Paper SD-06

Analyzing Multiway Models with ANOM Slicing

Peter Wludyka, University of North Florida

ABSTRACT

Multiway (multifactor) models with significant interaction can be analyzed using simple effect comparisons. These F-tests are multiple comparisons which are referred to as slice tests (e.g., in a two factor study one slices by factor A by comparing the levels of factor B for each level of A). Slicing uses the full model degrees of freedom and MSE. This paper shows how to use Analysis of Means (ANOM) methods from the multiple comparisons platform in JMP11 to create ANOM decision charts for each of the slice values. These ANOM charts tell more about the relationship among the factor levels than the F tests.

INTRODUCTION

Factorial studies with an interval continuous response and several explanatory variables are the subject of this paper. In particular we are interested in cases in which there is significant interaction between explanatory variables. We will introduce the idea using an example from *The Analysis of Means* (Nelson, et al, 2005, Example 5.3/5.8, page 89).

> A 3×2 factorial experiment was designed to study the effect of three monomers and two levels of UV exposure (UV versus no UV) on the percent yield for contact lens production. There were 4 replicates at each factor level combination. That is, there are a total of 24 observations in this study. The data is in Table 1.

Table 1: Data from Process Yield Study

	UV (A=1)		No UV (A = 2)	
monomer 1 (B = 1)	88.4	89.1	90.9	92.3
	90.9	90.8	92.3	92.3
monomer 2 (B = 2)	93.0	93.7	88.3	89.5
	93.4	92.9	88.0	89.6
monomer 3 (B =3)	94.2	95.1	91.0	90.0
	96.4	95.7	92.4	92.8

The means plot tells most of the story and helps keep the efforts to "prove" certain conclusions in perspective. Since the "lines" are not parallel —in fact, they intersect —the means plot (Figure 1) strongly suggests interaction

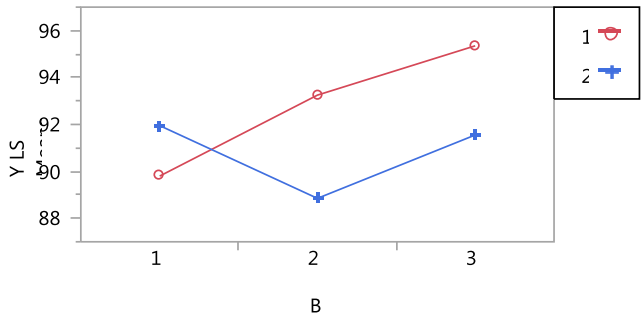


Figure 1: Means Plot for Process Yield Data.

The model for this study is:

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \epsilon_{ijk}$$

We will associate $\alpha_i, i = 1,2$ with factor A (in this example UV exposure) and β_j, j=1,2,3 with factor B (monomer). In general there are I levels of factor A and J levels of factor B and hence $I \times J$ factor level combinations. The term $(\alpha\beta)_{ij}$ is the interaction term, which when nonzero for some (i, j) indicates that the effect of B (monomer) depends on the level of factor A (UV) —and conversely. The three general null hypotheses of interest are:

$$H_A: \alpha_i = 0 \text{ for all } i.$$

$$H_B: \beta_i = 0 \text{ for all } j.$$

$$H_{AB}: (\alpha\beta)_{ij} = 0 \text{ for all } (i, j).$$

Table 2: ANOVA-F Tests for Process Yield Data; ANOVA Table

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
B	2	2	33.123333	18.4588	<.0001*
A	1	1	24.401667	27.1969	<.0001*
A*B	2	2	52.443333	29.2254	<.0001*

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	5	109.96833	21.9937	24.5131
Error	18	16.15000	0.8972	**Prob > F**
C. Total	23	126.11833		<.0001*

There is strong evidence for interaction (Table 2); that is H_{AB} is rejected (F = 29.22, p < 0.0001). When $H_{AB}: (\alpha\beta)_{ij} = 0$ is rejected, then interaction is present. Typically this means that the main effects hypotheses (H_A and H_B) are of little (or problematical) interest. For a two factor factorial with interaction one has the following analysis choices:

1. Convert to a 1-way layout in which there are now IJ factor level combinations explaining the response Y.
2. A simple effects analysis using “by analysis” which decomposes the problem into an independent set of sub-problems, one for each level of the “by” variable. Each sub-problem has fewer degrees of freedom than the full model; however, one need only assume that the row variances (or column variances) for the error term are equal.
3. A simple effects analysis using “Slicing” which is similar in appearance to “by analysis” but uses the entire full model degrees of freedom and an overall estimate for the variance of the error term (which implies belief that all IJ cell variances are equal).
4. Other choices, including specific comparisons (contrasts).

The choice is motivated by (1) the study goals (2) statistical considerations (assumptions underlying the method chosen), in particular the variance of the error term in the model. The advantage of slicing is the increase in the degrees of freedom (and increased precision in estimating the variance of the error term), which probably accounts for its recent popularity.

SLICING

The basic idea is to compare the levels of one factor for each level of the other factor. “Simple effects analysis” is the usual way to describe this.

Slicing using contrasts

Slicing is a set of simultaneous contrasts. The idea is simple. Suppose in our process yield example we slice by factor A (UV). That is we will first compare the levels of factor B for A = 1 and the repeat this for A = 2. The first contrast tests

$$H_0: \mu_{11} = \mu_{12} = \mu_{13}$$

which compares the monomers for UV present (A = 1). This is equivalent to 3 simultaneous tests:

$$\mu_{11} = \mu_{12};\ \mu_{11} = \mu_{13}; \mu_{12} = \mu_{13}$$

These three equalities are what the contrast statement tests. In SAS all is done in terms of the effects model, so $\mu_{11} - \mu_{12} = (\mu + \alpha_1 + \beta_1 + (\alpha\beta)_{11}) - (\mu + \alpha_1 + \beta_2 + (\alpha\beta)_{12}) = \beta_1 - \beta_2 + (\alpha\beta)_{11} - (\alpha\beta)_{12}$ which is used to build the first contrast (note the three contrasts are separated by commas).

```
PROC GLM data = ex5_3;
class A B;
model y = A B A*B ;
contrast 'Slice approach: slice by Factor A =1 (UV)/ compares monomers'
   B 1 -1 0  A*B 1 -1 0   0 0 0  ,
   B 1 0 -1  A*B 1 0 -1   0 0 0  ,
   B 0 1 -1  A*B 0 1 -1   0 0  0 ;
contrast 'Slice approach: slice by Factor A = 2 (no UV)/ compares monomers'
   B 1 -1 0  A*B 0 0 0  1 -1 0,
   B 1 0 -1  A*B 0 0 0  1 0 -1,
   B 0 1 -1  A*B 0 0 0  0 1 -1;
run;
```

The SAS output:

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
Slice approach: slice by Factor A =1 (UV)/ compares monomers	2	62.8200	31.410	35.01	<.0001
Slice approach: slice by Factor A = 2 (no UV)/ compares monomers	2	22.7466	11.373	12.68	0.0004

Slicing using PROC MIXED or the JMP Dropdown in the Least Squares Platform

Slicing is now easy to do in SAS using PROC GLM or PROC MIXED. An identical result can be produced using JMP within the least squares platform using the slice dropdown. The ideas will be illustrated by slicing by Factor A.

SAS PROC MIXED

```
Proc MIXED data=ex5_3;
 class A B;
 model y = A|B;
 lsmeans A*B/diff;
 lsmeans A*B/slice = A;
 ods output diffs=cld;
 title 'Proc MIxed with Slice';
run;
```

Tests of Effect Slices					
Effect	A	Num DF	Den DF	F Value	Pr > F
A*B	1	2	18	35.01	<.0001
A*B	2	2	18	12.68	0.0004

JMP Dropdown

In JMP using the dropdown and selecting "Test Slices" one gets the report below. Based on the p-values one concludes that the average yields differ for monomer for both A = 1 (UV) and A = 2 (no UV). The F statistics and p-values are identical to those produced with PROC MIXED.

Slice A=1
Test Detail

1,1	-1	-1
1,2	1	0
1,3	0	1
2,1	0	0
2,2	0	0
2,3	0	0
Estimate	3.45	5.55
Std Error	0.6698	0.6698
t Ratio	5.1509	8.2862
Prob>|t|	0.0001	1.5e-7
SS	23.805	61.605

SS	NumDF	DenDF	F Ratio	Prob > F
62.82	2	18	35.0080	<.0001*

Slice A=2
Test Detail

1,1	0	0
1,2	0	0
1,3	0	0
2,1	-1	-1
2,2	1	0
2,3	0	1
Estimate	-3.1	-0.4
Std Error	0.6698	0.6698
t Ratio	-4.628	-0.597
Prob>|t|	0.0002	0.5578
SS	19.22	0.32

SS	NumDF	DenDF	F Ratio	Prob > F
22.75	2	18	12.6762	0.0004*

ANOM Slicing

ANOM Slicing with SAS

```
title 'Slice Analysis: ANOM with Full Model MSE/df';
PROC ANOM  data = ex5_3;by A;
xchart y*B / mse = 0.8972222  dfe = 18;
run;
```

The basic idea is to do an ANOM chart for each level of factor A (the by statement) using the degrees of freedom from MSE in the full model (dfe = 18, see Table 2) and MSE from the full model (mse =0.8972). This differs from the by-analysis in as far as the degrees of freedom are greater. One of the two ANOM charts is below (Figure 2).

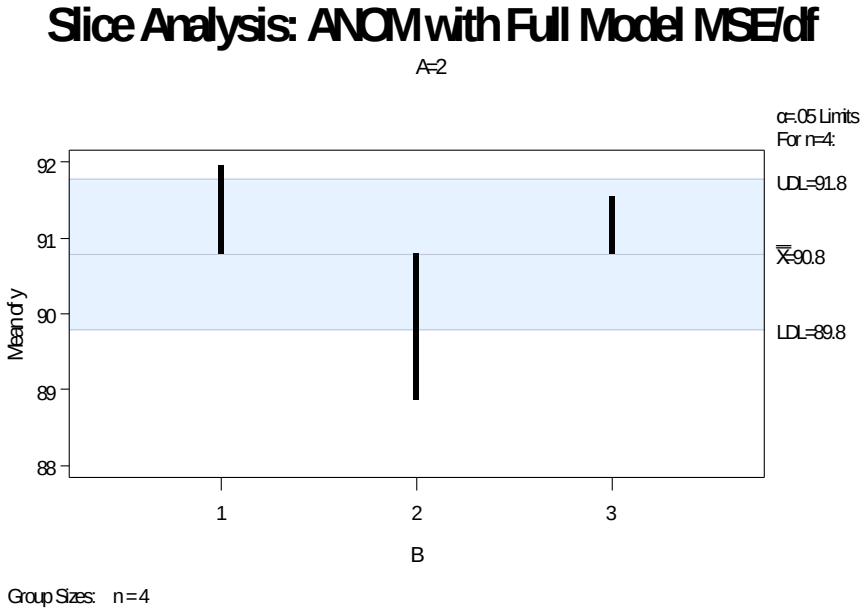
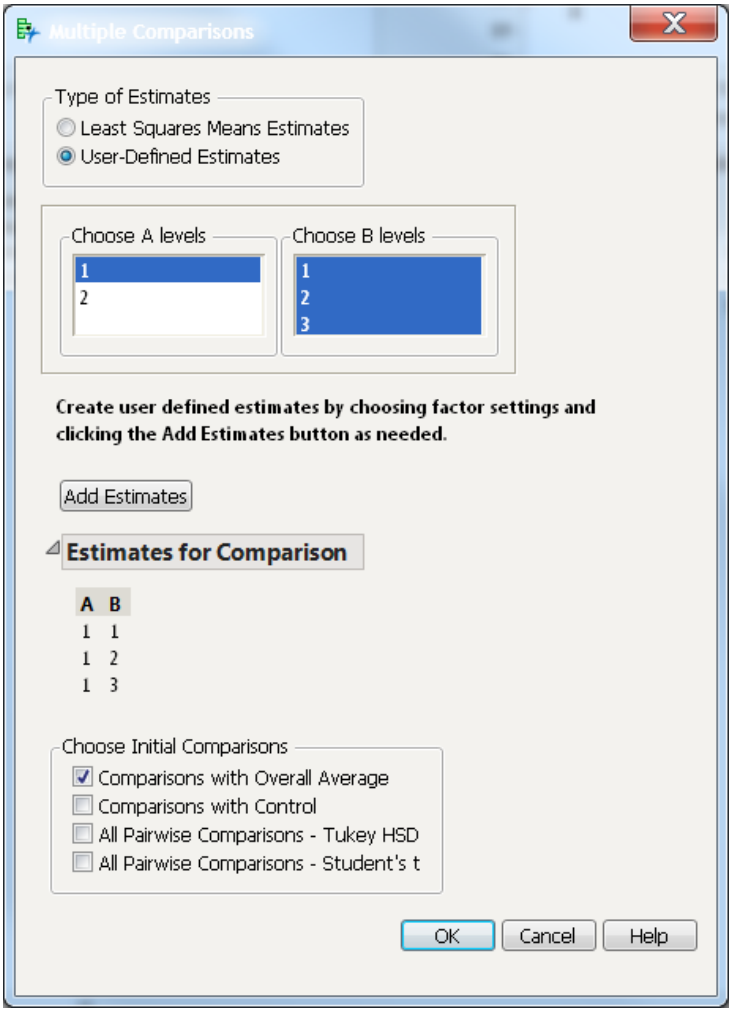


Figure 2: ANOM Decision Chart for Based on Slicing for A = 2 using SAS.

ANOM Slicing with the Multiple Comparisons Platform in JMP11

We will slice by factor A (UV versus no UV). To get the ANOM chart for the slices, select Multiple Comparisons from under the Estimates submenu in the Fit Least Squares platform (this is after analyze > fit model > arrow over A, B, A*B and the response). In the initial dialog there are radio buttons at the top for choosing the type of estimates. Switch the type to “User-Defined Estimates”. Now list boxes should appear for each effect. For “A” only choose “1”. For “B” choose all three levels. Now click on the “Add Estimates” button. The estimates that you have chosen will be listed in the dialog. Now you can check “Comparison with Overall Average” to get an ANOM chart when you launch the multiple comparisons. Here is a picture of the dialog right before I am about to click on the “OK” button.



Display 1: Dialog for ANOM Slicing.

The JMP report from this follows. The ANOM chart for A = 1 (Figure 3) shows that the three monomers differ. In particular, the average for monomer 1 is below the overall average and the average for monomer 3 is above the overall average. Note that the ANOM decision charts are identical to those produced using SAS.

Comparisons with Overall Average

A = 1

Quantile = 2.5522,
Avg = 92.8,
Adjustment = Nelson

Differences from Overall Average

B	-B	Difference	Std Error	DF	Lower 95%	Upper 95%
1	Avg	-3.00000	0.3867002	18	-3.98694	-2.01306
2	Avg	0.45000	0.3867002	18	-0.53694	1.43694
3	Avg	2.55000	0.3867002	18	1.56306	3.53694

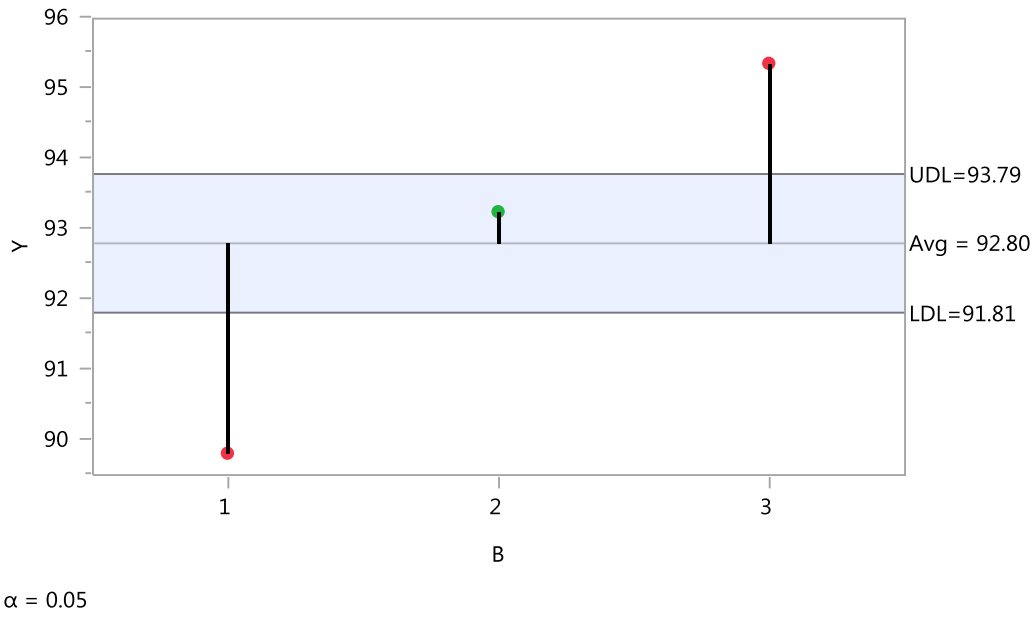


Figure 3: ANOM decision Chart using JMP11 Multiple Comparisons.

For completeness the JMP report for A = 2 is below. Note that for A = 2 (no UV) the monomers differ, but in an entirely different manner than in the A = 1 case — revealing the nature of the interaction. The average yield for monomer 1 is above the overall average and monomer 2 is below the overall average.

Multiple Comparisons
Comparisons with Overall Average

A = 2
Quantile = 2.5522,
Avg = 90.7833,
Adjustment = Nelson

Differences from Overall Average

B	-B	Difference	Std Error	DF	Lower 95%	Upper 95%
1	Avg	1.16667	0.3867002	18	0.17973	2.15360
2	Avg	-1.93333	0.3867002	18	-2.92027	-0.94640
3	Avg	0.76667	0.3867002	18	-0.22027	1.75360

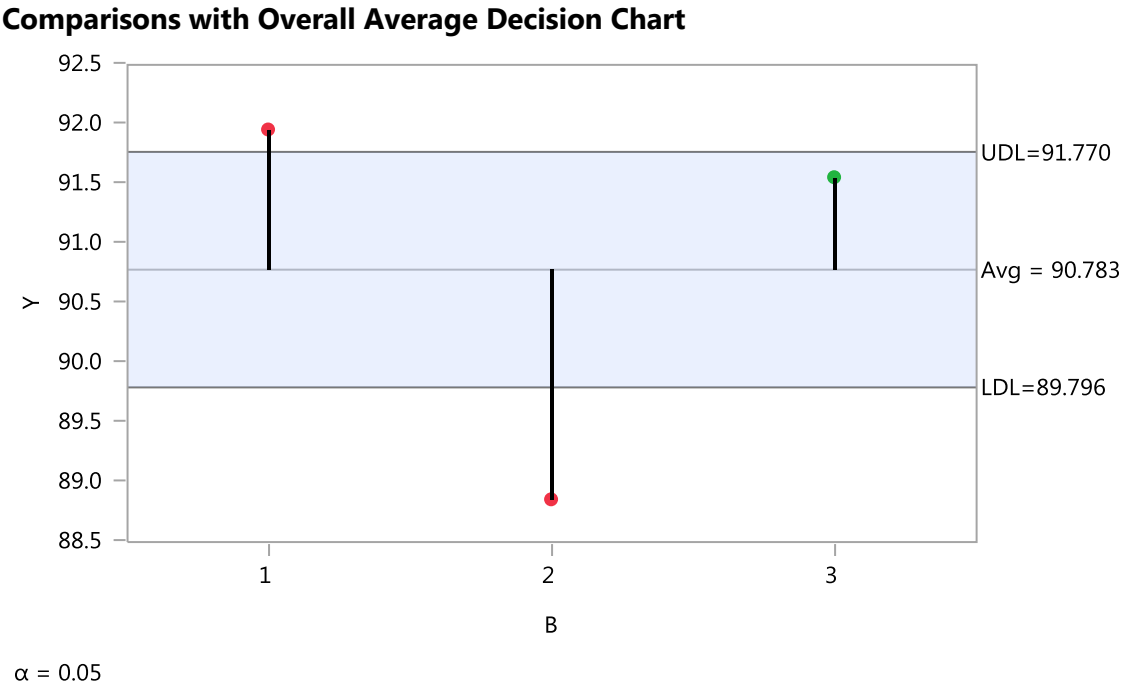


Figure 4: ANOM Decision Chart for A = 1 Using JMP 11.

ADVANTAGES OF ANOM SLICING

We have looked at slicing using contrasts, PROC MIXED, the JMP dropdown, and ANOM. The first three of these always produce the same F statistics and hence identical conclusions. The contrasts formulation is included to identify slicing as a multiple comparison procedure. ANOM is a natural choice for multiple comparisons and the ANOM decision chart exposes the nature of differences between the levels of "Factor B" for each level of "Factor A".

Assumptions for ANOM Slicing

The assumptions for ANOM are identical to those for the multiple comparison F tests.

1. The IJ cell variances are all equal; equivalently the variances of the error term in the model is constant.
2. The data in the IJ cells can reasonably me modeled as being a sample from a normal population with means μ_{ij}. Equivalently, the residuals are approximately normal.
3. The IJ samples are independent.

When normality is a safe assumption the cell variances can be tested using Analysis of Means for Variances (ANOMV). From the decision chart below (Figure 5) one cannot reject the equal variances hypothesis since all of the sample standard deviations plot within the decision limits.

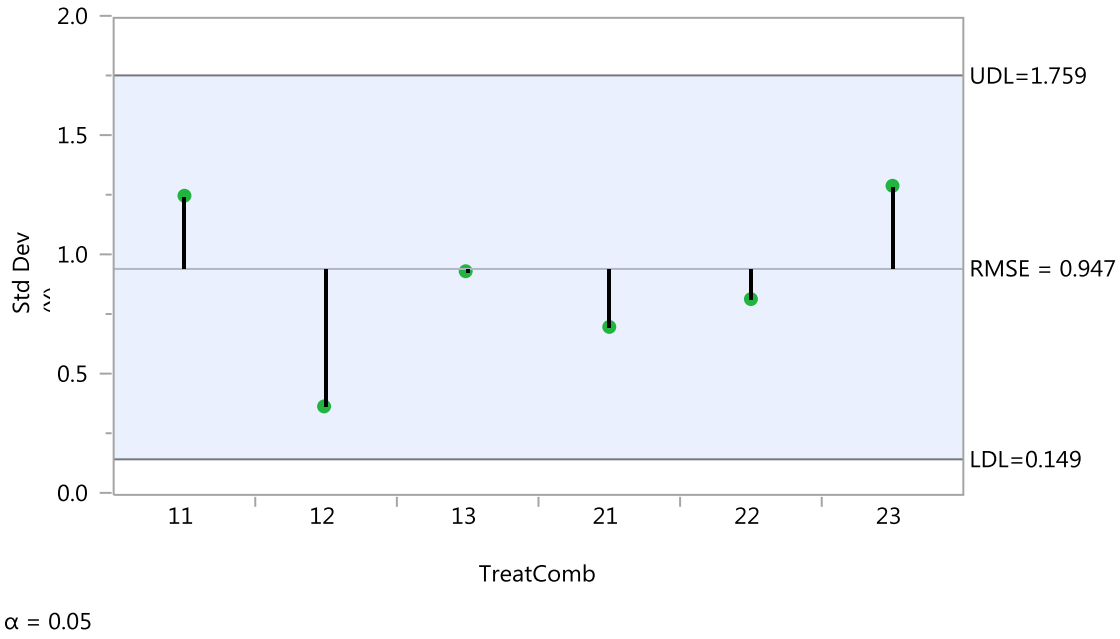


Figure 5: ANOMV Decision Chart FOR Comparing the Variances(JMP 11).

If there are concerns about normality (the tests on means are more robust to moderate departures from normality that variance tests), then a safer choice is the ANOM version of Levene's test. From the decision chart below (JMP11) one cannot reject the equal variances hypothesis since all of the ADMs plot within the decision limits.

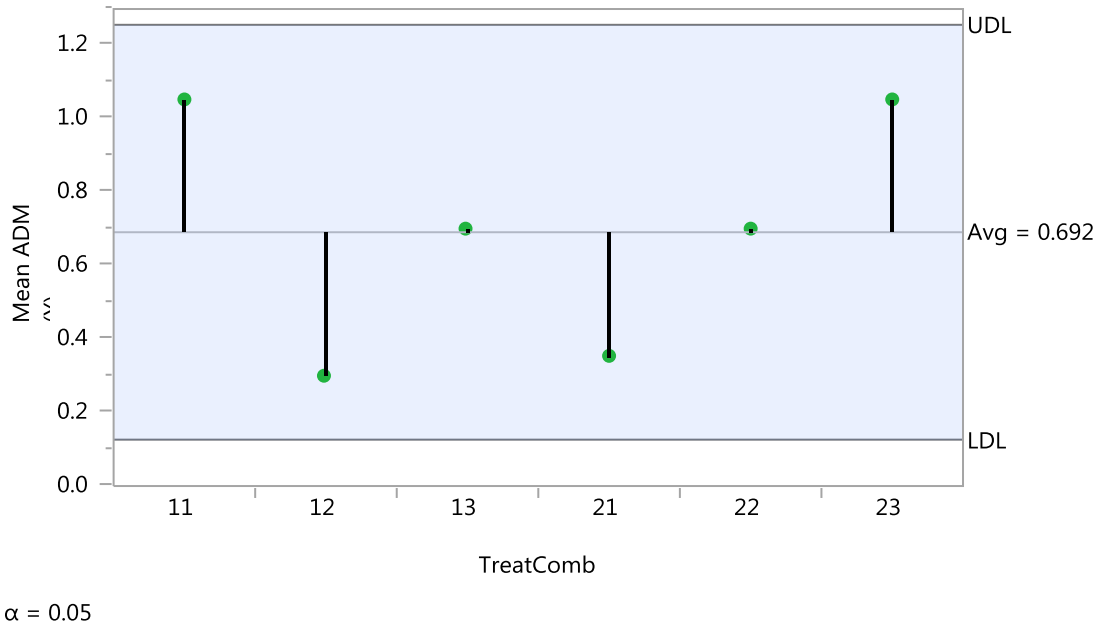


Figure 6: ANOM Decision Chart for Levene's Test.

The normal quantile plot (not shown) for the full model residuals indicates that the normality assumption is reasonable.

F-Tests and ANOM Conclusions are Potentially Different

Since the F-tests for slicing and ANOM are testing slightly different things there is the potential that the two approaches will not agree — even though both are using the same MSE and degrees of freedom. The two approaches have about the same power (see Nelson et all, 2005).

When Slicing is a Bad Idea

If the cell variances are significantly different and the data cannot be transformed to correct this then using MSE to estimate the variance of the error term is suspect. Often "by analysis" instead of the simple effects analysis based on slicing will work since then only the row or column variances need be equal. For example, in the process yield example, for A = 1, then only the variances for the three monomer types need be equal.

MORE THEN TWO FACTORS / UNBALANCED DESIGNS

The presentation in this paper has been for a balanced two factor study with significant interaction. The lack of balance creates not additional problems. For example, suppose two of the observations are missing for A = 2 (no UV) and B = 3 (monomer 3). Then slicing with A = 2 yields the ANOM Decision Chart below (Figure 7):

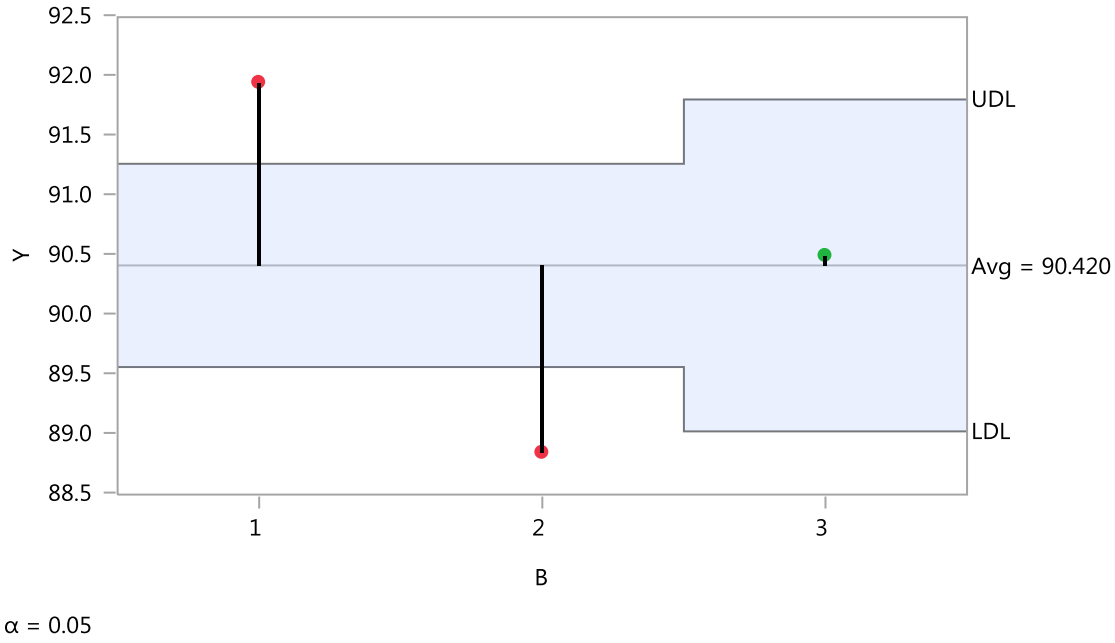


Figure 7: ANOM Decision Chart Slicing with A = 2 in an Unbalanced Design.

Note that there are now two pairs of ANOM decision lines. One for B = 1,2 (n = 4 replicates) and one for B = 3 (n = 2 replicates). The second pair of decision lines is wider since the sample size is smaller. One concludes that monomer does matter for A = 2 (no UV) since monomer 1 plots above the upper decision line indicating that it is above the overall average; and monomer 2 plots below the lower decision limit indicating it is lower than the overall average.

When there are more than two factors slicing is still an option; however, there are then several slicing strategies available to the analyst.

REFERENCES

Nelson, Peter R, Peter S. Wludyka, and Karen A. F. Copeland, *The Analysis of Means: A Graphical Method for Comparing Means, Rates, and Proportions*, ASA-SIAM Series on Statistics and Applied Probability, SIAM, Philadelphia, ASA, Alexandria, VA, 2005.

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CONTACT INFORMATION

Peter Wludyka, PhD

Professor of Statistics

Department of Mathematic & Statistics

University of North Florida

pwlufyka@unf.edu / www.wludyka.com