Indicator Variable Regression

R Handout

Derek H. Ogle

Laysan Teal Monitoring

Monitoring the abundance of animal populations can be expensive. Researchers often attempt to find methods for accurately predicting abundance from simple and inexpensive metrics. In one study, Reynolds *et al.* (2017) compared the abundance of Laysan Teal (*Anas laysanensis*) as estimated from the time-intensive Lincoln-Petersen mark-resight method to the maximum annual observed count of Laysan Teal made bi-monthly on Midway Atoll. They wanted to determine if there was a significantly positive relationship between the mark-resight abundance estimate and the maximum annual count, and if that relationship differed between the breeding and non-breeding seasons.

```
> library(NCStats)
> setwd("C:/aaaWork/Web/GitHub/NCMTH207/modules/IVRegression")
```

```
> df <- read.csv("LaysanTeal.csv")
> str(df)
```

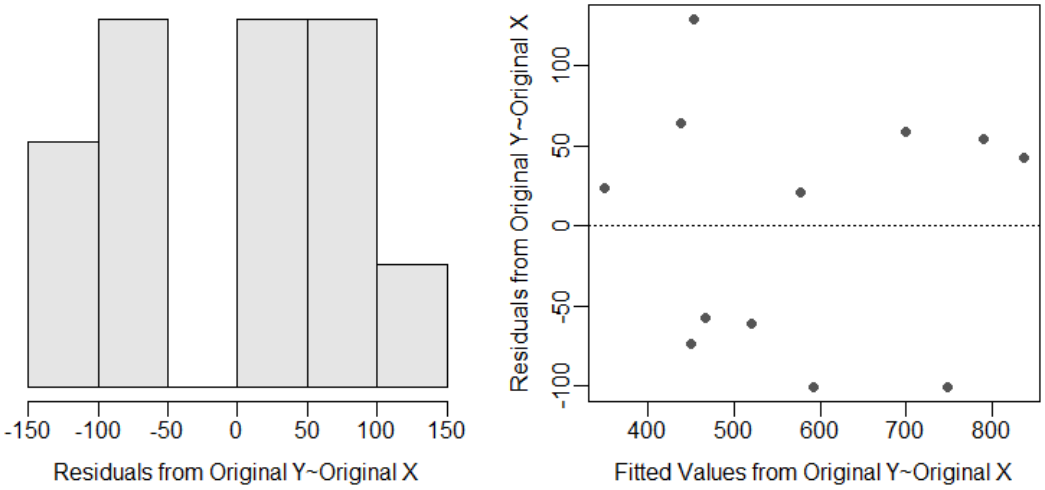
```
'data.frame':   12 obs. of  3 variables:
 $ max.count  : int  75 130 281 309 340 213 274 284 276 361 ...
 $ mr.estimate: int  502 459 647 844 879 374 376 409 582 492 ...
 $ season     : Factor w/ 2 levels "breeding","non-breeding": 1 1 1 1 1 2 2 2 2 2 ...
```

```
> xlbl <- "Maximum Count"
> ylbl <- "Lincoln-Petersen Abundance"
```

Fitting the Linear Model

```
> lm1 <- lm(mr.estimate~max.count*season,data=df)
```

```
> transChooser(lm1)
```



Lecture Support – ANOVA Demonstration

```
> lm1 <- lm(mr.estimate~max.count*season,data=df)
> anova(lm1)
```

```
                Df Sum Sq Mean Sq F value   Pr(>F)
max.count        1  83421   83421 10.6370 0.011503
season           1 190750  190750 24.3225 0.001147
max.count:season 1    359     359  0.0457 0.835991
Residuals        8  62740    7843
```

```
> lm2 <- lm(mr.estimate~max.count+season,data=df)
> anova(lm2)
```

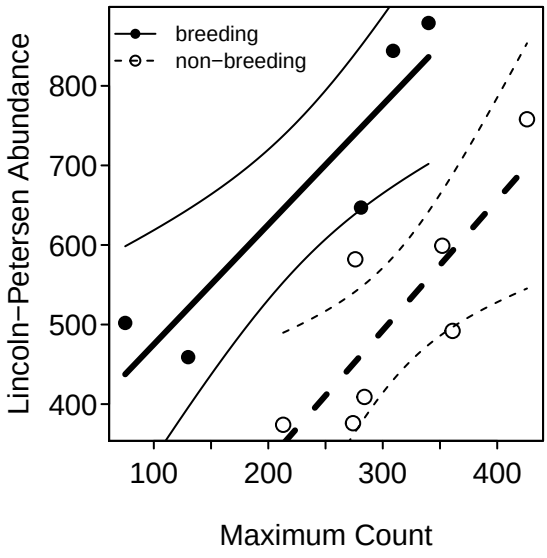
```
          Df Sum Sq Mean Sq F value    Pr(>F)
max.count  1  83421   83421  11.899 0.0072813
season     1 190750  190750  27.207 0.0005521
Residuals  9  63099    7011
```

```
> lm3 <- lm(mr.estimate~max.count,data=df)
> anova(lm3)
```

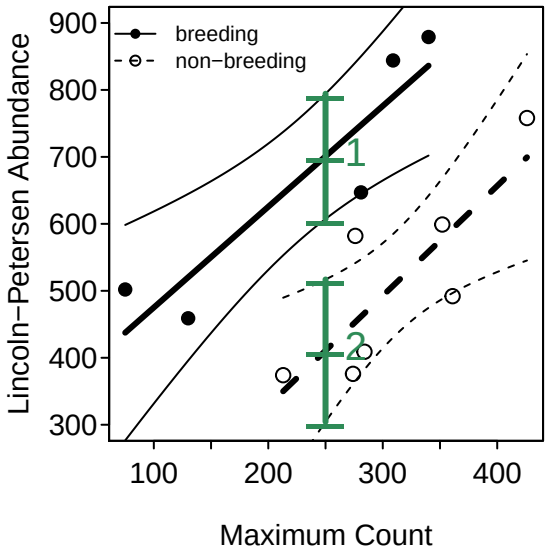
```
          Df Sum Sq Mean Sq F value  Pr(>F)
max.count  1  83421   83421  3.2862 0.09994
Residuals 10 253849   25385
```

Model Exploration and Summarization

```
> fitPlot(lm1,interval="confidence",xlab=xlbl,ylab=ylbl,legend="topleft",cex.leg=0.7)
```



```
> summary(lm1)

Coefficients:
                              Estimate Std. Error t value Pr(>|t|)
(Intercept)                   324.6130    94.4805   3.436  0.00888
max.count                       1.5048     0.3779   3.982  0.00405
seasonnon-breeding           -323.9986   187.8052  -1.725  0.12278
max.count:seasonnon-breeding    0.1355     0.6336   0.214  0.83599

Residual standard error: 88.56 on 8 degrees of freedom
Multiple R-squared: 0.814,  Adjusted R-squared: 0.7442
F-statistic: 11.67 on 3 and 8 DF,  p-value: 0.002718

> confint(lm1)

                                  2.5 %     97.5 %
(Intercept)                  106.7406493 542.485322
max.count                      0.6333927   2.376185
seasonnon-breeding          -757.0781733 109.081017
max.count:seasonnon-breeding   -1.3255575   1.596583

> ( nd <- data.frame(max.count=c(250,250),season=c("breeding","non-breeding")) )

  max.count       season
1       250     breeding
2       250 non-breeding

> predictionPlot(lm1,nd,interval="confidence",xlab=xlbl,ylab=ylbl,ylim=c(300,900),
                 legend="topleft",cex.leg=0.7)
```




```
  obs max.count       season      fit      lwr      upr
1   1       250     breeding 700.8101 607.3089 794.3114
2   2       250 non-breeding 410.6898 304.4186 516.9610
```

Fish Energy Density

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.

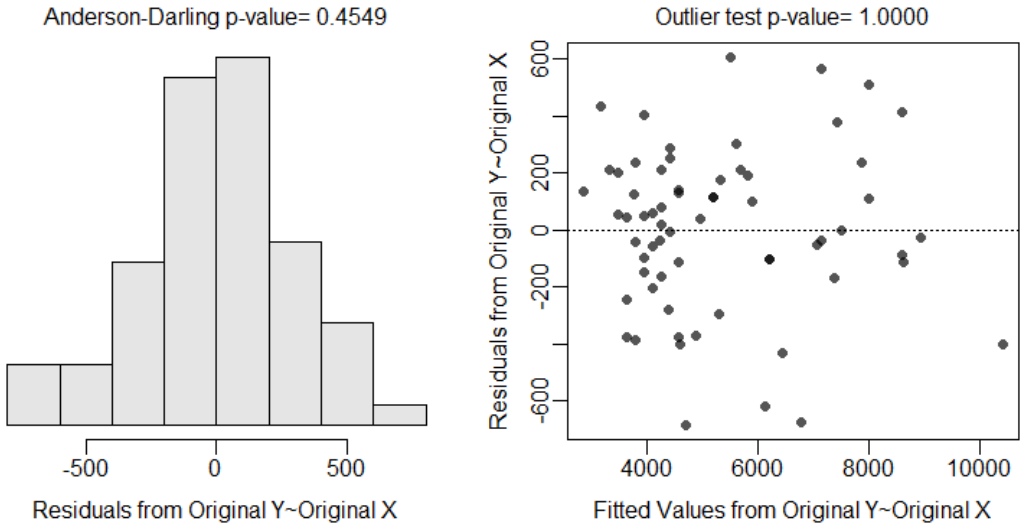
```
> FED <- read.csv("FishEnergyDensity.csv")
> str(FED)
```

```
'data.frame':   64 obs. of  3 variables:
 $ species: Factor w/ 4 levels "bayanchovy","bluefish",..: 2 2 2 2 2 2 2 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)
```

```
> transChooser(lm1)
```



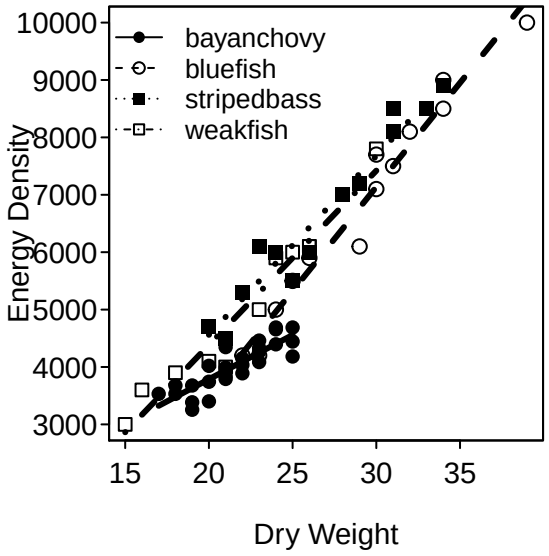

```
> anova(lm1)
```

```
           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",cex.leg=0.8)
```



Follow-Up Model Fitting and Analysis

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

```
           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
```

```
> fitPlot(lm2,xlab="Dry Weight",ylab="Energy Density",legend="topleft",cex.leg=0.8)
```