

Stat 217 Project 2

Due Wednesday September 23rd In Class

You must work in groups of 3 to 4. There will be a point deduction if you do not work in a group.

For this project we will look at data from a study in which researchers fed mice different doses of red dye number 40 and recorded the time until death in weeks (reference: Journal Natl. Cancer Inst., Vol. 66, p 197-212). The dose variable has four levels: control, low, medium, and high. We are interested in whether there is a difference among the groups in the average number of weeks until death and, if so, which groups differ from one another. For this project, we will use a significance level of 0.05. Note that the researchers randomized the mice into treatment groups and that lab mice are bred to be as nearly genetically identical as possible.

Summarize your results in a written report following the **Project Writing Guidelines** posted on D2L. The **Summary of Statistical Findings** section of your report should include the following:

- A decision sentence stating whether you would reject or fail to reject the null at a significance level of 0.05.
- **One** evidence sentence reporting the results of the One Way Analysis of Variance.
- **Four** estimate sentences - one sentence interpreting each of the coefficient estimates you get from R.
- A confidence interval and associated interpretation for any pairwise differences your Tukey's HSD analysis detects as being different from 0 (one sentence for each difference that is significant).

Begin by downloading the data file from D2L and saving it on your computer. Then read it in to R. The following code should get you started:

```
require(mosaic)
require(beanplot)
require(multcomp)

mice <- read.csv("../") ## insert the path for your saved mice.csv file
head(mice) ## shows you the first 6 lines of your mice data, so you can see how it is organized

favstats(weeks ~ dose, data = mice)
beanplot(weeks ~ dose, data = mice, method = "jitter", log = "", col = 7)

mice.lm <- lm(weeks ~ dose, data = mice)
summary(mice.lm)
anova(mice.lm)
par(mfrow = c(2, 2)) ## arranges the diagnostic plots in a 2x2 grid
plot(mice.lm)

mice.lm2 <- glht(mice.lm, linfct = mcp(dose = "Tukey"))
confint(mice.lm2, level = 0.95)
par(mfrow = c(1, 1)) ## makes only one plot appear at a time
old.par <- par(mai = c(1.5, 2.5, 1, 1)) ## makes room on the plot for the group names
plot(mice.lm2)
cld(mice.lm2)
```