The two way Anova model has two factors: A and B, and an interaction AB. In addition to response and residual plots, interaction plots are important.

The SAS example can be copied and pasted from (http://parker.ad.siu.edu/Olive/sasdoehw.txt). Only copy the program for this handout. 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).

In *SAS*, $Y = A|B$ is equivalent to $Y = A\ B\ AB$. 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;
```

For Minitab 19, a) copy and paste the SAS data with 3 columns into *Minitab*. (You could copy and paste data 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
.   .    .
.   .    .
.   .    .
3  80   60
```

b) Copy and paste the data into *Minitab* e.g., 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>Balanced ANOVA, select "C3 mvoltage" as the response and for Model use "material" "temp" and "material*temp." Click on storage and click on "residuals" and click on "fits." Then click on "OK." Copy and paste the output into *Word*.

d) To make a residual plot, select Graph>Scatterplot. Click on "ok." Select "Resi1" for "Y" and "Fits" for "X" and click on "OK." Copy and paste the residual plot into *Word*.

e) To make a response plot, select Graph>Scatterplot. Select "C3 mvoltage" for "Y" and "Fits1" for "X" and click on "OK." Copy and paste the residual plot into *Word*.

f) Use the file 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.

In *R*,

```
Y ~ A + B is equivalent to Y ~ . so the period indicates
use all main effects.  Y ~ A:B is equivalent to Y ~ A + B + A*B
and Y ~ A*B and Y ~ .^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.
```

The BHH (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. Use the source command to get the data set in R.

```
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.
plot(fitted(out1),resid(out1))
title("Residual Plot")
FIT <- poison$stime - out1$resid
plot(FIT,poison$stime)
abline(0,1)
title("Response Plot")
attach(poison)
interaction.plot(treat,ptype,stime)
out4 <- aov((1/stime)~ptype*treat,poison)
summary(out4)
plot(fitted(out4),resid(out4))
title("Residual Plot")
FIT <- 1/poison$stime - out4$resid
plot(FIT,(1/poison$stime))
abline(0,1)
title("Response Plot")
interaction.plot(treat,ptype,(1/stime))
out5 <- aov(log(stime)~ptype*treat,poison)
plot(fitted(out5),resid(out5))
title("Residual Plot")
FIT <- log(poison$stime) - out5$resid
plot(FIT,log(poison$stime))
abline(0,1)
title("Response Plot")
detach(poison)
```