**Winter, 2011 Biometry Quiz #1**

1. **[14 pts]** Use the information about the tree height experiment to answer (on a separate sheet) the lettered questions immediately below. For each question, as appropriate, show your work, refer to a specific part of the output, and describe your rationale.
2. What specific conclusion about tree heights should be made from the p-value in the ANOVA table?
3. What is the difference in sample mean height between the clipped and control groups? Make sure to explicitly say which one is larger.
4. Is there a significant difference in the population mean meight between the clipped and control groups?
5. Interpret the confidence interval related to the largest difference between groups?
6. What is the 95% CI for the clipped-fertilized parameter?
7. **[2 pts - XC]** Put letters on the fitPlot() plot that shows which means are statistical different?
8. **[10 pts]** Complete the following questions with the partial generic ANOVA table below.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Source** | **df** | **SS** | **MS** | **F** | **p-value** |
| **Among Groups** |  | 169.448 | 21.181 | 1.321 | 0.281 |
| **Within Groups** |  |  |  |  |  |
| **Total** | 34 |  |  |  |  |

* 1. Fill in the remainder of the ANOVA table above.
  2. How many individuals were in this analysis? \_\_\_\_\_\_\_\_\_
  3. What is the pooled estimate of the variance among individuals in each group? \_\_\_\_\_\_\_\_\_

1. **[12 pts]** Use the results and description from the *Daphnia* experiment to fully assess ALL assumptions of a one-way ANOVA.
2. **[15 pts]** Answer 3 of the 6 questions below (a-f) with COMPLETE SENTENCES.
   1. Completely compare and contrast the concepts of a “full” and a “simple” model. *Your statements should be general but you may refer to a specific instance as an example.*
   2. Completely compare and contrast the meanings of MSWithin, MSTotal, and MSAmong. *Your statements should be general but you may refer to a specific instance as an example.*
   3. Mathematically prove that SSTotal partitions exactly into SSWithin and SSAmong. *You do not need complete sentences for this question but you should show each step in the proof.*
   4. Define experiment-wise and comparison-wise error rates. Specifically identify the relative size of each error rate.
   5. Describe when a Tukey HSD and when a Dunnet’s procedure would be appropriate to use. For the Dunnet’s situation describe why the Dunnet’s method is “better” than Tukey’s method for the same situation.
   6. Mathematically show that the difference in two means of a log-transformed variable becomes a RATIO of two means on the original scale*.* *You do not need complete sentences for this question but you should show each step in the proof.*
3. **[3 pts]** Explain (thoughtfully) why you are taking this course (“because it is required” is not acceptable).

**Winter, 2011 Biometry Quiz #1**

The height of Scots pine trees in three treatment groups (clipped: all previous year’s shoots removed; fertilized: nitrogen added to the soil around the trees; shaded: top- and lateral-most branches covered with a cloth) and one control group (no manipulation) was recorded. Individual pine trees were randomly selected to be in one of the four groups. The author’s analysis of these data was repeated in R with the results given below.

**> library(NCStats)**

**> library(multcomp)**

**> m <- read.table("MooseBrowse.txt",header=TRUE)**

**> str(m)**

'data.frame': 140 obs. of 2 variables:

$ height: num 181 162 185 179 163 ...

$ treat : Factor w/ 4 levels "Clipped","Control",..: 3 3 3 3 3 3 3 3 3 3 ...

**> lm2 <- lm(height~treat,data=m)**

**> anova(lm2)**

Analysis of Variance Table

Response: height

Df Sum Sq Mean Sq F value Pr(>F)

treat 3 32728 10909.2 131.98 < 2.2e-16 \*\*\*

Residuals 136 11241 82.7

**> m.mc <- glht(lm2,mcp(treat="Tukey"))**

**> summary(m.mc)**

Linear Hypotheses:

Estimate Std. Error t value Pr(>|t|)

Control - Clipped == 0 33.420 2.173 15.378 < 0.001 \*\*\*

Fertilized - Clipped == 0 38.954 2.173 17.924 < 0.001 \*\*\*

Shaded - Clipped == 0 32.020 2.173 14.733 < 0.001 \*\*\*

Fertilized - Control == 0 5.534 2.173 2.547 0.05726 .

Shaded - Control == 0 -1.400 2.173 -0.644 0.91741

Shaded - Fertilized == 0 -6.934 2.173 -3.191 0.00927 \*\*

**> confint(m.mc)**

Linear Hypotheses:

Estimate lwr upr

Control - Clipped == 0 33.4200 27.7667 39.0733

Fertilized - Clipped == 0 38.9543 33.3010 44.6076

Shaded - Clipped == 0 32.0200 26.3667 37.6733

Fertilized - Control == 0 5.5343 -0.1190 11.1876

Shaded - Control == 0 -1.4000 -7.0533 4.2533

Shaded - Fertilized == 0 -6.9343 -12.5876 -1.2810

**> fitPlot(lm2,main=””)**



The effect of chlorine on the mortality rate of *Daphnia* spp. was tested. Ten tanks with 100 *Daphnia* each were set up and each was randomly selected to receive 1, 10, or 100 ppm of chlorine. The proportion of *Daphnia* that died after 48-h (*mort*) and the amount of chlorine injected (*dose*) was recorded for each tank. The author’s analysis of these data was repeated in R with the results given below (and on the next page).

**> library(NCStats)**

**> d <- read.table("DoseResponse.txt",header=TRUE)**

**> d$dose <- factor(d$dose)**

**> str(d)**

'data.frame': 30 obs. of 2 variables:

$ dose: Factor w/ 3 levels "1","10","100": 1 1 1 1 1 1 1 1 1 1 ...

$ mort: num 0.8 0.9 0.6 0.85 0.75 0.7 0.75 0.8 0.95 0.75 ...

**> lm1 <- lm(mort~dose,data=d)**

**> leveneTest(lm1)**

Levene's Test for Homogeneity of Variance (center = median)

Df F value Pr(>F)

group 2 4.2216 0.02539 \*

27

**> residPlot(lm1)**



**> adTest(lm1$residuals)**

Anderson-Darling normality test

data: lm1$residuals

A = 1.159, p-value = 0.004175

**> hist(lm1$residuals)**



**> outlierTest(lm1)**

rstudent unadjusted p-value Bonferonni p

3 -3.643678 0.0011755 0.035264