

Lab 8

2024-10-27

```
library(readr)
minnows <- read_table("minnows.txt",
  col_names = c("copper", "zinc", "protein"),
  col_types = cols(copper = col_factor(levels = c("0", "150")),
    zinc = col_factor(levels = c("0", "750", "1500")))
)
```

```
options(contrasts = c("contr.sum", "contr.sum"))
sumto0.anova <- aov(protein ~ copper + zinc + copper*zinc, data = minnows)
summary(sumto0.anova)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## copper         1    234      234   1.809 0.227264
## zinc          2  10234     5117  39.537 0.000351 ***
## copper:zinc    2    288     144   1.113 0.387957
## Residuals     6    777     129
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sumto0.anova$coefficients
```

```
##      (Intercept)      copper1          zinc1          zinc2 copper1:zinc1
##      155.750000      4.416667      27.250000      13.250000      6.083333
## copper1:zinc2
##      -5.916667
```

```
model.matrix(sumto0.anova)
```

```
##      (Intercept) copper1 zinc1 zinc2 copper1:zinc1 copper1:zinc2
## 1              1      1      1      0              1              0
## 2              1      1      1      0              1              0
## 3              1      1      0      1              0              1
## 4              1      1      0      1              0              1
## 5              1      1     -1     -1             -1             -1
## 6              1      1     -1     -1             -1             -1
## 7              1     -1      1      0             -1              0
## 8              1     -1      1      0             -1              0
## 9              1     -1      0      1              0             -1
## 10             1     -1      0      1              0             -1
## 11             1     -1     -1     -1              1              1
## 12             1     -1     -1     -1              1              1
## attr(,"assign")
```

```
## [1] 0 1 2 2 3 3
## attr("contrasts")
## attr("contrasts")$copper
## [1] "contr.sum"
##
## attr("contrasts")$zinc
## [1] "contr.sum"
```

```
options(contrasts = c("contr.treatment", "contr.treatment"))
baseline.anova <- aov(protein ~ copper + zinc + copper*zinc, data = minnows)
summary(baseline.anova)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## copper          1    234      234   1.809 0.227264
## zinc           2  10234     5117  39.537 0.000351 ***
## copper:zinc     2    288     144   1.113 0.387957
## Residuals      6    777     129
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

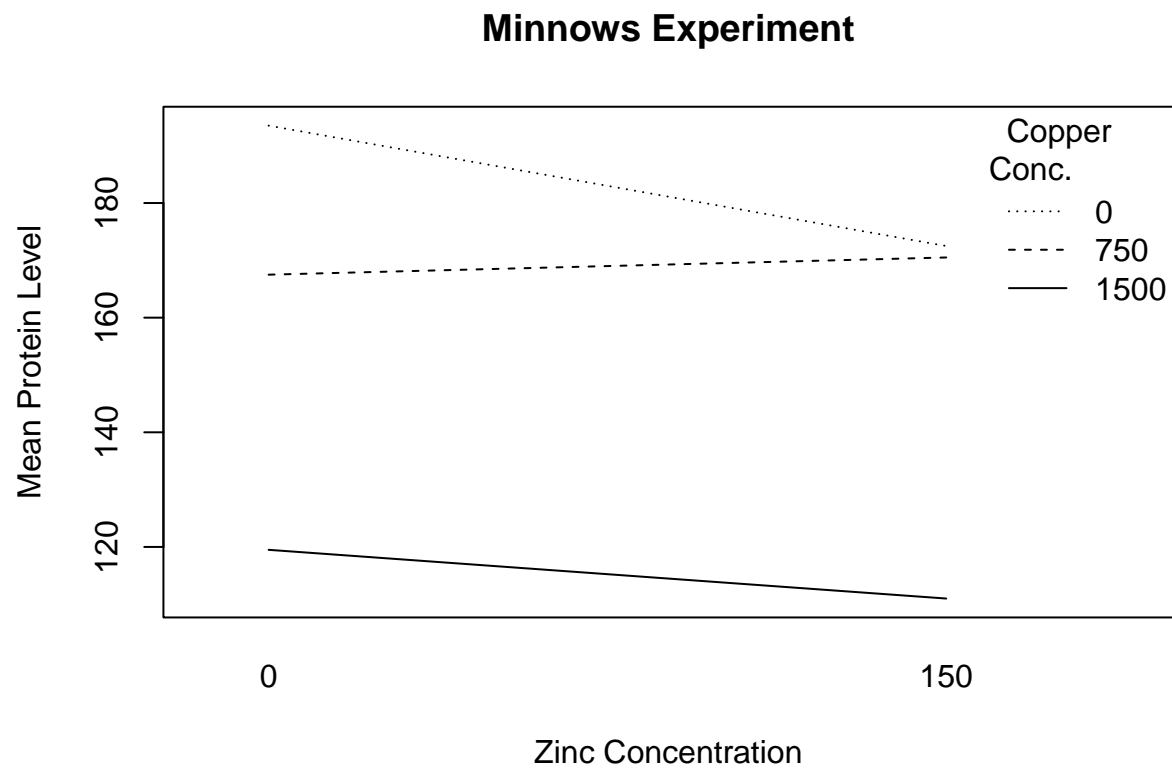
```
baseline.anova$coefficients
```

```
##      (Intercept)      copper150      zinc750      zinc1500
##           193.5          -21.0          -26.0          -74.0
## copper150:zinc750 copper150:zinc1500
##           24.0           12.5
```

```
model.matrix(baseline.anova)
```

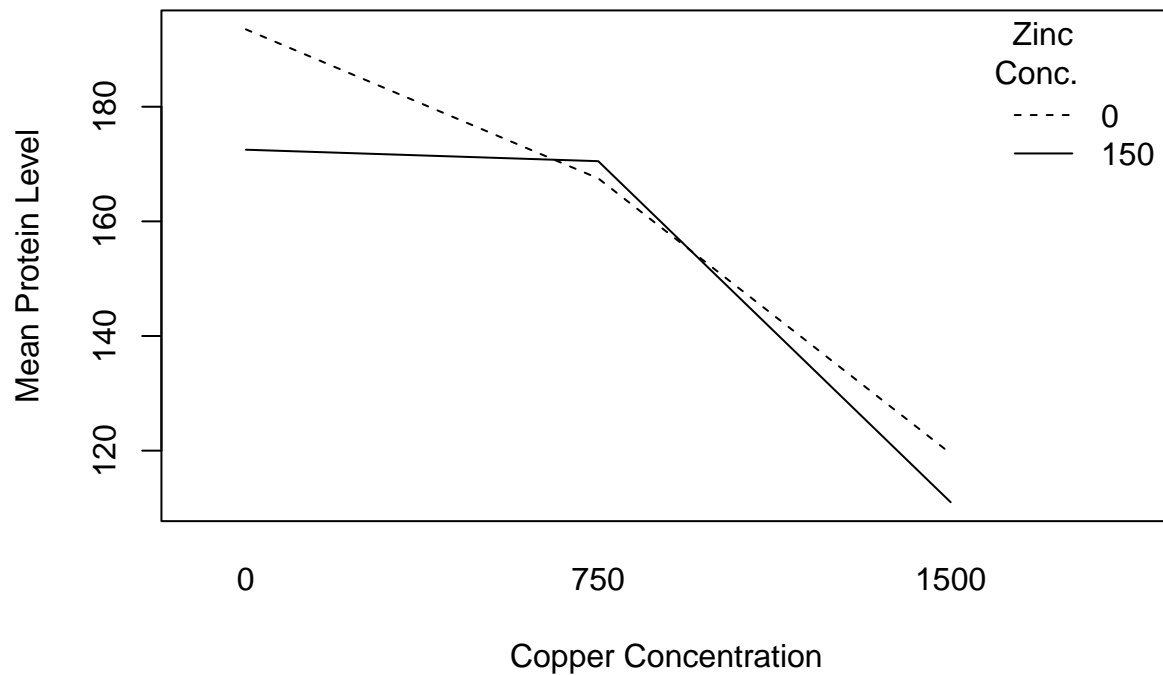
```
##      (Intercept) copper150 zinc750 zinc1500 copper150:zinc750 copper150:zinc1500
## 1             1         0       0         0              0              0
## 2             1         0       0         0              0              0
## 3             1         0       1         0              0              0
## 4             1         0       1         0              0              0
## 5             1         0       0         1              0              0
## 6             1         0       0         1              0              0
## 7             1         1       0         0              0              0
## 8             1         1       0         0              0              0
## 9             1         1       1         0              1              0
## 10            1         1       1         0              1              0
## 11            1         1       0         1              0              1
## 12            1         1       0         1              0              1
## attr("assign")
## [1] 0 1 2 2 3 3
## attr("contrasts")
## attr("contrasts")$copper
## [1] "contr.treatment"
##
## attr("contrasts")$zinc
## [1] "contr.treatment"
```

```
interaction.plot(minnows$copper, minnows$zinc, minnows$protein,
  main="Minnows Experiment",
  xlab="Zinc Concentration",
  ylab="Mean Protein Level",
  trace.label="Copper\n Conc.")
```



```
interaction.plot(minnows$zinc, minnows$copper, minnows$protein,
  main="Minnows Experiment",
  xlab="Copper Concentration",
  ylab="Mean Protein Level",
  trace.label="Zinc\n Conc.")
```

Minnows Experiment



```
library(emmeans)
```

```
## Welcome to emmeans.
## Caution: You lose important information if you filter this package's results.
## See '? untidy'
```

```
simple.effects <- emmeans(sumto0.anova, c("copper", "zinc"))
pairs(simple.effects, adjust=NULL)
```

## contrast	estimate	SE	df	t.ratio	p.value
## copper0 zinc0 - copper150 zinc0	21.0	11.4	6	1.846	0.1144
## copper0 zinc0 - copper0 zinc750	26.0	11.4	6	2.285	0.0623
## copper0 zinc0 - copper150 zinc750	23.0	11.4	6	2.022	0.0897
## copper0 zinc0 - copper0 zinc1500	74.0	11.4	6	6.505	0.0006
## copper0 zinc0 - copper150 zinc1500	82.5	11.4	6	7.252	0.0003
## copper150 zinc0 - copper0 zinc750	5.0	11.4	6	0.440	0.6757
## copper150 zinc0 - copper150 zinc750	2.0	11.4	6	0.176	0.8662
## copper150 zinc0 - copper0 zinc1500	53.0	11.4	6	4.659	0.0035
## copper150 zinc0 - copper150 zinc1500	61.5	11.4	6	5.406	0.0017
## copper0 zinc750 - copper150 zinc750	-3.0	11.4	6	-0.264	0.8008
## copper0 zinc750 - copper0 zinc1500	48.0	11.4	6	4.219	0.0056
## copper0 zinc750 - copper150 zinc1500	56.5	11.4	6	4.967	0.0025
## copper150 zinc750 - copper0 zinc1500	51.0	11.4	6	4.483	0.0042
## copper150 zinc750 - copper150 zinc1500	59.5	11.4	6	5.230	0.0020
## copper0 zinc1500 - copper150 zinc1500	8.5	11.4	6	0.747	0.4832

```
copper.effects <- emmeans(sumto0.anova, "copper")
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
pairs(copper.effects, adjust="tukey")
```

```
## contrast      estimate    SE df t.ratio p.value
## copper0 - copper150      8.83 6.57  6   1.345  0.2273
##
## Results are averaged over the levels of: zinc
```

```
zinc.effects <- emmeans(sumto0.anova, "zinc")
```

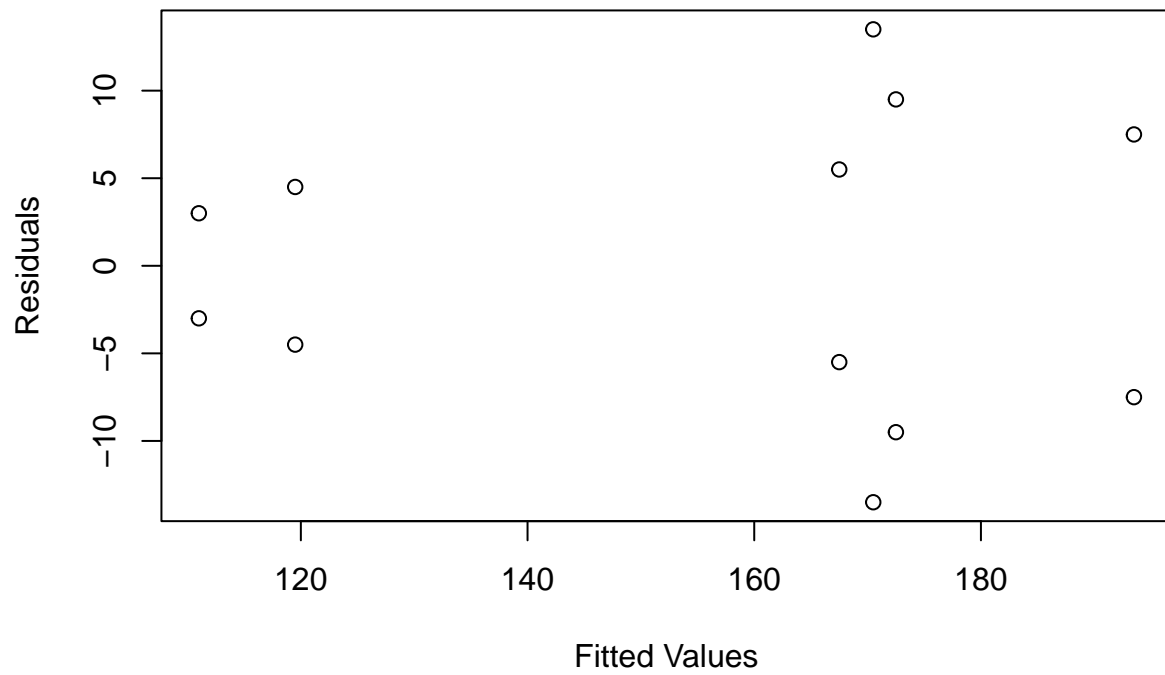
```
## NOTE: Results may be misleading due to involvement in interactions
```

```
pairs(zinc.effects, adjust="tukey")
```

```
## contrast      estimate    SE df t.ratio p.value
## zinc0 - zinc750      14.0 8.04  6   1.740  0.2666
## zinc0 - zinc1500      67.8 8.04  6   8.422  0.0004
## zinc750 - zinc1500     53.8 8.04  6   6.682  0.0013
##
## Results are averaged over the levels of: copper
## P value adjustment: tukey method for comparing a family of 3 estimates
```

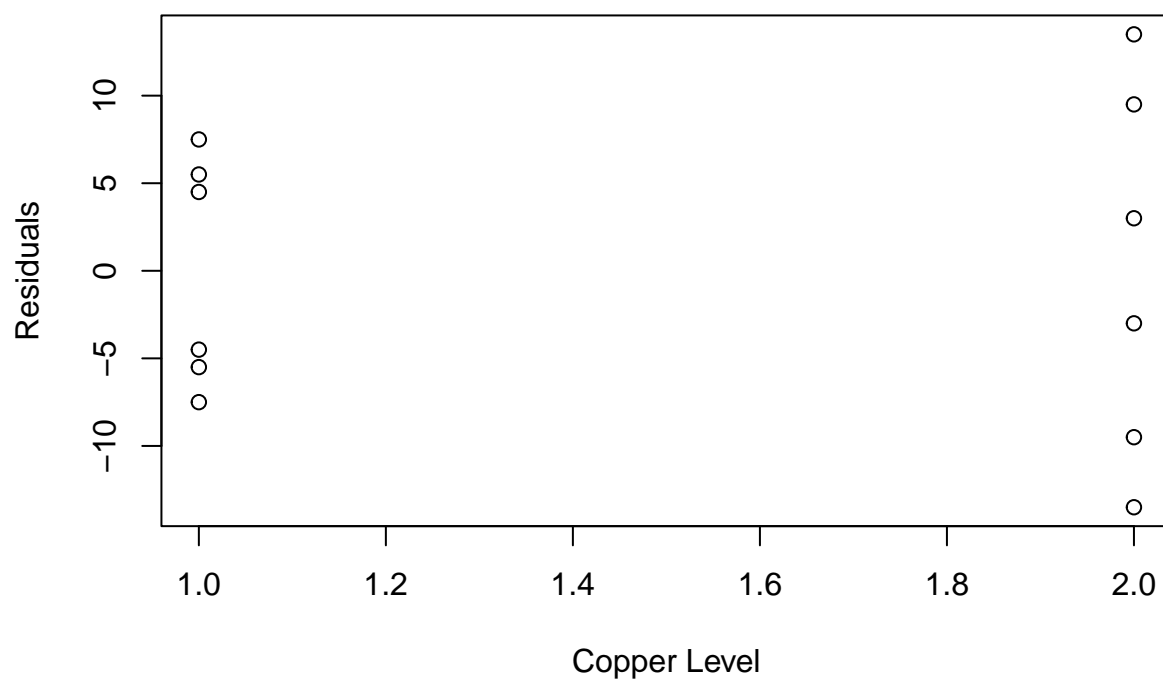
```
plot(sumto0.anova$fitted.values, sumto0.anova$residuals,
main="Diagnostic Plot for Minnows Experiment",
xlab="Fitted Values", ylab="Residuals")
```

Diagnostic Plot for Minnows Experiment



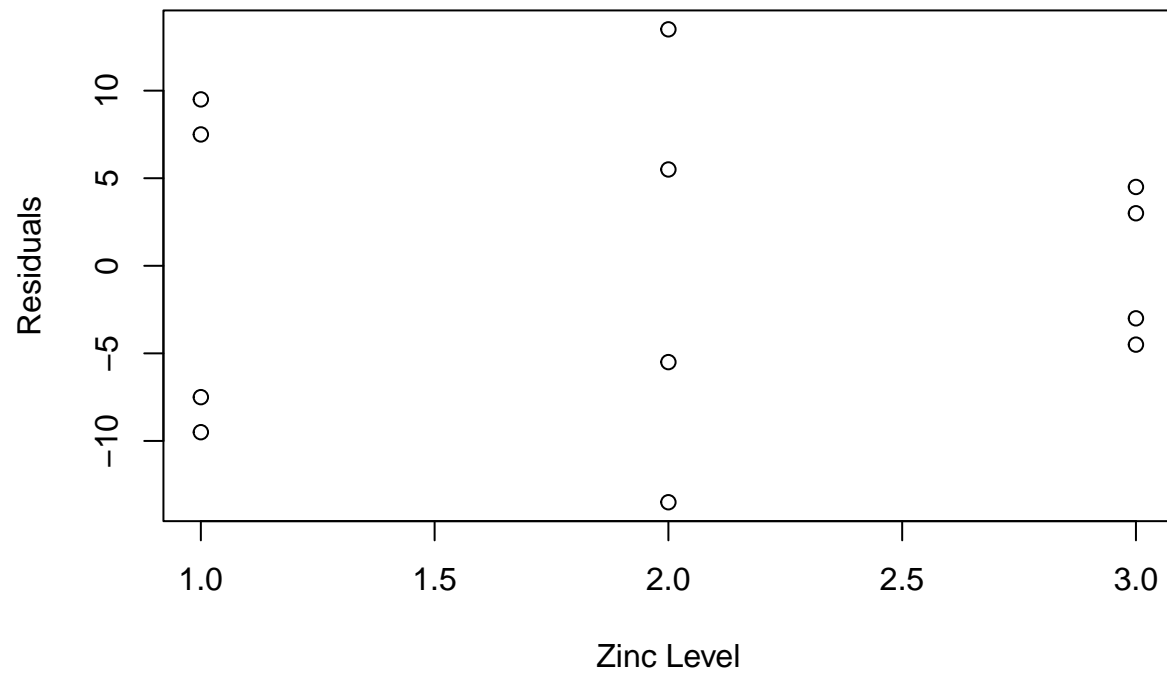
```
plot(as.numeric(minnows$copper), sumto0.anova$residuals,  
main="Diagnostic Plot for Minnows Experiment",  
xlab="Copper Level", ylab="Residuals")
```

Diagnostic Plot for Minnows Experiment



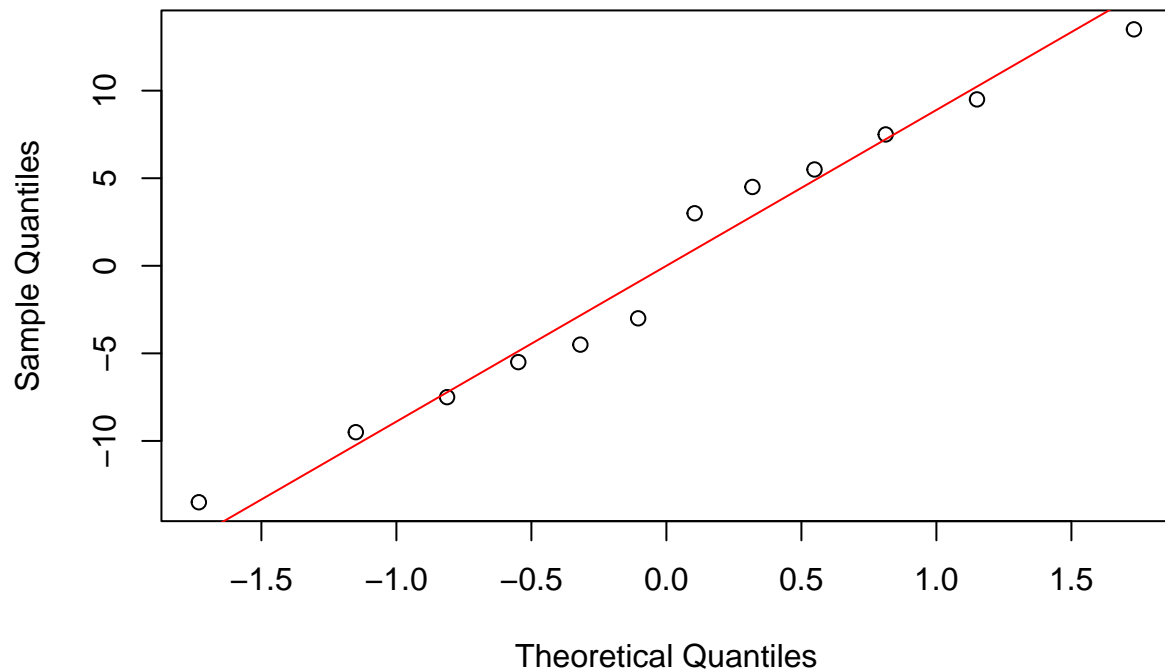
```
plot(as.numeric(minnows$zinc), sumto0.anova$residuals,  
main="Diagnostic Plot for Minnows Experiment",  
xlab="Zinc Level", ylab="Residuals")
```

Diagnostic Plot for Minnows Experiment



```
qqnorm(sumto0.anova$residuals)
qqline(sumto0.anova$residuals, col="red")
```


Normal Q-Q Plot



```
shapiro.test(sumto0.anova$residuals)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  sumto0.anova$residuals  
## W = 0.96538, p-value = 0.857
```

```
library(moments)  
mean(sumto0.anova$residuals)
```

```
## [1] 2.590159e-16
```

```
median(sumto0.anova$residuals)
```

```
## [1] 3.330669e-15
```

```
skewness(sumto0.anova$residuals)
```

```
## [1] -1.365054e-16
```

```
kurtosis(sumto0.anova$residuals)-3
```

```
## [1] -1.171783
```

1. Using baseline constraints, report the six unique rows in the design matrix X and the parameter vector β for this two-factor experiment.

2. Using sum-to-zero constraints, report the six unique rows in the design matrix X and the parameter vector β for this two-factor experiment.

3. Use the estimated parameters from the R output to calculate the six sample treatment means.

4. Use the ANOVA table from the R output to conduct the overall F-test for the effects of the six treatments on the minnow protein production. Interpret the results of the test in the context of the study.

5. Use the ANOVA table from the R output to test for the main effect of copper concentration on the minnow protein production. Assuming there is no significant interaction, interpret the results of the test in the context of the study.

6. Use the ANOVA table from the R output to test for the main effect of zinc concentration on the minnow protein production. Assuming there is no significant interaction, interpret the results of the test in the context of the study.

7. Use the ANOVA table from the R output to test for the interaction effect between copper and zinc concentrations on the minnow protein production. Interpret the results of the test in the context of the study.

8. Study the interaction plot in the R output. Explain why, based on this plot, the interaction is not significant in the model.

9. Use the LSD method to perform all pairwise comparisons of the cell means (simple effects) for the six treatments. Summarize any significant findings in the context of the study.

10. Use Tukey's HSD method to perform pairwise comparisons of the marginal means for the two copper concentrations (main effect of copper) and the marginal means for the three zinc concentrations (main effect of zinc). Summarize any significant findings in the context of the study.

11. Study the plots of the residuals versus: a) predicted value, b) the copper concentrations, and c) the zinc concentrations. Do these plots show any cause for concern?

12. Study the normal probability plot for the residuals. Is there anything of concern in this plot?