 = y3 then do;
			ctr = ctr + 0.5; end;
		if y2 < y3 then do;
			ctr = ctr + 1; end;
		if y2 = y3 then do;
			ctr = ctr + 0.5; end;
		if y4 < y3 then do;
			ctr = ctr + 1; end;
		if y4 = y3 then do;
			ctr = ctr + 0.5; end;
		output;
	end;
	end;
```

```
if rep > split then do;
        pl = 0;
        do j = 1 to &t;
        if data{j} > . then do;
                pl + 1;
                trt_value{pl} = data{j};
                trt_number{pl} = j;
                end;    end;
if C > B > A then do; rank{Ai} = 1; rank{Bi} = 2; rank{Ci} = 3; end;
else if A > B > C then do; rank{Ai} = 3; rank{Bi} = 2; rank{Ci} = 1; end;
else if B > C > A then do; rank{Ai} = 1; rank{Bi} = 3; rank{Ci} = 2; end;
else if B > A > C then do; rank{Ai} = 2; rank{Bi} = 3; rank{Ci} = 1; end;
else if A > C > B then do; rank{Ai} = 3; rank{Bi} = 1; rank{Ci} = 2; end;
else if C > A > B then do; rank{Ai} = 2; rank{Bi} = 1; rank{Ci} = 3; end;
        if &peak = II then do j=1 to (&t-1);
                if trt_number{j}=1 then rank1 = rank1*2;
                if trt_number{j}=2 then rank2 = rank2*3;
                if trt_number{j}=3 then rank3 = rank3*2;
        end;
        else if &peak = III then do j=1 to (&t-1);
                if trt_number{j}=2 then rank2 = rank2*2;
                if trt_number{j}=3 then rank3 = rank3*3;
                if trt_number{j}=4 then rank4 = rank4*2;
        end;
        T = sum(rank1, rank2, rank3, rank4);
        output; end;
run;
proc sort data=new;
        by sim rep;
run;
proc means data=new sum noprint;
        by sim;
        var ctr T;
        output out = one sum = KK sumT;
run;
data one;
        set one;
        if &split = 'Even' then split = 0.5 * &nrep;
                else if &split = 'MoreComplete' then split = 0.75 * &nrep;
                else if &split = 'LessComplete' then split = 0.25 * &nrep;
        Mu_T = 48*&nrep;
        Var_T = (16/3)*&nrep;
data final;
```

```
	set one;
	Mu_KK = &t * &nrep * (&peak**2 + (&t-&peak+1)**2 - &t - 1) / (4*(&nrep/split) );
	Var_KK = &t * &nrep * (2 * (&peak**3 + (&t-&peak+1)**3) +
3*(&peak**2 + (&t-&peak+1)**2) - 5*&t - 5 + 12*&peak*(&t-&peak+1) - 12*&t) / (72 *
(&nrep/split) );
	Z_KK = (KK - Mu_KK) / sqrt(Var_KK);
		if Z_KK > 1.645 then power_KK = 1;
	Mu_T1 = Mu_T / (&nrep/(&nrep-split));
	Var_T1 = Var_T / (&nrep/(&nrep-split));
	Z_T = (sumT - Mu_T1) / sqrt(Var_T1);
		if Z_T > 1.645 then power_Hemmer = 1;
	M1 = (Z_T + Z_KK) / sqrt(2);
		if M1 > 1.645 then power_M1 = 1;
	M2 = ((sumT + KK) - (Mu_T1 + Mu_KK)) / sqrt(Var_T1 + Var_KK);
		if M2 > 1.645 then power_M2 = 1;
run;
proc means data=final noprint;
	var power_M1 power_M2 power_KK power_Hemmer;
	output out=power sum= ;
run;
data power;
	set power;
	pH = sum(power_Hemmer) / &nsim;
		pH_CIupper = round(100 * (pH + 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
		pH_CIlower = round(100 * (pH - 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
	pKK = sum(power_KK) / &nsim;
	pKK_CIupper = round(100 * (pKK + 1.96*sqrt(pKK * (1-pKK) / &nsim) ), 0.01);
	pKK_CIlower = round(100 * (pKK - 1.96*sqrt(pKK * (1-pKK) / &nsim) ), 0.01);
	pM1 = sum(power_M1) / &nsim;
	pM1_CIupper = round(100 * (pM1 + 1.96*sqrt(pM1 * (1-pM1) / &nsim) ), 0.01);
	pM1_CIlower = round(100 * (pM1 - 1.96*sqrt(pM1 * (1-pM1) / &nsim) ), 0.01);
	pM2 = sum(power_M2) / &nsim;
	pM2_CIupper = round(100 * (pM2 + 1.96*sqrt(pM2 * (1-pM2) / &nsim) ), 0.01);
	pM2_CIlower = round(100 * (pM2 - 1.96*sqrt(pM2 * (1-pM2) / &nsim) ), 0.01);
run;
proc print data=power;
	var pH pH_CIlower pH_CIupper pKK pKK_CIlower pKK_CIupper;
	title2 "&dist Dist -- &split split -- Peak @ &peak";
	title3 "Mu1=&mu1 , Mu2=&mu2 , Mu3=&mu3 , Mu4=&mu4";
	title4 "Power Hemmer's			Power Kim-Kim";
run;
proc print data = power;
	var pM1 pM1_CIlower pM1_CIupper pM2 pM2_CIlower pM2_CIupper;
```

```
        title2 "&dist Dist -- &split split -- Peak @ &peak";
        title3 "Mu1=&mu1 , Mu2=&mu2 , Mu3=&mu3 , Mu4=&mu4";
        title4 "Power_Method 1                    Power_Method 2";
run;
%mend mixed4;
***     Peak = II        ***;
%mixed4(10000, 12, 'Normal', 'Even', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'Normal', 'Even', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'Normal', 'Even', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'Normal', 'Even', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'Normal', 'Even', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'Normal', 'Even', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'Even', 2, 0.5, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'Even', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Normal', 'Even', 2, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0.5, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 2, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0.5, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 2, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Exp', 'Even', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'Exp', 'Even', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'Exp', 'Even', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'Exp', 'Even', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'Exp', 'Even', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'Exp', 'Even', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Exp', 'Even', 2, 0.5, 0.5, 0.5, 0, 1)
```

```
%mixed4(10000, 12, 'Exp', 'Even', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Exp', 'Even', 2, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0.5, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 2, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0.5, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 2, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'T', 'Even', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'T', 'Even', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'T', 'Even', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'T', 'Even', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'T', 'Even', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'T', 'Even', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'T', 'Even', 2, 0.5, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'T', 'Even', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'T', 'Even', 2, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0.5, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 2, 0.75, 0.45, 0.5, 0.6, 1)
```

```
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0,0,0,0, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0.3, 0.5, 0.3, 0.1, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0.2, 0.5, 0.4, 0, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0.1, 0.5, 0.1, 0.05, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0, 0.5, 0, 0, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0.5, 0.5, 0.5, 0, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 2, 0.75, 0.45, 0.5, 0.6, 1)

***     Peak = III      ***;
%mixed4(10000, 12, 'Normal', 'Even', 3, 0,0,0,0, 1)
%mixed4(10000, 12, 'Normal', 'Even', 3, 0.1, 0.3, 0.5, 0.3, 1)
%mixed4(10000, 12, 'Normal', 'Even', 3, 0, 0.4, 0.5, 0.2, 1)
%mixed4(10000, 12, 'Normal', 'Even', 3, 0.05, 0.1, 0.5, 0.1, 1)
%mixed4(10000, 12, 'Normal', 'Even', 3, 0, 0, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'Even', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Normal', 'Even', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Normal', 'Even', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Normal', 'Even', 3, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0,0,0,0, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0.1, 0.3, 0.5, 0.3, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0, 0.4, 0.5, 0.2, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0.05, 0.1, 0.5, 0.1, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0, 0, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Normal', 'MoreComplete', 3, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0,0,0,0, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0.1, 0.3, 0.5, 0.3, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0, 0.4, 0.5, 0.2, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0.05, 0.1, 0.5, 0.1, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0, 0, 0.5, 0, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Normal', 'LessComplete', 3, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Exp', 'Even', 3, 0,0,0,0, 1)
%mixed4(10000, 12, 'Exp', 'Even', 3, 0.1, 0.3, 0.5, 0.3, 1)
```

```
%mixed4(10000, 12, 'Exp', 'Even', 3, 0, 0.4, 0.5, 0.2, 1)
%mixed4(10000, 12, 'Exp', 'Even', 3, 0.05, 0.1, 0.5, 0.1, 1)
%mixed4(10000, 12, 'Exp', 'Even', 3, 0, 0, 0.5, 0, 1)
%mixed4(10000, 12, 'Exp', 'Even', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Exp', 'Even', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Exp', 'Even', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Exp', 'Even', 3, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0,0,0,0, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0.1, 0.3, 0.5, 0.3, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0, 0.4, 0.5, 0.2, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0.05, 0.1, 0.5, 0.1, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0, 0, 0.5, 0, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Exp', 'MoreComplete', 3, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0,0,0,0, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0.1, 0.3, 0.5, 0.3, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0, 0.4, 0.5, 0.2, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0.05, 0.1, 0.5, 0.1, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0, 0, 0.5, 0, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'Exp', 'LessComplete', 3, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'T', 'Even', 3, 0,0,0,0, 1);
%mixed4(10000, 12, 'T', 'Even', 3, 0.1, 0.3, 0.5, 0.3, 1);
%mixed4(10000, 12, 'T', 'Even', 3, 0, 0.4, 0.5, 0.2, 1);
%mixed4(10000, 12, 'T', 'Even', 3, 0.05, 0.1, 0.5, 0.1, 1);
%mixed4(10000, 12, 'T', 'Even', 3, 0, 0, 0.5, 0, 1);
%mixed4(10000, 12, 'T', 'Even', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'T', 'Even', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'T', 'Even', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'T', 'Even', 3, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0,0,0,0, 1);
%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0.1, 0.3, 0.5, 0.3, 1);
%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0, 0.4, 0.5, 0.2, 1);
%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0.05, 0.1, 0.5, 0.1, 1);
%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0, 0, 0.5, 0, 1);
```

```
%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'T', 'MoreComplete', 3, 0.75, 0.45, 0.5, 0.6, 1)

%mixed4(10000, 12, 'T', 'LessComplete', 3, 0,0,0,0, 1);
%mixed4(10000, 12, 'T', 'LessComplete', 3, 0.1, 0.3, 0.5, 0.3, 1);
%mixed4(10000, 12, 'T', 'LessComplete', 3, 0, 0.4, 0.5, 0.2, 1);
%mixed4(10000, 12, 'T', 'LessComplete', 3, 0.05, 0.1, 0.5, 0.1, 1);
%mixed4(10000, 12, 'T', 'LessComplete', 3, 0, 0, 0.5, 0, 1);
%mixed4(10000, 12, 'T', 'LessComplete', 3, 0, 0, 0.5, 0.5, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 3, 0, 0.5, 0.5, 0.5, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 3, 0.05, 0.2, 0.05, 0.25, 1)
%mixed4(10000, 12, 'T', 'LessComplete', 3, 0.75, 0.45, 0.5, 0.6, 1)
```

APPENDIX VII. SAS CODE FOR MIXED DESIGN FOR 5 TREATMENTS WITH 4 TREATMENTS PER INCOMPLETE BLOCK

```
********************************************************************************
The following SAS code generates data from 5 treatments, with 4 treatments appearing within
each block that is incomplete.  The number of simulations, the number of combined complete
and incomplete block cycles, the ratio of complete to incomplete blocks, the treatment which is
assumed to be the peak, the underlying distribution and its associated parameters were passed in
as macro parameters.  The power of the Kim-Kim test would be calculated for complete blocks
and the power of Hemmer’s test will be calculated for the incomplete blocks.  The power of the
two proposed tests, Method 1 and Method 2, are calculated for all blocks.  All tests and
confidence intervals were conducted with a significance level of 5%.
*******************************************************************************;
%macro mixed5(nsim, nrep, dist, split, peak, mu1, mu2, mu3, mu4, mu5, sigma);
%let t = 5;
data raw;
	array seed{&t} seed1-seed&t;
	do i = 1 to &t;
		seed{i} = int(ranuni(0)*1e6);
	end;
	if &split = 'Even' then split = 0.5 * &nrep;
		else if &split = 'MoreComplete' then split = 0.75 * &nrep;
		else if &split = 'LessComplete' then split = 0.25 * &nrep;
	put seed1 - seed&t;
	do sim = 1 to &nsim;
	do rep = 1 to &nrep;
	do block = 1 to &t;
	if &dist = 'Normal' then do;
		call rannor(seed1, y1);
			y1 = &mu1 + &sigma*y1;
		call rannor(seed2, y2);
			y2 = &mu2 + &sigma*y2;
		call rannor(seed3, y3);
			y3 = &mu3 + &sigma*y3;
```

```
		call rannor(seed4, y4);
			y4 = &mu4 + &sigma*y4;
		call rannor(seed5, y5);
			y5 = &mu5 + &sigma*y5;
	end;
	else if &dist = 'Exp' then do;
		call ranexp(seed1, y1);
			y1 = &mu1 + y1;
		call ranexp(seed2, y2);
			y2 = &mu2 + y2;
		call ranexp(seed3, y3);
			y3 = &mu3 + y3;
		call ranexp(seed4, y4);
			y4 = &mu4 + y4;
		call ranexp(seed5, y5);
			y5 = &mu5 + y5;
	end;
	else if &dist = 'T' then do;
		call ranuni(seed1, y1);
			y1 = tinv(y1, 3);
			y1 = &mu1 + &sigma*y1;
		call ranuni(seed2, y2);
			y2 = tinv(y2, 3);
			y2 = &mu2 + &sigma*y2;
		call ranuni(seed3, y3);
			y3 = tinv(y3, 3);
			y3 = &mu3 + &sigma*y3;
		call ranuni(seed4, y4);
			y4 = tinv(y4, 3);
			y4 = &mu4 + &sigma*y4;
		call ranuni(seed5, y5);
			y5 = tinv(y5, 3);
			y5 = &mu5 + &sigma*y5;
	end;
	output; end; end; end;
run;
data raw;
	set raw;
	if rep > split then do;
		if block = 1 then do; y1 = .; end;
		else if block = 2 then do; y2 = .; end;
		else if block = 3 then do; y3 = .; end;
		else if block = 4 then do; y4 = .; end;
```

```
            else if block = 5 then do; y5 = .; end;
        end;
run;
data new;
        set raw;
        by sim rep;
        array data{&t} y1 - y&t;
        array trt_value{4} A B C D;
        array trt_number{4} Ai Bi Ci Di;
        array rank{&t} rank1 - rank&t;
if rep <= split then do;
        ctr = 0;
if &peak = II then do;
        if y1 < y2 then do;
            ctr = 1; end;
        if y1 = y2 then do;
            ctr = 0.5; end;
        if y3 < y2 then do;
            ctr = ctr + 1; end;
        if y3 = y2 then do;
            ctr = ctr + 0.5; end;
        if y4 < y2 then do;
            ctr = ctr + 1; end;
        if y4 = y2 then do;
            ctr = ctr + 0.5; end;
        if y4 < y3 then do;
            ctr = ctr + 1; end;
        if y4 = y3 then do;
            ctr = ctr + 0.5; end;
        if y5 < y2 then do;
            ctr = ctr + 1; end;
        if y5 = y2 then do;
            ctr = ctr + 0.5; end;
        if y5 < y3 then do;
            ctr = ctr + 1; end;
        if y5 = y3 then do;
            ctr = ctr + 0.5; end;
        if y5 < y4 then do;
            ctr = ctr + 1; end;
        if y5 = y4 then do;
            ctr = ctr + 0.5; end;
        output; end;
else if &peak = III then do;
```

```
        if y1 < y2 then do;
                ctr = 1; end;
        if y1 = y2 then do;
                ctr = 0.5; end;
        if y1 < y3 then do;
                ctr = ctr + 1; end;
        if y1 = y3 then do;
                ctr = ctr + 0.5; end;
        if y2 < y3 then do;
                ctr = ctr + 1; end;
        if y2 = y3 then do;
                ctr = ctr + 0.5; end;
        if y4 < y3 then do;
                ctr = ctr + 1; end;
        if y4 = y3 then do;
                ctr = ctr + 0.5; end;
        if y5 < y3 then do;
                ctr = ctr + 1; end;
        if y5 = y3 then do;
                ctr = ctr + 0.5; end;
        if y5 < y4 then do;
                ctr = ctr + 1; end;
        if y5 = y4 then do;
                ctr = ctr + 0.5; end;
        output; end;
else if &peak = IV then do;
        if y1 < y2 then do;
                ctr = 1; end;
        if y1 = y2 then do;
                ctr = 0.5; end;
        if y1 < y3 then do;
                ctr = ctr + 1; end;
        if y1 = y3 then do;
                ctr = ctr + 0.5; end;
        if y1 < y4 then do;
                ctr = ctr + 1; end;
        if y1 = y4 then do;
                ctr = ctr + 0.5; end;
        if y2 < y3 then do;
                ctr = ctr + 1; end;
        if y2 = y3 then do;
                ctr = ctr + 0.5; end;
        if y2 < y4 then do;
```

```
            ctr = ctr + 1; end;
        if y2 = y4 then do;
            ctr = ctr + 0.5; end;
        if y3 < y4 then do;
            ctr = ctr + 1; end;
        if y3 = y4 then do;
            ctr = ctr + 0.5; end;
        if y5 < y4 then do;
            ctr = ctr +1; end;
        if y5 = y4 then do;
            ctr = ctr + 0.5; end;
        output; end;
end;
if rep > split then do;
        pl = 0;
        do j = 1 to &t;
        if data{j} > . then do;
            pl + 1;
            trt_value{pl} = data{j};
            trt_number{pl} = j;
            end;    end;
if A > B > C > D then do; rank{Ai} = 4; rank{Bi} = 3; rank{Ci} = 2; rank{Di} = 1; end;
else if A > C > B > D then do; rank{Ai} = 4; rank{Bi} = 2; rank{Ci}=3; rank{Di}=1; end;
else if A > B > D > C then do; rank{Ai} = 4; rank{Bi} = 3; rank{Ci}=1; rank{Di}=2; end;
else if A > C > D > B then do; rank{Ai} = 4; rank{Bi} = 1; rank{Ci}=3; rank{Di}=2; end;
else if A > D > C > B then do; rank{Ai} = 4; rank{Bi} = 1; rank{Ci}=2; rank{Di}=3; end;
else if A > D > B > C then do; rank{Ai} = 4; rank{Bi} = 2; rank{Ci}=1; rank{Di}=3; end;

if B > A > C > D then do; rank{Ai} = 3; rank{Bi} = 4; rank{Ci} = 2; rank{Di} = 1; end;
else if B > C > A > D then do; rank{Ai} = 2; rank{Bi} = 4; rank{Ci}=3; rank{Di}=1; end;
else if B > A > D > C then do; rank{Ai} = 3; rank{Bi} = 4; rank{Ci}=1; rank{Di}=2; end;
else if B > C > D > A then do; rank{Ai} = 1; rank{Bi} = 4; rank{Ci}=3; rank{Di}=2; end;
else if B > D > C > A then do; rank{Ai} = 1; rank{Bi} = 4; rank{Ci}=2; rank{Di}=3; end;
else if B > D > A > C then do; rank{Ai} = 2; rank{Bi} = 4; rank{Ci}=1; rank{Di}=3; end;

if C > A > B > D then do; rank{Ai} = 3; rank{Bi} = 2; rank{Ci} = 4; rank{Di} = 1; end;
else if C > B > A > D then do; rank{Ai} = 2; rank{Bi} = 3; rank{Ci}=4; rank{Di}=1; end;
else if C > A > D > B then do; rank{Ai} = 3; rank{Bi} = 1; rank{Ci}=4; rank{Di}=2; end;
else if C > B > D > A then do; rank{Ai} = 1; rank{Bi} = 3; rank{Ci}=4; rank{Di}=2; end;
else if C > D > B > A then do; rank{Ai} = 1; rank{Bi} = 2; rank{Ci}=4; rank{Di}=3; end;
else if C > D > A > B then do; rank{Ai} = 2; rank{Bi} = 1; rank{Ci}=4; rank{Di}=3; end;

if D > A > B > C then do; rank{Ai} = 3; rank{Bi} = 2; rank{Ci} = 1; rank{Di} = 4; end;
```

```
else if D > B > A > C then do; rank{Ai} = 2; rank{Bi} = 3; rank{Ci}=1; rank{Di}=4; end;
else if D > A > C > B then do; rank{Ai} = 3; rank{Bi} = 1; rank{Ci}=2; rank{Di}=4; end;
else if D > B > C > A then do; rank{Ai} = 1; rank{Bi} = 3; rank{Ci}=2; rank{Di}=4; end;
else if D > C > B > A then do; rank{Ai} = 1; rank{Bi} = 2; rank{Ci}=3; rank{Di}=4; end;
else if D > C > A > B then do; rank{Ai} = 2; rank{Bi} = 1; rank{Ci}=3; rank{Di}=4; end;
	if &peak = II then do j=1 to (&t-1);
		if trt_number{j}=1 then rank1 = rank1*3;
		if trt_number{j}=2 then rank2 = rank2*4;
		if trt_number{j}=3 then rank3 = rank3*3;
		if trt_number{j}=4 then rank4 = rank4*2;
	end;
	else if &peak = III then do j=1 to (&t-1);
		if trt_number{j}=2 then rank2 = rank2*2;
		if trt_number{j}=3 then rank3 = rank3*3;
		if trt_number{j}=4 then rank4 = rank4*2;
	end;
	else if &peak = IV then do j=1 to (&t-1);
		if trt_number{j}=2 then rank2 = rank2*2;
		if trt_number{j}=3 then rank3 = rank3*3;
		if trt_number{j}=4 then rank4 = rank4*4;
		if trt_number{j}=5 then rank5 = rank5*3;
	end;
	T = sum(rank1, rank2, rank3, rank4, rank5);
	output; end;
run;
proc sort data=new;
	by sim rep;
run;
proc means data=new sum noprint;
	by sim;
	var ctr T;
	output out = one sum = KK sumT;
run;
data one;
	set one;
	if &split = 'Even' then split = 0.5 * &nrep;
		else if &split = 'MoreComplete' then split = 0.75 * &nrep;
		else if &split = 'LessComplete' then split = 0.25 * &nrep;
	if &peak = III then do;
		Mu_T = 90*&nrep;	Var_T = 18.2609*&nrep;	output; end;
	else then do;
		Mu_T = 130*&nrep;	Var_T = 32.5*&nrep; output; end;
data final;
```

```
	set one;
	Mu_KK = &t * &nrep * (&peak**2 + (&t-&peak+1)**2 - &t - 1) / (4*(&nrep/split) );
	Var_KK = &t * &nrep * (2 * (&peak**3 + (&t-&peak+1)**3) +
3*(&peak**2 + (&t-&peak+1)**2) - 5*&t - 5 + 12*&peak*(&t-&peak+1) - 12*&t) / (72 *
(&nrep/split) );
	Z_KK = (KK - Mu_KK) / sqrt(Var_KK);
		if Z_KK > 1.645 then power_KK = 1;
	Mu_T1 = Mu_T / (&nrep/(&nrep-split));
	Var_T1 = Var_T / (&nrep/(&nrep-split));
	Z_T = (sumT - Mu_T1) / sqrt(Var_T1);
		if Z_T > 1.645 then power_Hemmer = 1;
	M1 = (Z_T + Z_KK) / sqrt(2);
		if M1 > 1.645 then power_M1 = 1;
	M2 = ((sumT + KK) - (Mu_T1 + Mu_KK)) / sqrt(Var_T1 + Var_KK);
		if M2 > 1.645 then power_M2 = 1;
run;
proc means data=final noprint;
	var power_M1 power_M2 power_KK power_Hemmer;
	output out=power sum= ;
run;
data power;
	set power;
	pH = sum(power_Hemmer) / &nsim;
		pH_CIupper = round(100 * (pH + 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
		pH_CIlower = round(100 * (pH - 1.96*sqrt(pH * (1-pH) / &nsim) ), 0.01);
	pKK = sum(power_KK) / &nsim;
	pKK_CIupper = round(100 * (pKK + 1.96*sqrt(pKK * (1-pKK) / &nsim) ), 0.01);
	pKK_CIlower = round(100 * (pKK - 1.96*sqrt(pKK * (1-pKK) / &nsim) ), 0.01);
	pM1 = sum(power_M1) / &nsim;
		pM1_CIupper = round(100 * (pM1 + 1.96*sqrt(pM1 * (1-pM1) / &nsim) ), 0.01);
		pM1_CIlower = round(100 * (pM1 - 1.96*sqrt(pM1 * (1-pM1) / &nsim) ), 0.01);
	pM2 = sum(power_M2) / &nsim;
		pM2_CIupper = round(100 * (pM2 + 1.96*sqrt(pM2 * (1-pM2) / &nsim) ), 0.01);
		pM2_CIlower = round(100 * (pM2 - 1.96*sqrt(pM2 * (1-pM2) / &nsim) ), 0.01);
run;
proc print data=power;
	var pH pH_CIlower pH_CIupper pKK pKK_CIlower pKK_CIupper;
	title2 "&dist Dist -- &split split -- Peak @ &peak";
	title3 "Mu1=&mu1 , Mu2=&mu2 , Mu3=&mu3 , Mu4=&mu4 , Mu5=&mu5";
	title4 "Power Kim-Kim		Power Hemmer's";
run;
proc print data = power;
	var pM1 pM1_CIlower pM1_CIupper pM2 pM2_CIlower pM2_CIupper;
```

```
	title2 "&dist Dist -- &split split -- Peak @ &peak";
	title3 "Mu1=&mu1 , Mu2=&mu2 , Mu3=&mu3 , Mu4=&mu4 , Mu5=&mu5";
	title4 "Power_Method 1		Power_Method 2 ";
run;
%mend mixed5;

***		Peak = II		***;
%mixed5(10000, 12, 'Normal', 'Even', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'Even', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'Even', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 2, 0, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'Even', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'Even', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'Even', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'Even', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'Exp', 'Even', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'Exp', 'Even', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'Even', 2, 0, 0.3, 0.3, 0, 0, 1);
```

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%mixed5(10000, 12, 'Exp', 'Even', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'Even', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'Even', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'T', 'Even', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'Even', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'T', 'Even', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 2, 0, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'T', 'Even', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);
```

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%mixed5(10000, 12, 'T', 'LessComplete', 2, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'LessComplete', 2, 0.3, 0.4, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 2, 0.3, 0.4, 0.25, 0.15, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 2, 0.1, 0.4, 0.1, 0.05, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 2, 0, 0.3, 0, 0, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 2, 0, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 2, 0.3, 0.3, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 2, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 2, 0.75, 0, 0.3, 0.6, 0.1, 1);

***            Peak = III       ***;
%mixed5(10000, 12, 'Normal', 'Even', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'Even', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'Even', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'Normal', 'Even', 3, 0, 0.05, 0.3, 0.05, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'Even', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Normal', 'MoreComplete', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 3, 0, 0.05, 0.3, 0.05, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Normal', 'LessComplete', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 3, 0, 0.05, 0.3, 0.05, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'Even', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'Even', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'Even', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'Exp', 'Even', 3, 0, 0.05, 0.3, 0.05, 0, 1);
```

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%mixed5(10000, 12, 'Exp', 'Even', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'Even', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'Exp', 'Even', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'Even', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'MoreComplete', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 3, 0, 0.05, 0.3, 0.05, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'LessComplete', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 3, 0, 0.05, 0.3, 0.05, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'T', 'Even', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'Even', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'T', 'Even', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'T', 'Even', 3, 0, 0.05, 0.3, 0.05, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'T', 'Even', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'T', 'MoreComplete', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'MoreComplete', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 3, 0, 0.05, 0.3, 0.05, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'T', 'LessComplete', 3, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'LessComplete', 3, 0.1, 0.2, 0.3, 0.2, 0.1, 1);
```

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%mixed5(10000, 12, 'T', 'LessComplete', 3, 0.05, 0.25, 0.3, 0.2, 0.15, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 3, 0, 0.05, 0.3, 0.05, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 3, 0, 0, 0.3, 0, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 3, 0, 0, 0.3, 0.3, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 3, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 3, 0.75, 0, 0.3, 0.6, 0.1, 1);

***          Peak = IV     ***;
%mixed5(10000, 12, 'Normal', 'Even', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'Even', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'Even', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'Even', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'Even', 4, 0, 0, 0, 0.3, 0, 1);
%mixed5(10000, 12, 'Normal', 'Even', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'Even', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'Even', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'Even', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0, 0, 0, 0.3, 0, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'MoreComplete', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0, 0, 0, 0.3, 0, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Normal', 'LessComplete', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'Even', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'Even', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'Even', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'Even', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'Even', 4, 0, 0, 0, 0.3, 0, 1);
```

```
%mixed5(10000, 12, 'Exp', 'Even', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'Even', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'Even', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'Even', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0, 0, 0, 0.3, 0, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'MoreComplete', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0, 0, 0, 0.3, 0, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'Exp', 'LessComplete', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'T', 'Even', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'Even', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'T', 'Even', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'T', 'Even', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'T', 'Even', 4, 0, 0, 0, 0.3, 0, 1);
%mixed5(10000, 12, 'T', 'Even', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'T', 'Even', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'T', 'Even', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'T', 'Even', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0, 0, 0, 0.3, 0, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
```

```
%mixed5(10000, 12, 'T', 'MoreComplete', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);

%mixed5(10000, 12, 'T', 'LessComplete', 4, 0,0,0,0,0,1);
%mixed5(10000, 12, 'T', 'LessComplete', 4, 0.1, 0.2, 0.3, 0.4, 0.3, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 4, 0, 0.15, 0.25, 0.4, 0.3, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 4, 0, 0.05, 0.1, 0.4, 0.1, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 4, 0, 0, 0, 0.3, 0, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 4, 0, 0, 0, 0.3, 0.3, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 4, 0, 0, 0.3, 0.3, 0.3, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 4, 0.05, 0.2, 0.05, 0.25, 0.3, 1);
%mixed5(10000, 12, 'T', 'LessComplete', 4, 0.75, 0, 0.3, 0.6, 0.1, 1);
```