Question 2.6

a. The mean UTH is significantly different among the three groups ($p = 0.0017$; Table 1).

Table 1. Analysis of variance table for the UTH values by syndrome type with the 20th individual removed.

```
          Df Sum Sq Mean Sq F value   Pr(>F)
cause      2 181.12  90.561  9.4911 0.001706
Residuals 17 162.21   9.542
```

b. It appears that the mean UTH for the adenoma group is significantly different from the mean UTH for both the bilateral hyperplasia ($p = 0.0118$; Table 2) and carcinoma ($p = 0.0018$; Table 2) groups and that the mean UTH for the bilateral hyperplasia and carcinoma groups are NOT statistically different ($p = 0.2499$; Table 2). These results are shown visually in Figure 1.

Table 2. Tukey's multiple comparison results for the UTH values by syndrome type with the 20th individual removed.

```
                        Estimate Std. Error  t value    p value
BiHyper - Adenoma = 0   5.213333   1.595136 3.268268 0.01179697
Carcinoma - Adenoma = 0 8.233333   1.993920 4.129218 0.00178109
Carcinoma - BiHyper = 0 3.020000   1.827458 1.652568 0.24987006
```

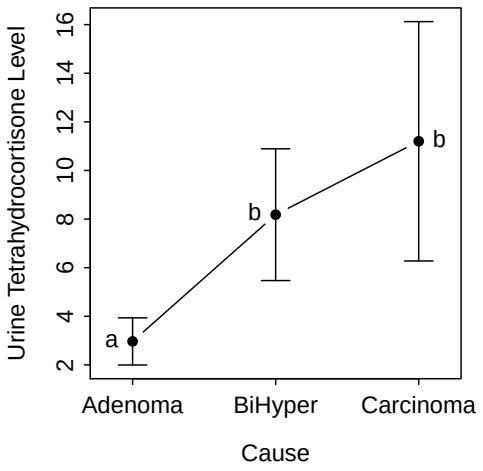

Figure 1. Plot of mean (with 95% CI) UTH level by syndrome type with the 20th individual removed. Different letters indicate means that are significantly different.

c. The mean of the bilateral hyperplasia group is between 1.13 and 9.30 units greater than the mean for the adenoma group (Table 3). The mean for the carcinoma group is between 3.13 and 13.34 units greater than the mean for the adenoma group (Table 3). The means for the bilateral hyperplasia and carcinoma groups are not statistically different.

Table 3. Tukey's confidence interval results for the difference in mean UTH values by syndrome type with the 20th individual removed.

```
                    Estimate       lwr       upr
BiHyper - Adenoma   5.213333  1.129973  9.296694
Carcinoma - Adenoma 8.233333  3.129132 13.337534
Carcinoma - BiHyper 3.020000 -1.658077  7.698077
```

R commands

```
> library(NCStats)
> library(multcomp)
> # the next four lines is just an alternative way to enter the data
> #   using read.table() is easier and more efficient
> d <- data.frame(cause=factor(c(rep("Adenoma",6),rep("BiHyper",10),rep("Carcinoma",5)),
                               levels= c("Adenoma","BiHyper","Carcinoma")),
                  uth=c(3.1,3,1.9,3.8,4.1,1.9,8.3,3.8,3.9,7.8,9.1,15.4,
                        7.7,6.5,5.7,13.6,10.2,9.2,9.6,53.8,15.8) )
> d2 <- d[-20,]
> lm2 <- lm(uth~cause,data=d2)
> anova(lm2)
> mc2 <- glht(lm2,mcp(cause="Tukey"))
> summary(mc2)
> confint(mc2)
> fitPlot(lm2,xlab="Cause",ylab="Urine Tetrahydrocortisone Level")
> addSigLetters(lm2,c("a","b","b"),pos=c(2,2,4))
```