R Handout - Simple Linear Regression

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Northland College

1 Initialization

```
> library(NCStats)
```

2 Salmon Sperm Example

2.1 Data Preparation

```
> ss <- read.csv("https://raw.githubusercontent.com/droglenc/NCData/master/SalmonSperm.csv")
```

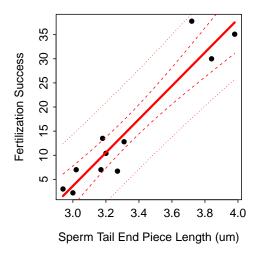
2.2 Lecture Support I – Model Fitting and Simple Predictions

```
Sperm Tail End Piece Length (um)
```

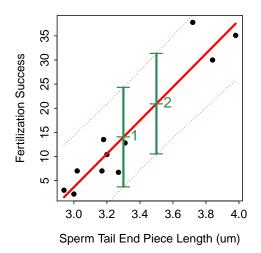
```
> predict(lm1,data.frame(step.len=3.5))
          1
20.92912
```

2.3 Lecture Support II – Sampling Variability

```
> summary(lm1)
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -100.205
                         13.015 -7.699 3.00e-05
step.len
              34.610
                          3.889
                                  8.901 9.35e-06
Residual standard error: 4.366 on 9 degrees of freedom
Multiple R-squared: 0.898, Adjusted R-squared: 0.8866
F-statistic: 79.22 on 1 and 9 DF, p-value: 9.35e-06
> confint(lm1)
                 2.5 %
                          97.5 %
(Intercept) -129.64815 -70.76202
step.len
              25.81336 43.40619
> fitPlot(lm1,interval="both",xlab=xlb1,ylab=ylb1,main="")
```



```
> predict(lm1,data.frame(step.len=3.5),interval="confidence")
      fit
              lwr
1 20.92912 17.5967 24.26153
> predict(lm1,data.frame(step.len=3.5),interval="prediction")
      fit
                lwr
                         upr
1 20.92912 10.50502 31.35321
> predictionPlot(lm1,data.frame(step.len=c(3.3,3.5)),interval="prediction",
xlab=xlbl,ylab=ylbl,main="")
  obs step.len
                   fit
                              lwr
   1
           3.3 14.00716 3.687506 24.32682
           3.5 20.92912 10.505016 31.35321
```



2.4 Lecture Support III – Model Comparisons

```
> anova(lm1)

Df Sum Sq Mean Sq F value Pr(>F)

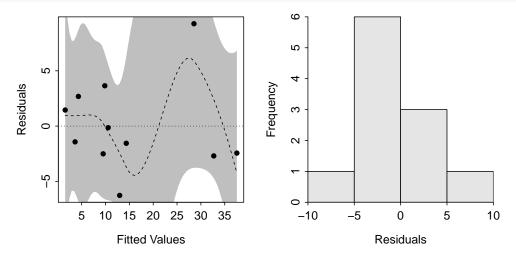
step.len 1 1510.23 1510.23 79.219 9.35e-06

Residuals 9 171.58 19.06

Total 10 1681.81
```

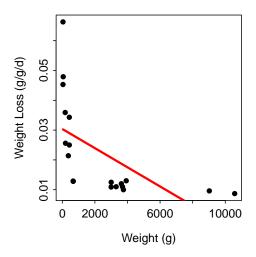
2.5 Lecture Support IV – Assumption Checking

```
> residPlot(lm1,main="")
```

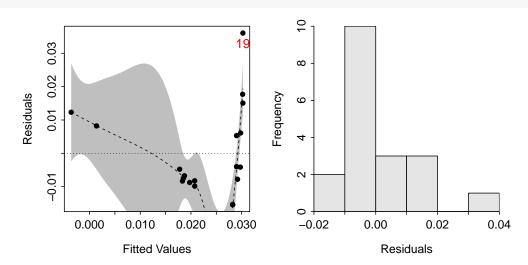


3 Petrels Example

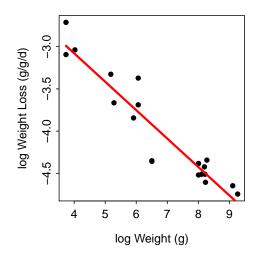
```
> petrels <- read.csv("https://raw.githubusercontent.com/droglenc/NCData/master/Petrels.csv")
> str(petrels)
'data.frame': 19 obs. of 4 variables:
    $ species : Factor w/ 13 levels "Diomedea chrysostoma",..: 2 2 4 4 1 1 3 3 3 9 ...
    $ sex : Factor w/ 4 levels "both","female",..: 3 2 3 2 3 2 3 2 1 3 ...
$ weight : int 10577 9022 3922 3694 3751 3624 3305 3000 2996 668 ...
$ weight.loss: num 0.0087 0.0096 0.013 0.011 0.01 0.012 0.011 0.0125 0.0109 0.0128 ...
> lm1 <- lm(weight.loss~weight,data=petrels)
> fitPlot(lm1,xlab="Weight (g)",ylab="Weight Loss (g/g/d)",main="")
```



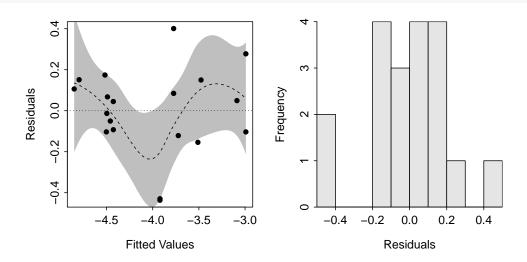
> residPlot(lm1,main="")



```
> with(petrels,max(weight)/min(weight))
[1] 251.8333
> ## transChooser(lm1) # interactive, results not shown
> petrels$log.wt <- log(petrels$weight)
> petrels$log.wtloss <- log(petrels$weight.loss)
> lm2 <- lm(log.wtloss~log.wt,data=petrels)
> fitPlot(lm2,xlab="log Weight (g)",ylab="log Weight Loss (g/g/d)",main="")
```



> residPlot(lm2,main="")



> adTest(lm2\$residuals) Anderson-Darling normality test with lm2\$residuals A = 0.3881, p-value = 0.3514 > anova(lm2) Df Sum Sq Mean Sq F value Pr(>F) 1 6.5113 6.5113 140.65 1.204e-09 log.wt Residuals 17 0.7870 0.0463 18 7.2983 Total > summary(lm2) Coefficients: Estimate Std. Error t value Pr(>|t|) 0.19792 -8.761 1.04e-07 (Intercept) -1.73403 -0.33632 0.02836 -11.860 1.20e-09 Residual standard error: 0.2152 on 17 degrees of freedom Multiple R-squared: 0.8922, Adjusted R-squared: 0.8858 F-statistic: 140.6 on 1 and 17 DF, p-value: 1.204e-09 > confint(lm2)

```
2.5 % 97.5 %
(Intercept) -2.1516113 -1.3164546
log.wt -0.3961507 -0.2764885
> ( p.log.wtloss <- predict(lm2,data.frame(log.wt=log(5000)),interval="confidence") )
    fit lwr upr
1 -4.598532 -4.746569 -4.450495
> exp(p.log.wtloss)*exp(anova(lm2)[2,3]/2)
    fit lwr upr
1 0.01030234 0.008884726 0.01194614
```