

Chapter 6

K Way ANOVA

6.1 Two Way ANOVA

Definition 6.1. The fixed effects **two way Anova model** has two factors A and B plus a response Y . Factor A has a levels and factor B has b levels. There are ab treatments.

Definition 6.2. The **cell means model** for two way Anova is $Y_{ijk} = \mu_{ij} + e_{ijk}$ where $i = 1, \dots, a$; $j = 1, \dots, b$; and $k = 1, \dots, m$. The sample size $n = abm$. The μ_{ij} are constants and the e_{ijk} are iid from a location family with mean 0 and variance σ^2 . Hence the $Y_{ijk} \sim f(y - \mu_{ij})$ come from a location family with location parameter μ_{ij} . The fitted values are $\hat{Y}_{ijk} = \bar{Y}_{ijo} = \hat{\mu}_{ij}$ while the residuals $r_{ijk} = Y_{ijk} - \hat{Y}_{ijk}$.

For one way Anova models, the cell sizes n_i need not be equal. For K way Anova models with $K \geq 2$ factors, the statistical theory is greatly simplified if all of the cell sizes are equal. Such designs are called balanced designs.

Definition 6.3. A **balanced design** has all of the cell sizes equal: for the two way Anova model, $n_{ij} \equiv m$.

In addition to randomization of units to treatments, another key principle of experimental design is factorial crossing. Factorial crossing allows for estimation of main effects and interactions.

Definition 6.4. A two way Anova design uses **factorial crossing** if each combination of an A level and a B level is used and called a treatment. There are ab treatments for the two way Anova model.

Experimental two way Anova designs randomly assign m of the $n = mab$ units to each of the ab treatments. Observational studies take random samples of size m from ab populations.

Definition 6.5. The **main effects** are A and B . The AB interaction is not a main effect.

Remark 6.1. If A and B are factors, then there are 5 possible models.

- i) The two way Anova model has terms A , B and AB .
- ii) The additive model or main effects model has terms A and B .
- iii) The one way Anova model that uses factor A .
- iv) The one way Anova model that uses factor B .
- v) The null model does not use any of the three terms A , B or AB . If the null model holds, then $Y_{ijk} \sim f(y - \mu_{00})$ so the Y_{ijk} form a random sample of size n from a location family and the factors have no effect on the response.

Remark 6.2. The response plot, residual plot and transformation plots for response transformations are used in the same way as Chapter 5. The plots work best if the MSE degrees of freedom $> \max(10, n/5)$. The model is overfitting if $1 < \text{MSE df} \leq \max(10, n/5)$, and then the plots may only be useful for detecting large deviations from the model. For the model that contains A , B and AB , there will be ab dot plots of size m , and need $m \geq 5$ to check for similar shape and spread. For the additive model, the response and residual plots often look like those for multiple linear regression. Then the plotted points should scatter about the identity line or $r = 0$ line in a roughly evenly populated band if the additive two way Anova model is reasonable.

Shown is an ANOVA table for the two way Anova model given in symbols. Sometimes “Error” is replaced by “Residual,” or “Within Groups.” A and B are the main effects while AB is the interaction. Sometimes “p-value” is replaced by “P”, “ $Pr(> F)$ ” or “PR > F.” The p-value for corresponding to F_A is for $H_0: \mu_{10} = \dots = \mu_{a0}$. The p-value for corresponding to F_B is for $H_0: \mu_{01} = \dots = \mu_{0b}$. The p-value for corresponding to F_{AB} is for H_0 : there is no interaction. The sample pvalue $\equiv pval$ is an estimator of the population pvalue.

Source	df	SS	MS	F	p-value
A	a-1	SSA	MSA	$F_A = \text{MSA}/\text{MSE}$	pval
B	b-1	SSB	MSB	$F_B = \text{MSB}/\text{MSE}$	pval
AB	$(a-1)(b-1)$	SSAB	MSAB	$F_{AB} = \text{MSAB}/\text{MSE}$	pval
Error	$n - ab = ab(m-1)$	SSE	MSE		

Be able to perform the 4 step test for AB interaction:

- i) H_0 no interaction H_A there is an interaction
- ii) F_{AB} is obtained from output.
- iii) The pvalue is obtained from output.
- iv) If pvalue $< \delta$ reject H_0 and conclude that there is an interaction between A and B , otherwise fail to reject H_0 and conclude that there is no interaction between A and B .

Remark 6.3. Keep A and B in the model if there is an AB interaction. The two tests for main effects (below) make the most sense if we fail to reject the test for interaction. The main effects tests are just like the F test for the fixed effects one way Anova model. If populations means are close, then larger sample sizes are needed for the F test to reject H_0 with high probability. If H_0 is rejected and the means are equal, then it is possible that the factor is unimportant, but it is also possible that the factor is important but the level is not. For example, factor A might be type of catalyst. The yield may be equally good for each type of catalyst, but there would be no yield if no catalyst was used.

Be able to perform the 4 step test for A main effects:

- i) $H_0 \mu_{10} = \dots = \mu_{a0}$ H_A not H_0
- ii) F_A is obtained from output.
- iii) The pvalue is obtained from output.
- iv) If pvalue $< \delta$ reject H_0 and conclude that the mean response depends on A , otherwise fail to reject H_0 and conclude that the mean response does not depend on A .

Be able to perform the 4 step test for B main effects:

- i) $H_0 \mu_{01} = \dots = \mu_{0b}$ H_A not H_0
- ii) F_B is obtained from output.
- iii) The pvalue is obtained from output.
- iv) If pvalue $< \delta$ reject H_0 and conclude that the mean response depends on

B , otherwise fail to reject H_0 and conclude that the mean response does not depend on B .

Remark 6.4. One could do a one way Anova on $p = ab$ treatments, but this procedure loses information about A , B and the AB interaction.

Definition 6.6. An **interaction plot** is made by plotting the levels of one factor (either $1, \dots, a$ or $1, \dots, b$) versus the cell sample means \bar{Y}_{ij0} . Typically the factor with more levels (eg A if $a > b$) is used on the horizontal axis. If the levels of A are on the horizontal axis, use line segments to join the a means that have the same j . There will be b curves on the plot. If the levels of B are on the horizontal axis, use line segments to join the b means that have the same i . There will be a curves on the plot. If **no interaction** is present, then the curves should be roughly parallel.

The interaction plot is rather hard to use, especially if the $n_{ij} = m$ are small. For small m , the curves can be far from parallel, even if there is no interaction. The further the curves are from being parallel, the greater the evidence of interaction. Intersection of curves suggests interaction unless the two curves are nearly the same. The two curves may be nearly the same if two levels of one factor give nearly the same mean response for each level of the other factor. Then the curves could cross several times even though there is no interaction. Software fills space. So the vertical axis needs to be checked to see whether the sample means for two curves are “close” with respect to the standard error MSE/m for the means.

The interaction plot is the most useful if the conclusions for the plot agree with the conclusions for the F test for no interaction.

Definition 6.7. The overparameterized two way Anova model has $Y_{ijk} = \mu_{ij} + e_{ijk}$ with $\mu_{ij} = \mu_{00} + \alpha_i + \beta_j + (\alpha\beta)_{ij}$ where the interaction parameters $(\alpha\beta)_{ij} = \mu_{ij} - \mu_{i0} - \mu_{0j} + \mu_{00}$. The A main effects are $\alpha_i = \mu_{i0} - \mu_{00}$ for $i = 1, \dots, a$. The B main effects are $\beta_j = \mu_{0j} - \mu_{00}$ for $j = 1, \dots, b$. Here $\sum_i \alpha_i = 0$, $\sum_j \beta_j = 0$, $\sum_i (\alpha\beta)_{ij} = 0$ for $j = 1, \dots, b$ and $\sum_j (\alpha\beta)_{ij} = 0$ for $i = 1, \dots, a$. Thus $\sum_i \sum_j (\alpha\beta)_{ij} = 0$.

The mean parameters have the following meaning. The parameter μ_{ij} is the population mean response for the ij th treatment. The means $\mu_{0j} = \sum_{i=1}^a \mu_{ij}/a$, and the means $\mu_{i0} = \sum_{j=1}^b \mu_{ij}/b$.

As was the case for multiple linear regression, interaction is rather difficult

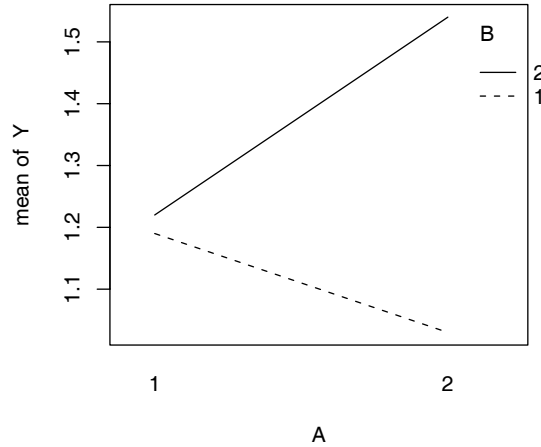


Figure 6.1: Interaction Plot for Example 6.1.

to understand. Note that if all of the interaction parameters $(\alpha\beta)_{ij} = 0$, then the factor effects are additive: $\mu_{ij} = \mu_{00} + \alpha_i + \beta_j$. Hence “no interaction” implies that the factor effects are additive while “interaction” implies that the factor effects are not additive. When there is no interaction, $\mu_{1j} = \mu_{00} + \alpha_1 + \beta_j$, $\mu_{2j} = \mu_{00} + \alpha_2 + \beta_j$, ..., $\mu_{aj} = \mu_{00} + \alpha_a + \beta_j$. Consider a plot with the μ_{ij} on the vertical axis and the levels 1, 2, ..., a of A on the horizontal axis. If there is no interaction and if the μ_{ij} with the same j are connected with line segments, then there will be b parallel curves with curve “height” depending on β_j . If there is interaction, then not all of the p curves will be parallel. The interaction plot replaces the μ_{ij} by the $\hat{\mu}_{ij} = \bar{Y}_{ij0}$.

Example 6.1. Cobb (1998, p. 200-212) describes an experiment on weight gain for baby pigs. The response Y was the average daily weight gain in pounds for each piglet (over a period of time). Factor A consisted of 0 mg of an antibiotic or 40 mg an antibiotic while factor B consisted of 0 mg of vitamin B12 or 5 mg of B12. Hence there were 4 diets $(A,B) = (0,0)$, $(40,0)$, $(0,5)$ or $(40,5)$. Hence level 1 corresponds to 0 mg and level 2 to more than 0 mg.

The interaction plot shown in Figure 6.1 suggests that there is an interaction. If no vitamin B12 is given, then the pigs given the antibiotic have

less mean weight gain than the pigs not given the antibiotic. For pigs given the diet with 5 mg of B12, the antibiotic was useful, with a mean gain near 1.6. Pigs with $A = 1$ (no antibiotic in the diet) had similar mean weight gains, but pigs with $A = 2$ (antibiotic in the diet) had greatly different mean weight gains. The best diet had both vitamin B12 and the antibiotic, while the worst diet had the antibiotic but no vitamin B12.

Source	DF	SS	MS	F	P
A	2	220.0200	110.0100	1827.86	0.000
B	2	123.6600	61.8300	1027.33	0.000
Interaction	4	29.4250	7.3562	122.23	0.000
Error	27	1.6250	0.0602		

Example 6.2. The above output uses data from Neter, Kutner, Nachtsheim and Wasserman (1996, problems 19.14-15). The output above is from an experiment on hay fever, and 36 volunteers were given medicine. The two active ingredients (factors A and B) in the medicine were varied at three levels each (low, medium, and high). The response is the number of hours of relief. (The factor names for this problem are “A” and “B.”)

- Give a four step test for the “A*B” interaction.
- Give a four step test for the A main effects.
- Give a four step test for the B main effects.

Solution: a) H_0 no interaction H_A there is an interaction

$$F_{AB} = 122.23$$

$$pval = 0.0$$

Reject H_0 , there is an interaction between the active ingredients A and B.

b) $H_0 \mu_{10} = \mu_{20} = \mu_{30}$ H_A not H_0

$$F_A = 1827.86$$

$$pval = 0.0$$

Reject H_0 , the mean hours of relief depends on active ingredient A.

c) $H_0 \mu_{01} = \mu_{02} = \mu_{03}$ H_A not H_0

$$F_B = 1027.33$$

$$pval = 0.0$$

Reject H_0 , the mean hours of relief depends on active ingredient B.

6.2 k Way Anova Models

Use **factorial crossing** to compare the effects (main effects, pairwise interactions, ..., k-fold interaction if there are k factors) of two or more factors. If A_1, \dots, A_k are the factors with l_i levels for $i = 1, \dots, k$; then there are $l_1 l_2 \cdots l_k$ treatments where each treatment uses exactly one level from each factor.

Below is a partial Anova table for a k way Anova design with the degrees of freedom left blank. For A, use $H_0 : \mu_{10\dots 0} = \cdots = \mu_{l_1 0 \dots 0}$. The other main effect have similar null hypotheses. For interaction, use $H_0 : \text{no interaction}$.

Source	df	SS MS	F	p-value
k main effects		eg SSA = MSA	F_A	p_A
$\binom{k}{2}$ 2 factor interactions		eg SSAB = MSAB	F_{AB}	p_{AB}
$\binom{k}{3}$ 3 factor interactions		eg SSABC = MSABC	F_{ABC}	p_{ABC}
\vdots	\vdots	\vdots	\vdots	\vdots
$\binom{k}{k-1}$ $k - 1$ factor interactions				
the k factor interaction		SSA \cdots L = MSA \cdots L	$F_{A\cdots L}$	$p_{A\cdots L}$
Error		SSE MSE		

These models get complex rapidly as k and the number of levels l_i increase. As k increases, there are a large number of models to consider. For experiments, usually the 3 way and higher order interactions are not significant. Hence a full model that includes all k main effects and $\binom{k}{2}$ 2 way interactions is a useful starting point for response, residual and transformation plots. The higher order interactions can be treated as potential terms and checked for significance. As a rule of thumb, significant interactions tend to involve significant main effects.

The sample size $n = m \prod_{i=1}^k l_i \geq m 2^k$ is minimized by taking $l_i = 2$ for $i = 1, \dots, k$. Hence the sample size grows exponentially fast with k . Designs that use the minimum number of levels 2 are discussed in Section 8.1.

6.3 Summary

1) The fixed effects two way Anova model has two factors A and B plus a response Y . Factor A has a levels and factor B has b levels. There are ab treatments. The cell means model is $Y_{ijk} = \mu_{ij} + e_{ijk}$ where $i = 1, \dots, a$;

$j = 1, \dots, b$; and $k = 1, \dots, m$. The sample size $n = abm$. The μ_{ij} are constants and the e_{ijk} are iid with mean 0 and variance σ^2 . Hence the $Y_{ijk} \sim f(y - \mu_{ij})$ come from a location family with location parameter μ_{ij} . The fitted values are $\hat{Y}_{ijk} = \bar{Y}_{ij\cdot} = \hat{\mu}_{ij}$ while the residuals $r_{ijk} = Y_{ijk} - \hat{Y}_{ijk}$.

2) **Know that the 4 step test for AB interaction is**

- i) H_0 no interaction H_A there is an interaction
- ii) F_{AB} is obtained from output.
- iii) The pvalue is obtained from output.
- iv) If pvalue $< \delta$ reject H_0 , and conclude that there is an interaction between A and B , otherwise fail to reject H_0 , and conclude that there is no interaction between A and B .

3) Keep A and B in the model if there is an AB interaction.

4) **Know that the 4 step test for A main effects is**

- i) $H_0 \mu_{10} = \dots = \mu_{a0}$ H_A not H_0
- ii) F_A is obtained from output.
- iii) The p-value is obtained from output.
- iv) If pvalue $< \delta$ reject H_0 and conclude that the mean response depends on A , otherwise fail to reject H_0 and conclude that the mean response does not depend on A .

5) **Know that the 4 step test for B main effects is**

- i) $H_0 \mu_{01} = \dots = \mu_{0b}$ H_A not H_0
- ii) F_B is obtained from output.
- iii) The pvalue is obtained from output.
- iv) If p-value $< \delta$ reject H_0 and conclude that the mean response depends on B , otherwise fail to reject H_0 and conclude that the mean response does not depend on B .

The tests for main effects (points 4) and 5)) do not always make sense if the test for interactions is rejected.

6) Shown is an ANOVA table for the two way Anova model given in symbols. Sometimes "Error" is replaced by "Residual," or "Within Groups." A and B are the main effects while AB is the interaction. Sometimes "p-value" is replaced by "P", " $Pr(> F)$ " or "PR > F." The p-value for corresponding to F_A is for $H_0: \mu_{10} = \dots = \mu_{a0}$. The p-value for corresponding to F_B is for $H_0: \mu_{01} = \dots = \mu_{0b}$. The p-value for corresponding to F_{AB} is for H_0 : there is no interaction.

Source	df	SS	MS	F	p-value
A	a-1	SSA	MSA	$F_A = \text{MSA}/\text{MSE}$	pval
B	b-1	SSB	MSB	$F_B = \text{MSB}/\text{MSE}$	pval
AB	$(a-1)(b-1)$	SSAB	MSAB	$F_{AB} = \text{MSAB}/\text{MSE}$	pval
Error	$n - ab = ab(m-1)$	SSE	MSE		

7) An **interaction plot** is made by plotting the levels of one factor (either $1, \dots, a$ or $1, \dots, b$) versus the cell sample means \bar{Y}_{ij0} . Typically the factor with more levels (eg A if $a > b$) is used on the horizontal axis. If the levels of A are on the horizontal axis, use line segments to join the a means that have the same j . There will be b curves on the plot. If the levels of B are on the horizontal axis, use line segments to join the b means that have the same i . There will be a curves on the plot. If **no interaction** is present, then the curves should be roughly parallel.

8) The interaction plot is rather hard to use, especially if the $n_{ij} = m$ are small. For small m , the curves could be far from parallel even if there is no interaction, but the further the curves are from being parallel, the greater the evidence of interaction. Intersection of curves suggests interaction unless the two curves are nearly the same. The two curves may be nearly the same if two levels of one factor give nearly the same mean response for each level of the other factor. Then the curves could cross several times even though there is no interaction. Software fills space. So the vertical axis needs to be checked to see whether the sample means for two curves are “close” with respect to the standard error MSE/m for the means.

9) The interaction plot is the most useful if the conclusions for the plot agree with the conclusions for the F test for no interaction.

10) The μ_{ij} of the cell means model can be parameterized as $\mu_{ij} = \mu_{00} + \alpha_i + \beta_j + (\alpha\beta)_{ij}$ for $i = 1, \dots, a$ and $j = 1, \dots, b$. Here the α_i are the A main effects and $\sum_i \alpha_i = 0$. The β_j are the B main effects and $\sum_j \beta_j = 0$. The $(\alpha\beta)_{ij}$ are the interaction effects and satisfy $\sum_i (\alpha\beta)_{ij} = 0$, $\sum_j (\alpha\beta)_{ij} = 0$ and $\sum_i \sum_j (\alpha\beta)_{ij} = 0$. The interaction effect $(\alpha\beta)_{ij} = \mu_{ij} - \mu_{i0} - \mu_{0j} + \mu_{00}$. Here the *row factor means* $\mu_{i0} = \sum_j \mu_{ij}/b$, the *column factor means* $\mu_{0j} = \sum_i \mu_{ij}/a$ and $\mu_{00} = \sum_i \sum_j \mu_{ij}/(ab)$.

11) If there is no interaction, then the factor effects are additive: $\mu_{ij} = \mu_{00} + \alpha_i + \beta_j$.

- 12) If A and B are factors, then there are 5 possible models.
- i) The two way Anova model has terms A , B and AB .
 - ii) The additive model or main effects model has terms A and B .
 - iii) The one way Anova model that uses factor A .
 - iv) The one way Anova model that uses factor B .
 - v) The null model does not use any of the three terms A , B or AB . If the null model holds, then $Y_{ijk} \sim f(y - \mu_{00})$ so the Y_{ijk} form a random sample of size n from a location family and the factors have no effect on the response.
- 13) A two way Anova model could be fit as a one way Anova model with $k = ab$ treatments, but for balanced models where $n_{ij} \equiv m$, this procedure loses information about A , B and the interaction AB .
- 14) Response, residual and transformation plots are used in the same way for the two way Anova model as for the one way Anova model.

6.4 Complements

Four good tests on the design and analysis of experiments are Box, Hunter and Hunter (2005), Cobb (1998), Kuehl (1994) and Ledolter and Swersey (2007). Also see Dean and Voss (2000), Kirk (1982), Montgomery (2005) and Oehlert (2000).

The software for k way Anova is often used to fit block designs. Each block is entered as if it were a factor and the main effects model is fit. The one way block design treats the block like one factor and the treatment factor as another factor and uses two way Anova software without interaction to get the correct sum of squares, F statistic and p-value. The Latin square design treats the row block as one factor, the column block as a second factor and the treatment factor as another factor. Then the three way Anova software for main effects is used to get the correct sum of squares, F statistic and p-value. These two designs are described in Chapter 7. The k way software is also used to get output for the split plot designs described in Chapter 9.

6.5 Problems

Problems with an asterisk * are especially important.

Output for 6.1.

Source	df	SS	MS	F	P
A	2	24.6	12.3	0.24	0.791
B	2	28.3	14.2	0.27	0.763
Interaction	4	1215.3	303.8	5.84	0.001
Error	36	1872.4	52.0		

6.1. The above output uses data from Neter, Kutner, Nachtsheim and Wasserman (1996, problems 19.16-17). A study measured the number of minutes to complete a repair job at a large dealership. The two explanatory variables were “A = technician” and “B = make of drive.” The output is given above.

- a) Give a four step test for no interaction.
- b) Give a four step test for the B main effects.

6.2. Suppose A has 5 levels and B has 4 levels. Sketch an interaction plot if there is no interaction.

Two Way Anova in SAS

In SAS, $Y = A|B$ is equivalent to $Y = A + B + A*B$. Thus the SAS model statement could be written in either of the following two forms.

```
proc glm;
  class material temp;
  model mvoltage = material|temp;
  output out =a p = pred r = resid;
```

```
proc glm;
  class material temp;
  model mvoltage = material temp material*temp;
  output out =a p = pred r = resid;
```

6.3. Cut and paste the SAS program from (www.math.siu.edu/olive/sasreg.txt) for 6.3 into the SAS Editor.

To execute the program, use the top menu commands “Run>Submit”. An output window will appear if successful. The data is from Montgomery (1984, p. 198) and gives the maximum output voltage for a typical type of storage battery. The two factors are material (1,2,3) and temperature (50, 65, 80 °F).

a) Copy and paste the SAS program into SAS, use the file command “Run>Submit.”

b) Click on the “Graph1” window and scroll down to the second interaction plot of “tmp” vs “ymn.” Press the printer icon to get the plot.

c) Is interaction present?

d) Click on the output window then click on the printer icon. This will produce 5 pages of output, but only hand in the Anova table, response plot and residual plots.

(Cutting and pasting the output into *Word* resulted in bad plots. Using *Notepad* gave better plots, but the printer would not easily put the Anova table and two plots on one page each.)

e) Do the residual and response plots look ok?

Two Way Anova in Minitab

6.4. a) Copy the SAS data for problem 6.3 into *Notepad*. Then hit “Enter” every three numbers so that the data is in 3 columns.

```
1  50  130
1  50  155
1  50   74
1  50  180
1  65   34
.   .   .
.   .   .
.   .   .
3  80   60
```

b) Copy and paste the data into *Minitab* using the menu commands Edit>Paste Cells and click on “OK.” Right below C1 type “material”, below C2 type “temp” and below C3 type “mvoltage”.

c) Select Stat>ANOVA>Two-way, select “C3 mvoltage” as the response and “C1 material” as the row factor and “C2 temp” as the column factor. Click on “Store residuals” and click on “Store fits.” Then click on “OK.” Click on the output and then click on the *printer* icon.

d) To make a residual plot, select Graph>Plot. Select “Resi1” for “Y” and “Fits1” for “X” and click on “OK.” Click on the *printer* icon to get a plot of the graph.

e) To make a response plot, select Graph>Plot. Select “C3 mvoltage” for “Y” and “Fits1” for “X” and click on “OK.” Click on the *printer* icon to get

a plot of the graph.

f) Use the menu commands “Stat>ANOVA>Interaction Plots” enter mvoltage in the “Responses” box and material and temp in the “Factors” box. Click on “OK” and print the plot.

g) Use the menu commands “Stat>ANOVA>Interaction Plots” enter mvoltage in the “Responses” box and material and temp in the “Factors” box. Click on “OK” and print the plot.

h) Do the 4 step test for interaction.

Problems using R/Splus.

In *R*,

$Y \sim A + B$ is equivalent to $Y \sim .$ so the period indicates use all main effects. $Y \sim A:B$ is equivalent to $Y \sim A + B + A*B$ and $Y \sim A*B$ and $Y \sim .^2$ which means fit all main effects and all two way interactions. A problem is that A and B need to be of type factor.

6.5. The Box, Hunter, and Hunter (2005, p. 318) poison data has 3 types of treatments (1,2,3,4) and 3 types of poisons (1,2,3). Each animal is given a poison and a treatment, and the response is survival in hours.

a) Type the following commands to see that the output for the three models is the same.

```
out1<-aov(stime~ptype*treat,poison)
summary(out1)
out2<-aov(stime~ptype + treat + ptype*treat,poison)
summary(out2)
out3<-aov(stime~.^2,poison)
summary(out3)
#The three models are the same.
```

b) Type the following commands to see the residual plot.

```
plot(fitted(out1),resid(out1))
title("Residual Plot")
```

c) Type the following commands to see the response plot.

```
FIT <- poison$stime - out1$resid
plot(FIT,poison$stime)
abline(0,1)
title("Response Plot")
```

d) Why is the two way Anova model inappropriate?

e) Now the response $Y = 1/stime$ will be used. Type the following commands to get the output. Copy the output into *Word*.

```
attach(poison)
out4 <- aov((1/stime)~ptype*treat,poison)
summary(out4)
```

f) Type the following commands to get the residual plot. Copy the plot into *Word*.

```
plot(fitted(out4),resid(out4))
title("Residual Plot")
```

g) Type the following commands to get the response plot. Copy the plot into *Word*.

```
FIT <- 1/poison$stime - out4$resid
plot(FIT,(1/poison$stime))
abline(0,1)
title("Response Plot")
```

h) Type the following commands to get the interaction plot. Copy the plot into *Word*.

```
interaction.plot(treat,ptype,(1/stime))
detach(poison)
```

i) Test whether there is an interaction using the output from e).