Introduction to Design and Analysis of Experiments with the SAS System
(Stat 7010 Lecture Notes)

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Chapter 1

Completely Randomized Design

1.1 Introduction

Suppose we have an experiment which compares $k$ treatments or $k$ levels of a single factor. Suppose we have $n$ experimental units to be included in the experiment. We can assign the first treatment to $n_1$ units randomly selected from among the $n$, assign the second treatment to $n_2$ units randomly selected from the remaining $n - n_1$ units, and so on until the $k$th treatment is assigned to the final $n_k$ units. Such an experimental design is called a completely randomized design (CRD).

We shall describe the observations using the linear statistical model

$$y_{ij} = \mu + \tau_i + \epsilon_{ij}, \quad i = 1, \ldots, k, \quad j = 1, \ldots, n_i,$$

(1.1)

where

- $y_{ij}$ is the $j$th observation on treatment $i$,
- $\mu$ is a parameter common to all treatments (overall mean),
- $\tau_i$ is a parameter unique to the $i$th treatment ($i$th treatment effect), and
- $\epsilon_{ij}$ is a random error component.

In this model the random errors are assumed to be normally and independently distributed with mean zero and variance $\sigma^2$, which is assumed constant for all treatments. The model is called the one-way classification analysis of variance (one-way ANOVA).

The typical data layout for a one-way ANOVA is shown below:

<table>
<thead>
<tr>
<th></th>
<th>Treatment</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>$y_{11}$</td>
<td>$y_{21}$</td>
<td>$y_{k1}$</td>
</tr>
<tr>
<td>$y_{11}$</td>
<td>$y_{21}$</td>
<td>$y_{k1}$</td>
</tr>
<tr>
<td>$\vdots$</td>
<td>$\vdots$</td>
<td>$\vdots$</td>
</tr>
<tr>
<td>$y_{1n_1}$</td>
<td>$y_{2n_2}$</td>
<td>$y_{kn_k}$</td>
</tr>
</tbody>
</table>

The model in Equation (1.1) describes two different situations:

1. **Fixed Effects Model**: The $k$ treatments could have been specifically chosen by the experimenter. The goal here is to test hypotheses about the treatment means and estimate the model parameters ($\mu$, $\tau_i$, and $\sigma^2$). Conclusions reached here only apply to the treatments considered and cannot be extended to other treatments that were not in the study.
2. Random Effects Model: The \( k \) treatments could be a random sample from a larger population of treatments. Conclusions here extend to all the treatments in the population. The \( \tau_i \) are random variables; thus, we are not interested in the particular ones in the model. We test hypotheses about the variability of \( \tau_i \).

Here are a few examples taken from Peterson: Design and Analysis of Experiments:

1. Fixed: A scientist develops three new fungicides. His interest is in these fungicides only.

   Random: A scientist is interested in the way a fungicide works. He selects, at random, three fungicides from a group of similar fungicides to study the action.

2. Fixed: Measure the rate of production of five particular machines.

   Random: Choose five machines to represent machines as a class.

3. Fixed: Conduct an experiment to obtain information about four specific soil types.

   Random: Select, at random, four soil types to represent all soil types.

1.2 The Fixed Effects Model

In this section we consider the ANOVA for the fixed effects model. The treatment effects, \( \tau_i \), are expressed as deviations from the overall mean, so that

\[
\sum_{i=1}^{k} \tau_i = 0 .
\]

Denote by \( \mu_i \) the mean of the \( i \)th treatment; \( \mu_i = E(y_{ij}) = \mu + \tau_i, \ i = 1, \ldots, k \). We are interested in testing the equality of the \( k \) treatment means;

\[
H_0 : \mu_1 = \mu_2 = \cdots = \mu_k \\
H_A : \mu_i \neq \mu_j \text{ for at least one } i, j
\]

An equivalent set of hypotheses is

\[
H_0 : \tau_1 = \tau_2 = \cdots = \tau_k = 0 \\
H_A : \tau_i \neq 0 \text{ for at least one } i
\]

1.2.1 Decomposition of the Total Sum of Squares

In the following let \( n = \sum_{i=1}^{k} n_i \). Further, let

\[
\bar{y}_i = \frac{1}{n_i} \sum_{j=1}^{n_i} y_{ij}, \quad \bar{y}_.. = \frac{1}{n} \sum_{i=1}^{k} \sum_{j=1}^{n_i} y_{ij}
\]

The total sum of squares (corrected) given by

\[
SS_T = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_.)^2,
\]

measures the total variability in the data.

The total sum of squares, \( SS_T \), may be decomposed as
1.2. THE FIXED EFFECTS MODEL

\[
\sum_{i=1}^{k} \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_i)^2 = \sum_{i=1}^{k} n_i (\bar{y}_i - \bar{y}_.)^2 + \sum_{i=1}^{k} \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_i)^2
\]

The proof is left as an exercise.

We will write

\[ SS_T = SS_B + SS_W \]

where \( SS_B = \sum_{i=1}^{k} n_i (\bar{y}_i - \bar{y}_.)^2 \) is called the between treatments sum of squares and \( SS_W = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_i)^2 \) is called the within treatments sum of squares.

One can easily show that the estimate of the common variance \( \sigma^2 \) is \( SS_W / (n - k) \).

Mean squares are obtained by dividing the sum of squares by their respective degrees of freedoms as

\[ MS_B = SS_B / (k - 1), \quad MS_W = SS_W / (n - k) \]

1.2.2 Statistical Analysis

Testing

Since we assumed that the random errors are independent, normal random variables, it follows by Cochran’s Theorem that if the null hypothesis is true, then

\[ F_0 = \frac{MS_B}{MS_W} \]

follows an \( F \) distribution with \( k - 1 \) and \( n - k \) degrees of freedom. Thus an \( \alpha \) level test of \( H_0 \) rejects \( H_0 \) if

\[ F_0 > F_{k-1,n-k}(\alpha) \]

The following ANOVA table summarizes the test procedure:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>( F_0 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between</td>
<td>( k - 1 )</td>
<td>( SS_B )</td>
<td>( MS_B )</td>
<td>( F_0 = MS_B / MS_W )</td>
</tr>
<tr>
<td>Within (Error)</td>
<td>( n - k )</td>
<td>( SS_W )</td>
<td>( MS_W )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( n - 1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Estimation

Once again consider the one-way classification model given by Equation (1.1). We now wish to estimate the model parameters \( (\mu, \tau_i, \sigma^2) \). The most popular method of estimation is the method of least squares (LS) which determines the estimators of \( \mu \) and \( \tau_i \) by minimizing the sum of squares of the errors

\[
L = \sum_{i=1}^{k} \sum_{j=1}^{n_i} \epsilon_{ij}^2 = \sum_{i=1}^{k} n_i \sum_{j=1}^{n_i} (y_{ij} - \mu - \tau_i)^2 .
\]

Minimization of \( L \) via partial differentiation provides the estimates \( \hat{\mu} = \bar{y}_. \) and \( \hat{\tau}_i = \bar{y}_i. - \bar{y}_. \) for \( i = 1, \cdots, k \).

By rewriting the observations as

\[ y_{ij} = \bar{y}_. + (\bar{y}_i. - \bar{y}_.) + (y_{ij} - \bar{y}_i.) \]

one can easily observe that it is quite reasonable to estimate the random error terms by

\[ \epsilon_{ij} = y_{ij} - \bar{y}_i. \]

These are the model residuals.
Alternatively, the estimator of $y_{ij}$ based on the model (1.1) is

$$\hat{y}_{ij} = \hat{\mu} + \hat{\tau}_i,$$

which simplifies to $\hat{y}_{ij} = \bar{y}_i$. Thus, the residuals are $y_{ij} - \hat{y}_{ij} = y_{ij} - \bar{y}_i$.

An estimator of the $i$th treatment mean, $\mu_i$, would be $\hat{\mu}_i = \hat{\mu} + \hat{\tau}_i = \bar{y}_i$.

Using $MS_W$ as an estimator of $\sigma^2$, we may provide a $100(1 - \alpha)%$ confidence interval for the treatment mean, $\mu_i$,

$$\bar{y}_i \pm t_{n-k}(\alpha/2)\sqrt{MS_W/n_i}.$$

A $100(1 - \alpha)%$ confidence interval for the difference of any two treatment means, $\mu_i - \mu_j$, would be

$$\bar{y}_i - \bar{y}_j \pm t_{n-k}(\alpha/2)\sqrt{MS_W(1/n_i + 1/n_j)}.$$

We now consider an example from Montgomery: Design and Analysis of Experiments.

Example

The tensile strength of a synthetic fiber used to make cloth for men’s shirts is of interest to a manufacturer. It is suspected that the strength is affected by the percentage of cotton in the fiber. Five levels of cotton percentage are considered: 15%, 20%, 25%, 30% and 35%. For each percentage of cotton in the fiber, strength measurements (time to break when subject to a stress) are made on five pieces of fiber.

<table>
<thead>
<tr>
<th></th>
<th>15</th>
<th>20</th>
<th>25</th>
<th>30</th>
<th>35</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>7</td>
<td>12</td>
<td>14</td>
<td>19</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>17</td>
<td>18</td>
<td>25</td>
<td>10</td>
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<td></td>
<td>15</td>
<td>12</td>
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<td>22</td>
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<td></td>
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<td>15</td>
</tr>
<tr>
<td></td>
<td>9</td>
<td>18</td>
<td>19</td>
<td>23</td>
<td>11</td>
</tr>
</tbody>
</table>

The corresponding ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>$F_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between</td>
<td>4</td>
<td>475.76</td>
<td>118.94</td>
<td>14.76</td>
</tr>
<tr>
<td>Within (Error)</td>
<td>20</td>
<td>161.20</td>
<td>8.06</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>24</td>
<td>636.96</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Performing the test at $\alpha = .01$ one can easily conclude that the percentage of cotton has a significant effect on fiber strength since $F_0 = 14.76$ is greater than the tabulated $F_{4,20}(.01) = 4.43$.

The estimate of the overall mean is $\bar{\mu} = \bar{y}_c = 15.04$. Point estimates of the treatment effects are

$$\hat{\tau}_1 = \bar{y}_1 - \bar{y}_c = 9.80 - 15.04 = -5.24$$
$$\hat{\tau}_2 = \bar{y}_2 - \bar{y}_c = 15.40 - 15.04 = 0.36$$
$$\hat{\tau}_3 = \bar{y}_3 - \bar{y}_c = 17.60 - 15.04 = 2.56$$
$$\hat{\tau}_4 = \bar{y}_4 - \bar{y}_c = 21.60 - 15.04 = 6.56$$
$$\hat{\tau}_5 = \bar{y}_5 - \bar{y}_c = 10.80 - 15.04 = -4.24$$

A 95% percent CI on the mean treatment 4 is

$$21.60 \pm (2.086)\sqrt{8.06/5},$$

which gives the interval $18.95 \leq \mu_4 \leq 24.25$. 
1.2.3 Comparison of Individual Treatment Means

Suppose we are interested in a certain linear combination of the treatment means, say,

\[ L = \sum_{i=1}^{k} l_i \mu_i, \]

where \( l_i, \ i = 1, \ldots, k, \) are known real numbers not all zero.

The natural estimate of \( L \) is

\[ \hat{L} = \sum_{i=1}^{k} l_i \hat{\mu}_i = \sum_{i=1}^{k} l_i \bar{y}_i. \]

Under the one-way classification model (1.1), we have:

1. \( \hat{L} \) follows a \( N(L, \sigma^2 \sum_{i=1}^{k} l_i^2 / n_i) \),
2. \( \frac{\hat{L} - L}{\sqrt{MS_W(\sum_{i=1}^{k} l_i^2 / n_i)}} \) follows a \( t_{n-k} \) distribution,
3. \( \hat{L} \pm t_{n-k}(\alpha/2) \sqrt{MS_W(\sum_{i=1}^{k} l_i^2 / n_i)} \),
4. An \( \alpha \)-level test of

\[ H_0 : L = 0 \]
\[ H_A : L \neq 0 \]

is

\[ \left| \frac{\hat{L}}{\sqrt{MS_W(\sum_{i=1}^{k} l_i^2 / n_i)}} \right| > t_{n-k}(\alpha/2). \]

A linear combination of all the treatment means

\[ \phi = \sum_{i=1}^{k} c_i \mu_i \]

is known as a contrast of \( \mu_1, \ldots, \mu_k \) if \( \sum_{i=1}^{k} c_i = 0 \). Its sample estimate is

\[ \hat{\phi} = \sum_{i=1}^{k} c_i \bar{y}_i. \]

Examples of contrasts are \( \mu_1 - \mu_2 \) and \( \mu_1 - \mu \).

Consider \( r \) contrasts of \( \mu_1, \ldots, \mu_k \), called planned comparisons, such as,

\[ \phi_i = \sum_{s=1}^{k} c_{is} \mu_s \quad \text{with} \quad \sum_{s=1}^{k} c_{is} = 0 \quad \text{for} \quad i = 1, \ldots, r, \]

and the experiment consists of

\[ H_0 : \phi_1 = 0 \quad \ldots \quad H_0 : \phi_r = 0 \]
\[ H_A : \phi_1 \neq 0 \quad \ldots \quad H_A : \phi_r \neq 0 \]
Example

The most common example is the set of all \( k^2 \) pairwise tests

\[
H_0 : \mu_i = \mu_j \\
H_A : \mu_i \neq \mu_j
\]

for \( 1 \leq i < j \leq k \) of all \( \mu_1, \ldots, \mu_k \). The experiment consists of all \( k^2 \) pairwise tests. An experimentwise error occurs if at least one of the null hypotheses is declared significant when \( H_0 : \mu_1 = \cdots = \mu_k \) is known to be true.

The Least Significant Difference (LSD) Method

Suppose that following an ANOVA \( F \) test where the null hypothesis is rejected, we wish to test \( H_0 : \mu_i = \mu_j \), for all \( i \neq j \). This could be done using the \( t \) statistic

\[
t_0 = \frac{\bar{y}_i - \bar{y}_j}{\sqrt{MS_W(1/n_i + 1/n_j)}}
\]

and comparing it to \( t_{n-k}(\alpha/2) \). An equivalent test declares \( \mu_i \) and \( \mu_j \) to be significantly different if \( |\bar{y}_i - \bar{y}_j| > LSD \), where

\[
LSD = t_{n-k}(\alpha/2)\sqrt{MS_W(1/n_i + 1/n_j)}.
\]

The following gives a summary of the steps.

Stage 1 : Test \( H_0 : \mu_1 = \cdots = \mu_k \) with \( F_0 = MS_B/MS_W \).

- if \( F_0 < F_{k-1,n-k}(\alpha) \), then declare \( H_0 : \mu_1 = \cdots = \mu_k \) true and stop.
- if \( F_0 > F_{k-1,n-k}(\alpha) \), then go to Stage 2.

Stage 2 : Test

\[
H_0 : \mu_i = \mu_j \\
H_A : \mu_i \neq \mu_j
\]

for all \( \binom{k}{2} \) pairs with

\[
|t_{ij}| = \frac{|\bar{y}_i - \bar{y}_j|}{\sqrt{MS_W(1/n_i + 1/n_j)}}
\]

- if \( |t_{ij}| < t_{n-k}(\alpha/2) \), then accept \( H_0 : \mu_i = \mu_j \).
- if \( |t_{ij}| > t_{n-k}(\alpha/2) \), then reject \( H_0 : \mu_i = \mu_j \).

Example

Consider the fabric strength example we considered above. The ANOVA \( F \)-test rejected \( H_0 : \mu_1 = \cdots = \mu_5 \). The LSD at \( \alpha = .05 \) is

\[
LSD = t_{20}(.025)\sqrt{MS_W(1/5 + 1/5)} = 2.086\sqrt{\frac{2(8.06)}{5}} = 3.75.
\]

Thus any pair of treatment averages that differ by more than 3.75 would imply that the corresponding pair of population means are significantly different. The \( \binom{5}{2} = 10 \) pairwise differences among the treatment means are
1.2. THE FIXED EFFECTS MODEL

\[ \bar{y}_1 - \bar{y}_2 = 9.8 - 15.4 = -5.6^* \]
\[ \bar{y}_1 - \bar{y}_3 = 9.8 - 17.6 = -7.8^* \]
\[ \bar{y}_1 - \bar{y}_4 = 9.8 - 21.6 = -11.8^* \]
\[ \bar{y}_1 - \bar{y}_5 = 9.8 - 10.8 = -1.0 \]
\[ \bar{y}_2 - \bar{y}_3 = 15.4 - 17.6 = -2.2 \]
\[ \bar{y}_2 - \bar{y}_4 = 15.4 - 21.6 = -6.2^* \]
\[ \bar{y}_2 - \bar{y}_5 = 15.4 - 10.8 = 4.6^* \]
\[ \bar{y}_3 - \bar{y}_4 = 17.6 - 21.6 = -4.0^* \]
\[ \bar{y}_3 - \bar{y}_5 = 17.6 - 10.8 = 6.8^* \]
\[ \bar{y}_4 - \bar{y}_5 = 21.6 - 10.8 = 10.8^* \]

Using underlining the result may be summarized as

\[
\begin{array}{cccc}
\bar{y}_1 & \bar{y}_2 & \bar{y}_3 & \bar{y}_4 \\
9.8 & 10.8 & 15.4 & 17.6 & 21.6
\end{array}
\]

As \( k \) gets large the experimentwise error becomes large. Sometimes we also find that the LSD fails to find any significant pairwise differences while the \( F \)-test declares significance. This is due to the fact that the ANOVA \( F \)-test considers all possible comparisons, not just pairwise comparisons.

Scheffé's Method for Comparing all Contrasts

Often we are interested in comparing different combinations of the treatment means. Scheffé (1953) has proposed a method for comparing all possible contrasts between treatment means. The Scheffé method controls the experimentwise error rate at level \( \alpha \).

Consider the \( r \) contrasts

\[ \phi_i = \sum_{s=1}^{k} c_{is} \mu_s \] with \( \sum_{s=1}^{k} c_{is} = 0 \) for \( i = 1, \ldots, r \),

and the experiment consists of

\[
\begin{align*}
H_0 : \phi_1 = 0 & \quad \cdots \quad H_0 : \phi_r = 0 \\
H_A : \phi_1 \neq 0 & \quad \cdots \quad H_A : \phi_r \neq 0
\end{align*}
\]

The Scheffé method declares \( \phi_i \) to be significant if

\[ |\hat{\phi}_i| > S_{\alpha,i} \]

where

\[ \hat{\phi}_i = \sum_{s=1}^{k} c_{is} \bar{y}_s. \]

and

\[ S_{\alpha,i} = \sqrt{(k - 1)F_{k-1, n-k}(\alpha) MSW \sum_{s=1}^{k} (c_{is}^2 / n_i)}. \]

Example

As an example, consider the fabric strength data and suppose that we are interested in the contrasts

\[ \phi_1 = \mu_1 + \mu_3 - \mu_4 - \mu_5 \]

and

\[ \phi_2 = \mu_1 - \mu_4. \]
The sample estimates of these contrasts are
\[ \hat{\phi}_1 = \bar{y}_1 + \bar{y}_3 - \bar{y}_4 - \bar{y}_5 = 5.00 \]
and
\[ \hat{\phi}_2 = \bar{y}_1 - \bar{y}_4 = -11.80 . \]

We compute the Scheffé 1% critical values as
\[ S_{.01,1} = \sqrt{(k - 1)F_{k-1,n-k}(.01)} \sqrt{MS_W \sum_{s=1}^{k} (c^2_{1s}/n_1)} \]
\[ = \sqrt{4(4.43)} \sqrt{8.06(1 + 1 + 1 + 1)/5} \]
\[ = 10.69 \]
and
\[ S_{.01,2} = \sqrt{(k - 1)F_{k-1,n-k}(.01)} \sqrt{MS_W \sum_{s=1}^{k} (c^2_{2s}/n_2)} \]
\[ = \sqrt{4(4.43)} \sqrt{8.06(1 + 1)/5} \]
\[ = 7.58 \]

Since \(|\hat{\phi}_1| < S_{.01,1}\), we conclude that the contrast \(\phi_1 = \mu_1 + \mu_3 - \mu_4 - \mu_5\) is not significantly different from zero. However, since \(|\hat{\phi}_2| > S_{.01,2}\), we conclude that \(\phi_2 = \mu_1 - \mu_2\) is significantly different from zero; that is, the mean strengths of treatments 1 and 4 differ significantly.

**The Tukey-Kramer Method**

The Tukey-Kramer procedure declares two means, \(\mu_i\) and \(\mu_j\), to be significantly different if the absolute value of their sample differences exceeds
\[ T_\alpha = q_{k,n-k}(\alpha) \sqrt{\frac{MS_W}{2} \left( \frac{1}{n_i} + \frac{1}{n_j} \right)} , \]
where \(q_{k,n-k}(\alpha)\) is the \(\alpha\) percentile value of the studentized range distribution with \(k\) groups and \(n - k\) degrees of freedom.

**Example**

Reconsider the fabric strength example. From the studentized range distribution table, we find that \(q_{4,20}(.05) = 4.23\). Thus, a pair of means, \(\mu_i\) and \(\mu_j\), would be declared significantly different if \(|\hat{y}_i - \hat{y}_j|\) exceeds
\[ T_{.05} = 4.23 \sqrt{\frac{8.06}{2} \left( \frac{1}{5} + \frac{1}{5} \right)} = 5.37 . \]

Using this value, we find that the following pairs of means do not significantly differ:
- \(\mu_1\) and \(\mu_5\)
- \(\mu_5\) and \(\mu_2\)
- \(\mu_2\) and \(\mu_3\)
- \(\mu_3\) and \(\mu_4\)

Notice that this result differs from the one reported by the LSD method.
1.2. THE FIXED EFFECTS MODEL

The Bonferroni Procedure

We start with the Bonferroni Inequality. Let $A_1, A_2, \ldots, A_k$ be $k$ arbitrary events with $P(A_i) \geq 1 - \alpha/k$. Then $P(A_1 \cap A_2 \cap \cdots \cap A_k) \geq 1 - \alpha$.

The proof of this result is left as an exercise.

We may use this inequality to make simultaneous inference about linear combinations of treatment means in a one-way fixed effects ANOVA set up.

Let $L_1, L_2, \cdots, L_r$ be $r$ linear combinations of $\mu_1, \cdots, \mu_k$ where $L_i = \sum_{j=1}^{k} l_{ij} \mu_j$ and $\hat{L}_i = \sum_{j=1}^{k} l_{ij} \bar{y}_j$. for $i = 1, \cdots, r$.

A $(1 - \alpha)100\%$ simultaneous confidence interval for $L_1, \cdots, L_r$ is

$$
\hat{L}_i \pm t_{n-k} \left( \frac{\alpha}{2r} \right) \sqrt{MSW \sum_{j=1}^{k} \frac{l_{ij}^2}{n_j}}.
$$

for $i = 1, \cdots, r$.

A Bonferroni $\alpha$-level test of

$$
H_0: \mu_1 = \mu_2 = \cdots = \mu_k
$$

is performed by testing

$$
H_0: \mu_i = \mu_j \quad \text{vs.} \quad H_A: \mu_i \neq \mu_j
$$

with

$$
t_{ij} \frac{|\bar{y}_i - \bar{y}_j|}{\sqrt{MSW(1/n_i + 1/n_j)}} > t_{n-k} \left( \frac{\alpha}{2(k)} \right),
$$

for $1 \leq i < j \leq k$.

There is no need to perform an overall $F$-test.

Example

Consider the tensile strength example considered above. We wish to test

$$
H_0: \mu_1 = \cdots = \mu_5
$$

at .05 level of significance. This is done using

$$
t_{20}(.05/(2 \times 10)) = t_{20}(.0025) = 3.153.
$$

So the test rejects $H_0 : \mu_i = \mu_j$ in favor of $H_A : \mu_i \neq \mu_j$ if $|\bar{y}_i - \bar{y}_j|$ exceeds

$$
3.153 \sqrt{MSW(2/5)} = 5.66.
$$

Exercise: Use underlining to summarize the results of the Bonferroni testing procedure.

Dunnett’s Method for Comparing Treatments to a Control

Assume $\mu_1$ is a control mean and $\mu_2, \cdots, \mu_k$ are $k - 1$ treatment means. Our purpose here is to find a set of $(1 - \alpha)100\%$ simultaneous confidence intervals for the $k - 1$ pairwise differences comparing treatment to control, $\mu_i - \mu_1$, for $i = 2, \cdots, k$.

Dunnett’s method rejects the null hypothesis $H_0 : \mu_i = \mu_1$ at level $\alpha$ if

$$
|\bar{y}_i - \bar{y}_1| > d_{k-1,n-k}(\alpha) \sqrt{MSW(1/n_i + 1/n_1)},
$$

for $i = 2, \cdots, k$.

The value $d_{k-1,n-k}(\alpha)$ is read from a table.
Example
Consider the tensile strength example above and let treatment 5 be the control. The Dunnett critical value is $d_{4,20}(0.05) = 2.65$. Thus the critical difference is

$$d_{4,20}(0.05)\sqrt{MS_W(2/5)} = 4.76$$

So the test rejects $H_0: \mu_i = \mu_5$ if

$$|\bar{y}_i - \bar{y}_5| > 4.76.$$

Only the differences $\bar{y}_3 - \bar{y}_5 = 6.8$ and $\bar{y}_4 - \bar{y}_5 = 10.8$ indicate any significant difference. Thus we conclude $\mu_3 \neq \mu_5$ and $\mu_4 \neq \mu_5$.

1.3 The Random Effects Model

The treatments in an experiment may be a random sample from a larger population of treatments. Our purpose is to estimate (and test, if any) the variability among the treatments in the population. Such a model is known as a random effects model. The mathematical representation of the model is the same as the fixed effects model:

$$y_{ij} = \mu + \tau_i + \epsilon_{ij}, \quad i = 1, \cdots, k, \quad j = 1, \cdots, n_i,$$

except for the assumptions underlying the model.

Assumptions

1. The treatment effects, $\tau_i$, are a random sample from a population that is normally distributed with mean 0 and variance $\sigma^2_\tau$, i.e. $\tau_i \sim N(0, \sigma^2_\tau)$.
2. The $\epsilon_{ij}$ are random errors which follow the normal distribution with mean 0 and common variance $\sigma^2$.

If the $\tau_i$ are independent of $\epsilon_{ij}$, the variance of an observation will be

$$\text{Var}(y_{ij}) = \sigma^2 + \sigma^2_\tau.$$ 

The two variances, $\sigma^2$ and $\sigma^2_\tau$ are known as variance components.

The usual partition of the total sum of squares still holds:

$$SS_T = SS_B + SS_W.$$ 

Since we are interested in the bigger population of treatments, the hypothesis of interest is

$$H_0: \sigma^2_\tau = 0$$

versus

$$H_A: \sigma^2_\tau > 0.$$ 

If the hypothesis $H_0: \sigma^2_\tau = 0$ is rejected in favor of $H_A: \sigma^2_\tau > 0$, then we claim that there is a significant difference among all the treatments.

Testing is performed using the same $F$ statistic that we used for the fixed effects model:

$$F_0 = \frac{MS_B}{MS_W}.$$ 

An $\alpha$-level test rejects $H_0$ if $F_0 > F_{k-1,n-k}(\alpha)$.

The estimators of the variance components are

$$\hat{\sigma}^2 = MS_W.$$
and
\[ \hat{\sigma}_r^2 = \frac{MS_B - MS_W}{n_0}, \]
where
\[ n_0 = \frac{1}{k-1} \left[ \sum_{i=1}^{k} n_i - \frac{\sum_{i=1}^{k} n_i^2}{\sum_{i=1}^{k} n_i} \right]. \]

We are usually interested in the proportion of the variance of an observation, \( \text{Var}(y_{ij}) \), that is the result of the differences among the treatments:
\[ \frac{\sigma_r^2}{\sigma^2 + \sigma_r^2}. \]

A 100(1 - \( \alpha \))% confidence interval for \( \sigma_r^2/(\sigma^2 + \sigma_r^2) \) is
\[ \left( \frac{L}{1+L}, \frac{U}{1+U} \right), \]
where
\[ L = \frac{1}{n_0} \left( \frac{MS_B}{MS_W F_{k-1,n-k}(\alpha/2)} - 1 \right), \]
and
\[ U = \frac{1}{n_0} \left( \frac{MS_B}{MS_W F_{k-1,n-k}(1-\alpha/2)} - 1 \right). \]

The following example is taken from Montgomery: Design and Analysis of Experiments.

**Example**
A textile company weaves a fabric on a large number of looms. They would like the looms to be homogeneous so that they obtain a fabric of uniform strength. The process engineer suspects that, in addition to the usual variation in strength within samples of fabric from the same loom, there may also be significant variations in strength between looms. To investigate this, he selects four looms at random and makes four strength determinations on the fabric manufactured on each loom. The data are given in the following table:

<table>
<thead>
<tr>
<th>Observations</th>
<th>Loom 1</th>
<th>Loom 2</th>
<th>Loom 3</th>
<th>Loom 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>98</td>
<td>97</td>
<td>99</td>
<td>96</td>
</tr>
<tr>
<td>2</td>
<td>91</td>
<td>90</td>
<td>93</td>
<td>92</td>
</tr>
<tr>
<td>3</td>
<td>96</td>
<td>95</td>
<td>97</td>
<td>95</td>
</tr>
<tr>
<td>4</td>
<td>95</td>
<td>96</td>
<td>99</td>
<td>98</td>
</tr>
</tbody>
</table>

The corresponding ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>( F_0 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between (Looms)</td>
<td>3</td>
<td>89.19</td>
<td>29.73</td>
<td>15.68</td>
</tr>
<tr>
<td>Within (Error)</td>
<td>12</td>
<td>22.75</td>
<td>1.90</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>15</td>
<td>111.94</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Since \( F_0 > F_{3,12}(.05) \), we conclude that the looms in the plant differ significantly. The variance components are estimated by
\[ \hat{\sigma}^2 = 1.90 \]
and
\[ \hat{\sigma}_r^2 = \frac{29.73 - 1.90}{4} = 6.96. \]
Thus, the variance of any observation on strength is estimated by $\hat{\sigma}^2 + \hat{\sigma}_\tau^2 = 8.86$. Most of this variability (about $6.96/8.86 = 79\%$) is attributable to the difference among looms. The engineer must now try to isolate the causes for the difference in loom performance (faulty set-up, poorly trained operators, . . . ).

Let's now find a 95% confidence interval for $\frac{\sigma^2_\tau}{\sigma^2 + \sigma^2_\tau}$. From properties of the $F$ distribution we have that $F_a,b(\alpha) = 1/F_{b,a}(1-\alpha)$. From the $F$ table we see that $F_{3,12(.025)} = 4.47$ and $F_{3,12(.975)} = 1/F_{12,3(.025)} = 1/5.22 = 0.192$. Thus

$$L = \frac{1}{4} \left[ \left( \frac{29.73}{1.90} \right) \left( \frac{1}{4.47} \right) - 1 \right] = 0.625$$

and

$$U = \frac{1}{4} \left[ \left( \frac{29.73}{1.90} \right) \left( \frac{1}{0.192} \right) - 1 \right] = 20.124$$

which gives the 95% confidence interval

$$\left( \frac{0.625}{1.625} = 0.39, \frac{20.124}{21.124} = 0.95 \right).$$

We conclude that the variability among looms accounts for between 39 and 95 percent of the variance in the observed strength of fabric produced.

**Using SAS**

The following SAS code may be used to analyze the tensile strength example considered in the fixed effects CRD case.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA MONT;
INPUT TS GROUP @@;
CARDS;
7 1 7 1 15 1 11 1 9 1
12 2 17 2 12 2 18 2 18 2
14 3 18 3 18 3 19 3 19 3
19 4 25 4 22 4 19 4 23 4
7 5 10 5 11 5 15 5 11 5
;
/* print the data */
PROC PRINT DATA=MONT;
RUN;
QUIT;

PROC GLM;
  CLASS GROUP;
  MODEL TS=GROUP;
  MEANS GROUP/ CLDIFF BON TUKEY SCHEFFE LSD DUNNETT('5');
  CONTRAST 'PHI1' GROUP 1 0 1 -1 -1;
  ESTIMATE 'PHI1' GROUP 1 0 1 -1 -1;
  CONTRAST 'PHI2' GROUP 1 0 0 -1 0;
  ESTIMATE 'PHI2' GROUP 1 0 0 -1 0;
RUN;
QUIT;
```

A random effects model may be analyzed using the RANDOM statement to specify the random factor:

```sas
PROC GLM DATA=A1;
  CLASS OFFICER;
  MODEL RATING=OFFICER;
  RANDOM OFFICER;
RUN;
```
1.3. **THE RANDOM EFFECTS MODEL**

**SAS Output**

```
The SAS System 1

Obs  TS  GROUP
1    7    1
2    7    1
3   15   1
4   11   1
5    9    1
6   12    2
7   17    2
8   12    2
9   18    2
10  18    2
11  14    3
12  18    3
13  18    3
14  19    3
15  19    3
16  19    4
17  25    4
18  22    4
19  19    4
20  23    4
21   7    5
22  10    5
23  11    5
24  15    5
25  11    5

The SAS System 2

The GLM Procedure

Class Level Information

Class       Levels  Values
GROUP     5  1 2 3 4 5

Number of observations  25

The SAS System 3

The GLM Procedure

Dependent Variable: TS

<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>4</td>
<td>475.7600000</td>
<td>118.9400000</td>
<td>14.76</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>20</td>
<td>161.2000000</td>
<td>8.0600000</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
```
CHAPTER 1. COMPLETELY RANDOMIZED DESIGN

Corrected Total 24 636.9600000

R-Square Coeff Var Root MSE TS Mean
0.746923 18.87642 2.839014 15.04000

Source DF Type I SS Mean Square F Value Pr > F
GROUP 4 475.7600000 118.9400000 14.76 <.0001

Source DF Type III SS Mean Square F Value Pr > F
GROUP 4 475.7600000 118.9400000 14.76 <.0001

The SAS System

The GLM Procedure

t Tests (LSD) for TS

NOTE: This test controls the Type I comparisonwise error rate, not the experimentwise error rate.

Alpha 0.05
Error Degrees of Freedom 20
Error Mean Square 8.06
Critical Value of t 2.08596
Least Significant Difference 3.7455

Comparisons significant at the 0.05 level are indicated by ***.

Difference
Comparison GROUP Between 95% Confidence
Means Limits

<table>
<thead>
<tr>
<th>GROUP</th>
<th>Comparison</th>
<th>Difference</th>
<th>Mean</th>
<th>Lower Limit</th>
<th>Upper Limit</th>
<th>Significance</th>
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<tbody>
<tr>
<td>4 - 3</td>
<td>4.000</td>
<td>0.255</td>
<td>7.745</td>
<td>***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4 - 2</td>
<td>6.200</td>
<td>2.455</td>
<td>9.945</td>
<td>***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4 - 5</td>
<td>10.800</td>
<td>7.055</td>
<td>14.545</td>
<td>***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4 - 1</td>
<td>11.800</td>
<td>8.055</td>
<td>15.545</td>
<td>***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3 - 4</td>
<td>-4.000</td>
<td>-7.745</td>
<td>-0.255</td>
<td>***</td>
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<td></td>
</tr>
<tr>
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<td>5.945</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3 - 5</td>
<td>6.800</td>
<td>3.055</td>
<td>10.545</td>
<td>***</td>
<td></td>
<td></td>
</tr>
<tr>
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<td>7.800</td>
<td>4.055</td>
<td>11.545</td>
<td>***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2 - 4</td>
<td>-6.200</td>
<td>-9.945</td>
<td>-2.455</td>
<td>***</td>
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<td></td>
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<tr>
<td>2 - 3</td>
<td>-2.200</td>
<td>-5.945</td>
<td>1.545</td>
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<td></td>
</tr>
<tr>
<td>2 - 5</td>
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<td>0.855</td>
<td>8.345</td>
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<td></td>
</tr>
<tr>
<td>2 - 1</td>
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<td>1.855</td>
<td>9.345</td>
<td>***</td>
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<td></td>
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<td>5 - 4</td>
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<td>4.745</td>
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</tbody>
</table>
### 1.3. THE RANDOM EFFECTS MODEL

<table>
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<tr>
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<th>4 - 3</th>
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<tbody>
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</tr>
<tr>
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<td>5.427</td>
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<td>-0.827 ***</td>
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<td>-16.173</td>
<td>-5.427 ***</td>
</tr>
<tr>
<td>GROUP</td>
<td>5 - 3</td>
<td>-6.800</td>
<td>-12.173</td>
<td>-1.427 ***</td>
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<td>1 - 5</td>
<td>-1.000</td>
<td>-6.373</td>
<td>4.373</td>
</tr>
</tbody>
</table>

**NOTE:** This test controls the Type I experimentwise error rate, but it generally
has a higher Type II error rate than Tukey’s for all pairwise comparisons.

### Alpha 0.05
### Error Degrees of Freedom 20
### Error Mean Square 8.06
### Critical Value of t 3.15340
### Minimum Significant Difference 5.6621

Comparisons significant at the 0.05 level are indicated by ***.

<table>
<thead>
<tr>
<th>GROUP</th>
<th>Between Means</th>
<th>Simultaneous 95% Confidence Limits</th>
</tr>
</thead>
<tbody>
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<td>-1.662 9.662</td>
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<tr>
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<td>10.800</td>
<td>5.138 16.462 ***</td>
</tr>
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<tr>
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<td>7.800</td>
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</tr>
<tr>
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<td>5 - 3</td>
<td>-6.800</td>
<td>-12.462 -1.138 ***</td>
</tr>
<tr>
<td>5 - 2</td>
<td>-4.600</td>
<td>-10.262 1.062</td>
</tr>
<tr>
<td>5 - 1</td>
<td>1.000</td>
<td>-4.662 6.662</td>
</tr>
<tr>
<td>1 - 4</td>
<td>-11.800</td>
<td>-17.462 -6.138 ***</td>
</tr>
<tr>
<td>1 - 3</td>
<td>-7.800</td>
<td>-13.462 -2.138 ***</td>
</tr>
<tr>
<td>1 - 2</td>
<td>-5.600</td>
<td>-11.262 0.062</td>
</tr>
<tr>
<td>1 - 5</td>
<td>-1.000</td>
<td>-6.662 4.662</td>
</tr>
</tbody>
</table>

The SAS System

The GLM Procedure

Scheffe’s Test for TS

NOTE: This test controls the Type I experimentwise error rate, but it generally has a higher Type II error rate than Tukey’s for all pairwise comparisons.

### Alpha 0.05
### Error Degrees of Freedom 20
### Error Mean Square 8.06
### Critical Value of F 2.86608
### Minimum Significant Difference 6.0796

Comparisons significant at the 0.05 level are indicated by ***.
### 1.3. THE RANDOM EFFECTS MODEL

#### Difference

<table>
<thead>
<tr>
<th>GROUP Comparison</th>
<th>Between Means</th>
<th>Simultaneous 95% Confidence Limits</th>
</tr>
</thead>
<tbody>
<tr>
<td>4 - 3</td>
<td>4.000</td>
<td>-2.080 10.080</td>
</tr>
<tr>
<td>4 - 2</td>
<td>6.200</td>
<td>0.120 12.280</td>
</tr>
<tr>
<td>4 - 5</td>
<td>10.800</td>
<td>4.720 16.880</td>
</tr>
<tr>
<td>4 - 1</td>
<td>11.800</td>
<td>5.720 17.880</td>
</tr>
<tr>
<td>3 - 4</td>
<td>-4.000</td>
<td>-10.080 2.080</td>
</tr>
<tr>
<td>3 - 2</td>
<td>2.200</td>
<td>-3.880 8.280</td>
</tr>
<tr>
<td>3 - 5</td>
<td>6.800</td>
<td>0.720 12.880</td>
</tr>
<tr>
<td>3 - 1</td>
<td>7.800</td>
<td>1.720 13.880</td>
</tr>
<tr>
<td>2 - 4</td>
<td>-6.200</td>
<td>-12.280 -0.120</td>
</tr>
<tr>
<td>2 - 3</td>
<td>-2.200</td>
<td>-8.280 3.880</td>
</tr>
<tr>
<td>2 - 5</td>
<td>4.600</td>
<td>-1.480 10.680</td>
</tr>
<tr>
<td>2 - 1</td>
<td>5.600</td>
<td>-0.480 11.680</td>
</tr>
<tr>
<td>5 - 4</td>
<td>-10.800</td>
<td>-16.880 -4.720</td>
</tr>
<tr>
<td>5 - 3</td>
<td>-6.800</td>
<td>-12.880 -0.720</td>
</tr>
<tr>
<td>5 - 2</td>
<td>-4.600</td>
<td>-10.680 1.480</td>
</tr>
<tr>
<td>5 - 1</td>
<td>1.000</td>
<td>-5.080 7.080</td>
</tr>
<tr>
<td>1 - 4</td>
<td>-11.800</td>
<td>-17.880 -5.720</td>
</tr>
<tr>
<td>1 - 3</td>
<td>-7.800</td>
<td>-13.880 -1.720</td>
</tr>
<tr>
<td>1 - 2</td>
<td>-5.600</td>
<td>-11.680 0.480</td>
</tr>
<tr>
<td>1 - 5</td>
<td>-1.000</td>
<td>-7.080 5.080</td>
</tr>
</tbody>
</table>

The SAS System

The GLM Procedure

Dunnett’s t Tests for TS

NOTE: This test controls the Type I experimentwise error for comparisons of all treatments against a control.

<table>
<thead>
<tr>
<th>Alpha</th>
<th>0.05</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error Degrees of Freedom</td>
<td>20</td>
</tr>
<tr>
<td>Error Mean Square</td>
<td>8.06</td>
</tr>
<tr>
<td>Critical Value of Dunnett’s t</td>
<td>2.65112</td>
</tr>
<tr>
<td>Minimum Significant Difference</td>
<td>4.7602</td>
</tr>
</tbody>
</table>

Comparisons significant at the 0.05 level are indicated by ***.
1.4 More About the One-Way Model

1.4.1 Model Adequacy Checking

Consider the one-way CRD model

\[ y_{ij} = \mu + \tau_i + \epsilon_{ij}, \quad i = 1, \ldots, k, \quad j = 1, \ldots, n_i, \]

where it is assumed that \( \epsilon_{ij} \sim_{\text{i.i.d.}} N(0, \sigma^2) \). In the random effects model, we additionally assume that \( \tau_i \sim_{\text{i.i.d.}} N(0, \sigma^2_\tau) \) independently of \( \epsilon_{ij} \).

Diagnostics depend on the residuals,

\[ \epsilon_{ij} = y_{ij} - \hat{y}_{ij} = y_{ij} - \bar{y}_i. \]

### The Normality Assumption

The simplest check for normality involves plotting the empirical quantiles of the residuals against the expected quantiles if the residuals were to follow a normal distribution. This is known as the normal QQ-plot. Other formal tests for normality (Kolmogorov-Smirnov, Shapiro-Wilk, Anderson-Darling, Cramer-von Mises) may also be performed to assess the normality of the residuals.

#### Example

The following SAS code and partial output checks the normality assumption for the tensile strength example considered earlier. The results from the QQ-plot as well as the formal tests (\( \alpha = .05 \)) indicate that the residuals are fairly normal.

#### SAS Code

```sas
OPTIONS LS=80 PS=66 NODATE; DATA MONT; INPUT TS GROUP@@; CARDS;
1 7 1 15 1 11 1 9 1 12 2 17 2 12 2 18 2 18 2 14 3 18 3 18 3 19 3 19
3 19 4 25 4 22 4 19 4 23 4 7 5 10 5 11 5 15 5 11 5 ;
TITLE1 'STRENGTH VS. PERCENTAGE'; SYMBOL1 V=CIRCLE I=NONE;
PROC GPLOT DATA=MONT; PLOT TS*GROUP/FRAME; RUN; QUIT;
```
1.4. MORE ABOUT THE ONE-WAY MODEL

PROC GLM;
   CLASS GROUP;
   MODEL TS=GROUP;
   OUTPUT OUT=DIAG R=RES P=PRED;
RUN;
QUIT;

PROC SORT DATA=DIAG;
   BY PRED;
RUN;
QUIT;

TITLE1 'RESIDUAL PLOT';
SYMBOL1 V=CIRCLE I=SM50;

PROC GPLOT DATA=DIAG;
   PLOT RES*PRED/FRAME;
RUN;
QUIT;

PROC UNIVARIATE DATA=DIAG NORMAL;
   VAR RES;
   TITLE1 'QQ-PLOT OF RESIDUALS';
   QQPLOT RES/NORMAL (L=1 MU=EST SIGMA=EST);
RUN;
QUIT;

Partial Output

The UNIVARIATE Procedure
Variable: RES

Moments

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>25</td>
<td>Sum Weights</td>
<td>25</td>
</tr>
<tr>
<td>Mean</td>
<td>0</td>
<td>Sum Observations</td>
<td>0</td>
</tr>
<tr>
<td>Std Deviation</td>
<td>2.59165327</td>
<td>Variance</td>
<td>6.71666667</td>
</tr>
<tr>
<td>Skewness</td>
<td>0.11239681</td>
<td>Kurtosis</td>
<td>-0.8683604</td>
</tr>
<tr>
<td>Uncorrected SS</td>
<td>161.2</td>
<td>Corrected SS</td>
<td>161.2</td>
</tr>
<tr>
<td>Coeff Variation</td>
<td>.</td>
<td>Std Error Mean</td>
<td>0.51833065</td>
</tr>
</tbody>
</table>

Basic Statistical Measures

<table>
<thead>
<tr>
<th>Location</th>
<th>Variability</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>0.00000</td>
</tr>
<tr>
<td>Median</td>
<td>0.40000</td>
</tr>
<tr>
<td>Mode</td>
<td>-3.40000</td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

NOTE: The mode displayed is the smallest of 7 modes with a count of 2.
Tests for Location: $\mu_0=0$

<table>
<thead>
<tr>
<th>Test</th>
<th>Statistic</th>
<th>$p$ Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Student’s t</td>
<td>t</td>
<td>0</td>
</tr>
<tr>
<td>Sign</td>
<td>M</td>
<td>2.5</td>
</tr>
<tr>
<td>Signed Rank</td>
<td>S</td>
<td>0.5</td>
</tr>
</tbody>
</table>

Tests for Normality

<table>
<thead>
<tr>
<th>Test</th>
<th>Statistic</th>
<th>$p$ Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shapiro-Wilk</td>
<td>W</td>
<td>0.943868</td>
</tr>
<tr>
<td>Kolmogorov-Smirnov</td>
<td>D</td>
<td>0.162123</td>
</tr>
<tr>
<td>Cramer-von Mises</td>
<td>W-Sq</td>
<td>0.080455</td>
</tr>
<tr>
<td>Anderson-Darling</td>
<td>A-Sq</td>
<td>0.518572</td>
</tr>
</tbody>
</table>
Constant Variance Assumption

Once again there are graphical and formal tests for checking the constant variance assumption. The graphical tool we shall utilize in this class is the plot of residuals versus predicted values. The hypothesis of interest is

\[ H_0 : \sigma_1^2 = \sigma_2^2 = \cdots = \sigma_k^2 \]

versus

\[ H_A : \sigma_i^2 \neq \sigma_j^2 \text{ for at least one pair } i \neq j . \]

One procedure for testing the above hypothesis is Bartlett’s test. The test statistic is

\[ B_0 = 2.3026 \frac{q}{c} \]

where

\[ q = (n - k) \log_{10} MS_W - \sum_{i=1}^{k} (n_i - 1) \log_{10} S_i^2 \]
We reject \( H_0 \) if

\[
B_0 > \chi^2_{k-1}(\alpha)
\]

where \( \chi^2_{k-1}(\alpha) \) is read from the chi-square table.

Bartlett’s test is too sensitive deviations from normality. So, it should not be used if the normality assumption is not satisfied.

A test which is more robust to deviations from normality is \textit{Levene's test}. Levene’s test proceeds by computing

\[
d_{ij} = |y_{ij} - m_i| ,
\]

where \( m_i \) is the median of the observations in group \( i \), and then running the usual ANOVA \( F \)-test using the transformed observations, \( d_{ij} \), instead of the original observations, \( y_{ij} \).

\[c = 1 + \frac{1}{3(k-1)} \left( \sum_{i=1}^{k} \left( \frac{1}{n_i - 1} - \frac{1}{n - k} \right) \right)\]

Example

Once again we consider the tensile strength example. The plot of residuals versus predicted values (see above) indicates no serious departure from the constant variance assumption. The following modification to the proc GLM code given above generates both Bartlett’s and Levene’s tests. The tests provide no evidence that indicates the failure of the constant variance assumption.

Partial SAS Code

```
PROC GLM;
   CLASS GROUP;
   MODEL TS=GROUP;
   MEANS GROUP/HOVTEST=BARTLETT HOVTEST=LEVENE;
RUN;
QUIT;
```

Partial SAS Output

The GLM Procedure

Levene’s Test for Homogeneity of TS Variance
ANOVA of Squared Deviations from Group Means

\[
\begin{array}{cccccc}
\text{Source} & \text{DF} & \text{Sum of Squares} & \text{Mean Square} & \text{F Value} & \text{Pr} > \text{F} \\
\hline
\text{GROUP} & 4 & 91.6224 & 22.9056 & 0.45 & 0.7704 \\
\text{Error} & 20 & 1015.4 & 50.7720 & & \\
\end{array}
\]

Bartlett’s Test for Homogeneity of TS Variance

\[
\begin{array}{cccc}
\text{Source} & \text{DF} & \text{Chi-Square} & \text{Pr} > \text{ChiSq} \\
\hline
\text{GROUP} & 4 & 0.9331 & 0.9198 \\
\end{array}
\]
1.4.2 Some Remedial Measures

The Kruskal-Wallis Test

When the assumption of normality is suspect, we may wish to use nonparametric alternatives to the $F$-test. The Kruskal-Wallis test is one such procedure based on the rank transformation.

To perform the Kruskal-Wallis test, we first rank all the observations, $y_{ij}$, in increasing order. Say the ranks are $R_{ij}$. The Kruskal-Wallis test statistic is

$$KW_0 = \frac{1}{S^2} \left[ \sum_{i=1}^{k} \frac{R_i^2}{n_i} - \frac{n(n+1)^2}{4} \right]$$

where $R_i$ is the sum of the ranks of group $i$, and

$$S^2 = \frac{1}{n-1} \left[ \sum_{i=1}^{k} \sum_{j=1}^{n_i} R_{ij}^2 - \frac{n(n+1)^2}{4} \right]$$

The test rejects $H_0: \mu_1 = \cdots = \mu_k$ if

$$KW_0 > \chi^2_{k-1}(\alpha).$$

Example

For the tensile strength data the ranks, $R_{ij}$, of the observations are given in the following table:

<table>
<thead>
<tr>
<th></th>
<th>15</th>
<th>20</th>
<th>25</th>
<th>30</th>
<th>35</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2.0</td>
<td>9.0</td>
<td>11.0</td>
<td>20.5</td>
<td>2.0</td>
</tr>
<tr>
<td>2</td>
<td>2.0</td>
<td>14.0</td>
<td>16.5</td>
<td>25.0</td>
<td>5.0</td>
</tr>
<tr>
<td>3</td>
<td>12.5</td>
<td>9.5</td>
<td>16.5</td>
<td>23.0</td>
<td>7.0</td>
</tr>
<tr>
<td>4</td>
<td>7.0</td>
<td>16.5</td>
<td>20.5</td>
<td>20.5</td>
<td>12.5</td>
</tr>
<tr>
<td>5</td>
<td>4.0</td>
<td>16.5</td>
<td>20.5</td>
<td>24.0</td>
<td>7.0</td>
</tr>
</tbody>
</table>

$R_i$ | 27.5 | 66.0 | 85.0 | 113.0 | 33.5 |

We find that $S^2 = 53.03$ and $KW_0 = 19.25$. From the chi-square table we get $\chi^2_{4}(0.01) = 13.28$. Thus we reject the null hypothesis and conclude that the treatments differ.

The SAS procedure NPAR1WAY may be used to obtain the Kruskal-Wallis test.

```sas
OPTIONS LS=80 PS=66 NODATE; DATA MONT; INPUT TS GROUP@@; CARDS; 7 1 7 1 15 1 11 1 9 1 12 2 17 2 12 2 18 2 18 2 14 3 18 3 18 3 19 3 19 3 19 4 25 4 22 4 19 4 23 4 7 5 10 5 11 5 15 5 11 5 ; PROC NPAR1WAY WILCOXON; CLASS GROUP; VAR TS; RUN; QUIT;
```
CHAPTER 1. COMPLETELY RANDOMIZED DESIGN

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable TS
Classified by Variable GROUP

<table>
<thead>
<tr>
<th>GROUP</th>
<th>N</th>
<th>Sum of Scores</th>
<th>Expected Under H0</th>
<th>Std Dev Under H0</th>
<th>Mean Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5</td>
<td>27.50</td>
<td>65.0</td>
<td>14.634434</td>
<td>5.50</td>
</tr>
<tr>
<td>2</td>
<td>5</td>
<td>66.00</td>
<td>65.0</td>
<td>14.634434</td>
<td>13.20</td>
</tr>
<tr>
<td>3</td>
<td>5</td>
<td>85.00</td>
<td>65.0</td>
<td>14.634434</td>
<td>17.00</td>
</tr>
<tr>
<td>4</td>
<td>5</td>
<td>113.00</td>
<td>65.0</td>
<td>14.634434</td>
<td>22.60</td>
</tr>
<tr>
<td>5</td>
<td>5</td>
<td>33.50</td>
<td>65.0</td>
<td>14.634434</td>
<td>6.70</td>
</tr>
</tbody>
</table>

Average scores were used for ties.

Kruskal-Wallis Test

<table>
<thead>
<tr>
<th>Chi-Square</th>
<th>DF</th>
<th>Pr &gt; Chi-Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>19.0637</td>
<td>4</td>
<td>0.0008</td>
</tr>
</tbody>
</table>

Variance Stabilizing Transformations

There are several variance stabilizing transformations one might consider in the case of heterogeneity of variance (heteroscedasticity). The common transformations are

$$\sqrt{y}, \log(y), 1/y, \arcsin(\sqrt{y}), 1/\sqrt{y}.$$  

A simple method of choosing the appropriate transformation is to plot \(\log S_i\) versus \(\log \bar{y}_i\) or regress \(\log S_i\) versus \(\log \bar{y}_i\). We then choose the transformation depending on the slope of the relationship. The following table may be used as a guide:

<table>
<thead>
<tr>
<th>Slope</th>
<th>Transformation</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>No Transformation</td>
</tr>
<tr>
<td>1/2</td>
<td>Square root</td>
</tr>
<tr>
<td>1</td>
<td>Log</td>
</tr>
<tr>
<td>3/2</td>
<td>Reciprocal square root</td>
</tr>
<tr>
<td>2</td>
<td>Reciprocal</td>
</tr>
</tbody>
</table>

A slightly more involved technique of choosing a variance stabilizing transformation is the Box-Cox transformation. It uses the maximum likelihood method to simultaneously estimate the transformation parameter as well as the overall mean and the treatment effects.
Chapter 2
Randomized Blocks, Latin Squares, and Related Designs

2.1 The Randomized Complete Block Design

2.1.1 Introduction
In a completely randomized design (CRD), treatments are assigned to the experimental units in a completely random manner. The random error component arises because of all the variables which affect the dependent variable except the one controlled variable, the treatment. Naturally, the experimenter wants to reduce the errors which account for differences among observations within each treatment. One of the ways in which this could be achieved is through blocking. This is done by identifying supplemental variables that are used to group experimental subjects that are homogeneous with respect to that variable. This creates differences among the blocks and makes observations within a block similar. The simplest design that would accomplish this is known as a randomized complete block design (RCBD). Each block is divided into \( k \) subblocks of equal size. Within each block the \( k \) treatments are assigned at random to the subblocks. The design is "complete" in the sense that each block contains all the \( k \) treatments.

The following layout shows a RCBD with \( k \) treatments and \( b \) blocks. There is one observation per treatment in each block and the treatments are run in a random order within each block.

<table>
<thead>
<tr>
<th>Block 1</th>
<th>Treatment 1</th>
<th>Treatment 2</th>
<th>( \cdots )</th>
<th>Treatment ( k )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Block 2</td>
<td>( y_{11} )</td>
<td>( y_{21} )</td>
<td>( \cdots )</td>
<td>( y_{k1} )</td>
</tr>
<tr>
<td>Block 3</td>
<td>( y_{12} )</td>
<td>( y_{22} )</td>
<td>( \cdots )</td>
<td>( y_{k2} )</td>
</tr>
<tr>
<td>\vdots</td>
<td>\vdots</td>
<td>\vdots</td>
<td>( \ddots )</td>
<td>( \vdots )</td>
</tr>
<tr>
<td>Block ( b )</td>
<td>( y_{1b} )</td>
<td>( y_{2b} )</td>
<td>( \cdots )</td>
<td>( y_{kb} )</td>
</tr>
</tbody>
</table>

The statistical model for RCBD is

\[
y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}, \quad i = 1, \cdots, k, \quad j = 1, \cdots, b
\]  

(2.1)

where

- \( \mu \) is the overall mean,
- \( \tau_i \) is the \( i \)th treatment effect,
- \( \beta_j \) is the effect of the \( j \)th block, and
- \( \epsilon_{ij} \) is the random error term associated with the \( ij \)th observation.
We make the following assumptions concerning the RCBD model:

- \( \sum_{i=1}^{k} \tau_i = 0 \),
- \( \sum_{j=1}^{b} \beta_j = 0 \), and
- \( \epsilon_{ij} \sim \text{i.i.d.} \ N(0, \sigma^2) \).

We are mainly interested in testing the hypotheses

\[ H_0 : \mu_1 = \mu_2 = \cdots = \mu_k \]
\[ H_A : \mu_i \neq \mu_j \text{ for at least one pair } i \neq j \]

Here the \( i \)th treatment mean is defined as

\[ \mu_i = \frac{1}{b} \sum_{j=1}^{b} (\mu + \tau_i + \beta_j) = \mu + \tau_i \]

Thus the above hypotheses may be written equivalently as

\[ H_0 : \tau_1 = \tau_2 = \cdots = \tau_k = 0 \]
\[ H_A : \tau_i \neq 0 \text{ for at least one } i \]

### 2.1.2 Decomposition of the Total Sum of Squares

Let \( n = kb \) be the total number of observations. Define

\[ \bar{y}_i = \frac{1}{b} \sum_{j=1}^{b} y_{ij}, \quad i = 1, \cdots, k \]
\[ \bar{y}_j = \frac{1}{k} \sum_{i=1}^{k} y_{ij}, \quad j = 1, \cdots, b \]
\[ \bar{y}_. = \frac{1}{n} \sum_{i=1}^{k} \sum_{j=1}^{b} y_{ij} = \frac{1}{k} \sum_{i=1}^{k} \bar{y}_i = \frac{1}{b} \sum_{j=1}^{b} \bar{y}_j \]

One may show that

\[ \sum_{i=1}^{k} \sum_{j=1}^{b} (y_{ij} - \bar{y}_.)^2 = b \sum_{i=1}^{k} (\bar{y}_i - \bar{y}_.)^2 + k \sum_{j=1}^{b} (\bar{y}_j - \bar{y}_.)^2 \]
\[ + \sum_{i=1}^{k} \sum_{j=1}^{b} (y_{ij} - \bar{y}_i - \bar{y}_j + \bar{y}_.)^2 \]

Thus the total sum of squares is partitioned into the sum of squares due to the treatments, the sum of squares due to the blocking, and the sum of squares due to error.

Symbolically,

\[ SS_T = SS_{\text{Treatments}} + SS_{\text{Blocks}} + SS_E \]

The degrees of freedom are partitioned accordingly as

\[ (n - 1) = (k - 1) + (b - 1) + (k - 1)(b - 1) \]
2.1. THE RANDOMIZED COMPLETE BLOCK DESIGN

2.1.3 Statistical Analysis

Testing

The test for equality of treatment means is done using the test statistic

$$F_0 = \frac{MS_{\text{Treatments}}}{MS_E}$$

where

$$MS_{\text{Treatments}} = \frac{SS_{\text{Treatments}}}{k-1}$$ and $$MS_E = \frac{SS_E}{(k-1)(b-1)}.$$ 

An $\alpha$ level test rejects $H_0$ if

$$F_0 > F_{k-1,(b-1)(k-1)}(\alpha).$$

The ANOVA table for RCBD is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>$F$-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatments</td>
<td>$k-1$</td>
<td>$SS_{\text{Treatments}}$</td>
<td>$MS_{\text{Treatments}}$</td>
<td>$F_0 = \frac{MS_{\text{Treatments}}}{MS_E}$</td>
</tr>
<tr>
<td>Blocks</td>
<td>$b-1$</td>
<td>$SS_{\text{Blocks}}$</td>
<td>$MS_{\text{Blocks}}$</td>
<td>$F_B = \frac{MS_{\text{Blocks}}}{MS_E}$</td>
</tr>
<tr>
<td>Error</td>
<td>$(k-1)(b-1)$</td>
<td>$SS_E$</td>
<td>$MS_E$</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>$n-1$</td>
<td>$SS_T$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Since there is no randomization of treatments across blocks the use of $F_B = MS_{\text{Blocks}}/MS_E$ as a test for block effects is questionable. However, a large value of $F_B$ would indicate that the blocking variable is probably having the intended effect of reducing noise.

Estimation

Estimation of the model parameters is performed using the least squares procedure as in the case of the completely randomized design. The estimators of $\mu$, $\tau_i$, and $\beta_j$ are obtained via minimization of the sum of squares of the errors

$$L = \sum_{i=1}^{k} \sum_{j=1}^{b} \epsilon_{ij}^2 = \sum_{i=1}^{k} \sum_{j=1}^{b} (y_{ij} - \mu - \tau_i - \beta_j)^2.$$ 

The solution is

$$\hat{\mu} = \bar{y}.,$$

$$\hat{\tau}_i = \bar{y}_i - \bar{y}. \quad i = 1, \cdots, k$$

$$\hat{\beta}_j = \bar{y}_j - \bar{y}. \quad j = 1, \cdots, b$$

From the model in (2.1), we can see that the estimated values of $y_{ij}$ are

$$\hat{y}_{ij} = \hat{\mu} + \hat{\tau}_i + \hat{\beta}_j$$

$$= \bar{y}. + \bar{y}_i - \bar{y}. + \bar{y}_j - \bar{y}.$$ 

$$= \bar{y}. + \bar{y}_j - \bar{y}.$$

Example

An experiment was designed to study the performance of four different detergents for cleaning clothes. The following ”cleanliness” readings (higher=cleaner) were obtained using a special device for three different types of common stains. Is there a significant difference among the detergents?
CHAPTER 2. RANDOMIZED BLOCKS

<table>
<thead>
<tr>
<th></th>
<th>Stain 1</th>
<th>Stain 2</th>
<th>Stain 3</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Detergent 1</td>
<td>45</td>
<td>43</td>
<td>51</td>
<td>139</td>
</tr>
<tr>
<td>Detergent 2</td>
<td>47</td>
<td>46</td>
<td>52</td>
<td>145</td>
</tr>
<tr>
<td>Detergent 3</td>
<td>48</td>
<td>50</td>
<td>55</td>
<td>153</td>
</tr>
<tr>
<td>Detergent 4</td>
<td>42</td>
<td>37</td>
<td>49</td>
<td>128</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>182</td>
<td>176</td>
<td>207</td>
<td>565</td>
</tr>
</tbody>
</table>

Using the formulæ for $SS$ given above one may compute:

$$SS_T = 265$$

$$SS_{Treatments} = 111$$

$$SS_{Blocks} = 135$$

$$SS_E = 265 - 111 - 135 = 19$$

Thus

$$F_0 = \frac{111/3}{19/6} = 11.6$$

which has a $p$-value < .01. Thus we claim that there is a significant difference among the four detergents.

The following SAS code gives the ANOVA table:

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA WASH;
INPUT STAIN SOAP Y @@;
CARDS;
1 1 45 1 2 47 1 3 48 1 4 42
2 1 43 2 2 46 2 3 50 2 4 37
3 1 51 3 2 52 3 3 55 3 4 49
;
PROC GLM;
CLASS STAIN SOAP;
MODEL Y = SOAP STAIN;
RUN;
QUIT;
```

The corresponding output is

The GLM Procedure

Dependent Variable: Y

<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>5</td>
<td>246.0833333</td>
<td>49.2166667</td>
<td>15.68</td>
<td>0.0022</td>
</tr>
<tr>
<td>Error</td>
<td>6</td>
<td>18.8333333</td>
<td>3.1388889</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>11</td>
<td>264.9166667</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>R-Square</th>
<th>Coeff Var</th>
<th>Root MSE</th>
<th>Y Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.928908</td>
<td>3.762883</td>
<td>1.771691</td>
<td>47.0833</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>SOAP</td>
<td>3</td>
<td>110.9166667</td>
<td>36.972222</td>
<td>11.78</td>
<td>0.0063</td>
</tr>
<tr>
<td>STAIN</td>
<td>2</td>
<td>135.1666667</td>
<td>67.583333</td>
<td>21.53</td>
<td>0.0018</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>SOAP</td>
<td>3</td>
<td>110.9166667</td>
<td>36.972222</td>
<td>11.78</td>
<td>0.0063</td>
</tr>
<tr>
<td>STAIN</td>
<td>2</td>
<td>135.1666667</td>
<td>67.583333</td>
<td>21.53</td>
<td>0.0018</td>
</tr>
</tbody>
</table>

The SAS Type I analysis gives the correct $F = 11.78$ with a $p$-value of .0063.

An incorrect analysis of the data using a one-way ANOVA set up (ignoring the blocking factor) is
2.1. THE RANDOMIZED COMPLETE BLOCK DESIGN

PROC GLM;
CLASS SOAP;
MODEL Y = SOAP;
RUN;
QUIT;

The corresponding output is

The GLM Procedure

Dependent Variable: Y

<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>3</td>
<td>110.9166667</td>
<td>36.9722222</td>
<td>1.92</td>
<td>0.2048</td>
</tr>
<tr>
<td>Error</td>
<td>8</td>
<td>154.0000000</td>
<td>19.2500000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>11</td>
<td>264.9166667</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Notice that $H_0$ is not rejected indicating no significant difference among the detergents.

2.1.4 Relative Efficiency of the RCBD

The example in the previous section shows that RCBD and CRD may lead to different conclusions. A natural question to ask is "How much more efficient is the RCBD compared to a CRD?" One way to define this relative efficiency is

$$ R = \frac{(df_b + 1)(df_r + 3)}{(df_b + 3)(df_r + 1)} \cdot \frac{\sigma^2_r}{\sigma^2_b} $$

where $\sigma^2$ and $\sigma^2_b$ are the error variances of the CRD and RCBD, respectively, and $df_r$ and $df_b$ are the corresponding error degrees of freedom. $R$ is the increase in the number of replications required if a CRD to achieve the same precision as a RCBD.

Using the ANOVA table from RCBD, we may estimate $\sigma^2$ and $\sigma^2_b$ as

$$ \hat{\sigma}^2_b = MS_E $$
$$ \hat{\sigma}^2_r = \frac{(b - 1)MS_{Blocks} + b(k - 1)MS_E}{kb - 1} $$

Example

Consider the detergent example considered in the previous section. From the ANOVA table for the RCBD we see that

$$ MS_E = 3.139, \quad df_b = (k - 1)(b - 1) = 6, \quad df_r = kb - k = 8 $$

Thus

$$ \hat{\sigma}^2_b = MS_E = 3.139 $$
$$ \hat{\sigma}^2_r = \frac{(b - 1)MS_{Blocks} + b(k - 1)MS_E}{kb - 1} = \frac{(2)(67.58) + (3)(3)(3.139)}{12 - 1} = 14.86 $$

The relative efficiency of RCBD to CRD is estimated to be

$$ \hat{R} = \frac{(df_b + 1)(df_r + 3)}{(df_b + 3)(df_r + 1)} \cdot \frac{\hat{\sigma}^2_r}{\hat{\sigma}^2_b} $$
$$ = \frac{(6 + 1)(8 + 3)(14.86)}{(6 + 3)(8 + 1)(3.139)} = 4.5 $$

This means that a CRD will need about 4.5 as many replications to obtain the same precision as obtained by blocking on stain types.
Another natural question is "What is the cost of blocking if the blocking variable is not really important, i.e., if blocking was not necessary?" The answer to this question lies in the differing degrees of freedom we use for the error variable. Notice that we are using \((k-1)(b-1)\) degrees of freedom in the RCBD as opposed to \(kb-k\) in the case of a CRD. Thus we lose \(b-1\) degrees of freedom unnecessarily. This makes the test on the treatment means less sensitive, i.e., differences among the means will remain undetected.

### 2.1.5 Comparison of Treatment Means

As in the case of CRD, we are interested in multiple comparisons to find out which treatment means differ. We may use any of the multiple comparison procedures discussed in Chapter 1. The only difference here is that we use the number of blocks \(b\) in place of the common sample size. Thus in all the equations we replace \(n_i\) by \(b\).

**Example**

Once again consider the detergent example of the previous section. Suppose we wish to make pairwise comparisons of the treatment means via the Tukey-Kramer procedure. The Tukey-Kramer procedure declares two treatment means, \(\mu_i\) and \(\mu_j\), to be significantly different if the absolute value of their sample differences exceeds

\[
T_\alpha = q_{k,b-1}(\alpha) \sqrt{\frac{MSE}{2} \left( \frac{2}{b} \right)},
\]

where \(q_{k,b-1}(\alpha)\) is the \(\alpha\) percentile value of the studentized range distribution with \(k\) groups and \((k-1)(b-1)\) degrees of freedom.

The sample treatment means are

\[
\bar{y}_1 = 46.33, \quad \bar{y}_2 = 48.33, \quad \bar{y}_3 = 51.00, \quad \bar{y}_4 = 42.67;
\]

We also have

\[
T_{.05} = q_{4,6}(.05)\sqrt{3.139/3} = (4.90)(1.023) = 5.0127
\]

Thus using underlining

\[
\begin{align*}
\bar{y}_4 &\quad \bar{y}_1 &\quad \bar{y}_2 &\quad \bar{y}_3 \\
42.67 &\quad 46.33 &\quad 48.33 &\quad 51.00
\end{align*}
\]

### 2.1.6 Model Adequacy Checking

**Additivity**

The initial assumption we made when considering the model

\[
y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}
\]

is that the model is additive. If the first treatment increases the expected response by 2 and the first block increases it by 4, then, according to our model, the expected increase of the response in block 1 and treatment 1 is 6. This setup rules out the possibility of interactions between blocks and treatments. In reality, the way the treatment affects the outcome may be different from block to block.

A quick graphical check for nonadditivity is to plot the residuals, \(e_{ij} = y_{ij} - \hat{y}_{ij}\), versus the fitted values, \(\hat{y}_{ij}\). Any nonlinear pattern indicates nonadditivity.

A formal test is Tukey’s one degree of freedom test for nonadditivity. We start out by fitting the model

\[
y_{ij} = \mu + \tau_i + \beta_j + \gamma \tau_i \beta_j + \epsilon_{ij}
\]

Then testing the hypothesis

\[
H_0 : \gamma = 0
\]

is equivalent to testing the presence of nonadditivity. We use the regression approach of testing by fitting the full and reduced models. Here is the procedure:
2.1. THE RANDOMIZED COMPLETE BLOCK DESIGN

- Fit the model
  \[ y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij} \]
- Let \( e_{ij} \) and \( \hat{y}_{ij} \) be the residual and the fitted value, respectively, corresponding to observation \( ij \) in resulting from fitting the model above.
- Let \( z_{ij} = \hat{y}_{ij}^2 \) and fit
  \[ z_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij} \]
- Let \( r_{ij} = z_{ij} - \hat{z}_{ij} \) be the residuals from this model.
- Regress \( e_{ij} \) on \( r_{ij} \), i.e, fit the model
  \[ e_{ij} = \alpha + \gamma r_{ij} + \epsilon_{ij} \]
  Let \( \hat{\gamma} \) be the estimated slope.
- The sum of squares due to nonadditivity is
  \[ SS_N = \hat{\gamma}^2 \sum_{i=1}^{k} \sum_{j=1}^{b} r_{ij}^2 \]
- The test statistic for nonadditivity is
  \[ F_0 = \frac{SS_N/1}{(SS_E - SS_N)/[(k-1)(b-1)-1]} \]

Example

The impurity in a chemical product is believed to be affected by pressure. We will use temperature as a blocking variable. The data is given below.

<table>
<thead>
<tr>
<th>Pressure</th>
<th>Temp</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>25</td>
</tr>
<tr>
<td>100</td>
<td>5</td>
</tr>
<tr>
<td>125</td>
<td>3</td>
</tr>
<tr>
<td>150</td>
<td>1</td>
</tr>
</tbody>
</table>

The following SAS code is used.

```sas
Options ls=80 ps=66 nodate;
title "Tukey's 1 DF Nonadditivity Test";
Data Chemical;
   Input Temp @;
   Do Pres = 25,30,35,40,45;
      Input Im @;
      output;
   end;
cards;
100 5 4 6 3 5
125 3 1 4 2 3
150 1 1 3 1 2
;
proc print;
run;
quit;
proc glm;
   class Temp Pres;
   model Im = Temp Pres;
```
output out=out1 predicted=Pred;
run;
quit;

/* Form a new variable called Psquare. */
Data Tukey;
  set out1;
    Psquare = Pred*Pred;
run;
quit;

proc glm;
  class Temp Pres;
  model Im = Temp Pres Psquare;
run;
quit;

The following is the corresponding output.

Tukey’s 1 DF Nonadditivity Test

The GLM Procedure
Dependent Variable: Im

<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>7</td>
<td>35.03185550</td>
<td>5.00455079</td>
<td>18.42</td>
<td>0.0005</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>1.90147783</td>
<td>0.27163969</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>14</td>
<td>36.93333333</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square  Coeff Var  Root MSE  Im Mean
0.948516   17.7676   0.521191  2.933333

Source    | DF | Type I SS | Mean Square | F Value | Pr > F |
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Temp</td>
<td>2</td>
<td>23.33333333</td>
<td>11.6666667</td>
<td>42.95</td>
<td>0.0001</td>
</tr>
<tr>
<td>Pres</td>
<td>4</td>
<td>11.60000000</td>
<td>2.90000000</td>
<td>10.68</td>
<td>0.0042</td>
</tr>
<tr>
<td>Psquare</td>
<td>1</td>
<td>0.09852217</td>
<td>0.09852217</td>
<td>0.36</td>
<td>0.5660</td>
</tr>
</tbody>
</table>

Source    | DF | Type III SS | Mean Square | F Value | Pr > F |
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Temp</td>
<td>2</td>
<td>1.25864083</td>
<td>0.62932041</td>
<td>2.32</td>
<td>0.1690</td>
</tr>
<tr>
<td>Pres</td>
<td>4</td>
<td>1.09624963</td>
<td>0.27406241</td>
<td>1.01</td>
<td>0.4634</td>
</tr>
<tr>
<td>Psquare</td>
<td>1</td>
<td>0.09852217</td>
<td>0.09852217</td>
<td>0.36</td>
<td>0.5660</td>
</tr>
</tbody>
</table>

Thus $F_0 = 0.36$ with 1 and 7 degrees of freedom. It has a p-value of 0.5660. Thus we have no evidence to declare nonadditivity.

Normality

The diagnostic tools for the normality of the error terms are the same as those use in the case of the CRD. The graphic tools are the QQ-plot and the histogram of the residuals. Formal tests like the Kolmogorov-Smirnov test may also be used to assess the normality of the errors.

Example

Consider the detergent example above. The following SAS code gives the normality diagnostics.
2.1. THE RANDOMIZED COMPLETE BLOCK DESIGN

```
OPTIONS LS=80 PS=66 NODATE;
DATA WASH;
INPUT STAIN SOAP Y @@;
CARDS;
1 1 45 1 2 47 1 3 48 1 4 42
2 1 43 2 2 46 2 3 50 2 4 37
3 1 51 3 2 52 3 3 55 3 4 49
;
PROC GLM;
   CLASS STAIN SOAP;
   MODEL Y = SOAP STAIN;
   MEANS SOAP/ TUKEY LINES;
   OUTPUT OUT=DIAG R=RES P=PRED;
RUN;
QUIT;
PROC UNIVARIATE NOPRINT;
   QQPLOT RES / NORMAL (L=1 MU=0 SIGMA=EST);
   HIST RES / NORMAL (L=1 MU=0 SIGMA=EST);
RUN;
QUIT;
PROC GPLOT;
   PLOT RES*SOAP;
   PLOT RES*STAIN;
   PLOT RES*PRED;
RUN;
QUIT;

The associated output is (figures given first):
```
CHAPTER 2. RANDOMIZED BLOCKS

Tukey’s Studentized Range (HSD) Test for Y

NOTE: This test controls the Type I experimentwise error rate, but it generally has a higher Type II error rate than REGWQ.

Alpha: 0.05  
Error Degrees of Freedom: 6  
Error Mean Square: 3.138889  
Critical Value of Studentized Range: 4.89559  
Minimum Significant Difference: 5.0076

Means with the same letter are not significantly different.

Tukey Grouping  

\[
\begin{array}{ccc}
\text{Group} & \text{Mean} & \text{N} & \text{SOAP} \\
A & 51.000 & 3 & 3 \\
A & 48.333 & 3 & 2 \\
B & A & 46.333 & 3 & 1 \\
B & & 42.667 & 3 & 4 \\
\end{array}
\]

RCBD Diagnostics

The UNIVARIATE Procedure  
Fitted Distribution for RES

Parameters for Normal Distribution

Parameter: Symbol, Estimate

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Symbol</th>
<th>Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>Mu</td>
<td>0</td>
</tr>
<tr>
<td>Std Dev</td>
<td>Sigma</td>
<td>1.252775</td>
</tr>
</tbody>
</table>

Goodness-of-Fit Tests for Normal Distribution

<table>
<thead>
<tr>
<th>Test</th>
<th>---Statistic---</th>
<th>------p Value------</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cramer-von Mises</td>
<td>W-Sq 0.01685612</td>
<td>Pr &gt; W-Sq &gt;0.250</td>
</tr>
<tr>
<td>Anderson-Darling</td>
<td>A-Sq 0.13386116</td>
<td>Pr &gt; A-Sq &gt;0.250</td>
</tr>
</tbody>
</table>

The QQ-plot and the formal tests do not indicate the presence of nonnormality of the errors.
2.1. THE RANDOMIZED COMPLETE BLOCK DESIGN

**Constant Variance**

The tests for constant variance are the same as those used in the case of the CRD. One may use formal tests, such as Levene’s test or perform graphical checks to see if the assumption of constant variance is satisfied. The plots we need to examine in this case are *residuals versus blocks*, *residuals versus treatments*, and *residuals versus predicted values*.

The plots below (produced by the SAS code above) suggest that there may be nonconstant variance. The spread of the residuals seems to differ from detergent to detergent. We may need to transform the values and rerun the analysis.
2.1.7 Missing Values

In a randomized complete block design, each treatment appears once in every block. A missing observation would mean a loss of the completeness of the design. One way to proceed would be to use a multiple regression analysis. Another way would be to estimate the missing value.

If only one value is missing, say $y_{ij}$, then we substitute a value

$$y'_{ij} = \frac{kT_i + bT_j - T_\cdot}{(k-1)(b-1)}$$

where

- $T_i$ is the total for treatment $i$,
- $T_j$ is the total for block $j$, and
- $T_\cdot$ is the grand total.

We then substitute $y'_{ij}$ and carry out the ANOVA as usual. There will, however, be a loss of one degree of freedom from both the total and error sums of squares. Since the substituted value adds no practical information to the design, it should not be used in computations of means, for instance, when performing multiple comparisons.

When more than one value is missing, they may be estimated via an iterative process. We first guess the values of all except one. We then estimate the one missing value using the procedure above. We then estimate the second one using the one estimated value and the remaining guessed values. We proceed to estimate the rest in a similar fashion. We repeat this process until convergence, i.e. difference between consecutive estimates is small.

If several observations are missing from a single block or a single treatment group, we usually eliminate the block or treatment in question. The analysis is then performed as if the block or treatment is nonexistent.

Example

Consider the detergent comparison example. Suppose $y_{4,2} = 37$ is missing. Note that the totals (without 37) are $T_4 = 91$, $T_2 = 139$, $T_\cdot = 528$. The estimate is

$$y'_{4,2} = \frac{4(91) + 3(139) - 528}{6} = 42.17$$
Now we just plug in this value and perform the analysis. We then need to modify the $F$ value by hand using the correct degrees of freedom. The following SAS code will perform the RCBD ANOVA.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA WASH;
INPUT STAIN SOAP Y @@;
CARDS;
1 1 45 1 2 47 1 3 48 1 4 42
2 1 43 2 2 46 2 3 50 2 4 .
3 1 51 3 2 52 3 3 55 3 4 49 ;
/* Replace the missing value with the estimated value. */
DATA NEW;
SET WASH;
IF Y = . THEN Y = 42.17;
RUN;
QUIT;
PROC GLM;
CLASS STAIN SOAP;
MODEL Y = SOAP STAIN;
RUN;
QUIT;
```

The following is the associated SAS output.

```
The SAS System
The GLM Procedure

Dependent Variable: Y

          Source    DF    Type I SS  Mean Square   F Value  Pr > F
          Model     5   71.9305583  23.9768528  26.22  0.0008
          Error     6   107.7398167  53.8699083  58.92  0.0001
          Corrected Total 11 185.1564917

          Source    DF    Type III SS   Mean Square     F Value  Pr > F
          SOAP      3   71.9305583   23.9768528  26.22  0.0008
          STAIN     2  107.7398167  53.8699083   58.92  0.0001
```

So, the correct $F$ value is

$$F_0 = \frac{71.93/3}{5.49/5} = 21.84$$

which exceeds the tabulated value of $F_{3.5}(0.05) = 5.41$. 

2.2 The Latin Square Design

The RCBD setup allows us to use only one factor as a blocking variable. However, sometimes we have two or more factors that can be controlled.

Consider a situation where we have two blocking variables, row and column hereafter, and treatments. One design that handles such a case is the Latin square design. To build a Latin square design for \( p \) treatments, we need \( p^2 \) observations. These observations are then placed in a \( p \times p \) grid made up of, \( p \) rows and \( p \) columns, in such a way that each treatment occurs once, and only once, in each row and column.

Say we have 4 treatments, \( A, B, C, \) and \( D \) and two factors to control. A basic \( 4 \times 4 \) Latin square design is

\[
\begin{array}{cccc}
\text{Row} & 1 & 2 & 3 & 4 \\
1 & A & B & C & D \\
2 & B & C & D & A \\
3 & C & D & A & B \\
4 & D & A & B & C \\
\end{array}
\]

The SAS procedure \texttt{Proc PLAN} may be used in association with \texttt{Proc TABULATE} to generate designs, in particular the Latin square design. The following SAS code gives the above basic \( 4 \times 4 \) design.

```sas
OPTIONS LS=80 PS=66 NODATE;
TITLE 'A 4 BY 4 LATIN SQUARE DESIGN';
PROC PLAN SEED=12345;
   FACTORS ROWS=4 ORDERED COLS=4 ORDERED /NOPRINT;
   TREATMENTS TMTS=4 CYCLIC;
   OUTPUT OUT=LAT44
       ROWS NVALS=(1 2 3 4)
       COLS NVALS=(1 2 3 4)
       TMTS NVALS=(1 2 3 4);
RUN;
QUIT;
PROC TABULATE;
   CLASS ROWS COLS;
   VAR TMTS;
   TABLE ROWS, COLS*TMTS;
RUN;
QUIT;
```

---

\[A 4 BY 4 LATIN SQUARE DESIGN\]

```
<table>
<thead>
<tr>
<th>COLS</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TMTS</td>
<td>TMTS</td>
<td>TMTS</td>
<td>TMTS</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sum</td>
<td>Sum</td>
<td>Sum</td>
<td>Sum</td>
</tr>
<tr>
<td>ROWS</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
```

The statistical model for a Latin square design is

\[ y_{ijk} = \mu + \alpha_i + \tau_j + \beta_k + \epsilon_{ijk} \]

where

- \( \mu \) is the grand mean,
- \( \alpha_i \) is the \( i \)th block 1 (row) effect,
- \( \tau_j \) is the \( j \)th treatment effect,
- \( \beta_k \) is the \( k \)th block 2 (column) effect, and
- \( \epsilon_{ijk} \sim i.i.d. N(0, \sigma^2) \).

There is no interaction between rows, columns, and treatments; the model is completely additive.

2.2.1 Statistical Analysis

The total sum of squares, \( SS_T \), partitions into sums of squares due to columns, rows, treatments, and error. An intuitive way of identifying the components is (since all the cross products are zero)

\[ y_{ijk} = \bar{y} + (\bar{y}_i - \bar{y}) + (\bar{y}_j - \bar{y}) + (\bar{y}_k - \bar{y}) + (y_{ijk} - \bar{y}_i - \bar{y}_j - \bar{y}_k + 2\bar{y}) \]

We have

\[ SS_T = SS_{Row} + SS_{Trt} + SS_{Col} + SS_E \]

where

\[ SS_T = \sum \sum \sum (y_{ijk} - \bar{y})^2 \]
\[ SS_{Row} = p \sum (\bar{y}_i - \bar{y})^2 \]
\[ SS_{Trt} = p \sum (\bar{y}_j - \bar{y})^2 \]
\[ SS_{Col} = p \sum (\bar{y}_k - \bar{y})^2 \]
\[ SS_E = \sum \sum \sum (y_{ijk} - \bar{y}_i - \bar{y}_j - \bar{y}_k + 2\bar{y})^2 \]

Thus the ANOVA table for the Latin square design is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatments</td>
<td>( p - 1 )</td>
<td>( SS_{Trt} )</td>
<td>( MS_{Trt} )</td>
<td>( F_0 = \frac{MS_{Trt}}{MS_E} )</td>
</tr>
<tr>
<td>Rows</td>
<td>( p - 1 )</td>
<td>( SS_{Row} )</td>
<td>( MS_{Row} )</td>
<td></td>
</tr>
<tr>
<td>Columns</td>
<td>( p - 1 )</td>
<td>( SS_{Col} )</td>
<td>( MS_{Col} )</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>((p - 2)(p - 1))</td>
<td>( SS_E )</td>
<td>( MS_E )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( p^2 - 1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The test statistic for testing for no differences in the treatment means is \( F_0 \). An \( \alpha \) level test rejects null hypothesis if \( F_0 > F_{p-1,(p-2)(p-1)}(\alpha) \).

Multiple comparisons are performed in a similar manner as in the case of RCBD. The only difference is that \( b \) is replaced by \( p \) and the error degrees of freedom becomes \((p - 2)(p - 1)\) instead of \((k - 1)(b - 1)\).
Example

Consider an experiment to investigate the effect of four different diets on milk production of cows. There are four cows in the study. During each lactation period the cows receive a different diet. Assume that there is a washout period between diets so that previous diet does not affect future results. Lactation period and cows are used as blocking variables.

A $4 \times 4$ Latin square design is implemented.

<table>
<thead>
<tr>
<th>Period</th>
<th>Cow 1</th>
<th>Cow 2</th>
<th>Cow 3</th>
<th>Cow 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A=38</td>
<td>B=39</td>
<td>C=45</td>
<td>D=41</td>
</tr>
<tr>
<td>2</td>
<td>B=32</td>
<td>C=37</td>
<td>D=38</td>
<td>A=30</td>
</tr>
<tr>
<td>3</td>
<td>C=35</td>
<td>D=36</td>
<td>A=37</td>
<td>B=32</td>
</tr>
<tr>
<td>4</td>
<td>D=33</td>
<td>A=30</td>
<td>B=35</td>
<td>C=33</td>
</tr>
</tbody>
</table>

The following gives the SAS analysis of the data.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA NEW;
  INPUT COW PERIOD DIET MILK @@;
  CARDS;
  1 1 1 38 1 2 2 32 1 3 3 35 1 4 4 33 2 1 3 39 2 2 3 37 2 3 4 36 2 4 1 30 3 1 3 45 3 2 4 38 3 3 1 37 3 4 2 35 4 1 4 41 4 2 1 30 4 3 2 32 4 4 3 33 ;
  RUN;
QUIT;
PROC GLM;
  CLASS COW DIET PERIOD;
  MODEL MILK = DIET PERIOD COW;
  MEANS DIET/ LINES TUKEY;
RUN;
QUIT;
```

---

**Dependent Variable: MILK**

<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>9</td>
<td>242.5625000</td>
<td>26.9513889</td>
<td>33.17</td>
<td>0.0002</td>
</tr>
<tr>
<td>Error</td>
<td>6</td>
<td>4.8750000</td>
<td>0.8125000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>15</td>
<td>247.4375000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square  | Coeff Var | Root MSE | MILK Mean |
----------|-----------|----------|-----------|
0.980298  | 2.525780  | 0.901388 | 35.68750  |

**Source**

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>DIET</td>
<td>3</td>
<td>40.6875000</td>
<td>13.5625000</td>
<td>16.69</td>
<td>0.0026</td>
</tr>
<tr>
<td>PERIOD</td>
<td>3</td>
<td>147.187500</td>
<td>49.0625000</td>
<td>60.38</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>COW</td>
<td>3</td>
<td>54.6875000</td>
<td>18.2291667</td>
<td>22.44</td>
<td>0.0012</td>
</tr>
</tbody>
</table>

**Source**

<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>DIET</td>
<td>3</td>
<td>40.6875000</td>
<td>13.5625000</td>
<td>16.69</td>
<td>0.0026</td>
</tr>
<tr>
<td>PERIOD</td>
<td>3</td>
<td>147.187500</td>
<td>49.0625000</td>
<td>60.38</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>COW</td>
<td>3</td>
<td>54.6875000</td>
<td>18.2291667</td>
<td>22.44</td>
<td>0.0012</td>
</tr>
</tbody>
</table>

Tukey’s Studentized Range (HSD) Test for MILK

Alpha | 0.05
2.2. THE LATIN SQUARE DESIGN

<table>
<thead>
<tr>
<th>Error Degrees of Freedom</th>
<th>6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error Mean Square</td>
<td>0.8125</td>
</tr>
<tr>
<td>Critical Value of Studentized Range</td>
<td>4.89559</td>
</tr>
<tr>
<td>Minimum Significant Difference</td>
<td>2.2064</td>
</tr>
</tbody>
</table>

Means with the same letter are not significantly different.

<table>
<thead>
<tr>
<th>Tukey Grouping</th>
<th>Mean</th>
<th>N</th>
<th>DIET</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>37.5000</td>
<td>4</td>
<td>3</td>
</tr>
<tr>
<td>A</td>
<td>37.0000</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>B</td>
<td>34.5000</td>
<td>4</td>
<td>2</td>
</tr>
<tr>
<td>B</td>
<td>33.7500</td>
<td>4</td>
<td>1</td>
</tr>
</tbody>
</table>

Thus there diet has a significant effect ($p$-value=0.0026) on milk production. The Tukey-Kramer multiple comparison procedure indicates that diets $C$ and $D$ do not differ significantly. The same result holds for diets $A$ and $B$. All other pairs are declared to be significantly different.

2.2.2 Missing Values

Missing values are estimated in a similar manner as in RCBD’s. If only $y_{ijk}$ is missing, it is estimated by

$$y_{ijk} = \frac{p(T_{i.} + T_{.j} + T_{..k}) - 2T_{..}}{(p - 1)(p - 2)}$$

where $T_{i.}, T_{.j}, T_{..k}$, and $T_{..}$ are the row $i$, treatment $j$, column $k$, and grand totals of the available observations, respectively.

If more than one value is missing, we employ an iterative procedure similar to the one in RCBD.

2.2.3 Relative Efficiency

The relative efficiency of the Latin square design with respect to other designs is considered next.

The estimated relative efficiency of a Latin square design with respect to a RCBD with the rows omitted and the columns as blocks is

$$\hat{R}(\text{Latin, RCBD}_{col}) = \frac{MS_{Row} + (p - 1)MS_{E}}{pMS_{E}}$$

Similarly, the estimated relative efficiency of a Latin square design with respect to a RCBD with the columns omitted and the rows as blocks is

$$\hat{R}(\text{Latin, RCBD}_{row}) = \frac{MS_{Col} + (p - 1)MS_{E}}{pMS_{E}}$$

Furthermore, the estimated relative efficiency of a Latin square design with respect to a CRD

$$\hat{R}(\text{Latin, CRD}) = \frac{MS_{Row} + MS_{Col} + (p - 1)MS_{E}}{(p + 1)MS_{E}}$$

For instance, considering the milk production example, we see that if we just use cows as blocks, we get

$$\hat{R}(\text{Latin, RCBD}_{cows}) = \frac{MS_{Period} + (p - 1)MS_{E}}{pMS_{E}} = \frac{49.06 + 3(0.8125)}{4(0.8125)} = 15.85$$

Thus a RCBD design with just cows as blocks would cost about 16 times as much as the present Latin square design to achieve the same sensitivity.
2.2.4 Replicated Latin Square

Replication of a Latin square is done by forming several Latin squares of the same dimension. This may be done using

- same row and column blocks
- new rows and same columns
- same rows and new columns
- new rows and new columns

Examples

The following $3 \times 3$ Latin square designs are intended to illustrate the techniques of replicating Latin squares.

**same rows; same columns** :

```
  1  2  3  replication
1  A  B  C
2  B  C  A   1
3  C  A  B

  1  2  3
1  C  B  A
2  B  A  C   2
3  A  C  B

  1  2  3
1  B  A  C
2  A  C  B   3
3  C  B  A
```

**different rows; same columns** :

```
  1  2  3  replication
1  A  B  C
2  B  C  A   1
3  C  A  B

  1  2  3
4  C  B  A
5  B  A  C   2
6  A  C  B

  1  2  3
7  B  A  C
8  A  C  B   3
9  C  B  A
```

**different rows; different columns** :
2.2. THE LATIN SQUARE DESIGN

1 2 3 replication
1 A B C
2 B C A 1
3 C A B
4 5 6
4 C B A
5 B A C 2
6 A C B
7 8 9
7 B A C
8 A C B 3
9 C B A

Replication increases the error degrees of freedom without increasing the number of treatments. However, it adds a parameter (or parameters) in our model, thus increasing the complexity of the model.

The analysis of variance depends on the type of replication.

Replicated Square

This uses the same rows and columns and different randomization of the treatments within each square. The statistical model is

\[ y_{ijkl} = \mu + \alpha_i + \tau_j + \beta_k + \psi_l + \epsilon_{ijkl} \]

where \( r \) is the number of replications. Here \( \psi_l \) represents the effect of the \( l \)th replicate. The associated ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatments</td>
<td>( p - 1 )</td>
<td>( SS_{Trt} )</td>
<td>( MS_{Trt} )</td>
<td>( F_0 = \frac{MS_{Trt}}{MS_E} )</td>
</tr>
<tr>
<td>Rows</td>
<td>( p - 1 )</td>
<td>( SS_{Row} )</td>
<td>( MS_{Row} )</td>
<td></td>
</tr>
<tr>
<td>Columns</td>
<td>( p - 1 )</td>
<td>( SS_{Col} )</td>
<td>( MS_{Col} )</td>
<td></td>
</tr>
<tr>
<td>Replicate</td>
<td>( r - 1 )</td>
<td>( SS_{Rep} )</td>
<td>( MS_{Rep} )</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>((p - 1)[r(p + 1) - 3])</td>
<td>( SS_E )</td>
<td>( MS_E )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( rp^2 - 1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

where

\[ SS_T = \sum \sum \sum \sum (y_{ijkl} - \bar{y}_{...})^2 \]

\[ SS_{Trt} = np \sum_{j=1}^{p} (\bar{y}_{j..} - \bar{y}_{...})^2 \]

\[ SS_{Row} = np \sum_{i=1}^{p} (\bar{y}_{i...} - \bar{y}_{...})^2 \]

\[ SS_{Col} = np \sum_{k=1}^{p} (\bar{y}_{..k} - \bar{y}_{...})^2 \]

\[ SS_{Rep} = p^2 \sum_{l=1}^{r} (\bar{y}_{...l} - \bar{y}_{...})^2 \]

and \( SS_E \) is found by subtraction.
Example

Three gasoline additives (TREATMENTS, A B & C) were tested for gas efficiency by three drivers (ROWS) using three different tractors (COLUMNS). The variable measured was the yield of carbon monoxide in a trap. The experiment was repeated twice. Here is the SAS analysis.

```sas
DATA ADDITIVE;
  INPUT SQUARE COL ROW TREAT YIELD;
  CARDS;
  1 1 1 2 26.0
  1 1 2 3 28.7
  1 1 3 1 25.3
  1 2 1 3 25.0
  1 2 2 1 23.6
  1 2 3 2 28.4
  1 3 1 1 21.3
  1 3 2 2 28.5
  1 3 3 3 30.1
  2 1 1 3 32.4
  2 1 2 1 31.7
  2 1 3 1 24.9
  2 2 1 2 28.7
  2 2 2 1 24.3
  2 2 3 2 29.3
  2 3 1 1 25.8
  2 3 2 3 30.5
  2 3 3 2 29.2
;
PROC GLM;
  TITLE 'SINGLE LATIN SQUARES';
  CLASS COL ROW TREAT;
  MODEL YIELD= COL ROW TREAT;
  BY SQUARE;
RUN;
QUIT;

PROC GLM;
  TITLE 'REPLICATED LATIN SQUARES SHARING BOTH ROWS AND COLUMNS';
  CLASS SQUARE COL ROW TREAT;
  MODEL YIELD= SQUARE COL ROW TREAT;
RUN;
QUIT;
```

SINGLE LATIN SQUARES 1

----------------------------------------------------------------------------------------------------- SQUARE=1 -----------------------------------------------------------------------------------------------------

The GLM Procedure

Dependent Variable: YIELD

<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>6</td>
<td>64.22000000</td>
<td>10.70333333</td>
<td>72.43</td>
<td>0.0137</td>
</tr>
<tr>
<td>Error</td>
<td>2</td>
<td>0.29555556</td>
<td>0.14777778</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>8</td>
<td>64.51555556</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square Coeff Var Root MSE YIELD Mean

0.995419 1.460443 0.384419 26.32222

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>COL</td>
<td>2</td>
<td>1.93555556</td>
<td>0.96777778</td>
<td>6.55</td>
<td>0.1325</td>
</tr>
<tr>
<td>ROW</td>
<td>2</td>
<td>23.72222222</td>
<td>11.86111111</td>
<td>80.26</td>
<td>0.0123</td>
</tr>
<tr>
<td>TREAT</td>
<td>2</td>
<td>38.56222222</td>
<td>19.28111111</td>
<td>130.47</td>
<td>0.0076</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>
</table>
2.2. THE LATIN SQUARE DESIGN

<table>
<thead>
<tr>
<th></th>
<th>COL</th>
<th>ROW</th>
<th>TREAT</th>
</tr>
</thead>
<tbody>
<tr>
<td>Area</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>1</td>
<td>1.93555556</td>
<td>23.72222222</td>
<td>38.56222222</td>
</tr>
<tr>
<td>2</td>
<td>0.96777778</td>
<td>11.86111111</td>
<td>19.28111111</td>
</tr>
<tr>
<td>3</td>
<td>6.55</td>
<td>80.26</td>
<td>130.47</td>
</tr>
<tr>
<td>4</td>
<td>0.1325</td>
<td>0.0123</td>
<td>0.0076</td>
</tr>
</tbody>
</table>

------------------------------------------- SQUARE=2 --------------------------------------------

The GLM Procedure

Dependent Variable: YIELD

<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>6</td>
<td>67.240000000</td>
<td>11.20666667</td>
<td>17.79</td>
<td>0.0542</td>
</tr>
<tr>
<td>Error</td>
<td>2</td>
<td>1.260000000</td>
<td>0.63000000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>8</td>
<td>68.500000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square: 0.981606
Coeff Var: 2.781748
Root MSE: 0.793725
YIELD Mean: 28.5333

Source DF Type I SS Mean Square F Value Pr > F
COL 2 7.48666667 3.74333333 5.94 0.1441
ROW 2 2.44666667 1.22333333 1.94 0.3399
TREAT 2 57.30666667 28.65333333 45.48 0.0215

Source DF Type III SS Mean Square F Value Pr > F
COL 2 7.48666667 3.74333333 5.94 0.1441
ROW 2 2.44666667 1.22333333 1.94 0.3399
TREAT 2 57.30666667 28.65333333 45.48 0.0215

REPLICATED LATIN SQUARES SHARING BOTH ROWS AND COLUMNS

The GLM Procedure

Dependent Variable: YIELD

<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>7</td>
<td>132.0038889</td>
<td>18.8576984</td>
<td>8.19</td>
<td>0.0018</td>
</tr>
<tr>
<td>Error</td>
<td>10</td>
<td>23.01222222</td>
<td>2.30122222</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>17</td>
<td>155.0161111</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square: 0.851549
Coeff Var: 5.530809
Root MSE: 1.516978
YIELD Mean: 27.42778

Source DF Type I SS Mean Square F Value Pr > F
SQUARE 1 22.00055556 22.00055556 9.56 0.0114
COL 2 8.01444444 4.00722222 1.74 0.2244
ROW 2 7.20111111 3.60055556 1.56 0.2563
TREAT 2 94.78777778 47.39388889 20.60 0.0003

Source DF Type III SS Mean Square F Value Pr > F
SQUARE 1 22.00055556 22.00055556 9.56 0.0114
COL 2 8.01444444 4.00722222 1.74 0.2244
ROW 2 7.20111111 3.60055556 1.56 0.2563
TREAT 2 94.78777778 47.39388889 20.60 0.0003
Replicated Rows

In this instance the rows of different squares are independent but the columns are shared; i.e. different rows but same columns. Thus, the treatment effect may be different for each square. The statistical model in shows this by nesting row effects within squares. The model is

\[ y_{ijkl} = \mu + \alpha_i(l) + \tau_j + \beta_k + \psi_l + \epsilon_{ijkl} \]

where \( \alpha_i(l) \) represents the effect of row \( i \) nested within replicate (square) \( l \).

The associated ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatments</td>
<td>( p - 1 )</td>
<td>( SS_{Trt} )</td>
<td>( MS_{Trt} )</td>
<td>( F_0 = \frac{MS_{Trt}}{MS_E} )</td>
</tr>
<tr>
<td>Rows</td>
<td>( r(p-1) )</td>
<td>( SS_{Row} )</td>
<td>( MS_{Row} )</td>
<td></td>
</tr>
<tr>
<td>Columns</td>
<td>( p - 1 )</td>
<td>( SS_{Col} )</td>
<td>( MS_{Col} )</td>
<td></td>
</tr>
<tr>
<td>Replicate</td>
<td>( r - 1 )</td>
<td>( SS_{Rep} )</td>
<td>( MS_{Rep} )</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>( (p-1)[rp-2] )</td>
<td>( SS_{E} )</td>
<td>( MS_{E} )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( rp^2 - 1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Example

We will reanalyze the previous example; this time assuming we have six different drivers.

DATA ADDITIVE;
INPUT SQUARE COL ROW TREAT YIELD;
CARDS;
1 1 2 26.0
1 1 2 3 28.7
1 1 3 1 25.3
1 2 1 3 25.0
1 2 2 1 23.6
1 2 3 2 28.4
1 3 1 1 21.3
1 3 2 2 28.5
1 3 3 3 30.1
2 1 4 3 32.4
2 1 5 2 31.7
2 1 6 1 24.9
2 2 4 2 28.7
2 2 5 1 24.3
2 2 6 3 29.3
3 3 4 1 25.8
3 3 5 3 30.5
3 3 6 2 29.2;
PROC GLM;
TITLE 'REPLICATED LATIN SQUARES SHARING ONLY COLUMNS';
CLASS SQUARE COL ROW TREAT;
MODEL YIELD= SQUARE COL ROW(SQUARE) TREAT;
RUN;
QUIT;

The GLM Procedure

Dependent Variable: YIELD

<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>9</td>
<td>150.9716667</td>
<td>16.7746296</td>
<td>33.18</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>
2.2. THE LATIN SQUARE DESIGN

Error  8  4.0444444  0.5055556
Corrected Total 17  155.0161111

R-Square  Coeff Var  Root MSE  YIELD Mean
0.973910  2.592351  0.711024  27.42778

Source  DF  Type I SS  Mean Square  F Value  Pr > F
SQUARE  1  22.00055556  22.00055556  43.52  0.0002
COL  2  8.01444444  4.00722222  7.93  0.0127
ROW(SQUARE)  4  26.16888889  6.54222222  12.94  0.0014
TREAT  2  94.78777778  47.39388889  93.75 <.0001

Source  DF  Type III SS  Mean Square  F Value  Pr > F
SQUARE  1  22.00055556  22.00055556  43.52  0.0002
COL  2  8.01444444  4.00722222  7.93  0.0127
ROW(SQUARE)  4  26.16888889  6.54222222  12.94  0.0014
TREAT  2  94.78777778  47.39388889  93.75 <.0001

Replicated Rows and Columns

The different Latin squares are now independent. Both row and column effects are nested within the squares. The statistical model is

\[ y_{ijkl} = \mu + \alpha_i(l) + \tau_j + \beta_k(l) + \psi_l + \epsilon_{ijkl} \]

\[ i = 1, \ldots, p \]
\[ j = 1, \ldots, r \]
\[ k = 1, \ldots, p \]
\[ l = 1, \ldots, r \]

The associated ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatments</td>
<td>p - 1</td>
<td>SSTrt</td>
<td>MSTrt</td>
<td>( F_0 = \frac{MSTrt}{MS_E} )</td>
</tr>
<tr>
<td>Rows</td>
<td>r(p - 1)</td>
<td>SSSrow</td>
<td>MSrow</td>
<td></td>
</tr>
<tr>
<td>Columns</td>
<td>r(p - 1)</td>
<td>SSScol</td>
<td>MScol</td>
<td></td>
</tr>
<tr>
<td>Replicate</td>
<td>r - 1</td>
<td>SSSrep</td>
<td>MSrep</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>(p - 1)[r(p - 1) - 1]</td>
<td>SSE</td>
<td>MSE</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>rp^2 - 1</td>
<td>SST</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Example

Lets reanalyze the previous example; this time assuming six different drivers and six different tractors.

DATA ADDITIVE;
INPUT SQUARE COL ROW TREAT YIELD;
CARDS;
  1 1 1 2 26.0
  1 1 2 3 28.7
  1 1 3 1 25.3
  1 2 1 3 25.0
  1 2 2 1 23.6
  1 2 3 2 28.4
  1 3 1 1 21.3
  1 3 2 2 28.5
  1 3 3 3 30.1
  2 4 4 3 32.4
  2 4 5 2 31.7
  2 4 6 1 24.9
  2 5 4 2 28.7
  2 5 5 1 24.3
2.3 The Graeco-Latin Square Design

Graeco-Latin squares are used when we have three blocking variables. Greek letters are used to represent the blocking in the third direction. Thus we investigate four factors: rows, columns, Greek letters, and treatments.

In a Graeco-Latin square, each treatment appears once, and only once, in each column, each row, and with each Greek letter. Graeco-Latin squares exist for each $p \geq 3$, with the exception of $p = 6$. An example of a Graeco-Latin square for $p = 4$ is

$$
\begin{array}{cccc}
C & \gamma & A & \beta \\
D & \delta & B & \alpha \\
A & \alpha & C & \delta \\
B & \beta & D & \gamma \\
\end{array}
$$

The statistical model is
\[ y_{ijkl} = \mu + \alpha_i + \tau_j + \beta_k + \psi_l + \epsilon_{ijkl} \]

\[
\begin{align*}
&i = 1, \ldots, p \\
&j = 1, \ldots, p \\
&k = 1, \ldots, p \\
&l = 1, \ldots, p 
\end{align*}
\]

where \( \psi_l \) is the effect of the \( l \)th Greek letter.

The associated ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatments</td>
<td>( p - 1 )</td>
<td>( SS_{Trt} )</td>
<td>( MS_{Trt} )</td>
<td>( F_0 = \frac{MS_{Trt}}{MS_E} )</td>
</tr>
<tr>
<td>Greek letters</td>
<td>( p - 1 )</td>
<td>( SS_G )</td>
<td>( MS_G )</td>
<td></td>
</tr>
<tr>
<td>Rows</td>
<td>( p - 1 )</td>
<td>( SS_{Row} )</td>
<td>( MS_{Row} )</td>
<td></td>
</tr>
<tr>
<td>Columns</td>
<td>( p - 1 )</td>
<td>( SS_{Col} )</td>
<td>( MS_{Col} )</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>( (p - 1)(p - 3) )</td>
<td>( SS_E )</td>
<td>( MS_E )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( p^2 - 1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

where

\[
SS_T = \sum \sum \sum \sum (y_{ijkl} - \bar{y}_{...})^2
\]

\[
SS_{Trt} = p \sum_{j=1}^{p} (\bar{y}_{..j} - \bar{y}_{...})^2
\]

\[
SS_{Row} = p \sum_{i=1}^{p} (\bar{y}_{i..} - \bar{y}_{...})^2
\]

\[
SS_{Col} = p \sum_{k=1}^{p} (\bar{y}_{..k} - \bar{y}_{...})^2
\]

\[
SS_G = p \sum_{l=1}^{r} (\bar{y}_{...l} - \bar{y}_{...})^2
\]

and \( SS_E \) is found by subtraction.

The following example is taken from Petersen: Design and Analysis of Experiments (1985).

**Example**

A food processor wanted to determine the effect of package design on the sale of one of his products. He had five designs to be tested: A, B, C, D, E. There were a number of sources of variation. These included: (1) day of the week, (2) differences among stores, and (3) effect of shelf height. He decided to conduct a trial using a Graeco-Latin square design with five weekdays corresponding to the row classification, five different stores assigned to the column classification, and five shelf heights corresponding to the Greek letter classification. The following table contains the results of his trial.

<table>
<thead>
<tr>
<th>Day</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mon</td>
<td>E ( \alpha ) (238)</td>
<td>C ( \delta ) (228)</td>
<td>B ( \gamma ) (158)</td>
<td>D ( \epsilon ) (188)</td>
<td>A ( \beta ) (74)</td>
</tr>
<tr>
<td>Tue</td>
<td>D ( \delta ) (149)</td>
<td>B ( \beta ) (220)</td>
<td>A ( \alpha ) (92)</td>
<td>C ( \gamma ) (169)</td>
<td>E ( \epsilon ) (282)</td>
</tr>
<tr>
<td>Wed</td>
<td>B ( \epsilon ) (222)</td>
<td>E ( \gamma ) (295)</td>
<td>D ( \beta ) (104)</td>
<td>A ( \delta ) (54)</td>
<td>C ( \alpha ) (213)</td>
</tr>
<tr>
<td>Thur</td>
<td>C ( \beta ) (187)</td>
<td>A ( \epsilon ) (66)</td>
<td>E ( \delta ) (242)</td>
<td>B ( \alpha ) (122)</td>
<td>D ( \gamma ) (90)</td>
</tr>
<tr>
<td>Fri</td>
<td>A ( \gamma ) (65)</td>
<td>D ( \alpha ) (118)</td>
<td>C ( \epsilon ) (279)</td>
<td>E ( \beta ) (278)</td>
<td>B ( \gamma ) (176)</td>
</tr>
</tbody>
</table>

The following is the SAS analysis.
OPTIONS LS=80 PS=66 NODATE;
DATA GL;
INPUT ROW COL TRT GREEK Y;
CARDS;
1 1 5 1 238
1 2 3 4 228
1 3 2 3 158
1 4 4 5 188
1 5 1 2 74
2 1 4 4 149
2 2 2 2 220
2 3 1 1 92
2 4 3 3 169
2 5 5 5 282
3 1 2 5 222
3 2 5 3 295
3 3 4 2 104
3 4 1 4 54
3 5 3 1 213
4 1 3 2 187
4 2 1 5 66
4 3 5 4 242
4 4 2 1 122
4 5 4 3 90
5 1 1 3 65
5 3 1 1 118
5 4 3 5 279
5 5 2 4 176
;
PROC GLM;
   CLASS ROW COL TRT GREEK;
   MODEL Y = ROW COL TRT GREEK;
RUN;
QUIT;

The SAS System
2
The GLM Procedure
Dependent Variable: Y

<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>16</td>
<td>131997.8400</td>
<td>8249.8650</td>
<td>8.92</td>
<td>0.0019</td>
</tr>
<tr>
<td>Error</td>
<td>8</td>
<td>7397.9200</td>
<td>924.7400</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>24</td>
<td>139395.7600</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square  Coef Var  Root MSE  Y Mean
0.946929  17.64304  30.40954  172.3600

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS  Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>ROW</td>
<td>4</td>
<td>6138.5600 1534.6400</td>
<td>1.66</td>
<td>0.2510</td>
</tr>
<tr>
<td>COL</td>
<td>4</td>
<td>1544.9600 386.2400</td>
<td>0.42</td>
<td>0.7919</td>
</tr>
<tr>
<td>TRT</td>
<td>4</td>
<td>115462.1600 28865.5400</td>
<td>31.21</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>GREEK</td>
<td>4</td>
<td>8852.1600 2213.0400</td>
<td>2.39</td>
<td>0.1366</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>ROW</td>
<td>4</td>
<td>6138.5600 1534.6400</td>
<td>1.66</td>
<td>0.2510</td>
<td></td>
</tr>
<tr>
<td>COL</td>
<td>4</td>
<td>1544.9600 386.2400</td>
<td>0.42</td>
<td>0.7919</td>
<td></td>
</tr>
<tr>
<td>TRT</td>
<td>4</td>
<td>115462.1600 28865.5400</td>
<td>31.21</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>GREEK</td>
<td>4</td>
<td>8852.1600 2213.0400</td>
<td>2.39</td>
<td>0.1366</td>
<td></td>
</tr>
</tbody>
</table>
There are highly significant differences in mean sales among the five package designs.

2.4 Incomplete Block Designs

Some experiments may consist of a large number of treatments and it may not be feasible to run all the treatments in all the blocks. Designs where only some of the treatments appear in every block are known as *incomplete block designs*.

2.4.1 Balanced Incomplete Block Designs (BIBD’s)

In a BIBD setup, each block is selected in a balanced manner so that any pair of treatments occur together the same number of times as any other pair. Suppose there are $k$ treatments and $b$ blocks. Each block can hold $a$ treatments, where $a < k$.

One way to construct a BIBD is by using $\binom{k}{a}$ blocks and assigning different combination of treatments to every block. The following two examples illustrate this procedure.

**Examples**

Consider three treatments, $A$, $B$, and $C$ where two treatments are run in every block. There are $\binom{3}{2} = 3$ ways of choosing 2 out of three. Thus using three blocks

<table>
<thead>
<tr>
<th>block</th>
<th></th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>-</td>
<td>A</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>B</td>
<td>-</td>
<td>C</td>
</tr>
<tr>
<td>C</td>
<td></td>
<td>C</td>
<td>C</td>
</tr>
</tbody>
</table>

Now consider five treatments, $A, B, C, D,$ and $E$ where 3 treatments appear per block. We use 10 blocks.

<table>
<thead>
<tr>
<th>block</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>-</td>
<td></td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>-</td>
<td>A</td>
<td>A</td>
<td></td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>B</td>
<td>B</td>
<td>-</td>
<td>B</td>
<td>B</td>
<td>-</td>
<td>B</td>
<td>B</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>-</td>
<td>C</td>
<td>C</td>
<td>-</td>
<td>-</td>
<td>C</td>
<td>-</td>
<td>C</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>D</td>
<td>-</td>
<td>D</td>
<td>D</td>
<td>D</td>
<td>-</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>E</td>
<td>E</td>
<td>E</td>
<td>-</td>
<td>E</td>
<td>-</td>
<td>E</td>
<td>E</td>
<td>E</td>
<td></td>
</tr>
</tbody>
</table>

Usually, however, BIBD’s may be obtained using fewer than $\binom{k}{a}$ blocks.

**Statistical Analysis**

We begin by introducing some notation.

- Let $r$ be the number of blocks in which each treatment appears.
- Let $\lambda$ be the number of times each pair of treatments appear together in the same block.

Thus the total sample size is $ab = kr$. We can also show that $\lambda(k - 1) = r(a - 1)$ and thus $\lambda = r(a - 1)/(k - 1)$.

The statistical model is

$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij} \quad \left\{ \begin{array}{l} i = 1, \ldots, k \\ j = 1, \ldots, b \end{array} \right.$$ 

with the same assumptions as the RCBD model.
We partition the total sum of squares in the usual manner; into sum of square due to treatments, blocks, and error. The difference here is that the sum of squares due to treatments needs to be adjusted for incompleteness. Thus, we have

\[ SS_T = SS_{\text{Trt(adj)}} + SS_{\text{Blocks}} + SS_E \]

where

- \( SS_T = \sum_{i=1}^{k} \sum_{j=1}^{b} (y_{ij} - \bar{y})^2 \)
- \( SS_{\text{Blocks}} = k \sum_{j=1}^{b} (\bar{y}_j - \bar{y})^2 \)
- Let \( T_i \) and \( T_j \) be the \( i \)th treatment and the \( j \)th block totals, respectively, and
  \[ \phi_{ij} = \begin{cases} 
    1 & \text{if trt } i \text{ in block } j \\
    0 & \text{otherwise}
  \end{cases} \]

Let

\[ Q_i = T_i - \frac{1}{a} \sum_{j=1}^{b} \phi_{ij} T_j \]

The quantity \( Q_i \) is the \( i \)th treatment total minus the average of the block totals containing treatment \( i \). Now

\[ SS_{\text{Trt(adj)}} = \frac{a}{\lambda k} \sum_{i=1}^{k} Q_i^2 \]

- \( SS_E = SS_T - SS_{\text{Trt(adj)}} - SS_{\text{Blocks}} \)

The corresponding ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatments</td>
<td>( k - 1 )</td>
<td>( SS_{\text{Trt(adj)}} )</td>
<td>( MS_{\text{Trt(adj)}} )</td>
<td>( F_0 = \frac{MS_{\text{Trt(adj)}}}{MS_E} )</td>
</tr>
<tr>
<td>Blocks</td>
<td>( b - 1 )</td>
<td>( SS_{\text{Blocks}} )</td>
<td>( MS_{\text{Blocks}} )</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>( kr - k - b + 1 )</td>
<td>( SS_E )</td>
<td>( MS_E )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( kr - 1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Estimates of the model are

\[ \hat{\mu} = \bar{y} \text{., } \hat{\tau}_i = \frac{aQ_i}{\lambda k} \text{, } \hat{\beta}_j = \frac{rQ'_j}{\lambda b} \]

where

\[ Q'_j = T_j - \frac{1}{r} \sum_{i=1}^{k} \phi_{ij} T_i. \]

**Multiple Comparisons**

The standard error of the adjusted treatment \( i \) mean, \( \hat{\tau}_i \), is

\[ \sqrt{\frac{aMS_E}{\lambda k}}. \]

Thus individual as well as simultaneous inference may be made concerning the treatment means. For instance, we declare treatment \( i \) and \( j \) to be significantly different, while making all pairwise comparisons, with MEER=\( \alpha \), if \( |\hat{\tau}_i - \hat{\tau}_j| \) exceeds

- Bonferroni: \( t_{kr-k-b+1} \left( \frac{\alpha}{2(\frac{k}{2})} \right) \sqrt{MS_E \frac{2a}{\lambda k}} \)
- Tukey: \( q_{k,kr-k-b+1}(\alpha) \sqrt{2 MS_E \frac{2a}{\lambda k}} \)

The following example is taken from em Montgomery: Design and Analysis of Experiments.
Example

A chemical engineer thinks that the time of reaction for a chemical process is a function of the type of catalyst employed. Four catalysts are being investigated. The experimental procedure consists of selecting a batch of raw material, loading the pilot plant, applying each catalyst in a separate run of the pilot plant, and observing the reaction time. Since variations in the batches of raw material may affect the performance of the catalysts, the engineer decides to use batches of raw materials as blocks. However, each batch is only large enough to permit three catalysts to be run. The following table summarizes the results.

<table>
<thead>
<tr>
<th>Block (Batch)</th>
<th>Treatment (Catalyst)</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td>73</td>
<td>74</td>
<td>-</td>
<td>71</td>
</tr>
<tr>
<td>2</td>
<td></td>
<td>-</td>
<td>75</td>
<td>67</td>
<td>72</td>
</tr>
<tr>
<td>3</td>
<td></td>
<td>73</td>
<td>75</td>
<td>68</td>
<td>-</td>
</tr>
<tr>
<td>4</td>
<td></td>
<td>75</td>
<td>-</td>
<td>72</td>
<td>75</td>
</tr>
</tbody>
</table>

Thus \( k = 4, r = 3, a = 3, \lambda = 2, b = 4 \). This is known as a symmetric design since \( k = b \).

The following SAS code is used to analyze the above data.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA CHEM;
  INPUT CATALYST BATCH TIME;
  CARDS;
  1 1 73
  1 2 74
  1 4 71
  2 2 75
  2 3 67
  2 4 72
  3 1 73
  3 2 75
  3 3 68
  4 1 75
  4 3 72
  4 4 75
;
PROC GLM;
  CLASS CATALYST BATCH;
  MODEL TIME = CATALYST BATCH;
  LSMEANS CATALYST / TDIFF PDIFF ADJUST=BON STDERR;
  LSMEANS CATALYST / TDIFF ADJUST=TUKEY;
  CONTRAST '1 VS 2' CATALYST 1 -1 0 0;
  ESTIMATE '1 VS 2' CATALYST 1 -1 0 0;
RUN;
QUIT;
```

The associated SAS output is

```
The SAS System 52

The GLM Procedure

Dependent Variable: TIME

<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>6</td>
<td>77.75000000</td>
<td>12.95833333</td>
<td>19.94</td>
<td>0.0024</td>
</tr>
</tbody>
</table>
```
## ERROR

<table>
<thead>
<tr>
<th></th>
<th>5</th>
<th>3.25000000</th>
<th>0.65000000</th>
</tr>
</thead>
<tbody>
<tr>
<td>Corrected Total</td>
<td>11</td>
<td>81.00000000</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>R-Square</th>
<th>Coeff Var</th>
<th>Root MSE</th>
<th>TIME Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.959877</td>
<td>1.112036</td>
<td>0.806226</td>
<td>72.50000</td>
</tr>
</tbody>
</table>

### Source DF Type I SS Mean Square F Value Pr > F

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>CATALYST</td>
<td>3</td>
<td>11.66666667</td>
<td>3.88888889</td>
<td>5.98</td>
<td>0.0415</td>
</tr>
<tr>
<td>BATCH</td>
<td>3</td>
<td>66.08333333</td>
<td>22.02777778</td>
<td>33.89</td>
<td>0.0010</td>
</tr>
</tbody>
</table>

### Source DF Type III SS Mean Square F Value Pr > F

<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>CATALYST</td>
<td>3</td>
<td>22.75000000</td>
<td>7.58333333</td>
<td>11.67</td>
<td>0.0107</td>
</tr>
<tr>
<td>BATCH</td>
<td>3</td>
<td>66.08333333</td>
<td>22.02777778</td>
<td>33.89</td>
<td>0.0010</td>
</tr>
</tbody>
</table>

The SAS System

The GLM Procedure

Least Squares Means

Adjustment for Multiple Comparisons: Bonferroni

<table>
<thead>
<tr>
<th>CATALYST</th>
<th>TIME LSMEAN</th>
<th>Error</th>
<th>Pr &gt;</th>
<th>1/2</th>
<th>3/4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>71.37500000</td>
<td>0.4868051</td>
<td>&lt;.0001</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>71.62500000</td>
<td>0.4868051</td>
<td>&lt;.0001</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>72.00000000</td>
<td>0.4868051</td>
<td>&lt;.0001</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>75.00000000</td>
<td>0.4868051</td>
<td>&lt;.0001</td>
<td>4</td>
<td></td>
</tr>
</tbody>
</table>

Least Squares Means for Effect CATALYST

Dependent Variable: TIME

\( t \) for \( H_0: \text{LSMean}(i) = \text{LSMean}(j) / \text{Pr} > |t|\)

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-0.35806</td>
<td>-0.89514</td>
<td>-5.19183</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.358057</td>
<td>-0.53709</td>
<td>-4.83378</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0.895144</td>
<td>0.537086</td>
<td>-4.29669</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>5.191833</td>
<td>4.833775</td>
<td>4.29669</td>
<td></td>
</tr>
</tbody>
</table>

The SAS System

The GLM Procedure

Least Squares Means

Adjustment for Multiple Comparisons: Tukey-Kramer

<table>
<thead>
<tr>
<th>CATALYST</th>
<th>TIME LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>71.37500000</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>71.62500000</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>72.00000000</td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>75.00000000</td>
<td>4</td>
</tr>
</tbody>
</table>

Least Squares Means for Effect CATALYST

Dependent Variable: TIME

\( t \) for \( H_0: \text{LSMean}(i) = \text{LSMean}(j) / \text{Pr} > |t|\)

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-0.35806</td>
<td>-0.89514</td>
<td>-5.19183</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.358057</td>
<td>-0.53709</td>
<td>-4.83378</td>
<td></td>
</tr>
</tbody>
</table>
2.4. INCOMPLETE BLOCK DESIGNS

\begin{verbatim}
0.9825 0.9462 0.0175
3 0.895144 0.537086 -4.29669
0.8085 0.9462 0.0281
4 5.191833 4.833775 4.296689
0.0130 0.0175 0.0281
\end{verbatim}

The SAS System 55
The GLM Procedure

Dependent Variable: TIME

\begin{verbatim}
Contrast DF Contrast SS Mean Square F Value Pr > F
1 VS 2 1 0.08333333 0.08333333 0.13 0.7349
\end{verbatim}

\begin{verbatim}
Parameter Standard
   Estimate Error t Value Pr > |t|
1 VS 2 -0.25000000 0.69821200 -0.36 0.7349
\end{verbatim}

We may see from the output that $F_0 = 11.67$ with a $p$-value of 0.0107. Thus we declare the catalysts to be significantly different.

Both the Bonferroni and the Tukey-Kramer procedures give us

$\bar{y}_1 = 71.375, \bar{y}_2 = 71.625, \bar{y}_3 = 72.000, \bar{y}_4 = 75.000$

2.4.2 Youden Squares

These are incomplete Latin squares, in which the number of columns is not equal to the number of rows. The following example shows a Youden square with 5 treatments, 4 columns, and 5 rows.

\begin{verbatim}
Column
Row 1 2 3 4
1 A B C D
2 B C D E
3 C D E A
4 D E A B
5 E A B C
\end{verbatim}

A Youden square may be considered as a symmetric BIBD with rows corresponding to blocks and each treatment occurring exactly once in each position of the block.

2.4.3 Other Incomplete Designs

There are other incomplete designs that will not be discussed here. These include the partially balanced incomplete block design and lattice designs such as square, cubic, and rectangular lattices.
Chapter 3

Factorial Designs

3.1 Introduction

This chapter focuses on the study of the effects of two or more factors using factorial designs. A factorial design is a design in which every combination of the factors is studied in every trial (replication). For example, we may have two factors $A$ and $B$, say, with $a$ and $b$ levels, respectively. Each replicate in a two-factor factorial design will contain all the $a \times b$ treatment combinations.

The effect of factor $A$ is the change in response due to a change in the level of $A$. For instance, consider a two-factor experiment in which the two factors $A$ and $B$ have two levels each. Then the experiment is run once. The following is the resulting output.

<table>
<thead>
<tr>
<th></th>
<th>$B_1$</th>
<th>$B_2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A_1$</td>
<td>30</td>
<td>20</td>
</tr>
<tr>
<td>$A_2$</td>
<td>40</td>
<td>30</td>
</tr>
</tbody>
</table>

The average effect of factor $A$ is then

$$\frac{40 + 30}{2} - \frac{30 + 20}{2} = 10$$

Thus, increasing factor $A$ from level 1 to level 2 causes an increase of 10 units in the response. This is known as the main effect of factor $A$. In a similar fashion, the main effect of $B$ is

$$\frac{40 + 30}{2} - \frac{30 + 20}{2} = 10$$

In this case there is no interaction since the effect of factor $A$ is the same at all levels of $B$: $40 - 30 = 10$ and $30 - 20 = 10$.

Sometimes the effect of the first factor may depend on the level of the second factor under consideration. The following table shows two interacting factors.

<table>
<thead>
<tr>
<th></th>
<th>$B_1$</th>
<th>$B_2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A_1$</td>
<td>20</td>
<td>25</td>
</tr>
<tr>
<td>$A_2$</td>
<td>40</td>
<td>30</td>
</tr>
</tbody>
</table>

The effect of factor $A$ at the first level of $B$ is

$$40 - 20 = 20$$

and at the second level

$$10 - 25 = -15$$

The effect of $A$ depends on the level of $B$ chosen. The following plots, known as profile plots, display the two situations.
The following example taken from Montgomery: Design and Analysis of Experiments considers two factors, each with 3 levels, and the experiment repeated 4 times.

**Example**

The maximum output voltage of a particular battery is thought to be influenced by the material used in the plates and the temperature in the location at which the battery is installed. Four batteries are tested at each combination of plate material and temperature, and all 36 tests are run in random order. The results are shown below.

<table>
<thead>
<tr>
<th>Material</th>
<th>Temperature 15</th>
<th>Temperature 65</th>
<th>Temperature 80</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>130, 155, 74, 180</td>
<td>34, 40, 80, 75</td>
<td>20, 70, 82, 58</td>
</tr>
<tr>
<td>2</td>
<td>150, 188, 159, 126</td>
<td>136, 122, 106, 115</td>
<td>25, 70, 58, 45</td>
</tr>
<tr>
<td>3</td>
<td>138, 110, 168, 160</td>
<td>174, 120, 150, 139</td>
<td>96, 104, 82, 60</td>
</tr>
</tbody>
</table>
As the following profile plot shows the interaction between temperature and material type may be significant. We will perform formal statistical tests to determine whether the interaction is significant in the next section.

The profile plot is constructed using the average response for each cell.

3.2 The Two-Factor Factorial Design

We shall now study the statistical properties of the two-factor design. Let the factors be $A$ and $B$ each with $a$ and $b$ levels. Suppose the experiment is run $n$ times at each combination of the levels of $A$ and $B$. The following table displays the data arrangement of such an experiment.

<table>
<thead>
<tr>
<th>Factor $A$</th>
<th>1</th>
<th>2</th>
<th>...</th>
<th>$b$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>$y_{111}, \ldots, y_{11n}$</td>
<td>$y_{121}, \ldots, y_{12n}$</td>
<td>$y_{1b1}, \ldots, y_{1bn}$</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>$y_{211}, \ldots, y_{21n}$</td>
<td>$y_{221}, \ldots, y_{22n}$</td>
<td>$y_{2b1}, \ldots, y_{2bn}$</td>
<td></td>
</tr>
<tr>
<td>...</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$a$</td>
<td>$y_{a11}, \ldots, y_{a1n}$</td>
<td>$y_{a21}, \ldots, y_{a2n}$</td>
<td>$y_{ab1}, \ldots, y_{abn}$</td>
<td></td>
</tr>
</tbody>
</table>

The statistical model is

$$y_{ijk} = \mu + \tau_i + \beta_j + (\tau\beta)_{ij} + \epsilon_{ijk}, \quad \begin{cases} i = 1, \ldots, a \\ j = 1, \ldots, b \\ k = 1, \ldots, n \end{cases}$$ (3.1)

where $\mu$ is the overall mean, $\tau_i$ is the effect of the $i$th level of factor $A$, $\beta_j$ is the effect of the $j$th level of factor $B$, $(\tau\beta)_{ij}$ is the effect of the interaction between the $i$th level of factor $A$ and the $j$th level of factor $B$, and $\epsilon_{ijk}$ is the random error associated with the $k$th replicate in cell $(i,j)$. 

3.2.1 The Fixed Effects Model

The fixed effects model is given by (3.1) along with the assumptions

\[ \sum_{i=1}^{a} \tau_i = \sum_{j=1}^{b} \beta_j = \sum_{i=1}^{a} (\tau \beta)_{ij} = \sum_{j=1}^{b} (\tau \beta)_{ij} = 0. \]

and \( \epsilon_{ijk} \sim_{iid} N(0, \sigma^2) \).

**Estimation**

The estimators of the model parameters are obtained via the least squares procedure. They are

\[
\hat{\mu} = \bar{y} \dots \\
\hat{\tau}_i = \bar{y}_{i.} - \bar{y} \dots, \quad i = 1, \ldots, a \\
\hat{\beta}_j = \bar{y}_{.j} - \bar{y} \dots, \quad j = 1, \ldots, b \\
(\hat{\tau} \beta)_{ij} = \bar{y}_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y} \dots,
\]

Using the model in (3.1), we can easily see that the observation \( y_{ijk} \) is estimated by

\[ \hat{y}_{ijk} = \hat{\mu} + \hat{\tau}_i + \hat{\beta}_j + (\hat{\tau} \beta)_{ij} = \bar{y}_{ij}. \]

Thus, every observation in cell \((i, j)\) is estimated by the cell mean. The model residuals are obtained as

\[ e_{ijk} = y_{ijk} - \hat{y}_{ijk} = y_{ijk} - \bar{y}_{ij}. \]

**Inference**

In the two-factor fixed effects model, we are interested in the hypotheses

\begin{align*}
A \text{ main effect:} & \\
H_0 : \tau_1 = \cdots = \tau_a = 0 \\
H_A : \text{at least one } \tau_i \neq 0 \\
B \text{ main effect:} & \\
H_0 : \beta_1 = \cdots = \beta_b = 0 \\
H_A : \text{at least one } \beta_j \neq 0 \\
AB \text{ interaction effect:} & \\
H_0 : (\tau \beta)_{11} = \cdots = (\tau \beta)_{ab} = 0 \\
H_A : \text{at least one } (\tau \beta)_{ij} \neq 0
\end{align*}

The following is the two-factor fixed effects ANOVA table:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>(a - 1)</td>
<td>(SS_A)</td>
<td>(MS_A)</td>
<td>(F_A = \frac{MS_A}{MS_E})</td>
</tr>
<tr>
<td>B</td>
<td>(b - 1)</td>
<td>(SS_B)</td>
<td>(MS_B)</td>
<td>(F_B = \frac{MS_B}{MS_E})</td>
</tr>
<tr>
<td>AB</td>
<td>((a - 1)(b - 1))</td>
<td>(SS_{AB})</td>
<td>(MS_{AB})</td>
<td>(F_{AB} = \frac{MS_{AB}}{MS_E})</td>
</tr>
<tr>
<td>Error</td>
<td>(ab(a - 1))</td>
<td>(SS_E)</td>
<td>(MS_E)</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>(abn - 1)</td>
<td>(SS_T)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
3.2. THE TWO-FACTOR FACTORIAL DESIGN

where

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

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

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

$$SS_E = \sum_{i=1}^{a} \sum_{j=1}^{b} \sum_{k=1}^{n} (y_{ijk} - \bar{y}_{ij.})^2$$

$$SS_T = \sum_{i=1}^{a} \sum_{j=1}^{b} \sum_{k=1}^{n} (y_{ijk} - \bar{y}_{..})^2$$

We then declare the $A$, $B$, or $AB$ effect to be significant if $F_A > F_{a-1,ab(n-1)}(\alpha)$, $F_B > F_{b-1,ab(n-1)}(\alpha)$, or $F_{AB} > F_{(a-1)(b-1),ab(n-1)}(\alpha)$, respectively.

Example

Consider the battery life experiment given above and assume that the material type and temperatures under consideration are the only ones we are interested in. The following SAS code may be used to produce the two-factor factorial ANOVA table along with an interaction plot (given above).

```sas
OPTIONS PS=66 LS=80 NODATE;

DATA BATTERY;
INPUT MAT TEMP LIFE;
DATALINES;
1 1 130
1 1 155
...
3 3 60
;

PROC GLM;
CLASS MAT TEMP;
MODEL LIFE=MAT TEMP MAT*TEMP;
RUN;
QUIT;

PROC MEANS NOPRINT;
VAR LIFE;
BY MAT TEMP;
OUTPUT OUT=OUTMEAN MEAN=MN;
RUN;
QUIT;

SYMBOL I=JOIN;
PROC GGRAPH;
    PLOT MN*TEMP=MAT;
RUN;
QUIT;

The corresponding SAS output is

<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>8</td>
<td>59416.222222</td>
<td>7427.02778</td>
<td>11.00</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>
```
Therefore, we declare that both main effects as well as the interaction effect are significant.

**Multiple Comparisons**

The manner in which we perform multiple comparisons is dependent on whether or not the interaction effect is significant. In the case where the interaction between factors $A$ and $B$ is not significant, we may compare the means of factor $A$ pooled over all levels of factor $B$ ($\bar{y}_{i.}$’s) and the means of factor $B$ pooled over all levels of factor $A$ ($\bar{y}_{.j}$’s). On the other hand, if the interaction between $A$ and $B$ is significant, we need to compare the means of one factor within each level of the other factor ($\bar{y}_{ij}$’s).

The following example shows the need for comparing the means of one factor within each level of the other.

\[
\begin{array}{c|c|c|c|c}
A & B & \bar{y}_{i.} & \bar{y}_{.j} \\
\hline
1 & 10, 20, 30 & 30, 40, 50 & 30 \\
& \bar{y}_{11} = 20 & \bar{y}_{12} = 40 & \\
2 & 40, 50, 60 & 0, 10, 20 & 30 \\
& \bar{y}_{21} = 50 & \bar{y}_{22} = 10 & \\
\end{array}
\]

\[
\begin{array}{c|c|c}
\bar{y}_{ij} & 35 & 25 \\
\hline
& \bar{y}_{..} = 30 &
\end{array}
\]
The interaction plot shows that factor \( A \) may have an effect on the response; however, \( \bar{y}_{2.} - \bar{y}_{1.} = 0 \). Notice that within each level of \( B \), the effect of \( A \) is nonzero:

\[
\bar{y}_{21} - \bar{y}_{11} = 30, \quad \bar{y}_{22} - \bar{y}_{12} = -30.
\]

Generally, when interaction is not present, we use the following standard errors in our comparisons of means:

\[
SE(\bar{y}_{i.} - \bar{y}_{i'.}) = \sqrt{\frac{2MS_E}{nb}}
\]

and

\[
SE(\bar{y}_{j.} - \bar{y}_{j'.}) = \sqrt{\frac{2MS_E}{na}}
\]

Thus, for example, the \( a \) factor \( A \) means may be compared via the Tukey-Kramer procedure as: declare \( \tau_i \) to be significantly different from \( \tau_{i'} \) if

\[
|\bar{y}_{i.} - \bar{y}_{i'.}| > q_{a,ab(n-1)}(\alpha) \sqrt{\frac{2MS_E}{nb}}.
\]

Similarly, we declare \( \beta_j \) to be significantly different from \( \beta_{j'} \) if

\[
|\bar{y}_{j.} - \bar{y}_{j'.}| > q_{b,ab(n-1)}(\alpha) \sqrt{\frac{2MS_E}{na}}.
\]

When interaction is present we use the \( ab \) cell means. The standard errors are

\[
SE(\bar{y}_{ij} - \bar{y}_{i'j'}) = \sqrt{\frac{2MS_E}{n}},
\]

where \((i,j) \neq (i',j')\).

The Tukey-Kramer method declares \( \tau_i \) to be significantly different from \( \tau_{i'} \) in level \( j \) of factor \( B \) if

\[
|\bar{y}_{ij} - \bar{y}_{i'j'}| > q_{ab,ab(n-1)}(\alpha) \sqrt{\frac{2MS_E}{n}}.
\]

The following SAS code provides the Tukey-Kramer intervals for the battery life example considered above.
CHAPTER 3. FACTORIAL DESIGNS

PROC GLM;
  CLASS MAT TEMP;
  MODEL LIFE=MAT TEMP MAT*TEMP;
  LSMEANS MAT | TEMP /TDIFF ADJUST=TUKEY;
RUN;
QUIT;

Adjustment for Multiple Comparisons: Tukey

<table>
<thead>
<tr>
<th>MAT</th>
<th>LIFE LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>83.166667</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>108.333333</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>125.083333</td>
<td>3</td>
</tr>
</tbody>
</table>

Least Squares Means for Effect MAT

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-2.37236</td>
<td>-3.95132</td>
<td>0.0628</td>
</tr>
<tr>
<td>2</td>
<td>2.37236</td>
<td>-1.57896</td>
<td>0.0628</td>
</tr>
<tr>
<td>3</td>
<td>3.951318</td>
<td>1.578956</td>
<td>0.0014</td>
</tr>
</tbody>
</table>

Adjustment for Multiple Comparisons: Tukey

<table>
<thead>
<tr>
<th>TEMP</th>
<th>LIFE LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>144.833333</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>107.583333</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>64.166667</td>
<td>3</td>
</tr>
</tbody>
</table>

Least Squares Means for Effect TEMP

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3.51141</td>
<td>7.604127</td>
<td>0.0044</td>
</tr>
<tr>
<td>2</td>
<td>-3.51141</td>
<td>4.092717</td>
<td>0.0044</td>
</tr>
<tr>
<td>3</td>
<td>-7.60413</td>
<td>-4.09272</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Adjustment for Multiple Comparisons: Tukey

<table>
<thead>
<tr>
<th>MAT</th>
<th>TEMP</th>
<th>LIFE LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>134.750000</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>57.250000</td>
<td>2</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>57.500000</td>
<td>3</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>155.750000</td>
<td>4</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>119.750000</td>
<td>5</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>49.500000</td>
<td>6</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>144.000000</td>
<td>7</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>145.750000</td>
<td>8</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>85.500000</td>
<td>9</td>
</tr>
</tbody>
</table>

Least Squares Means for Effect MAT*TEMP
3.2. THE TWO-FACTOR FACTORIAL DESIGN

### Least Squares Means for Effect MAT*TEMP

**t for H0: LSMean(i)=LSMean(j) / Pr > |t|**

**Dependent Variable: LIFE**

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4.2179</td>
<td>4.204294</td>
<td>-1.14291</td>
<td>0.816368</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.0065</td>
<td>0.0067</td>
<td>0.9616</td>
<td>0.9953</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>-4.2179</td>
<td>-0.01361</td>
<td>-5.36082</td>
<td>-3.40153</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.0065</td>
<td>1.0000</td>
<td>0.0003</td>
<td>0.0460</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>-4.20429</td>
<td>0.013606</td>
<td>-5.34721</td>
<td>-3.38793</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.0067</td>
<td>1.0000</td>
<td>0.0004</td>
<td>0.0475</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>1.142915</td>
<td>5.360815</td>
<td>5.347209</td>
<td>1.959283</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.9616</td>
<td>0.0003</td>
<td>0.0004</td>
<td>0.5819</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>-0.81637</td>
<td>3.401533</td>
<td>3.387926</td>
<td>-1.95928</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.9953</td>
<td>0.0460</td>
<td>0.0475</td>
<td>0.5819</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>-4.63969</td>
<td>-0.42179</td>
<td>-4.70772</td>
<td>-5.78261</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1.0000</td>
<td>1.0000</td>
<td>1.0000</td>
<td>0.0001</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>0.503427</td>
<td>4.721327</td>
<td>4.707721</td>
<td>-0.63949</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.9999</td>
<td>0.0018</td>
<td>0.0019</td>
<td>0.9991</td>
<td></td>
</tr>
</tbody>
</table>

**Adjustment for Multiple Comparisons: Tukey**

Least Squares Means for Effect MAT*TEMP

**t for H0: LSMean(i)=LSMean(j) / Pr > |t|**

**Dependent Variable: LIFE**

<table>
<thead>
<tr>
<th></th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4.63969</td>
<td>-0.50343</td>
<td>-0.59867</td>
<td>2.680408</td>
</tr>
<tr>
<td></td>
<td>0.0022</td>
<td>0.9999</td>
<td>0.9995</td>
<td>0.2017</td>
</tr>
<tr>
<td>2</td>
<td>0.42179</td>
<td>-4.72133</td>
<td>-4.81657</td>
<td>-1.53749</td>
</tr>
<tr>
<td></td>
<td>1.0000</td>
<td>0.0018</td>
<td>0.0014</td>
<td>0.8282</td>
</tr>
<tr>
<td>3</td>
<td>0.435396</td>
<td>-4.70772</td>
<td>-4.80296</td>
<td>-1.52389</td>
</tr>
<tr>
<td></td>
<td>1.0000</td>
<td>0.0019</td>
<td>0.0015</td>
<td>0.8347</td>
</tr>
<tr>
<td>4</td>
<td>5.782605</td>
<td>0.639488</td>
<td>0.544245</td>
<td>3.823323</td>
</tr>
<tr>
<td></td>
<td>0.0001</td>
<td>0.9991</td>
<td>0.9997</td>
<td>0.0172</td>
</tr>
<tr>
<td>5</td>
<td>3.823323</td>
<td>-1.31979</td>
<td>-1.41504</td>
<td>1.86404</td>
</tr>
<tr>
<td></td>
<td>0.0172</td>
<td>0.9165</td>
<td>0.8823</td>
<td>0.6420</td>
</tr>
<tr>
<td>6</td>
<td>-5.14312</td>
<td>-5.23836</td>
<td>-1.95928</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.0006</td>
<td>0.0005</td>
<td>0.5819</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>5.143117</td>
<td>-0.09524</td>
<td>3.183834</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.0006</td>
<td>1.0000</td>
<td>0.0743</td>
<td></td>
</tr>
</tbody>
</table>

Notice that SAS has labelled the 9 cells consecutively as
We use underlining to summarize the results.

Temperature within Material:

<table>
<thead>
<tr>
<th>Material</th>
<th>$\bar{y}_{12}$</th>
<th>$\bar{y}_{13}$</th>
<th>$\bar{y}_{11}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>57.25</td>
<td>57.50</td>
<td>134.75</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Material</th>
<th>$\bar{y}_{23}$</th>
<th>$\bar{y}_{22}$</th>
<th>$\bar{y}_{21}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>49.50</td>
<td>119.75</td>
<td>155.75</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Material</th>
<th>$\bar{y}_{33}$</th>
<th>$\bar{y}_{31}$</th>
<th>$\bar{y}_{32}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>85.5</td>
<td>144.00</td>
<td>145.75</td>
</tr>
</tbody>
</table>

Material within Temperature:

<table>
<thead>
<tr>
<th>Temperature</th>
<th>$\bar{y}_{11}$</th>
<th>$\bar{y}_{31}$</th>
<th>$\bar{y}_{21}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>134.75</td>
<td>144.00</td>
<td>155.75</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Temperature</th>
<th>$\bar{y}_{12}$</th>
<th>$\bar{y}_{22}$</th>
<th>$\bar{y}_{32}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>57.25</td>
<td>119.75</td>
<td>145.75</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Temperature</th>
<th>$\bar{y}_{23}$</th>
<th>$\bar{y}_{13}$</th>
<th>$\bar{y}_{33}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>49.50</td>
<td>57.50</td>
<td>85.5</td>
</tr>
</tbody>
</table>

Model Diagnostics

Diagnostics are run the usual way via residual analysis. Recall that the residuals for the two-factor factorial model are given by

$$e_{ijk} = y_{ijk} - \bar{y}_{ij}.$$  

Graphical checks for equality of variances as well as unusual observations are plots of residuals versus

- $\bar{y}_{ij}$,
- factor $A$, and
- factor $B$.

The graphical check for normality is the QQ-plot of the residuals. For the battery life example the following SAS code may be used to produce the required plots.

**PROC GLM:**
```sas
PROC GLM;
  CLASS MAT TEMP;
  MODEL LIFE=MAT TEMP MAT*TEMP;
  OUTPUT OUT=DIAG R=RES P=PRED;
RUN;
QUIT;
```

**SYMBOL V=CIRCLE:**
```sas
PROC UNIVARIATE NOPRINT;
  QQPLOT RES / NORMAL (L=1 MU=0 SIGMA=EST);
  HIST RES / NORMAL (L=1 MU=0 SIGMA=EST);
RUN;
QUIT;
```

**PROC GLOT:**
```sas
PROC GLOT;
  PLOT RES*MAT;
  PLOT RES*TEMP;
  PLOT RES*PRED;
RUN;
QUIT;
```
Formal tests for normality indicate no deviation from normality. The QQ-plot shows no signs of non-normality. The residual plots show a mild deviation from constant variance. We may need to transform the data.

<table>
<thead>
<tr>
<th>Test</th>
<th>Statistic</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cramer-von Mises</td>
<td>W-Sq 0.05586092</td>
<td>Pr &gt; W-Sq &gt;0.250</td>
</tr>
<tr>
<td>Anderson-Darling</td>
<td>A-Sq 0.34769847</td>
<td>Pr &gt; A-Sq &gt;0.250</td>
</tr>
</tbody>
</table>
There is no command in SAS to perform Levene's test for equality of variances. The following trick of relabelling the cells and running a one-factor ANOVA model may be used to perform Levene's test. The partial SAS code is given along with the output.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA BATTERY;
  INPUT MAT TEMP LIFE;
  CELL = 3*(MAT - 1) + TEMP;
DATALINES;
  1 1 130
  1 1 155
  ...
  3 3 82
  3 3 60
;
PROC GLM;
  CLASS CELL;
  MODEL LIFE=CELL;
  MEANS CELL/ HOVTEST=LEVENE;
RUN;
QUIT;
```

Levene's Test for Homogeneity of LIFE Variance
ANOVA of Squared Deviations from Group Means
### 3.2. THE TWO-FACTOR FACTORIAL DESIGN

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Squares</th>
<th>Sq Mean</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>CELL</td>
<td>8</td>
<td>5407436</td>
<td>675929</td>
<td>1.48</td>
<td>0.2107</td>
</tr>
<tr>
<td>Error</td>
<td>27</td>
<td>12332885</td>
<td>456774</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
3.2.2 Random and Mixed Models

We shall now consider the case where the levels of factor A or the levels of factor B are randomly chosen from a population of levels.

The Random Effects Model

In a random effects model the \( a \) levels of factor A and the \( b \) levels of factor B are random samples from populations of levels. The statistical model is the same as the one given in (3.1) where \( \tau_i \), \( \beta_j \), \((\tau\beta)_{ij}\), and \( \epsilon_{ijk} \) are randomly sampled from \( N(0, \sigma^2_\tau) \), \( N(0, \sigma^2_\beta) \), \( N(0, \sigma^2_{\tau\beta}) \), and \( N(0, \sigma^2) \) distributions, respectively. Thus, the variance of any observation is

\[ \text{Var}(y_{ijk}) = \sigma^2_\tau + \sigma^2_\beta + \sigma^2_{\tau\beta} + \sigma^2 \]

The hypotheses of interest are

A main effect:

\[ H_0 : \sigma^2_\tau = 0 \quad H_A : \sigma^2_\tau \neq 0 \]

B main effect:

\[ H_0 : \sigma^2_\beta = 0 \quad H_A : \sigma^2_\beta \neq 0 \]

AB interaction effect:

\[ H_0 : \sigma^2_{\tau\beta} = 0 \quad H_A : \sigma^2_{\tau\beta} \neq 0 \]

The ANOVA table needs some modifications. This is seen examining the expected mean squares.

\begin{align*}
E(MS_A) &= \sigma^2 + n\sigma^2_{\tau\beta} + bn\sigma^2_\tau \\
E(MS_B) &= \sigma^2 + n\sigma^2_{\tau\beta} + an\sigma^2_\beta \\
E(MS_{AB}) &= \sigma^2 + n\sigma^2_{\tau\beta} \\
E(MS_E) &= \sigma^2
\end{align*}

Therefore, the two-factor random effects ANOVA table is:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>( a - 1 )</td>
<td>( SS_A )</td>
<td>( MS_A )</td>
<td>( F_A = \frac{MS_A}{MS_{AB}} )</td>
</tr>
<tr>
<td>B</td>
<td>( b - 1 )</td>
<td>( SS_B )</td>
<td>( MS_B )</td>
<td>( F_B = \frac{MS_B}{MS_{AB}} )</td>
</tr>
<tr>
<td>AB</td>
<td>((a - 1)(b - 1))</td>
<td>( SS_{AB} )</td>
<td>( MS_{AB} )</td>
<td>( F_{AB} = \frac{MS_{AB}}{MS_E} )</td>
</tr>
<tr>
<td>Error</td>
<td>( ab(n - 1) )</td>
<td>( SS_E )</td>
<td>( MS_E )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( abn - 1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

From the expected mean squares, we get the estimates of the variance components as

\begin{align*}
\hat{\sigma}^2 &= MS_E \\
\hat{\sigma}^2_{\tau\beta} &= \frac{MS_{AB} - MS_E}{n} \\
\hat{\sigma}^2_\tau &= \frac{MS_A - MS_{AB}}{bn} \\
\hat{\sigma}^2_\beta &= \frac{MS_B - MS_{AB}}{an}
\end{align*}
3.2. THE TWO-FACTOR FACTORIAL DESIGN

Example

Consider the battery life example once again. This time assume that the material types and temperatures are randomly selected out of several possibilities. We may then use the RANDOM statement in PROC GLM of SAS to analyze the data as a random effects model. Here are the SAS code and associated output.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA BATTERY;
INPUT MAT TEMP LIFE;
DATALINES;
1 1 130
1 1 155
........
3 3 60
;
PROC GLM;
CLASS MAT TEMP;
MODEL LIFE=MAT TEMP MAT*TEMP;
RANDOM MAT TEMP MAT*TEMP / TEST;
RUN;
QUIT;
```

The GLM Procedure

<table>
<thead>
<tr>
<th>Source</th>
<th>Type III Expected Mean Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAT</td>
<td>Var(Error) + 4 Var(MAT*TEMP) + 12 Var(MAT)</td>
</tr>
<tr>
<td>TEMP</td>
<td>Var(Error) + 4 Var(MAT*TEMP) + 12 Var(TEMP)</td>
</tr>
<tr>
<td>MAT*TEMP</td>
<td>Var(Error) + 4 Var(MAT*TEMP)</td>
</tr>
</tbody>
</table>

The GLM Procedure

Tests of Hypotheses for Random Model Analysis of Variance

Dependent Variable: LIFE

<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>MAT</td>
<td>2</td>
<td>10684</td>
<td>5341.861111</td>
<td>2.22</td>
<td>0.2243</td>
</tr>
<tr>
<td>TEMP</td>
<td>2</td>
<td>39119</td>
<td>19559</td>
<td>8.14</td>
<td>0.0389</td>
</tr>
<tr>
<td>Error: MS(MAT*TEMP)</td>
<td>4</td>
<td>9613.777778</td>
<td>2403.444444</td>
<td></td>
<td></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>MAT*TEMP</td>
<td>4</td>
<td>9613.777778</td>
<td>2403.444444</td>
<td>3.56</td>
<td>0.0186</td>
</tr>
<tr>
<td>Error: MS(Error)</td>
<td>27</td>
<td>18231</td>
<td>675.212963</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Notice that variability among material types is the only factor that is not significant.

The estimates of the components of variance are (values in parentheses are percent contributions of the components)

\[
\hat{\sigma}^2 = MS_E = 675.21 (24.27\%)
\]
\[
\hat{\sigma}_{\tau}^2 = n \frac{MS_{AB} - MS_E}{4} = \frac{2403.44 - 675.21}{4} = 432.06 (15.53\%)
\]
\[
\hat{\sigma}_{\tau_1}^2 = \frac{MS_A - MS_{AB}}{b} = \frac{5341.86 - 2403.44}{12} = 244.87 (8.80\%)
\]
\[
\hat{\sigma}_{\tau_2}^2 = \frac{MS_B - MS_{AB}}{a} = \frac{19559 - 2403.44}{12} = 1429.58 (51.39\%)
\]
**Mixed Models**

Let us now consider the case where one factor is fixed and the other is random. Without loss of generality, assume that factor $A$ is fixed and factor $B$ is random. When a factor is random, its interaction with any other factor is also random.

The statistical model, once again, has the same form given in (3.1). This time we assume that

- $\tau_i$ are fixed effects such that $\sum \tau_i = 0$,
- $\beta_j \sim_{iids} N(0, \sigma_\beta^2)$, $(\tau\beta)_{ij} \sim_{iids} N(0, \frac{a-1}{a} \sigma_\tau^2 \sigma_\beta^2)$, and $\epsilon_{ijk} \sim_{iids} N(0, \sigma^2)$.

The hypotheses of interest are

$$H_0 : \tau_1 = \cdots = \tau_a = 0, \quad H_0 : \sigma_\beta^2 = 0, \quad H_0 : \sigma_{\tau\beta}^2 = 0$$

The expected mean squares are given by

$$E(MS_A) = \sigma_\tau^2 + a \sigma_\beta^2 + \frac{bn}{a-1} \sum \tau_i^2$$
$$E(MS_B) = \sigma_\tau^2 + a n \sigma_\beta^2$$
$$E(MS_{AB}) = \sigma_\tau^2 + a \sigma_\beta^2$$
$$E(MS_E) = \sigma^2$$

The fixed factor effects are estimated the usual way as

$$\hat{\mu} = \bar{y} \ldots, \quad \hat{\tau}_i = \bar{y}_{i..} - \bar{y} \ldots$$

and the variance components are estimated as

$$\hat{\sigma}^2 = MS_E, \quad \hat{\sigma}_{\tau\beta}^2 = \frac{MS_{AB} - MS_E}{n}, \quad \text{and} \quad \hat{\sigma}_\beta^2 = \frac{MS_B - MS_E}{an}$$

The ANOVA table for the mixed model is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>$F$-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>A (fixed)</td>
<td>$a-1$</td>
<td>$SS_A$</td>
<td>$MS_A$</td>
<td>$F_A = \frac{MS_A}{MS_{AB}}$</td>
</tr>
<tr>
<td>B (random)</td>
<td>$b-1$</td>
<td>$SS_B$</td>
<td>$MS_B$</td>
<td>$F_B = \frac{MS_B}{MS_{AB}}$</td>
</tr>
<tr>
<td>AB</td>
<td>$(a-1)(b-1)$</td>
<td>$SS_{AB}$</td>
<td>$MS_{AB}$</td>
<td>$F_{AB} = \frac{MS_{AB}}{MS_E}$</td>
</tr>
<tr>
<td>Error</td>
<td>$ab(n-1)$</td>
<td>$SS_E$</td>
<td>$MS_E$</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>$abn-1$</td>
<td>SS_T</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Example**

Consider the battery life example and assume that temperature is a random factor while material type is a fixed factor. We use **PROC MIXED** in SAS to generate the output. **PROC GLM** does not provide the correct analysis!

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA BATTERY;
  INPUT MAT TEMP LIFE;
  DATALINES;
    1 1 130
    1 1 155
    .......
    3 3 60;
PROC MIXED COVTEST;
CLASS MAT TEMP;
PROC MIXED;
```
3.2. THE TWO-FACTOR FACTORIAL DESIGN

MODEL LIFE=MAT;
RANDOM TEMP MAT*TEMP;
RUN;
QUIT;

The Mixed Procedure

Model Information
Data Set             WORK.BATTERY
Dependent Variable   LIFE
Covariance Structure Variance Components
Estimation Method     REML
Residual Variance Method Profile
Fixed Effects SE Method Model-Based
Degrees of Freedom Method Containment

Class Level Information

<table>
<thead>
<tr>
<th>Class</th>
<th>Levels</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAT</td>
<td>3</td>
<td>1 2 3</td>
</tr>
<tr>
<td>TEMP</td>
<td>3</td>
<td>1 2 3</td>
</tr>
</tbody>
</table>

Dimensions

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Covariance Parameters</td>
<td>3</td>
</tr>
<tr>
<td>Columns in X</td>
<td>4</td>
</tr>
<tr>
<td>Columns in Z</td>
<td>12</td>
</tr>
<tr>
<td>Subjects</td>
<td>1</td>
</tr>
<tr>
<td>Max Obs Per Subject</td>
<td>36</td>
</tr>
<tr>
<td>Observations Used</td>
<td>36</td>
</tr>
<tr>
<td>Observations Not Used</td>
<td>0</td>
</tr>
<tr>
<td>Total Observations</td>
<td>36</td>
</tr>
</tbody>
</table>

Iteration History

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Evaluations</th>
<th>-2 Res Log Like</th>
<th>Criterion</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1</td>
<td>352.41258855</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>327.91147422</td>
<td>0.00000000</td>
</tr>
</tbody>
</table>

Convergence criteria met.

Covariance Parameter Estimates

<table>
<thead>
<tr>
<th>Cov Parm</th>
<th>Estimate</th>
<th>Error</th>
<th>Z</th>
<th>Pr Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>TEMP</td>
<td>1429.66</td>
<td>1636.09</td>
<td>0.87</td>
<td>0.1911</td>
</tr>
<tr>
<td>MAT*TEMP</td>
<td>432.06</td>
<td>427.35</td>
<td>1.01</td>
<td>0.1560</td>
</tr>
<tr>
<td>Residual</td>
<td>675.21</td>
<td>183.77</td>
<td>3.67</td>
<td>0.0001</td>
</tr>
</tbody>
</table>

Fit Statistics

-2 Res Log Likelihood 327.9
AIC (smaller is better) 333.9
AICC (smaller is better) 334.7
BIC (smaller is better) 331.2

The Mixed Procedure

Type 3 Tests of Fixed Effects

<table>
<thead>
<tr>
<th>Effect</th>
<th>DF</th>
<th>DF</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAT</td>
<td>2</td>
<td>4</td>
<td>2.22</td>
<td>0.2243</td>
</tr>
</tbody>
</table>
From the output we observe that the fixed effect (MAT) is not significant. Neither of the random effects are significant ($p$-values of 0.1911 and 0.1560).

Proc Mixed uses the restricted maximum likelihood (REML) technique to estimate the variance components. In a balanced design the REML method gives identical estimates as those obtained using the expected mean squares. When there is imbalance, however, the results are not the same.

**Exercise:** For this example, show that the estimates of the variance components obtained here are identical to those using the expected mean squares.
### 3.3 Blocking in Factorial Designs

Blocking may be implemented in factorial designs using the same principles. In a randomized block design, every block contains all possible treatment combinations.

The statistical model for a two-factor blocked factorial design with 1 replication per block is

\[ y_{ijk} = \mu + \tau_i + \beta_j + (\tau\beta)_{ij} + \delta_k + \epsilon_{ijk} \]

where \( i = 1, \ldots, a, \quad j = 1, \ldots, b, \quad \text{and} \quad k = 1, \ldots, n. \) \( \delta_k \) is the effect of the \( k \)-th block.

The model assumes that treatment-block interactions are negligible. The ANOVA table for a random effects model is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>( F )-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>( a - 1 )</td>
<td>( SS_A )</td>
<td>( MS_A )</td>
<td>( F_A = \frac{MS_A}{MS_E} )</td>
</tr>
<tr>
<td>B</td>
<td>( b - 1 )</td>
<td>( SS_B )</td>
<td>( MS_B )</td>
<td>( F_B = \frac{MS_B}{MS_E} )</td>
</tr>
<tr>
<td>AB</td>
<td>((a - 1)(b - 1))</td>
<td>( SS_{AB} )</td>
<td>( MS_{AB} )</td>
<td>( F_{AB} = \frac{MS_{AB}}{MS_E} )</td>
</tr>
<tr>
<td>Blocks</td>
<td>( n - 1 )</td>
<td>( SS_{Blocks} )</td>
<td>( MS_{Blocks} )</td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>((ab - 1)(n - 1))</td>
<td>( SS_E )</td>
<td>( MS_E )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( abn - 1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

where

\[ SS_{Blocks} = ab \sum_{k=1}^{n} (\bar{y}_{..k} - \bar{y}_{..})^2. \]

**Example**

An agronomist wanted to study the effect of different rates of phosphorous fertilizer on two types of broad bean plants. He thought that the plant types might respond differently to fertilization; so, he decided to do a factorial experiment with two factors:

1. Plant type \( (T) \) at two levels
   - \( T_1 = \) short, bushy
   - \( T_2 = \) tall, erect

2. Phosphorous rate \( (P) \) at three levels
   - \( P_1 = \) none
   - \( P_2 = 25kg/ha \)
   - \( P_3 = 50kg/ha \)

Using the full factorial set of combinations he had six treatments:

\[ T_1P_1, \ T_1P_2, \ T_1P_3, \ T_2P_1, \ T_2P_2, \ T_2P_3 \]

He conducted the experiment using a randomized block design with four blocks of six plots each. The field layout and the yield in \( kg/ha \) are shown below:

<table>
<thead>
<tr>
<th>BLOCK</th>
<th>I</th>
<th>II</th>
<th>III</th>
<th>IV</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>( T_2P_2(8.3) )</td>
<td>( T_2P_1(11.2) )</td>
<td>( T_1P_2(17.6) )</td>
<td>( T_1P_3(18.9) )</td>
</tr>
<tr>
<td></td>
<td>( T_2P_1(11.0) )</td>
<td>( T_2P_2(10.5) )</td>
<td>( T_1P_1(14.3) )</td>
<td>( T_2P_2(12.8) )</td>
</tr>
<tr>
<td></td>
<td>( T_1P_2(11.5) )</td>
<td>( T_2P_3(16.7) )</td>
<td>( T_2P_1(12.1) )</td>
<td>( T_2P_3(17.5) )</td>
</tr>
<tr>
<td></td>
<td>( T_2P_3(15.7) )</td>
<td>( T_1P_2(17.6) )</td>
<td>( T_1P_3(18.2) )</td>
<td>( T_2P_1(12.6) )</td>
</tr>
<tr>
<td></td>
<td>( T_1P_3(18.2) )</td>
<td>( T_1P_1(13.6) )</td>
<td>( T_2P_3(16.6) )</td>
<td>( T_1P_2(18.1) )</td>
</tr>
<tr>
<td></td>
<td>( T_1P_2(17.1) )</td>
<td>( T_1P_3(17.6) )</td>
<td>( T_2P_2(9.1) )</td>
<td>( T_1P_1(14.5) )</td>
</tr>
</tbody>
</table>
The data layout is (observations in a cell are in increasing block order I, II, III, IV)

<table>
<thead>
<tr>
<th>Type</th>
<th>$P_1$</th>
<th>Phosphorous</th>
<th>$P_2$</th>
<th>$P_3$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$T_1$</td>
<td>11.5, 13.6, 14.3, 14.5</td>
<td>17.1, 17.6, 17.6, 18.1</td>
<td>18.2, 17.6, 18.2, 18.9</td>
<td></td>
</tr>
<tr>
<td>$T_2$</td>
<td>11.0, 11.2, 12.1, 12.6</td>
<td>8.3, 10.5, 9.1, 12.8</td>
<td>15.7, 16.7, 16.6, 17.5</td>
<td></td>
</tr>
</tbody>
</table>

The following SAS code and output give the analysis.
3.3. BLOCKING IN FACTORIAL DESIGNS

OPTIONS LS=80 PS=66 NODATE;

DATA FERT;
INPUT TYPE PH BLOCK YIELD;
DATALINES;
  1 1 1 11.5
  1 1 2 13.6
  1 1 3 14.3
  1 1 4 14.5
  1 2 1 17.1
  1 2 2 17.6
  1 2 3 17.6
  1 2 4 18.1
  1 3 1 18.2
  1 3 2 17.6
  1 3 3 18.2
  1 3 4 18.9
  2 1 1 11.0
  2 1 2 11.2
  2 1 3 12.1
  2 1 4 12.6
  2 2 1 8.3
  2 2 2 10.5
  2 2 3 9.1
  2 2 4 12.8
  2 3 1 15.7
  2 3 2 16.7
  2 3 3 16.6
  2 3 4 17.5
;

PROC GLM;
  CLASS TYPE PH BLOCK;
  MODEL YIELD=BLOCK TYPE|PH;
RUN;
QUIT;
CHAPTER 3. FACTORIAL DESIGNS

The interaction between plant type and phosphorous level is significant. This means that all comparisons of means of one factor would have to be done within the levels of the other factor. Different plant types respond differently to different levels of the fertilizer. Short, bushy plants seem to show their greatest yield increase with the first increment of added phosphorous, while tall, erect plants seem to show no yield increase with 25 kg/ha of phosphorous.

Blocking seems to be working here judging from the corresponding $F$ value. The efficiency needs to be investigated further.

The main effects are also significant. The rates of phosphorous fertilizer and the type of plant both affect yield significantly.
A Factorial Experiment with Two Blocking Factors

This is dealt with by implementing a Latin square design in a similar manner as one factor experiments. The only difference here is that every factor combination is considered to be a treatment. To illustrate this, consider a two-factor factorial experiment with 3 levels of factor A and 2 levels of factor B. We will use Latin letters to represent the $3 \times 2 = 6$ treatment combinations.

<table>
<thead>
<tr>
<th>$A$</th>
<th>$B$</th>
<th>Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A_1$</td>
<td>$B_1$</td>
<td>A</td>
</tr>
<tr>
<td>$A_1$</td>
<td>$B_2$</td>
<td>B</td>
</tr>
<tr>
<td>$A_2$</td>
<td>$B_1$</td>
<td>C</td>
</tr>
<tr>
<td>$A_2$</td>
<td>$B_2$</td>
<td>D</td>
</tr>
<tr>
<td>$A_3$</td>
<td>$B_1$</td>
<td>E</td>
</tr>
<tr>
<td>$A_3$</td>
<td>$B_2$</td>
<td>F</td>
</tr>
</tbody>
</table>

We then form the $6 \times 6$ basic Latin square cyclically as

<table>
<thead>
<tr>
<th>Row</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>B</td>
<td>C</td>
<td>D</td>
<td>E</td>
<td>F</td>
</tr>
<tr>
<td>2</td>
<td>B</td>
<td>C</td>
<td>D</td>
<td>E</td>
<td>F</td>
<td>A</td>
</tr>
<tr>
<td>3</td>
<td>C</td>
<td>D</td>
<td>E</td>
<td>F</td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>E</td>
<td>F</td>
<td>A</td>
<td>B</td>
<td>C</td>
</tr>
<tr>
<td>3</td>
<td>E</td>
<td>F</td>
<td>A</td>
<td>B</td>
<td>C</td>
<td>D</td>
</tr>
<tr>
<td>3</td>
<td>F</td>
<td>A</td>
<td>B</td>
<td>C</td>
<td>D</td>
<td>E</td>
</tr>
</tbody>
</table>

We then randomize the rows and the columns.

In general, consider two factors: factor $A$ with $a$ levels and factor $B$ with $b$ levels. The statistical model is

$$
y_{ijkl} = \mu + \tau_i + \beta_j + \gamma_k + (\tau \beta)_{ij} + (\tau \gamma)_{ik} + (\beta \gamma)_{jk} + (\tau \beta \gamma)_{ijk} + \epsilon_{ijkl}
$$

where

- $\tau_i$, $i = 1, \ldots, a$ is the effect of the $i$th level of factor $A$,
- $\beta_j$, $j = 1, \ldots, b$ is the effect of the $j$th level of factor $B$,
- $\gamma_k$ and $\delta_l$, $k, l = 1, \ldots, ab$, are the effects of the $k$th row and the $l$th column, respectively.

### 3.4 The General Factorial Design

Consider an experiment in which we have $t$ factors $F_1, \ldots, F_t$ with $f_1, \ldots, f_t$ levels, respectively. The statistical model is

$$
y_{i_1i_2\ldots i_t} = \mu + \tau_{i_1} + \tau_{i_2} + \cdots + \tau_{i_t} + (\tau_1 \tau_2)_{i_1i_2} + \cdots + (\tau_{t-1} \tau_t)_{i_{t-1}i_t} + \cdots + (\tau_1 \tau_2 \cdots \tau_t)_{i_1i_2\ldots i_t} + \epsilon_{i_1i_2\ldots i_t}
$$

where $i_1 = 1, \ldots, f_1; i_2 = 1, \ldots, f_2$, etc.

A special case is the 3 factor factorial design with factors $A$, $B$, and $C$ with levels $a$, $b$, and $c$, respectively. We need two or more replications to be able to test for all possible interactions. The statistical model is

$$
y_{ijkl} = \mu + \tau_i + \beta_j + \gamma_k + (\tau \beta)_{ij} + (\tau \gamma)_{ik} + (\beta \gamma)_{jk} + (\tau \beta \gamma)_{ijk} + \epsilon_{ijkl}
$$

where $i = 1, \ldots, a; j = 1, \ldots, b; k = 1, \ldots, c; \text{ and } l = 1, \ldots, n$.

Considering a fixed effects model, the ANOVA table is...
CHAPTER 3. FACTORIAL DESIGNS

<table>
<thead>
<tr>
<th>Source df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>A (a-1)</td>
<td>(SS_A)</td>
<td>(MS_A)</td>
<td>(F_A = \frac{MS_A}{MS_E})</td>
</tr>
<tr>
<td>B (b-1)</td>
<td>(SS_B)</td>
<td>(MS_B)</td>
<td>(F_B = \frac{MS_B}{MS_E})</td>
</tr>
<tr>
<td>C (c-1)</td>
<td>(SS_C)</td>
<td>(MS_C)</td>
<td>(F_C = \frac{MS_C}{MS_E})</td>
</tr>
<tr>
<td>AB ((a-1)(b-1))</td>
<td>(SS_{AB})</td>
<td>(MS_{AB})</td>
<td>(F_{AB} = \frac{MS_{AB}}{MS_E})</td>
</tr>
<tr>
<td>AC ((a-1)(c-1))</td>
<td>(SS_{AC})</td>
<td>(MS_{AC})</td>
<td>(F_{AC} = \frac{MS_{AC}}{MS_E})</td>
</tr>
<tr>
<td>BC ((b-1)(c-1))</td>
<td>(SS_{BC})</td>
<td>(MS_{BC})</td>
<td>(F_{BC} = \frac{MS_{BC}}{MS_E})</td>
</tr>
<tr>
<td>ABC ((a-1)(b-1)(c-1))</td>
<td>(SS_{ABC})</td>
<td>(MS_{ABC})</td>
<td>(F_{ABC} = \frac{MS_{ABC}}{MS_E})</td>
</tr>
<tr>
<td>Error (abc(n-1))</td>
<td>(SS_E)</td>
<td>(MS_E)</td>
<td></td>
</tr>
<tr>
<td>Total (abcn-1)</td>
<td>(SS_T)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The following example is taken from Montgomery: Design and Analysis of Experiments

Example

A soft drink bottler is studying the effect of percent carbonation \((A)\), operating pressure \((B)\), and line speed \((C)\) on the volume of beverage packaged in each bottle. Three levels of \(A\), two levels of \(B\) and two levels of \(C\) are considered to set up a \(3 \times 2 \times 2\) factorial experiment. This experiment is run twice and the deviations from the target volume are recorded. The data are given below.

<table>
<thead>
<tr>
<th>Pressure (B)</th>
<th>25 psi</th>
<th>30 psi</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carbonation (A)</td>
<td>Line Speed (C)</td>
<td>Line Speed (C)</td>
</tr>
<tr>
<td>10</td>
<td>-3, -1</td>
<td>-1, 0</td>
</tr>
<tr>
<td>12</td>
<td>0, 1</td>
<td>2, 3</td>
</tr>
<tr>
<td>14</td>
<td>5, 4</td>
<td>7, 9</td>
</tr>
</tbody>
</table>

We will use SAS to analyze the data. The SAS code and output are as follows:

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA BOTTLE;
INPUT CARB PRES SPEED VOL;
CARDS;
1 1 1 -3
1 1 2 -1
1 1 2 0
1 2 1 -1
1 2 1 0
1 2 2 1
1 2 2 1
2 1 1 0
2 1 1 1
2 1 2 2
2 1 2 1
2 2 1 2
2 2 1 2
2 2 1 3
2 2 2 6
2 2 2 5
3 1 1 5
3 1 1 4
3 1 2 7
3 1 2 6
3 2 1 7
3 2 1 9
3 2 2 10
3 2 2 11
;
PROC GLM;
CLASS CARB PRES SPEED;
MODEL VOL = CARB|PRES|SPEED;
RUN;
```
3.4. THE GENERAL FACTORIAL DESIGN

As we can see, none of the interactions is significant. However, all the main effects appear to be significant. One may perform multiple comparisons at the highest level of the factors. As an example we will run the Tukey-Kramer procedure on factor A. PROC GLM of SAS is modified as follows:

```
PROC GLM;
CLASS CARB PRES SPEED;
MODEL VOL = CARB|PRES|SPEED;
LSMEANS CARB/PDIFF ADJUST=TUKEY;
RUN;
QUIT;
```

Adjustment for Multiple Comparisons: Tukey

<table>
<thead>
<tr>
<th>CARB</th>
<th>VOL</th>
<th>LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-0.5000000</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>2.5000000</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>7.3750000</td>
<td>3</td>
<td></td>
</tr>
</tbody>
</table>

Least Squares Means for effect CARB

Pr > |t| for H0: LSMean(i)=LSMean(j)

Dependent Variable: VOL

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
</tbody>
</table>

Thus, all pairwise comparisons comparisons of the levels of factor A, percent carbonation, are significantly different at MEER = 0.05.
Chapter 4

$2^k$ and $3^k$ Factorial Designs

4.1 Introduction

Often we consider general factorial designs with $k$ factors each with 2 levels, denoted by $+$ and $-$. This involves a $2 \times 2 \times \cdots \times 2 = 2^k$ factorial experiment. This is known as a $2^k$ factorial design. A similar situation where each of the $k$ factors has three levels (0, 1, 2) is known as a $3^k$ factorial design.

4.2 The $2^k$ Factorial Design

This is particularly useful in the early stages of an experiment as a factor screening mechanism, i.e. to identify important factors. Every interaction term has only 1 degree of freedom. We shall consider special cases where $k = 2, 3$ before looking at the general $2^k$ factorial design.

4.2.1 The $2^2$ Design

Let $A$ and $B$ denote the two factors of interest with two levels ("low (−)" and "high (+)") each. There are $2^2 = 4$ treatments designated as:

<table>
<thead>
<tr>
<th>Treatment</th>
<th>A</th>
<th>B</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1)</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>$a$</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>$b$</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>$ab$</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>

The presence of a letter indicates that the factor is at a high level. The absence of letter indicates the factor is at a low level. The symbol (1) is used to represent the treatment where every factor is at a low level.

As an example consider an experiment where the time a chemical reaction takes is investigated. The two factors of interest are reactant concentration ($A$ at 15% (−) and 25% (+)) and catalyst ($B$ with absence (−) and presence (+)). The experiment is replicated three times.

<table>
<thead>
<tr>
<th>Factor</th>
<th>Replicate</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A$ $B$</td>
<td>Treatment</td>
</tr>
<tr>
<td>− −</td>
<td>(1)</td>
</tr>
<tr>
<td>+ −</td>
<td>$a$</td>
</tr>
<tr>
<td>− +</td>
<td>$b$</td>
</tr>
<tr>
<td>+ +</td>
<td>$ab$</td>
</tr>
</tbody>
</table>
Let $\bar{y}(A_+) \equiv \bar{y}(A + B_+)$ denote the mean of the response where factor $A$ is at high level. A similar notation is used for all the other means. For example, $\bar{y}(A_-B_+)$ is the mean of the response in the case where factor $A$ is at low level and factor $B$ is at high level.

We can now define the main effects of a factor. The main effect of $A$ is

$$\bar{y}(A_+) - \bar{y}(A_-)$$

This is equivalent to

$$\frac{1}{2} \left\{ \bar{y}(A_+ + B_+ + B_-) + \bar{y}(A_+ - B_+ - B_-) \right\} - \frac{1}{2} \left\{ \bar{y}(A_- + B_+ + B_-) + \bar{y}(A_- - B_+ - B_-) \right\} = 8.33$$

Using the treatment means, this may be given as a contrast with coefficients $(−0.5, 0.5, −0.5, 0.5)$.

Similarly, the main effect of $B$ is given by

$$\bar{y}(B_+) - \bar{y}(B_-)$$

which is equivalent to

$$\frac{1}{2} \left\{ \bar{y}(A_+ + B_+ + B_-) + \bar{y}(A_+ - B_+ - B_-) \right\} - \frac{1}{2} \left\{ \bar{y}(A_- + B_+ + B_-) + \bar{y}(A_- - B_+ - B_-) \right\} = −5.00$$

Now the contrast coefficients are $(−0.5, −0.5, 0.5, 0.5)$.

The $AB$ interaction effect is the average difference between the effect of $A$ at the high level of $B$ and the effect of $A$ at the low level of $B$

$$\frac{1}{2} \left\{ \bar{y}(A_+ + B_+) - \bar{y}(A_- + B_-) \right\} - \frac{1}{2} \left\{ \bar{y}(A_+ + B_-) - \bar{y}(A_- + B_+) \right\} = 1.67$$

Using the treatment means, the contrast coefficients become $(0.5, −0.5, −0.5, 0.5)$.

The sum of squares for each factor and the interaction may be obtained in a very simple manner. Let $n$ be the number of replicates in the study.

$$SS_A = n \times (\text{Main effect of } A)^2$$
$$SS_B = n \times (\text{Main effect of } B)^2$$
$$SS_{AB} = n \times (\text{Interaction effect of } AB)^2$$

The total sum of squares is defined as usual

$$SS_T = 2 \sum_{i=1}^{2} \sum_{j=1}^{2} \sum_{k=1}^{n} (y_{ijk} - \bar{y}_{...})^2$$

and the error sum of squares is obtained by subtraction as

$$SS_E = SS_T - SS_A - SS_B - SS_{AB}.$$

For the example above these yield

$$SS_A = 208.33, \quad SS_B = 75.00, \quad SS_{AB} = 8.33, \quad SS_T = 323.00, \quad SS_E = 31.34$$

The ANOVA table is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F-statistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
<td>$SS_A = 208.33$</td>
<td>$MS_A = 208.33$</td>
<td>$F_A = \frac{MS_A}{MS_E} = 53.15$</td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>$SS_B = 75.00$</td>
<td>$MS_B = 75.00$</td>
<td>$F_B = \frac{MS_B}{MS_E} = 19.13$</td>
</tr>
<tr>
<td>AB</td>
<td>1</td>
<td>$SS_{AB} = 8.33$</td>
<td>$MS_{AB} = 8.33$</td>
<td>$F_{AB} = \frac{MS_{AB}}{MS_E} = 2.13$</td>
</tr>
<tr>
<td>Error</td>
<td>$4(n-1) = 8$</td>
<td>$SS_E = 31.34$</td>
<td>$MS_E = 3.92$</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>$4n - 1 = 11$</td>
<td>$SS_T = 323.00$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
4.2. THE $2^K$ FACTORIAL DESIGN

Using SAS

```
OPTIONS LS=80 PS=66 NODATE;
DATA BOTTLE;
  INPUT A B Y @@;
  CARDS:
    -1 -1  28  -1 -1  25  -1 -1  27
    -1  1  36  -1  1  32  -1  1  32
    1 -1  18  1 -1  19  -1  1  23
    1  1  31  1  1  30  1  1  29
;
PROC GLM;
  CLASS A B;
  MODEL Y = A|B;
RUN;
QUIT;
```

```
-----------------------------------------------
<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
<td>208.3333333</td>
<td>208.3333333</td>
<td>53.19</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>75.0000000</td>
<td>75.0000000</td>
<td>19.15</td>
<td>0.0024</td>
</tr>
<tr>
<td>A*B</td>
<td>1</td>
<td>8.3333333</td>
<td>8.3333333</td>
<td>2.13</td>
<td>0.1828</td>
</tr>
</tbody>
</table>
-----------------------------------------------
```

One may use a multiple regression model to estimate the effects in a $2^2$ design. This is done by forming two variables $(x_1, x_2)$ as

$$
\begin{align*}
A_- & \quad x_1 = -.5 \\
A_+ & \quad x_1 = .5 \\
B_- & \quad x_2 = -.5 \\
B_+ & \quad x_2 = .5
\end{align*}
$$

and fitting the regression model

$$
y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} (2x_1 x_2) + \epsilon.
$$

The estimated model coefficient are now

$$
\hat{\beta}_0 = \bar{y}
\hat{\beta}_1 = \text{Main effect of } A
\hat{\beta}_2 = \text{Main effect of } B
\hat{\beta}_{12} = AB \text{ Interaction effect}
$$

Using SAS

```
OPTIONS LS=80 PS=66 NODATE;
DATA BOTTLE;
  INPUT A B Y @@;
  X1 = A/2;
  X2 = B/2;
  X1X2 = 2*X1*X2;
  CARDS:
    -1 -1  28  -1 -1  25  -1 -1  27
    -1  1  36  -1  1  32  -1  1  32
    1 -1  18  1 -1  19  -1  1  23
    1  1  31  1  1  30  1  1  29
;
PROC GLM;
  MODEL Y = X1 X2 X1X2;
RUN;
QUIT;
```

```
CHAPTER 4. $2^K$ AND $3^K$ FACTORIAL DESIGNS

Dependent Variable: Y

<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>3</td>
<td>291.6666667</td>
<td>97.2222222</td>
<td>24.82</td>
<td>0.0002</td>
</tr>
<tr>
<td>Error</td>
<td>8</td>
<td>31.3333333</td>
<td>3.9166667</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>11</td>
<td>323.0000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square  Coeff Var Root MSE Y Mean
0.902993  7.196571  1.979057  27.50000

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>X1</td>
<td>1</td>
<td>208.333333</td>
<td>208.333333</td>
<td>53.19</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>X2</td>
<td>1</td>
<td>75.000000</td>
<td>75.000000</td>
<td>19.15</td>
<td>0.0024</td>
</tr>
<tr>
<td>X1X2</td>
<td>1</td>
<td>8.333333</td>
<td>8.333333</td>
<td>2.13</td>
<td>0.1828</td>
</tr>
</tbody>
</table>

Parameter Estimate Error t Value Pr > |t|
Intercept 27.50000000 0.57130455 48.14 <.0001
X1 8.33333333 1.14260910 7.29 <.0001
X2 -5.00000000 1.14260910 -4.38 0.0024
X1X2 1.66666667 1.14260910 1.46 0.1828

4.2.2 The $2^3$ Design

In this subsection we consider 3-factor factorial experiments each with two levels. This setup uses a total of $2^3 = 8$ experiments that are represented as

<table>
<thead>
<tr>
<th>Treatment</th>
<th>A</th>
<th>B</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1)</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>a</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>b</td>
<td>-</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>c</td>
<td>-</td>
<td>c</td>
<td>+</td>
</tr>
</tbody>
</table>

The following table gives the contrast coefficients for calculating the effects.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>I</th>
<th>A</th>
<th>B</th>
<th>AB</th>
<th>C</th>
<th>AC</th>
<th>BC</th>
<th>ABC</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1)</td>
<td>1/4</td>
<td>-1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>-1/4</td>
</tr>
<tr>
<td>a</td>
<td>1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
</tr>
<tr>
<td>b</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
</tr>
<tr>
<td>ab</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
</tr>
<tr>
<td>c</td>
<td>1/4</td>
<td>-1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
</tr>
<tr>
<td>ac</td>
<td>1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
</tr>
<tr>
<td>bc</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
<td>1/4</td>
<td>-1/4</td>
</tr>
<tr>
<td>abc</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
</tr>
</tbody>
</table>

For example, the main effect of $A$ is

$$\frac{1}{4}[-\bar{y}(A_-B_-C_-) + \bar{y}(A_+B_-C_-) - \bar{y}(A_-B_+C_-) + \bar{y}(A_+B_+C_-)]$$

The sum of squares are

$$SS_{\text{effect}} = 2n(\text{effect})^2$$

Consider the bottling experiment in Chapter 3. With only the first two levels of factor $A$, the data is
4.2. THE $2^K$ FACTORIAL DESIGN

<table>
<thead>
<tr>
<th>Carbonation (A)</th>
<th>Pressure (B)</th>
<th>Line Speed (C)</th>
<th>Line Speed (C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>25 psi</td>
<td>200</td>
<td>200</td>
</tr>
<tr>
<td>12</td>
<td>30 psi</td>
<td>250</td>
<td>250</td>
</tr>
</tbody>
</table>

(1): -3, -1  
$c$: -1, 0  
$b$: -1, 0  
$bc$: 1, 1  

$a$: 0, 1  
$ac$: 2, 1  
$ab$: 2, 3  
$abc$: 6, 5

The SAS analysis is given below:

OPTIONS LS=80 PS=66 NODATE;
DATA BOTTLE;
INPUT A B C VOL;
CARDS;
   -1 -1 -1 -3
   -1 -1 -1 -1
   -1 -1 1 -1
   -1 1 1 1
   -1 1 -1 0
   -1 -1 -1
   -1 1 1 1
   1 1 -1 2
   1 1 1 6
   1 1 1 5
PROC GLM;
   CLASS A B C;
   MODEL VOL = A|B|C;
RUN;
QUIT;

<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>7</td>
<td>73.00000000</td>
<td>10.42857143</td>
<td>16.69</td>
<td>0.0003</td>
</tr>
<tr>
<td>Error</td>
<td>8</td>
<td>5.00000000</td>
<td>0.62500000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>15</td>
<td>78.00000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

R-Square  Coeff Var  Root MSE  VOL Mean
0.935897  79.05694  0.790569  1.000000

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
<td>36.00000000</td>
<td>36.00000000</td>
<td>57.60</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>2.25000000</td>
<td>2.25000000</td>
<td>32.40</td>
<td>0.0005</td>
</tr>
<tr>
<td>A*B</td>
<td>1</td>
<td>1.25000000</td>
<td>1.25000000</td>
<td>9.60</td>
<td>0.0022</td>
</tr>
<tr>
<td>A*C</td>
<td>1</td>
<td>0.25000000</td>
<td>0.25000000</td>
<td>0.40</td>
<td>0.5447</td>
</tr>
<tr>
<td>B*C</td>
<td>1</td>
<td>1.00000000</td>
<td>1.00000000</td>
<td>1.60</td>
<td>0.2415</td>
</tr>
<tr>
<td>A<em>B</em>C</td>
<td>1</td>
<td>1.00000000</td>
<td>1.00000000</td>
<td>1.60</td>
<td>0.2415</td>
</tr>
</tbody>
</table>

To employ multiple regression, one may consider the following coding:

$$A_+ x_1 = -0.5$$
$$A_- x_1 = 0.5$$
$$B_+ x_2 = -0.5$$
$$B_- x_2 = 0.5$$
$$C_+ x_3 = -0.5$$
$$C_- x_3 = 0.5$$
The regression model is

\[ y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_{12}(2x_1 x_2) + \beta_{13}(2x_1 x_3) + \beta_{23}(2x_2 x_3) + \beta_{123}(4x_1 x_2 x_3) + \epsilon \]

Once again, the estimate of the regression coefficients correspond to the effects of the factors. For example, \( \hat{\beta}_{12} \) is the \( AB \) interaction effect. Considering the bottling experiment, the following SAS code is an implementation the regression approach.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA BOTTLE;
INPUT A B C VOL;
X1 = A/2;
X2 = B/2;
X3 = C/2;
X1X2 = 2*X1*X2;
X1X3 = 2*X1*X3;
X2X3 = 2*X2*X3;
X1X2X3 = 4*X1*X2*X3;
CARDS;
-1 -1 -1 -3
-1 -1 -1 -1
-1 -1 1 -1
-1 -1 -1 0
-1 1 -1 0
-1 1 1 1
-1 1 1 1
1 -1 -1 0
1 -1 -1 1
1 -1 1 2
1 -1 1 1
1 1 -1 2
1 1 -1 3
1 1 1 6
1 1 1 5
;
PROC REG;
MODEL VOL = X1 X2 X3 X1X2 X1X3 X2X3 X1X2X3;
RUN;
QUIT;

Dependent Variable: VOL

Analysis of Variance

<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>7</td>
<td>73.00000</td>
<td>10.42857</td>
<td>16.69</td>
<td>0.0003</td>
</tr>
<tr>
<td>Error</td>
<td>8</td>
<td>5.00000</td>
<td>0.62500</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>15</td>
<td>78.00000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Root MSE 0.79057  R-Square 0.9359
Dependent Mean 1.00000  Adj R-Sq 0.8798
Coeff Var 79.05694

Parameter Estimates

| Variable | DF | Parameter Estimate | Standard Error | t Value | Pr > |t| |
|----------|----|--------------------|----------------|---------|-------|
| Intercept| 1  | 1.00000            | 0.19764        | 5.06    | 0.0010|
| X1       | 1  | 3.00000            | 0.39528        | 7.59    | <0.0001|
| X2       | 1  | 2.25000            | 0.39528        | 5.69    | 0.0005|
| X3       | 1  | 1.75000            | 0.39528        | 4.43    | 0.0022|
| X1X2     | 1  | 0.75000            | 0.39528        | 1.90    | 0.0943|
| X1X3     | 1  | 0.25000            | 0.39528        | 0.63    | 0.5447|
| X2X3     | 1  | 0.50000            | 0.39528        | 1.26    | 0.2415|
| X1X2X3   | 1  | 0.50000            | 0.39528        | 1.26    | 0.2415|
```
4.2. THE $2^k$ FACTORIAL DESIGN

One may obtain sums of squares using

$$SS = 2n(\text{effect})^2.$$ 

For example, in the bottling experiment,

$$SS_A = 2 \times 2 \times 3^2 = 36.$$ 

4.2.3 The General $2^k$ Design

Consider $k$ factors $F_1, \cdots, F_k$ each with 2 levels. Suppose the experiment is replicated $n$ times. There are $k = \binom{k}{1}$ main effects, $\binom{k}{2}$ two-factor interaction effects, $\binom{k}{3}$ three-factor interaction effects, \ldots, $\binom{k}{k} = 1$ $k$-factor interaction. Each main effect as well as interaction effect has one degree of freedom. Thus the sum of the degrees of freedom due to the factors (main and interaction) is

$$\sum_{i=1}^{k} \binom{k}{i} = 2^k - 1$$

and the total degrees of freedom are $2^kn - 1$. Thus we get the error degrees of freedom to be

$$(2^kn - 1) - (2^k - 1) = 2^k(n - 1).$$

The partial ANOVA table for the $2^k$ design is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
</tr>
</thead>
<tbody>
<tr>
<td>$k$ main effects</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_1$</td>
<td>1</td>
<td>$SS_{F_1}$</td>
</tr>
<tr>
<td>$F_2$</td>
<td>1</td>
<td>$SS_{F_2}$</td>
</tr>
<tr>
<td>\vdots</td>
<td></td>
<td>\vdots</td>
</tr>
<tr>
<td>$F_k$</td>
<td>1</td>
<td>$SS_{F_k}$</td>
</tr>
<tr>
<td>$\binom{k}{2}$ two-factor interactions</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_1F_2$</td>
<td>1</td>
<td>$SS_{F_1F_2}$</td>
</tr>
<tr>
<td>$F_1F_3$</td>
<td>1</td>
<td>$SS_{F_1F_3}$</td>
</tr>
<tr>
<td>\vdots</td>
<td></td>
<td>\vdots</td>
</tr>
<tr>
<td>$F_{k-1}F_k$</td>
<td>1</td>
<td>$SS_{F_{k-1}F_k}$</td>
</tr>
<tr>
<td>\vdots</td>
<td></td>
<td>\vdots</td>
</tr>
<tr>
<td>$\binom{k}{1}$ = 1 $k$-factor interaction</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_1F_2\cdots F_k$</td>
<td>1</td>
<td>$SS_{F_1F_2\cdots F_k}$</td>
</tr>
<tr>
<td>Error</td>
<td>$2^k(n - 1)$</td>
<td>$SS_E$</td>
</tr>
<tr>
<td>Total</td>
<td>$2^kn - 1$</td>
<td>$SS_T$</td>
</tr>
</tbody>
</table>

We denote the $2^k$ treatments using the standard notation, i.e.

$$(1), f_1, \cdots, f_1 \cdots f_k.$$ 

As always contrasts are of interest since they represent factor effects. We will use contrast coefficients $\pm 2^{1-k}$ to linearly combine the $2^k$ cell means. For instance, in the $2^2$ design ($k = 2$), the coefficients are $\pm 2^{1-2} = \pm 2^{-1} = \pm 1/2$. Similarly, in the $2^3$ design, the coefficients become $\pm 1/4$ as expected.

The sums of squares are now

$$SS_{\text{effect}} = n \times 2^{k-2} \times (\text{effect})^2.$$ 

We will use the regression approach to estimate the effects. We will now create $k$ variables $x_1, \cdots, x_k$ each taking values $\pm 1/2$ depending on whether the corresponding factor is at high or low level. We then fit the regression equation

$$y = \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k + \beta_{12}(2x_1x_2) + \cdots + \beta_{k-1,k}(2x_{k-1}x_k) + \cdots$$
CHAPTER 4. $2^K$ AND $3^K$ FACTORIAL DESIGNS

The multiplier is obtained as $2^{(\text{number of factors in interaction} - 1)}$.

Now the estimates, $\hat{\beta}$'s, are the effects of the corresponding factor.

4.2.4 The Unreplicated $2^k$ Design

Since the number of factor level combinations in a $2^k$ design may be large, it is often impossible to find enough subjects to replicate the design. In such a situation it is impossible to estimate the error; which in turn means that hypotheses cannot be tested. An approach is to ignore some high-order interactions, i.e. assume that interactions with three or higher factors do not exist. Another approach is to use a QQ-plot to identify the significant factors.

The following example, taken from Petersen: Design and Analysis of Experiments, illustrates these approaches.

Example

A research chemist wanted to study the effect of a number of factors on the yield of a new high-impact plastic. The plastic is produced by mixing resin with an extender in a solvent. The process takes place in a heated reaction vat. The materials are allowed to react for a period of time, and the plastic settles to the bottom of the vat, filtered on a screen, and dried.

The chemist worked in a laboratory that contained 32 experimental vats and a filter and dryer with each vat. He knew that he could run one trial per day in each vat. He decided to study five factors using a single replication of a $2^5$ design. He selected the following factors:

- $A = \text{reaction temperature} : 300^\circ C, 150^\circ C$
- $B = \text{reaction time} : 4hr, 2hr$
- $C = \text{filter pressure} : 1\text{atm}, 2\text{atm}$
- $D = \text{drying temperature} : 200^\circ C, 100^\circ C$
- $E = \text{resin/extender ratio} : 2/1, 1/1$

The following table gives the results:

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>Yield</th>
</tr>
</thead>
<tbody>
<tr>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td>246</td>
</tr>
<tr>
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<td>-1</td>
<td>-1</td>
<td>-1</td>
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<td>-1</td>
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<tr>
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<td>1</td>
<td>-1</td>
<td>-1</td>
<td>258</td>
</tr>
<tr>
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<td>-1</td>
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<td>344</td>
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<td>-1</td>
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</tr>
<tr>
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<td>-1</td>
<td>313</td>
</tr>
<tr>
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<td>-1</td>
<td>1</td>
<td>-1</td>
<td>249</td>
</tr>
<tr>
<td>1</td>
<td>-1</td>
<td>-1</td>
<td>1</td>
<td>-1</td>
<td>310</td>
</tr>
<tr>
<td>-1</td>
<td>1</td>
<td>-1</td>
<td>1</td>
<td>-1</td>
<td>318</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>-1</td>
<td>1</td>
<td>-1</td>
<td>363</td>
</tr>
<tr>
<td>-1</td>
<td>-1</td>
<td>1</td>
<td>1</td>
<td>-1</td>
<td>212</td>
</tr>
<tr>
<td>1</td>
<td>-1</td>
<td>1</td>
<td>1</td>
<td>-1</td>
<td>249</td>
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<tr>
<td>-1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>-1</td>
<td>283</td>
</tr>
<tr>
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<td>1</td>
<td>1</td>
<td>-1</td>
<td>219</td>
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<td>-1</td>
<td>379</td>
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<td>-1</td>
<td>1</td>
<td>-1</td>
<td>326</td>
</tr>
<tr>
<td>-1</td>
<td>1</td>
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<td>-1</td>
<td>1</td>
<td>344</td>
</tr>
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<td>1</td>
<td>-1</td>
<td>-1</td>
<td>1</td>
<td>349</td>
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<tr>
<td>-1</td>
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<td>1</td>
<td>389</td>
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<td>-1</td>
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<td>-1</td>
<td>1</td>
<td>359</td>
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<td>1</td>
<td>-1</td>
<td>1</td>
<td>283</td>
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<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>-1</td>
<td>1</td>
<td>363</td>
</tr>
</tbody>
</table>
4.2. THE $2^K$ FACTORIAL DESIGN

\[ y = \beta_0 + \beta_1 x_1 + \cdots + \beta_{12345}(2^4 x_1 x_2 x_3 x_4 x_5) + \epsilon \]

We save the above data as it is in a file called `chem.dat`, without the line which contains the names of the variables, and we call the file using the SAS command `infile`. The following code gives the analysis:

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA CHEM;
INFILE "C:\ASH\S7010\SAS\CHEM.DAT";
INPUT A B C D E YIELD;
RUN;
QUIT;
DATA CHEM2;
SET CHEM;
AB=A*B; AC=A*C; AD=A*D; AE=A*E;
BC=B*C; BD=B*D; BE=B*E;
CD=C*D; CE=C*E;
DE=D*E;
ABCD=A*B*C*D; ABCE=A*B*C*E; ABDE=A*B*D*E; ACDE=A*C*D*E;
BCDE = B*C*D*E;
ABCDE=A*B*C*D*E;
RUN;
QUIT;
PROC REG;
MODEL YIELD = A B C D E
AB AC AD AE BC BD BE CD CE DE
ABD ABD ABE ABD ACD ACE ACD ADE ADE BCDE ACDE BCDE
ABCD ABCE ABDE ACDE BCDE
ABCD;
RUN;
QUIT;
```

The SAS System

The REG Procedure
Model: MODEL1
Dependent Variable: YIELD

Analysis of Variance

<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>
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<tbody>
<tr>
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<td>2380.86694</td>
<td>.</td>
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</tr>
<tr>
<td>Error</td>
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<td>0</td>
<td>.</td>
<td>.</td>
<td>.</td>
</tr>
</tbody>
</table>
CHAPTER 4. $2^K$ AND $3^K$ FACTORIAL DESIGNS

Corrected Total 31 73807

| Variable | DF | Parameter Estimate | Standard Error | t Value | Pr > |t| |
|----------|----|--------------------|----------------|---------|-------|---|
| Intercept| 1  | 315.81250          |                |         |       |   |
| A        | 1  | 11.18750           |                |         |       |   |
| B        | 1  | 6.62500            |                |         |       |   |
| C        | 1  | -6.31250           |                |         |       |   |
| D        | 1  | -5.00000           |                |         |       |   |
| E        | 1  | 31.81250           |                |         |       |   |
| AB       | 1  | -2.00000           |                |         |       |   |
| AC       | 1  | 0.93750            |                |         |       |   |
| AD       | 1  | -4.62500           |                |         |       |   |
| AE       | 1  | -9.43750           |                |         |       |   |
| BC       | 1  | -7.75000           |                |         |       |   |
| BD       | 1  | 11.31250           |                |         |       |   |
| BE       | 1  | -6.00000           |                |         |       |   |
| CD       | 1  | -7.25000           |                |         |       |   |
| CE       | 1  | 9.81250            |                |         |       |   |
| DE       | 1  | 3.62500            |                |         |       |   |
| ABC      | 1  | -1.25000           |                |         |       |   |
| ABD      | 1  | -10.31250          |                |         |       |   |
| ABE      | 1  | 7.50000            |                |         |       |   |
| ACD      | 1  | -6.25000           |                |         |       |   |
| ACE      | 1  | 8.18750            |                |         |       |   |
| ADE      | 1  | 6.12500            |                |         |       |   |
| BCD      | 1  | 3.31250            |                |         |       |   |
| BCE      | 1  | 2.75000            |                |         |       |   |
| BDE      | 1  | 3.56250            |                |         |       |   |
| CDE      | 1  | 11.25000           |                |         |       |   |
| ABCD     | 1  | -1.93750           |                |         |       |   |
| ABCE     | 1  | 6.62500            |                |         |       |   |
| ABDE     | 1  | -5.18750           |                |         |       |   |
| ACDE     | 1  | 3.12500            |                |         |       |   |
| BCDE     | 1  | 2.93750            |                |         |       |   |
| ABCDE    | 1  | 0.81250            |                |         |       |   |

The estimates of the effects are now the parameter estimate multiplied by 2. For instance, the ABE effect is $2 \times 7.5 = 15$. 
4.2. THE $2^K$ FACTORIAL DESIGN

We will now analyze the data ignoring 3 and higher factor interactions. The following partial SAS code follows the one given above.

```
PROC GLM;
CLASS A B C D E AB AC AD AE BC BD BE CD CE DE;
MODEL YIELD = A B C D E AB AC AD AE BC BD BE CD CE DE;
RUN;
QUIT;
```

The following partial SAS code that provides the QQ-plot of the effects in the full model in an effort to identify the important factors.

```
PROC REG OUTEST=EFFECTS;
MODEL YIELD = A B C D E AB AC AD AE BC BD BE CD CE DE ABC ABD ABE ACD ACE ADE BCD BCE BDE CDE ABCDE;
RUN;
QUIT;
```

The only significant factor appears to be resin/extender ratio.

Let us now plot the QQ-plot of the effects in the full model in an effort to identify the important factors. The following SAS code that provides the QQ-plot continues the above:

```
PROC REG OUTTEST=EFFECTS;
MODEL YIELD = A B C D E AB AC AD AE BC BD BE CD CE DE ABC ABD ABE ACD ACE ADE BCD BCE BDE CDE ABCDE;
RUN;
QUIT;
```

```
DATA EFFECTS;
SET EFFECTS;
DROP YIELD INTERCEPT _RMSE_;
RUN;
```
QUIT;

PROC TRANSPOSE DATA=EFFECTS OUT=EFFECTS;
RUN;
QUIT;

DATA EFFECTS;
  SET EFFECTS;
  EFFECT = COL1*2;
  DROP COL1;
RUN;
QUIT;

PROC SORT DATA=EFFECTS;
  BY EFFECT;
RUN;
QUIT;

PROC RANK DATA=EFFECTS NORMAL=BLOM;
  VAR EFFECT;
  RANKS RANKEFF;
RUN;
QUIT;

GOPTION COLORS=(NONE);
SYMBOL V=CIRCLE;

PROC GPLOT;
  PLOT RANKEFF*EFFECT=_NAME_;
RUN;
QUIT;
4.2. THE $2^k$ FACTORIAL DESIGN
Once again the only variable that appears to be significant is resin/extender ratio. The following example is taken from Montgomery : Design and Analysis of Experiments.

Example

A chemical product is produced in a pressure vessel. A factorial experiment was conducted in the pilot plant to study the factors thought to influence the filtration rate of this product. The four factors are temperature (A), pressure (B), reactant concentration (C), and stirring rate (D). The data are given below:

<table>
<thead>
<tr>
<th></th>
<th>B0</th>
<th>C0</th>
<th>C1</th>
<th>B1</th>
<th>A0</th>
<th>C0</th>
<th>C1</th>
<th>A1</th>
</tr>
</thead>
<tbody>
<tr>
<td>D0</td>
<td>45</td>
<td>48</td>
<td>80</td>
<td>71</td>
<td>65</td>
<td>60</td>
<td>86</td>
<td>104</td>
</tr>
<tr>
<td>D1</td>
<td>43</td>
<td>75</td>
<td>45</td>
<td>100</td>
<td>65</td>
<td>60</td>
<td>104</td>
<td>96</td>
</tr>
</tbody>
</table>

This is an unreplicated $2^4$ design. We start by drawing the QQ plot of the effects to identify the potentially significant factors.
4.2. THE $2^K$ FACTORIAL DESIGN

\begin{verbatim}
EFFECT = COL1*2;
DROP COL1;
RUN;
QUIT;

PROC SORT DATA=EFFECTS;
   BY EFFECT;
RUN;
QUIT;

PROC RANK DATA=EFFECTS NORMAL=BLOM;
   VAR EFFECT;
   RANKS RANKEFF;
RUN;
QUIT;

GOPTION COLORS=(NONE);
SYMBOL V=CIRCLE;

PROC GPLOT;
   PLOT RANKEFF*EFFECT=_NAME_;
RUN;
QUIT;
\end{verbatim}
4.3 THE $3^k$ DESIGN

The QQ-plot identifies $A, C, D, AC, AD$ as significant. Thus, ignoring factor $B$ and any interactions involving factor $B$ we run the analysis. This means the resulting analysis is a $2^3$ design with factors $A, C, D$ and 2 replications. The following partial SAS code performs the analysis.

```
PROC GLM DATA=FILTER;
    CLASS A C D;
    MODEL Y = A|C|D;
RUN;
QUIT;
```

Dependent Variable: Y

<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>
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<td>5551.437500</td>
<td>793.062500</td>
<td>35.35</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>8</td>
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<td>22.437500</td>
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<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>15</td>
<td>5730.937500</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Source | DF | Type I SS | Mean Square | F Value | Pr > F |
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<th></th>
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<th></th>
<th></th>
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</thead>
<tbody>
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<td>83.37</td>
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</tr>
<tr>
<td>C</td>
<td>1</td>
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<td>390.062500</td>
<td>17.38</td>
<td>0.0031</td>
</tr>
<tr>
<td>A*C</td>
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<td>1314.062500</td>
<td>58.57</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>D</td>
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<td>855.562500</td>
<td>855.562500</td>
<td>38.13</td>
<td>0.0003</td>
</tr>
<tr>
<td>A*D</td>
<td>1</td>
<td>1105.562500</td>
<td>1105.562500</td>
<td>49.27</td>
<td>0.0001</td>
</tr>
<tr>
<td>C*D</td>
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<td>5.062500</td>
<td>5.062500</td>
<td>0.23</td>
<td>0.6475</td>
</tr>
<tr>
<td>A<em>C</em>D</td>
<td>1</td>
<td>10.562500</td>
<td>10.562500</td>
<td>0.47</td>
<td>0.5120</td>
</tr>
</tbody>
</table>

4.3 The $3^k$ Design

We now consider the analysis of a $k$-factor factorial design where each factor has 3 levels: 0 (low), 1 (intermediate), and 2 (high). We now have $3^k$ treatments which we denote by $k$ digit combinations of 0, 1, and 2 instead of the standard notation (1), a, b, ab, . . . . For example, for a $3^2$ design the treatments are 00, 10, 20, 01, 11, 21, 02, 12, 22. The treatment 01, for instance, is the combination of the low level of factor $A$ and the intermediate level of factor $B$. Computations of effects and sums of squares are direct extensions of the $2^k$ case.

The ANOVA table for a $3^k$ design with $n$ replications is
## CHAPTER 4. $2^K$ AND $3^K$ FACTORIAL DESIGNS

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
</tr>
</thead>
<tbody>
<tr>
<td>$k$ main effects</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_1$</td>
<td>2</td>
<td>$SS_{F_1}$</td>
</tr>
<tr>
<td>$F_2$</td>
<td>2</td>
<td>$SS_{F_2}$</td>
</tr>
<tr>
<td>$\vdots$</td>
<td>$\vdots$</td>
<td>$\vdots$</td>
</tr>
<tr>
<td>$F_k$</td>
<td>2</td>
<td>$SS_{F_k}$</td>
</tr>
<tr>
<td>$(^2)$ two-factor interactions</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_1F_2$</td>
<td>4</td>
<td>$SS_{F_1F_2}$</td>
</tr>
<tr>
<td>$F_1F_3$</td>
<td>4</td>
<td>$SS_{F_1F_3}$</td>
</tr>
<tr>
<td>$\vdots$</td>
<td>$\vdots$</td>
<td>$\vdots$</td>
</tr>
<tr>
<td>$F_{k-1}F_k$</td>
<td>4</td>
<td>$SS_{F_{k-1}F_k}$</td>
</tr>
<tr>
<td>$(^3)$ three-factor interactions</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_1F_2F_3$</td>
<td>8</td>
<td>$SS_{F_1F_2F_3}$</td>
</tr>
<tr>
<td>$F_1F_2F_4$</td>
<td>8</td>
<td>$SS_{F_1F_2F_4}$</td>
</tr>
<tr>
<td>$\vdots$</td>
<td>$\vdots$</td>
<td>$\vdots$</td>
</tr>
<tr>
<td>$F_{k-2}F_{k-1}F_k$</td>
<td>8</td>
<td>$SS_{F_{k-2}F_{k-1}F_k}$</td>
</tr>
<tr>
<td>$\vdots$</td>
<td>$\vdots$</td>
<td>$\vdots$</td>
</tr>
<tr>
<td>$(^1) = 1$ $k$-factor interaction</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$F_1F_2\cdots F_k$</td>
<td>$2^k$</td>
<td>$SS_{F_1F_2\cdots F_k}$</td>
</tr>
<tr>
<td>Error</td>
<td>$3^k(n-1)$</td>
<td>$SS_E$</td>
</tr>
<tr>
<td>Total</td>
<td>$3^k n - 1$</td>
<td>$SS_T$</td>
</tr>
</tbody>
</table>
Chapter 5

Repeated Measurement Designs

5.1 Introduction

Sometimes we take observations repeatedly on the same experimental subjects under several treatments. Such observations are rarely independent as they are measured on the same subject. These designs are extensions of the randomized complete block design where blocks are random.

5.1.1 The Mixed RCBD

Consider a single factor experiment with \( a \) levels of the factor, say \( A \). Suppose we have a blocking variable \( B \) that is random. This situation is sometimes referred to as the one-way repeated measurement design.

We assume that a random sample of \( b \) blocks (subjects) is available from a large population of blocks (subjects). Each of the \( a \) levels of factor \( A \) is observed with each subject. Let \( y_{ij} \) be the observation on level \( i \) of \( A \) for the \( j \)th subject.

The statistical model for the mixed randomized complete block design is

\[
y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}, \quad \begin{cases} i = 1, \ldots, a \\ j = 1, \ldots, b \end{cases}
\]

where

- \( \sum_{i=1}^{a} \tau_i = 0 \),
- \( \beta_1, \ldots, \beta_b \) is a random sample from a \( N(0, \sigma^2) \) distribution,
- \( \epsilon_{ij} \) are iid \( N(0, \sigma^2) \) random variables, and
- all the \( b + ab \) random variables (blocks and errors) are independent.

Under these conditions, one obtains

\[
\text{Var}(y_{ij}) = \sigma^2 + \sigma_B^2
\]

and

\[
\text{Cov}(y_{ij}, y_{i'j}) = \sigma_B^2, \quad \text{for } i \neq i'.
\]

Thus,

\[
\rho = \frac{\sigma_B^2}{\sigma^2 + \sigma_B^2}
\]

is the common correlation of measurements made on the same subject for any pair of distinct treatment \( A \) levels, \( i \) and \( i' \). All variances of observations are equal within a block and all covariances within a block are equal. The variance-covariance matrix of observations on each subject \( y'_j = (y_{1j}, \ldots, y_{aj}) \) is
CHAPTER 5. REPEATED MEASUREMENT DESIGNS

\[ \Sigma = \begin{bmatrix} \sigma_{11} & \sigma_{12} & \cdots & \sigma_{1a} \\ \sigma_{21} & \sigma_{22} & \cdots & \sigma_{2a} \\ \vdots & \vdots & \ddots & \vdots \\ \sigma_{a1} & \sigma_{a2} & \cdots & \sigma_{aa} \end{bmatrix} \]

Under the assumptions of the mixed RCBD \( \Sigma \) satisfies \textit{compound symmetry}. Compound symmetry (CS) is the case where all variances are equal and all covariances are equal:

\[ \Sigma = \begin{bmatrix} \sigma_y^2 & \rho \sigma_y^2 & \cdots & \rho \sigma_y^2 \\ \rho \sigma_y^2 & \sigma_y^2 & \cdots & \rho \sigma_y^2 \\ \vdots & \vdots & \ddots & \vdots \\ \rho \sigma_y^2 & \rho \sigma_y^2 & \cdots & \sigma_y^2 \end{bmatrix} \]

where \( \sigma_y^2 = \sigma^2 + \sigma_\beta^2 \).

\textbf{\( \alpha \)-level Tests}

Recalling the situation in the mixed two factor analysis, we have

1. An \( \alpha \)-level test of \( H_0: \tau_1 = \cdots = \tau_a = 0 \) is

\[ \frac{MS_A}{MS_{AB}} > F_{a-1, (a-1)(b-1)}(\alpha) \]

2. An \( \alpha \)-level test of \( H_0: \tau_i = \tau_{i'} \) is

\[ \frac{|\bar{y}_i - \bar{y}_{i'}|}{\sqrt{2MS_{AB}}} > t_{(a-1)(b-1)}(\alpha/2) \]

3. An \( \alpha \)-level simultaneous Tukey-Kramer test of \( H_0: \tau_i = \tau_{i'} \) for \( 1 \leq i < i' \leq a \) is

\[ \frac{|\bar{y}_i - \bar{y}_{i'}|}{\sqrt{2MS_{AB}}} > \frac{q_{a,(a-1)(b-1)}(\alpha)}{\sqrt{2}} \]

4. An \( \alpha \)-level simultaneous Dunnett test of \( H_0: \tau_i = \tau_1 \) for \( 2 \leq i \leq a \), where level 1 of \( a \) is control, is

\[ \frac{|\bar{y}_i - \bar{y}_1|}{\sqrt{2MS_{AB}}} > d_{a-1,(a-1)(b-1)}(\alpha) \]

5. An \( \alpha \)-level test of \( H_0: \sigma_\beta^2 = 0 \) is

\[ \frac{MS_B}{MS_{AB}} > F_{b-1, (a-1)(b-1)}(\alpha) \]

It can be shown that these tests remain valid for a more general variance-covariance, \( \Sigma \), structure called the Huynh-Feldt sphericity (S) structure. RCBD’s that satisfy the (S) condition are known as one-way repeated measurement (RM) designs. It is recommended that all mixed RCBD’s be analyzed as one-way RM designs since we can test for the (S) condition in a similar manner as Levene’s test.
5.2 One-Way Repeated Measurement Designs

The major difference between the mixed RCBD and the one-way RM design is in the conceptualization of a 'block'. In many cases the 'block' is a human or an animal and all the $a$ levels of $A$ are observed on the same subject. The $a$ levels of $A$ may be $a$ different drugs, or $a$ different dosages of the same drug, or measurements of the same drug at the same dosage level over a period of $a$ times, say $t_1, \cdots, t_a$. In all these cases the drug (dosage) mean responses are to be compared for these $a$ levels. That is, a test of

$$H_0 : \tau_1 = \cdots = \tau_a = 0$$

is needed.

Usually, the subjects are assumed to be randomly selected from a population of subjects. Hence, the subject factor ($B$) will be considered random in RM designs.

The major difference between mixed RCBD’s and RM designs is that in RM designs the levels of factor $A$ cannot be observed simultaneously. The following example illustrates a typical RM design.

**Example**

Suppose three drugs $D_1, D_2,$ and $D_3$ are to be compared with respect to suppression of enzyme $X$, which is produced and secreted by the liver. Assume each of $n = 6$ subjects is to be observed with each of the three drugs.

Subject 1 takes the drugs in the order $D_1, D_2, D_3$. It is assumed that $D_1$ is administered and then enzyme $X$ measured ($y_{11}$). After the effect of $D_1$ is worn-off, $D_2$ is administered and enzyme $X$ measured, etc. Note that $y_{11}, y_{21}, y_{31}$ for subject 1 cannot be obtained simultaneously.

This raises another issue to be considered and controlled in RM designs. This is the *order effect*. If all the six subjects are treated with $D_1$ followed by $D_2$ followed by $D_3$, then how can one distinguish observed differences between $D_1, D_2,$ and $D_3$ from the fact that the drugs were given in the order $(D_1, D_2, D_3)$? Are these differences due to true differences between the drugs or the order in which they are observed?

In RM designs, it is important to control the possible order effects. In the above example, this may be done as follows.

Consider three orders: $(D_1, D_2, D_3), (D_2, D_3, D_1), (D_3, D_1, D_2)$ and randomly assign two subjects to each order. The following table is one possible randomization:

<table>
<thead>
<tr>
<th>subject</th>
<th>order</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>$D_1$</td>
</tr>
<tr>
<td>2</td>
<td>$D_2$</td>
</tr>
<tr>
<td>3</td>
<td>$D_1$</td>
</tr>
<tr>
<td>4</td>
<td>$D_3$</td>
</tr>
<tr>
<td>5</td>
<td>$D_3$</td>
</tr>
<tr>
<td>6</td>
<td>$D_2$</td>
</tr>
</tbody>
</table>

Note that each drug is observed first by two subjects, second by two subjects, and third by two subjects.

In certain RM designs the order effect is impossible to eliminate. For example, let $t_1 < t_2 < \cdots < t_a$ be $a$ times and let $\tau_i$ be the effect of the drug $D$ at time $t_i$. Assume the drug, $D$, is given to all subjects at the same dosage level. The following is an example for $a = 4$: 
### 5.2.1 The Huynh-Feldt Sphericity (S) Structure

The Huynh-Feldt sphericity structure is given by

\[
\sigma_{ii'} = \begin{cases} 
2\gamma_i + \delta & \text{if } i = i' \\
\gamma_i + \gamma_{i'} & \text{if } i \neq i' 
\end{cases}
\]

Of course, for \(j \neq j', \text{Cov}(y_{ij}, y_{ij'}) = 0\), i.e. observations taken on different subjects are independent. The (S) structure implies the following (prove!):

1. All pairwise comparisons of treatments have the same variance
   \[\text{Var}(\bar{y}_i - \bar{y}_{i'}) = \frac{2\delta}{b}.\]

2. The variance of any sample contrast \(\hat{\phi} = \sum_{i=1}^a c_i \bar{y}_i\), \(\sum c_i = 0\), is free of \(\gamma_1, \ldots, \gamma_a\). It is given by
   \[\text{Var}(\hat{\phi}) = \frac{\delta}{b} \sum_{i=1}^a c_i^2.\]

3. The covariance between any two contrasts, \(\hat{\phi}_c = \sum_{i=1}^a c_i \bar{y}_i\) and \(\hat{\phi}_d = \sum_{i=1}^a d_i \bar{y}_i\), say, is free of \(\gamma_1, \ldots, \gamma_a\). It is given by
   \[\text{Cov}(\hat{\phi}_c, \hat{\phi}_d) = \frac{\delta}{b} \sum_{i=1}^a c_id_i.\]

### 5.2.2 The One-Way RM Design : (S) Structure

The statistical model for the one way RM design under the (S) structure is

\[y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}\]

where

- \(\sum_{i=1}^a \tau_i = 0\),
- the \(b\) subjects are a random sample from a population of subjects following a normal distribution with...
5.2. ONE-WAY REPEATED MEASUREMENT DESIGNS

1. \( E(y_{ij}) = \mu + \tau_i \)
2. The variance-covariance matrix of the observations on the same subject, \( y_j' = (y_{1j}, \ldots, y_{aj}) \), satisfies the (S) condition.

Under the one-way RM model where \( \Sigma \) satisfies the (S) condition we have

1. an \( \alpha \)-level test of \( H_0 : \tau_1 = \cdots = \tau_a = 0 \) is
   \[
   MS_A/MS_{AB} > F_{a-1,(a-1)(b-1)}(\alpha) ;
   \]
2. an \( \alpha \)-level test of \( H_0 : \tau_i = \tau_{i'} \) is
   \[
   \frac{|\bar{y}_i - \bar{y}_{i'}|}{\sqrt{2MS_{AB}/b}} > t_{(a-1)(b-1)}(\alpha/2) ;
   \]
3. a set of \( (1-\alpha)100\% \) Tukey-Kramer confidence intervals for all \( \binom{a}{2} \) pairwise comparisons \( \tau_i - \tau_{i'} \) is
   \[
   (\bar{y}_i - \bar{y}_{i'}) \pm q_{a-1,(a-1)(b-1)}(\alpha) \sqrt{MS_{AB}/b} ,
   \]
i.e. a test of \( H_0 : \tau_i = \tau_{i'} \) at MEER=\( \alpha \) is
   \[
   \frac{|\bar{y}_i - \bar{y}_{i'}|}{\sqrt{2MS_{AB}/b}} > q_{a-1,(a-1)(b-1)}(\alpha) \sqrt{2} ;
   \]
and
4. a set of \( (1-\alpha)100\% \) Dunnet confidence intervals for all \( a-1 \) comparisons \( \tau_i - \tau_1 \) (treatments versus control) is
   \[
   (\bar{y}_i - \bar{y}_1) \pm d_{a-1,(a-1)(b-1)}(\alpha) \sqrt{2MS_{AB}/b} ,
   \]
i.e. a test of \( H_0 : \tau_i = \tau_1 \) at MEER=\( \alpha \) is
   \[
   \frac{|\bar{y}_i - \bar{y}_1|}{\sqrt{2MS_{AB}/b}} > d_{a-1,(a-1)(b-1)}(\alpha) .
   \]

These results depend on the (S) condition. Actually, in the one-way RM design, for all the tests to hold a necessary and sufficient condition is that \( \Sigma \) satisfies the (S) condition. For the proof of this, please see


The following example is taken from Mike Stoline’s class notes.

Example
In a pre-clinical trial pilot study \( b = 6 \) dogs are randomly selected and each dog is given a standard dosage of each of 4 drugs \( D_1, D_2, D_3, \) and \( D_4 \). These drugs are compounds that are chemically quite similar and each is hypothesized to be effective in the stabilization of the heart function. Four measures of the stabilization of the heart function are obtained for each dog for each drug type, assuming the effect of previously-administered drugs have worn off. These measures are differences between rates measured immediately prior the injection of the drug and rates measured one hour after injection in all cases. The order effect was partially removed by selecting one of the four drug orders below for each dog:
The data are (a large entry indicates high stabilization of heart-rate)

The following SAS code is used to perform the ANOVA $F$-test as well as follow-up Tukey-Kramer analysis.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA RM1;
INPUT DOG DRUG Y @@;
CARDS;
1 1 2.6 1 2 4.6 1 3 5.2 1 4 4.2
2 1 3.9 2 2 5.1 2 3 6.3 2 4 5.0
3 1 4.2 3 2 5.8 3 3 7.1 3 4 5.8
4 1 2.4 4 2 3.9 4 3 5.1 4 4 4.0
5 1 3.3 5 2 5.2 5 3 6.3 5 4 3.8
6 1 3.9 6 2 5.6 6 3 5.2 6 4 4.5
;
PROC GLM;
CLASS DRUG DOG;
MODEL Y=DRUG DOG;
LSMEANS DRUG/PDIFF ADJUST=TUKEY;
RUN;
QUIT;
```

---

**Sum of Squares**

<table>
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<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>
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<td>3.52520833</td>
<td>22.71</td>
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<tr>
<td>Error</td>
<td>15</td>
<td>2.32791667</td>
<td>0.15519444</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>23</td>
<td>30.52958333</td>
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</table>

**Model Type III SS**

<table>
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<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>3</td>
<td>19.30458333</td>
<td>6.43486111</td>
<td>41.46</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>DOG</td>
<td>5</td>
<td>8.89708333</td>
<td>1.77941667</td>
<td>11.47</td>
<td>0.0001</td>
</tr>
</tbody>
</table>

Adjustment for Multiple Comparisons: Tukey

<table>
<thead>
<tr>
<th>DRUG</th>
<th>Y LSMEAN Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3.38333333</td>
</tr>
<tr>
<td>2</td>
<td>5.01666667</td>
</tr>
<tr>
<td>3</td>
<td>5.86666667</td>
</tr>
<tr>
<td>4</td>
<td>4.55000000</td>
</tr>
</tbody>
</table>

Least Squares Means for effect DRUG

Pr > |t| for HO: LSMean(i)=LSMean(j)

Dependent Variable: Y
Thus, there is a significant difference among the four drugs ($F = 41.46$, $p$-value < .0001). From the Tukey-Kramer procedure, we get the following:

- Drug 3 is superior to all other drugs.
- Drug 1 is inferior to the other drugs.
- Drugs 2 and 4 are the same.

5.2.3 One-way RM Design: General

An estimate of the departure of $\Sigma$ from the (S) structure is

$$ e = \frac{a^2(\bar{\sigma} - \bar{\sigma}_j)^2}{(a - 1)\left[\sum \sum \sigma_{ij}^2 - 2a \sum \sigma_{j}^2 + a^2 \bar{\sigma}^2\right]} $$

where

- $\bar{\sigma}$ is the mean of all $a^2$ entries of $\Sigma$.
- $\bar{\sigma}_j$ is the mean of row $j$ entries of $\Sigma$.
- $\bar{\sigma}_j$ is the mean of the diagonal entries of $\Sigma$.

The value of $e$ satisfies $1/(a - 1) \leq e \leq 1.0$. The (S) condition is satisfied if and only if $e = 1.0$. The question now is "How can it be determined whether $\Sigma$ satisfies (S), i.e. $e = 1$?" The answer to this question is the Huynh-Feldt modification of the Mauchly (1940) test for sphericity.

Whenever the (S) condition is not met we use the Greenhouse-Geisser (G-G) $e$-adjusted test of

$$ H_0 : \tau_1 = \cdots = \tau_a = 0 $$

given by

$$ \frac{MS_A}{MS_{AB}} > F_{(a-1)e, (a-1)(b-1)e}(\alpha) \cdot $$

The G-G $e$-adjusted test reduces to the usual $F$-test if $\hat{e} = 1$. Hence, in this class, we will always use the G-G $e$-adjusted test regardless of the result of Mauchly’s test.

Example

We will reconsider the dogs’ heart-rate example once more. The following SAS code produces Mauchly’s test as well as the G-G $e$-adjusted $F$-test.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA RM2;
INPUT D1 D2 D3 D4;
CARDS:
2.6 4.6 5.2 4.2
3.9 5.1 6.3 5.0
4.2 5.8 7.1 5.8
2.4 3.9 5.1 4.0
3.3 5.2 6.3 3.8
3.9 5.5 5.2 4.5;
PROC GLM;
MODEL D1-D4 = /NOUNI;
```

CHAPTER 5. REPEATED MEASUREMENT DESIGNS

```sas
REPEATED DRUG/PRINTE NOH;
RUN;
QUIT;
```

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 Variates</td>
<td>5</td>
<td>0.1627138</td>
<td>6.7586721</td>
<td>0.2392</td>
</tr>
<tr>
<td>Orthogonal Components</td>
<td>5</td>
<td>0.426476</td>
<td>3.1720748</td>
<td>0.6735</td>
</tr>
</tbody>
</table>

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>
</tr>
</thead>
<tbody>
<tr>
<td>DRUG</td>
<td>3</td>
<td>19.30458333</td>
<td>6.43486111</td>
<td>41.46</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error(DRUG)</td>
<td>15</td>
<td>2.32791667</td>
<td>0.15519444</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Greenhouse-Geisser Epsilon 0.7576
Huynh-Feldt Epsilon 1.4225

Thus the test for \( H_0 : e = 1 \) is not rejected using Mauchly's criterion (\( p \)-value = 0.6735). The G-G estimate of \( e \) is \( \hat{e} = 0.7576 \). The G-G \( e \)-adjusted test for \( H_0 : \tau_1 = \tau_3 = \tau_4 = 0 \) is rejected with \( p \)-value < .0001.

Follow-up \( t \)-tests may be performed without assuming equality of variances. This is done using \textit{PROC MEANS} in SAS to get pairwise \( t \)-test statistics.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA RM2;
INPUT D1 D2 D3 D4;
D12 = D2-D1;
D13 = D3-D1;
D14 = D4-D1;
D23 = D3-D2;
D24 = D4-D2;
D34 = D4-D3;
CARDS;
   2.6 4.6 5.2 4.2
   3.9 5.1 6.3 5.0
   4.2 5.8 7.1 5.8
   2.4 3.9 5.1 4.0
   3.3 5.2 6.3 3.8
   3.9 5.5 5.2 4.5
;
PROC MEANS N MEAN STDERR T PRT;
VAR D12 D13 D14 D23 D24 D34;
RUN;
QUIT;
```

The MEANS Procedure

| Variable | N | Mean     | Std Error | t Value | Pr > |t| |
|----------|---|----------|-----------|---------|------|----|
| D12      | 6 | 1.6333333| 0.1173788 | 13.92   | <.0001 |
| D13      | 6 | 2.4833333| 0.2522124 | 9.85    | 0.0002 |
| D14      | 6 | 1.1666667| 0.2108185 | 5.63    | 0.0026 |
| D23      | 6 | 0.8500000| 0.2513298 | 3.38    | 0.0196 |
| D24      | 6 | -0.4666667| 0.2472066 | -1.69   | 0.1177 |
Once again the only drugs that are not significantly different are $D_2$ and $D_4$.

## 5.3 Two-Way Repeated Measurement Designs

In this section we will consider the two-way RM model with repeated measures on one factor. We will define the model for the general unbalanced case but we will confine our attention to the balanced case as it is the most common design. Let $A$ be the between-subject factor with $a$ fixed levels and $B$ be the within-subject (repeated) factor with $b$ levels. A random sample of $n_i$ subjects are selected and assigned to the $i$th level of $A$. The $b$ levels of $B$ are observed for each subject in each $A$ group. This is known as the classic two-way RM design.

The layout for the classic two-way RM design looks like the following:

<table>
<thead>
<tr>
<th>Groups $(A)$</th>
<th>Treatments $(B)$</th>
<th>Group Means</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_1$</td>
<td>$y_{11}$</td>
<td>$y_{1b}$</td>
</tr>
<tr>
<td>$S_{n_1}$</td>
<td>$y_{11n_1}$</td>
<td>$y_{1bn_1}$</td>
</tr>
<tr>
<td>$S_2$</td>
<td>$y_{21}$</td>
<td>$y_{2b}$</td>
</tr>
<tr>
<td>$S_{n_2}$</td>
<td>$y_{21n_2}$</td>
<td>$y_{2bn_2}$</td>
</tr>
</tbody>
</table>

This is a very widely used design. Between group comparisons involve distinct subjects and hence are similar to such comparisons in the single factor CRD model. Within treatment comparisons involve the same subjects and are analyzed similarly to the one-way RM design.

Sometimes it is important to consider an unbalanced case. For instance, suppose the groups are 3 clinics serving different subjects in different cities. Suppose that two of the three clinics serve cities that are medium-sized while the third clinic is serving a large metropolitan population. Suppose that the third clinic services a population that is four times as large as the other two. The recommended sample sizes are: $n_1 = n_2 = n$ and $n_3 = 4n$.

The classic two-way RM model is

\[
y_{ijk} = \mu + \tau_i + \beta_j + (\tau \beta)_{ij} + \pi_{k(i)} + (\beta \pi)_{jk(i)} + \epsilon_{ijk},
\]

where

- $\tau_i$ is the $i$th group effect ($\sum_i \tau_i = 0$)
- $\beta_j$ is the $j$th treatment effect ($\sum_j \beta_j = 0$)
• \((\tau\beta)_{ij}\) is the interaction of the \(i\)th group and the \(j\)th treatment \(\sum_i(\tau\beta)_{ij} = \sum_j(\tau\beta)_{ij} = 0\)

• \(\pi_{k(i)}\) is the random effect of subject \(k\) nested within group \(i\). The \(N = \sum_{i=1}^a n_i\) \(\pi_{k(i)}\) random variables are assumed to follow a \(N(0, \sigma^2_\pi)\) distribution.

• \((\beta\pi)_{jk(i)}\) is the random joint interaction effect of subject \(k\) and treatment \(j\) nested within group \(i\). \((\beta\pi)\)'s are assumed to satisfy
  
  1. \((\beta\pi)_{jk(i)}\) follows a \(N(0, \frac{b-1}{b} \sigma^2_\beta)\).
  2. \(\text{Cov}((\beta\pi)_{jk(i)}, (\beta\pi)_{j'k(i)}) = -\frac{\sigma^2_\beta}{b}\) for \(j \neq j'\).
  3. \(\text{Cov}((\beta\pi)_{jk(i)}, (\beta\pi)_{j'k'(i')}) = 0\) if \(k \neq k'\) or \(i \neq i'\).

• \(\epsilon_{ijk}\) is a random error term which is assumed to follow a \(N(0, \sigma^2)\) distribution.

• The \(\pi_{k(i)}, (\beta\pi)_{jk(i)},\) and \(\epsilon_{ijk}\) are mutually independent.

Note that the variables \((\beta\pi)_{jk(i)}\) have a (CS) structure similar to the (CS) structure of \((\tau\beta)_{ij}\) in the mixed two factor model:

\[ y_{ijk} = \mu + \tau_i + \beta_j + (\tau\beta)_{ij} + \epsilon_{ijk} \]

where \(\tau_i\) is fixed and \(\beta_j\) is random. In this model we have

\[ \text{Var}((\tau\beta)_{ij}) = \frac{a-1}{a} \sigma^2_\tau\beta \quad \text{and} \quad \text{Cov}((\tau\beta)_{ij}, (\tau\beta)_{i'j'}) = -\frac{\sigma^2_\tau\beta}{a}. \]

Let \(N = \sum_{i=1}^a n_i\), \(df_1 = N - a\), and \(df_2 = (N - a)(b - 1)\). Further, let

\[ MS_1 = \sum_{i=1}^a \sum_{k=1}^{n_i} \frac{b(y_{ik} - \bar{y}_{..})^2}{df_1} \]

and

\[ MS_2 = \sum_{i=1}^a \sum_{j=1}^b \sum_{k=1}^{n_i} \frac{(y_{ijk} - \bar{y}_{ik} - \bar{y}_{i.} + \bar{y}_{..})^2}{df_2}. \]

The ANOVA table for the classic two-way RM design is

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>df</th>
<th>MS</th>
<th>E(MS)</th>
<th>(F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between Subjects</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(A)</td>
<td>(N - 1)</td>
<td>(a - 1)</td>
<td>(MS_A)</td>
<td>(MS_A/MS_1)</td>
</tr>
<tr>
<td>Subjects within groups</td>
<td>(df_1)</td>
<td>(MS_1)</td>
<td>(\frac{\sigma^2 + b\sigma^2_\pi + \frac{b\sum_{i=1}^a n_i r^2}{a-1}}{\sum_{i=1}^a n_i r^2})</td>
<td></td>
</tr>
<tr>
<td>Within Subjects</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(B)</td>
<td>(b - 1)</td>
<td>(MS_B)</td>
<td>(\frac{\sigma^2 + b^2_\beta + \frac{N\sum_{i=1}^a \sigma^2_\beta}{b^2}}{\sum_{i=1}^a \frac{b-1}{b} \sum_{k=1}^{n_i} r^2_{ik}\sum_{j=1}^b n_{ik}(\tau\beta)_{ij}^2}{(a-1)(b-1)})</td>
<td>(MS_B/MS_2)</td>
</tr>
<tr>
<td>(AB)</td>
<td>((a - 1)(b - 1))</td>
<td>(MS_{AB})</td>
<td>(\frac{\sigma^2 + \frac{b^2_\beta}{a} + \frac{\sum_{i=1}^a \sigma^2_\beta}{b^2}}{\sum_{i=1}^a \frac{b-1}{b} \sum_{k=1}^{n_i} r^2_{ik}\sum_{j=1}^b n_{ik}(\tau\beta)_{ij}^2}{(a-1)(b-1)})</td>
<td>(MS_{AB}/MS_2)</td>
</tr>
<tr>
<td>(B\times Subjects within groups)</td>
<td>(df_2)</td>
<td>(MS_2)</td>
<td>(\frac{\sigma^2 + \frac{b^2_\beta}{a}}{\sum_{i=1}^a \frac{b-1}{b} \sum_{k=1}^{n_i} r^2_{ik}\sum_{j=1}^b n_{ik}(\tau\beta)_{ij}^2}{(a-1)(b-1)})</td>
<td></td>
</tr>
</tbody>
</table>

Comparisons of means may be in order if the main effects are significant. If the interaction effect is not significant, then we have the following \(\alpha\)-level tests:

1. A test of \(H_0: \tau_i = \tau_i'\) is

\[ \frac{|\bar{y}_{..} - \bar{y}_{i.}|}{\sqrt{\frac{MS_1}{b} \left(\frac{1}{n_i} + \frac{1}{n_i'}\right)}} > t_{df_1} (\alpha/2) \]
5.3. TWO-WAY REPEATED MEASUREMENT DESIGNS

2. A test of $H_0 : \beta_j = \beta_{j'}$ is

$$\frac{|\bar{y}_{ij} - \bar{y}_{ij'}|}{\sqrt{\frac{2MS_2}{n_i}}} > t_{df_2}(\alpha/2)$$

One may make simultaneous comparisons by making the appropriate adjustments in the above tests. If the AB interaction effect is significant, comparisons of the means of one factor needs to be performed within the levels of the other factor. Let $\mu_{ij}$ be the mean of cell $(i, j)$. The estimator of $\mu_{ij}$ is $\bar{y}_{ij}$.

Since

$$\text{Var}(\bar{y}_{ij}, \bar{y}_{ij'}) = \frac{2MS_2}{n_i}$$

the $\alpha$-level test of $H_0 : \mu_{ij} = \mu_{i'j'}$ (comparison of treatments $j$ and $j'$ within Group $i$)

$$\frac{|\bar{y}_{ij} - \bar{y}_{ij'}|}{\sqrt{2MS_2/n_i}} > t_{df_2}(\alpha/2).$$

The comparison of groups $i$ and $i'$ is, however, slightly more problematic since

$$\text{Var}(\bar{y}_{ij}, \bar{y}_{ij'}) = \left(\frac{1}{n_i} + \frac{1}{n_{i'}}\right)\left(\sigma^2 + \sigma_{\pi}^2 + \frac{b-1}{b}\sigma_{\beta\pi}^2\right) =: \left(\frac{1}{n_i} + \frac{1}{n_{i'}}\right)M$$

and $M$ cannot be unbiasedly estimated by either $MS_1$ or $MS_2$. However,

$$MS_3 = \frac{(df_1)(MS_1) + (df_2)(MS_2)}{df_1 + df_2}$$

is an unbiased estimate of $M$. Using the Satterthwaite approximation formula, we get the degrees of freedom associated with $MS_3$ as

$$df_3 = \frac{[(df_1)(MS_1) + (df_2)(MS_2)]^2}{(df_1)(MS_1)^2 + (df_2)(MS_2)^2}$$

Thus an $\alpha$-level test of $H_0 : \mu_{ij} = \mu_{i'j'}$ is

$$\frac{|\bar{y}_{ij} - \bar{y}_{ij'}|}{\sqrt{MS_3\left(\frac{1}{n_i} + \frac{1}{n_{i'}}\right)}} > t_{df_3}(\alpha/2).$$

For the balanced case, i.e. $n_1 = n_2 = \cdots = n_a = n$, $N = na$ and the ANOVA table is

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>df</th>
<th>MS</th>
<th>$F$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between Subjects</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A (Groups)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Subjects within groups</td>
<td>$N-1$</td>
<td>$a-1$</td>
<td>$MS_A$</td>
</tr>
<tr>
<td></td>
<td></td>
<td>$a(n-1)$</td>
<td>$MS_1$</td>
</tr>
<tr>
<td>Within Subjects</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B</td>
<td></td>
<td>$N(b-1)$</td>
<td>$MS_B$</td>
</tr>
<tr>
<td>AB</td>
<td></td>
<td>$(a-1)(b-1)$</td>
<td>$MS_{AB}$</td>
</tr>
<tr>
<td>B× Subjects within groups</td>
<td></td>
<td>$a(n-1)(b-1)$</td>
<td>$MS_2$</td>
</tr>
</tbody>
</table>

Comparisons of means in the balanced case are summarized in the following table:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Estimator</th>
<th>Standard Error of Estimator</th>
<th>df</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\tau_i - \tau_{i'}$</td>
<td>$\bar{y}<em>{i..} - \bar{y}</em>{i'..}$</td>
<td>$\sqrt{\frac{2MS_1}{bn}}$</td>
<td>$df_1$</td>
</tr>
<tr>
<td>$\beta_j - \beta_{j'}$</td>
<td>$\bar{y}<em>{..j} - \bar{y}</em>{..j'}$</td>
<td>$\sqrt{\frac{2MS_2}{am}}$</td>
<td>$df_2$</td>
</tr>
<tr>
<td>$\mu_{ij} - \mu_{i'j'}$</td>
<td>$\bar{y}<em>{i..j} - \bar{y}</em>{i'..j'}$</td>
<td>$\sqrt{\frac{2MS_n}{n}}$</td>
<td>$df_2$</td>
</tr>
<tr>
<td>$\mu_{ij} - \mu_{i'j}$</td>
<td>$\bar{y}<em>{i..j} - \bar{y}</em>{i'..j}$</td>
<td>$\sqrt{\frac{2MS_n}{n}}$</td>
<td>$df_3$</td>
</tr>
</tbody>
</table>
In the balanced case $MS_3$ and $df_3$ are given by

$$MS_3 = \frac{MS_1 + (b-1)MS_2}{b}$$

and

$$df_3 = \frac{a(n-1)(MS_1 + (b-1)MS_2)^2}{MS_1^2 + (b-1)MS_2^2}$$

The following example is taken from *Milliken and Johnson: The Analysis of Messy Data (Vol 1)*

**Example**

An experiment involving $d$ drugs was conducted to study each drug effect on the heart rate of humans. After the drug was administered, the heart rate was measured every five minutes for a total of $t$ times. At the start of the study, $n$ female human subjects were randomly assigned to each drug. The following table contains results from one such study.

<table>
<thead>
<tr>
<th>Person</th>
<th></th>
<th>DRUG</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>DRUG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td></td>
<td>AX23</td>
<td></td>
<td>T1</td>
<td>T2</td>
<td>T3</td>
<td>T4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td></td>
<td>BWW9</td>
<td></td>
<td>T1</td>
<td>T2</td>
<td>T3</td>
<td>T4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td></td>
<td>CONTROL</td>
<td></td>
<td>T1</td>
<td>T2</td>
<td>T3</td>
<td>T4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td>72</td>
<td>86</td>
<td>81</td>
<td>77</td>
<td>85</td>
<td>86</td>
</tr>
<tr>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td>78</td>
<td>83</td>
<td>88</td>
<td>81</td>
<td>82</td>
<td>86</td>
</tr>
<tr>
<td>6</td>
<td></td>
<td></td>
<td></td>
<td>71</td>
<td>82</td>
<td>81</td>
<td>75</td>
<td>71</td>
<td>78</td>
</tr>
<tr>
<td>7</td>
<td></td>
<td></td>
<td></td>
<td>72</td>
<td>83</td>
<td>83</td>
<td>69</td>
<td>83</td>
<td>88</td>
</tr>
<tr>
<td>8</td>
<td></td>
<td></td>
<td></td>
<td>66</td>
<td>79</td>
<td>77</td>
<td>66</td>
<td>86</td>
<td>76</td>
</tr>
<tr>
<td>9</td>
<td></td>
<td></td>
<td></td>
<td>74</td>
<td>83</td>
<td>84</td>
<td>77</td>
<td>85</td>
<td>82</td>
</tr>
<tr>
<td>10</td>
<td></td>
<td></td>
<td></td>
<td>62</td>
<td>73</td>
<td>78</td>
<td>70</td>
<td>79</td>
<td>83</td>
</tr>
<tr>
<td>11</td>
<td></td>
<td></td>
<td></td>
<td>69</td>
<td>75</td>
<td>76</td>
<td>70</td>
<td>83</td>
<td>84</td>
</tr>
</tbody>
</table>

The following SAS code performs the analyses:

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA RM;
INPUT S @;
DO A=1,2,3;
  DO B = 1,2,3,4;
    INPUT Y @@;
    OUTPUT;
  END;
END;
CARDS;
  1 72 86 81 77 85 86 83 80 69 73 72 74
  2 78 83 88 81 82 86 80 84 66 62 67 73
  3 71 82 81 75 71 78 70 75 84 90 88 87
  4 72 83 83 69 83 88 79 81 80 81 77 72
  5 66 79 77 66 86 85 76 76 72 72 69 70
  6 74 83 84 77 85 82 83 80 65 62 65 61
  7 62 73 78 70 79 83 80 81 75 69 69 68
  8 69 75 76 70 83 84 78 81 71 70 65 65
PROC SORT DATA=RM;
  BY A B S;
RUN;
QUIT;
PROC MEANS MEAN NOPRINT;
  VAR Y;
  BY A B;
  OUTPUT OUT=OUTMEAN MEAN=YM;
RUN;
QUIT;
```
GOPTIONS DISPLAY;
PROC G PLOT DATA=OUTMEAN;
   PLOT Y*M=B=A;
   SYMBOL1 V= DIAMOND L=1 I= JOIN CV= BLUE;
   SYMBOL2 V= TRIANGLE L=1 I= JOIN CV= BLACK;
   SYMBOL3 V= CIRCLE L=1 I= JOIN CV= ORANGE;
   TITLE3 ‘DRUG BY TIME’;
RUN;
QUIT;

TITLE1 ‘HEART RATE DATA’;
PROC GLM DATA=RM;
   CLASS A B S;
   MODEL Y = A S(A) B A*B B*S(A);
   TEST H=A E=S(A);
   TEST H=B A*B E=B*S(A);
   LSMEANS A*B;
RUN;
QUIT;

Dependent Variable: Y

<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>95</td>
<td>4907.489583</td>
<td>51.657785</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>Error</td>
<td>0</td>
<td>0.000000</td>
<td>.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>95</td>
<td>4907.489583</td>
<td></td>
<td></td>
<td></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>A</td>
<td>2</td>
<td>1315.083333</td>
<td>657.541667</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>S(A)</td>
<td>21</td>
<td>2320.156250</td>
<td>110.483631</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>B</td>
<td>3</td>
<td>282.614583</td>
<td>94.204861</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>A*B</td>
<td>6</td>
<td>531.166667</td>
<td>88.527778</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>B*S(A)</td>
<td>63</td>
<td>458.468750</td>
<td>7.277282</td>
<td>.</td>
<td>.</td>
</tr>
</tbody>
</table>

Tests of Hypotheses Using the Type III MS for S(A) 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>A</td>
<td>2</td>
<td>1315.083333</td>
<td>657.541667</td>
<td>5.95</td>
<td>0.0090</td>
</tr>
</tbody>
</table>

Tests of Hypotheses Using the Type III MS for B*S(A) 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>B</td>
<td>3</td>
<td>282.614583</td>
<td>94.204861</td>
<td>12.95</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>A*B</td>
<td>6</td>
<td>531.166667</td>
<td>88.527778</td>
<td>12.16</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Least Squares Means

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>Y LSMEAN</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>70.5000000</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>80.5000000</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>81.0000000</td>
</tr>
<tr>
<td>1</td>
<td>4</td>
<td>73.1250000</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>81.7500000</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>84.0000000</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>78.6250000</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>79.7500000</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>72.7500000</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>72.3750000</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>71.5000000</td>
</tr>
<tr>
<td>3</td>
<td>4</td>
<td>71.2500000</td>
</tr>
</tbody>
</table>
The interaction plot as well as the $F$-test show a significant interaction.

**Compare times within drugs**

The common standard error is

$$se(\bar{y}_{ij} - \bar{y}_{ij'}) = \sqrt{\frac{2 MS_2}{n}} = \sqrt{\frac{(2)(7.28)}{8}} = 1.35$$

The least significant difference (LSD) is

$$LSD = t_{63}(0.025)\sqrt{\frac{2 MS_2}{n}} = 2.00(1.35) = 2.70.$$ 

Thus any $|\bar{y}_{ij} - \bar{y}_{ij'}|$ that exceeds 2.70 indicates a significant difference between $\mu_{ij}$ and $\mu_{ij'}$. 

This gives us the following set of underlining patterns:

**DRUG 1 : AX23**

<table>
<thead>
<tr>
<th>T1</th>
<th>T4</th>
<th>T2</th>
<th>T3</th>
</tr>
</thead>
<tbody>
<tr>
<td>70.5</td>
<td>73.1</td>
<td>80.5</td>
<td>81.0</td>
</tr>
</tbody>
</table>

**DRUG 2 : BWW9**

<table>
<thead>
<tr>
<th>T3</th>
<th>T4</th>
<th>T1</th>
<th>T2</th>
</tr>
</thead>
<tbody>
<tr>
<td>78.6</td>
<td>79.8</td>
<td>81.8</td>
<td>84.0</td>
</tr>
</tbody>
</table>

**DRUG 3 : CONTROL**

<table>
<thead>
<tr>
<th>T4</th>
<th>T3</th>
<th>T2</th>
<th>T1</th>
</tr>
</thead>
<tbody>
<tr>
<td>71.3</td>
<td>71.5</td>
<td>72.4</td>
<td>72.8</td>
</tr>
</tbody>
</table>
5.3. TWO-WAY REPEATED MEASUREMENT DESIGNS

---

Compare drugs within times

The common standard error is

\[
se(\bar{y}_{ij} - \bar{y}_{i'j'}) = \sqrt{\frac{2MS_3}{n}} = \sqrt{\frac{2(MS_1 + (b-1)MS_2)}{nb}} = \sqrt{\frac{2(110.5 + (3)(7.28))}{(2)(8)}} = 2.876
\]

with

\[
df_3 = \frac{a(n-1)[MS_1 + (b-1)MS_2]^2}{MS_2^2 + (b-1)MS_2^2} = \frac{3(7)[110.5 + (3)(7.28)]^2}{(110.5)^2 + (3)(7.28)^2} = 29.7 \approx 30
\]

The least significant difference (LSD) is

\[
LSD = t_{30}(0.025)\sqrt{\frac{2MS_3}{n}} = 2.042(2.876) = 5.87.
\]

Thus any \(|\bar{y}_{ij} - \bar{y}_{i'j'}|\) that exceeds 5.87 indicates a significant difference between \(\mu_{ij}\) and \(\mu_{i'j}\).

This gives us the following set of underlining patterns:

**TIME 1**

<table>
<thead>
<tr>
<th>AX23</th>
<th>CONTROL</th>
<th>BW9</th>
</tr>
</thead>
<tbody>
<tr>
<td>70.5</td>
<td>72.8</td>
<td>81.75</td>
</tr>
</tbody>
</table>

**TIME 2**

<table>
<thead>
<tr>
<th>CONTROL</th>
<th>AX23</th>
<th>BW9</th>
</tr>
</thead>
<tbody>
<tr>
<td>72.4</td>
<td>80.5</td>
<td>84.0</td>
</tr>
</tbody>
</table>

**TIME 3**

<table>
<thead>
<tr>
<th>CONTROL</th>
<th>BW9</th>
<th>AX23</th>
</tr>
</thead>
<tbody>
<tr>
<td>71.5</td>
<td>78.6</td>
<td>81.0</td>
</tr>
</tbody>
</table>

**TIME 4**

<table>
<thead>
<tr>
<th>CONTROL</th>
<th>AX23</th>
<th>BW9</th>
</tr>
</thead>
<tbody>
<tr>
<td>71.3</td>
<td>73.1</td>
<td>79.8</td>
</tr>
</tbody>
</table>

The following example taken from *Milliken and Johnson* illustrates how SAS can be used to make comparisons of means in the absence of a significant interaction.

**Example**

This experiment involved studying the effect of a dose of a drug on the growth of rats. The data set consists of the growth of 15 rats, where 5 rats were randomly assigned to each of the 3 doses of the drug. The weights were obtained each week for 4 weeks.
## CHAPTER 5. REPEATED MEASUREMENT DESIGNS

<table>
<thead>
<tr>
<th>Dose</th>
<th>Rat</th>
<th>Week 1</th>
<th>Week 2</th>
<th>Week 3</th>
<th>Week 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>54</td>
<td>60</td>
<td>63</td>
<td>74</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>69</td>
<td>75</td>
<td>81</td>
<td>90</td>
</tr>
<tr>
<td>3</td>
<td>77</td>
<td>81</td>
<td>87</td>
<td>94</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>64</td>
<td>69</td>
<td>77</td>
<td>83</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>51</td>
<td>58</td>
<td>62</td>
<td>71</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>62</td>
<td>71</td>
<td>75</td>
<td>81</td>
</tr>
<tr>
<td>2</td>
<td>68</td>
<td>73</td>
<td>81</td>
<td>91</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>94</td>
<td>102</td>
<td>109</td>
<td>112</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>81</td>
<td>90</td>
<td>95</td>
<td>104</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>64</td>
<td>69</td>
<td>72</td>
<td>78</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>59</td>
<td>63</td>
<td>66</td>
<td>75</td>
</tr>
<tr>
<td>2</td>
<td>56</td>
<td>66</td>
<td>70</td>
<td>81</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>71</td>
<td>77</td>
<td>84</td>
<td>80</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>59</td>
<td>64</td>
<td>69</td>
<td>76</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>65</td>
<td>70</td>
<td>73</td>
<td>77</td>
<td></td>
</tr>
</tbody>
</table>

The SAS code and output are given below:

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA RM1;
  DO A=1,2,3;
    DO S=1,2,3,4,5;
      DO B = 1,2,3,4;
        INPUT Y @@;
      OUTPUT;
    END;
  END;
END;
CARDS;
54 60 63 74
69 75 81 90
77 81 87 94
64 69 77 83
51 58 62 71
62 71 75 81
68 73 81 91
94 102 109 112
81 90 96 104
64 69 72 78
59 63 66 75
56 66 70 81
71 77 84 80
59 64 69 76
65 70 73 77
;
PROC SORT DATA=RM1;
  BY A B S;
RUN;
QUIT;
PROC MEANS MEAN NOPRINT;
  VAR Y;
  BY A B;
  OUTPUT OUT=OUTMEAN MEAN=YM;
RUN;
QUIT;
GOPTIONS DISPLAY;
PROC GPlot DATA=OUTMEAN;
  PLOT YM*B=A;
  SYMBOL1 V=Diamond L=1 I=JOIN CV=Blue;
  SYMBOL2 V=Triangle L=1 I=JOIN CV=Black;
  SYMBOL3 V=Circle L=1 I=JOIN CV=Orange;
```
## 5.3. TWO-WAY REPEATED MEASUREMENT DESIGNS

**RUN**;
QUIT;

**TITLE1 'RAT BODY WEIGHT DATA';**
**PROC GLM DATA=RM1;**
**CLASS A B S;**
**MODEL Y = A S(A) B A*B B*S(A);**
**TEST H=A E=S(A);**
**TEST H=B A*B E=B*S(A);**
**LSMEANS A/PDIFF E=S(A);**
**LSMEANS B/PDIFF E=B*S(A);**
**RUN;**
QUIT;

---

### Dependent Variable: Y

<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>Model</td>
<td>59</td>
<td>10440.18333</td>
<td>176.95226</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>Corrected Total</td>
<td>59</td>
<td>10440.18333</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Tests of Hypotheses Using the Type III MS for S(A) 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>A</td>
<td>2</td>
<td>2146.433333</td>
<td>1073.216667</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>S(A)</td>
<td>12</td>
<td>5405.500000</td>
<td>450.458333</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>B</td>
<td>3</td>
<td>2678.183333</td>
<td>892.727778</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>A*B</td>
<td>6</td>
<td>32.366667</td>
<td>5.394444</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>B*S(A)</td>
<td>36</td>
<td>177.700000</td>
<td>4.936111</td>
<td>.</td>
<td>.</td>
</tr>
</tbody>
</table>

**Tests of Hypotheses Using the Type III MS for B*S(A) 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>B</td>
<td>3</td>
<td>2678.183333</td>
<td>892.727778</td>
<td>180.86</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>A*B</td>
<td>6</td>
<td>32.366667</td>
<td>5.394444</td>
<td>1.09</td>
<td>0.3854</td>
</tr>
</tbody>
</table>

---

### Least Squares Means

<table>
<thead>
<tr>
<th>Source</th>
<th>Y LSMEAN Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>2</td>
</tr>
<tr>
<td></td>
<td>3</td>
</tr>
<tr>
<td></td>
<td>23</td>
</tr>
</tbody>
</table>

**Least Squares Means for effect A**

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.1095</td>
<td>0.7764</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.1095</td>
<td>0.0664</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.7764</td>
<td>0.0664</td>
<td></td>
</tr>
</tbody>
</table>

---

**The GLM Procedure**

**Least Squares Means**

**Standard Errors and Probabilities Calculated Using the Type III MS for S(A) as an Error Term**

**Least Squares Means for effect A**

| Pr > |t| for H0: LSMean(i)=LSMean(j) |
|------|----------------------------|
| 1/2  | 0.1095 | 0.7764 |
| 2    | 0.1095 | 0.0664 |
| 3    | 0.7764 | 0.0664 |
CHAPTER 5. REPEATED MEASUREMENT DESIGNS

Least Squares Means
Standard Errors and Probabilities Calculated Using the Type III MS for B*S(A)
as an Error Term

<table>
<thead>
<tr>
<th>B</th>
<th>Y LSMEAN</th>
<th>LSMEAN Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>66.266667</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>72.533333</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>77.600000</td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>84.466667</td>
<td>4</td>
</tr>
</tbody>
</table>

Least Squares Means for effect B
Pr > |t| for H0: LSMean(i)=LSMean(j)
Dependent Variable: Y

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
</tbody>
</table>

Since there is no significant interaction, the means of $A$ and $B$ can be compared at the highest level. Using the output from *LSMEANS* one obtains the following underlining patterns:

DOSES : D3  D1  D2
70.1  72.0  83.6

WEEKS : W1  W2  W3  W4
66.3  72.5  77.6  84.5

Two-Way RM Design : General Case
So far, we have considered the analysis of the classic two-way RM design under the assumption that the (S) condition is satisfied for each level of $A$. Here we consider the analysis of a two-way RM design where the (S) condition may not hold.
The analysis strategy will be as follows:

1. Test the $B$ main effect and the $AB$ interaction effect using the G-G $e$-adjusted $F$-test.

2. Run a complete one-way ANOVA of the the levels of $A$ within each level of $B$. That is, for level $j$ of $B$, we test $H_0 : \mu_{1j} = \cdots = \mu_{aj}$ and make multiple comparisons of means using the data

\[
\begin{array}{cccc}
  A & i & \cdots & a \\
  y_{ij1} & \cdots & y_{ij1} & \cdots & y_{aj1} \\
  \vdots & & \vdots & & \vdots \\
  y_{ijn} & \cdots & y_{ijn} & \cdots & y_{ajn}
\end{array}
\]

3. Run a complete one-way RM analysis of the levels of $B$ within each level of $A$ using the G-G $e$-adjusted one-way RM $F$-tests followed by multiple comparisons of means. That is, for level $i$ of $A$, we test $H_0 : \mu_{i1} = \cdots = \mu_{ib}$ using the data

\[
\begin{array}{cccc}
  B & j & \cdots & a \\
  \text{Subject} & i & \cdots & j & \cdots & a \\
  1 & y_{i11} & \cdots & y_{ij1} & \cdots & y_{ib1} \\
  \vdots & & \vdots & & \vdots & & \vdots \\
  k & y_{ik1} & \cdots & y_{ijk} & \cdots & y_{ibk} \\
  \vdots & & \vdots & & \vdots & & \vdots \\
  n_i & y_{i1n_i} & \cdots & y_{ijn_i} & \cdots & y_{ibn_i}
\end{array}
\]

Example

We will revisit the body weight of rats data considered above. The following SAS code is used to get the tests for $B$ and $AB$ effects.

```sas
OPTIONS LS=80 PS=66 NODATE;
DATA RM3;
   INPUT A Y1 Y2 Y3 Y4;
   CARDS;
   1 54 60 63 74
   1 69 75 81 90
   1 77 81 87 94
   1 64 69 77 83
   1 51 58 62 71
   2 62 71 75 81
   2 68 73 81 91
   2 94 102 109 112
   2 81 90 95 104
   2 64 69 72 78
   3 59 63 66 75
   3 56 66 70 81
   3 71 77 84 90
   3 59 64 69 76
   3 65 70 73 77
   ;
   TITLE1 'RAT BODY WEIGHT DATA : 2';
PROC GLM DATA=RM3;
   CLASS A;
   MODEL Y1-Y4 = A;
   REPEATED B 4/ PRINTE;
RUN;
QUIT;
```

---

SELECTED OUTPUT

---

RAT BODY WEIGHT DATA : 2
Sphericity Tests

<table>
<thead>
<tr>
<th>Variables</th>
<th>Mauchly's DF</th>
<th>Criterion</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transformed Variates</td>
<td>5</td>
<td>0.0459293</td>
<td>33.031436</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Orthogonal Components</td>
<td>5</td>
<td>0.3345438</td>
<td>11.740697</td>
<td>0.0385</td>
</tr>
</tbody>
</table>

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>A</td>
<td>2</td>
<td>2146.433333</td>
<td>1073.216667</td>
<td>2.38</td>
<td>0.1345</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>5405.500000</td>
<td>450.458333</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

RAT BODY WEIGHT DATA : 2

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>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>3</td>
<td>2678.183333</td>
<td>892.727778</td>
<td>180.86</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>B*A</td>
<td>6</td>
<td>32.366667</td>
<td>5.394444</td>
<td>1.09</td>
<td>0.3854</td>
</tr>
<tr>
<td>Error(B)</td>
<td>36</td>
<td>177.700000</td>
<td>4.936111</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Using the G-G ε-adjusted tests one observes that the AB interaction effect is not significant while the B main effect is significant both at \( \alpha = .05 \). Mauchly’s test for the (S) condition is significant indicating that the analyses run earlier may not be the appropriate ones.

We now run one-way RM analyses of B within each level of A.

PROC SORT DATA=RM3;
BY A;
RUN;
QUIT;

PROC GLM DATA=RM3;
MODEL Y1-Y4=/NOUNI;
REPEATED B 4/PRINTE;
BY A;
RUN;
QUIT;

SELECTED OUTPUT

RAT BODY WEIGHT DATA : 2

------------------------------------- A=1 --------------------------------------

Sphericity Tests

<table>
<thead>
<tr>
<th>Variables</th>
<th>Mauchly's DF</th>
<th>Criterion</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transformed Variates</td>
<td>5</td>
<td>0.1626147</td>
<td>4.9445682</td>
<td>0.4227</td>
</tr>
<tr>
<td>Orthogonal Components</td>
<td>5</td>
<td>0.27398</td>
<td>3.5244612</td>
<td>0.6197</td>
</tr>
</tbody>
</table>
5.3. TWO-WAY REPEATED MEASUREMENT DESIGNS

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>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>3</td>
<td>1023.600000</td>
<td>341.200000</td>
<td>284.33</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error(B)</td>
<td>12</td>
<td>14.400000</td>
<td>1.200000</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Adj Pr > F
Source
G - G   H - F
B       <.0001  <.0001
Error(B)

Greenhouse-Geisser Epsilon 0.6286
Huynh-Feldt Epsilon 1.1713

------------------------------------- A=2 --------------------------------------

Sphericity Tests
Mauchly's

<table>
<thead>
<tr>
<th>Variables</th>
<th>DF</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transformed Variates</td>
<td>5</td>
<td>7.2149884</td>
<td>0.2051</td>
</tr>
<tr>
<td>Orthogonal Components</td>
<td>5</td>
<td>2.6252267</td>
<td>0.7575</td>
</tr>
</tbody>
</table>

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>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>3</td>
<td>1014.000000</td>
<td>338.000000</td>
<td>78.00</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error(B)</td>
<td>12</td>
<td>52.000000</td>
<td>4.333333</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Adj Pr > F
Source
G - G   H - F
B       <.0001  <.0001
Error(B)

Greenhouse-Geisser Epsilon 0.6370
Huynh-Feldt Epsilon 1.2055

------------------------------------- A=3 --------------------------------------

Sphericity Tests
Mauchly's

<table>
<thead>
<tr>
<th>Variables</th>
<th>DF</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transformed Variates</td>
<td>5</td>
<td>14.15447</td>
<td>0.0147</td>
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<tr>
<td>Orthogonal Components</td>
<td>5</td>
<td>8.0126045</td>
<td>0.1555</td>
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</tbody>
</table>

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>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>3</td>
<td>672.950000</td>
<td>224.3186676</td>
<td>24.19</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error(B)</td>
<td>12</td>
<td>111.300000</td>
<td>9.275000</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Adj Pr > F
Source
G - G   H - F
B       0.0021  0.0004
Error(B)

Greenhouse-Geisser Epsilon 0.4800
Sphericity is satisfied in all the three cases. The repeated factor $B$ is also significant in all the cases. Thus, we may compare the means of $B$ using the $MS_E$ as a denominator. In the situation where the (S) condition is not satisfied in one or more of the groups, one uses Welch $t$-tests, as shown in the last example of Section 5.2, to compare the means of $B$ in the particular group which does not satisfy the (S) condition.

The following SAS code re-creates the data as $A, B, S, Y$ columns and runs:

- the one-way ANOVA for the factor $A$ within each level of $B$;
- comparisons of the $A$ means for each level of $B$; and
- comparisons of the $B$ means within each level of $A$.

```sas
DATA RM4;
  SET RM3;
  ARRAY Z Y1-Y4;
  DO B=1,2,3,4;
    S = _N_;
    Y = Z(B);
    OUTPUT;
  END;
  DROP Y1-Y4;
RUN;
QUIT;
PROC SORT DATA=RM4;
  BY B;
RUN;
QUIT;
PROC GLM DATA=RM4;
  CLASS A;
  MODEL Y=A;
  LSMEANS A/PDIFF;
  BY B;
RUN;
QUIT;
PROC SORT DATA=RM4;
  BY A;
RUN;
QUIT;
PROC GLM DATA=RM4;
  CLASS B S;
  MODEL Y=B S;
  LSMEANS B/ PDIFF;
  BY A;
RUN;
QUIT;
```

---

**SELECTED OUTPUT**

---

RAT BODY WEIGHT DATA : 2

------------------------------------- B=1 --------------------------------------

The GLM Procedure

<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>2</td>
<td>428.133333</td>
<td>214.066667</td>
<td>1.93</td>
<td>0.1876</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>1330.800000</td>
<td>110.900000</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### 5.3. Two-Way Repeated Measurement Designs

<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>A</td>
<td>2</td>
<td>428.133333</td>
<td>214.066667</td>
<td>1.93</td>
<td>0.1876</td>
</tr>
</tbody>
</table>

The GLM Procedure
Least Squares Means

<table>
<thead>
<tr>
<th>A</th>
<th>Y</th>
<th>LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Y</td>
<td>63.0000000</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>Y</td>
<td>73.8000000</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>Y</td>
<td>62.0000000</td>
<td>3</td>
</tr>
</tbody>
</table>

Least Squares Means for effect A
Pr > |t| for H0: LSmean(i)=LSmean(j)

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.1309</td>
<td>0.8831</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.1309</td>
<td>0.1018</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0.8831</td>
<td>0.1018</td>
<td></td>
</tr>
</tbody>
</table>

---

### B=2

The GLM Procedure
Dependent Variable: Y

<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>Model</td>
<td>2</td>
<td>538.533333</td>
<td>269.266667</td>
<td>2.41</td>
<td>0.1319</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>1341.200000</td>
<td>111.766667</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Corrected Total 14 1879.733333

The GLM Procedure
Least Squares Means

<table>
<thead>
<tr>
<th>A</th>
<th>Y</th>
<th>LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Y</td>
<td>68.6000000</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>Y</td>
<td>81.0000000</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>Y</td>
<td>68.0000000</td>
<td>3</td>
</tr>
</tbody>
</table>

Least Squares Means for effect A
Pr > |t| for H0: LSmean(i)=LSmean(j)

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.0884</td>
<td>0.9300</td>
<td></td>
</tr>
<tr>
<td>2</td>
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<td>0.0757</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0.9300</td>
<td>0.0757</td>
<td></td>
</tr>
</tbody>
</table>

---

### B=3

The GLM Procedure
Dependent Variable: Y

<table>
<thead>
<tr>
<th>Source</th>
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<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>2</td>
<td>538.533333</td>
<td>269.266667</td>
<td>2.41</td>
<td>0.1319</td>
</tr>
<tr>
<td>Error</td>
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<td>111.766667</td>
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<td></td>
</tr>
</tbody>
</table>

Corrected Total 14 1879.733333

The GLM Procedure
Least Squares Means

<table>
<thead>
<tr>
<th>A</th>
<th>Y</th>
<th>LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Y</td>
<td>68.6000000</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>Y</td>
<td>81.0000000</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>Y</td>
<td>68.0000000</td>
<td>3</td>
</tr>
</tbody>
</table>

Least Squares Means for effect A
Pr > |t| for H0: LSmean(i)=LSmean(j)

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.0884</td>
<td>0.9300</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.0884</td>
<td>0.0757</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0.9300</td>
<td>0.0757</td>
<td></td>
</tr>
</tbody>
</table>
CHAPTER 5. REPEATED MEASUREMENT DESIGNS

Model 2 587.200000 293.600000 2.15 0.1589
Error 12 1636.400000 136.366667
Corrected Total 14 2223.600000

Source DF Type III SS Mean Square F Value Pr > F
A 2 587.200000 293.600000 2.15 0.1589

The GLM Procedure
Least Squares Means

<table>
<thead>
<tr>
<th>A</th>
<th>LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>74.0000000</td>
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<tr>
<td>2</td>
<td>86.4000000</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>72.4000000</td>
<td>3</td>
</tr>
</tbody>
</table>

Least Squares Means for effect A
Pr > |t| for H0: LSMeans(i)=LSMeans(j)

Dependent Variable: Y

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.1190</td>
<td>0.8321</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.1190</td>
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</tr>
<tr>
<td>3</td>
<td>0.8321</td>
<td>0.0824</td>
<td></td>
</tr>
</tbody>
</table>

RAT BODY WEIGHT DATA : 2

--- A=1 --------------------------------------

The GLM Procedure

Sum of

Source DF Squares Mean Square F Value Pr > F
Model 2 624.933333 312.466667 2.94 0.0913
Error 12 1274.800000 106.233333
Corrected Total 14 1899.733333

The GLM Procedure
Least Squares Means

<table>
<thead>
<tr>
<th>A</th>
<th>LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>82.4000000</td>
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</tr>
<tr>
<td>2</td>
<td>93.2000000</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>77.8000000</td>
<td>3</td>
</tr>
</tbody>
</table>

Least Squares Means for effect A
Pr > |t| for H0: LSMeans(i)=LSMeans(j)

Dependent Variable: Y

<table>
<thead>
<tr>
<th>i/j</th>
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<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.1235</td>
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</tr>
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<td>0.4939</td>
<td>0.0359</td>
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--- A*4 --------------------------------------

The GLM Procedure

Dependent Variable: Y

Sum of

--- A*1 --------------------------------------

The GLM Procedure

Dependent Variable: Y
### 5.3. TWO-WAY REPEATED MEASUREMENT DESIGNS

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>7</td>
<td>2733.600000</td>
<td>390.514286</td>
<td>325.43</td>
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</tr>
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<td>Error</td>
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<td>1.200000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>19</td>
<td>2748.000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
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<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>3</td>
<td>1023.600000</td>
<td>341.200000</td>
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<tr>
<td>S</td>
<td>4</td>
<td>1710.000000</td>
<td>427.500000</td>
<td>356.25</td>
<td>&lt;.0001</td>
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#### The GLM Procedure

<table>
<thead>
<tr>
<th>Least Squares Means</th>
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<tbody>
<tr>
<td>B</td>
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<tr>
<td>Y</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
</tbody>
</table>

#### Least Squares Means for effect B

Pr > |t| for H0: LSMean(i)=LSMean(j)

<table>
<thead>
<tr>
<th>Dependent Variable: Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>i/j</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
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</table>

---

A*2

---

#### The GLM Procedure

<table>
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<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>7</td>
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<tr>
<td>Corrected Total</td>
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<table>
<thead>
<tr>
<th>Source</th>
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<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>3</td>
<td>1014.000000</td>
<td>338.000000</td>
<td>78.00</td>
<td>&lt;.0001</td>
</tr>
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<td>S</td>
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#### The GLM Procedure

<table>
<thead>
<tr>
<th>Least Squares Means</th>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
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<tr>
<td>Y</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
</tbody>
</table>

#### Least Squares Means for effect B

Pr > |t| for H0: LSMean(i)=LSMean(j)

<table>
<thead>
<tr>
<th>Dependent Variable: Y</th>
</tr>
</thead>
<tbody>
<tr>
<td>i/j</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
</tbody>
</table>
### Chapter 5. Repeated Measurement Designs

---

**The GLM Procedure**

**Dependent Variable:** Y

<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>
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<td>1055.650000</td>
<td>150.807143</td>
<td>16.26</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>111.300000</td>
<td>9.275000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>19</td>
<td>1166.950000</td>
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<td></td>
<td></td>
</tr>
</tbody>
</table>

**Source: DF Type III SS Mean Square F Value Pr > F**

<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>B</td>
<td>3</td>
<td>672.950000</td>
<td>224.316667</td>
<td>24.19</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>S</td>
<td>4</td>
<td>382.700000</td>
<td>95.675000</td>
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<td>0.0007</td>
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</tbody>
</table>

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**The GLM Procedure**

**Least Squares Means**

<table>
<thead>
<tr>
<th>B</th>
<th>Y LSMEAN Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>62.0000000 1</td>
</tr>
<tr>
<td>2</td>
<td>68.0000000 2</td>
</tr>
<tr>
<td>3</td>
<td>72.4000000 3</td>
</tr>
<tr>
<td>4</td>
<td>77.8000000 4</td>
</tr>
</tbody>
</table>

---

**Least Squares Means for effect B**

Pr > |t| for H0: LSMean(i)=LSMean(j)

<table>
<thead>
<tr>
<th>Dependent Variable: Y</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
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<tbody>
<tr>
<td>i/j</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>0.0089</td>
<td>0.0002</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.0089</td>
<td>0.0414</td>
<td>0.0003</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0.0002</td>
<td>0.0414</td>
<td>0.0159</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>&lt;.0001</td>
<td>0.0003</td>
<td>0.0159</td>
<td></td>
</tr>
</tbody>
</table>

---

Using underlining to summarize the results:

**Group(A)**

---

| B levels |
|----------|----------|
| 1        | B1 B2 B3 B4 |
| 2        | B1 B2 B3 B4 |
| 3        | B1 B2 B3 B4 |

**Treatment(B)**

---

| A levels |
|----------|----------|
| 1        | A3 A1 A2 |
| 2        | A3 A1 A2 |
| 3        | A3 A1 A2 |
| 4        | A3 A1 A2 |
Chapter 6

More on Repeated Measurement Designs

In this chapter we will further investigate one- and two-way repeated measurement designs. Since RM designs usually involve a time factor, one may be interested in the pattern of the response variable over time. Thus, we shall consider trend analysis in one- and two-way RM designs as our first section. Later sections consider special cases of the two-way RM design.

6.1 Trend Analyses in One- and Two-way RM Designs

6.1.1 Regression Components of the Between Treatment SS ($SS_B$)

Often the treatments in an experiment consist of levels of a quantitative variable. For instance, in a one-way CRD model, the treatments may be several dosages of the same drug. One is usually interested in developing an equation for a curve that describes the dose-response relationship. This may be used to find the optimal dosage level. To this end we want to consider applications of regression procedures within the ANOVA framework.

As an illustration, consider the fabric strength experiment considered in Chapter 1. The treatment consists of five different levels of cotton percentages and the response is the strength of the fabric produced. Each percentage of cotton is randomly assigned to five randomly selected experimental units. This is the usual CRD framework that is represented by the model

$$y_{ij} = \mu + \tau_i + \epsilon_{ij}, \quad i = 1, \cdots, 5, \quad j = 1, \cdots, 5,$$

where our interest lies in testing

$$H_0 : \tau_1 = \tau_2 = \cdots = \tau_5 = 0$$
$$H_A : \tau_i \neq 0 \text{ for at least one } i$$

which is tested using $F_0 = MS_B/MS_W$.

We can get more insight into the nature of the relationship of the response, $y$, and the levels of the treatment variable, $x$, if we consider a regression type relationship between $x$ and $y$; i.e

$$y = f(x) + \epsilon$$

For example, one may consider the simple linear regression model

$$y = \beta_0 + \beta_1 x + \epsilon$$

and test

$$H_0 : \beta_1 = 0$$

to determine if the response is linearly related to the levels of the treatment.
Partitioning $SS_B$

The variability in the response that is explained by the treatment may now be partitioned into that due to the linear regression and that due to the remainder that cannot be explained by the regression model. Thus,

$$SS_B = SS_R + SS_L$$

where $SS_R$ is the sum of squares due to the linear regression and $SS_L$ is the sum of squares due to lack of fit (i.e., failure of the linear regression to describe the relationship between $x$ and $y$).

The ANOVA table for the CRD is

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>$F_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between</td>
<td>$k-1$</td>
<td>$SS_B$</td>
<td>$MS_B$</td>
<td>$F_0 = MS_B/MS_W$</td>
</tr>
<tr>
<td>Linear Regression</td>
<td>1</td>
<td>$SS_R$</td>
<td>$MS_R$</td>
<td>$F_R = MS_R/MS_W$</td>
</tr>
<tr>
<td>Lack of Fit</td>
<td>$k-2$</td>
<td>$SS_L$</td>
<td>$MS_L$</td>
<td>$F_L = MS_L/MS_W$</td>
</tr>
<tr>
<td>Within (Error)</td>
<td>$n-k$</td>
<td>$SS_W$</td>
<td>$MS_W$</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>$n-1$</td>
<td>$SS_T$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

One may obtain $SS_R$ by fitting an ordinary linear regression model of $y$ on $x$. This, however, seems to be the hard way as the $F$ values may have to be computed by hand. An easier way is to find a set of coefficients to define a contrast among the treatment means. To use this approach we may define contrasts using the deviations of the treatment levels from the treatment mean as our contrast coefficients. Without loss of generality, assume that we have a balanced CRD model where $r$ represents the number of replications per treatment level. Assume also that we have $k$ treatment levels. Then

$$\hat{\phi}_R = \sum_{i=1}^{k} (x_i - \bar{x}) \mu_i$$

is a contrast ($\sum_{i=1}^{k} (x_i - \bar{x}) = 0$) whose estimator is

$$\hat{\phi}_R = \sum_{i=1}^{k} (x_i - \bar{x}) \bar{y}_i$$

From $\hat{\phi}_R$ we get

$$SS_R = \frac{r \hat{\phi}_R^2}{\sum_{i=1}^{k} (x_i - \bar{x})^2}$$

and

$$SS_L = SS_B - SS_R .$$

The $F$ ratios in the above ANOVA table are used to test the following hypotheses:

1. $F_0$ is a test statistic for testing
   $$H_0 : \tau_1 = \cdots = \tau_k = 0 ,$$
   the hypothesis that all the treatment means are the same against the alternative that at least two are different.

2. $F_R$ is a test statistic for testing
   $$H_0 : \beta_1 = 0 ,$$
   the hypothesis that there is no linear relationship between the response and the levels of the treatment against the alternative that there is a significant linear relationship.

3. $F_L$ is the test statistic for testing
   $$H_0 : E(y) = \beta_0 + \beta_1 x ,$$
   the hypothesis that the simple linear regression model describes the data against the alternative that a simple linear model is not sufficient.
6.1. TREND ANALYSES IN ONE- AND TWO-WAY RM DESIGNS

Orthogonal Polynomials

The fitting of curves within the ANOVA framework can be greatly simplified if

1. the design is balanced; and,
2. the treatment levels are equally spaced.

In such a case we may replace \((x_i - \bar{x})\) by a simple set of multipliers known as *orthogonal polynomial coefficients*. These coefficients are extensively tabulated but we will use Proc IML in SAS to generate them. These coefficients enable us to partition \(SS_B\) into orthogonal linear, quadratic, cubic, quartic, etc. components each with one degree of freedom. This means that \(SS_B\) can be completely decomposed using a polynomial of degree \(k - 1\) with no lack of fit term. The usual procedure is to fit successive terms of the polynomial starting with the linear term until lack of fit becomes non-significant. This is very widely used in practice even though it sometimes entail premature stopping.

Assume that \(c_{ij}, i = 1, \ldots, k-1, j = 1, \ldots, k\) be the \(i\)th order polynomial coefficient for the \(j\)th treatment level. Then

\[
L_i = \sum_{j=1}^{k} c_{ij} \bar{y}_j
\]

is the contrast of means associated with the \(i\)th order term of the polynomial, and

\[
S_i^2 = \frac{rL_i^2}{\sum_{j=1}^{k} c_{ij}^2}
\]

is the 1 df sum of squares associated with the \(i\)th term.

Proc IML in SAS may be used to generate orthogonal polynomial coefficients. For instance, consider a case where the treatment has \(k = 4\) levels, say, 10, 20, 30, 40, and 50. The orthogonal polynomial coefficients for all four terms of the polynomial

\[
y = \beta_0 + \beta_1 x + \beta_{11} x^2 + \beta_{111} x^3 + \beta_{1111} x^4
\]

are computed as

```sas
proc iml;
x={10 20 30 40 50};
xp=orpol(x,4);
print xp;
run;
quit;
```

The output is

\[
0.4472136 -0.632456 0.5345225 -0.316228 0.1195229
0.4472136 -0.316228 -0.267261 0.6324555 -0.478091
0.4472136 3.588E-18 -0.534522 1.86E-16 0.7171372
0.4472136 0.3162278 -0.267261 -0.632456 -0.478091
0.4472136 0.6324555 0.5345225 0.3162278 0.1195229
\]

The first column represents the intercept term.

Note that in SAS the treatment levels need not be equally spaced. For example

```sas
proc iml;
x={0 25 75 100};
xp=orpol(x,3);
print xp;
run;
quit;
```
The following code and associated plot show how the contrast coefficients are related to the polynomial terms.

```
Title1 "Orthogonal Polynomials";
Title2 "5 Equallyspaced Levels";
Data Five;
Length Trend $9;
Input Trend @;
Do X=4,5,6,7,8;
Input Coef @;
Output;
End;
Datalines;
linear  -0.632456  0.5 -0.316228 0.5 -0.316228 1.969E-17 0.3162278 0.6324555
quadratic 0.5345225 -0.267261 -0.534522 -0.267261 0.5345225
Cubic -0.316228 0.6324555 6.501E-17 -0.632456 0.3162278
quartic 0.1195229 -0.478091 0.7171372 -0.478091 0.1195229
;
proc print;
run;
quit;
Proc GPlot Data=Five;
Plot Coef*X=Trend / VAxis=Axis1;
Axis1 Label=(A=90 "Coefficient") Order=(-1 To 1 By .1);
Symbol1 C=Black V=Triangle L=1 I=Spline;
Symbol2 C=Black V=Square L=1 I=Spline;
Symbol3 C=Black V=Diamond L=1 I=Spline;
Symbol4 C=Black V=Circle L=1 I=Spline;
Run;
Quit;
```
EXAMPLE: An experiment was conducted to determine the effect of storage temperature on potency of an antibiotic. Fifteen samples of the antibiotic were obtained and three samples, selected at random, were stored at each of five temperatures. After 30 days of storage the samples were tested for potency. The results are given below:

<table>
<thead>
<tr>
<th>Temperature</th>
<th>10°C</th>
<th>30°C</th>
<th>50°C</th>
<th>70°C</th>
<th>90°C</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>62</td>
<td>26</td>
<td>16</td>
<td>10</td>
<td>13</td>
</tr>
<tr>
<td></td>
<td>55</td>
<td>36</td>
<td>15</td>
<td>11</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td>57</td>
<td>31</td>
<td>23</td>
<td>18</td>
<td>9</td>
</tr>
</tbody>
</table>

The contrast coefficients in the following code were generated using Proc IML in SAS.

data potency;
input temp pot @@;
cards;
10 62 10 55 10 57
30 26 30 36 30 31
50 16 50 15 50 23
70 10 70 11 70 18
90 13 90 11 90 9
;

proc glm;
class temp;
model pot = temp;
contrast 'linear' temp -0.632456 -0.316228 1.969E-17 0.3162278 0.6324555;
contrast 'quadratic' temp 0.5345225 -0.267261 -0.534522 -0.267261 0.5345225;
contrast 'cubic' temp -0.316228 0.6324555 6.501E-17 -0.632456 0.3162278;
contrast 'quartic' temp 0.1195229 -0.478091 0.7171372 -0.478091 0.1195229;
run; quit;

proc glm;
model pot=temp temp*temp;
output out=quadmod p=p;
run;
The following is the ANOVA table that is produced by SAS:

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>temp</td>
<td>4</td>
<td>4520.400000</td>
<td>1130.100000</td>
<td>70.63</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>linear</td>
<td>1</td>
<td>3763.199609</td>
<td>3763.199609</td>
<td>235.20</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>quadratic</td>
<td>1</td>
<td>720.859329</td>
<td>720.859329</td>
<td>45.05</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>cubic</td>
<td>1</td>
<td>36.300220</td>
<td>36.300220</td>
<td>2.27</td>
<td>0.1629</td>
</tr>
<tr>
<td>quartic</td>
<td>1</td>
<td>0.042866</td>
<td>0.042866</td>
<td>0.00</td>
<td>0.9597</td>
</tr>
</tbody>
</table>

The following is the ANOVA table that is produced by SAS:

Over the 30 day storage period used in this study temperature had a highly significant effect on the potency of the antibiotic ($P < .0001$). The linear and quadratic terms are the only significant trend components. So we will fit a quadratic model using SAS' Proc GLM. Over the temperature range $10^\circ$ to $90^\circ$, potency may be described by the equation

$$
\hat{y} = 71.80 - 1.60x + .01x^2
$$

where $\hat{y}$ is the expected potency and $x$ is the 30-day storage temperature.

The issue of trend analysis involving more than one independent variable, and response surface methodology in general, will be investigated in a greater detail in a later chapter.

### 6.1.2 RM Designs

Consider those cases where the within subject factor, denoted by $B$ hereafter, involves $b$ time measurements at times $t_1 < t_2 < \ldots < t_b$. Let $\phi = \sum_{i=1}^b c_j \mu_{ij}$ or $\phi = \sum_{i=1}^b c_j \mu_{ij}$ be a polynomial contrast of the main $B$ means or the simple $B$ means specific to Group $i$, respectively. Let $\phi_1, \phi_2, \ldots, \phi_{b-1}$ be the $b - 1$ orthogonal polynomial contrasts, where $\phi_i$ is degree $i$.

One may use the POLYNOMIAL transformation option of SAS to obtain trend analysis. In the following we will consider two examples: one- and two-way RM designs.

The following is due to Michael Stoline, Personal Communication.

#### Example : One-way RM Design

In a small pilot clinical trial dose-response drug study, a pharmaceutical company research team is concerned with the quickness that a new drug can sedate a person so that they can go to sleep. A sample $b = 8$ people is selected from a population of insomniacs, who have no medically-diagnosed physical or mental disease or symptoms, which may cause or explain the insomnia. A Likert scale is used to determine ease in going to sleep. The scale used in the study is:
Each of the subjects in the insomniac population has chronic sleep difficulties, and each consistently scores a value of 4 in their daily evaluation of time required to go to sleep, using the above instrument. A standard dosage of the new drug is administered daily to each of the eight subjects under the care of a physician. Sleep difficulty, in the above Likert scale, is measured for each patient after one, two, four, and eight weeks. The goal of the study is to assess the relationship of the ease of going to sleep as a function of the length of time under medication. In particular we would like to test the significance of the linear quadratic and cubic orthogonal trend components of sleep difficulty as a function of time. The data are given below:

The following SAS code is used to perform orthogonal trend analysis.

DATA RM1;
  INPUT B1 B2 B3 B4;
  CARDS;
  4 2 2 1
  2 2 1 1
  2 2 2 2
  4 3 3 2
  3 2 1 1
  3 1 2 1
  1 1 2 1
  2 2 1 2
;
TITLE 'ONE-WAY RM TREND'; PROC GLM DATA=RM1;
  MODEL B1-B4 = / NOUNI;
  REPEATED TIME 4 (1 2 4 8) POLYNOMIAL / PRINTM SUMMARY;
RUN; QUIT;

The related output is

<table>
<thead>
<tr>
<th>Scale</th>
<th>Time to go to sleep (in minutes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>&lt; 10</td>
</tr>
<tr>
<td>2</td>
<td>10 – 20</td>
</tr>
<tr>
<td>3</td>
<td>20 – 40</td>
</tr>
<tr>
<td>4</td>
<td>&gt; 40</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Subject</th>
<th>1 week</th>
<th>2 weeks</th>
<th>4 weeks</th>
<th>8 weeks</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4</td>
<td>2</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>4</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>5</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>6</td>
<td>3</td>
<td>1</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>7</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>8</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>2</td>
</tr>
</tbody>
</table>
CHAPTER 6. MORE ON REPEATED MEASUREMENT DESIGNS

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>
</tr>
</thead>
<tbody>
<tr>
<td>TIME</td>
<td>3</td>
<td>6.59375000</td>
<td>2.19791667</td>
<td>5.66</td>
<td>0.0053</td>
</tr>
<tr>
<td>Error(TIME)</td>
<td>21</td>
<td>8.15625000</td>
<td>0.38839286</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Adj Pr > F

Source       G - G  H - F

TIME          0.0153  0.0061
Error(TIME)

Greenhouse-Geisser Epsilon  0.6766
Huynh-Feldt Epsilon        0.9549

The GLM Procedure
Repeated Measures Analysis of Variance
Analysis of Variance of Contrast Variables

TIME_N represents the nth degree polynomial contrast for TIME

Contrast Variable: TIME_1

<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>Mean</td>
<td>1</td>
<td>4.95244565</td>
<td>4.95244565</td>
<td>9.75</td>
<td>0.0168</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>3.55407609</td>
<td>0.50772516</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Contrast Variable: TIME_2

<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>Mean</td>
<td>1</td>
<td>0.82477209</td>
<td>0.82477209</td>
<td>2.78</td>
<td>0.1391</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>2.07354488</td>
<td>0.29622070</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Contrast Variable: TIME_3

<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>Mean</td>
<td>1</td>
<td>0.81653226</td>
<td>0.81653226</td>
<td>2.26</td>
<td>0.1764</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>2.52862903</td>
<td>0.36123272</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The linear trend is the only significant trend (P = .0168).
Example: Two-way RM Design

Consider again the experiment involving \( d \) drugs was conducted to study each drug effect on the heart rate of humans. After the drug was administered, the heart rate was measured every five minutes for a total of \( t \) times. At the start of the study, \( n \) female human subjects were randomly assigned to each drug. The following table contains results from one such study.

<table>
<thead>
<tr>
<th>Person within drug</th>
<th>AX23</th>
<th>BWW9</th>
<th>CONTROL</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>( T_1 )</td>
<td>( T_2 )</td>
<td>( T_3 )</td>
</tr>
<tr>
<td>1</td>
<td>72</td>
<td>86</td>
<td>81</td>
</tr>
<tr>
<td>2</td>
<td>78</td>
<td>83</td>
<td>88</td>
</tr>
<tr>
<td>3</td>
<td>71</td>
<td>82</td>
<td>81</td>
</tr>
<tr>
<td>4</td>
<td>72</td>
<td>83</td>
<td>83</td>
</tr>
<tr>
<td>5</td>
<td>66</td>
<td>79</td>
<td>77</td>
</tr>
<tr>
<td>6</td>
<td>74</td>
<td>83</td>
<td>84</td>
</tr>
<tr>
<td>7</td>
<td>62</td>
<td>73</td>
<td>78</td>
</tr>
<tr>
<td>8</td>
<td>69</td>
<td>75</td>
<td>76</td>
</tr>
</tbody>
</table>

The profile plot (given below) indicates that the trend patterns may be different for all the three levels of \( A \). The significance of the \( AB \) interaction implies that the three levels of \( A \) must be treated separately.

An inspection of the above profile plot shows that:

1. AX23 may have a quadratic trend
2. BWW9 may have a cubic trend
3. Control may have a constant trend

The following is the SAS analysis of the trend components:

\[
\text{OPTIONS LS=80 PS=66 NODATE;}
\text{DATA RM1;}
\]
INPUT A Y1 Y2 Y3 Y4 @0;
CARDS;
 1 72 86 81 77 2 85 86 83 80 3 69 73 72 74
 1 78 83 88 81 2 82 86 80 84 3 66 62 67 73
 1 71 82 81 75 2 71 78 70 75 3 84 90 88 87
 1 72 83 83 69 2 83 88 79 81 3 80 81 77 72
 1 66 79 77 66 2 86 85 76 76 3 72 72 69 70
 1 74 83 84 77 2 85 82 83 80 3 65 62 65 61
 1 62 73 78 70 2 79 83 80 81 3 75 69 69 68
 1 69 75 76 70 2 83 84 78 81 3 71 70 65 65
;
TITLE 'HEART RATE DATA : TREND';
PROC SORT DATA=RM1;
  BY A;
RUN;
QUIT;
PROC GLM DATA=RM1;
  CLASS A;
  MODEL Y1-Y4 = /NOUNI;
  REPEATED B 4 POLYNOMIAL/ PRINTM SUMMARY;
  BY A;
RUN;
QUIT;

Selected output

------------------------------------- A=1 --------------------------------------
B_N represents the nth degree polynomial contrast for B

Contrast Variable: B_1

<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>Mean</td>
<td>1</td>
<td>28.05625000</td>
<td>28.05625000</td>
<td>4.37</td>
<td>0.0748</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>44.89375000</td>
<td>6.41339286</td>
<td></td>
<td></td>
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</tbody>
</table>

Contrast Variable: B_2

<table>
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</tr>
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<tbody>
<tr>
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<td>1</td>
<td>639.0312500</td>
<td>639.0312500</td>
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<td>&lt;.0001</td>
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<tr>
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<td>40.7187500</td>
<td>5.8169643</td>
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</tbody>
</table>

Contrast Variable: B_3

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<th>F Value</th>
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</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>1</td>
<td>0.50625000</td>
<td>0.50625000</td>
<td>0.10</td>
<td>0.7564</td>
</tr>
<tr>
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<td>7</td>
<td>34.04375000</td>
<td>4.86339286</td>
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</tr>
</tbody>
</table>
6.1. TREND ANALYSES IN ONE- AND TWO-WAY RM DESIGNS

<table>
<thead>
<tr>
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<th>F Value</th>
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</tr>
</thead>
<tbody>
<tr>
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<td>51.75625000</td>
<td>51.75625000</td>
<td>5.18</td>
<td>0.0570</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>69.99375000</td>
<td>9.99910714</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Contrast Variable: B_2

<table>
<thead>
<tr>
<th>Source</th>
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<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>1</td>
<td>2.53125000</td>
<td>2.53125000</td>
<td>2.16</td>
<td>0.1855</td>
</tr>
<tr>
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<td>7</td>
<td>8.21875000</td>
<td>1.17410714</td>
<td></td>
<td></td>
</tr>
</tbody>
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Contrast Variable: B_3

<table>
<thead>
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<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>1</td>
<td>79.80625000</td>
<td>79.80625000</td>
<td>11.65</td>
<td>0.0112</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>47.94375000</td>
<td>6.84910714</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

----------------------------- A=3 -----------------------------

Contrast Variable: B_1

<table>
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<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>1</td>
<td>11.5562500</td>
<td>11.5562500</td>
<td>0.62</td>
<td>0.4566</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>130.2937500</td>
<td>18.6133929</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Contrast Variable: B_2

<table>
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<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>1</td>
<td>0.03125000</td>
<td>0.03125000</td>
<td>0.00</td>
<td>0.9511</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>54.2187500</td>
<td>7.74553571</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Contrast Variable: B_3

<table>
<thead>
<tr>
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<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>Mean</td>
<td>1</td>
<td>0.50625000</td>
<td>0.50625000</td>
<td>0.13</td>
<td>0.7332</td>
</tr>
<tr>
<td>Error</td>
<td>7</td>
<td>28.1437500</td>
<td>4.02053571</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The results match our prior expectations:

1. AX23 - quadratic
2. BWW9 - cubic
3. Control - No trend
6.2 The Split-Plot Design

In some multi-factor designs that involve blocking, we may not be able to completely randomize the order of runs within each block. This results in a design known as the split-plot design which is a generalization of the RCBD (or a subset of the classic two-way RM design, as we shall see later).

We shall only consider the simplest split-plot design that involves two factors and an incomplete block. There are two sizes of experimental units: whole plots are the larger units and subplots or split-plots are the smaller units. The levels of one factor are assigned at random to large experimental units within blocks of such units. The large units are then divided into smaller units, and the levels of the second factor are assigned at random to the small units within the larger units.

An agronomist may be interested in the effect of tillage treatments and fertilizers on yield. Tillage machinery requires large plots while fertilizers can be applied to small plots. One such experiment considers three methods of seedbed preparation ($S_1, S_2, S_3$) as a whole-plot factor and four rates of nitrogen fertilizer applied by hand ($N_0, N_1, N_2, N_3$) as the subplot factor. The analysis is divided into two parts: whole plot and subplot. The three methods of land preparation are applied to the whole plots in random order. Then each plot is divided into four subplots and the four different fertilizers are applied in random order.

\[
\begin{array}{cccccc}
& S_3 & S_1 & S_2 & S_1 & S_3 \\
N_3 & N_2 & N_0 & N_3 & N_0 & N_1 \\
N_2 & N_3 & N_3 & N_2 & N_1 & N_0 \\
N_1 & N_0 & N_2 & N_0 & N_3 & N_4 \\
N_0 & N_1 & N_1 & N_2 & N_0 & N_2 \\
\end{array}
\]

The statistical model associated with the split-plot design is

\[
y_{ijk} = \mu + \tau_i + \epsilon_{ij} + \beta_j + (\tau\beta)_{ij} + e_{ijk},
\]

where $\mu + \tau_i + \epsilon_{ij}$ is the whole plot part of the model and $\beta_j + (\tau\beta)_{ij} + e_{ijk}$ is the subplot part. Here $a$ is the number of levels of the whole plot factor, $b$ is the number of levels of the subplot factor, and $r$ is the number of times a whole plot factor is repeated. Notice that our design restricts the number of whole plots to be a multiple of $a$. We may have unequal number of repetitions of the whole plot factor if the number of whole plots is not a multiple of $a$.

The ANOVA table for this split-plot design is

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>df</th>
</tr>
</thead>
<tbody>
<tr>
<td>Whole Plot Analysis</td>
<td></td>
</tr>
<tr>
<td>$A$</td>
<td>$a - 1$</td>
</tr>
<tr>
<td>Error(Whole Plot)</td>
<td>$a(r - 1)$</td>
</tr>
<tr>
<td>Subplot Analysis</td>
<td></td>
</tr>
<tr>
<td>$B$</td>
<td>$b - 1$</td>
</tr>
<tr>
<td>$AB$</td>
<td>$(a - 1)(b - 1)$</td>
</tr>
<tr>
<td>Error(Subplot)</td>
<td>$a(b - 1)(r - 1)$</td>
</tr>
</tbody>
</table>

Notice that the ANOVA table looks like a two-way RM design ANOVA where the whole plot analysis here corresponds to the between subject analysis of the RM design and the subplot analysis corresponds to the within subject analysis of the RM design.

The following example is taken from Milliken and Johnson.
6.2. THE SPLIT-PLOT DESIGN

Example

The following data are taken from an experiment where the amount of dry matter was measured on wheat plants grown in different levels of moisture and different amounts of fertilizer. There were 48 different peat pots and 12 plastic trays; 4 pots could be put into each tray. The moisture treatment consisted of adding 10, 20, 30, or 40 ml of water per pot per day to the *tray*, where the water was absorbed by the peat pots. The levels of moisture were randomly assigned to the trays. The levels of fertilizer were 2, 4, 6, or 8 mg per pot. The four levels of fertilizer were randomly assigned *to the four pots in each tray* so that each fertilizer occurred once in each tray. The wheat seeds were planted in each pot and after 30 days the dry matter of each pot was measured.

<table>
<thead>
<tr>
<th>Level of Moisture</th>
<th>Tray</th>
<th>Level of Fertilizer</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>4.0444</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>4.0444</td>
</tr>
<tr>
<td>10</td>
<td>4</td>
<td>5.0490</td>
</tr>
<tr>
<td>2</td>
<td>5</td>
<td>5.91310</td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>6.95113</td>
</tr>
<tr>
<td>30</td>
<td>7</td>
<td>6.56933</td>
</tr>
<tr>
<td>40</td>
<td>8</td>
<td>8.29741</td>
</tr>
<tr>
<td></td>
<td>9</td>
<td>5.27853</td>
</tr>
</tbody>
</table>

The data was placed in a file called "split2.dat" in the following format:

```
moist fert tray yield
10 2 1 3.3458
10 2 2 4.0444
10 2 3 1.97584
10 4 1 4.3170
10 4 2 4.1413
10 4 3 3.8397

...  
40 8 10 12.5144
40 8 11 12.5034
40 8 12 10.2811
```

The following SAS code uses two ways (PROC GLM and PROC MIXED) to perform the split-plot analysis.

```sas
OPTIONS LINESIZE=80 PAGESIZE=37; /* SPLIT PLOT MJ 24.2 */
DATA EXPT;
  INFILE 'C:\ASH\S7010\SAS\SPLIT2.DAT' FIRSTOBS=2;
  INPUT MOIST FERT TRAY YIELD;
RUN;
QUIT;

PROC GLM; /* SPLIT PLOT USING GLM */
  CLASS TRAY FERT MOIST;
  MODEL YIELD = MOIST TRAY(MOIST) FERT MOIST*FERT / SS1;
  RANDOM TRAY(MOIST) / TEST; /* TESTS USING RANDOM STATEMENT */
  TEST H = MOIST E = TRAY(MOIST); /* TESTS USING TEST STATEMENT */
  MEANS MOIST / LSD E = TRAY(MOIST); /* MEANS OK FOR BALANCED DATA */
```
CHAPTER 6. MORE ON REPEATED MEASUREMENT DESIGNS

MEANS FERT / LSD;
LSMEANS MOIST*FERT / PDIFFT STDERR OUT=LSM; /* SAVE LS MEANS DATASET */
RUN;
QUIT;

PROC PLOT DATA=LSM; /* INTERACTION PLOTS FROM GLM */
PLOT LSMEAN*FERT=MOIST;
PLOT LSMEAN*MOIST=FERT;
RUN;
QUIT;

PROC MIXED DATA=EXPT; /* SPLIT PLOT USING MIXED */
CLASS TRAY FERT MOIST;
MODEL YIELD = MOIST | FERT;
RANDOM TRAY(MOIST);
RUN;
QUIT;

----------------------------------------------------------------

<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>23</td>
<td>631.5513647</td>
<td>27.4587550</td>
<td>36.51</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>24</td>
<td>18.0513405</td>
<td>0.7521392</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>47</td>
<td>649.6027051</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>moist</td>
<td>3</td>
<td>269.1895496</td>
<td>89.7298499</td>
<td>119.30</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>tray(moist)</td>
<td>8</td>
<td>27.2515182</td>
<td>3.4064398</td>
<td>4.53</td>
<td>0.0019</td>
</tr>
<tr>
<td>fert</td>
<td>3</td>
<td>297.0540027</td>
<td>99.0180009</td>
<td>131.65</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>fert*moist</td>
<td>9</td>
<td>38.0562942</td>
<td>4.2284771</td>
<td>5.62</td>
<td>0.0003</td>
</tr>
</tbody>
</table>

Plot of LSMEAN*moist. Symbol is value of fert.

The Mixed Procedure

Type 3 Tests of Fixed Effects

<table>
<thead>
<tr>
<th>Effect</th>
<th>Num</th>
<th>Den</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>moist</td>
<td>3</td>
<td>8</td>
<td>26.34</td>
<td>0.0002</td>
</tr>
<tr>
<td>fert</td>
<td>3</td>
<td>24</td>
<td>131.65</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>fert*moist</td>
<td>9</td>
<td>24</td>
<td>5.62</td>
<td>0.0003</td>
</tr>
</tbody>
</table>
6.2. THE SPLIT-Plot DESIGN

We may add grouping in the split-plot design to reduce the whole plot variability. Consider once again the land preparation and fertilizers example. Now a block of land is divided into three whole-plots and the three methods of land preparation are applied to the plots in random order. Then each plot is divided into four subplots and the four different fertilizers are applied in random order. This is done (replicated) for two blocks of land. The following table shows the experimental plan:

<table>
<thead>
<tr>
<th>Block</th>
<th>II</th>
<th></th>
<th>II</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>S1</td>
<td>S2</td>
<td>S1</td>
</tr>
<tr>
<td></td>
<td>N3</td>
<td>N2</td>
<td>N0</td>
</tr>
<tr>
<td></td>
<td>N2</td>
<td>N3</td>
<td>N3</td>
</tr>
<tr>
<td></td>
<td>N1</td>
<td>N0</td>
<td>N2</td>
</tr>
<tr>
<td></td>
<td>N0</td>
<td>N1</td>
<td>N1</td>
</tr>
</tbody>
</table>

The following rearrangement of the above table shows that a split-plot design is analyzed as a classic two-way RM design with blocks treated as "subjects":

<table>
<thead>
<tr>
<th>S1</th>
<th>S2</th>
<th>S3</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>II</td>
<td>I</td>
</tr>
<tr>
<td>N2</td>
<td>N3</td>
<td>N0</td>
</tr>
<tr>
<td>N3</td>
<td>N2</td>
<td>N3</td>
</tr>
<tr>
<td>N0</td>
<td>N0</td>
<td>N2</td>
</tr>
<tr>
<td>N1</td>
<td>N1</td>
<td>N2</td>
</tr>
</tbody>
</table>

The model for such designs is

\[ y_{ijk} = \mu + \tau_i + \beta_j + \epsilon_{ij} \]

whole plot part of the model

\[ + \pi_k + (\tau\pi)_{ik} + \epsilon_{ijk} \]

subplot part of the model

where \( \tau_i \) is the effect of the \( i \)th level of the whole plot factor, \( \beta_j \) is the effect of the \( j \)th block, and \( \pi_k \) is the effect of the \( k \)th level of the subplot factor.

The ANOVA table for this split-plot design is:

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>df</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>( r - 1 )</td>
</tr>
<tr>
<td>A</td>
<td>( a - 1 )</td>
</tr>
<tr>
<td>Error(Whole Plot)</td>
<td>( (a - 1)(r - 1) )</td>
</tr>
<tr>
<td>B</td>
<td>( b - 1 )</td>
</tr>
<tr>
<td>AB</td>
<td>( (a - 1)(b - 1) )</td>
</tr>
<tr>
<td>Error(Subplot)</td>
<td>( a(b - 1)(r - 1) )</td>
</tr>
</tbody>
</table>

One final note here is that there is no appropriate error term to test for significance of replication effect.

Example

Two varieties of wheat (\( B \)) are grown in two different fertility regimes (\( A \)). The field was divided into two blocks with four whole plots. Each of the four fertilizer levels was randomly assigned to one whole plot within a block. Each whole plot was divided into two subplots, and each variety of wheat was randomly assigned to one subplot within each whole plot.
### Chapter 6. More on Repeated Measurement Designs

Block 1

<table>
<thead>
<tr>
<th>Variety</th>
<th>Block 1</th>
<th>Block 2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$B_1$</td>
<td>$B_2$</td>
</tr>
<tr>
<td>$A_1$</td>
<td>35.4</td>
<td>37.9</td>
</tr>
<tr>
<td>$A_2$</td>
<td>36.7</td>
<td>38.2</td>
</tr>
<tr>
<td>$A_3$</td>
<td>34.8</td>
<td>36.4</td>
</tr>
<tr>
<td>$A_4$</td>
<td>39.5</td>
<td>40.0</td>
</tr>
</tbody>
</table>

Block 2

<table>
<thead>
<tr>
<th>Variety</th>
<th>Block 1</th>
<th>Block 2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$B_1$</td>
<td>$B_2$</td>
</tr>
<tr>
<td>$A_1$</td>
<td>41.6</td>
<td>40.3</td>
</tr>
<tr>
<td>$A_2$</td>
<td>42.7</td>
<td>41.6</td>
</tr>
<tr>
<td>$A_3$</td>
<td>43.6</td>
<td>42.8</td>
</tr>
<tr>
<td>$A_4$</td>
<td>44.5</td>
<td>47.6</td>
</tr>
</tbody>
</table>

SAS was used to analyze the data.

```sas
OPTIONS NOCENTER PS=64 LS=76; /* SPLIT PLOT MJ 24.1 */
DATA SPLIT;
  INPUT FERT N1 N2 N3 N4;
CARDS;
1 35.4 37.9 41.6 40.3
2 36.7 38.2 42.7 41.6
3 34.8 36.4 43.6 42.8
4 39.5 40.0 44.5 47.6
;
DATA B; SET SPLIT;
  YIELD = N1; BLOCK=1; VAR=1; OUTPUT;
  YIELD = N2; BLOCK=1; VAR=2; OUTPUT;
  YIELD = N3; BLOCK=2; VAR=1; OUTPUT;
  YIELD = N4; BLOCK=2; VAR=2; OUTPUT;
  DROP N1--N4;
RUN;
QUIT;
PROC GLM;
  CLASS BLOCK VAR FERT;
  MODEL YIELD = BLOCK FERT BLOCK*FERT VAR VAR*FERT;
  RANDOM BLOCK BLOCK*FERT;
  TEST H = BLOCK FERT E = BLOCK*FERT;
  LSMEANS FERT / PDIFF STDERR E = BLOCK*FERT;
  LSMEANS VAR VAR*FERT / PDIFF STDERR;
RUN;
QUIT;
PROC MIXED;
  CLASS BLOCK VAR FERT;
  MODEL YIELD = FERT VAR VAR*FERT;
  RANDOM BLOCK BLOCK*FERT;
  LSMEANS FERT | VAR;
RUN;
QUIT;
```

---

Dependent Variable: YIELD

<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>11</td>
<td>182.02000000</td>
<td>16.5472727</td>
<td>7.85</td>
<td>0.0306</td>
</tr>
<tr>
<td>Error</td>
<td>4</td>
<td>8.43000000</td>
<td>2.1075000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>15</td>
<td>190.45000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
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<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>1</td>
<td>131.10250000</td>
<td>131.1025000</td>
<td>62.21</td>
<td>0.0014</td>
</tr>
<tr>
<td>FERT</td>
<td>3</td>
<td>40.19000000</td>
<td>13.3966667</td>
<td>6.36</td>
<td>0.0530</td>
</tr>
<tr>
<td>BLOCK*FERT</td>
<td>3</td>
<td>6.92750000</td>
<td>2.3091667</td>
<td>1.10</td>
<td>0.4476</td>
</tr>
<tr>
<td>VAR</td>
<td>1</td>
<td>2.25000000</td>
<td>2.2500000</td>
<td>1.07</td>
<td>0.3599</td>
</tr>
<tr>
<td>VAR*FERT</td>
<td>3</td>
<td>1.55000000</td>
<td>0.5166667</td>
<td>0.25</td>
<td>0.8612</td>
</tr>
</tbody>
</table>

Tests of Hypotheses Using the Type III MS for BLOCK*FERT 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>BLOCK</td>
<td>1</td>
<td>131.10250000</td>
<td>131.1025000</td>
<td>56.77</td>
<td>0.0048</td>
</tr>
<tr>
<td>FERT</td>
<td>3</td>
<td>40.19000000</td>
<td>13.3966667</td>
<td>5.80</td>
<td>0.0914</td>
</tr>
</tbody>
</table>
We may reorganize the ANOVA table in the output as

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>BLOCK</td>
<td>1</td>
<td>131.1025000</td>
<td>131.1025000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>FERT</td>
<td>3</td>
<td>40.1900000</td>
<td>13.3966667</td>
<td>5.80</td>
<td>0.0914</td>
</tr>
<tr>
<td>BLOCK*FERT=Error(Whole plot)</td>
<td>3</td>
<td>6.9275000</td>
<td>2.3091667</td>
<td></td>
<td></td>
</tr>
<tr>
<td>VAR</td>
<td>1</td>
<td>2.2500000</td>
<td>2.2500000</td>
<td>1.07</td>
<td>0.3599</td>
</tr>
<tr>
<td>VAR*FERT</td>
<td>3</td>
<td>1.5500000</td>
<td>0.5166667</td>
<td>0.25</td>
<td>0.8612</td>
</tr>
<tr>
<td>Error(Subplot)</td>
<td>4</td>
<td>8.4300000</td>
<td>2.1075000</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

There is no significant difference among fertilizers. If this test were significant, then multiple comparisons would have to be carried out to determine the significant differences. A slight modification of the SAS code above will provide the necessary tests. This is left as an exercise.
6.3 Crossover Designs

A crossover design is a two-way RM design in which the order (A) of administration of the repeated levels of a single factor (B) is accounted for as a between subject factor in the design. Hence, a crossover design is a basic one-way RM design on the levels of B that has been analyzed as a two way RM design to account for the order or sequence effect caused by the fact that the B levels are given one at a time in different orders.

A Latin square type design approach is used in the construction of the order effects so that each level of B occurs equally often as the ith observation for \( i = 1, \ldots, b \).

We will only consider the two-period crossover design as an illustration. Here the repeated factor B has two levels \( b_1 \) and \( b_2 \) which are observed in the order \( b_1, b_2 \) by subjects in sequence level 1 \( (a_1) \) and in the order \( b_2, b_1 \) by subjects in sequence level 2 \( (a_2) \) as shown below:

<table>
<thead>
<tr>
<th>Sequence: A</th>
<th>( c_1 )</th>
<th>( c_2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( a_1 )</td>
<td>( b_1 )</td>
<td>( b_2 )</td>
</tr>
<tr>
<td>( a_2 )</td>
<td>( b_2 )</td>
<td>( b_1 )</td>
</tr>
</tbody>
</table>

There are three factors: sequence \( A \) \( (a_1 \) and \( a_2) \), period \( C \) \( (c_1 \) and \( c_2) \), and treatment \( B \) \( (b_1 \) and \( b_2) \) in the experiment. Let \( \beta_j \) be the \( j \)th treatment effect, \( j = 1, 2 \), and \( \gamma_k \) be the \( k \)th period effect, \( k = 1, 2 \). Further, let \( \tau_1 \) be the effect on the second observation if \( b_1 \) is observed first and \( \tau_2 \) be the effect on the second observation if \( b_2 \) is observed first. Thus \( \tau_1 \) and \( \tau_2 \) are the carry-over effects observed in the second observation whenever \( b_1 \) and \( b_2 \) are observed first, respectively. Let \( Y_{ijk} \) be the random variable which represents the observation corresponding to sequence \( i \), treatment \( j \) and period \( k \). The following table gives the observations:

<table>
<thead>
<tr>
<th>Sequence: A</th>
<th>Period: C</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>( a_1 = (b_1, b_2) )</td>
<td>( Y_{111} ) ( Y_{122} )</td>
<td>( \bar{Y}_{1.} )</td>
</tr>
<tr>
<td>( a_2 = (b_2, b_1) )</td>
<td>( Y_{221} ) ( Y_{212} )</td>
<td>( \bar{Y}_{2.} )</td>
</tr>
</tbody>
</table>

The model incorporates carry-over effects in the second observations but not in the observations made first.

\[
E(Y_{111}) = \mu + \beta_1 + \gamma_1 \\
E(Y_{122}) = \mu + \tau_1 + \beta_2 + \gamma_2 \\
E(Y_{221}) = \mu + \beta_2 + \gamma_1 \\
E(Y_{212}) = \mu + \tau_2 + \beta_1 + \gamma_2
\]

One can show that

\[
E(\bar{Y}_{1..} - \bar{Y}_{2..}) = \frac{\tau_1 - \tau_2}{2} \\
E(\bar{Y}_{1.} - \bar{Y}_{2.}) = (\beta_1 - \beta_2) - \frac{\tau_1 - \tau_2}{2} \\
E(\bar{Y}_{111} - \bar{Y}_{221}) = \beta_1 - \beta_2 \\
E(\bar{Y}_{1.} - \bar{Y}_{2.}) = E \left( \frac{Y_{111} - Y_{122}}{2} - \frac{Y_{212} - Y_{221}}{2} \right) = (\tau_1 - \tau_2) - \frac{\tau_1 + \tau_2}{2}
\]

The last expression shows that the \( AB \) and \( C \) effects are identical, i.e. \( AB \) and \( C \) are confounded. If there is no sequence effect \( (H_0 : \tau_1 = \tau_2) \), then

\[
A : E(\bar{Y}_{1..} - \bar{Y}_{2..}) = \frac{\tau_1 - \tau_2}{2} = 0 \\
B : E(\bar{Y}_{1.} - \bar{Y}_{2.}) = (\beta_1 - \beta_2)
\]
Thus, the $B$ main effect is a valid test if there is no sequence effect. Otherwise, $E(\bar{Y}_{11} - \bar{Y}_{22})$ is a biased estimate of $\beta_1 - \beta_2$. In this case the test $H_0 : \mu_{111} = \mu_{221}$ of the simple $B$ effects is a valid test of $H_0 : \beta_1 = \beta_2$ since $E(\bar{Y}_{111} - \bar{Y}_{221}) = \beta_1 - \beta_2$ even when $H_0 : \tau_1 = \tau_2$ is not true.

Now assume that there are $n_1 + n_2$ subjects available, and $n_1$ are randomly assigned to sequence 1 while the remaining $n_2$ are assigned to sequence 2. The data layout is

<table>
<thead>
<tr>
<th>Sequence : $A$</th>
<th>Subject</th>
<th>Treatment : $B$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$a_1 = (b_1, b_2)$</td>
<td>$1$</td>
<td>$y_{111}$ $y_{121}$</td>
</tr>
<tr>
<td></td>
<td>$\vdots$</td>
<td>$\vdots$ $\vdots$</td>
</tr>
<tr>
<td>$n_1$</td>
<td>$y_{11n_1}$ $y_{12n_1}$</td>
<td></td>
</tr>
<tr>
<td>$a_2 = (b_2, b_1)$</td>
<td>$1$</td>
<td>$y_{211}$ $y_{221}$</td>
</tr>
<tr>
<td></td>
<td>$\vdots$</td>
<td>$\vdots$ $\vdots$</td>
</tr>
<tr>
<td>$n_2$</td>
<td>$y_{21n_2}$ $y_{22n_2}$</td>
<td></td>
</tr>
</tbody>
</table>

One can immediately observe that this is a classic two-way RM layout discussed in Chapter 5. The ANOVA table is

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>df</th>
<th>MS</th>
<th>$F$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A$ : Sequence</td>
<td>1</td>
<td>$MS_A$</td>
<td>$F_A = MS_A/MS_1$</td>
</tr>
<tr>
<td>Subjects within $A$</td>
<td>$n_1 + n_2 - 2$</td>
<td>$MS_1$</td>
<td></td>
</tr>
<tr>
<td>$B$</td>
<td>1</td>
<td>$MS_B$</td>
<td>$F_B = MS_B/MS_2$</td>
</tr>
<tr>
<td>$AB$</td>
<td>1</td>
<td>$MS_{AB}$</td>
<td>$F_{AB} = MS_{AB}/MS_2$</td>
</tr>
<tr>
<td>$B \times$ Subjects within $A$</td>
<td>$n_1 + n_2 - 2$</td>
<td>$MS_2$</td>
<td></td>
</tr>
</tbody>
</table>

The recommended analysis strategy is

**Step 1:** Test for sequence effects $H_0 : \mu_1 = \mu_2$, using $F_A$.

- If $F_A$ is not significant, then go to **Step 2A**.
- If $F_A$ is significant, then go to **Step 2B**.

**Step 2A:** Test for $B$ main effects using $\mu_1 - \mu_2$

1. An $\alpha$ level test rejects $H_0$ if $F_B > F_{1, n_1 + n_2 - 2}(\alpha)$ using SAS Type III SS.
2. A $100(1 - \alpha)%$ confidence interval for $\mu_1 - \mu_2$ is

\[
(\bar{y}_{11} - \bar{y}_{22}) \pm t_{n_1 + n_2 - 2}(\alpha/2) \sqrt{MS_2 \left( \frac{1}{n_1} + \frac{1}{n_2} \right)}
\]

where $\bar{y}_{11} = (\bar{y}_{111} + \bar{y}_{121})/2$, the unweighted mean.

**Step 2B:** Test for $B$ main effects using $\mu_{11} - \mu_{22}$

The standard error of the estimator of $\mu_{11} - \mu_{22}$ is

\[
se(\bar{y}_{11} - \bar{y}_{22}) = \sqrt{\left( MS_1 + MS_2 \right) \left( \frac{1}{n_1} + \frac{1}{n_2} \right)}
\]

with the approximate degrees of freedom

\[
df_w = \frac{(n_1 + n_2 - 2)(MS_1 + MS_2)}{(MS_1)^2 + (MS_2)^2}
\]
CHAPTER 6. MORE ON REPEATED MEASUREMENT DESIGNS

1. An \( \alpha \)-level test of \( H_0: \mu_{11} = \mu_{22} \) rejects \( H_0 \) if

\[
\frac{|\bar{y}_{11} - \bar{y}_{22}|}{se(\bar{y}_{11} - \bar{y}_{22})} > t_{df}(\alpha/2)
\]

2. A 100(1 - \( \alpha \))\% confidence interval for \( \mu_{11} - \mu_{22} \) is

\[
(\bar{y}_{11} - \bar{y}_{22}) \pm t_{df}(\alpha/2)se(\bar{y}_{11} - \bar{y}_{22})
\]

Example

The following data are taken from Grizzle - Biometrics - 1965, pp 467-480. The responses are differences between pre-treatment and post-treatment hemoglobin levels.

<table>
<thead>
<tr>
<th>Period</th>
<th>Treatment</th>
<th>Subject</th>
<th>Total</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>0.2 0.0 -0.8 0.6 0.3 1.5</td>
<td>1.8 .3000</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>B</td>
<td>1.0 -0.7 0.2 1.1 0.4 1.2</td>
<td>3.2 .5333</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>1.2 -0.7 -0.6 1.7 0.7 2.7</td>
<td>5.0</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Period</th>
<th>Treatment</th>
<th>Subject</th>
<th>Total</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>B</td>
<td>1.3 -2.3 0.0 -0.8 -0.4 -2.9 -1.9 -2.9</td>
<td>-9.9 -1.2375</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>A</td>
<td>0.9 1.0 0.6 -0.3 -1.0 1.7 -0.3 0.9</td>
<td>3.5 0.4375</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>2.2 -1.3 0.6 -1.1 -1.4 -1.2 -2.2 -2.0</td>
<td>-6.4</td>
<td></td>
</tr>
</tbody>
</table>

The SAS code and partial output are given below

```sas
OPTIONS LINESIZE=80 PAGESIZE=66;
DATA CROSS;
INPUT SEQ PERSON A B;
CARDS;
1 1 .2 1
1 2 0 -.7
1 3 -.8 .2
1 4 .6 1.1
1 5 .3 .4
1 6 1.5 1.2
2 1 .9 1.3
2 2 .1 -2.3
2 3 .6 0
2 4 -.3 -.8
2 5 -1 -.4
2 6 1.7 -2.9
2 7 -3 -1.9
2 8 .9 -2.9
;
DATA CROSS2;
SET CROSS;
TRT = 'A'; Y = A; OUTPUT;
TRT = 'B'; Y = B; OUTPUT;
DROP A B;
RUN;
QUIT;

PROC GLM;
CLASS TRT SEQ PERSON;
MODEL Y = SEQ PERSON(SEQ) TRT TRT*SEQ;
RANDOM PERSON(SEQ) / TEST;
TEST H=SEQ E=PERSON(SEQ);
LSMEANS SEQ / E=PERSON(SEQ);
LSMEANS TRT TRT*SEQ;
RUN;
QUIT;
```

---

\( \bar{y} \): sample mean, \( \bar{y}_{ij} \): sample mean for the \( i \)-th treatment and \( j \)-th subject, \( t_{df}(\alpha) \): critical value of the t-distribution with \( df \) degrees of freedom.
### 6.3. CROSSOVER DESIGNS

#### Dependent Variable: Y

<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>15</td>
<td>27.96583333</td>
<td>1.86438889</td>
<td>1.50</td>
<td>0.2435</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>14.94166667</td>
<td>1.2454722</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>27</td>
<td>42.91000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

#### Source

<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>SEQ</td>
<td>1</td>
<td>4.57333333</td>
<td>4.57333333</td>
<td>3.67</td>
<td>0.0794</td>
</tr>
<tr>
<td>PERSON(SEQ)</td>
<td>12</td>
<td>12.00666667</td>
<td>1.00055556</td>
<td>0.80</td>
<td>0.6446</td>
</tr>
<tr>
<td>TRT</td>
<td>1</td>
<td>3.56297619</td>
<td>3.56297619</td>
<td>2.86</td>
<td>0.1165</td>
</tr>
<tr>
<td>TRT*SEQ</td>
<td>1</td>
<td>6.24297619</td>
<td>6.24297619</td>
<td>5.01</td>
<td>0.0449</td>
</tr>
</tbody>
</table>

Tests of Hypotheses for Mixed Model Analysis of Variance

#### Dependent Variable: Y

<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>* SEQ</td>
<td>1</td>
<td>4.57333333</td>
<td>4.57333333</td>
<td>3.67</td>
<td>0.0538</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>12.00666667</td>
<td>1.00055556</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* This test assumes one or more other fixed effects are zero.

#### Least Squares Means

<table>
<thead>
<tr>
<th>SEQ</th>
<th>Y LSEMEAN</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.416667</td>
</tr>
<tr>
<td>2</td>
<td>-0.400000</td>
</tr>
</tbody>
</table>

#### Least Squares Means

<table>
<thead>
<tr>
<th>TRT</th>
<th>Y LSEMEAN</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>0.3687500</td>
</tr>
<tr>
<td>B</td>
<td>-0.352083</td>
</tr>
</tbody>
</table>

#### TRT*SEQ Y LSEMEAN

<table>
<thead>
<tr>
<th>TRT</th>
<th>SEQ</th>
<th>Y LSEMEAN</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
<td>0.300000</td>
</tr>
<tr>
<td>A</td>
<td>2</td>
<td>0.437600</td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>0.533333</td>
</tr>
<tr>
<td>B</td>
<td>2</td>
<td>-1.237500</td>
</tr>
</tbody>
</table>

Using SAS Type III analysis we get the following summary for \( \alpha = .05 \) and \( \alpha = .10 \) (for illustrative purposes):

**\( \alpha = .05 \):** Sequence effects are not significant (\( p\)-value = .0538). Analyze treatment effects using \( \bar{y}_1 = .3688 \) and \( \bar{y}_2 = -.3521 \). The difference is not significant (\( p\)-value = .1165). Therefore, there are no treatment effects at \( \alpha = .05 \) level of significance.

**\( \alpha = .10 \):** Sequence effects are significant (\( p\)-value = .0538). Analyze treatment effects at time period 1 using \( \bar{y}_{11} = .3000 \) and \( \bar{y}_{22} = -1.2375 \). We have

\[
se(\bar{y}_{11} - \bar{y}_{22}) = \sqrt{\left(\frac{1}{6} + \frac{1}{8}\right)\frac{1.000 + 1.245}{2}} = 0.572,
\]

and

\[
df_w = \frac{12(1 + 1.245)^2}{(1)^2 + (1.245)^2} = 23.7 \approx 24.
\]

Therefore, the \( t \)-statistic is

\[
\frac{.3000 - (-1.2375)}{.572} = 2.69
\]
which has a two-sided $p$-value of 0.0128.
Thus, the difference is significant at $\alpha = .10$. Therefore, there are treatment effects at $\alpha = .10$ level of significance.
### 6.4 Two-Way Repeated Measurement Designs with Repeated Measures on Both Factors

Consider a design where factors $B$ and $C$ are within subject factors with levels $b$ and $c$, respectively. Assume that a random sample of $n$ subjects are observed on each of the $bc$ crossed levels of $B$ and $C$. The following table gives the data layout of such designs.

<table>
<thead>
<tr>
<th>Treatments ($B$)</th>
<th>$B_1$</th>
<th>( B_{b} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Subjects</td>
<td>$C_1$</td>
<td>( C_{c} )</td>
</tr>
<tr>
<td>$1$</td>
<td>$y_{111}$</td>
<td>$y_{1c1}$</td>
</tr>
<tr>
<td>\vdots</td>
<td>\vdots</td>
<td>\vdots</td>
</tr>
<tr>
<td>$n$</td>
<td>$y_{11n}$</td>
<td>$y_{1cn}$</td>
</tr>
</tbody>
</table>

The statistical model for such designs is

\[
y_{jkl} = \mu + \beta_j + \gamma_k + (\beta \gamma)_{jk} + S_l + (\beta S)_{jl} + (\gamma S)_{kl} + (\beta \gamma S)_{jkl} + e_{jkl}
\]

for \( j = 1, \ldots, b, \ k = 1, \ldots, c, \) and \( l = 1, \ldots, n, \) where

**Fixed Effects** :
- $\beta_j$ and $\gamma_k$ ate the $B_j$ and $C_k$ main effects and
- $(\beta \gamma)_{jk}$ is the $B_j C_k$ interaction effect.

**Random Effects** :
- $S_l \sim N(0, \sigma^2_1)$ = subject $l$ effect
- $(\beta S)_{jl} \sim N(0, d_2 \sigma^2_2) = B_j$ by subject $l$ interaction.
- $(\gamma S)_{kl} \sim N(0, d_3 \sigma^2_3) = C_k$ by subject $l$ interaction.
- $(\beta \gamma S)_{jkl} \sim N(0, d_4 \sigma^2_4) = B_j$ by $C_k$ by subject $l$ interaction.
- $e_{jkl} \sim N(0, \sigma^2)$.

We assume that the random effects interactions satisfy some (CS) conditions while all other random variables are assumed to be independent. One should notice that the $e_{jkl}$ are confounded with $(\beta \gamma S)_{jkl}$ and hence cannot be estimated.

The following table contains the expected MS for the two-way RM design with repeated measures on both factors. These are used in the construction of $F$ tests.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>MS</th>
<th>$E(\text{MS})$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between Subjects</td>
<td>( n - 1 )</td>
<td>$MS_S$</td>
<td>$\sigma^2 + bc\sigma^2_1$</td>
</tr>
<tr>
<td>Subjects (S)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Within Subjects</td>
<td>( b - 1 )</td>
<td>$MS_b$</td>
<td>$\sigma^2 + bc\sigma^2_1 + \frac{nc}{b-1} \sum \beta_j^2$</td>
</tr>
<tr>
<td>$B$</td>
<td>( (b - 1)(n - 1) )</td>
<td>$MS_{b1}$</td>
<td>$\sigma^2 + \sigma_b^2 + \frac{n}{b-1} \sum \beta_j^2$</td>
</tr>
<tr>
<td>$B \times S$</td>
<td>( c - 1 )</td>
<td>$MS_c$</td>
<td>$\sigma^2 + b \sigma_c^2 + \frac{nb}{c-1} \sum \gamma_k^2$</td>
</tr>
<tr>
<td>$C \times S$</td>
<td>( (c - 1)(n - 1) )</td>
<td>$MS_{bc}$</td>
<td>$\sigma^2 + b \sigma_c^2 + \frac{n}{(b-1)(c-1)} \sum (\beta \gamma)_{jk}$</td>
</tr>
<tr>
<td>$BC \times S$</td>
<td>( (b - 1)(c - 1)(n - 1) )</td>
<td>$MS_3$</td>
<td>$\sigma^2 + \sigma_b^2 + \sigma_c^2 + \frac{n}{(b-1)(c-1)} \sum (\beta \gamma)_{jk}$</td>
</tr>
</tbody>
</table>

The following ANOVA table gives the $F$ tests to test for main effects:
CHAPTER 6. MORE ON REPEATED MEASUREMENT DESIGNS

Source | df | MS | F
--- | --- | --- | ---
Between Subjects
Subjects (S) | n − 1 | MS_S |
Within Subjects
B | b − 1 | MS_b | F_b = MS_b / MS_1
B × S | (b − 1)(n − 1) = df_1 | MS_1 |
C | c − 1 | MS_c | F_c = MS_c / MS_2
C × S | (c − 1)(n − 1) = df_2 | MS_bc | F_bc = MS_bc / MS_3
BC | (b − 1)(c − 1) | MS_3 |
BC × S | (b − 1)(c − 1)(n − 1) = df_3 | MS_3 |

Mean comparisons are made using the following standard errors:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>df</th>
</tr>
</thead>
<tbody>
<tr>
<td>Main Effects</td>
<td>( \beta_j - \beta_{j'} )</td>
<td>( \bar{y}<em>{j..} - \bar{y}</em>{j'..} )</td>
<td>( \sqrt{\frac{2MS_c}{cn}} )</td>
</tr>
<tr>
<td></td>
<td>( \gamma_k - \gamma_{k'} )</td>
<td>( \bar{y}<em>{k.} - \bar{y}</em>{k'} )</td>
<td>( \sqrt{\frac{2MS_b}{bn}} )</td>
</tr>
<tr>
<td>Simple Main Effects</td>
<td>( \mu_{jk} - \mu_{j'k} )</td>
<td>( \bar{y}<em>{jk} - \bar{y}</em>{j'k} )</td>
<td>( \sqrt{\frac{2(df_1MS_1 + df_3MS_3)}{n(df_1 + df_3)}} )</td>
</tr>
<tr>
<td></td>
<td>( \mu_{jk} - \mu_{jk'} )</td>
<td>( \bar{y}<em>{jk} - \bar{y}</em>{jk'} )</td>
<td>( \sqrt{\frac{2(df_2MS_2 + df_3MS_3)}{n(df_2 + df_3)}} )</td>
</tr>
</tbody>
</table>

The degrees of freedoms for the simple main effects are approximated using Satterthwaite approximation formulae:

\[
df_4 = \frac{(df_1MS_1 + df_3MS_3)^2}{df_1(MS_1)^2 + df_3(MS_3)^2}
\]

\[
df_5 = \frac{(df_2MS_2 + df_3MS_3)^2}{df_2(MS_2)^2 + df_3(MS_3)^2}
\]

Three sphericity conditions corresponding to \( F_b \), \( F_c \), and \( F_{bc} \) need to be checked. If the (S) condition is not satisfied, then G-G e-adjusted \( F \) tests followed by paired \( t \) tests for mean comparisons need to be performed.

The generic SAS Proc GLM code for analyzing two-way repeated measurement designs with repeated measures on both subjects is

```
PROC GLM;
MODEL Y11 Y12 ... Ybc = / NOUNI;
REPEATED B b, C c;
```

The following is part of an example taken from Milliken and Johnson, *The Analysis of Messy Data, Vol. I*.

The attitudes of families were measured every six months for three time periods. The data were obtained for seven families, each family consisting of a son, father, and mother. The data are given as follows:

<table>
<thead>
<tr>
<th>Person</th>
<th>Family</th>
<th>T_1</th>
<th>T_2</th>
<th>T_3</th>
<th>T_1</th>
<th>T_2</th>
<th>T_3</th>
<th>T_1</th>
<th>T_2</th>
<th>T_3</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
<td>12</td>
<td>11</td>
<td>14</td>
<td>19</td>
<td>12</td>
<td>16</td>
<td>16</td>
<td>19</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>13</td>
<td>13</td>
<td>17</td>
<td>18</td>
<td>19</td>
<td>22</td>
<td>16</td>
<td>16</td>
<td>19</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>12</td>
<td>13</td>
<td>16</td>
<td>19</td>
<td>18</td>
<td>22</td>
<td>17</td>
<td>16</td>
<td>20</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>18</td>
<td>18</td>
<td>21</td>
<td>22</td>
<td>23</td>
<td>18</td>
<td>17</td>
<td>16</td>
<td>20</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>15</td>
<td>14</td>
<td>16</td>
<td>15</td>
<td>15</td>
<td>19</td>
<td>17</td>
<td>17</td>
<td>20</td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>6</td>
<td>6</td>
<td>10</td>
<td>15</td>
<td>16</td>
<td>19</td>
<td>18</td>
<td>19</td>
<td>21</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>16</td>
<td>17</td>
<td>18</td>
<td>17</td>
<td>17</td>
<td>21</td>
<td>18</td>
<td>20</td>
<td>23</td>
</tr>
</tbody>
</table>
The SAS analysis of the data is given as follows:

```sas
DATA RM;
INPUT Y1-Y9;
CARDS;
12 11 14 18 19 22 16 16 19
13 13 17 18 19 22 16 16 19
12 13 16 19 18 22 17 16 20
18 18 21 23 23 26 23 22 26
15 14 16 15 19 17 17 20
6 6 10 15 19 18 19 21
16 17 18 17 21 18 20 23
;
PROC GLM;
MODEL Y1--Y9 = / NOUNI;
REPEATED B 3, C 3/ PRINTE NOM;
RUN;
QUIT;

DATA RM2;
SET RM;
ARRAY Z Y1--Y9;
DO I=1 TO 9;
  Y = Z[I];
  S = _N_;  
  IF (MOD(I,3) = 0) THEN DO;
    B = ROUND(I/3);
    C = ROUND(I/B);
    OUTPUT;
  END;
  ELSE DO;
    B = FLOOR(I/3) + 1;
    C = MOD(I,3);
    OUTPUT;
  END;
END;
DROP Y1-Y9;
RUN;
QUIT;

PROC GLM DATA = RM2;
CLASS S B C;
MODEL Y = B|C|S;
TEST H=B E=B*S;
TEST H=C E=C*S;
TEST H=B*C E=B*C*S;
LSMEANS B/ PDIFF E=B*S;
LSMEANS C/PDIFF E=C*S;
LSMEANS B*C/PDIFF E=B*C*S;
RUN;
QUIT;
```

Some selected output from a run of the above program is:

Sphericity Tests(B)
### Sphericity Tests (C)

<table>
<thead>
<tr>
<th>Variables</th>
<th>DF</th>
<th>Criterion</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transformed Variates</td>
<td>2</td>
<td>0.947328</td>
<td>0.2705497</td>
<td>0.8735</td>
</tr>
<tr>
<td>Orthogonal Components</td>
<td>2</td>
<td>0.6578854</td>
<td>2.0936229</td>
<td>0.3511</td>
</tr>
</tbody>
</table>

### Sphericity Tests (BC)

<table>
<thead>
<tr>
<th>Variables</th>
<th>DF</th>
<th>Criterion</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transformed Variates</td>
<td>9</td>
<td>0.0508148</td>
<td>13.159756</td>
<td>0.1555</td>
</tr>
<tr>
<td>Orthogonal Components</td>
<td>9</td>
<td>0.0948413</td>
<td>10.403681</td>
<td>0.3188</td>
</tr>
</tbody>
</table>

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>G - G</th>
<th>H - F</th>
<th>Adj Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>2</td>
<td>350.3809524</td>
<td>175.1904762</td>
<td>14.35</td>
<td>0.0007</td>
<td>0.0012</td>
<td>0.0007</td>
<td></td>
</tr>
<tr>
<td>Error(B)</td>
<td>12</td>
<td>146.5079365</td>
<td>12.2089947</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Greenhouse-Geisser Epsilon 0.8819
Huynh-Feldt Epsilon 1.2212

<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>G - G</th>
<th>H - F</th>
<th>Adj Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>2</td>
<td>144.8571429</td>
<td>72.4285714</td>
<td>258.28</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Error(C)</td>
<td>12</td>
<td>3.3650794</td>
<td>0.2804233</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Greenhouse-Geisser Epsilon 0.7451
Huynh-Feldt Epsilon 0.9348

<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>G - G</th>
<th>H - F</th>
<th>Adj Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>B*C</td>
<td>4</td>
<td>1.33333333</td>
<td>0.33333333</td>
<td>0.82</td>
<td>0.5262</td>
<td>0.4780</td>
<td>0.5237</td>
<td></td>
</tr>
<tr>
<td>Error(B*C)</td>
<td>24</td>
<td>9.77777778</td>
<td>0.40740741</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### Least Squares Means for effect B

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.0005</td>
<td>0.0007 0.0007</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.0005</td>
<td>0.8627 0.8627</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0.0007</td>
<td>0.8627 0.8627</td>
<td></td>
</tr>
</tbody>
</table>

### Least Squares Means for effect C

<table>
<thead>
<tr>
<th>i/j</th>
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<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.3992</td>
<td>&lt;.0001 &lt;.0001</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.3992</td>
<td>&lt;.0001 &lt;.0001</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>&lt;.0001</td>
<td>&lt;.0001 &lt;.0001</td>
<td></td>
</tr>
</tbody>
</table>

### Least Squares Means for effect B C

<table>
<thead>
<tr>
<th>B</th>
<th>C</th>
<th>Y</th>
<th>LSMEAN Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>13.1428571</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
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<td>2</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>16.0000000</td>
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</tr>
<tr>
<td>2</td>
<td>1</td>
<td>17.8571429</td>
<td>4</td>
</tr>
<tr>
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<td>2</td>
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</tr>
<tr>
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<td>3</td>
<td>21.5714286</td>
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</tr>
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<td>17.8571429</td>
<td>7</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>18.0000000</td>
<td>8</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>21.1428571</td>
<td>9</td>
</tr>
</tbody>
</table>
### Chapter 6. More on Repeated Measurement Designs

Least Squares Means for effect B*C
Pr > |t| for H0: LSMean(i)=LSMean(j)

<table>
<thead>
<tr>
<th>1/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1.0000</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1.0000</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>0.4106</td>
<td>&lt;.0001</td>
<td>1.0000</td>
<td>0.6791</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>0.4106</td>
<td>&lt;.0001</td>
<td>0.4106</td>
<td>0.6791</td>
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<td></td>
</tr>
<tr>
<td>6</td>
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<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>0.2212</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>1.0000</td>
<td>0.4106</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>0.2212</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>0.6791</td>
<td>0.6791</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td>&lt;.0001</td>
<td></td>
</tr>
</tbody>
</table>

The following is a summary of the results:

1. The (S) condition is satisfied for all three tests B, C, and BC.
2. The BC(Person by Time) interaction is not significant ($P = 0.5262$).
3. The BC interaction is not significant ($P = 0.5262$).
4. The B(Person) main effect is significant ($P = 0.0007$)
5. Comparison of B(Person) means

<table>
<thead>
<tr>
<th>B1</th>
<th>B3</th>
<th>B2</th>
</tr>
</thead>
<tbody>
<tr>
<td>14.1</td>
<td>19.0</td>
<td>19.2</td>
</tr>
</tbody>
</table>

6. The C(Time) main effect is significant ($P < 0.0001$)
7. Comparison of C(Time) means

<table>
<thead>
<tr>
<th>C1</th>
<th>C2</th>
<th>C3</th>
</tr>
</thead>
<tbody>
<tr>
<td>16.3</td>
<td>16.4</td>
<td>19.6</td>
</tr>
</tbody>
</table>
Chapter 7

Introduction to the Analysis of Covariance

Analysis of covariance (ANCOVA) methods combine regression and ANOVA techniques to investigate the relationship of a response variable with a set of 'treatments' as well as other additional 'background' variables.

7.1 Simple Linear Regression

Let \( y \) be a measured response variable that is believed to depend on a predictor \( x \) up to a random error; that is,

\[
y = f(x) + \varepsilon;.
\]

In a data setting, suppose we have \( n \) experimental units giving rise to observations \((x_1, y_1), (x_2, y_2), \ldots, (x_n, y_n)\). Then our model becomes

\[
y_i = f(x_i) + \varepsilon_i, \quad i = 1, 2, \ldots, n.
\]

In this chapter we will focus our attention to situations where \( y \) depends on \( x \) in a linear fashion; that is,

\[
f(x) = \beta_0 + \beta_1 x,
\]

where \( \beta_0 \) is the intercept and \( \beta_1 \) is the slope. In a data setting,

\[
y_i = \beta_0 + \beta_1 x_i + \varepsilon_i, \quad i = 1, 2, \ldots, n,
\]

where \( \beta_0 \) and \( \beta_1 \) are unknown. We will assume that the random errors, \( \varepsilon_i \), are independent random variables with mean 0 and constant variance \( \sigma^2 \).

Our goal is to estimate and make inferences about the unknown regression coefficients, \( \beta_0 \) and \( \beta_1 \).

7.1.1 Estimation: The Method of Least Squares

The least squares (LS) estimators \( \hat{\beta}_0 \) and \( \hat{\beta}_1 \) of \( \beta_0 \) and \( \beta_1 \), respectively, are the values of \( \beta_0 \) and \( \beta_1 \) that minimize

\[
L(\beta_0, \beta_1) = \sum_{i=1}^{n} \varepsilon_i^2 = \sum_{i=1}^{n} (y_i - \beta_0 - \beta_1 x_i)^2.
\]

Thus the observation \( y_i \) is estimated by the fitted value

\[
\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i.
\]

In other words, the method of least squares gives the least possible sum of squared residuals, \( y_i - \hat{y}_i \).

Using differential calculus, we get the LS estimators as

157
\[ \hat{\beta}_1 = \frac{S_{xy}}{S_{xx}}, \] and \[ \hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x} , \]

where \[ S_{xy} = \sum_{i=1}^{n} (x_i - \bar{x})(y_i - \bar{y}) \] and \[ S_{xx} = \sum_{i=1}^{n} (x_i - \bar{x})^2 . \]

### 7.1.2 Partitioning the Total SS

Similar to ANOVA models, the total sum of squares \( \sum (y_i - \bar{y})^2 \) partitions into smaller variabilities: the variability in the response explained by the regression model and the unexplained variability. This is done as

\[ \sum_{i=1}^{n} (y_i - \bar{y})^2 = \sum_{i=1}^{n} (\hat{y}_i - \bar{y})^2 + \sum_{i=1}^{n} (y_i - \hat{y})^2 \]

i.e.,

\[ SS_T = SS_R + SS_E . \]

Here \( SS_R \) represents the sum of squares due to regression while \( SS_T \) and \( SS_E \) are the familiar SS’s due to total and error, respectively. As before the degrees of freedom for \( SS_T \) partitions into regression df and error df as

\[ n - 1 = 1 + (n - 2) . \]

### 7.1.3 Tests of Hypotheses

One very important question is "Does \( x \) truly influence \( y \)?". Since this is under an assumption of a linear relationship, another way to pose the question will be "Is there a significant linear relationship between \( x \) and \( y \)?" In terms of statistical hypotheses, we are interested in testing

\[ H_0 : \beta_1 = 0 \]
\[ H_A : \beta_1 \neq 0 \]

The rejection of \( H_0 \) indicates that there is a significant linear relationship between \( x \) and \( y \). It does not, however, imply that the model is "good".

Using the partition of the total variability, one may set up an ANOVA table as follows:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>( F )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Regression</td>
<td>1</td>
<td>( SS_R )</td>
<td>( MS_R = SS_R/1 )</td>
<td>( F = MS_R/MS_E )</td>
</tr>
<tr>
<td>Residual</td>
<td>( n-2 )</td>
<td>( SS_E )</td>
<td>( MS_E = SS_E/(n-2) )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>( n-1 )</td>
<td>( SS_T )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

We reject the null if the \( F \)-test is significant at the desired level of significance.

#### Example

Let \( X \) be the length (cm) of a laboratory mouse and let \( Y \) be its weight (gm). Consider the data for \( X \) and \( Y \) given below.

<table>
<thead>
<tr>
<th>( X )</th>
<th>( Y )</th>
</tr>
</thead>
<tbody>
<tr>
<td>16</td>
<td>32</td>
</tr>
<tr>
<td>15</td>
<td>26</td>
</tr>
<tr>
<td>20</td>
<td>40</td>
</tr>
<tr>
<td>13</td>
<td>27</td>
</tr>
<tr>
<td>15</td>
<td>30</td>
</tr>
</tbody>
</table>
The following SAS code is used to perform the simple linear regression.

```sas
DATA SLR;
INPUT X Y;
CARDS;
16 32
15 26
20 40
13 27
15 30
17 38
16 34
21 43
22 64
23 45
24 46
18 39
;
SYMBOL V=CIRCLE I=NONE;
PROC GPLOT;
   TITLE1 'SCATTER PLOT OF Y VS X';
   PLOT Y*X;
RUN;
QUIT;

PROC GLM;
   TITLE1 'REGRESSION OF Y ON X';
   MODEL Y = X;
   OUTPUT OUT=REGOUT R=R P=P;
RUN;
QUIT;

SYMBOL V=CIRCLE I=R;
PROC GPLOT DATA=SLR;
   TITLE1 'SCATTER PLOT OF Y VS X OVERLAYED WITH REGRESSION FIT';
   PLOT Y*X;
RUN;
QUIT;

PROC GPLOT DATA=REGOUT;
   TITLE1 'RESIDUAL PLOT';
   PLOT R*P;
RUN;
QUIT;
```

Selected output from SAS is given below:
Dependent Variable: Y

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type I SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>1</td>
<td>813.763823</td>
<td>813.763823</td>
<td>21.36</td>
<td>0.0009</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>X</td>
<td>1</td>
<td>813.763823</td>
<td>813.763823</td>
<td>21.36</td>
<td>0.0009</td>
</tr>
</tbody>
</table>

Parameter Estimate     Error       t Value   Pr > |t|
Intercept -5.428909953 9.70503506   -0.56     0.5882
X 2.405213270 0.52036911  4.62      0.0009

SCATTER PLOT OF Y VS X
The fitted regression line is

\[ y = -5.43 + 2.41x \]

The length of a mouse is significantly linearly related to the weight of a mouse \((P = 0.0009)\). From the scatter plot and the fitted line, one observes that the relationship between length and weight is an increasing relationship.
7.2 Single Factor Designs with One Covariate

Analysis of Covariance (ANCOVA) unites analysis of variance (ANOVA) and regression. In the one-way ANOVA model, suppose that for each experimental a covariate, $X_{ij}$, is measured along with the response variable, $Y_{ij}$. A covariate is a variable that is thought to have an effect on the response. The ANCOVA model which includes the covariate in a linear model is

$$Y_{ij} = \mu_i + \tau_i + \beta(X_{ij} - \bar{X}) + \epsilon_{ij}$$

This model may be written as

$$Y_{ij} = \mu_i + \beta(X_{ij} - \bar{X}) + \epsilon_{ij}$$

where $\mu_i = \mu + \tau_i$ is the mean of treatment $i$.

The data layout for a single factor ANCOVA model is

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>...</th>
<th>k</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y</td>
<td>$Y_{11}$</td>
<td>$Y_{21}$</td>
<td>...</td>
<td>$Y_{k1}$</td>
</tr>
<tr>
<td>X</td>
<td>$X_{11}$</td>
<td>$X_{21}$</td>
<td>...</td>
<td>$X_{k1}$</td>
</tr>
<tr>
<td></td>
<td>$Y_{12}$</td>
<td>$Y_{22}$</td>
<td>...</td>
<td>$Y_{k2}$</td>
</tr>
<tr>
<td>X</td>
<td>$X_{12}$</td>
<td>$X_{22}$</td>
<td>...</td>
<td>$X_{k2}$</td>
</tr>
<tr>
<td></td>
<td>$Y_{1n_1}$</td>
<td>$Y_{2n_2}$</td>
<td>...</td>
<td>$Y_{kn_k}$</td>
</tr>
<tr>
<td>X</td>
<td>$X_{1n_1}$</td>
<td>$X_{2n_2}$</td>
<td>...</td>
<td>$X_{kn_k}$</td>
</tr>
</tbody>
</table>

In the one-way ANOVA model, $\mu_i$ is unbiasedly estimated by $\hat{\mu}_i = \bar{y}_i$. However, in the ANCOVA model $\bar{y}_i$ is an unbiased estimator of $\mu_i + \beta(\bar{X}_i - \bar{X})$. Thus, $\hat{\mu}_{i,adj} = \bar{y}_i - \hat{\beta}(\bar{X}_i - \bar{X})$ is the adjusted estimator of $\mu_i$ in the ANCOVA model, where $\hat{\beta}$ is the least squares estimator of the common slope parameter, $\beta$.

An essential assumption in the ANCOVA is that there is a common slope parameter, $\beta$. This says that if we were to fit regression lines for each one of the $k$ groups independently, then these lines would be parallel to each other. This assumption is known as the parallelism assumption. The homogeneity of the group slope parameters is an assumption that needs to be tested, i.e., $H_0: \beta_1 = \beta_2 = \cdots = \beta_k$. If this hypothesis is true, then we need a follow up test of the importance of the covariate variable as a predictor, i.e., $H_0: \beta = 0$.

Let $A$ denote the factor of interest. The following is the analysis strategy to follow:

1. **Test whether the covariate $X$ is important:**
   
   (a) Assuming heterogeneous slopes, we test
   
   $$H_0: \beta_1 = \beta_2 = \cdots = \beta_k = 0.$$ 
   
   In SAS
   
   ```sas
   PROC GLM;
   CLASS A;
   MODEL Y = A A*X /NOINT;
   ```
   
   The $P$-value corresponding to $A * X$ is the $P$-value for the test of interest.
   
   (b) Assuming homogeneous slopes, we test
   
   $$H_0: \beta = 0.$$ 
   
   In SAS
   
   ```sas
   PROC GLM;
   CLASS A;
   MODEL Y = A X;
   ```
7.2. SINGLE FACTOR DESIGNS WITH ONE COVARIATE

If both are non-significant, then the covariate $X$ is not needed. If either one of the tests is significant, the we use the ANCOVA model. Go to Step 2.

2. **Test whether there is a common slope:**

   We test
   
   $H_0 : \beta_1 = \beta_2 = \cdots = \beta_k$

   using
   
   \begin{verbatim}
   PROC GLM;
   CLASS A;
   MODEL Y = A X A*X;
   \end{verbatim}

   The $P$-value of interest corresponds to the $A \times X$ term.

   (a) If the test is significant, then we follow a Johnson-Neyman analysis. This will be addressed in a later section.

   (b) If the test is not significant, then we perform the ANCOVA analysis. Using SAS
   
   \begin{verbatim}
   PROC GLM;
   CLASS A;
   MODEL Y = A X;
   \end{verbatim}

   fits the classic ANCOVA model
   
   $Y_{ij} = \mu + \tau_i + \beta(X_{ij} - \bar{X}.) + \epsilon_{ij}$

   and tests $H_0 : \tau_1 = \tau_2 = \cdots = \tau_k = 0$.

   Follow-up pairwise comparisons ($H_0 : \tau_i = \tau_j$) may be performed by including
   
   \begin{verbatim}
   LSMEANS A/PDIFF;
   \end{verbatim}

   in the preceding SAS code.

The following example is adapted from Snedecor and Cochran (1967) (See also SAS Online Documentation).

**Example**

Ten patients are selected for each treatment (Drug), and six sites on each patient are measured for leprosy bacilli. The variables in the study are

- Drug - two antibiotics (A and D) and a control (F)
- PreTreatment - a pre-treatment score of leprosy bacilli
- PostTreatment - a post-treatment score of leprosy bacilli

The covariate (a pretreatment score) is included in the model for increased precision in determining the effect of drug treatments on the posttreatment count of bacilli.

The following is the SAS code used to analyze the data. It is given along with a partial output.

\begin{verbatim}
DATA DRUGTEST;
  input DRUG $ PRE POST @@;
  CARDS;
  A 11 6 A 8 0 A 5 2 A 14 8 A 19 11
  A 6 4 A 10 13 A 6 1 A 11 8 A 3 0
  D 6 0 D 6 2 D 7 3 D 8 1 D 18 18
\end{verbatim}
CHAPTER 7. INTRODUCTION TO THE ANALYSIS OF COVARIANCE

```
D  8  4  D 19 14  D  8  9  D  5  1  D 15  9
F 16 13  F 13 10  F 11 18  F  9  5  F 21 23
F 16 12  F 12  5  F 12 16  F  7  1  F 12 20

; PROC GLM;
CLASS DRUG;
MODEL POST = DRUG DRUG*PRE / NOINT;
RUN;
QUIT;

PROC GLM;
CLASS DRUG;
MODEL POST = DRUG PRE DRUG*PRE;
RUN;
QUIT;

PROC GLM;
CLASS DRUG;
MODEL POST = DRUG PRE;
MEANS DRUG;
LSMEANS DRUG/ STDERR PDIFF TDIFF;
RUN;
QUIT;
```

---

**Dependent Variable: POST**

<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>DRUG</td>
<td>3</td>
<td>2165.90000000</td>
<td>721.966667</td>
<td>43.58</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>PRE*DRUG</td>
<td>3</td>
<td>597.542048</td>
<td>199.180683</td>
<td>12.02</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>24</td>
<td>397.557952</td>
<td>16.564915</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>30</td>
<td>3161.00000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Dependent Variable: POST**

<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>DRUG</td>
<td>2</td>
<td>293.60000000</td>
<td>146.800000</td>
<td>8.86</td>
<td>0.0013</td>
</tr>
<tr>
<td>PRE</td>
<td>1</td>
<td>577.897403</td>
<td>577.897403</td>
<td>34.89</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>PRE*DRUG</td>
<td>2</td>
<td>19.646451</td>
<td>9.8223226</td>
<td>0.59</td>
<td>0.5606</td>
</tr>
<tr>
<td>Error</td>
<td>24</td>
<td>397.557952</td>
<td>16.564915</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>29</td>
<td>1288.700000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Dependent Variable: POST**

<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>DRUG</td>
<td>2</td>
<td>293.60000000</td>
<td>146.800000</td>
<td>9.15</td>
<td>0.0010</td>
</tr>
<tr>
<td>PRE</td>
<td>1</td>
<td>577.897403</td>
<td>577.897403</td>
<td>36.01</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>
7.2. SINGLE FACTOR DESIGNS WITH ONE COVARIATE

<table>
<thead>
<tr>
<th>Level of</th>
<th>POST</th>
<th>PRE</th>
</tr>
</thead>
<tbody>
<tr>
<td>DRUG</td>
<td>Mean Std Dev</td>
<td>Mean Std Dev</td>
</tr>
<tr>
<td>A</td>
<td>5.30 4.64399254</td>
<td>9.30 4.76211904</td>
</tr>
<tr>
<td>D</td>
<td>6.10 6.15449249</td>
<td>10.00 5.24933858</td>
</tr>
<tr>
<td>F</td>
<td>12.30 7.14998057</td>
<td>12.90 3.95671019</td>
</tr>
</tbody>
</table>

Standard LSMEAN

<table>
<thead>
<tr>
<th>DRUG</th>
<th>POST LSMEAN</th>
<th>Error</th>
<th>Pr &gt;</th>
<th>t</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>6.7149635</td>
<td>1.2884943</td>
<td>&lt;.0001</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>6.8239348</td>
<td>1.2724690</td>
<td>&lt;.0001</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>10.1611017</td>
<td>1.3159234</td>
<td>&lt;.0001</td>
<td>3</td>
<td></td>
</tr>
</tbody>
</table>

Least Squares Means for Effect DRUG

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-0.0607</td>
<td>-1.82646</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.9521</td>
<td>0.0793</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.060704</td>
<td>-1.80011</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.9521</td>
<td>0.0835</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>1.826465</td>
<td>1.800112</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.0793</td>
<td>0.0835</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

An observation is that the results of MEANS and LSMEANS are quite different. LSMEANS gives the adjusted means while MEANS gives the raw means. Here is a summary of the results:

1. Is the covariate important?
   (a) The hypothesis $H_0: \beta_1 = \beta_2 = \beta_3 = 0$ is rejected ($F = 12.02, P < 0.0001$).
   (b) The hypothesis $H_0: \beta = 0$ is rejected ($F = 36.01, P < 0.0001$).

   Thus, the covariate is important and needs to be included in the model.

2. Do we have a common slope?
   We fail to reject the hypothesis $H_0: \beta_1 = \beta_2 = \beta_3$ ($F = 0.59, P = 0.5606$). Thus, the assumption of a common slope is a valid assumption.

   The test for treatment effects, $H_0: \tau_1 = \tau_2 = \tau_3 = 0$, is significant ($F = 9.15, P = 0.0010$).

   None of the pairwise differences is significant at $\alpha = .05$. 
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7.3 ANCOVA in Randomized Complete Block Designs

We will consider the case where a single covariate is observed along with the response in a RCBD. The analysis of such a design proceeds in the same manner as the single factor design considered above.

The statistical model for the RCBD ANCOVA is

\[ Y_{ij} = \mu + \tau_i + \gamma_j + \beta(X_{ij} - \bar{X}) + \epsilon_{ij} \]

where \( i = 1, \cdots, k \), \( j = 1, \cdots, n \), and \( \gamma_j \) is the effect of the \( j \)th block of \( n \) blocks.

Let \( A \) denote the factor of interest and \( B \) be the blocking factor. The following is the analysis strategy to follow:

1. **Test whether the covariate \( X \) is important:**
   - **(a)** Assuming heterogeneous slopes, we test
     \[ H_0 : \beta_1 = \beta_2 = \cdots = \beta_k = 0 \, . \]
     In SAS
     ```sas
     PROC GLM;
     CLASS A;
     MODEL Y = A B A*X /NOINT;
     ```
     The \( P \)-value corresponding to \( A \times X \) is the \( P \)-value for the test of interest.
   - **(b)** Assuming homogeneous slopes, we test
     \[ H_0 : \beta = 0 \, . \]
     In SAS
     ```sas
     PROC GLM;
     CLASS A;
     MODEL Y = A B X;
     ```
     If both are non-significant, then the covariate \( X \) is not needed. If either one of the tests is significant, we use the ANCOVA model. Go to Step 2.

2. **Test whether there is a common slope:**
   We test
   \[ H_0 : \beta_1 = \beta_2 = \cdots = \beta_k \]
   using
   ```sas
   PROC GLM;
   CLASS A;
   MODEL Y = A B X A*X;
   ```
   The \( P \)-value of interest corresponds to the \( A \times X \) term.
   - **(a)** If the test is significant, then we follow a Johnson-Neyman type analysis.
   - **(b)** If the test is not significant, then we perform the ANCOVA analysis. Using SAS
     ```sas
     PROC GLM;
     CLASS A;
     MODEL Y = A B X;
     ```
7.3. ANCOVA IN RANDOMIZED COMPLETE BLOCK DESIGNS

fits the RCBD ANCOVA model

\[ Y_{ij} = \mu + \tau_i + \gamma_j + \beta(X_{ij} - \bar{X}_.) + \epsilon_{ij} \]

and tests \( H_0 : \tau_1 = \tau_2 = \cdots = \tau_k = 0 \).

Follow-up pairwise comparisons (\( H_0 : \tau_i = \tau_j \)) may be performed by including

\textsc{lsmeans a/pdiff;}

in the preceding SAS code.

The following example is taken from Wishart (1949).

**Example**

Yields for 3 varieties of a certain crop in a randomized complete block design with 4 blocks are considered. The variables of interest are

- \( X \) = yield of a plot in a previous year
- \( Y \) = yield on the same plot for the experimental year

The data are as follows:

<table>
<thead>
<tr>
<th>Varieties</th>
<th>Block</th>
<th>A</th>
<th>B</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
<td>54</td>
<td>51</td>
<td>57</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Y</td>
<td>64</td>
<td>65</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>62</td>
<td>64</td>
<td>60</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Y</td>
<td>68</td>
<td>69</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>51</td>
<td>47</td>
<td>46</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Y</td>
<td>54</td>
<td>60</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>53</td>
<td>50</td>
<td>41</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Y</td>
<td>62</td>
<td>66</td>
</tr>
</tbody>
</table>

The SAS analysis of the data is as follows:

\texttt{DATA CROP;}
\texttt{INPUT A \$ B Y X;}
\texttt{CARDS;}
\texttt{ A 1 64 54}
\texttt{ A 2 68 62}
\texttt{ A 3 54 51}
\texttt{ A 4 62 53}
\texttt{ B 1 65 51}
\texttt{ B 2 69 64}
\texttt{ B 3 60 47}
\texttt{ B 4 66 50}
\texttt{ C 1 72 57}
\texttt{ C 2 70 60}
\texttt{ C 3 57 46}
\texttt{ C 4 61 41}

;
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PROC GLM;
   CLASS A B;
   MODEL Y = A B A*X / NOINT;
RUN;
QUIT;

PROC GLM;
   CLASS A B;
   MODEL Y = A B X A*X;
RUN;
QUIT;

PROC GLM;
   CLASS A B;
   MODEL Y = A B X;
   LSMEANS A / STDERR PDIFF TDIFF;
RUN;
QUIT;

Dependent Variable: Y

<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>
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<td>16392.00000</td>
<td>8503.32</td>
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</tr>
<tr>
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<td>3</td>
<td>252.00000</td>
<td>84.00000</td>
<td>43.57</td>
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</tr>
<tr>
<td>X*A</td>
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<td>42.21685</td>
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<td>7.30</td>
<td>0.0684</td>
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<tr>
<td>Error</td>
<td>3</td>
<td>5.78315</td>
<td>1.92772</td>
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<td></td>
</tr>
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</table>

Dependent Variable: Y

<table>
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<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
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<td>24.0000000</td>
<td>12.0000000</td>
<td>6.22</td>
<td>0.0856</td>
</tr>
<tr>
<td>B</td>
<td>3</td>
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<td>84.0000000</td>
<td>43.57</td>
<td>0.0057</td>
</tr>
<tr>
<td>X</td>
<td>1</td>
<td>24.6046512</td>
<td>24.6046512</td>
<td>12.76</td>
<td>0.0375</td>
</tr>
<tr>
<td>X*A</td>
<td>2</td>
<td>17.6121953</td>
<td>8.8060976</td>
<td>4.57</td>
<td>0.1229</td>
</tr>
<tr>
<td>Error</td>
<td>3</td>
<td>5.7831535</td>
<td>1.9277178</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>11</td>
<td>324.0000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Dependent Variable: Y

<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>A</td>
<td>2</td>
<td>24.0000000</td>
<td>12.0000000</td>
<td>2.56</td>
<td>0.1712</td>
</tr>
<tr>
<td>B</td>
<td>3</td>
<td>252.0000000</td>
<td>84.0000000</td>
<td>17.95</td>
<td>0.0042</td>
</tr>
<tr>
<td>X</td>
<td>1</td>
<td>24.6046512</td>
<td>24.6046512</td>
<td>5.26</td>
<td>0.0704</td>
</tr>
<tr>
<td>Error</td>
<td>5</td>
<td>23.3953488</td>
<td>4.6790698</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>11</td>
<td>324.0000000</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
7.3. ANCOVA IN RANDOMIZED COMPLETE BLOCK DESIGNS

Least Squares Means

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th></th>
<th>B</th>
<th></th>
<th>C</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Y LSMEAN</td>
<td>Error</td>
<td>Pr &gt;</td>
<td>t</td>
<td></td>
<td>Number</td>
</tr>
<tr>
<td>A</td>
<td>60.9302326</td>
<td>1.1778789</td>
<td>&lt;.0001</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>65.0000000</td>
<td>1.0815579</td>
<td>&lt;.0001</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>66.0697674</td>
<td>1.1778789</td>
<td>&lt;.0001</td>
<td>3</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Least Squares Means for Effect A

\[
t \text{for H0: LSMean(i)=LSMean(j) / Pr > |t|}
\]

Dependent Variable: Y

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-2.54501</td>
<td>-2.86858</td>
<td>0.0516</td>
</tr>
<tr>
<td>2</td>
<td>2.545014</td>
<td>-0.66898</td>
<td>0.0516</td>
</tr>
<tr>
<td>3</td>
<td>2.868582</td>
<td>0.668975</td>
<td>0.0351</td>
</tr>
</tbody>
</table>

The covariate \( X \) does not appear to be very important (\( P = 0.0684 \) for heterogeneous slopes and \( P = 0.0704 \) for a single slope). However, we will keep it in the analysis for the sake of illustration. Besides, with \( P \)-values close to 0.05, this is the conservative route to follow.

The test for the equality of slopes is not rejected (\( P = 0.1229 \)). Thus, the assumption of a common slope is justified.

The test for treatment effect is not significant. Hence, we fail to detect any difference in yield among the 3 different crop varieties after adjusting for yield differences of the previous year.

The results of the pairwise testing are summarized below using underlining.

<table>
<thead>
<tr>
<th>Group</th>
<th>A</th>
<th>B</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>60.9302326</td>
<td>65.0000000</td>
<td>66.0697674</td>
</tr>
</tbody>
</table>

--------------------------
7.4 ANCOVA in Two-Factor Designs

We will start by recalling the balanced two-factor fixed effects analysis of variance model

\[ y_{ijk} = \mu + \tau_i + \gamma_j + (\tau\gamma)_{ij} + \epsilon_{ijk}, \]

where

\[
\sum_{i=1}^{a} \tau_i = \sum_{j=1}^{b} \gamma_j = \sum_{i=1}^{a} (\tau\gamma)_{ij} = \sum_{j=1}^{b} (\tau\gamma)_{ij} = 0.
\]

and \( \epsilon_{ijk} \sim iid \ N(0, \sigma^2). \)

We shall consider the case where a covariate \( x_{ijk} \) is observed along with the response for each experimental unit. The corresponding two-factor fixed effects ANCOVA model is

\[ y_{ijk} = \mu + \tau_i + \gamma_j + (\tau\gamma)_{ij} + \beta_{ij}(x_{ijk} - \bar{x}) + \epsilon_{ijk}, \]

under the same assumptions.

As in the one-way model, the means \( \mu_i, \mu_j, \) and \( \mu_{ij} \) are estimated by the adjusted means

\[
\hat{\mu}_i = \bar{y}_i - \bar{\beta}(\bar{x}_i - \bar{x})
\]

\[
\hat{\mu}_j = \bar{y}_j - \bar{\beta}(\bar{x}_j - \bar{x})
\]

\[
\hat{\mu}_{ij} = \bar{y}_{ij} - \bar{\beta}(\bar{x}_{ij} - \bar{x})
\]

The major assumption, once again, is the homogeneity of the slopes. If that assumption is not satisfied, then our model may be written as

\[ y_{ijk} = \mu + \tau_i + \gamma_j + (\tau\gamma)_{ij} + \beta_{ij}(x_{ijk} - \bar{x}) + \epsilon_{ijk}, \]

under the same assumptions as above. Thus, the hypothesis

\[ H_0 : \beta_{11} = \ldots = \beta_{ab} = \beta \]

is of interest. We may use the one-way ANCOVA methods to perform the test by rewriting the model as

\[ y_{sk} = \mu_s + \beta_s(x_{sk} - \bar{x}) + \epsilon_{sk}, \]

which is obtained by "rolling-out" the cells into one big vector as

\[
(i,j) \quad (1,1) \quad (1,2) \quad \ldots \quad (a, b-1) \quad (a,b)
\]

\[
s \quad 1 \quad 2 \quad \ldots \quad ab - 1 \quad ab
\]

The correspondence between \( s \) and \( (i,j) \) is according to the formula

\[ s = b(i - 1) + j. \]

The analysis of two-way ANCOVA is performed as follows:

1. Test for the homogeneity of the slopes.
2. If the slopes are not heterogeneous, test main and simple effects using the adjusted means. If the slopes are heterogeneous, use a Johnson-Neyman analysis.

The following example is taken from Neter, Kutner, Nachtsheim, and Wasserman. Applied Linear Statistical Models.
Example

A horticulturist conducted an experiment to study the effects of flower variety (factor $A$) and moisture level (factor $B$) on yield of salable flowers ($Y$). Because the plots were not of the same size, the horticulturist wished to use plot size ($X$) as the concomitant variable. Six replications were made for each treatment. The data are presented below:

<table>
<thead>
<tr>
<th>Factor A</th>
<th>B₁ (low) $Y_{i1k}$</th>
<th>X₁₁k</th>
<th>B₂ (high) $Y_{i2k}$</th>
<th>X₁₂k</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A_1$ (variety LP)</td>
<td>98 15 71 10</td>
<td>60 4 80 12</td>
<td>77 7 86 14</td>
<td>80 9 82 13</td>
</tr>
<tr>
<td>$A_2$ (variety WB)</td>
<td>55 4 76 11</td>
<td>60 5 68 10</td>
<td>75 8 43 2</td>
<td>65 7 47 3</td>
</tr>
</tbody>
</table>

The following SAS code is used to analyze the above example. A partial output is given following the code:

```sas
DATA FLOWERS;
INPUT A B Y X @@;
C = 2*(A-1)+B;
CARDS;
1 1 98 15 1 2 71 10
1 1 60 4 1 2 80 12
1 1 77 7 1 2 86 14
1 1 80 9 1 2 82 13
1 1 95 14 1 2 46 2
1 1 64 5 1 2 55 3
2 1 55 4 2 2 76 11
2 1 60 5 2 2 68 10
2 1 75 8 2 2 43 2
2 1 65 7 2 2 47 3
2 1 87 13 2 2 62 7
2 1 78 11 2 2 70 9
;
PROC GLM;
  TITLE1 'HOMOGENEITY OF SLOPES';
  CLASS C;
  MODEL Y = C X C*X;
RUN;
QUIT;

PROC GLM;
  TITLE1 'TWO-WAY ANCOVA';
```
CHAPTER 7. INTRODUCTION TO THE ANALYSIS OF COVARIANCE

CLASS A B;
MODEL Y = A B A*B X;
LSMEANS A B A*B / STDERR PDIFF TDIFF;
RUN;
QUIT;

HOMOGENEITY OF SLOPES

Dependent Variable: Y

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
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<td>87.399785</td>
<td>29.133262</td>
<td>4.29</td>
<td>0.0212</td>
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<tr>
<td>X</td>
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<tr>
<td>X*C</td>
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<td>10.733375</td>
<td>3.577792</td>
<td>0.53</td>
<td>0.6704</td>
</tr>
<tr>
<td>Error</td>
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<td>108.747808</td>
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</tr>
<tr>
<td>Total</td>
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<td></td>
</tr>
</tbody>
</table>

TWO-WAY ANCOVA

Dependent Variable: Y

<table>
<thead>
<tr>
<th>Source</th>
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<th>Pr &gt; F</th>
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</thead>
<tbody>
<tr>
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<td>96.601826</td>
<td>96.601826</td>
<td>15.36</td>
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<td>B</td>
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<td>323.849473</td>
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<td>3994.518817</td>
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<tr>
<td>Total</td>
<td>23</td>
<td>5086.000000</td>
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<td></td>
<td></td>
</tr>
</tbody>
</table>

Least Squares Means

<table>
<thead>
<tr>
<th>Standard</th>
<th>H0:LSMEAN=0</th>
<th>H0:LSMean1=LSMean2</th>
</tr>
</thead>
<tbody>
<tr>
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<td>Y LSMEAN</td>
<td>Error Pr &gt;</td>
</tr>
<tr>
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<tr>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Standard</th>
<th>H0:LSMEAN=0</th>
<th>H0:LSMean1=LSMean2</th>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>Y LSMEAN</td>
<td>Error Pr &gt;</td>
</tr>
<tr>
<td>1</td>
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<td>0.7246356 &lt;.0001 7.18 &lt;.0001</td>
</tr>
<tr>
<td>2</td>
<td>66.3192204</td>
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</table>

<table>
<thead>
<tr>
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<th>LSMEAN</th>
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</thead>
<tbody>
<tr>
<td>A</td>
<td>B</td>
</tr>
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<td>76.5423387</td>
</tr>
<tr>
<td>1 2</td>
<td>67.5423387</td>
</tr>
<tr>
<td>2 1</td>
<td>70.8192204</td>
</tr>
<tr>
<td>2 2</td>
<td>65.0961022</td>
</tr>
</tbody>
</table>

Least Squares Means for Effect A*B
7.4. ANCOVA IN TWO-FACTOR DESIGNS

\[ t \text{ for } H_0: \text{LSMean}(i) = \text{LSMean}(j) \] 
\[ / \Pr > |t| \]

Dependent Variable: Y

<table>
<thead>
<tr>
<th>i/j</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
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</thead>
<tbody>
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<td>1</td>
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<tr>
<td></td>
<td>&lt;.0001</td>
<td>0.0009</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>2</td>
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<td>-2.254261</td>
<td>1.662999</td>
<td></td>
</tr>
<tr>
<td></td>
<td>&lt;.0001</td>
<td>0.0362</td>
<td>0.1127</td>
<td></td>
</tr>
<tr>
<td>3</td>
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<td>2.254261</td>
<td>3.937098</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.0009</td>
<td>0.0362</td>
<td>0.0009</td>
<td></td>
</tr>
<tr>
<td>4</td>
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<td>-1.663</td>
<td>-3.9371</td>
<td></td>
</tr>
<tr>
<td></td>
<td>&lt;.0001</td>
<td>0.1127</td>
<td>0.0009</td>
<td></td>
</tr>
</tbody>
</table>

Thus

1. The parallelism hypothesis

\[ H_0 : \beta_{11} = \beta_{12} = \beta_{21} = \beta_{22} = \beta \]

is not rejected \((P = 0.6704)\). The ANCOVA model with a common slope is valid.

2. Comparisons of means results:

   (a) The \(AB\) interaction effect fails to be significant \((P = 0.1267)\). We may compare \(A\) and \(B\) means at the main effect level.

   (b) The \(A\) main effect is significant \((P = 0.0009)\).

   (c) The \(B\) main effect is significant \((P < 0.0001)\).

   (d) The hypothesis \(H_0 : \beta = 0\) is rejected \((P < 0.0001)\). Thus the inclusion of the covariate is justified.
7.5 The Johnson-Neyman Technique: Heterogeneous Slopes

7.5.1 Two Groups, One Covariate

We shall now consider ANCOVA designs where the assumption of equal slopes is not satisfied. This happens when the treatment effect is dependent upon the value of the covariate, \( X \). In other words, there is a significant interaction between the levels of the treatment and the covariate variable. Heterogeneous slopes present a problem in ANCOVA in that it is impossible to claim significance or non-significance of the treatment effect throughout the range of the covariate under consideration.

The following plot gives a case where the heterogeneity of the slopes is clear. The difference between the two lines is clearly not significant for values of \( X \) near 6.5; however, there may be a significant difference between the lines for values of \( X \) around 2.

Thus we wish to test if there is a significant treatment effect for a chosen value of the covariate \( X \). The Johnson-Neyman procedure generalizes this process by identifying the values of the covariate for which there is a significant difference between the levels of the treatment.

The following example is taken from Huitema (1980): *The Analysis of Covariance and Alternatives*.

**Example**

Suppose that the data in the following table are based on an experiment in which the treatments consist of two methods of therapy. Scores on a sociability scale are employed as a covariate. The dependent variable is the aggressiveness score on a behavioral checklist.
Using SAS, we get the following two regression lines:

![Graph showing two regression lines](image)

The slopes are heterogeneous. The following SAS code may be used to fit the heterogeneous slope ANCOVA and test for significance of the difference between the two methods of therapy on a case by case basis. A partial output is given following the code.

```sas
data jn;
  input grp x y;
  cards;
  1 1 10
  1 2 10
  1 2 11
  1 3 10
  1 4 11
  1 5 11
  1 5 10
  1 6 11
```

The slopes are heterogeneous. The following SAS code may be used to fit the heterogeneous slope ANCOVA and test for significance of the difference between the two methods of therapy on a case by case basis. A partial output is given following the code.

```sas
data jn;
  input grp x y;
  cards;
  1 1 10
  1 2 10
  1 2 11
  1 3 10
  1 4 11
  1 5 11
  1 5 10
  1 6 11
```
CHAPTER 7. INTRODUCTION TO THE ANALYSIS OF COVARIANCE

1  6  11.5
1  7  12
1  8  12
1  8  11
1  9  11
1 10  12.5
1 11  12
2  1  5
2  1.5  6
2  2.5  6
2  3.5  7
2  4.5  8
2  4.5  9
2  5  9
2  6  9
2  6  10.5
2  7  11
2  7  12.5
2  7.5  12.5
2  8  14
2  9  14.5
2 10  16

; goptions reset=symbol;
symbol1 c=black v=dot l=1 i=r;
symbol2 c=black v=square l=1 i=r;

proc gplot;
  plot y*x=grp;
run;
quit;

PROC GLM DATA=JN;
  CLASS GRP;
  MODEL Y = GRP X GRP*X;
  LSMEANS GRP/ AT X=5 PDIFF;
  LSMEANS GRP/ AT X=6.5 PDIFF TDIFF;
  LSMEANS GRP/ AT X=6.7 PDIFF TDIFF;
  LSMEANS GRP/ AT X=8 PDIFF TDIFF;
RUN;
QUIT;

<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>grp</td>
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<td>64.1707155</td>
<td>64.1707155</td>
<td>152.79</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>x</td>
<td>1</td>
<td>117.7551731</td>
<td>117.7551731</td>
<td>280.37</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>x*grp</td>
<td>1</td>
<td>59.5963693</td>
<td>59.5963693</td>
<td>141.90</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>26</td>
<td>10.9199841</td>
<td>0.4199994</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
7.5. THE JOHNSON-NEYMAN TECHNIQUE: HETEROGENEOUS SLOPES

Total 29 176.9666667

**Least Squares Means at x=5**

\[ H_0: \text{LSMean}_1 = \text{LSMean}_2 \]

| grp | y LSMEAN | Pr > |t| |
|-----|----------|-------|
| 1   | 10.8997955 | <.0001 |
| 2   | 9.3402754  |       |

**Least Squares Means at x=6.5**

\[ H_0: \text{LSMean}_1 = \text{LSMean}_2 \]

| grp | y LSMEAN | t Value | Pr > |t| |
|-----|----------|---------|-------|
| 1   | 11.2126789 | 0.07 | 0.9461 |
| 2   | 11.1957508 |       |       |

**Least Squares Means at x=6.7**

\[ H_0: \text{LSMean}_1 = \text{LSMean}_2 \]

| grp | y LSMEAN | t Value | Pr > |t| |
|-----|----------|---------|-------|
| 1   | 11.2543967 | -0.74 | 0.4636 |
| 2   | 11.4431475 |       |       |

**Least Squares Means at x=8**

\[ H_0: \text{LSMean}_1 = \text{LSMean}_2 \]

| grp | y LSMEAN | t Value | Pr > |t| |
|-----|----------|---------|-------|
| 1   | 11.5255624 | -4.89 | <.0001 |
| 2   | 13.0512261 |       |       |

Thus, there is a significant difference between the two methods of therapy for an individual with a sociability scale of 5 (\( P < 0.0001 \)), while we fail to find a significant treatment effect for an individual with a sociability scale of 6.5 (\( P = 0.9461 \)).

Let the regression lines fitted individually for groups 1 and 2 be \( \hat{Y}_1 = \hat{\alpha}_1 + \hat{\beta}_1 X_1 \) and \( \hat{Y}_2 = \hat{\alpha}_2 + \hat{\beta}_2 X_2 \), respectively. Let \( \bar{X}_1 \) and \( \bar{X}_2 \) be the sample means of the covariate associated with the two groups while

\[
S_{XX_1} = \sum_{i=1}^{n_1} (X_{1i} - \bar{X}_1)^2, \quad S_{XX_2} = \sum_{i=1}^{n_2} (X_{2i} - \bar{X}_2)^2
\]

where \( n_1 \) and \( n_2 \) are the respective sample sizes.

We can identify the lower and upper limits, \( X_L \) and \( X_U \), of the region of non-significance on \( X \) using the following formulæ:

\[
X_L = \frac{-B - \sqrt{B^2 - 4AC}}{2A}
\]

\[
X_U = \frac{-B + \sqrt{B^2 - 4AC}}{2A}
\]

where

\[
A = -d \left( \frac{1}{S_{XX_1}} + \frac{1}{S_{XX_2}} \right) + (\hat{\beta}_1 - \hat{\beta}_2)^2
\]

\[
B = d \left( \frac{\bar{X}_1}{S_{XX_1}} + \frac{\bar{X}_2}{S_{XX_2}} \right) + (\hat{\alpha}_1 - \hat{\alpha}_2)(\hat{\beta}_1 - \hat{\beta}_2)
\]

\[
C = -d \left( \frac{1}{n_1} + \frac{1}{n_2} + \frac{\bar{X}_1^2}{S_{XX_1}} + \frac{\bar{X}_2^2}{S_{XX_2}} \right) + (\hat{\alpha}_1 - \hat{\alpha}_2)^2
\]
Here
\[ d = (t_{n_1+n_2-4}(\alpha/2))^2 s_p^2 \]
where
\[ s_p^2 = \frac{(n_1-2)s_1^2 + (n_2-2)s_2^2}{n_1 + n_2 - 4} \]
is the pooled variance. The values of \( s_1^2 \) and \( s_2^2 \) represent the error mean of squares when the two individual regression lines are fit.

**Example**
Consider the preceding example. The following SAS code can be used to compute the quantities in the formula.

```sas
PROC SORT;
   BY GRP;
RUN;
QUIT;
PROC MEANS MEAN CSS N;
   VAR X;
   BY GRP;
RUN;
QUIT;
PROC GLM DATA=JN;
   MODEL Y = X;
   BY GRP;
RUN;
QUIT;
/* Get t value squared from the T-table*/
DATA T;
   TVAL = TINV(.975, 26);
   TVAL = TVAL*TVAL;
RUN;
QUIT;
PROC PRINT DATA=T;
RUN;
QUIT;
```

<table>
<thead>
<tr>
<th>Analysis Variable : x</th>
<th>Mean</th>
<th>Corrected SS</th>
<th>N</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>5.8000000</td>
<td>130.4000000</td>
<td>15</td>
</tr>
</tbody>
</table>

**grp=2**

Analysis Variable : x
We may now compute $X_L$ and $X_U$. A summary the quantities needed is

<table>
<thead>
<tr>
<th>Group 1</th>
<th>Group 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>$n_1 = 15$</td>
<td>$n_2 = 15$</td>
</tr>
<tr>
<td>$\bar{X}_1 = 5.8$</td>
<td>$\bar{X}_2 = 5.533$</td>
</tr>
<tr>
<td>$S_{XX_1} = 130.4$</td>
<td>$S_{XX_2} = 99.23$</td>
</tr>
<tr>
<td>$\hat{\alpha}_1 = 9.857$</td>
<td>$\hat{\alpha}_2 = 3.155$</td>
</tr>
<tr>
<td>$\hat{\beta}_1 = 0.209$</td>
<td>$\hat{\beta}_2 = 1.237$</td>
</tr>
<tr>
<td>$s^2_1 = 0.289$</td>
<td>$s^2_2 = 0.551$</td>
</tr>
</tbody>
</table>

$t_{26(.025)} = 4.225$
The values of $s_p^2, d, A, B,$ and $C$ are computed as

\[ s_p^2 = \frac{(13 \times 0.289) + (13 \times 0.551)}{26} = 0.42 \]

\[ d = 4.225 \times 0.42 = 1.7745 \]

\[ A = -1.7745 \times \left( \frac{1}{130.4} + \frac{1}{99.23} \right) + (0.209 - 1.237)^2 = 1.0253 \]

\[ B = 1.7745 \times \left( \frac{5.8}{130.4} + \frac{5.533}{99.23} \right) + (9.857 - 3.155) \times (0.209 - 1.237) = -6.712 \]

\[ C = -1.7745 \times \left( \frac{1}{15} + \frac{1}{15} + \frac{5.8^2}{130.4} + \frac{5.533^2}{99.23} \right) + (9.857 - 3.155)^2 = 43.675 \]

These give

\[ X_L = -B - \sqrt{B^2 - AC} \]

\[ X_U = -B + \sqrt{B^2 - AC} \]

\[ X_L = \frac{6.712 - 0.533}{1.0253} = 6.03 \]

\[ X_U = \frac{6.712 + 0.533}{1.0253} = 7.07 \]

Thus, using $\alpha = 0.05$, the region of non-significance is $(6.03, 7.07)$. For subjects with sociability score between 6.03 and 7.07, we fail to detect a difference between the two methods of therapy. Method 1 appears to be superior for subjects with sociability score below 6.03, while method 2 seems to work better for subjects above the sociability score of 7.07.

### 7.5.2 Multiple Groups, One Covariate

Two procedures extending the Johnson-Neyman strategy to incorporate several groups were proposed by Potthoff (1964). We shall consider the simpler of the two which uses the above technique along with a Bonferroni correction. The idea is to make all pairwise comparisons using the Bonferroni technique.

Let $a$ be the number of groups under consideration. There are \( \binom{a}{2} = a(a - 1)/2 \) possible pairwise comparisons. One compares each pair of groups using a Johnson-Neyman procedure at level $\alpha/\binom{a}{2}$. If the specific value of $X$ is known, this may be done at once using the \textit{BONFERRONI} adjustment of \textit{LSMEANS} in SAS. However, to determine regions of non-significance with simultaneous confidence $\alpha$, one uses the formula given above.

The lower and upper limits for comparing groups $r$ and $s$, $X_L(r, s)$ and $X_U(r, s)$, for $1 \leq r < s \leq a$ are:

\[ X_L(r, s) = -B_{rs} - \sqrt{B_{rs}^2 - A_{rs}C_{rs}} \]

\[ X_U(r, s) = -B_{rs} + \sqrt{B_{rs}^2 - A_{rs}C_{rs}} \]

where

\[ A_{rs} = -d \left( \frac{1}{S_{XX_r}} + \frac{1}{S_{XX_s}} \right) + (\hat{\beta}_r - \hat{\beta}_s)^2 \]

\[ B_{rs} = d \left( \frac{\bar{X}_r}{S_{XX_r}} + \frac{\bar{X}_s}{S_{XX_s}} \right) + (\hat{\alpha}_r - \hat{\alpha}_s)(\hat{\beta}_r - \hat{\beta}_s) \]

\[ C_{rs} = -d \left( \frac{1}{n_r} + \frac{1}{n_s} + \frac{\bar{X}_r^2}{S_{XX_r}} + \frac{\bar{X}_s^2}{S_{XX_s}} \right) + (\hat{\alpha}_r - \hat{\alpha}_s)^2 \]

Here

\[ d = \left[ t(a-1) - 2a \right] \left( \frac{\alpha}{a(a-1)} \right) \right]^2 \]

\[ s_p^2 = \frac{\sum_{i=1}^{a} (n_i - 2a) s_i^2}{\sum_{i=1}^{a} n_i - 2a} \]
Chapter 8

Nested Designs

We have already seen some examples of nesting in the analysis of repeated measurement models as well as split-plot designs. Nested designs, or hierarchical designs, are used in experiments where it is difficult or impossible to measure response on the experimental unit. Instead, smaller sampling units (subsamples) are selected from each experimental unit on which the response is measured. Another instance of nesting involves two or more factors in which one or more of the factors are nested within the other structurally.

8.1 Nesting in the Design Structure

The type of nesting where there are two or more sizes of experimental units is known as nesting in the design structure. These involve smaller sampling units obtained via subsampling. This subsampling process introduces a new source of variability due to the subsamples within the experimental units in our model in addition to the variation among the experimental units.

As an illustration, consider a situation where the treatments are several diets that are taken by humans in a completely randomized manner. The response is the level of a certain hormone in the blood of a subject’s body. Since it is difficult to measure the level of the hormone in all of the blood of an individual, we take several blood samples from each individual and measure the hormone in each sample. The experimental error now consists of the variability among the blood samples per individual and the variability among the individuals themselves.

Suppose we are interested in comparing the $a$ levels of factor $A$. Assume there are $r$ subjects available for each level of $A$. Responses are measured on $n$ subsamples for each subject. The data layout looks like the following:
The statistical model for a one-way CRD with subsampling is

\[ y_{ijk} = \mu + \tau_i + \epsilon_{j(i)} + \delta_{k(ij)} \]

where \( i = 1, \ldots, a, \ j = 1, \ldots, r, \ k = 1, \ldots, n \). Here \( \mu \) is the overall mean, \( \tau_i \) is the effect of level \( i \) of the treatment, \( \epsilon_{j(i)} \) is the random variation of the \( j \)th experimental unit on the \( i \)th treatment, and \( \delta_{k(ij)} \) is the random variation of the \( k \)th sampling unit within the \( j \)th unit on the \( i \)th treatment.

We assume that the random errors follow normal distributions with mean 0 and constant variances, i.e.

\[ \epsilon_{j(i)} \sim N(0, \sigma^2) \quad \text{and} \quad \delta_{k(ij)} \sim N(0, \sigma^2_\delta). \]

One can show that the expected mean squares are those given in the following table:

<table>
<thead>
<tr>
<th>Source</th>
<th>MS</th>
<th>E(MS)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatment</td>
<td>( MS_A )</td>
<td>( \sigma^2 + na^2 + (rn \sum \tau_i^2)/(a - 1) )</td>
</tr>
<tr>
<td>Experimental Error</td>
<td>( MS_E )</td>
<td>( \sigma^2 + na^2 )</td>
</tr>
<tr>
<td>Sampling Error</td>
<td>( MS_S )</td>
<td>( \sigma^2_\delta )</td>
</tr>
</tbody>
</table>

Using the expected MS, we find the following ANOVA table:

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>MS</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treatment</td>
<td>( a - 1 )</td>
<td>( MS_A )</td>
<td>( F_A = MS_A/MS_E )</td>
</tr>
<tr>
<td>Experimental Error</td>
<td>( a(r - 1) )</td>
<td>( MS_E )</td>
<td>( F_E = MS_E/MS_S )</td>
</tr>
<tr>
<td>Sampling Error</td>
<td>( ar(n - 1) )</td>
<td>( MS_S )</td>
<td>( F = MS_S/MS_A )</td>
</tr>
</tbody>
</table>

The following example is taken from Peterson: *Design and Analysis of Experiments*.

**Example**

A chemist wanted to measure the ability of three chemicals to retard the spread of fire when used to treat plywood panels. He obtained 12 panels and sprayed 4 of the panels with each of the three chemicals. He then cut two small pieces from each panel and measured the time required for each to be completely consumed in a standard flame. The data is given as follows:
The SAS analysis of the data is given as follows. It is followed by the output.

```
DATA NEW;
INPUT TRT PANEL SUB RESP;
CARDS;
  1 1 1 10.3
  2 1 1 4.4
  3 1 1 3.1
  1 1 2 9.8
  2 1 2 4.7
  3 1 2 3.3
  1 2 1 5.8
  2 2 1 2.7
  3 2 1 6.5
  1 2 2 5.4
  2 2 2 1.6
  3 2 2 5.4
  1 3 1 8.7
  2 3 1 4.6
  3 3 1 5.1
  1 3 2 10.0
  2 3 2 4.0
  3 3 2 7.5
  1 4 1 8.9
  2 4 1 5.6
  3 4 1 5.6
  1 4 2 9.4
  2 4 2 3.4
  3 4 2 4.2
;
PROC GLM;
  CLASS TRT PANEL SUB;
  MODEL RESP=TRT PANEL(TRT);
  TEST H=TRT E=PANEL/TRT);
RUN;
QUIT;
```

Dependent Variable: RESP
CHAPTER 8. NESTED DESIGNS

### ANOVA Table

<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>11</td>
<td>137.1633333</td>
<td>12.4693939</td>
<td>16.79</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>8.9100000</td>
<td>0.7425000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>23</td>
<td>146.0733333</td>
<td>9.7804333</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Type III SS 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>TRT</td>
<td>2</td>
<td>93.63083333</td>
<td>46.81541667</td>
<td>63.05</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>PANEL(TRT)</td>
<td>9</td>
<td>43.53250000</td>
<td>4.83694444</td>
<td>6.51</td>
<td>0.0019</td>
</tr>
</tbody>
</table>

Tests of Hypotheses Using the Type III MS for PANEL(TRT) 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>TRT</td>
<td>2</td>
<td>93.63083333</td>
<td>46.81541667</td>
<td>9.68</td>
<td>0.0057</td>
</tr>
</tbody>
</table>

Thus, there were highly significant differences among the three chemicals in their ability to retard the spread of fire ($P = 0.0057$). There is also a significant difference among the panels treated alike ($P = 0.0019$).

Mean comparisons can be made by using SAS’ LSMEANS with the appropriate error term.

**LSMEANS TRT / PDIFF E=PANEL(TRT);**

The corresponding output is

<table>
<thead>
<tr>
<th>TRT</th>
<th>RESP</th>
<th>LSMEAN</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>8.53750000</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>3.87500000</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>5.08750000</td>
<td>3</td>
<td></td>
</tr>
</tbody>
</table>

i/j  

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.0022</td>
<td>0.0120</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0.0022</td>
<td>0.2988</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0.0120</td>
<td>0.2988</td>
<td></td>
</tr>
</tbody>
</table>

Thus there is a significant difference between treatment A and the remaining two. Thus, treatment A appears to be the most effective fire retardant.
8.2 Nesting in the Treatment Structure

Consider two factors, $A$ and $B$. The levels of factor $B$ are nested within the levels of factor $A$ if each level of $B$ occurs with only one level of $A$. In this case $B$ needs to have more levels than $A$. The data has the following format:

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td></td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Assuming that factor $A$ has $a$ levels and the nested factor $B$ has a total of $b$ levels with $m_i$ levels appearing with level $i$ if $A$. Further assume that there are $n_i$ replications for each level of $B$ nested within level $i$ of $A$. Further assume that there are $n_i$ replications for each level of $B$ nested within level $i$ of $A$. In the above representation $a = 3, m_1 = 2, m_2 = 3, m_3 = 2, b = \sum m_i = 7$. A more general case that will not be considered here is the case of unequal replications for each $B$ nested within $A$.

The statistical model for this case is

\[
y_{ijk} = \mu + \tau_i + \beta_{j(i)} + \epsilon_{ijk},
\]

where $y_{ijk}$ is the observed response from the $k$th replication of level $j$ of $B$ within level $i$ of $A$, $\mu$ is the overall mean, $\tau_i$ is the effect of the $i$th level of $A$, $\beta_{j(i)}$ is the effect of the $j$th level of $B$ contained within level $i$ of $A$, and $\epsilon_{ijk} \sim N(0, \sigma^2)$ are random errors.

Note that, in contrast to nesting in the design structure, there is only one error term. In the current case, the sampling unit and the experimental unit coincide.

The total sum of squares decomposes into component sum of squares in a natural way. Let $N = \sum_{i=1}^{a} m_i n_i$ be the total number of observations. Then we have

\[
SS_T = SS_A + SS_{B(A)} + SS_E
\]

where (given with the associated df)

\[
SS_T = \sum_{i=1}^{a} \sum_{j=1}^{m_i} \sum_{k=1}^{n_i} (y_{ijk} - \bar{y}_{..})^2, \quad df = N - 1
\]

\[
SS_A = \sum_{i=1}^{a} m_i n_i (\bar{y}_{i..} - \bar{y}_{..})^2, \quad df = a - 1
\]

\[
SS_{B(A)} = \sum_{i=1}^{a} \sum_{j=1}^{m_i} n_i (y_{ij.} - \bar{y}_{i..})^2, \quad df = \sum_{i=1}^{a} (m_i - 1) = b - a
\]

\[
SS_E = \sum_{i=1}^{a} \sum_{j=1}^{m_i} \sum_{k=1}^{n_i} (y_{ijk} - \bar{y}_{ij.})^2, \quad df = \sum_{i=1}^{a} m_i (n_i - 1) = N - b
\]

The following ANOVA table may be used to test if there are any treatment differences. The correct $F$ is derived using the expected mean squares. This is left as an exercise.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>MS</th>
<th>$F$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A$</td>
<td>$a - 1$</td>
<td>$MS_A$</td>
<td>$F_A = MS_A/MS_{B(A)}$</td>
</tr>
<tr>
<td>$B(A)$</td>
<td>$b - a$</td>
<td>$MS_{B(A)}$</td>
<td>$F_{B(A)} = MS_{B(A)}/MS_E$</td>
</tr>
<tr>
<td>Error</td>
<td>$N - b$</td>
<td>$MS_E$</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>$N - 1$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The following example is taken from Milliken and Johnson: The Analysis of Messy Data, Vol I.
Example

Four chemical companies produce insecticides in the following manner:

- Company A produces three insecticides,
- Companies B and C produce two insecticides each,
- Company D produces four insecticides, and
- no company produces an insecticide exactly like that of another.

The treatment structure is a two-way with the data given as follows:

<table>
<thead>
<tr>
<th>Company</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>151</td>
<td>118</td>
<td>131</td>
<td>135</td>
<td>132</td>
<td>137</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>137</td>
<td>135</td>
<td>121</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>140</td>
<td>151</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>152</td>
<td>132</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>133</td>
<td>139</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>96</td>
<td>84</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>108</td>
<td>87</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>94</td>
<td>82</td>
<td></td>
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Thus in this example

\[ a = 4, \quad b = 11, \quad m_1 = 3, m_2 = m_3 = 2, m_4 = 4, \quad n_1 = n_2 = n_3 = n_4 = 3 \]

The following SAS code (given with edited output) may be used to analyze the data:

data insect;
input A $ B Y @@;
cards;
A 1 151 A 2 118 A 3 131
A 1 135 A 2 132 A 3 137
A 1 137 A 2 135 A 3 121
B 4 140 B 5 151
B 4 152 B 5 132
B 4 133 B 5 139
C 6 96 C 7 84
C 6 108 C 7 87
C 6 94 C 7 82
D 8 79 D 9 67 D 10 90 D 11 83
D 8 74 D 9 78 D 10 81 D 11 89
D 8 73 D 9 63 D 10 96 D 11 94
;

proc glm;
  class A B;
  model y = A B(A);
  test H=A E=B(A);
8.2. NESTING IN THE TREATMENT STRUCTURE

run;
quit;

--------------------------------------------------------------------------
Source  DF  Sum of  Mean Square  F Value  Pr > F
        Squares   
A   3   22813.29545  7604.43182  35.47  0.0001
B(A) 7   1500.58333  214.36905  3.74  0.0081
Error 22  1260.00000  57.27273
Total 32  25573.87879

Thus there are significant differences among the companies ($P = 0.0001$) and there are significant differences among the insecticides produced by the same company ($P = 0.0081$).