Indicator Variable Regression

R Handout

Derek H. Ogle

Initialization

```
> library(NCStats)
```

Salmon Sperm Example

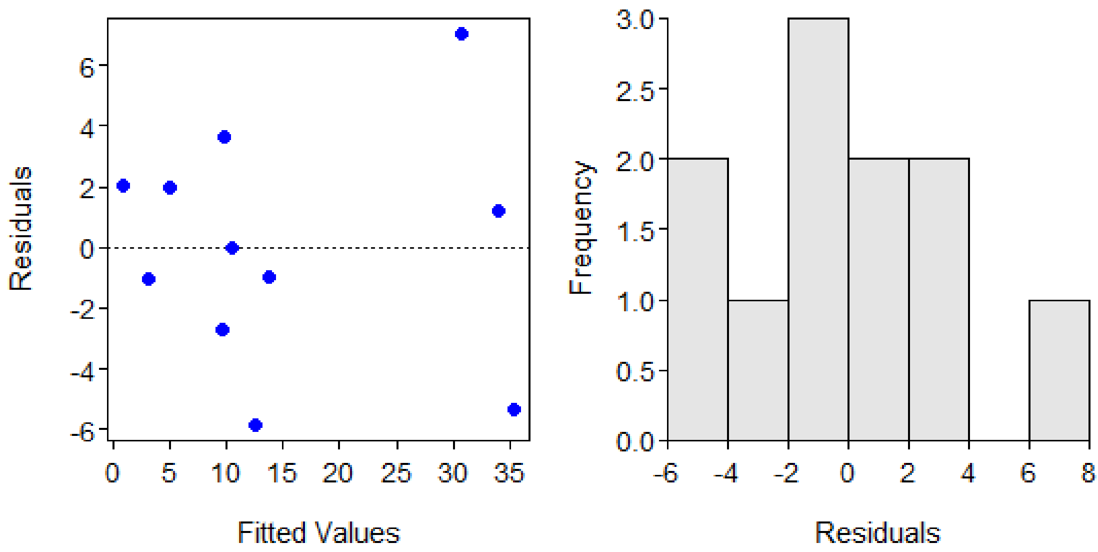
Background

Vladic *et al.* (2002) recorded (in `SalmonSperm.csv`) the probability of successful egg fertilization (`fert.success`) and the length of sperm tail end piece (`step.len`). They asked "Are fertilization success and length of sperm related and does that relationship differ between adult and parr salmon?"

```
> setwd("C:/aaaWork/Web/GitHub/NCMTH207/modules/IVRegression")
> ss <- read.csv("SalmonSperm.csv")
> ss <- ss[-c(1,10,11),]  # only for class demo purposes
> str(ss)

'data.frame':   11 obs. of  3 variables:
 $ step.len : num  2.94 3 3.02 3.17 3.18 3.2 3.27 3.31 3.72 3.84 ...
 $ fert.succ: num  3 2.2 7 7 13.5 10.4 6.7 12.8 37.8 30 ...
 $ mat      : Factor w/ 2 levels "Adult","Parr": 2 2 1 2 1 1 1 1 2 2 ...

> xlbl <- "Sperm Tail End Piece Length (um)"
> ylbl <- "Fertilization Success"
```

Fitting the Linear Model

```
> lm1 <- lm(fert.succ~step.len*mat,data=ss)
> residPlot(lm1,legend=FALSE,loess=FALSE)
```

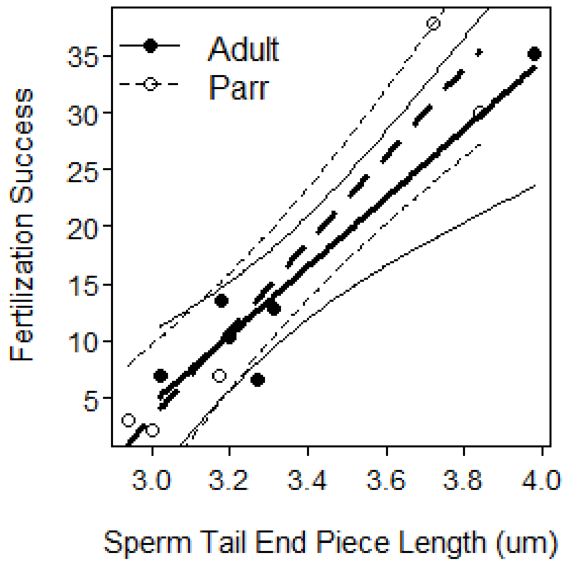


```
> adTest(lm1$residuals)

Anderson-Darling normality test with x
A = 0.1784, p-value = 0.8932

> outlierTest(lm1)

No Studentized residuals with Bonferonni p < 0.05
Largest |rstudent|:
   rstudent unadjusted p-value Bonferonni p
12 2.905895           0.027125      0.29838
```

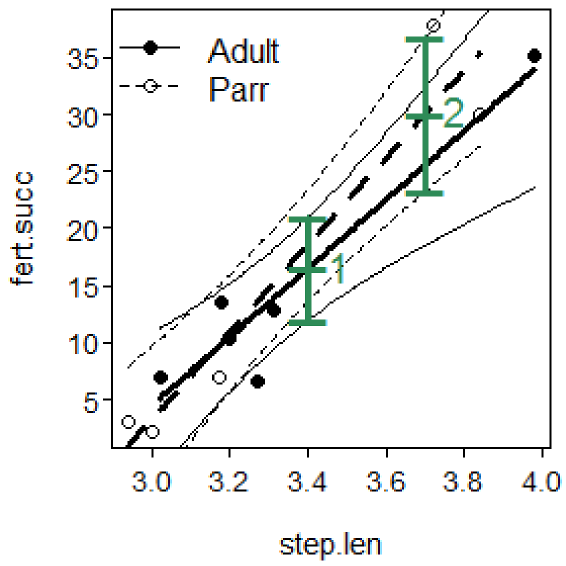
Model Exploration and Summarization

```
> summary(lm1)

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       -85.769     20.266  -4.232  0.00388
step.len           30.066      6.066   4.956  0.00164
matParr           -25.661     27.273  -0.941  0.37809
step.len:matParr    8.155      8.148   1.001  0.35022

Residual standard error: 4.547 on 7 degrees of freedom
Multiple R-squared: 0.9139, Adjusted R-squared: 0.877
F-statistic: 24.78 on 3 and 7 DF,  p-value: 0.0004207

> confint(lm1)

                      2.5 %    97.5 %
(Intercept)      -133.68997 -37.84811
step.len           15.72132  44.41036
matParr           -90.15097  38.82930
step.len:matParr  -11.11233  27.42328
```

```
> fitPlot(lm1,interval="confidence",xlab=xlbl,ylab=ylbl,legend="topleft")
```



```
> ( nd <- data.frame(step.len=c(3.4,3.7),mat=c("Adult","Parr")) )

  step.len   mat
1      3.4 Adult
2      3.7  Parr

> predictionPlot(lm1,nd,interval="confidence",legend="topleft")
```



```
  obs step.len   mat      fit      lwr      upr
1   1      3.4 Adult 16.45483 11.94067 20.96899
2   2      3.7  Parr 29.98900 23.25902 36.71899
```

Lecture Support -- ANOVA Demonstration

```
> lm1 <- lm(fert.succ~step.len*mat,data=ss)
> anova(lm1)

Analysis of Variance Table

Response: fert.succ
             Df  Sum Sq Mean Sq F value    Pr(>F)
step.len      1 1510.23 1510.23 73.0316 5.966e-05
mat           1    6.11    6.11  0.2953    0.6037
step.len:mat  1   20.72   20.72  1.0017    0.3502
Residuals     7  144.75   20.68



> lm2 <- lm(fert.succ~step.len+mat,data=ss)
> anova(lm2)

Analysis of Variance Table

Response: fert.succ
          Df  Sum Sq Mean Sq F value    Pr(>F)
step.len   1 1510.23 1510.23 73.0157 2.709e-05
mat        1    6.11    6.11  0.2952    0.6017
Residuals  8  165.47   20.68



> lm3 <- lm(fert.succ~step.len,data=ss)
> anova(lm3)

Analysis of Variance Table

Response: fert.succ
          Df  Sum Sq Mean Sq F value   Pr(>F)
step.len   1 1510.23 1510.23  79.219 9.35e-06
Residuals  9  171.58   19.06
```

Fish Energy Density Example

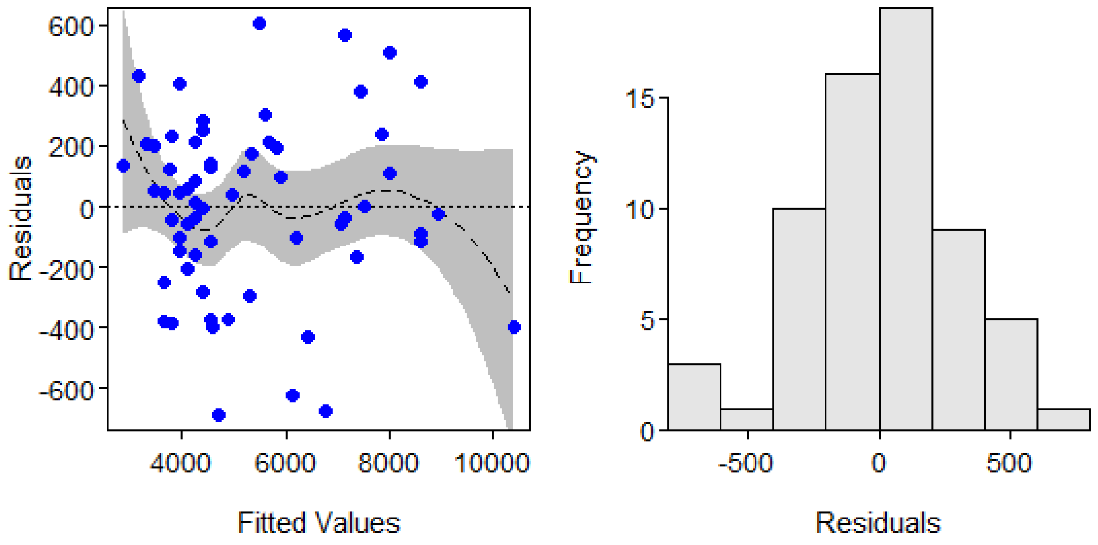
Background

Hartman and Brandt (1995) examined the relationship between energy density and percent dry weight for four species of fish -- Bay Ancovy (*Anchoa mitchilli*), Bluefish (*Pomatomus saltatrix*), Striped Bass (*Morone saxatilis*), and Weakfish (*Cynoscion regalis*). They wanted to describe the relationship between these two variables and determine if there were any differences among species.

```
> FED <- read.csv("FishEnergyDensity.csv")
> str(FED)

'data.frame':   64 obs. of  3 variables:
 $ species: Factor w/ 4 levels "bayanchovy","bluefish",..: 2 2 2 2 2 2 2 ...
 $ dw     : int  39 34 34 32 31 30 30 29 26 25 ...
 $ ed     : int  10000 9000 8500 8100 7500 7100 7700 6100 5900 5500 ...
```

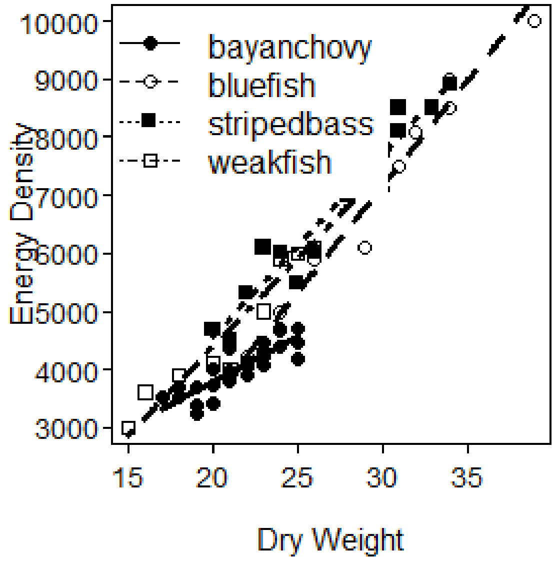
Model Fitting and Analysis

```
> lm1 <- lm(ed~dw*species,data=FED)
> residPlot(lm1,legend=FALSE)
```



```
> adTest(lm1$residuals)

Anderson-Darling normality test with x
A = 0.353, p-value = 0.4549

> outlierTest(lm1)

No Studentized residuals with Bonferonni p < 0.05
Largest |rstudent|:
    rstudent unadjusted p-value Bonferonni p
20 -2.492888           0.015711           NA
```

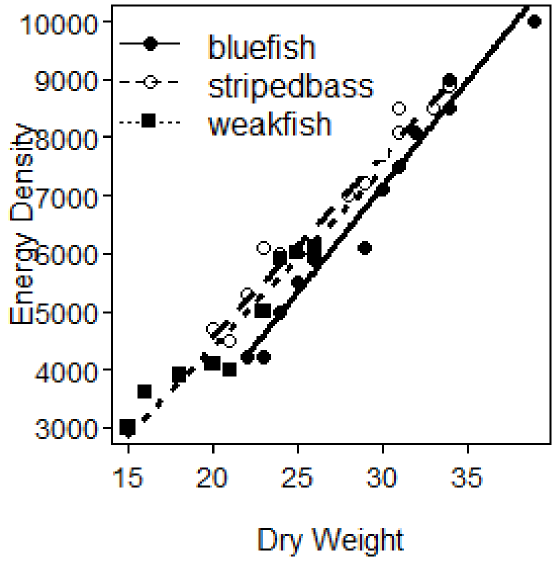
```
> anova(lm1)

Analysis of Variance Table

Response: ed
           Df    Sum Sq   Mean Sq  F value    Pr(>F)
dw          1 170693154 170693154 1858.966 < 2.2e-16
species     3  10592036   3530679   38.452 1.258e-13
dw:species  3   4105617   1368539   14.904 3.002e-07
Residuals  56   5142008     91822

> compSlopes(lm1)

Multiple Slope Comparisons (using the 'holm' adjustment)

              comparison      diff    95% LCI   95% UCI p.unadj   p.adj
1    bluefish-bayanchovy 208.30952  145.62788 270.99117 0.00000 0.00000
2 stripedbass-bayanchovy 157.62055   94.29774 220.94336 0.00001 0.00005
3    weakfish-bayanchovy 149.60379   83.20906 215.99852 0.00003 0.00012
4   stripedbass-bluefish -50.68898 -101.08569  -0.29227 0.04873 0.10290
5      weakfish-bluefish -58.70573 -112.91192  -4.49955 0.03430 0.10290
6   weakfish-stripedbass  -8.01676  -62.96310  46.92958 0.77116 0.77116


Slope Information (using the 'holm' adjustment)

        level   slopes  95% LCI  95% UCI p.unadj p.adj
1  bayanchovy 154.1905 102.2341 206.1469       0     0
4    weakfish 303.7943 262.4567 345.1318       0     0
3 stripedbass 311.8110 275.6128 348.0092       0     0
2    bluefish 362.5000 327.4355 397.5645       0     0

> fitPlot(lm1,xlab="Dry Weight",ylab="Energy Density",legend="topleft")
```



Follow-Up Model Fitting and Analysis

```
> FED1 <- filterD(FED,species!="bayanchovy")
> lm2 <- lm(ed~dw*species,data=FED1)
> anova(lm2)

Analysis of Variance Table

Response: ed
           Df    Sum Sq   Mean Sq  F value    Pr(>F)
dw          1 104962559 104962559 838.6208 < 2.2e-16
species     2   2583571   1291785  10.3210 0.0003476
dw:species  2    556352    278176   2.2225 0.1247887
Residuals  32   4005150    125161

> compIntercepts(lm2)

Warning: Removed an interaction term from 'mdl' (i.e., assumed
 parallel lines) to test intercepts.

Tukey HSD on means adjusted assuming parallel lines

            comparison      diff   95% LCI  95% UCI        p.adj
1 stripedbass-bluefish  631.3980  291.1082 971.6878 0.0001843341
2    weakfish-bluefish  506.4749  144.5318 868.4180 0.0044160914
3 weakfish-stripedbass -124.9231 -480.8922 231.0461 0.6693967026


Mean ed when dw=26.10526

   bluefish stripedbass    weakfish
   5828.663    6460.061    6335.138

> compIntercepts(lm2,common.cov=0)

Warning: Removed an interaction term from 'mdl' (i.e., assumed
 parallel lines) to test intercepts.

Tukey HSD on means adjusted assuming parallel lines

            comparison      diff   95% LCI  95% UCI        p.adj
1 stripedbass-bluefish  631.3980  291.1082 971.6878 0.0001843341
2    weakfish-bluefish  506.4749  144.5318 868.4180 0.0044160914
3 weakfish-stripedbass -124.9231 -480.8922 231.0461 0.6693967026


Mean ed when dw=0

   bluefish stripedbass    weakfish
  -2752.451   -2121.053   -2245.976
```

```
> compIntercepts(lm2,common.cov=20)

Warning: Removed an interaction term from 'mdl' (i.e., assumed
 parallel lines) to test intercepts.

Tukey HSD on means adjusted assuming parallel lines

            comparison      diff   95% LCI   95% UCI         p.adj
1 stripedbass-bluefish  631.3980  291.1082 971.6878 0.0001843341
2    weakfish-bluefish  506.4749  144.5318 868.4180 0.0044160914
3 weakfish-stripedbass -124.9231 -480.8922 231.0461 0.6693967026


Mean ed when dw=      20

   bluefish stripedbass    weakfish
   3821.790    4453.188    4328.265



> fitPlot(lm2,xlab="Dry Weight",ylab="Energy Density",legend="topleft")
```


bluefish
stripedbass
weakfish
Energy Density
Dry Weight