General Factorial Design

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• General Factorial Design
Three Way Interactions

We say factor A, B, and C have **three-way interactions** if
- AB interaction changes with the levels of C, or
- BC interaction changes with the levels of A, or
- AC interaction changes with the levels of B.

E.g., in a 3-way design, based on the means model

\[ y_{ijkl} = \mu_{ijk} + \varepsilon_{ijkl} \]

3-way interaction of level \((i_1, i_2)\) for factor A, level \((j_1, j_2)\) for factor B, and level \((k_1, k_2)\) for factor C is

\[
\begin{align*}
\mu_{i_1j_1k_1} - \mu_{i_2j_1k_1} - \mu_{i_1j_2k_1} + \mu_{i_1j_1k_2} + \mu_{i_2j_2k_1} + \mu_{i_2j_1k_2} + \mu_{i_1j_2k_2} - \mu_{i_2j_2k_2}
= (\mu_{i_1j_1k_1} - \mu_{i_2j_1k_1} - \mu_{i_1j_2k_1} + \mu_{i_2j_2k_1}) - (\mu_{i_1j_1k_2} - \mu_{i_2j_1k_2} - \mu_{i_1j_2k_2} + \mu_{i_2j_2k_2})
\end{align*}
\]

**AB interaction at level \(k_1\) of C**

\[
= (\mu_{i_1j_1k_1} - \mu_{i_1j_2k_1} - \mu_{i_1j_1k_2} + \mu_{i_1j_2k_2}) - (\mu_{i_2j_1k_1} - \mu_{i_2j_2k_1} - \mu_{i_2j_1k_2} + \mu_{i_2j_2k_2})
\]

**BC interaction at level \(i_1\) of A**

\[
= (\mu_{i_1j_1k_1} - \mu_{i_2j_1k_1} - \mu_{i_1j_1k_2} + \mu_{i_2j_1k_2}) - (\mu_{i_1j_2k_1} - \mu_{i_2j_2k_1} - \mu_{i_1j_2k_2} + \mu_{i_2j_2k_2})
\]

**AC interaction at level \(j_1\) of B**

\[
= (\mu_{i_1j_1k_1} - \mu_{i_2j_1k_1} - \mu_{i_1j_1k_2} + \mu_{i_2j_1k_2}) - (\mu_{i_1j_2k_1} - \mu_{i_2j_2k_1} - \mu_{i_1j_2k_2} + \mu_{i_2j_2k_2})
\]

**AC interaction at level \(j_2\) of B**

\[
= (\mu_{i_1j_1k_1} - \mu_{i_2j_1k_1} - \mu_{i_1j_1k_2} + \mu_{i_2j_1k_2}) - (\mu_{i_1j_2k_1} - \mu_{i_2j_2k_1} - \mu_{i_1j_2k_2} + \mu_{i_2j_2k_2})
\]
Higher Order Interactions

- We say 4 factors have 4-way interactions means the 3-way interaction of any 3 of the 4 factors changes with the levels of a 4th factor.

- We say $k$ factors have $k$-way interactions means the $(k - 1)$-way interaction of any $(k - 1)$ of the $k$ factors changes with the levels of a $k$th factor.

Hierarchy

- Since $k$-way interactions are defined on $(k - 1)$-way interactions, we cannot skip orders.

- E.g., when we say there are no AB interactions, we also imply that there are no higher order interactions that involve AB interactions, like ABD interactions, or ABCD interactions.
General Factorial Designs

The model and analysis of multi-way factorial are generalization of those of two-way factorial. E.g., consider a 4-way factorial with factors A, B, C, and D.

means model: \( y_{ijklm} = \mu_{ijkl} + \varepsilon_{ijklm} \) for \( \{ i = 1, \ldots, a, j = 1, \ldots, b, \) 
\( k = 1, \ldots, c, l = 1, \ldots, d, \) 
\( m = 1, \ldots, n. \) 

effects model: \( y_{ijklm} = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l \) 
\( \text{grand mean} \) 
\( \text{main effects} \) 
\( + \alpha \beta_{ij} + \alpha \gamma_{ik} + \alpha \delta_{il} + \beta \gamma_{jk} + \beta \delta_{jl} + \gamma \delta_{kl} \) 
\( \text{2-way interactions} \) 
\( + \alpha \beta \gamma_{ijk} + \alpha \beta \delta_{ijl} + \alpha \gamma \delta_{ikl} + \beta \gamma \delta_{jkl} \) 
\( \text{3-way interactions} \) 
\( + \alpha \beta \gamma \delta_{ijkl} + \varepsilon_{ijklm} \) 
\( \text{4-way interaction} \) 
\( \text{error} \)
General Factorial Designs

\[ y_{ijklm} = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l \]
\[ + \alpha \beta_{ij} + \alpha \gamma_{ik} + \alpha \delta_{il} + \beta \gamma_{jk} + \beta \delta_{jl} + \gamma \delta_{kl} \]
\[ + \alpha \beta \gamma_{ijk} + \alpha \beta \delta_{ijl} + \alpha \gamma \delta_{ikl} + \beta \gamma \delta_{jkl} \]
\[ + \alpha \beta \gamma \delta_{ijkl} + \varepsilon_{ijklm} \]

All the effects have zero-sum constraints that they will add to 0 when summed over any subscript, e.g.,

> \[ \sum_i \alpha_i = \sum_j \beta_j = \sum_k \gamma_k = \sum_l \delta_l = 0 \]

> \[ \sum_i \alpha \gamma_{ik} = \sum_k \alpha \gamma_{ik} = 0, \text{ for all } i, k, \]
so do other 2-way interactions

> \[ \sum_i \alpha \gamma \delta_{ikl} = \sum_k \alpha \gamma \delta_{ikl} = \sum_l \alpha \gamma \delta_{ikl} = 0, \text{ for all } i, k, l, \]
so do other 3-way interactions

> \[ \sum_i \alpha \beta \gamma \delta_{ijkl} = \sum_j \alpha \beta \gamma \delta_{ijkl} = \sum_k \alpha \beta \gamma \delta_{ijkl} = \sum_l \alpha \beta \gamma \delta_{ijkl} = 0, \]
for all \( i, j, k, l \).
Sum of Squares

The SST can be decomposed into SS of main effects and interactions of all orders, e.g., in a 4-way design:

\[
SST = SS_A + SS_B + SS_C + SS_D
+ SS_{AB} + SS_{AC} + SS_{AD} + SS_{BC} + SS_{BD} + SS_{CD}
+ SS_{ABC} + SS_{ACD} + SS_{ABD} + SS_{BCD}
+ SS_{ABCD}
+ SSE
\]

- \(\text{SST} = \sum_{ijklm} (y_{ijklm} - \overline{y}_{\ldots\ldots})^2\)
- \(\text{SSE} = \sum_{ijklm} (y_{ijklm} - \overline{y}_{ijkl\cdot})^2\)
- \(\text{SS}_C = \sum_{ijklm} (\overline{y}_{\cdot\cdot k\cdot\cdot} - \overline{y}_{\cdot\cdot\cdot\cdot})^2\)
- \(\text{SS}_{BC} = \sum_{ijklm} (\overline{y}_{\cdot jk\cdot\cdot} - \overline{y}_{\cdot j\cdot\cdot\cdot} - \overline{y}_{\cdot\cdot k\cdot\cdot} + \overline{y}_{\cdot\cdot\cdot\cdot})^2\)
- \(\text{SS}_{ACD} = \sum_{ijklm} (\overline{y}_{i\cdot kl\cdot} - \overline{y}_{i\cdot k\cdot\cdot} - \overline{y}_{i\cdot l\cdot\cdot} - \overline{y}_{i\cdot kl\cdot}
+ \overline{y}_{i\cdot\cdot\cdot\cdot} + \overline{y}_{\cdot\cdot k\cdot\cdot} + \overline{y}_{\cdot\cdot\cdot l\cdot} - \overline{y}_{\cdot\cdot\cdot\cdot\cdot})^2\)
- \(\text{SS}_{ABCD} = \sum_{ijklm} (\ldots 16 \text{ terms} \ldots)^2\)
Degrees of Freedom

Say factor A, B, C, and D have respectively \( a, b, c, d \) levels, and there are \( n \) replicates.

- d.f. of a main effect = number of levels \(-1\).
  e.g., \( df_A = a - 1, \ df_C = c - 1 \).

- d.f. of an interaction = product of d.f.’s for the main effects of the involved factors, e.g.,
  - \( df_{AD} = (a - 1)(d - 1) \),
  - \( df_{BCD} = (b - 1)(c - 1)(d - 1) \),
  - \( df_{ABCD} = (a - 1)(b - 1)(c - 1)(d - 1) \).

- d.f. of SST = total \# of observation \(-1\) = \( abcdn - 1 \)

- d.f. of SSE = total \# of observation \(-\) total \# of treatments
  = \( abcdn - abcd = abcd(n - 1) \)
Example 8.10  Amylase data (p.195)

- Goal: to study the amylase specific activity of sprouted maize
- An $8 \times 2 \times 2$ factorial design with 3 factors:
  - analysis temperature (40, 35, 30, 25, 20, 15, 13, or $10^\circ\text{C}$)
  - growth temperature of the sprouts (25 or $13^\circ\text{C}$)
  - variety of maize (B73 or Oh43)
- 3 replicates per treatment
- Response: the amylase specific activities (IU)
- Data file:
  http://users.stat.umn.edu/~gary/book/fcdae.data/exmpl8.10
Table 8.9: Amylase specific activity (IU), for two varieties of sprouted maize under different growth and analysis temperatures (degrees C).

<table>
<thead>
<tr>
<th>GT</th>
<th>Var.</th>
<th>Analysis Temperature</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>40</td>
</tr>
<tr>
<td>25</td>
<td>B73</td>
<td>391.8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>311.8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>367.4</td>
</tr>
<tr>
<td></td>
<td>O43</td>
<td>301.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>271.4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>300.3</td>
</tr>
<tr>
<td>13</td>
<td>B73</td>
<td>292.7</td>
</tr>
<tr>
<td></td>
<td></td>
<td>283.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>348.1</td>
</tr>
<tr>
<td></td>
<td>O43</td>
<td>269.7</td>
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<tr>
<td></td>
<td></td>
<td>284.0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>235.3</td>
</tr>
</tbody>
</table>
Example 8.10  Amylase data — Interaction Plots

Does the main effect at appear significant?

How about the main effect gt?

How about at:gt interaction?

Does the main effect at appear significant?

and the main effect v?

at:v interaction?
Example 8.10  Amylase data — Interaction Plots (2)

▶ Does the main effect $gt$ appear significant?
▶ and main effect $v$?
▶ $gt:v$ interaction?
> attach(mydata)
> at = as.factor(mydata$atemp)
> gt = as.factor(mydata$gtemp)
> v = as.factor(mydata$variety)

To make the variance constant, the response is log-transformed (see p.215-216 in the textbook).

We fit a full model with all 2-way and 3-way interactions.

> logfit1 = lm(log(y) ~ at + gt + v + at:gt + at:v + gt:v + at:gt:v)

A simpler syntax is 

> logfit1 = lm(log(y) ~ at*gt*v)

The syntax at*gt*v will automatically include all relevant main effects and lower order interactions in the model.
Example 8.10 Amylase data — ANOVA Table

```r
> logfit1 = lm(log(y) ~ at*gt*v)
> anova(logfit1)
```

Analysis of Variance Table

Response: log(y)

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>at</td>
<td>7</td>
<td>3.01613</td>
<td>0.43088</td>
<td>78.8628</td>
<td>&lt; 2.2e-16 ***</td>
</tr>
<tr>
<td>gt</td>
<td>1</td>
<td>0.00438</td>
<td>0.00438</td>
<td>0.8016</td>
<td>0.3739757</td>
</tr>
<tr>
<td>v</td>
<td>1</td>
<td>0.58957</td>
<td>0.58957</td>
<td>107.9085</td>
<td>2.305e-15 ***</td>
</tr>
<tr>
<td>at:gt</td>
<td>7</td>
<td>0.08106</td>
<td>0.01158</td>
<td>2.1195</td>
<td>0.0539203 .</td>
</tr>
<tr>
<td>at:v</td>
<td>7</td>
<td>0.02758</td>
<td>0.00394</td>
<td>0.7212</td>
<td>0.6543993</td>
</tr>
<tr>
<td>gt:v</td>
<td>1</td>
<td>0.08599</td>
<td>0.08599</td>
<td>15.7392</td>
<td>0.0001863 ***</td>
</tr>
<tr>
<td>at:gt:v</td>
<td>7</td>
<td>0.04764</td>
<td>0.00681</td>
<td>1.2457</td>
<td>0.2916176</td>
</tr>
<tr>
<td>Residuals</td>
<td>64</td>
<td>0.34967</td>
<td>0.00546</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Only analysis temperature (at), variety (v), and the growth temperature by variety interaction (gt:v) are highly significant.

Can I fit a model like $y_{ijkl} = \mu + \alpha_i + \gamma_k + \beta\gamma_j + \varepsilon_{ijkl}$?

```r
> logfit2 = lm(log(y) ~ at + v + gt:v)
```

Chapter 08B - 13
8.11 Hierarchy

A model is *hierarchical* if any term in the model implies the presence of all the composite lower-order terms.

- $y_{ijkl} = \mu + \alpha_i + \gamma_k + \beta \gamma_{jk} + \varepsilon_{ijkl}$ is not hierarchical because including the term $\beta \gamma_{jk}$ must includes *both* $\beta_j$ and $\gamma_k$ as well.

- $y_{ijk} = \mu + \alpha_i + \beta_j + \alpha \beta_{ij} + \varepsilon_{ijk}$ is hierarchical.

- A hierarchical model with a term $\alpha \beta \gamma_{ijk}$ must also include:
  - the included main effects: $\alpha_i + \beta_j + \gamma_k$
  - and the included two-way effects: $\alpha \beta_{ij} + \alpha \gamma_{ik} + \beta \gamma_{jk}$.

Unless having a specific reason, we should stick to hierarchical models.

- This is because a $k$-way interaction in defined upon its composite lower-order terms. It is strange to consider a ABC interaction while claiming A and B have no 2-way interaction.
Back to the Amylase Data

Here is a model that is still hierarchical, but leaves off non-significant model terms.

```r
> logfit2 = lm(log(y) ~ at + gt + v + at:gt + gt:v)
> anova(logfit2)
```

Analysis of Variance Table

Response: log(y)

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>at</td>
<td>7</td>
<td>3.0161</td>
<td>0.4309</td>
<td>79.098</td>
<td>&lt;2.2e-16 ***</td>
</tr>
<tr>
<td>gt</td>
<td>1</td>
<td>0.0044</td>
<td>0.0044</td>
<td>0.804</td>
<td>0.373</td>
</tr>
<tr>
<td>v</td>
<td>1</td>
<td>0.5896</td>
<td>0.5896</td>
<td>108.23</td>
<td>&lt;2.2e-16 ***</td>
</tr>
<tr>
<td>at:gt</td>
<td>7</td>
<td>0.0811</td>
<td>0.0115</td>
<td>2.126</td>
<td>0.050</td>
</tr>
<tr>
<td>gt:v</td>
<td>1</td>
<td>0.0859</td>
<td>0.0859</td>
<td>15.786</td>
<td>&lt;2.2e-16 ***</td>
</tr>
<tr>
<td>Residuals</td>
<td>78</td>
<td>0.4249</td>
<td>0.0054</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Though insignificant, the main effect `gt` cannot be left out since the two-way interaction `gt:v` is significant.

The SS’s and d.f.’s of the left-out terms are pooled into SSE, while the SS’s and d.f.’s of the remaining stay unchanged.
Comparing the reduced model with the full 3-way model, the large $P$-value indicates the adequacy of the reduced model.

```
> anova(logfit2,logfit1)
Analysis of Variance Table

Model 1: log(y) ~ at + gt + v + at:gt + gt:v
Model 2: log(y) ~ at * gt * v

  Res.Df RSS Df Sum of Sq  F Pr(>F)
1     78 0.42489
2     64 0.34967 14 0.075223 0.9834 0.4801
```
More On Model Formula in R (1)

Instead of writing terms explicitly in the model formula

```r
> logfit2 = lm(log(y) ~ at + gt + v + at:gt + gt:v)
```

here is another simpler expression for the same model. R will automatically create the smallest hierarchical model that include both `at:gt` and `gt:v` interactions.

```r
> logfit2a = lm(log(y) ~ at*gt + gt*v)
> anova(logfit2a)
Analysis of Variance Table

Response: log(y)

<table>
<thead>
<tr>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>at</td>
<td>7</td>
<td>3.01613</td>
<td>0.43088</td>
<td>79.0981 &lt; 2.2e-16 ***</td>
</tr>
<tr>
<td>gt</td>
<td>1</td>
<td>0.00438</td>
<td>0.00438</td>
<td>0.8040 0.3726670</td>
</tr>
<tr>
<td>v</td>
<td>1</td>
<td>0.58957</td>
<td>0.58957</td>
<td>108.2305 &lt; 2.2e-16 ***</td>
</tr>
<tr>
<td>at:gt</td>
<td>7</td>
<td>0.08106</td>
<td>0.01158</td>
<td>2.1258 0.0503809 .</td>
</tr>
<tr>
<td>gt:v</td>
<td>1</td>
<td>0.08599</td>
<td>0.08599</td>
<td>15.7861 0.0001571 ***</td>
</tr>
<tr>
<td>Residuals</td>
<td>78</td>
<td>0.42489</td>
<td>0.00545</td>
<td></td>
</tr>
</tbody>
</table>
```
If want a model without 3-way interaction but including all two-way interactions, one can explicitly write down every term

```r
> logfit3a = lm(log(y) ~ at + gt + v + at:gt + gt:v + at:v)
```

Here is another way to obtain everything up to the 2-way interactions

```r
> logfit3b = lm(log(y) ~ (at + gt + v)^2)
```

Here is another way to “leave out” the 3-way interaction

```r
> logfit3c = lm(log(y) ~ at*gt*v - at:gt:v)
```

You can verify that the 3 model formula are identical to R.

```r
> anova(logfit3a)
> anova(logfit3b)
> anova(logfit3c)
```
Example 8.10  Amylase data — Model Checking

Always check model assumptions!

Recall that we took log of the original response. If we didn’t...

```r
> fit1 = lm(y ~ at*gt*v); anova(fit1)
```

Analysis of Variance Table

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>at</td>
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<td>327811</td>
<td>46830</td>
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<td>&lt; 2.2e-16  ***</td>
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<tr>
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<td>1</td>
<td>1155</td>
<td>1155</td>
<td>1.7988</td>
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<tr>
<td>v</td>
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<td>63809</td>
<td>63809</td>
<td>99.3801</td>
<td>1.192e-14  ***</td>
</tr>
<tr>
<td>at:gt</td>
<td>7</td>
<td>7158</td>
<td>1023</td>
<td>1.5925</td>
<td>0.1537663</td>
</tr>
<tr>
<td>at:v</td>
<td>7</td>
<td>1174</td>
<td>168</td>
<td>0.2611</td>
<td>0.9665902</td>
</tr>
<tr>
<td>gt:v</td>
<td>1</td>
<td>10648</td>
<td>10648</td>
<td>16.5839</td>
<td>0.0001305  ***</td>
</tr>
<tr>
<td>at:gt:v</td>
<td>7</td>
<td>6257</td>
<td>894</td>
<td>1.3922</td>
<td>0.2240596</td>
</tr>
<tr>
<td>Residuals</td>
<td>64</td>
<td>41092</td>
<td>642</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Don’t drop non-significant terms before checking model assumptions. If any assumption is violated, the ANOVA table is not reliable.
Example 8.10  Amylase data — Model Checking (2)

- The residual plot indicates non-constant variance — the size of residuals increases with fitted values.
- The QQ plot looks symmetric but a bit short-tailed.
- The Box-Cox method suggests a log-transformation.
We check the model again after log-transformation but before dropping terms (i.e. for the model \( \text{logfit1} = \text{lm}(\log(y) \sim at*v*gt) \)).

- The non-constant variance problem is alleviated
- The QQ plot still looks short-tailed. Residuals often appear short-tailed when fitting a “large” model, which tends to overfit the data, making residuals too close to zero.
- Box-Cox suggests no transformation (\( \lambda = 1 \) is in the 95% C.I.), i.e., the log-transformed response is fine.

So the ANOVA table based on the log-transformed data seems trustworthy and we can make inference or drop terms based on it.
We check the model again after log-transformation and dropping non-significant terms (i.e. for \( \text{logfit2} = \text{lm}(\log(y) \sim \text{at} \times \text{gt} + \text{gt} \times v) \)).

- The residual plot looks fine
- After removing non-significant terms, residuals no longer appear short-tailed
- Box-Cox shows the 95% C.I. still contains \( \lambda = 1 \). Okay.

**Remark about Box-Cox:** R by default will only plot \( \lambda \) for the range \((-2, 2)\). The range of \( \lambda \) can be changed, like -2 to 10 in steps 0.25 in the command below.

> library(MASS)
> boxcox(logfit2, lambda=seq(-2,10,0.25))
Some factorial experiments have only ONE replicate per treatment.

- No degree of freedom for error, cannot estimate $\sigma^2$
- All sum of squares (SS) can be computed as usual except that $\text{SSE} = 0$.
- ANOVA $F$-tests for main effects and interactions of all orders cannot be done!

Remedy — Pool higher order interactions into error
Problem 8.6 (p. 222, Oehlert’s)

- Response: dry matter yield in hundreds of pounds per acre over a 54-week study period
- Factors:
  - height of cut (1, 3, or 6 inches),
  - the cutting interval (1, 3, 6, or 9 weeks), and
  - the amount of nitrogen fertilizer (0, 8, 16, or 32 hundred pounds of ammonium sulfate per acre per year).

<table>
<thead>
<tr>
<th></th>
<th>Cutting Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1 wks.</td>
</tr>
<tr>
<td>Ht 1</td>
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</tr>
<tr>
<td></td>
<td>F 8</td>
</tr>
<tr>
<td></td>
<td>F 16</td>
</tr>
<tr>
<td></td>
<td>F 32</td>
</tr>
<tr>
<td>Ht 3</td>
<td>F 0</td>
</tr>
<tr>
<td></td>
<td>F 8</td>
</tr>
<tr>
<td></td>
<td>F 16</td>
</tr>
<tr>
<td></td>
<td>F 32</td>
</tr>
<tr>
<td>Ht 6</td>
<td>F 0</td>
</tr>
<tr>
<td></td>
<td>F 8</td>
</tr>
<tr>
<td></td>
<td>F 16</td>
</tr>
<tr>
<td></td>
<td>F 32</td>
</tr>
</tbody>
</table>
> pr8.6 = read.table("http://users.stat.umn.edu/~gary/book/fcdae.data/pr8.6", header=T)
> pr8.6$Ht = c(1,3,6)[pr8.6$ht]
> pr8.6$Fert = c(0,8,16,32)[pr8.6$fert]
> pr8.6$Int = c(1,3,6,9)[pr8.6$int]
> pr8.6$HT = factor(pr8.6$ht, labels=c(1,3,6))
> pr8.6$FERT = factor(pr8.6$fert, labels=c(0,8,16,32))
> pr8.6$INT = factor(pr8.6$int, labels=c(1,3,6,9))
> lm1 = lm(y ~ HT*FERT*INT, data=pr8.6)
> anova(lm1)

Analysis of Variance Table

Response: y

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HT</td>
<td>2</td>
<td>29</td>
<td>14.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>FERT</td>
<td>3</td>
<td>42072</td>
<td>14023.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>INT</td>
<td>3</td>
<td>73887</td>
<td>24629.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>HT:FERT</td>
<td>6</td>
<td>406</td>
<td>67.7</td>
<td></td>
<td></td>
</tr>
<tr>
<td>HT:INT</td>
<td>6</td>
<td>3005</td>
<td>500.9</td>
<td></td>
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</tr>
<tr>
<td>FERT:INT</td>
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<td>5352</td>
<td>594.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>HT:FERT:INT</td>
<td>18</td>
<td>3155</td>
<td>175.3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Residuals</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Warning message:
In anova.lm(lm1) :
   ANOVA F-tests on an essentially perfect fit are unreliable
We pool the 3-way interaction terms as errors to get a conservative estimate of the MSE.

```r
> lm2 = lm(y ~ (HT+FERT+INT)^2, data=pr8.6)
> anova(lm2)
Analysis of Variance Table

Response: y

<table>
<thead>
<tr>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HT</td>
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<td>29</td>
<td>14.6</td>
<td>0.0830</td>
</tr>
<tr>
<td>FERT</td>
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<td>42072</td>
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<td>80.0153</td>
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<tr>
<td>INT</td>
<td>3</td>
<td>73887</td>
<td>24629.0</td>
<td>140.5241</td>
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<td>406</td>
<td>67.7</td>
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<td>594.6</td>
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<tr>
<td>Residuals</td>
<td>18</td>
<td>3155</td>
<td>175.3</td>
<td></td>
</tr>
</tbody>
</table>
---
```
Before examining the treatment effects, first check if the model assumptions are met.

```R
> library(MASS)
> boxcox(lm2)
```

The Box-Cox method below suggest a square-root transformation of the response (since 0.5 is in the 95% confidence interval for $\lambda$).

![Box-Cox Transform. for Linear Models](image-url)
```r
> lm2s = lm(sqrt(y) ~ (HT+FERT+INT)^2, data=pr8.6)
> anova(lm2s)
```

Analysis of Variance Table

Response: sqrt(y)

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HT</td>
<td>2</td>
<td>0.103</td>
<td>0.052</td>
<td>0.1763</td>
<td>0.83979</td>
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<tr>
<td>FERT</td>
<td>3</td>
<td>82.222</td>
<td>27.407</td>
<td>93.8199</td>
<td>3.510e-11 ***</td>
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<tr>
<td>INT</td>
<td>3</td>
<td>132.738</td>
<td>44.246</td>
<td>151.4617</td>
<td>5.865e-13 ***</td>
</tr>
<tr>
<td>HT:FERT</td>
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<td>0.089</td>
<td>0.3062</td>
<td>0.92553</td>
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<tr>
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<td>4.873</td>
<td>0.812</td>
<td>2.7800</td>
<td>0.04303 *</td>
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<tr>
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<td>0.03962 *</td>
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<tr>
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<td>0.292</td>
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