Preliminaries

```
> library(FSA)      # for Subset(), wrVal(), psdVal()
> library(car)      # for outlierTest(), leveneTest()
> library(multcomp) # for glht(), mcp()
> library(plotrix)  # for plotCI(), cld()
```

```
> setwd("C:/aaaWork/Web/fishR/courses/Vermont2014/CourseMaterial/") # Derek's Computer
> d <- read.csv("Data/Keuska99.csv",header=TRUE)
> str(d)
'data.frame': 2391 obs. of  10 variables:
 $ species  : Factor w/ 4 levels "BG","LMB","WAE",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ date     : Factor w/ 12 levels "3/31/1999","4/1/1999",..: 6 6 6 6 4 4 6 6 6 6 ...
 $ geartype : Factor w/ 2 levels "BOOM SHOCKER",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ sex      : Factor w/ 3 levels "F","M","U": NA NA NA NA NA NA NA NA NA NA ...
 $ inches   : num  0.9 1 1 1 1 1 1.1 1.1 1.1 1.1 ...
 $ pounds   : num  0.001 0.001 0.001 0.001 0.001 0.001 0 0 0.001 0.001 ...
 $ mm       : int  23 25 25 25 25 25 28 28 28 28 ...
 $ grams    : int  0 0 0 0 1 1 0 0 0 0 ...
 $ age      : int  NA NA NA NA NA NA NA NA NA NA ...
 $ agestruct: Factor w/ 2 levels "SCALE","SPINE": NA NA NA NA NA NA NA NA NA NA ...
> levels(d$species)
[1] "BG"  "LMB" "WAE" "YEP"
>
> # Focus on LMB and remove some variables (only to make the handout easier to read)
> lmb <- Subset(d,species=="LMB",select=c("species","geartype","mm","grams"))
>
> # Identify which fish had both mm and grams recorded, show first 10
> complete.cases(lmb[,c("mm","grams")])[1:10]
 [1]  TRUE FALSE  TRUE  TRUE FALSE FALSE FALSE  TRUE  TRUE  TRUE
>
> # Retain only those with both measures
> lmb <- Subset(lmb,complete.cases(lmb[,c("mm","grams")]))
> str(lmb)
'data.frame': 541 obs. of  4 variables:
 $ species : Factor w/ 1 level "LMB": 1 1 1 1 1 1 1 1 1 1 ...
 $ geartype: Factor w/ 2 levels "BOOM SHOCKER",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ mm      : int  81 91 91 107 107 112 132 137 137 137 ...
 $ grams   : int  6 8 8 9 14 15 28 24 24 36 ...
> view(lmb)
    species      geartype  mm grams
79      LMB BOOM SHOCKER 178    67
153     LMB BOOM SHOCKER 241   172
289     LMB BOOM SHOCKER 284   304
306     LMB     FYKE NET 292   297
415     LMB BOOM SHOCKER 315   428
512     LMB BOOM SHOCKER 361   600
```

Data Prep for Relative Weight Analysis

```
> ( wsLMB <- wsVal("Largemouth Bass") )
          species  units    type ref    int  slope quad min.len max.len measure
75 Largemouth Bass metric linear  75 -5.528  3.273   NA     150      NA      TL
   method comment       source
75    RLP    none Henson, 1991
> lmb1 <- Subset(lmb,mm>=150)
>
> lmb1 <- within(lmb1,{
         Ws <- 10^(wsLMB$int)*mm^wsLMB$slope
         Wr <- grams/Ws*100
       })
> view(lmb1)
    species      geartype  mm grams     Wr     Ws
69      LMB BOOM SHOCKER 180    69  96.68  71.37
145     LMB BOOM SHOCKER 246   169  85.18 198.39
288     LMB BOOM SHOCKER 290   371 109.13 339.96
363     LMB BOOM SHOCKER 307   380  92.76 409.64
437     LMB     FYKE NET 330   519 100.02 518.91
450     LMB BOOM SHOCKER 335   516  94.66 545.09
```

```
> ( wsPSD <- psdVal("Largemouth Bass") )
     zero     stock   quality preferred memorable    trophy
        0       200       300       380       510       630
> lmb1 <- lencat(~mm,data=lmb1,breaks=wsPSD)
> view(lmb1)
    species      geartype  mm grams    Wr     Ws LCat
10      LMB BOOM SHOCKER 152    40 97.47  41.04    0
178     LMB BOOM SHOCKER 257   213 93.04 228.93  200
271     LMB BOOM SHOCKER 284   293 92.29 317.48  200
314     LMB BOOM SHOCKER 297   303 82.43 367.56  200
325     LMB BOOM SHOCKER 300   331 87.14 379.86  300
467     LMB     FYKE NET 343   516 87.63 588.87  300
> xtabs(~LCat,data=lmb1)
LCat
  0 200 300 380 510
 80 242 184  18   3
>
> lmb1 <- lencat(~mm,data=lmb1,breaks=c(0,200,300,380,1000))
> view(lmb1)
    species      geartype  mm grams     Wr     Ws LCat LCat1
20      LMB     FYKE NET 157    47 103.02  45.62    0     0
77      LMB BOOM SHOCKER 191    81  93.47  86.66    0     0
104     LMB     FYKE NET 226   138  91.81 150.31  200   200
264     LMB BOOM SHOCKER 282   290  93.48 310.22  200   200
390     LMB BOOM SHOCKER 312   411  95.16 431.88  300   300
513     LMB BOOM SHOCKER 399  1009 104.45 966.02  380   380
> xtabs(~LCat1,data=lmb1)
LCat1
  0 200 300 380
 80 242 184  21
```
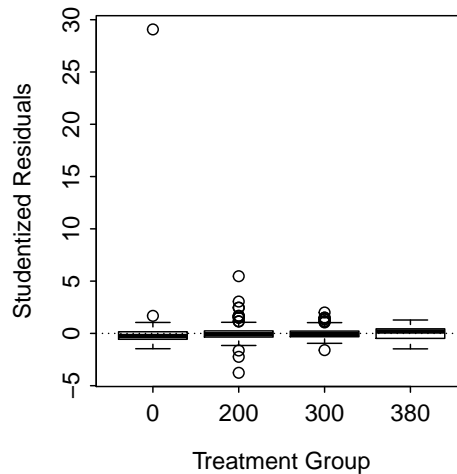
One-Way ANOVA of Wr by PSD Category

```
> lm1 <- lm(Wr~LCat1,data=lmb1)
> residPlot(lm1)
```



```
> outlierTest(lm1)

    rstudent unadjusted p-value Bonferonni p
80     29.07         3.266e-111    1.721e-108
122     5.47          6.986e-08     3.682e-05
> lmb1[80,]                            # Outlier?

   species     geartype  mm grams  Wr   Ws LCat LCat1
80     LMB BOOM SHOCKER 198   350 359 97.5    0     0
> lmb1[lmb1$mm>=195 & lmb1$mm<=205,]  # Fish w/ similar lengths

   species     geartype  mm grams     Wr     Ws LCat LCat1
78     LMB BOOM SHOCKER 196    87  92.25  94.31    0     0
79     LMB     FYKE NET 196    92  97.55  94.31    0     0
80     LMB BOOM SHOCKER 198   350 358.99  97.50    0     0
81     LMB     FYKE NET 203    97  91.69 105.79  200   200
> lmb2 <- lmb1[-80,]                    # Remove the fish
```
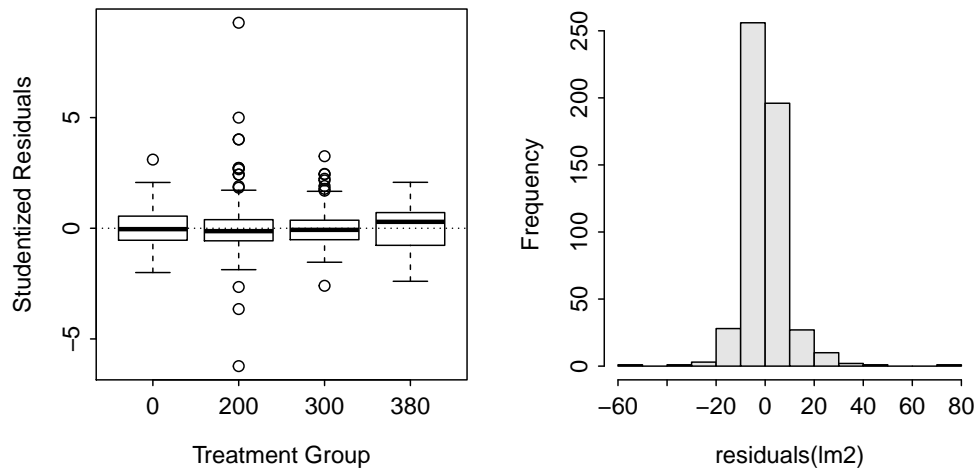
```
> lm2 <- lm(Wr~LCat1,data=lmb2)
> leveneTest(lm2)

Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group   3    1.72   0.16
      522
> residPlot(lm2)        # Left
> hist(~residuals(lm2)) # Right
```

```
> anova(lm2)
Analysis of Variance Table

Response: Wr
          Df Sum Sq Mean Sq F value Pr(>F)
LCat1      3   1342     447    5.47  0.001
Residuals 522  42673      82
> mc1 <- glht(lm2,mcp(LCat1="Tukey"))
> summary(mc1)


 Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = Wr ~ LCat1, data = lmb2)

Linear Hypotheses:
              Estimate Std. Error t value Pr(>|t|)
200 - 0 == 0    -1.862      1.172   -1.59   0.3660
300 - 0 == 0    -2.743      1.216   -2.26   0.1004
380 - 0 == 0     4.883      2.220    2.20   0.1139
300 - 200 == 0  -0.882      0.884   -1.00   0.7368
380 - 200 == 0   6.745      2.057    3.28   0.0055
380 - 300 == 0   7.626      2.083    3.66   0.0013
(Adjusted p values reported -- single-step method)
> cld(mc1)
   0  200  300  380
"ab"  "a"  "a"  "b"
> confint(mc1)


 Simultaneous Confidence Intervals

Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = Wr ~ LCat1, data = lmb2)
```

```
Quantile = 2.54
95% family-wise confidence level


Linear Hypotheses:
               Estimate lwr     upr
200 - 0 == 0    -1.862   -4.838  1.115
300 - 0 == 0    -2.743   -5.833  0.346
380 - 0 == 0     4.883   -0.756 10.522
300 - 200 == 0  -0.882   -3.128  1.365
380 - 200 == 0   6.745    1.519 11.970
380 - 300 == 0   7.626    2.336 12.917
```

```
> ( sumWr <- Summarize(Wr~LCat1,data=lmb2,digits=1) )
  LCat1   n mean   sd  min   Q1 median   Q3 max percZero
1     0  79 94.5  8.0 76.6 89.6   94.1 99.4 122        0
2   200 242 92.6 10.4 38.4 87.5   91.4 96.1 170        0
3   300 184 91.7  7.2 68.4 87.1   91.1 95.0 121        0
4   380  21 99.4 10.5 78.3 92.6  102.0 106.0 118       0

> sumWr <- within(sumWr, {
  LCI <- mean-1.96*sd/sqrt(n)
  UCI <- mean+1.96*sd/sqrt(n)
 })
> sumWr
  LCat1   n mean   sd  min   Q1 median   Q3 max percZero    UCI    LCI
1     0  79 94.5  8.0 76.6 89.6   94.1 99.4 122        0  96.26 92.74
2   200 242 92.6 10.4 38.4 87.5   91.4 96.1 170        0  93.91 91.29
3   300 184 91.7  7.2 68.4 87.1   91.1 95.0 121        0  92.74 90.66
4   380  21 99.4 10.5 78.3 92.6  102.0 106.0 118       0 103.89 94.91

> with(sumWr,plotCI(1:4,mean,ui=UCI,li=LCI,pch=16,xlim=c(0.5,4.5),xaxt="n",
                  ylim=c(89,105),xlab="Length Category",ylab="Mean Wr"))
> axis(1,1:4,c("Sub-Stock","Stock","Quality","Preferred"))
> abline(h=100,col="red",lty=3,lwd=2)
> text(1:4,sumWr$mean,c("ab","a","a","b"),pos=c(4,4,4,4))
> text(1:4,89,paste("n=",sumWr$n,sep=""))
```