

A COMPARISON OF TYPE I ERROR AND POWER OF THE ALIGNED RANK METHOD
USING MEANS AND MEDIANS FOR ALIGNMENT

by

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Abstract

A simulation study was done to compare the Type I error and power of standard analysis of variance (ANOVA), the aligned rank transform procedure (ART), and the aligned rank transform procedure where alignment is done using medians (ART + Median). The methods were compared in the context of a balanced two-way factorial design with interaction when errors have a normal distribution and outliers are present in the data and when errors have the Cauchy distribution. The simulation results suggest that the nonparametric methods are more outlier-resistant and valid when errors have heavy tails in comparison to ANOVA. The ART + Median method appears to provide greater resistance to outliers and is less affected by heavy-tailed distributions than the ART method and ANOVA.

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Dedication

I dedicate this work to my loving wife, Chunfang Xu Yates. She has shown the patience, strength, and wisdom to carry me through all these times. As for my son, William, I dedicate this to him in love.

Chapter 1 - Introduction

1.1 Analysis of Variance in Two Way

The two way factorial effects model with interaction, as defined in Kuehl (2000) is

$$y_{ijr} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \varepsilon_{ijr}$$

where

$$\varepsilon_{ijr} \sim N(0, \sigma^2)$$

$$i = 1, 2, 3, \dots, a$$

$$j = 1, 2, 3, \dots, b$$

$$r = 1, 2, 3, \dots, n$$

a is the number of levels in effect A,

b is the number of levels in effect B,

n is the number of replications,

μ is equal to the overall mean

α_i denotes the i^{th} level of A,

β_j denotes the j^{th} level of B,

γ_{ij} denotes the interaction between the i^{th} level of A and j^{th} level of B,

It is important to also note that the parameters are not unique without restrictions on the parameters. We will use the sum-to-zero restrictions as follows:

$$\sum_{i=1}^a \alpha_i = 0$$

$$\sum_{j=1}^b \beta_j = 0$$

$$\sum_{i=1}^a \gamma_{ij} = 0$$

$$\sum_{j=1}^b \gamma_{ij} = 0$$

The analysis of variance (ANOVA) may be seen in Table 1.1.1

Table 1.1.1 Analysis of Variance

<i>Source of Variation</i>	<i>Df</i>	<i>SS</i>	<i>Mean Square</i>	<i>F</i>
<i>Total</i>	$nab - 1$	<i>SS Total</i>		
<i>Main Effect A</i>	$a - 1$	<i>SSA</i>	<i>MSA</i>	F_A
<i>Main Effect B</i>	$b - 1$	<i>SSB</i>	<i>MSB</i>	F_B
<i>Interactive Effect AB</i>	$(a - 1)(b - 1)$	<i>SSAB</i>	<i>MSAB</i>	F_{AB}
<i>Error</i>	$ab(n - 1)$	<i>SSE</i>	<i>MSE</i>	

The sums of squares as given in the table are defined below.

$$SSA = nb \sum_{i=1}^a (\bar{y}_{i..} - \bar{y}_{...})^2$$

$$SSB = na \sum_{j=1}^b (\bar{y}_{.j.} - \bar{y}_{...})^2$$

$$SSAB = n \sum_{i=1}^a (\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...})^2$$

where,

$$\bar{y}_{ij.} = \frac{\sum_{r=1}^n y_{ijr}}{n}$$

$$\bar{y}_{i..} = \frac{\sum_{j=1}^b \sum_{r=1}^n y_{ijr}}{bn}$$

$$\bar{y}_{.j.} = \frac{\sum_{i=1}^a \sum_{r=1}^n y_{ijr}}{an}$$

$$\bar{y}_{...} = \frac{\sum_{i=1}^a \sum_{j=1}^b \sum_{r=1}^n y_{ijr}}{abn}$$

Analysis of Variance allows us to test for main effects and interactions. The main effect A is tested by hypotheses:

$$H_0 : \alpha_i = 0$$

$$H_\alpha : \alpha_i \neq 0$$

where the hypotheses are tested by rejecting the null when $F_A = \frac{MSA}{MSE} > F_{\alpha, (a-1), ab(n-1)}$.

The main effect B is tested by hypothesis:

$$H_0 : \beta_i = 0$$

$$H_\alpha : \beta_i \neq 0$$

where the hypotheses are tested by rejecting the null when $F_B = \frac{MSB}{MSE} > F_{\alpha, (b-1), ab(n-1)}$.

The interaction between main effect A and main effect B is tested by hypotheses:

$$H_0 : \gamma_{ij} = 0$$

$$H_\alpha : \gamma_{ij} \neq 0$$

where the hypotheses are tested by rejecting the null when $F_{AB} = \frac{MSB}{MSE} > F_{\alpha, (a-1)(b-1), ab(n-1)}$.

The method may produce misleading results if the normality assumption is violated or if outliers are present, as p-values for effects may be incorrect. As a result of these limitations other methods are available when there is nonnormality of the error distribution or outliers are present in the data.

1.2 Aligned Rank Transform using Means and Medians in Two Way

The development of the Aligned Rank Transform (ART) comes from the application of nonparametric techniques to factorial experimental designs. The predecessor of ART was the Rank Transform (RT) method introduced by Conover and Iman (1981). The RT method was first introduced as an extremely simple and straightforward nonparametric technique in which data are ranked and standard parametric ANOVA is applied to ranks. This simplicity is very attractive given that the Rank Transform test performs similarly to other nonparametric tests such as the Wilcoxon rank-sum test and the Kruskal-Wallis test in the one-way ANOVA setting (Higgins, 2004). However, the RT method can run into problems in doing ANOVA involving two or more factors. It has been shown that the process may provide incorrect tests for main

effects and interaction as shown by Higgins and Tatshtoush (1994). As a consequence of this, ART was introduced to deal with this problem.

The ART method begins by first aligning the data and then ranking according to the effect of interest. After it has been ranked, the standard parametric ANOVA analysis is applied to the aligned ranked data (Higgins, 2004). ART provides an effective nonparametric method for dealing with both main effects and interaction (Mansouri et al. 2004). The asymptotic results of ART have been shown to give the correct significance levels and data simulation studies have shown that ART provides tests which give approximately the correct levels for moderate sample sizes (Higgins and Tashtoush, 1994).

Let us consider the ART procedure in the context of the two way factorial with interaction. As in section 1.1 we begin with the following two way factorial model:

$$y_{ijr} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \varepsilon_{ijr}$$

The terms are defined exactly the way they were in Section 1.1. ART aligns the data first. The procedure aligns the data according the factor we wish to test. Suppose we want to test for interaction. The observations are aligned by subtracting the main effects of A and B from the observations. The aligned data are then ranked and the standard two-way ANOVA is applied to the ranks. Significance is determined by the p-value of the F-test for interaction. Tests for A and B main effects are ignored. A similar procedure is applied to the main effects for A and B. Details are shown below.

We can estimate the effects of α_i , β_j and γ_{ij} with the sum to zero restrictions. The estimates for the case where all sample sizes are equal to n are

$$\hat{\alpha}_i = \hat{\mu}_{i\cdot} - \hat{\mu}$$

$$\hat{\beta}_j = \hat{\mu}_{\cdot j} - \hat{\mu}$$

$$\hat{\gamma}_{ij} = \hat{\mu}_{ij} - \hat{\mu}_{i\cdot} - \hat{\mu}_{\cdot j} + \hat{\mu}$$

$$\hat{\varepsilon}_{ijr} = \mu_{ijr} - \hat{\mu}_{ij}$$

where

$$\hat{\mu}_{i\cdot} = \frac{1}{nb} \sum_{j=1}^b \sum_{r=1}^n y_{ijr} = \bar{y}_{i\cdot}$$

$$\hat{\mu}_{\cdot j} = \frac{1}{na} \sum_{i=1}^a \sum_{r=1}^n y_{ijr} = \bar{y}_{\cdot j}$$

$$\hat{\mu}_{ij} = \frac{1}{n} \sum_{r=1}^n y_{ijr} = \bar{y}_{ij}$$

$$\hat{\mu} = \frac{1}{nab} \sum_{i=1}^a \sum_{j=1}^b \sum_{r=1}^n y_{ijr} = \bar{y}_{\dots}$$

If we want to test for interaction, then the data are aligned as follows:

$$\begin{aligned} y_{ijr(\text{aligned})} &= y_{ijr} - (\hat{\mu} + \hat{\alpha}_i + \hat{\beta}_j) \\ &= y_{ijr} - (\hat{\mu} + \hat{\alpha}_i + \hat{\beta}_j + \hat{\gamma}_{ij}) + \hat{\gamma}_{ij} \\ &= (y_{ijr} - \bar{y}_{ij}) + \hat{\gamma}_{ij} \\ &= \hat{\epsilon}_{ijr} + \hat{\gamma}_{ij} \end{aligned}$$

We may align the data for main effects as well. In order to test for the A main effect, the data are aligned as follows:

$$\begin{aligned} y_{ijr(\text{aligned})} &= y_{ijr} - (\hat{\mu} + \hat{\beta}_j + \hat{\gamma}_{ij}) \\ &= y_{ijr} - (\hat{\mu} + \hat{\beta}_j + \hat{\gamma}_{ij} + \hat{\alpha}_i) + \hat{\alpha}_i \\ &= (y_{ijr} - \bar{y}_{ij}) + \hat{\alpha}_i \\ &= \hat{\epsilon}_{ijr} + \hat{\alpha}_i \end{aligned}$$

To test for the B main effect the data are aligned as follows:

$$\begin{aligned} y_{ijr(\text{aligned})} &= y_{ijr} - (\hat{\mu} + \hat{\alpha}_i + \hat{\gamma}_{ij}) \\ &= y_{ijr} - (\hat{\mu} + \hat{\alpha}_i + \hat{\beta}_j + \hat{\gamma}_{ij}) + \hat{\beta}_j \\ &= (y_{ijr} - \bar{y}_{ij}) + \hat{\beta}_j \\ &= \hat{\epsilon}_{ijr} + \hat{\beta}_j \end{aligned}$$

As a result, it follows that we must perform three separate aligned ranked procedures. That is, two for the main effects and one for the interaction. We select the p-value of interest based on what effect we aligned for.

The aligned rank transform with medians is a very simple method that replaces the cell means instead with the corresponding cell medians. After alignment by medians, the method is

exactly the same as ordinary ART. Namely, once the data are aligned and ranked, then the standard ANOVA method is applied. The idea behind using cell medians instead of cell means is that cell medians are less affected by outliers than are cell means. This in turn ought to reduce the effect of outliers on significance levels of the tests for main effects and interactions. This procedure is denoted as ART + Median.

1.3 Comparison between ANOVA and Aligned Rank Transform using Means and Median in Two-Way Model

The comparison between ANOVA and Aligned Rank Transform using means and medians will be demonstrated by data sets simulated for our purposes. One data set was simulated with underlying assumptions of normality. The other data sets were obtained by introducing outliers of various sizes into original data. The data set without outliers was generated from the following model:

$$y_{ijr} = \mu + AX_A + ABX_{AB} + \varepsilon_{ijr}$$

where

$$\varepsilon_{ijr} \sim N(0,1)$$

$$i = 1, 2$$

$$j = 1, 2$$

$$r = 1, 2, 3, 4, 5, 6$$

$$\mu = 5$$

$$A = 0.5$$

$$AB = 0.4$$

$$X_A = \begin{cases} 1 & \text{if } i = 1 \\ -1 & \text{if } i = 2 \end{cases}$$

$$X_{AB} = \begin{cases} 1 & \text{if } i = j \\ -1 & \text{otherwise} \end{cases}$$

The data sets with outliers were obtained by adding $k \times rmse$ to the largest observation in the data set where $k = 1, 2, \dots, 8$ and $rmse$ is the square root of the MSE of the generated data set.

The simulated data without outliers and the alignment for testing for interaction are shown in Table 1.3.1. For instance, consider the first observation. The estimated interaction effect is $(4.8083 - 4.3484 - 4.7635 + 4.7427) = 0.4391$. The error is $5.2327 - 4.8083 = 0.4244$. So the aligned observation for interaction is $0.4244 + 0.4391 = 0.8635$ which has the rank 21 among the aligned observations. This data set and the data sets with outliers were analyzed and p-values for the tests for main effects and interaction were obtained. The ANOVA, ART and ART + Median p-values are shown in are shown in Tables 1.3.2, 1.3.3, and 1.3.4. The plots of the p-values are shown in Figures 1.3.1, 1.3.2, and 1.3.3.

Table 1.3.1 Data with Aligned and Ranked Data with Effects

X_A	X_B	y_{ijr}	$\bar{y}_{ij\cdot}$	$\bar{y}_{i\cdot\cdot}$	$\bar{y}_{\cdot j\cdot}$	$\bar{y}_{\cdot\cdot\cdot}$	$\hat{\epsilon}_{ijr}$	$\hat{y}_{ijr}(AB \text{ aligned})$	<i>AB Rank</i>
-1	-1	5.2327	4.8083	4.3484	4.7635	4.7427	0.4244	0.8635	21
-1	-1	4.6220	4.8083	4.3484	4.7635	4.7427	-0.1863	0.2528	14
-1	-1	4.3399	4.8083	4.3484	4.7635	4.7427	-0.4683	-0.0293	12
-1	-1	5.3282	4.8083	4.3484	4.7635	4.7427	0.5199	0.9590	22
-1	-1	4.1277	4.8083	4.3484	4.7635	4.7427	-0.6805	-0.2415	9
-1	-1	5.1991	4.8083	4.3484	4.7635	4.7427	0.3908	0.8299	20
1	-1	4.5173	4.7187	5.1370	4.7635	4.7427	-0.2014	-0.6405	5
1	-1	4.6186	4.7187	5.1370	4.7635	4.7427	-0.1002	-0.5392	6
1	-1	3.8542	4.7187	5.1370	4.7635	4.7427	-0.8645	-1.3036	4
1	-1	4.8345	4.7187	5.1370	4.7635	4.7427	0.1158	-0.3233	8
1	-1	4.6661	4.7187	5.1370	4.7635	4.7427	-0.0526	-0.4917	7
1	-1	5.8217	4.7187	5.1370	4.7635	4.7427	1.1029	0.6639	18
-1	1	4.6301	3.8886	4.3484	4.7220	4.7427	0.7415	0.3024	15
-1	1	2.4424	3.8886	4.3484	4.7220	4.7427	-1.4462	-1.8853	1
-1	1	5.8824	3.8886	4.3484	4.7220	4.7427	1.9938	1.5547	23
-1	1	4.8273	3.8886	4.3484	4.7220	4.7427	0.9387	0.4996	16
-1	1	2.7663	3.8886	4.3484	4.7220	4.7427	-1.1223	-1.5614	2
-1	1	2.7832	3.8886	4.3484	4.7220	4.7427	-1.1054	-1.5445	3
1	1	5.8143	5.5553	5.1370	4.7220	4.7427	0.2590	0.6981	19
1	1	4.9464	5.5553	5.1370	4.7220	4.7427	-0.6090	-0.1699	10
1	1	5.0554	5.5553	5.1370	4.7220	4.7427	-0.5000	-0.0609	11
1	1	6.6715	5.5553	5.1370	4.7220	4.7427	1.1162	1.5552	24
1	1	5.2223	5.5553	5.1370	4.7220	4.7427	-0.3330	0.1060	13
1	1	5.6222	5.5553	5.1370	4.7220	4.7427	0.0668	0.5059	18

An outlier was introduced into this data set in order to compare the performance of ANOVA and ART. The outlier was produced by multiplying a constant to the standard deviation of the response and adding that value to the largest value found data set in Table 1.3.1. The ANOVA, ART and ART + Median p-values may be observed in Table 1.3.2, Table 1.3.3 and Table 1.3.4.

Table 1.3.2 Main Effect A Reported P-Values

	Main Effect A		
Test	ANOVA	ART	ART + Median
<i>k</i>			
0	0.0395	0.0533	0.0459
1	0.0377	0.0418	0.0459
2	0.0405	0.0460	0.0459
3	0.0463	0.0313	0.0459
4	0.0540	0.0247	0.0459
5	0.0629	0.0280	0.0459
6	0.0552	0.0380	0.0459
7	0.0820	0.0339	0.0459
8	0.0916	0.0377	0.0459

Table 1.3.3 Main Effect B Reported P-Values

	Main Effect B		
Test	ANOVA	ART	ART + Median
<i>k</i>			
0	0.9088	0.7901	0.7092
1	0.9359	0.7900	0.7092
2	0.8088	0.5935	0.7092
3	0.7120	0.5566	0.7092
4	0.6400	0.5197	0.7092
5	0.5865	0.4479	0.7092
6	0.5463	0.4082	0.7092
7	0.5155	0.4017	0.7092
8	0.4915	0.3991	0.7092

Table 1.3.4 Interaction Effect AB Reported P-Values

Interaction Effect AB			
Effects	ANOVA	ART	ART + Median
<i>k</i>			
0	0.0235	0.0157	0.0127
1	0.0232	0.0184	0.0127
2	0.0262	0.0178	0.0127
3	0.0315	0.0283	0.0127
4	0.0384	0.0270	0.0127
5	0.0465	0.0275	0.0127
6	0.0723	0.0380	0.0127
7	0.0644	0.0490	0.0127
8	0.0737	0.0397	0.0127

Figure 1.3.1 Main Effect A

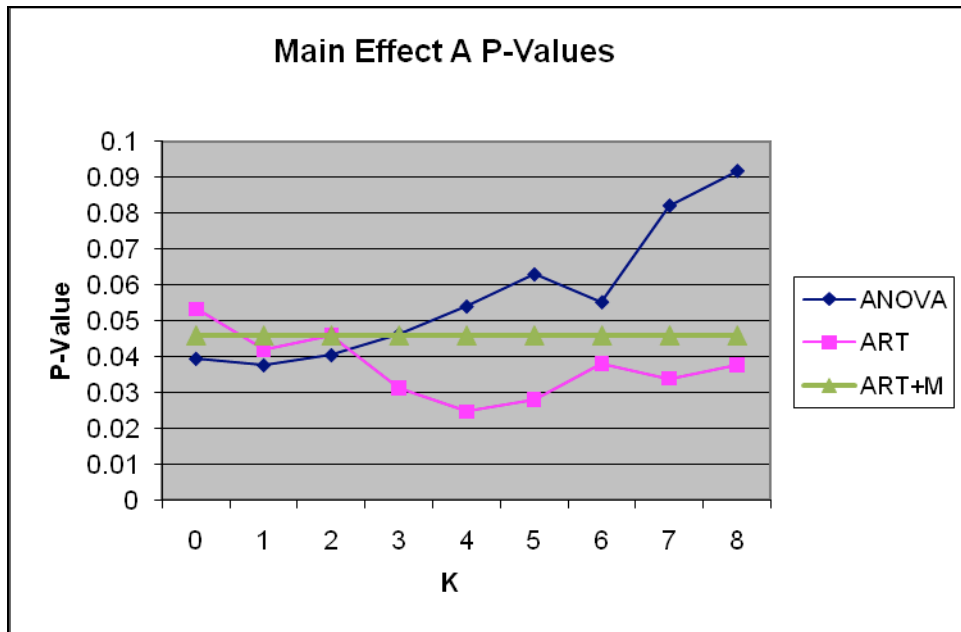


Figure 1.3.2 Main Effect B

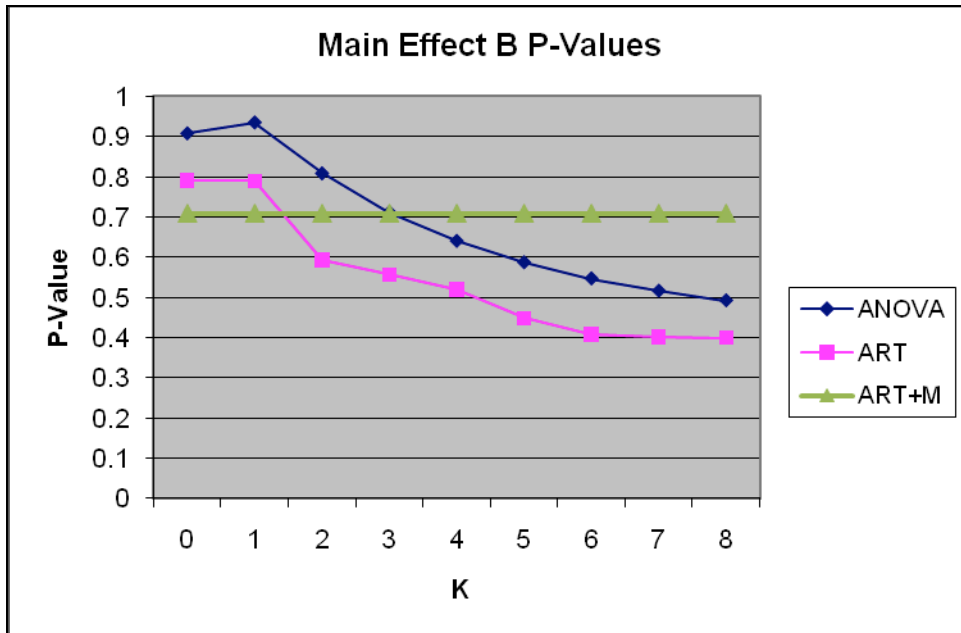
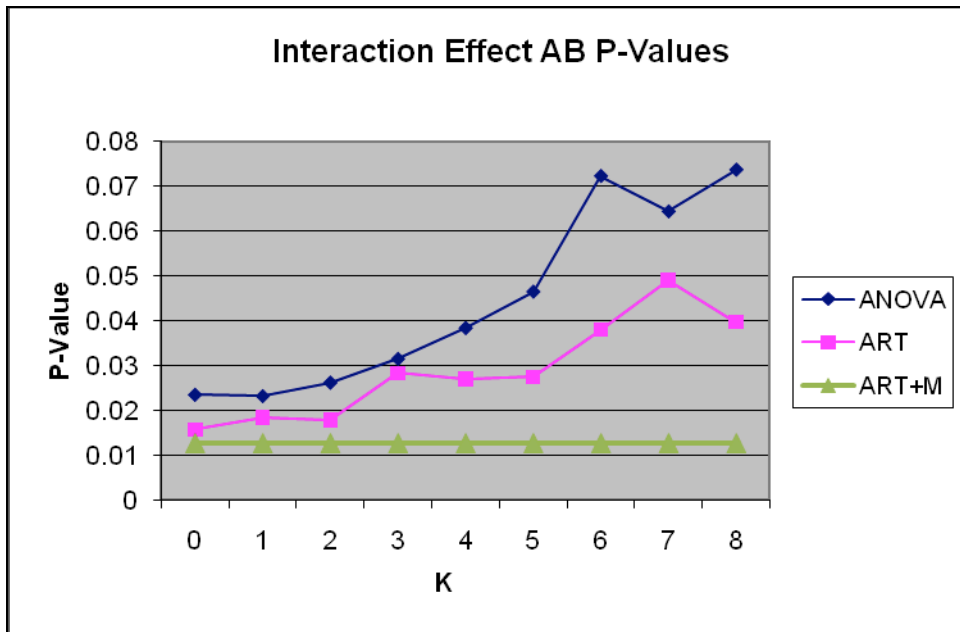


Figure 1.3.3 Interaction Effect AB



In Figure 1.3.1, then the main effect A is significant initially for ANOVA, but as the magnitude of the outlier increases, the p-value is inflated and it is not significant. ART resists the influence of the outlier and still reports a statistically significant main effect. We can see that

ART with medians is consistently resisting the outlier while the p-value for standard ANOVA is increasingly inflated.

In Figure 1.3.2, the main effect B is clearly not significant. However, as the outlier increases it follows that ANOVA p-value is on a decreasing trend. It should be noted that ART also follows this trend and reports a smaller p-value than ANOVA. However, ART + Median effectively resists the change.

In Figure 1.3.3 the AB interaction is significant. As the outlier increases, it can be seen that the p-value increases and becomes insignificant for ANOVA. The p-value for ART also increases but the p-value is less than ANOVA p-values. However, ART + Median effectively resists this trend.

We would like to use procedures where p-values do not appreciably change with increasing magnitudes of outliers. The ART did better in this regard than standard ANOVA, but it was not adequately resistant to outliers. Given the simplicity and ease by which ART may be implemented, ART can be seen to be an extremely attractive method and option to apply in data under these situations.

Chapter 2 - Simulation and Power Study

The concept of power is defined for single tests as the probability of rejecting the null hypothesis. If the null hypothesis is true, power is the probability of a Type I error. A simulation study was done to examine the power of single tests in a two way factorial design for standard ANOVA, ART, and ART + Median.

2.1 Power vs Replication Size

The two-way factorial design selected for the data simulation is based on the model in Chapter One where means from $y_{ijr} = 5 + 0.5X_A + 0.4X_{AB}$ are shown in Table 2.1.1. The error was not considered as only the cell means were of interest. The errors would be included in the data simulation.

Table 2.1.1 Cell Means

i	j	X_A	X_B	X_{AB}	μ_{ij}
1	1	1	1	1	5.9
1	2	1	-1	-1	5.1
2	1	-1	1	-1	4.1
2	2	-1	-1	1	4.9

The cell means from the table above were used in the model $y_{ijr} = \mu_{ij} + \epsilon_{ijr}$ with standard normal errors where 1000 data sets were generated with $n = 6$ and $n = 16$ replications. This was accomplished in SAS with the use of a macro program. The program used two nested loops and created 1000 data sets and organized them by the iteration of the set. The data sets were placed into PROC GLM, and PROC SQL was used to count the proportion of p-values that were less than $\alpha = 0.05$. As for ART and ART + Median, the data sets were processed by PROC MEANS and PROC RANK by iterations. We used PROC MEANS to calculate cell means, row means, and column means. As for ART + MEDIAN, it uses medians instead of cell means in PROC MEANS. Since the main effect B is not in the model from the data generated, then it follows that the proportion of tests with $p \leq 0.05$ (rejection of the null for B) is equal to the Type I error rate. Furthermore, given that the main effect A and interaction term AB is present in the model it

follows the proportion of tests with p-values less than 0.05 estimates the power of the tests for the alternative given by the model.

Table 2.1.2 Proportion of tests out of 1000 that at $\alpha = 0.05$ given model

$$y_{ijr} = 5 + 0.5X_A + 0.4X_{AB} + \varepsilon_{ijr} \text{ and no outliers}$$

		Replications	
Test	Effect	$n = 6$	$n = 16$
ANOVA	A	0.648	0.975
ART	A	0.625	0.970
ART + M	A	0.650	0.972
ANOVA	B	0.046	0.043
ART	B	0.047	0.048
ART + M	B	0.049	0.049
ANOVA	AB	0.460	0.898
ART	AB	0.450	0.889
ART + M	AB	0.458	0.889

The table above organized the tests by the effects with corresponding levels of power. The maximum margin of error for this data simulation is approximately 0.03. Hence, it can be seen above that the power for main effect A is relatively comparable across testing methods for $n = 6$. Similarly, this is also seen for the interaction effect AB across testing methods for $n = 6$. Given that there is no B main effect model present in the data simulated, then it follows that power here is also the Type I error. The expected range in the Type I error for this data simulation is between 0.036 and 0.064. The levels observed for B main effects are comparable to each other across testing methods and are hovering near the expected Type I error level of 0.05. The expected range in the Type I error rate is between 0.036 and 0.064. It would also be expected that as the number of replications increased, that we would observe an increase in power. This was indeed observed when we saw an increase in power for $n = 16$. It also becomes apparent that regardless of the test employed for the effects, the power is comparable between the tests.

2.2 Presence of Outliers and Power

The cell means from the Table 2.1.1 were used in the model $y_{ijr} = \mu_{ij} + \varepsilon_{ijr}$ with standard normal errors for first data simulation where 1000 data sets were generated with replications $n = 6$. This was accomplished in SAS with the use of the same macro program in Section 2.1. The program used two nested loops and created 1000 data sets and organized them by the iteration of the set.

There were two kinds of outliers that were considered. The first outlier is to take the maximum value in a data set and add a constant $k \times rmse$ where $rmse$ is the root mean square error. That is, the outlier is defined as $outlier = \max(y_{ijr}) + k \times rmse$ where $k = 0, 1, 2, \dots, 8$. Let us consider the case where $k = 1$. The data simulation used the same randomly generated data, and SAS calculates the outlier for the first data set as $9.076662 = 8.07442 + 1.002242$. SAS will replace the old value 8.07442 with the new outlier 9.076662 and then proceed to the next data set and repeat the process. After this, we will have 1000 data sets with outliers when $k = 1$. The data simulation did this for each value of k . The motivation in this procedure was to compare the performance between standard ANOVA, ART, and ART + Median on the randomly generated data sets with outliers.

The second outlier considered was to take the 15th observation in a data set and add a constant k times the $rmse$. The outlier is defined as $outlier = 15^{th} obs(y_{ijr}) + k \times rmse$ where $k = 0, 1, 2, \dots, 8$. The process in SAS was exactly the same as for the maximum outlier except we chose the 15th observation in each data set. The same 1000 data sets randomly generated produced the outliers based on the constant k . The motivation in this procedure, as with the other outlier, was to compare the performance between standard ANOVA, ART, and ART + Median.

After outliers were added to the data sets, the simulation was carried out as outlined in Section 2.1. Since the main effect B is not in the model from the data generated, then it follows that the Type I error present is also power. Since main effect A and interaction AB are present in the model, then power is obtained by tabulating the proportion of p-values less than 0.05.

Table 2.2.1 Proportion of tests out of 1000 that at $\alpha = 0.05$ given model

$y_{ijr} = 5 + 0.5X_A + 0.4X_{AB} + \varepsilon_{ijr}$ and outliers with $n = 6$

Maximum Outlier where $\max(y_{ijr}) + k \times rmse$										
Test	Effect	Probability to Reject Null								
		$k = 0$	$k = 1$	$k = 2$	$k = 3$	$k = 4$	$k = 5$	$k = 6$	$k = 7$	$k = 8$
ANOVA	A	0.648	0.635	0.614	0.584	0.549	0.508	0.447	0.403	0.347
ART	A	0.625	0.634	0.640	0.636	0.627	0.627	0.619	0.617	0.609
ART+M	A	0.650	0.646	0.646	0.646	0.646	0.646	0.646	0.646	0.646
ANOVA	B	0.046	0.043	0.036	0.032	0.022	0.019	0.016	0.011	0.010
ART	B	0.047	0.042	0.042	0.047	0.042	0.043	0.041	0.042	0.040
ART+M	B	0.049	0.046	0.047	0.047	0.047	0.047	0.047	0.047	0.047
ANOVA	AB	0.460	0.454	0.433	0.404	0.369	0.330	0.292	0.250	0.204
ART	AB	0.440	0.444	0.442	0.448	0.448	0.442	0.440	0.440	0.436
ART+M	AB	0.458	0.460	0.461	0.461	0.461	0.461	0.461	0.461	0.461
Observation where $15^{th} obs + k \cdot rmse$										
Test	Effect	Probability to Reject Null								
		$k = 0$	$k = 1$	$k = 2$	$k = 3$	$k = 4$	$k = 5$	$k = 6$	$k = 7$	$k = 8$
ANOVA	A	0.648	0.648	0.461	0.335	0.335	0.335	0.070	0.037	0.010
ART	A	0.625	0.547	0.457	0.390	0.343	0.318	0.303	0.289	0.267
ART+M	A	0.650	0.570	0.483	0.422	0.398	0.389	0.389	0.387	0.387
ANOVA	B	0.046	0.046	0.056	0.058	0.058	0.058	0.040	0.028	0.018
ART	B	0.047	0.052	0.057	0.053	0.052	0.049	0.049	0.052	0.055
ART+M	B	0.049	0.053	0.059	0.056	0.057	0.057	0.057	0.052	0.055
ANOVA	AB	0.460	0.460	0.281	0.198	0.198	0.198	0.021	0.009	0.006
ART	AB	0.440	0.358	0.289	0.235	0.207	0.186	0.168	0.156	0.141
ART+M	AB	0.458	0.382	0.306	0.262	0.241	0.234	0.234	0.234	0.234

The first part of Table 2.2.1 considers the probability of rejecting the null when the outliers were produced from maximum observations. First consider the main effect A. The tests are comparable until $k = 2$ where the power of standard ANOVA in comparison of ART and ART + Median begins to decrease. ART + Median resists the outlier more effectively than both standard ANOVA and ART. It maintains a power level of around 0.646. The probability of rejection for the null given the main effect B continues to decline as the outlier increases for standard ANOVA. ART and ART + Median resist the outlier and are comparable to each other.

ART and ART + Median maintain a level more around the expected Type I error and resist the influence of the outlier. The probability of rejecting the null when given interaction effect AB for standard ANOVA does not resist the outlier as it increases. The standard ANOVA is comparable with the other methods until the outlier is large. ART does a much better job than standard ANOVA, but does not resist the outlier as well as ART + Median. ART + Median is comparable to other methods for smaller outliers, but as the outlier increases it effectively maintains a level around 0.234 and outperforms ART and standard ANOVA. The probability to reject the null hypothesis given any effect is highest for ART + Median.

The second part of Table 2.2.1 considers the probability of rejecting the null hypothesis when the 15th observation was used for producing the outlier. The probability of rejecting the null hypothesis for main effect A for standard ANOVA declines substantially. ART and ART + Median resist the outlier more effectively than standard ANOVA, but still decline. ART + Median resists the outlier better than ART. The probability of rejecting the null hypothesis for main effect B for standard ANOVA declines as the outlier increases. ART and ART + Median resist the outlier more effectively and are comparable to each other. However, ART + Median has a slightly higher observed probability of rejecting the null than ART. The probability of rejecting the null when given interaction effect AB for standard ANOVA does not resist the outlier as it increases. The standard ANOVA is comparable with the other methods until the outlier is large. ART does a much better job than standard ANOVA, but does not resist the outlier as well as ART + Median. ART + Median is comparable to other methods until outliers are large, but as the outlier increases it effectively maintains a level around 0.234 and outperforms ART and standard ANOVA. The probability of rejecting the null hypothesis given any effect is highest for ART + Median

2.3 Power under Cauchy Errors

The values of the cell means from the Table 2.1.1 were used in the model $y_{ijk} = \mu_{ij} + \varepsilon_{ijk}$ with Cauchy errors where 1000 data sets were generated with replications $n = 6$ and $n = 16$. This distribution was chosen since it has heavy tails. The SAS program used to generate the random samples for this data was nearly identical to the code used in Section 2.1 except the errors were defined as RANCAU(%Seed).

Table 2.3.1 Proportion of tests out of 1000 that at $\alpha = 0.05$ given model

$y_{ijr} = 5 + 0.5X_A + 0.4X_{AB} + \varepsilon_{ijr}$ **and where error is Cauchy**

Test	Effect	Replications	
		$n = 6$	$n = 16$
ANOVA	A	0.066	0.075
ART	A	0.111	0.259
ART + M	A	0.227	0.533
ANOVA	B	0.019	0.015
ART	B	0.038	0.033
ART + M	B	0.063	0.059
ANOVA	AB	0.061	0.048
ART	AB	0.113	0.191
ART + M	AB	0.206	0.390

The probability of rejecting the null hypothesis for main effect A is higher for ART and ART + Median than standard ANOVA. ART + Median has the highest probability of rejection. The probability of rejecting the null for main effect B is also higher for ART and ART + Median than standard ANOVA. The ART + Median is also closer to the desired type I error level. The probability for rejecting the null given interaction effect AB is highest for ART + Median with ART next. The power of ANOVA for tests for A and AB is essentially the same as the nominal level of significance. Given that ART + Median uses medians and not cell means, then it deals with the parametric difficulties of the Cauchy much better than standard ANOVA and ART.

2.4 Summary

The data simulation compared standard ANOVA, ART, and ART + Median with normal errors, normal errors plus outliers, and Cauchy errors.

Examining the tests for the B effect where the null hypothesis is true, we see that the standard ART, and ART + Median maintained Type I errors near the nominal 5% level with normal errors and no outliers. With outliers, the standard ANOVA Type I error declined with larger outliers, but the ART and ART + Median maintained their levels of significance near the nominal level.

The power of the ANOVA tests for A and AB declined with increasing size of the outliers. The extent to which ART and ART+ Median resisted the effect of outliers depended on where the outlier was located. If the outlier was added to the largest value in the data set, the power of ART + Median was unchanged, but the power of the ART declined somewhat with increasing size of the outlier. When the outlier appeared in the middle of the data, the power of both ART and ART + Median declined with increasing size of the outlier but less so with ART + Median.

With Cauchy errors, the Type I error and power of the ANOVA were essentially unaffected by sample size and poor in all cases. As the results for the B effect showed, the Type I error for the ART was a bit lower than the nominal level, and as the tests for A and AB showed, and the power was a bit lower than the ART + Median.

In the cases considered the ART + Median was overall the best procedure. It maintained Type I errors near the nominal level, and the power was more stable than the other procedures in the presence of outliers. It also had the best Type I error and power for the Cauchy distribution.

References

- Kuehl, R. (2000). Design of Experiments: Statistical Principles of Research Design and Analysis. Belmont, CA. Brooks/Cole.
- Conover, W.J., & Imam, R.L. (1981) Rank Transformations as a Bridge Between Parametric and Nonparametric Statistics. The American Statistician, Vol.35, No.3, 124-129
- Higgins, J. J. & Tashtoush, S. (1994). An Aligned Rank Transform Test for Interaction. Nonlinear World 1 (2), pp. 201-211.
- Mansouri,H., Paige, R.L. and Surles, J.G. (2004). Aligned Rank Transform Techniques for Analysis of Variance and Multiple Comparisons. Communications in Statistics: Theory and Methods (9), pp. 2217-2232.
- Higgins, J.J.(2004). Introduction to Modern Nonparametric Statistics. Pacific Grove, California: Duxbury Press.

Appendix A - Chapter 1 SAS Code

```
options nocenter;

data one;
block=1;
input A      B Y;
datalines;
1      1      5.814331864
1      -1     4.517298878
-1     1      4.630063986
-1     -1     5.232686018
1      1      4.94635751
1      -1     4.618559924
-1     1      2.442381959
-1     -1     4.621970711
1      1      5.055369635
1      -1     3.854195726
-1     1      5.882358627
-1     -1     4.339943816
1      1      6.671487958
1      -1     4.834501398
-1     1      4.827313335
-1     -1     5.328174464
1      1      5.222311974
1      -1     4.666116349
-1     1      2.766279181
-1     -1     4.127724982
1      1      5.622166662
1      -1     5.821650317
-1     1      2.783172617
-1     -1     5.199118635
;
run;
```

```

data one;
    set one;
    K=8;
    RMSE= 0.876904;
    if Y=3.671487958 then Y=Y+K*RMSE; *adds outlier to the data set
    drop RMSE K;
Run;

proc print data=one;
run;

proc glm Data=one;*Standard ANOVA with outlier;
    class A B;
    model Y = A B A*B;
run;

*****
*ART          *
*****;

Proc sort data = one;
    by A B;
run;
proc means noprint data = one;
    by A B;
    var Y;
    output out = cellmeans mean = cell_mean;*Calculates Cell Means
run;
data two;
    merge one cellmeans;
    by A B;
run;
proc print data = two;
run;
proc sort data = two;
    by A;

```

```

run;
proc means noprint data = two;
    by A;
    var cell_mean;
    output out = Ameans mean = A_mean;*Calculates row mean
run;
data three;
    merge two Ameans;
    by A;
run;
proc print data = three;
run;

proc sort data = three;
    by B;
run;
proc means noprint data = three;
    by B;
    var cell_mean;
    output out = Bmeans mean = B_mean;*Calculates column mean
run;
data four;
    merge three Bmeans;
    by B;
run;
proc print data = four;
run;
proc sort data = four;
    by block;
run;
proc means data = four noprint;
    var cell_mean;
    by block;
    output out = grandmean mean = g_mean;
run;
data five;
    merge four grandmean;
    by block;

```

```

        run;
proc print data = five;
run;
data align;
    set five;
error = Y - cell_mean;
A_align = error + (A_mean - G_mean);*Aligns data for A effect;
B_align = error + (B_mean - G_mean);*Aligns data for B effect;
AB_align = error + (cell_mean - A_mean - B_mean + g_mean);*Aligns data
for AB effect
run;
proc print data = align;
run;
proc rank data = align out = alignrank;
    var A_align B_align AB_align;
    ranks AR_align BR_align ABR_align;
run;
proc print data = alignrank;
run;
proc glm;
    class A B;
    model AR_align BR_align ABR_align = A B A*B;
run;
quit;

```

Appendix B - Chapter 2 SAS Code

```
%let rep = 1000;
%let n = 6;
%let seed = 1066;

%let mu11=5.9;
%let mu12=5.1;
%let mu21=4.1;
%let mu22=4.9;

*****
*Standard ANOVA No Outliers*
*****;

%macro sim(out=);
  data dat1;
    do rep = 1 to &rep;*Macro generates 1000 data sets by rep
      do n = 1 to &n;
        %do A = 1 %to 2;
          %do B = 1 %to 2;
            A = &A;
            B = &B;
            error = rannor(&seed);
            y=&&mu&A&B+error;
            output;
          %end;
        %end;
      end;
    end;
  run;

  proc sort data=dat1; by rep A B n; run;
  proc print data=dat1; run;

  *ods trace on; *Turn this on to see table names of any SAS
  procedure.;
```



```

*ods listing close;
proc glm data=dat1; by rep;
    class A B;
    model y = A|B;
    lsmeans A|B/pdiff;
    ods output modelanova = anova(where=(HypothesisType=3) keep
                                = HypothesisType source probf rep)
                                differencematrix = diffs;

run;
quit;
*ods listing;

*Count number of significant tests.;
proc sql;
    create table &out as select source, (count(rep))/&rep as
    propsign from anova where probf le 0.05
    group by source;
quit;

proc print data=&out;run;

%mend;

%sim(out=set1);

```

```

%let rep = 1000;
%let n = 6;
%let seed = 1066;

%let mu11=5.9;
%let mu12=5.1;
%let mu21=4.1;
%let mu22=4.9;

*****
*ART Data Simulation      *
*****;

%macro sim(artout=);
  data dat1;
    do rep = 1 to &rep;
      do n = 1 to &n;
        %do A = 1 %to 2;
          %do B = 1 %to 2;
            A = &A;
            B = &B;
            error = rannor(&seed);
            y=&&mu&A&B+error;
            output;
          %end;
        %end;
      end;
    end;
  run;

  proc sort data=dat1; by rep A B n; run;
  proc print data=dat1; run;

  proc means noprint data = dat1;
    by rep A B;
    var Y;
  output out = cellmeans mean = cell_mean;
  run;

```

```

*proc print data=cellmeans;*run;

data two;
    merge dat1 cellmeans;
    by rep A B;
run;

*proc print data=two;*run;

proc sort data=two;
    by rep A;
run;

proc means noprint data=two;
    by rep A;
    var cell_mean;
    output out=Ameans mean=A_mean;
run;

data three;
    merge two Ameans;
    by rep A;
run;

*proc print data=three;*run;

proc sort data=three;
    by rep B;
run;

proc means noprint data=three;
    by rep B;
    var cell_mean;
    output out=Bmeans mean=B_mean;
run;

*proc print data=Bmeans;*run;

```

```

data four;
    merge three Bmeans;
    by rep B;
run;

*proc print data=four;*run;

proc sort data=four;
    by rep;
run;

proc means data=four noprint;
    by rep;
    var cell_mean;
    output out=grandmean mean=g_mean;
run;

*proc print data=grandmean;*run;

data five;
    merge four grandmean;
    by rep;
run;

*proc print data=five;*run;

data align;
    set five;
    error = y - cell_mean;
    A_align = error + (A_mean - G_mean);
    B_align = error + (B_mean - G_mean);
    AB_align = error + (cell_mean - A_mean - B_mean + g_mean);
run;

*proc print data=align;*run;

proc rank data = align out = alignrank;

```

```

        by rep;
        var A_align B_align AB_align;
        ranks AR_align BR_align ABR_align;
run;

*proc print data=alignrank;*run;

*ods trace on; *Turn this on to see table names of any SAS
                procedure.;
*ods listing close;
proc glm data=alignrank; by rep;
    class A B;
    model AR_align BR_align ABR_align = A|B;
    lsmeans A|B/pdiff;
    ods output modelanova = anova(where=(HypothesisType=3) keep
                                = HypothesisType dependent source probf rep)
                                differencematrix = diffs;

run;
quit;
*ods listing;

*Count number of significant tests.;
proc sql;
    create table &artout as select dependent, source,
(count(rep))/&rep as propsign from anova where probf le 0.05
    group by dependent, source;
quit;

Title 'Proportion of factors that tested at a 0.05 level of
        significance';
proc print data=&artout noobs;run;

%mend;

%sim(artout=set1);

```

```

%let rep = 1000;
%let n = 6;
%let seed = 1066;

%let mu11=5.9;
%let mu12=5.1;
%let mu21=4.1;
%let mu22=4.9;

*****
*ANOVA with Max Outlier*
*****;

%macro sim(out=);
  data dat1;
    do rep = 1 to &rep;
      do n = 1 to &n;
        %do A = 1 %to 2;
          %do B = 1 %to 2;
            A = &A;
            B = &B;
            error = rannor(&seed);
            y=&&mu&A&B+error;
            output;
          %end;
        %end;
      end;
    end;
  run;

  proc sort data=dat1; by rep A B n; run;
  proc print data=dat1; run;

  *ods trace on; *Turn this on to see table names of any SAS
  procedure.;

```

```

ods listing close;
proc glm data=dat1; by rep;
    class A B;
    model y = A|B;
    lsmeans A|B/pdiff;
    ods output modelanova = anova(where=(HypothesisType=3) keep
        = HypothesisType source probf rep)
        differencematrix = diffs;
run;
quit;
ods listing;

*Count number of significant tests.;
proc sql;
    create table &out as select source, (count(rep))/&rep as
        propsign from anova where probf le 0.05
    group by source;
    /*order by source*/;
quit;

proc print data=&out;run;

%mend;

%sim(out=set1);

```

```

%let rep = 1000;
%let n = 6;
%let seed = 1066;

%let mu11=5.9;
%let mu12=5.1;
%let mu21=4.1;
%let mu22=4.9;

*****
*ANOVA with MAX Outlier*
*****;

%macro sim(artout=);
  data dat1;
    do rep = 1 to &rep;
      do n = 1 to &n;
        %do A = 1 %to 2;
          %do B = 1 %to 2;
            A = &A;
            B = &B;
            error = rannor(&seed);
            y=&&mu&A&B+error;
            output;
          %end;
        %end;
      end;
    end;
  run;

  proc sort data=dat1; by rep A B n; run;
  proc print data=dat1; run;

  *ods trace on; *Turn this on to see table names of any SAS
  procedure.;
  *ods trace ouput;

```



```

ods listing close;

proc glm data=dat1; by rep;
    class A B;
    model y = A|B;
    lsmeans A|B/pdiff;
    *ods output modelanova = anova(where=(HypothesisType=3)
    keep = HypothesisType source ms probf rep)
        differencematrix = diffs;
    *ods output OverallANOVA= rootmse;
    ods output FitStatistics=rootmse(keep= RootMSE rep);

run;
quit;
ods listing;
ods close;

*proc print data=rootmse;*run;

*mergese dataset and rootmse by rep;
data dat1rmse;
    merge dat1 rootmse;
    by rep;
run;

*proc print data=dat1rmse;*run;

*finds maximum value by rep;
proc means data=dat1 noprint max;
    class rep;
    var y;
    output out=dat1max(where=(_type_=1)) max=maxy;
run;

*proc print data=dat1max;*run;

*merge dat1rmse and maximum values;

```

```

data datlmaxrmse;
    merge datlrmse datlmax;
    by rep;
run;

*proc print data=datlmaxrmse ;*run;

*adds outlier(this demonstrates its working);
/*
data datlout;
    set datlmaxrmse;
    by rep;
    k=1;
    if y=maxy then y1=y+k*RootMSE;
run;

proc print data=datlout;run;
*/

*adds outliers;
data datlout;
    set datlmaxrmse;
    by rep;
    k=0;
    if y=maxy then y=y+k*RootMSE;
    keep rep error n A B y;
run;

proc sort data=datlout; by rep A B n; run;
*proc print data=datlout; run;

proc means noprint data = datlout;
    by rep A B;
    var Y;
    output out = cellmeans mean = cell_mean;
run;

```

```

*proc print data=cellmeans;*run;

data two;
    merge dat1out cellmeans;
    by rep A B;
run;

*proc print data=two;*run;

proc sort data=two;
    by rep A;
run;

proc means noprint data=two;
    by rep A;
    var cell_mean;
    output out=Ameans mean=A_mean;
run;

data three;
    merge two Ameans;
    by rep A;
run;

*proc print data=three;*run;

proc sort data=three;
    by rep B;
run;

proc means noprint data=three;
    by rep B;
    var cell_mean;
    output out=Bmeans mean=B_mean;
run;

*proc print data=Bmeans;*run;

```

```

data four;
    merge three Bmeans;
    by rep B;
run;

*proc print data=four;*run;

proc sort data=four;
    by rep;
run;

proc means data=four noprint;
    by rep;
    var cell_mean;
    output out=grandmean mean=g_mean;
run;

*proc print data=grandmean;*run;

data five;
    merge four grandmean;
    by rep;
run;

*proc print data=five;*run;

data align;
    set five;
    error = y - cell_mean;
    A_align = error + (A_mean - G_mean);
    B_align = error + (B_mean - G_mean);
    AB_align = error + (cell_mean - A_mean - B_mean + g_mean);
run;

*proc print data=align;*run;

```

```

proc rank data = align out = alignrank;
    by rep;
    var A_align B_align AB_align;
    ranks AR_align BR_align ABR_align;
run;

*proc print data=alignrank;*run;

*ods trace on; *Turn this on to see table names of any SAS
procedure.;
*ods listing close;
proc glm data=alignrank; by rep;
    class A B;
    model AR_align BR_align ABR_align = A|B;
    lsmeans A|B/pdiff;
    ods output modelanova = anova(where=(HypothesisType=3) keep
    = HypothesisType dependent source probf rep)
        differencematrix = diffs;
run;
quit;
*ods listing;

*Count number of significant tests.;
proc sql;
    create table &artout as select dependent, source,
(count(rep))/&rep as propsign from anova where probf le 0.05
    group by dependent, source;
quit;

Title 'Proportion of factors that tested at a 0.05 level of
    significance';
proc print data=&artout noobs;run;
quit;

proc print data=&artout;run;
%mend;
%sim(artout=set1);

```

```

%let rep = 1000;
%let n = 6;
%let seed = 1066;

%let mu11=5.9;
%let mu12=5.1;
%let mu21=4.1;
%let mu22=4.9;

*****
*ANOVA with 15th Obs Outlier*
*****;

%macro sim(out=);
  data dat1;
    do rep = 1 to &rep;
      do n = 1 to &n;
        %do A = 1 %to 2;
          %do B = 1 %to 2;
            A = &A;
            B = &B;
            error = rannor(&seed);
            y=&&mu&A&B+error;
            output;
          %end;
        %end;
      end;
    end;
  run;

  proc sort data=dat1; by rep A B n; run;
  proc print data=dat1; run;

  data dat1;
    set dat1;
    count+1;
    by rep;

```

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        if first.rep then count=1;
run;

*proc print data=dat1;run;

*ods trace on; *Turn this on to see table names of any SAS
procedure.;
*ods trace ouput;
ods listing close;

proc glm data=dat1; by rep;
    class A B;
    model y = A|B;
    lsmeans A|B/pdiff;
    *ods output modelanova = anova(where=(HypothesisType=3)
        keep = HypothesisType source ms probf rep)
        differencematrix = diffs;
    *ods output OverallANOVA= rootmse;
    ods output FitStatistics=rootmse(keep= RootMSE rep);

run;
quit;
ods listing;
ods close;

*proc print data=rootmse;*run;

*merge dataset and rootmse by rep;
data dat1rmse;
    merge dat1 rootmse;
    by rep;
run;

*proc print data=dat1rmse;*run;

```

```

*adds outlier(this demonstrates its working);
/*
data datlout;
    set datlrmse;
    by rep;
    k=1;
    if count=15 then y1=y+k*RootMSE;
run;

proc print data=datlout;run;
*/

*adds outliers;
data datlout;
    set datlrmse;
    by rep;
    k=0;
    if count=15 then y=y+k*RootMSE;
    keep rep error n A B y;
run;

*proc sort data=datlout; by rep A B n; run;
*proc print data=datlout; *run;

*proc print data=datlout;*run;

*ods trace on; *Turn this on to see table names of any SAS procedure.;
*ods trace ouput;
ods listing close;
proc glm data=datlout; by rep;
    class A B;
    model y = A|B;
    lsmeans A|B/pdiff;
    ods output modelanova = anova(where=(HypothesisType=3) keep
    = HypothesisType source ms probf rep)
        differencematrix = diffs;
run;

```



```
quit;
ods listing;

*Count number of significant tests.;
proc sql;
    create table &out as select source, (count(rep))/&rep as
    propsign from anova where probf le 0.05
    group by source;
    /*order by source*/
quit;

proc print data=&out;run;

%mend;

%sim(out=set1);
```

```

%let rep = 1000;
%let n = 6;
%let seed = 1066;

%let mu11=5.9;
%let mu12=5.1;
%let mu21=4.1;
%let mu22=4.9;

*****
*ART with 15th obs Outlier*
*****;

%macro sim(artout=);
  data dat1;
    do rep = 1 to &rep;
      do n = 1 to &n;
        %do A = 1 %to 2;
          %do B = 1 %to 2;
            A = &A;
            B = &B;
            error = rannor(&seed);
            y=&&mu&A&B+error;
            output;
          %end;
        %end;
      end;
    end;
  run;

  proc sort data=dat1; by rep A B n; run;
  proc print data=dat1; run;

  data dat1;
    set dat1;
    count+1;

```

```

        by rep;
        if first.rep then count=1;
run;

*proc print data=dat1;run;

*ods trace on; *Turn this on to see table names of any SAS
  procedure.;
*ods trace ouput;
ods listing close;

proc glm data=dat1; by rep;
    class A B;
    model y = A|B;
    lsmeans A|B/pdiff;
    *ods output modelanova = anova(where=(HypothesisType=3)
      keep = HypothesisType source ms probf rep)
      differencematrix = diffs;
    *ods output OverallANOVA= rootmse;
    ods output  FitStatistics=rootmse(keep= RootMSE rep);

run;
quit;
ods listing;
*ods close;

*proc print data=rootmse;*run;

*merge dataset and rootmse by rep;
data dat1rmse;
    merge dat1 rootmse;
    by rep;
run;

*proc print data=dat1rmse;*run;

```

```

*adds outlier(this demonstrates its working);
/*
data datlout;
    set datlrmse;
    by rep;
    k=1;
    if count=15 then y1=y+k*RootMSE;
run;

proc print data=datlout;run;
*/

*adds outliers;
data datlout;
    set datlrmse;
    by rep;
    k=3;
    if count=15 then y=y+k*RootMSE;
    keep rep error n A B y;
run;

proc sort data=datlout; by rep A B n; run;
*proc print data=datlout; run;

proc means noprint data = datlout;
    by rep A B;
    var Y;
    output out = cellmeans mean = cell_mean;
run;

*proc print data=cellmeans;*run;

data two;
    merge datlout cellmeans;
    by rep A B;
run;

```

```

*proc print data=two;*run;

proc sort data=two;
    by rep A;
run;

proc means noprint data=two;
    by rep A;
    var cell_mean;
    output out=Ameans mean=A_mean;
run;

data three;
    merge two Ameans;
    by rep A;
run;

*proc print data=three;*run;

proc sort data=three;
    by rep B;
run;

proc means noprint data=three;
    by rep B;
    var cell_mean;
    output out=Bmeans mean=B_mean;
run;

*proc print data=Bmeans;*run;

data four;
    merge three Bmeans;
    by rep B;
run;

*proc print data=four;*run;

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proc sort data=four;
    by rep;
run;

proc means data=four noprint;
    by rep;
    var cell_mean;
    output out=grandmean mean=g_mean;
run;

*proc print data=grandmean;*run;

data five;
    merge four grandmean;
    by rep;
run;

*proc print data=five;*run;

data align;
    set five;
    error = y - cell_mean;
    A_align = error + (A_mean - G_mean);
    B_align = error + (B_mean - G_mean);
    AB_align = error + (cell_mean - A_mean - B_mean + g_mean);
run;

*proc print data=align;*run;

proc rank data = align out = alignrank;
    by rep;
    var A_align B_align AB_align;
    ranks AR_align BR_align ABR_align;
run;

*proc print data=alignrank;*run;

*ods trace on; *Turn this on to see table names of any SAS

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    procedure.;
ods listing close;
proc glm data=alignrank; by rep;
    class A B;
    model AR_align BR_align ABR_align = A|B;
    lsmeans A|B/pdiff;
    ods output modelanova = anova(where=(HypothesisType=3) keep
        = HypothesisType dependent source probf rep);
run;
quit;
ods listing;

*Count number of significant tests.;
proc sql;
    create table &artout as select dependent, source,
        (count(rep))/&rep as propsign from anova where probf le 0.05
        group by dependent, source;
quit;

Title 'Proportion of factors that tested at a 0.05 level of
    significance';
proc print data=&artout noobs;run;

quit;

proc print data=&artout;run;

%mend;

%sim(artout=set1);

```