Quiz 2 Handout

Background

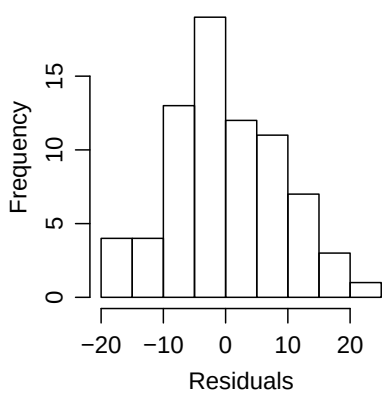
Sanz (2001) examined the nesting behavior and success for male and female pied flycatchers (*Ficedula hypoleuca*). He hypothesized that males would be more involved in nesting activities as the level of brood demand increased and as the "attractiveness" of the male decreased. The author manipulated brood demand by removing two eggs from randomly selected nests and placing these eggs into other randomly selected nests. This created two levels for a "clutch-size manipulation" factor - reduced and enlarged clutch sizes. A third level consisted of nests where the number of eggs was not manipulated (called the "control" level). The author manipulated the "attractiveness" of the male by reducing the size of the white patch on the forehead. The forehead patch was reduced in size on randomly selected males by clipping approximately two-thirds of the white feathers. Thus, the experiment consisted of two levels of the "forehead patch" factor - "unmanipulated" and "reduced." In one aspect of the experiment, Sanz recorded the feeding rate of the male flycatchers on the 13th day post-hatch. The feeding rate was recorded as the number of times the male fed the hatchlings per hour. The author tested his hypotheses by examining the data for clutch-size manipulation (*csm*), forehead manipulation (*fh*), and interaction effects on feeding rates (*mfr*).

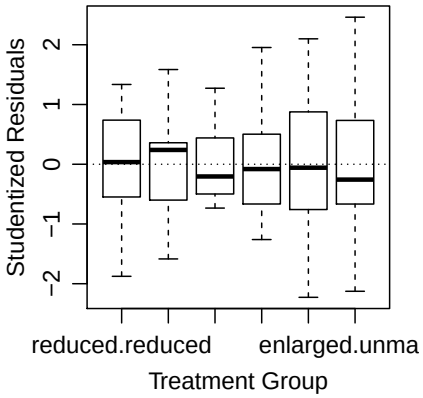
R Results

```
> library(NCStats)
> library(multcomp)

> pfc <- read.table("PiedFlycatcher1.txt",head=TRUE)
> str(pfc)

'data.frame':        74 obs. of  3 variables:
 $ csm: Factor w/ 3 levels "control","enlarged",..: 1 1 1 1 1 1 1 1 1 ...
 $ fh : Factor w/ 2 levels "reduced","unmanip": 2 2 2 2 2 2 2 2 2 ...
 $ mfr: int  0 13 11 3 24 12 26 36 17 19 ...

> pfc$csm <- factor(pfc$csm,levels=c("reduced","control","enlarged"))
> lm1 <- lm(mfr~csm*fh,data=pfc)
> leveneTest(lm1)

Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  5  0.8643 0.5097
      68

> adTest(lm1$residuals)

        Anderson-Darling normality test

data:  lm1$residuals
A = 0.261, p-value = 0.6989

> outlierTest(lm1)
```

```
No Studentized residuals with Bonferonni p < 0.05
Largest |rstudent|:
   rstudent unadjusted p-value Bonferonni p
24 2.461379           0.016422           NA
```

```
> hist(lm1$residuals,main="",xlab="Residuals")
> residualPlot(lm1,main="")
```

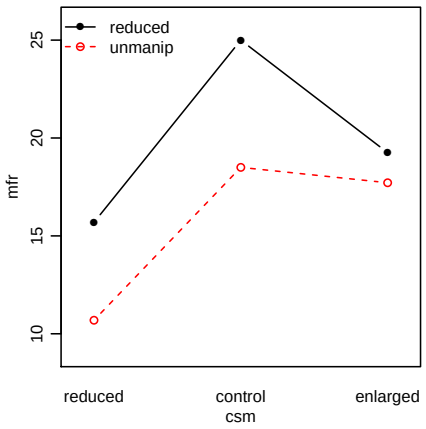


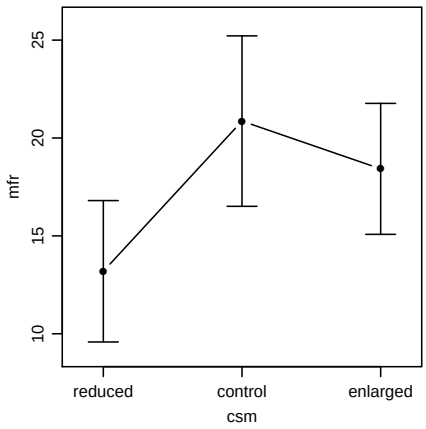


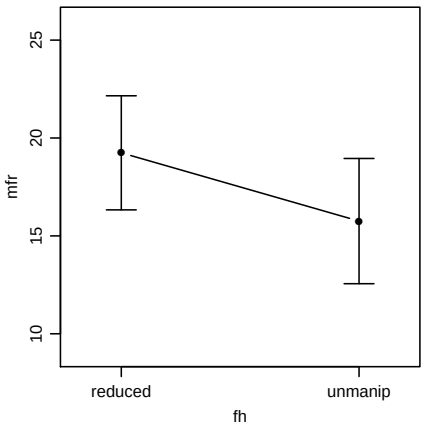

```
> anova(lm1)
```

```
          Df Sum Sq Mean Sq F value  Pr(>F)
csm        2  750.9  375.44  4.7771 0.01145
fh         1  315.9  315.88  4.0193 0.04897
csm:fh     2   77.0   38.48  0.4896 0.61503
Residuals 68 5344.1   78.59
```

```
> fitPlot(lm1,legend="topleft",ylim=c(9,26),main="",interval=FALSE)
> fitPlot(lm1,which="csm",ylim=c(9,26),main="")
> fitPlot(lm1,which="fh",ylim=c(9,26),main="")
```







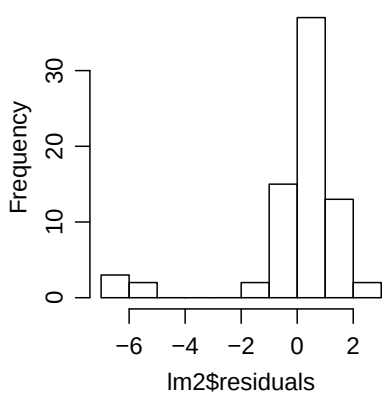

```
> mc1 <- glht(lm1,mcp(csm="Tukey"))
> summary(mc1)
```

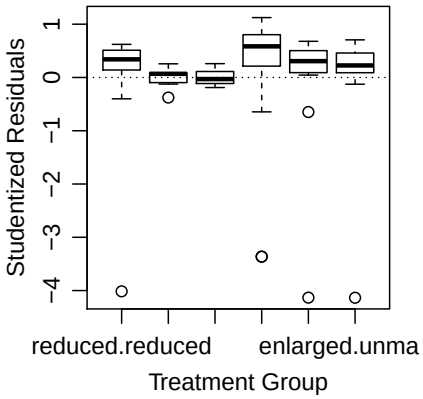
```
                       Estimate Std. Error   t value     p value
control - reduced = 0   8.241742   2.564876  3.213310 0.005475138
enlarged - reduced = 0  5.391655   2.442048  2.207842 0.076664737
enlarged - control = 0 -2.850087   2.557330 -1.114478 0.508294723
```

```
> pfc$comb <- pfc$csm:pfc$fh
> lm1a <- lm(mfr~comb,data=pfc)
> mc1a <- glht(lm1a,mcp(comb="Tukey"))
> summary(mc1a)
```

```
                                          Estimate Std. Error    t value     p value
reduced:unmanip - reduced:reduced = 0   -5.0000000   3.477187 -1.4379441 0.702573150
control:reduced - reduced:reduced = 0    9.3076923   3.983618  2.3364923 0.192779682
control:unmanip - reduced:reduced = 0    2.8076923   3.414530  0.8222779 0.962144218
enlarged:reduced - reduced:reduced = 0   3.5576923   3.548889  1.0024806 0.914997266
enlarged:unmanip - reduced:reduced = 0   2.0219780   3.414530  0.5921688 0.991168825
control:reduced - reduced:unmanip = 0   14.3076923   3.983618  3.5916328 0.007796999
control:unmanip - reduced:unmanip = 0    7.8076923   3.414530  2.2866085 0.212569829
enlarged:reduced - reduced:unmanip = 0   8.5576923   3.548889  2.4113724 0.165799466
enlarged:unmanip - reduced:unmanip = 0   7.0219780   3.414530  2.0564994 0.320874928
control:unmanip - control:reduced = 0   -6.5000000   3.929045 -1.6543460 0.564443257
enlarged:reduced - control:reduced = 0  -5.7500000   4.046356 -1.4210317 0.712914972
enlarged:unmanip - control:reduced = 0  -7.2857143   3.929045 -1.8543219 0.437172894
enlarged:reduced - control:unmanip = 0   0.7500000   3.487520  0.2150525 0.999933257
enlarged:unmanip - control:unmanip = 0  -0.7857143   3.350701 -0.2344925 0.999897684
enlarged:unmanip - enlarged:reduced = 0 -1.5357143   3.487520 -0.4403456 0.997798702
```

```
> pfc$logmfr <- log(pfc$mfr+0.01)
> lm2 <- lm(logmfr~csm*fh,data=pfc)
> leveneTest(lm2)

Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  5  0.9781 0.4376
      68

> adTest(lm2$residuals)

        Anderson-Darling normality test

data:  lm2$residuals
A = 9.7963, p-value < 2.2e-16

> hist(lm2$residuals,main="")
> residualPlot(lm2,main="")
```

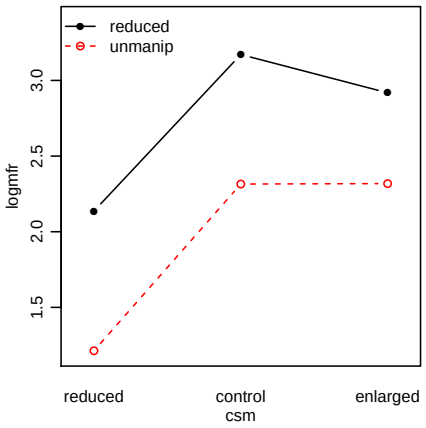


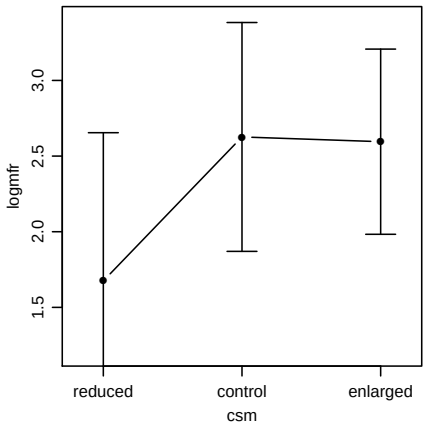


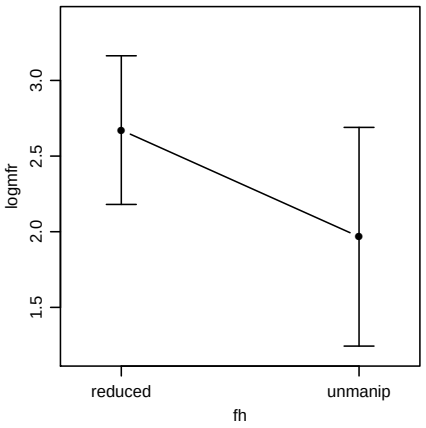

```
> anova(lm2)
```

```
          Df  Sum Sq Mean Sq F value  Pr(>F)
csm        2  14.739  7.3694  1.9733 0.14688
fh         1  11.229 11.2289  3.0067 0.08745
csm:fh     2   0.371  0.1857  0.0497 0.95153
Residuals 68 253.951  3.7346
```

```
> fitPlot(lm2,legend="topleft",ylim=c(1.2,3.4),main="",interval=FALSE)
> fitPlot(lm2,which="csm",ylim=c(1.2,3.4),main="")
> fitPlot(lm2,which="fh",ylim=c(1.2,3.4),main="")
```








```
> mc2a <- glht(lm2,mcp(csm="Tukey"))
> summary(mc2a)
```

```
                       Estimate Std. Error    t value   p value
control - reduced = 0   1.0344433  0.8683878  1.1912227 0.4615795
enlarged - reduced = 0  0.7813633  0.7736213  1.0100075 0.5723424
enlarged - control = 0 -0.2530799  0.8820640 -0.2869179 0.9555398
```

```
> mc2b <- glht(lm2,mcp(fh="Tukey"))
> summary(mc2b)
```

```
                       Estimate Std. Error   t value   p value
unmanip - reduced = 0 -0.9235421   0.757991 -1.218408 0.2272795
```

```
> lm2a <- lm(logmfr~comb,data=pfc)
> mc2c <- glht(lm2a,mcp(comb="Tukey"))
> summary(mc2c)
```

```
                                          Estimate Std. Error      t value   p value
reduced:unmanip - reduced:reduced = 0   -0.923542109  0.7579910 -1.218407762 0.8254227
control:reduced - reduced:reduced = 0    1.034443253  0.8683878  1.191222727 0.8386153
control:unmanip - reduced:reduced = 0    0.178445506  0.7443324  0.239739009 0.9998859
enlarged:reduced - reduced:reduced = 0   0.781363341  0.7736213  1.010007511 0.9124943
enlarged:unmanip - reduced:reduced = 0   0.181387911  0.7443324  0.243692088 0.9998763
control:reduced - reduced:unmanip = 0    1.957985362  0.8683878  2.254736212 0.2258995
control:unmanip - reduced:unmanip = 0    1.101987615  0.7443324  1.480504741 0.6762910
enlarged:reduced - reduced:unmanip = 0   1.704905450  0.7736213  2.203798437 0.2482281
enlarged:unmanip - reduced:unmanip = 0   1.104930020  0.7443324  1.484457820 0.6736755
control:unmanip - control:reduced = 0   -0.855997747  0.8564915 -0.999423528 0.9160202
enlarged:reduced - control:reduced = 0  -0.253079912  0.8820640 -0.286917852 0.9997238
enlarged:unmanip - control:reduced = 0  -0.853055342  0.8564915 -0.995988112 0.9171282
enlarged:reduced - control:unmanip = 0   0.602917834  0.7602436  0.793058774 0.9675611
enlarged:unmanip - control:unmanip = 0   0.002942405  0.7304184  0.004028383 1.0000000
enlarged:unmanip - enlarged:reduced = 0 -0.599975429  0.7602436 -0.789188429 0.9682227
```