Homework 2

Quantitative Analysis of Vertebrate Populations

1. Using the iris data, make a new dataframe called iris_petal with just the petal length and width columns.

```
iris_petal <- iris[ , c("Petal.Length", "Petal.Width")]
str(iris_petal)

## 'data.frame': 150 obs. of 2 variables:
## $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...</pre>
```

Note that depending on the order you add Petal.Length and Petal.Width will change the order of the columns. This can be useful but it also hints at a challenge or confusion that can arise from using column numbers to select columns (e.g. iris[, 3:4]).

2. Now add a new column to iris_petal called Random filled with normally distributed random numbers.

```
iris_petal$Random <- rnorm(n = ncol(iris_petal), mean = 0, sd = 3)</pre>
```

3. Display the first 15 rows of the iris_petal dataframe.

```
iris_petal[1:15, ]
      Petal.Length Petal.Width
##
                                    Random
## 1
               1.4
                            0.2 -1.466416
## 2
               1.4
                            0.2 -3.823607
                            0.2 -1.466416
## 3
                1.3
## 4
                1.5
                            0.2 -3.823607
                            0.2 -1.466416
## 5
                1.4
## 6
                1.7
                            0.4 -3.823607
## 7
                1.4
                            0.3 -1.466416
## 8
                1.5
                            0.2 -3.823607
## 9
                1.4
                            0.2 -1.466416
## 10
               1.5
                            0.1 -3.823607
## 11
                1.5
                            0.2 - 1.466416
## 12
                1.6
                            0.2 -3.823607
## 13
                1.4
                            0.1 -1.466416
## 14
                1.1
                            0.1 -3.823607
## 15
                1.2
                            0.2 -1.466416
```

4. Print a summary of the iris_petal dataframe.

```
summary(iris_petal)
```

```
##
    Petal.Length
                   Petal.Width
                                      Random
                         :0.100 Min.
          :1.000
                                         :-3.824
## Min.
                 Min.
## 1st Qu.:1.600
                 1st Qu.:0.300
                                  1st Qu.:-3.824
## Median :4.350
                 Median :1.300
                                  Median :-2.645
## Mean
          :3.758
                  Mean
                         :1.199
                                  Mean
                                         :-2.645
## 3rd Qu.:5.100
                  3rd Qu.:1.800
                                  3rd Qu.:-1.466
## Max.
          :6.900
                         :2.500
                                        :-1.466
                 Max.
                                  Max.
```

5. Select just the values of Petal.Length greater than the mean petal length. Then print the new summary.

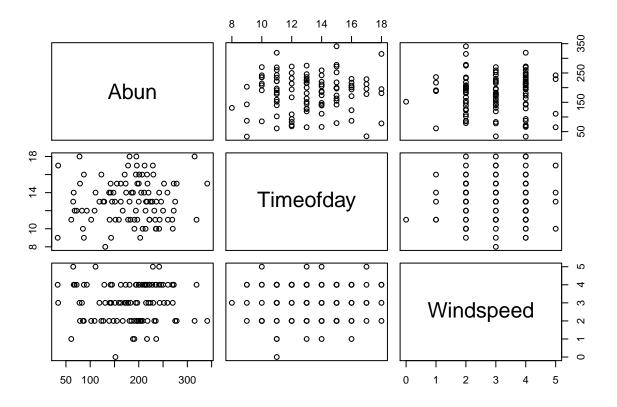
```
pl_mean <- mean(iris_petal$Petal.Length)</pre>
pl_big <- iris_petal[which(iris_petal$Petal.Length > pl_mean), ]
summary(pl_big)
##
    Petal.Length
                    Petal.Width
                                       Random
## Min.
          :3.800
                  Min.
                          :1.000
                                   Min.
                                         :-3.824
## 1st Qu.:4.500
                   1st Qu.:1.400
                                   1st Qu.:-3.824
## Median :4.900 Median :1.700
                                   Median :-1.466
## Mean
          :5.018 Mean
                          :1.723
                                   Mean
                                          :-2.632
## 3rd Qu.:5.600
                   3rd Qu.:2.000
                                   3rd Qu.:-1.466
          :6.900 Max.
                          :2.500
## Max.
                                   Max.
                                          :-1.466
```

6. Read a file into R and save the dataframe as an object. Be sure to use stringsAsFactors = FALSE.

```
seals <- read.table("Data/Seals.txt", header = TRUE, stringsAsFactors = FALSE)</pre>
str(seals)
## 'data.frame':
                 98 obs. of 10 variables:
## $ Abun : int 232 235 191 207 236 155 242 195 196 236 ...
            : int 1 1 1 1 1 1 1 1 1 1 ...
## $ Site
## $ Month : int 4 5 6 6 6 7 7 7 8 8 ...
            ## $ Year
## $ Week
            : int 16 22 24 25 26 27 29 30 32 33 ...
## $ WeekTime : num 2003 2003 2003 2003 ...
## $ Timeofday: int 12 10 10 16 10 15 14 18 17 13 ...
## $ Winddir : int 4 6 6 7 8 8 8 7 8 6 ...
## $ Windspeed: int 2 2 2 4 4 2 4 4 2 1 ...
## $ Weather : int 3 3 3 3 2 3 2 1 3 3 ...
```

7. Make a scatterplot matrix of three variables from the new dataframe.

```
pairs(seals[ , c("Abun", "Timeofday", "Windspeed")])
```

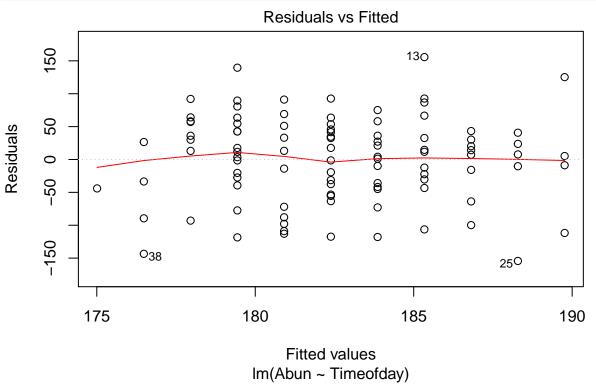


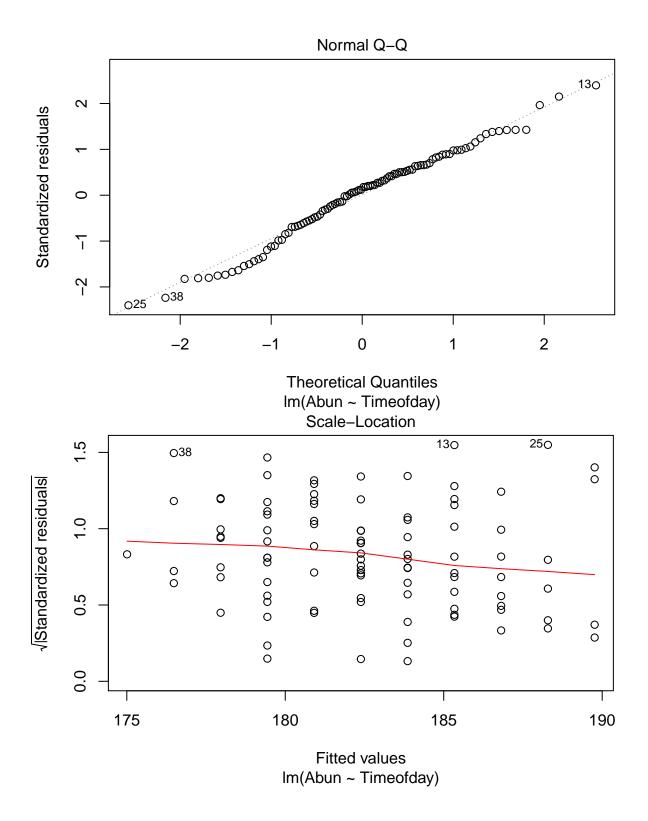
8. Run a linear regression and print the summary table.

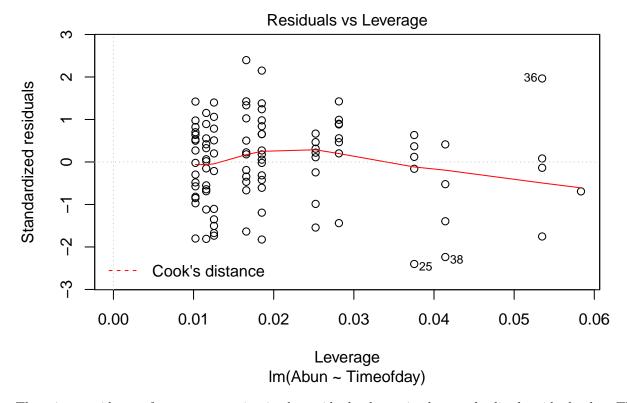
```
lm_seals <- lm(Abun ~ Timeofday, data = seals)</pre>
summary(lm_seals)
##
## Call:
## lm(formula = Abun ~ Timeofday, data = seals)
## Residuals:
##
       Min
                       Median
                                            Max
                  1Q
                                    3Q
  -154.287 -41.255
                        9.639
                                        155.663
                                42.565
##
  Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 163.206
                            37.367
                                     4.368 3.17e-05 ***
## Timeofday
                  1.475
                             2.800
                                     0.527
                                                0.6
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 65.51 on 96 degrees of freedom
## Multiple R-squared: 0.002883, Adjusted R-squared:
## F-statistic: 0.2776 on 1 and 96 DF, p-value: 0.5995
```

9. Are the linear model assumptions met and how do you know (Hint: make diagnostic plots using plot(Model_Name) and interpret the output. You won't lose points if you correctly explain the plots even if I disagree with your judgement on whether things are normal or homogenous enough.

plot(lm_seals)







There is no evidence of strong patterning in the residuals plot or in the standardized residuals plot. The QQ-plot shows evidence of normality and there are no clear outliers identified by Cook's distance. As such, there seems to be a good match between the data and the model (this is probably not true since there is likely some problems of independence in the experimental design that needs to be accounted for but it's not apparent from these plots).