Topic 12: Split plot design and its relatives

- A comment on error
- Split plot design as an RCBD
- Another way to think about the main plot error
- Split plot design as a CRD
- Split plot design as a Latin Square
- Split plot approach to repeated measurements (time as a subplot effect)
- Repeated measurements using the REPEATED statement
- APPENDIX: The standard split plot analysis for Example 8.4

A Comment on Error

How you randomize your experimental units determines your experimental design, and your experimental design determines the error terms for all tests – there is no way around this, end of story. So, once you decide on an experimental design, the error terms associated with that design must be used consistently in F-tests, contrasts, mean separations, everything.

Split Plot Design as an RCBD

A split plot design results from a two-stage randomization process of a factorial treatment structure. Because of this two-stage process, there is higher sensitivity in detecting differences among subplot treatments (the second level), as well as the significance of the MainPlot*Subplot interaction. There is less sensitivity in detecting differences among main plot treatments (the first level of randomization).

Example 8.1

This experiment is an example of a split plot design organized as an RCBD. A significant interaction is found between main plots and subplots; thus an analysis of simple effects is required. In this study, four different seed lots of oats (main plots) are randomized within four blocks, and four different seed treatments (subplots) are randomized within each of the sixteen main plots:

<table>
<thead>
<tr>
<th>Blocks:</th>
<th>Four</th>
</tr>
</thead>
<tbody>
<tr>
<td>Main plots (seed lots):</td>
<td>Four</td>
</tr>
<tr>
<td>Subplots (seed treatments):</td>
<td>Four (includes one control)</td>
</tr>
</tbody>
</table>

![Diagram of split plot design](image-url)
Note that in this case the greater precision is afforded to the seed treatments (subplots) and the lesser to the seed lots (main plots). If the primary intention is to investigate differences among seed treatments, one possible reason to choose this design would be to extend the scope of the experiment across seed lots.

**Data** SPRCBD;
Do Block = 1 to 4;
Do SeedLotA = 1 to 4; * We will have less precision here;
Do TrtmtB = 1 to 4; * We will have more precision here;
Input Yield @@;
Output;
End;
End;
End;
Cards;
42.9  53.8  49.5  44.4  28.9  43.9  40.7  28.3
53.3  57.6  59.8  64.1  45.4  42.4  41.4  44.1
62.3  63.4  64.5  63.6  44.6  45.0  62.6  52.7
75.4  70.3  68.8  71.6  54.0  57.6  45.6  56.6
41.6  58.5  53.8  41.8  30.8  46.3  39.4  34.7
69.6  69.6  65.8  57.4  35.1  51.9  45.4  51.6
58.5  50.4  46.1  56.1  50.3  46.7  50.3  51.8
65.6  67.3  65.3  69.4  52.7  58.5  51.0  47.4

**Proc GLM Data = SPRCBD;**
Class Block SeedLotA TrtmtB;
Model Yield = Block SeedLotA Block*SeedLotA /* Correct error term for A */ TrtmtB SeedLotA*TrtmtB;
Test h = SeedLotA e = Block*SeedLotA; * Specify the correct error for testing A;
Run;
Quit;

As we have seen before in some previous examples (nested experiments, mixed models), in a split plot design we need to use the Test statement in order to carry out the appropriate F-tests. As before, the generic syntax for this statement is

```
Test h = Numerator e = Denominator;
```

where "Numerator" and "Denominator" refer to the numerator and denominator in a specialized F-test. For this split plot, the main plot SeedLotA is the “Numerator.” Since the main plots were randomized according to an RCBD, the “Denominator” is Block*SeedLotA. If the main plots had been randomized according to a CRD, the “Denominator” would be Replication*SeedLotA.

**Output**

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>27</td>
<td>7066.191875</td>
<td>261.710810</td>
<td>12.89</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>36</td>
<td>731.202500</td>
<td>20.311181</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>63</td>
<td>7797.394375</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>R-Square</td>
<td></td>
<td>0.906225</td>
<td>8.534077</td>
<td>4.506793</td>
<td>52.80938</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Block</td>
<td>3</td>
<td>2842.873125</td>
<td>947.624375</td>
<td>46.66</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>SeedLotA</td>
<td>3</td>
<td>2842.873125</td>
<td>947.624375</td>
<td>46.66</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Block*SeedLotA</td>
<td>9</td>
<td>618.294375</td>
<td>68.699375</td>
<td>3.38</td>
<td>0.0042</td>
</tr>
<tr>
<td>TrtmtB</td>
<td>3</td>
<td>170.536875</td>
<td>56.845625</td>
<td>2.80</td>
<td>0.0539 NS</td>
</tr>
<tr>
<td>SeedLotA*TrtmtB</td>
<td>9</td>
<td>586.465625</td>
<td>65.162847</td>
<td>3.21</td>
<td>0.0059 *</td>
</tr>
</tbody>
</table>

---

PLS205 2012

Lab 8 (Topic 12)
Tests of Hypotheses Using the Type III MS for Block*SeedLotA as an Error Term

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>SeedLotA</td>
<td>3</td>
<td>2848.021875</td>
<td>949.340625</td>
<td>13.82</td>
<td>0.0010 **</td>
</tr>
</tbody>
</table>

The F values indicate significant differences among seed lots (p = 0.001), no significant differences (barely) among seed treatments (p = 0.0539), and a significant interaction (p = 0.0059). If there were no significant interaction, we could analyze the main effects of the main plot and subplot by adding the following lines to the Proc GLM:

```sas
Means SeedLotA / Tukey e = Block*SeedLotA;
Means TrtmtB / Dunnett;
```

BUT, since the interaction is significant, we cannot make comparisons among the main effects. Rather, we can use Dunnett's Test to compare the simple effects of each seed treatment against the control within each seed lot:

```
Example 8.1b  [Lab8ex1b.sas]
```

```
Proc Sort;
   By SeedLotA;
Proc GLM Data = SPRCBD;
Class Block TrtmtB;
Model Yield = Block TrtmtB;
Means TrtmtB / Dunnett; * Control will be #1 if not specified;
By SeedLotA; * Draw conclusions within each seed lot separately;
```

**Output Summary**

<table>
<thead>
<tr>
<th>SeedLotA</th>
<th>TrtmtB p-value</th>
<th>S / NS</th>
</tr>
</thead>
<tbody>
<tr>
<td>a1</td>
<td>0.0001</td>
<td>***</td>
</tr>
<tr>
<td>a2</td>
<td>0.7312</td>
<td>NS</td>
</tr>
<tr>
<td>a3</td>
<td>0.6093</td>
<td>NS</td>
</tr>
<tr>
<td>a4</td>
<td>0.2109</td>
<td>NS</td>
</tr>
</tbody>
</table>

**Rankings and pairwise comparisons of treatments (2, 3, 4) vs. control (1) within each seed lot**

```
<table>
<thead>
<tr>
<th>SeedLot A</th>
</tr>
</thead>
<tbody>
<tr>
<td>a1</td>
</tr>
<tr>
<td>2 *</td>
</tr>
<tr>
<td>3 *</td>
</tr>
<tr>
<td>4</td>
</tr>
</tbody>
</table>
```

Notice that the seed treatment (Factor B) is found to have a significant effect in Seed Lot 1, in contradiction to the original NS ANOVA result for the subplot (p = 0.0539). This is why it is important to look at simple effects when there is a significant interaction.
Another way to think about the Main Plot error

Chew on this: The correct error term produces the same F- and p-values for the main plot effect (A) that you get if you simply average the subplots (B). Let's look again at the RCBD example from above; but this time we'll average over the subplots, essentially removing the subplot treatments from the experiment:

Example 8.2

Data SPRCBD;
  Do SeedLotA = 1 to 4;
  Do Block = 1 to 4;
    Input AveYield @@;
    Output;
  End;
End;
Cards;
47.65 58.7 63.45 71.525
48.925 65.6 52.775 66.9
35.45 43.325 51.225 53.45
37.8 46 49.775 52.4
;
Proc GLM Data = SPRCBD;
  Class Block SeedLotA;
  Model AveYield = Block SeedLotA;
Run;
Quit;

Lo and behold, the output we get matches the previous results exactly:

Source                      DF     Type III SS     Mean Square    F Value    Pr > F
Block                        3     710.7182813     236.9060938      13.79    0.0010
SeedLotA                     3     712.0054688     237.3351563      13.82    0.0010

In addition to confirming that Block*SeedLotA is the appropriate error term to use for SeedLotA, this result illustrates that in a split plot design the main plot effect is totally insensitive to the variation among subplots (i.e. when comparing main plot effects, subplots act as subsamples).

Split Plot Design as a CRD

Recall that in a CRD, “Replication” does not appear in the Class or Model statements because variation among replications within a given treatment level is the source of error for the experiment. In a split plot design organized as a CRD, however, the Replication*A interaction is needed as the appropriate error term for the main plot; to use it in this way, we must include it in the Model statement. **BE AWARE:** When you include "Replication*A" in the Model without including "Replication" by itself, SAS automatically produces a SS labeled "Replication*A" that includes SS for "Replication" AND "Replication*A" combined. In general:

- **Model y = A A*B;**  
  * Produces SS called “(A*B)” = SS (A*B) + SS (B);
- **Model y = B A*B;**  
  * Produces SS called “(A*B)” = SS (A*B) + SS (A);
- **Model y = A*B;**  
  * Produces SS called “(A*B)” = SS (A*B) + SS (A) + SS (B);
Here is how the experiment above might look had the main plots been randomized as a CRD.

To accommodate this new design, the SAS code would be changed by first substituting Reps for Blocks in the input and then modifying the Class and Model statements appropriately:

**Example 8.3**

```
Data SPCRD;
  Do Rep = 1 to 4;
    Do SeedLotA = 1 to 4; /* We will have less precision here;*/
      Do TrtmtB = 1 to 4; /* We will have more precision here;*/
        Input Yield @@;
      ;
    ;
  ;
Input Yield @@;
...
Proc GLM Data = SPCRD;
  Class Rep SeedLotA TrtmtB;
  Model Yield = SeedLotA /*Correct error term for A*/
      Rep*SeedLotA /*Correct error term for A*/
      TrtmtB
      SeedLotA*TrtmtB; /* Notice "Rep" alone does not appear in the Model;*/
  Test h = SeedLotA e = Rep*SeedLotA; /* Specify the correct error for testing A;*/
Run;
Quit;
```

Again, "Rep" appears in the Class statement only because we need Rep*SeedLotA as the error term for the main plot, not because we in some way want to test for significant differences among replications. It is also worth mentioning that the inclusion of the Rep*SeedLotA term in the model is what distinguishes this experiment from a CRD factorial.

**Output**

```
Source            DF     Type III SS     Mean Square    F Value    Pr > F
SeedLotA          3     2812.51825        937.50625      46.74    <.0001
Rep*SeedLotA      12     3461.16750        288.43062      14.20    <.0001
TrtmtB            3      170.53687        56.84562        2.80    0.0539  NS
SeedLotA*TrtmtB   9      586.46562        65.16284        3.21    0.0059  **
```

R-Square  Coeff Var  Root MSE  Yield Mean
0.906225  8.534077  4.506793  52.80938

Source            DF     Type III SS     Mean Square    F Value    Pr > F
Model             27     7066.19187        261.71081      12.89    <.0001
Error             36     731.20250         20.31118
Corrected Total   63     7797.39437
Tests of Hypotheses Using the Type III MS for Rep*SeedLotA as an Error Term

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>SeedLotA</td>
<td>3</td>
<td>2848.021875</td>
<td>949.340625</td>
<td>3.29</td>
<td>0.0581</td>
</tr>
</tbody>
</table>

Analyzing this set of data as though it were a CRD leads to a NS main effect of seed lot (p = 0.0581), in contrast to its significant effect under the RCBD. Does this make sense? Now, because there is a significant interaction, our analysis must continue with the simple effects. The code is similar to the RCBD case:

**Example 8.3b**

```
Proc Sort Data = SPCRD;
   By SeedLotA;
Proc GLM Data = SPCRD;
   Class TrtmtB;  * we eliminate Rep from Class b/c we no longer need it as an error term;
   Model Yield = TrtmtB;
   Means TrtmtB / Dunnett;
   By SeedLotA;
```

And the results can be summarized in a manner similar to the one shown above for the RCBD case.

**Split Plot Design as a Latin Square**

How would this split plot look as a Latin Square?

```
+-----+-----+-----+-----+
| Col | Col | Col | Col |
+-----+-----+-----+-----+
| MP3 | MP1 | MP4 | MP2 |
+-----+-----+-----+-----+
| MP2 | SP4 | SP1 | MP3 | MP1 |
| SP3 | SP2 |     |     |     |
+-----+-----+-----+-----+
| MP2 | MP3 | MP1 | MP2 |
| MP1 | MP2 | MP2 | MP3 |
+-----+-----+-----+-----+
```

In a Latin Square, “Row” and "Col" are both blocking variables and therefore both need to appear in the MODEL statement. The error term for the main plot (SeedLotA) is now "Row*Col*SeedLotA," and SAS
will automatically include in this term all possible two-way interactions among these effects (e.g. Row*Col, Row*SeedLotA, and Col*SeedLotA):

```
Proc GLM Data = SPLS;
  Class Row Col SeedLotA TrtmtB;
  Model Yield = Row Col SeedLotA Row*Col*SeedLotA /*Correct error term for A*/ TrtmtB SeedLotA*TrtmtB;
  Test h = SeedLotA e = Row*Col*SeedLotA; * Specify the correct error for testing A;
```

**Repeated Measurements (time as a subplot effect)**

By repeatedly measuring the same experimental unit at different points in time, one can gain insight into the effect of time on the observations. In this way, "time" is similar to a subplot effect in a split plot design; there are two major differences, however:

1. Whereas true subplots can be assigned randomly, "time" cannot.
2. Because the observations are made on the same experimental units, the observations are not independent from one another and the degrees of freedom must be adjusted appropriately.

Before going through a specific example, let's first take a moment and outline the analysis protocol you should follow if you have an experiment in which you are carrying out repeated measures:

1. First, treat the repeated measures as a subplot effect of time in a split plot design, run the analysis as you would any split plot, and look at the resultant ANOVA.

2. Then, *by hand*, reduce the subplot degrees of freedom to 1 (this will also affect the mainplot*subplot interaction df and the error df) and recalculate p-values for the subplot and the mainplot*subplot interaction(s). Note that this procedure will not affect your F-values; it only affects the df of the critical F-value and thus the corresponding p-values.

3. Next, compare the results of the normal split plot ANOVA [from Step 1] and the conservative df ANOVA [from Step 2]:
   - If both are significant, the effects are significant. [STOP]
   - If both are NS, the effects are NS. [STOP]
   - If the full df ANOVA is significant but the conservative df ANOVA is not, perform a repeated measures analysis using SAS. [Go to Step 4]

4. When you perform a repeated measures analysis, you will obtain two tables in the output:
   - **Between subjects effects**: This corresponds to the main plot effects in your experiment. The F- and p-values in this table will match those in the full df ANOVA, as long as the correct error term is specified in the "Test" statement. These results are valid.
   - **Within subjects effects**: This corresponds to the subplot effects. There are three columns of p-values in this table:
     - **"p"**: These values are the p-values generated using the full df; they match the p-values in your original split plot ANOVA and should not be used. They should not be used because they result from assuming that all the measurements in your experiment are
perfectly independent from one another (not the case when taking repeated measures on the same experimental units).

2) "G-G" These p-values are generated using adjusted df based on the actual correlations found in the data. In reality, your measurements are not perfectly independent (full df) or perfectly correlated (conservative df) – they are somewhere in between. The G-G procedure tries to find this middle ground. **USE THESE P-VALUES.**

3) "H-F" Another method of adjusting df, but not as conservative as G-G.

A Final Comment: All this being said, if you have a significant Orthogonal Components Sphericity Test, you should not use any of the results from the Within-Subjects table, not even the G-G values. Failing this test is akin to failing Levene’s for an ANOVA. Either some remediation needs to be done to the data so that you no longer fail it (i.e. transformation), or you need to find some other way to analyze your data.

**Repeated Measures Using the REPEATED Statement**

So, your full-df ANOVA was significant but your conservative-df ANOVA was not. SAS to the rescue: The **Repeated** statement in **Proc GLM** provides a slick way of adjusting for correlations among repeated observations of the same experimental units.

**Example 8.4**

In this example, the main plot itself has an underlying 2x2 factorial treatment structure; the subplot is Time. Specifically, sixteen dogs (experimental units) were randomly assigned to four groups (main plots). Within each group, dogs received either morphine or trimethaphan (levels M or T, variable DRUG) and had either depleted or intact histamine levels (levels D or I, variable HIST). The response variable was the blood concentration of histamine at 0, 1, 3, and 5 minutes after injection of the drug.

**Data** RepMeas;
    Input Drug $ Hist $ h0 h1 h2 h3; *Same animal measured 4 times at minute 0, 1, 3, and 5; Cards;
    M D 3.02 2.89 2.80 2.88
    M D 3.25 2.69 2.89 3.07
    M D 3.29 2.67 2.66 2.90
    M D 3.31 2.70 2.68 2.87
    M I 4.36 3.88 3.67 3.99
    M I 4.67 4.04 3.82 3.84
    M I 4.42 4.09 3.86 3.85
    M I 4.53 3.85 4.11 4.16
    T D 2.10 1.78 1.81 1.89
    T D 2.06 1.83 1.83 1.73
    T D 2.22 1.68 1.80 1.74
    T D 2.37 2.03 1.73 1.73
    T I 2.81 2.52 2.50 2.55
    T I 2.60 2.45 2.80 2.71
    T I 2.75 2.29 2.56 2.76
    T I 2.79 2.31 2.67 2.52
; * This order is needed for repeated measurements;

**Proc GLM** Data = RepMeas;
    Class Drug Hist; * h0, h1, etc. are all dependent variables;
    Model h0 h1 h2 h3 = Drug Hist Drug*Hist / nouni; * NO UNivariate analysis;
    Repeated Time / printe nom; * Sphericity Test, NO Multivariate analysis;

**Run;**
**Quit;**
Output and Commentary

The GLM Procedure
Repeated Measures Analysis of Variance
Tests of Hypotheses for Between Subjects Effects

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Drug</td>
<td>1</td>
<td>24.73818906</td>
<td>24.73818906</td>
<td>2205.79</td>
<td>&lt;.0001 ***</td>
</tr>
<tr>
<td>Hist</td>
<td>1</td>
<td>13.90357656</td>
<td>13.90357656</td>
<td>1239.72</td>
<td>&lt;.0001 ***</td>
</tr>
<tr>
<td>Drug*Hist</td>
<td>1</td>
<td>0.83493906</td>
<td>0.83493906</td>
<td>74.45</td>
<td>&lt;.0001 ***</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>0.13458125</td>
<td>0.01121510</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

This section reports the main plot effects, ignoring the within-dog effects. The F-values here are correct since under the Repeated procedure it is unnecessary to specify the correct error term. The results here match the results you would obtain by running the data as a simple split plot with Time as the subplot effect [see Appendix]. The significant Drug*Hist interaction requires you to analyze the simple effects of these two factors.

The GLM Procedure
Repeated Measures Analysis of Variance
Univariate Tests of Hypotheses for Within Subject Effects

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
<th>Adj Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time</td>
<td>3</td>
<td>1.86815469</td>
<td>0.62271823</td>
<td>38.49</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Time*Drug</td>
<td>3</td>
<td>0.17417969</td>
<td>0.05805990</td>
<td>3.59</td>
<td>0.0229</td>
<td>0.0332</td>
</tr>
<tr>
<td>Time*Hist</td>
<td>3</td>
<td>0.01459219</td>
<td>0.00486406</td>
<td>0.30</td>
<td>0.8247</td>
<td>0.7820</td>
</tr>
<tr>
<td>Time<em>Drug</em>Hist</td>
<td>3</td>
<td>0.23615469</td>
<td>0.07871823</td>
<td>4.87</td>
<td>0.0061</td>
<td>0.0110</td>
</tr>
<tr>
<td>Error(Time)</td>
<td>36</td>
<td>0.58249375</td>
<td>0.01618038</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Greenhouse-Geisser Epsilon 0.8048

This section reports the subplot effects (i.e. within-dog effects of Time). Looking at the G-G column, the results indicate that Time, Time*Drug, and Time*Drug*Hist are all significant. The significant Time*Drug interaction, for example, indicates that the effect of time on the blood concentration of histamine is different for the two drugs being studied. Notice that the p-values in the first column are the ones you obtain under a split plot analysis using full df [see Appendix].

Now, before this analysis is used to make conclusions about the data (specifically the Time*Drug interaction), the results of the sphericity test, generated by the \texttt{/printe} option, should be examined:

The GLM Procedure
Repeated Measures Analysis of Variance
Sphericity Tests

<table>
<thead>
<tr>
<th>Variables</th>
<th>DF</th>
<th>Mauchly's Criterion</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transformed Var</td>
<td>5</td>
<td>0.4005856</td>
<td>9.308983</td>
<td>0.0808</td>
</tr>
<tr>
<td>Orthogonal Components</td>
<td>5</td>
<td>0.6442253</td>
<td>4.7146334</td>
<td>0.4517</td>
</tr>
</tbody>
</table>

Somewhat simplified, the Sphericity Test tests the assumptions that the variances and correlations are homogeneous across the various dependent variables. You can think of it as an assumption test for Repeated analysis the same way Levene's is an assumption test for ANOVA. If the Orthogonal Components Sphericity Test is NS (p > 0.05), one can use the G-G p-values. [Note: The Greenhouse-Geisser Epsilon is used to multiply the numerator and denominator degrees of freedom before determining significance levels for the F-tests.]
Appendix: The standard split plot analysis for Example 8.4

If you were given the histamine data (Example 12.4) to analyze, the first thing you would do is to treat it like a standard split plot. In this case, the main plot effect has a factorial treatment structure and the SAS code would look something like this:

```
Data RepMeas;
Input Drug $ Hist $ Dog Time Resp; *Same animal measured 4 times at minute 0, 1, 3, and 5;
Cards;
M D 1 0 3.02 M I 1 0 4.36 T D 1 0 2.10 T I 1 0 2.81
M D 1 1 2.89 M I 1 1 3.88 T D 1 1 1.78 T I 1 1 1.52
M D 1 2 2.80 M I 1 2 3.67 T D 1 2 1.81 T I 1 2 2.50
M D 1 3 2.88 M I 1 3 3.99 T D 1 3 1.89 T I 1 3 2.55
M D 2 0 3.25 M I 2 0 4.67 T D 2 0 2.06 T I 2 0 2.60
M D 2 1 2.69 M I 2 1 4.04 T D 2 1 1.83 T I 2 1 2.45
M D 2 2 2.89 M I 2 2 3.82 T D 2 2 1.83 T I 2 2 2.80
M D 2 3 3.07 M I 2 3 3.84 T D 2 3 1.73 T I 2 3 3.71
M D 3 0 3.20 M I 3 0 4.42 T D 3 0 2.22 T I 3 0 2.75
M D 3 1 2.67 M I 3 1 4.09 T D 3 1 1.68 T I 3 1 2.29
M D 3 2 2.66 M I 3 2 3.86 T D 3 2 1.80 T I 3 2 2.56
M D 3 3 2.90 M I 3 3 3.85 T D 3 3 1.74 T I 3 3 2.76
M D 4 0 3.31 M I 4 0 4.53 T D 4 0 2.37 T I 4 0 2.79
M D 4 1 2.70 M I 4 1 3.85 T D 4 1 2.03 T I 4 1 2.31
M D 4 2 2.68 M I 4 2 4.11 T D 4 2 1.73 T I 4 2 2.67
M D 4 3 2.87 M I 4 3 4.16 T D 4 3 1.73 T I 4 3 2.52
;
Proc GLM Data = Repmeas;
Class Dog Drug Hist Time;
Model Resp = Drug Hist Drug*Hist /*Correct error term for A*/
Dog*Drug*Hist /* Notice "Dog" alone does not appear in the Model;
Time Drug|Time|Hist; /* Specify the correct error for testing A;
Test h = Drug e = Dog*Drug*Hist; * Specify the correct error for testing A;
Test h = Hist e = Dog*Drug*Hist; * Specify the correct error for testing A;
Test h = Drug*Hist e = Dog*Drug*Hist; * Specify the correct error for testing A;
Run;
Quit;
```

Output

```
<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>27</td>
<td>41.90436719</td>
<td>1.55201360</td>
<td>95.92</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>36</td>
<td>0.58249375</td>
<td>0.01618038</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>63</td>
<td>42.48686094</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>R-Square</td>
<td></td>
<td>0.986290</td>
<td>4.433337</td>
<td>0.127202</td>
<td>2.869219</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Drug</td>
<td>1</td>
<td>24.73818906</td>
<td>24.73818906</td>
<td>1528.90</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Hist</td>
<td>1</td>
<td>13.90387656</td>
<td>13.90387656</td>
<td>859.29</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Drug*Hist</td>
<td>1</td>
<td>0.83493906</td>
<td>0.83493906</td>
<td>51.60</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Dog<em>Drug</em>Hist</td>
<td>12</td>
<td>0.33458125</td>
<td>0.028121510</td>
<td>0.69</td>
<td>0.7429</td>
</tr>
<tr>
<td>Time</td>
<td>3</td>
<td>1.68015469</td>
<td>0.56271823</td>
<td>38.49</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Drug*Time</td>
<td>3</td>
<td>0.17417969</td>
<td>0.05805990</td>
<td>3.59</td>
<td>0.0229</td>
</tr>
<tr>
<td>Hist*Time</td>
<td>3</td>
<td>0.01459219</td>
<td>0.00486406</td>
<td>0.30</td>
<td>0.8247</td>
</tr>
<tr>
<td>Drug<em>Hist</em>Time</td>
<td>3</td>
<td>0.23615469</td>
<td>0.07871823</td>
<td>4.87</td>
<td>0.0061</td>
</tr>
</tbody>
</table>
```
Tests of Hypotheses Using the Type III MS for Dog\*Drug\*Hist as an Error Term

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Drug</td>
<td>1</td>
<td>24.73818906</td>
<td>24.73818906</td>
<td>2205.79</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Hist</td>
<td>1</td>
<td>13.90357656</td>
<td>13.90357656</td>
<td>1239.72</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Drug*Hist</td>
<td>1</td>
<td>0.83493906</td>
<td>0.83493906</td>
<td>74.45</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Notice first of all that the F- and p-values of the main plot effects (Drug, Hist, and Drug\*Hist) exactly match those found in the "Between Subjects Effects" table produced by the Repeated option within Proc GLM. This is a nice verification that our split plot programming and error term assignments are correct.

At this point, recompute the p-values by hand for the subplot effect (and interactions) using conservative degrees of freedom. The adjusted table:

<table>
<thead>
<tr>
<th>Adj</th>
<th>Source</th>
<th>DF</th>
<th>DF</th>
<th>F Value</th>
<th>df den</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Time</td>
<td>3</td>
<td>1</td>
<td>38.49</td>
<td>(1, 12)</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td></td>
<td>Drug*Time</td>
<td>3</td>
<td>1</td>
<td>3.59</td>
<td>(1, 12)</td>
<td>0.0825 NS</td>
</tr>
<tr>
<td></td>
<td>Hist*Time</td>
<td>3</td>
<td>1</td>
<td>0.30</td>
<td>(1, 12)</td>
<td>0.5939 NS</td>
</tr>
</tbody>
</table>
|     | Drug\*Hist\*Time | 3 | 1  | 4.87    | (1, 12) | 0.0476 | *

Now compare the results of the full df analysis with those of the conservative df analysis. Due to agreement between the two approaches, you can declare the Time\*Hist\*Drug interaction to be significant; you can also declare the Hist\*Time interaction to be NS. The Drug\*Time interaction, however, was found to be significant (p = 0.0229) with full df but NS (p = 0.0825) with conservative df. Because of this discrepancy, we needed to carry out the repeated measures analysis documented in the lab.