HW2 Peer Assessment Solutions

Background

The fishing industry uses numerous measurements to describe a specific fish. Our goal is to predict the weight of a fish based on a number of these measurements and determine if any of these measurements are insignificant in determining the weigh of a product. See below for the description of these measurments.

Data Description

The data consists of the following variables:

1. **Weight**: weight of fish in g (numerical)
2. **Species**: species name of fish (categorical)
3. **Body.Height**: height of body of fish in cm (numerical)
4. **Total.Length**: length of fish from mouth to tail in cm (numerical)
5. **Diagonal.Length**: length of diagonal of main body of fish in cm (numerical)
6. **Height**: height of head of fish in cm (numerical)
7. **Width**: width of head of fish in cm (numerical)

Read the data

```
# Import library you may need
library(car)
```

```
## Loading required package: carData
```

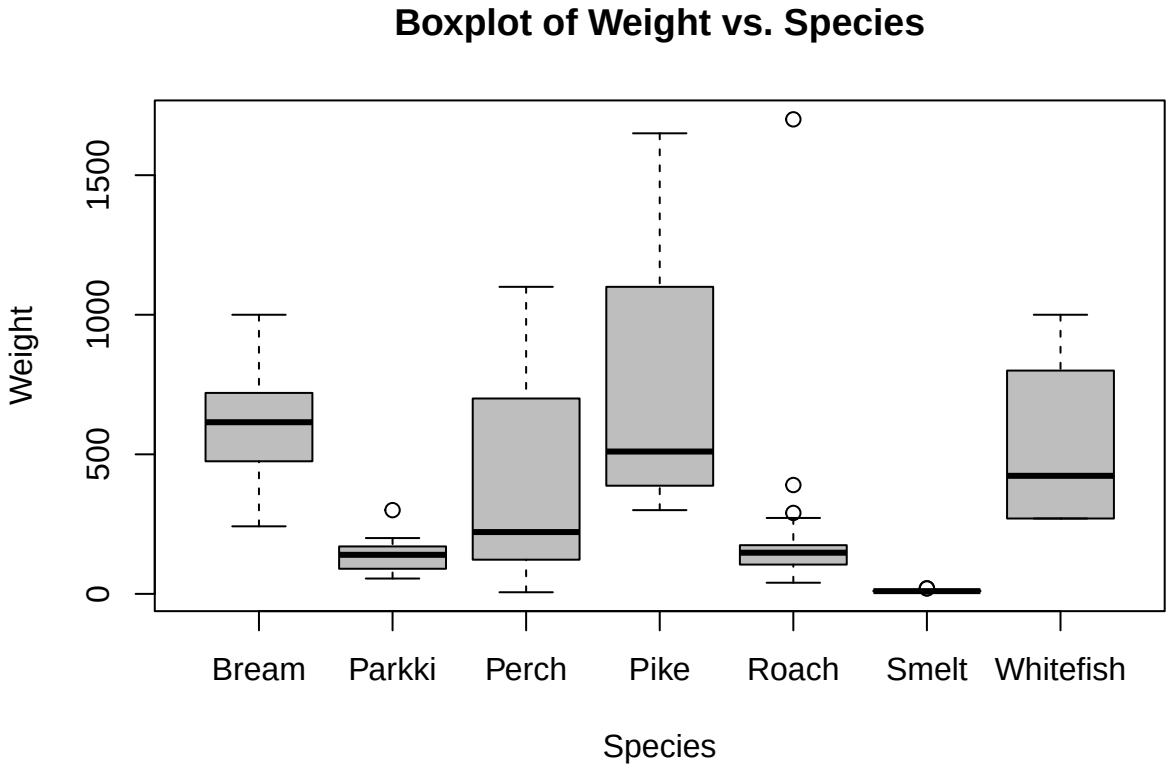
```
# Read the data set
fishfull = read.csv("Fish.csv",header=T, fileEncoding = 'UTF-8-BOM')
row.cnt = nrow(fishfull)
# Split the data into training and testing sets
fishtest = fishfull[(row.cnt-9):row.cnt,]
fish = fishfull[1:(row.cnt-10),]
```

Please use fish as your data set for the following questions unless otherwise stated.

Question 1: Exploratory Data Analysis [8 points]

(a) Create a box plot comparing the response variable, *Weight*, across the multiple *species*. Based on this box plot, does there appear to be a relationship between the predictor and the response?

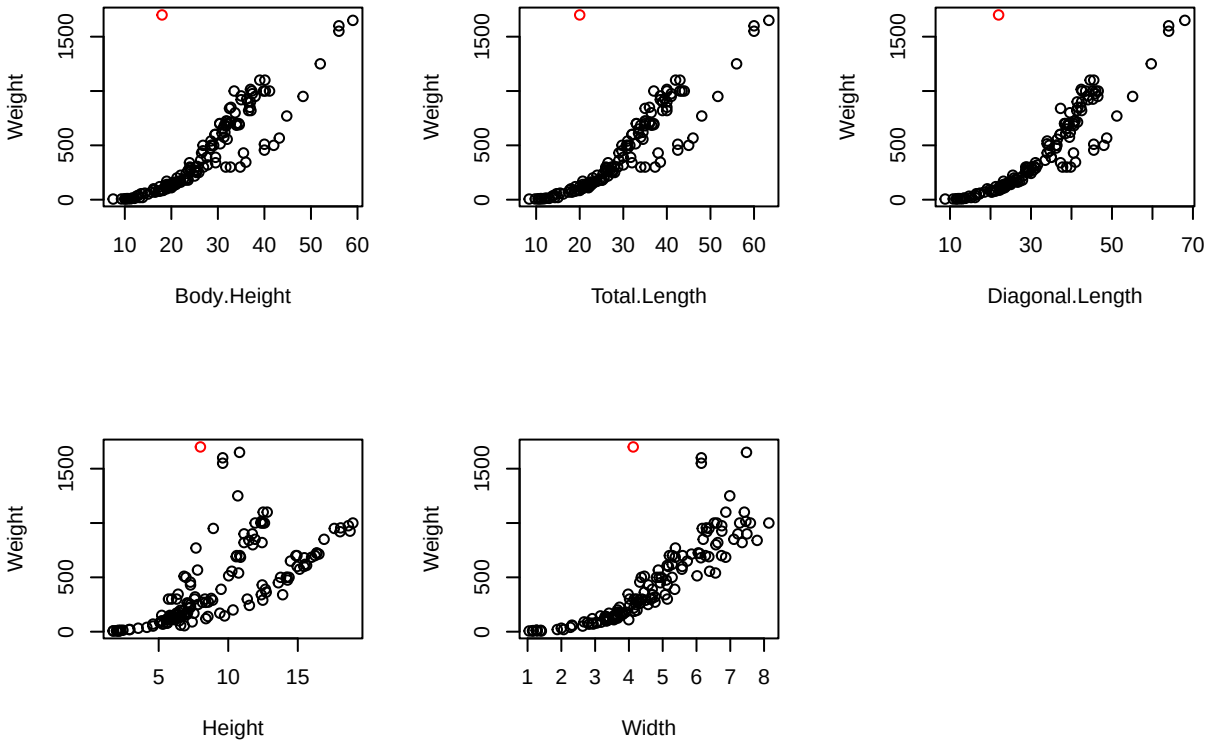
```
# Create boxplot
boxplot(Weight~Species, data=fish, col='grey',
        main ="Boxplot of Weight vs. Species")
```



From the plot, we see the medians vary across all species of fish.Hence, there appears to be a relationship between the predictor, Species and the response, Weight. Specifically, Parkki, Roach, and Smelt have lower weights, while Bream, Whitefish, and Pike have higher weights.

(b) Create scatterplots of the response, *Weight*, against each quantitative predictor, namely Body.Height**,** Total.Length**,** Diagonal.Length**,** Height**, and** Width**. Describe the general trend of each plot. Are there any potential outliers?**

```
# Creat scatterplots
par(mfrow=c(2,3))
for (i in c(3:7)){
  col_name = names(fish[i])
  plot(fish[,i], fish$Weight, xlab= col_name, ylab = "Weight",
       col=ifelse(fish$Weight== max(fish$Weight), 'red', 'black'))
}
```



General trend:

- Graphically, it appears that all five predictors have a strong positive relationship with the Weight of the fish.
- It seems that these relationships are non-linear, since each plot suggests a curved relationship between the response and each quantitative predictor.
- Also, some of the plots show heteroscedasticity with variability of the weights increasing as the values of the predictors increase.
- The plots for Weight vs. Body.Height, Total.Length and Diagonal.Lenght are very similar, which suggest that these three predicting variables might be strongly correlated with each other.

Outliers: We also may have a possible outlier with a large weight of over 1500 grams in the upper left portions of the graphs (highlighted in red) that will need further investigation.

(c) Display the correlations between each of the quantitative variables. Interpret the correlations in the context of the relationships of the predictors to the response and in the context of multicollinearity.

```
# Correlation matrix
round(cor(fish[-2]),4)
```

```
##                Weight Body.Height Total.Length Diagonal.Length Height  Width
## Weight         1.0000      0.8617       0.8655          0.8688 0.6880 0.8457
## Body.Height    0.8617      1.0000       0.9995          0.9920 0.6269 0.8662
## Total.Length   0.8655      0.9995       1.0000          0.9941 0.6422 0.8728
## Diagonal.Length 0.8688     0.9920       0.9941          1.0000 0.7052 0.8770
## Height         0.6880      0.6269       0.6422          0.7052 1.0000 0.7908
## Width          0.8457      0.8662       0.8728          0.8770 0.7908 1.0000
```

We see moderate to very strong positive correlation between the predicting variables and the response variable. The least strong linear relationship is between Weight and Height (r=0.6880).

In addition, we see moderate to very strong correlation among all the pairs of predicting variables. Body.Height and Total.Length (r= 0.9995), Diagonal.Length and Total.Length (r= 0.9941), and Diagonal.Length and Body.Height(r= 0.9920) have a nearly perfect correlation. This suggests that multicollinearity might be a problem in a model that uses all predictors.

(d) Based on this exploratory analysis, is it reasonable to assume a multiple linear regression model for the relationship between *Weight* and the predictor variables?

Yes, numerous of these factors will be able to help determine the weight of the fish. We can attempt a multiple linear regression model first, but we are likely going to want to attempt a Box-Cox transformation to reduce the heteroskedasticity and/or incorporate non-linear associations in the linear model by including transformed versions of the predictors in the model.

Question 2: Fitting the Multiple Linear Regression Model [8 points]

Create the full model without transforming the response variable or predicting variables using the fish data set. Do not use fishtest

(a) Build a multiple linear regression model, called model1, using the response and all predictors. Display the summary table of the model.

```
# fit full model
model1<-lm(Weight~., data=fish)
# Display summary
summary(model1)
```

```
##
## Call:
## lm(formula = Weight ~ ., data = fish)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -211.37  -70.59  -23.50   42.42 1335.87
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -813.90     218.34  -3.728 0.000282 ***
## SpeciesParkki       79.34     132.71   0.598 0.550918
## SpeciesPerch        10.41     206.26   0.050 0.959837
## SpeciesPike         16.76     233.06   0.072 0.942775
## SpeciesRoach       194.03     156.84   1.237 0.218173
## SpeciesSmelt       455.78     204.92   2.224 0.027775 *
## SpeciesWhitefish    28.31     164.91   0.172 0.863967
## Body.Height       -176.87      61.36  -2.882 0.004583 **
## Total.Length       266.70      77.75   3.430 0.000797 ***
## Diagonal.Length    -72.49      49.48  -1.465 0.145267
## Height              38.27      22.09   1.732 0.085448 .
## Width               29.63      40.54   0.731 0.466080
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 156.1 on 137 degrees of freedom
## Multiple R-squared:  0.8419, Adjusted R-squared:  0.8292
## F-statistic:  66.3 on 11 and 137 DF,  p-value: < 2.2e-16
```

(b) Is the overall regression significant at an α level of 0.01? Explain.

Because the p-value associated to the F-statistic (<2.2e-16) is less than the α level, we reject the null hypothesis that all slope coefficients are equal to zero, and state that the model is statistically significant at an α level of 0.01.

(c) What is the coefficient estimate for *Body.Height*? Interpret this coefficient.

$\hat{\beta}_{Body.Height} = -176.87$, which means for every centimeter increase in Body.Height, the expected weight of the fish DECREASES by 176.87 grams holding all other variables constant. This intepretation seems surprising suggesting that multicollinearity might be a problem in this model.

(d) What is the coefficient estimate for the *Species* category Parkki? Interpret this coefficient.

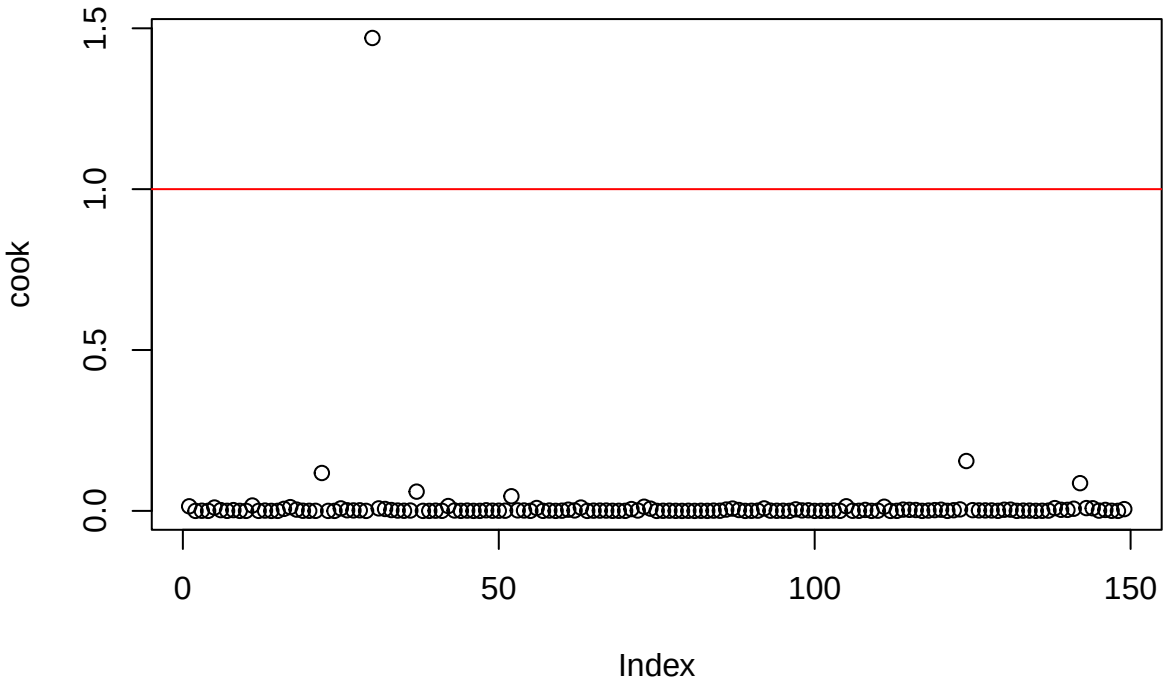
$\hat{\beta}_{SpeciesParkki} = 79.34$, which means that if the fish is categorized as Parkki, then the expected weight of the fish would be 79.34 grams greater than the baseline species Bream holding all other variables constant.

Question 3: Checking for Outliers and Multicollinearity [6 points]

(a) Create a plot for the Cook's Distances. Using a threshold Cook's Distance of 1, identify the row numbers of any outliers.

```
# Calculating Cook's distances
cook=cooks.distance(model1)

# Plotting Cook's distances
plot(cook)
abline(h=1, col="red")
```




```
#Identify outliers
cat("Observation", which(cook>1), "has a cook's distance that is greater than 1")
```

```
## Observation 30 has a cook's distance that is greater than 1
```

(b) Remove the outlier(s) from the data set and create a new model, called model2, using all predictors with *Weight* as the response. Display the summary of this model.

```r
# Remove outlier
fish2<-fish[-30,]

# Fit model2
model2<-lm(Weight~., data=fish2)

# Display summary
summary(model2)
```

```
##
## Call:
## lm(formula = Weight ~ ., data = fish2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -211.10  -50.18  -14.44   34.04  433.68
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -969.766    131.601  -7.369 1.51e-11 ***
## SpeciesParkki      195.500     80.105   2.441 0.015951 *
## SpeciesPerch       174.241    124.404   1.401 0.163608
## SpeciesPike       -175.936    140.605  -1.251 0.212983
## SpeciesRoach       141.867     94.319   1.504 0.134871
## SpeciesSmelt       489.714    123.174   3.976 0.000113 ***
## SpeciesWhitefish   122.277     99.293   1.231 0.220270
## Body.Height        -76.321     37.437  -2.039 0.043422 *
## Total.Length        74.822     48.319   1.549 0.123825
## Diagonal.Length     34.349     30.518   1.126 0.262350
## Height              10.000     13.398   0.746 0.456692
## Width               -8.339     24.483  -0.341 0.733924
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 93.84 on 136 degrees of freedom
## Multiple R-squared:  0.9385, Adjusted R-squared:  0.9335
## F-statistic: 188.6 on 11 and 136 DF,  p-value: < 2.2e-16
```

(c) Display the VIF of each predictor for model2. Using a VIF threshold of max(10, 1/(1-R^2) what conclusions can you draw?

```r
# VIF Threshold
cat("VIF Threshold:", max(10, 1/(1-summary(model2)$r.squared)), "\n")
```

```
## VIF Threshold: 16.25583
```

```r
# Calculate VIF
vif(model2)
```

```
##                       GVIF Df GVIF^(1/(2*Df))
## Species         1545.55017  6        1.843983
## Body.Height     2371.15420  1       48.694499
## Total.Length    4540.47698  1       67.383062
## Diagonal.Length 2126.64985  1       46.115614
## Height            56.21375  1        7.497583
## Width             29.01683  1        5.386727
```

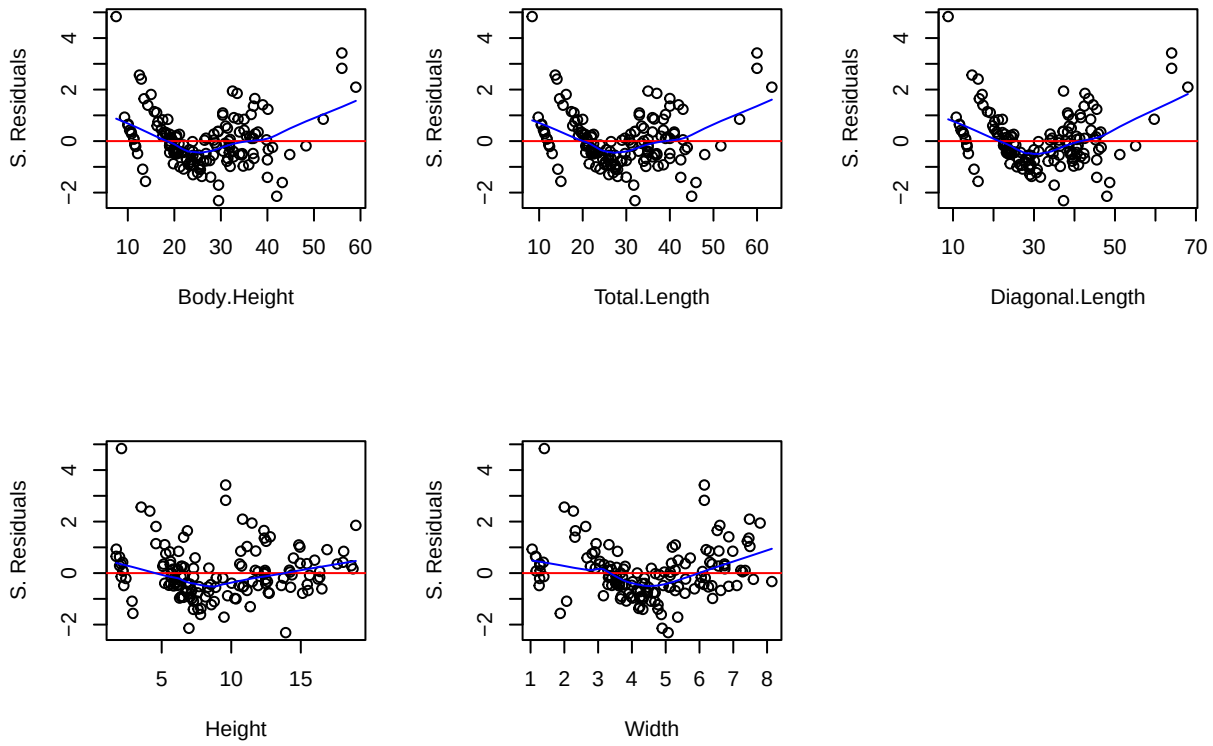
The VIF for all predictors is notably higher than the VIF threshold of 16.26, suggesting that all predictors are highly correlated with at least one of the other predictors in the model. We can conclude that a high degree of multicollinearity is present in this model.

Question 4: Checking Model Assumptions [6 points]

Please use the cleaned data set, which have the outlier(s) removed, and model2 for answering the following questions.

(a) Create scatterplots of the standardized residuals of model2 versus each quantitative predictor. Does the linearity assumption appear to hold for all predictors?

```
# Get standardized residuals
resids =rstandard(model2)
par(mfrow=c(2,3))
for (i in c(3:7)){
  col_name = names(fish2[i])
  plot(fish2[,i], resids, xlab= col_name, ylab = "S. Residuals")
  abline(h=0, col="red")
  lines(lowess(fish2[,i], resids), col='blue')
}
```



Note: The blue line is a smooth fit to the residuals, intended to make it easier to identify a trend.

From the scatterplots for Body.Height, Total.Length, Diagonal.Lenght, and Width we can see that the residuals exhibit an U-shape, which provides a indication of non-linearity. Specifically,

Body.Height: A possible concern between 20-30cm, where the majority of the residuals are below the zero line.

Total.Length: A possible concern between 20-30cm, where the majority of the residuals are below the zero line.

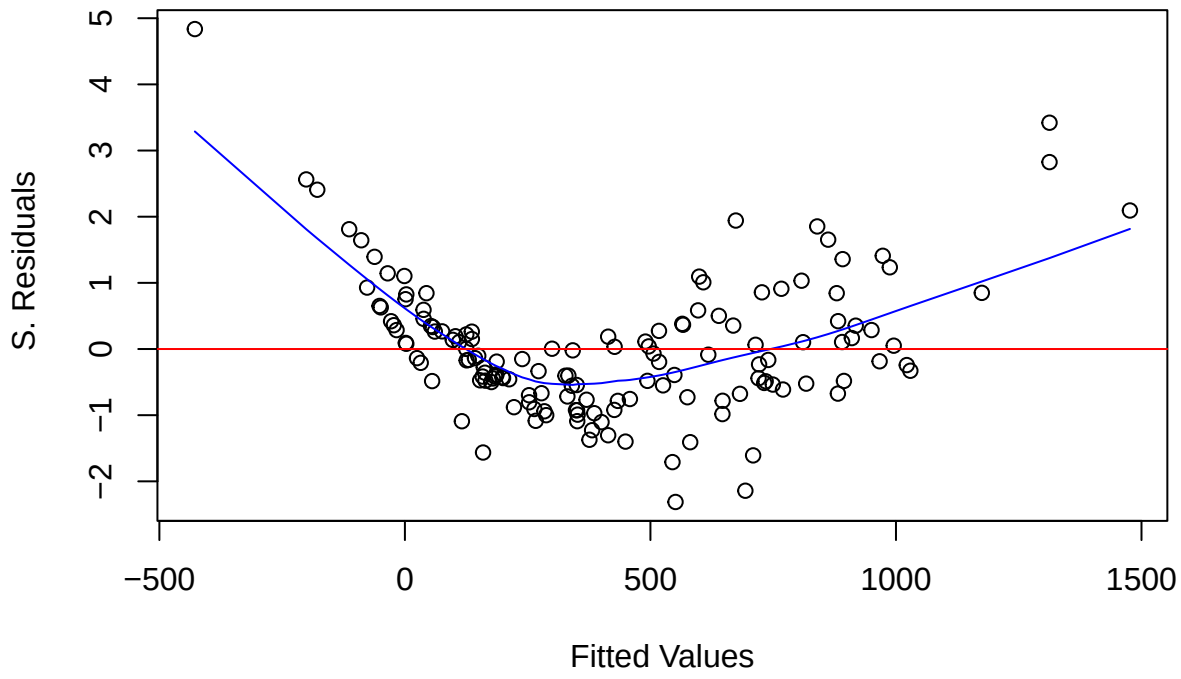
Diagonal.Length: A possible concern between 27-35cm, where the majority of the residuals are below the zero line.

Width: A possible concern between 3.9-5cm, where the majority of the residuals are below the zero line.

Overall, the linearity assumption does not seem to hold.

(b) Create a scatter plot of the standardized residuals of model2 versus the fitted values of model2. Does the constant variance assumption appear to hold? Do the errors appear uncorrelated?

```
# Plot of std. residuals versus fitted values
plot(model2$fitted.values, resids, xlab="Fitted Values", ylab=" S. Residuals")
lines(lowess(model2$fitted.values, resids), col='blue')
abline(h=0, col="red")
```



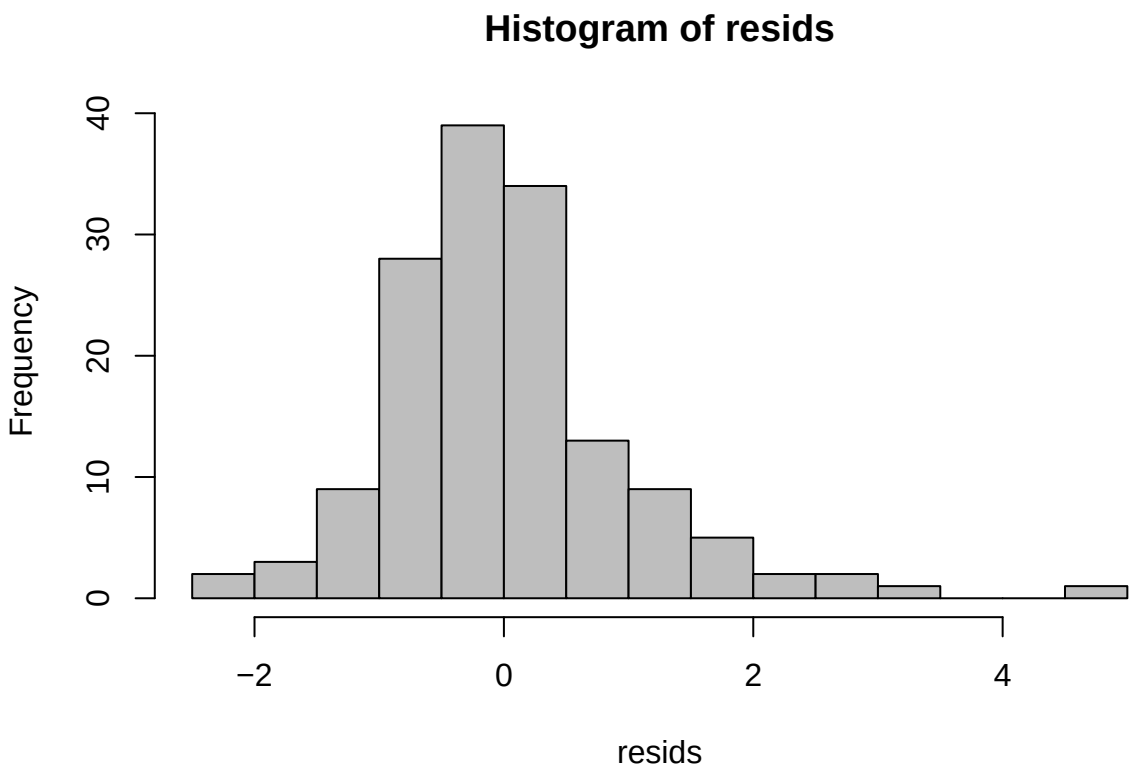
From the plot of the standardized residuals vs. fitted values, we also see a U-shaped pattern which confirms that the linearity assumption does not hold.

Also the plot shows that the spread of the residuals is not roughly equal per fitted value, with the variance increasing as the fitted values increase. Constant variance does not appear to hold.

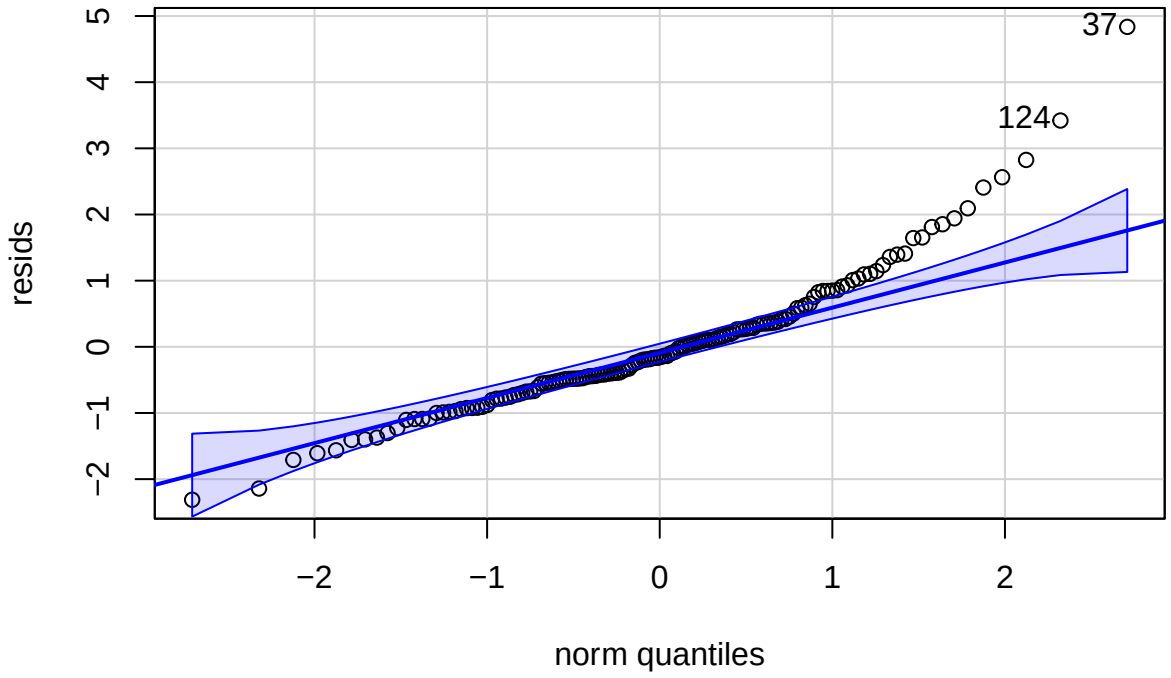
There does not appear to be any clear clustering in the residuals. This suggests that the errors might be uncorrelated.

(c) Create a histogram and normal QQ plot for the standardized residuals. What conclusions can you draw from these plots?

```
# Histogram of standardized residuals
hist(resids, col="grey", nclass=15)
```




```
# Q-q plot of standardized residuals
qqPlot(resids)
```




```
##  37 124
##  36 123
```

From the histogram, we see a normal peak but with a heavy right tail. The heavy right tail can be confirmed with the QQ Plot. The normality assumption does not appear to hold. Thus a transformation on the response variable may better our model.

Question 5: Partial F Test [6 points]

(a) Build a third multiple linear regression model using the cleaned data set without the outlier(s), called model3, using only *Species* and *Total.Length* as predicting variables and *Weight* as the response. Display the summary table of the model3.

```
# Fit model3
model3<-lm(Weight~Species+Total.Length, data=fish2)

# Dsiplay summary
summary(model3)
```

```
##
## Call:
## lm(formula = Weight ~ Species + Total.Length, data = fish2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -233.83  -56.59  -10.13   34.58  418.30
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -730.977     42.449 -17.220  < 2e-16 ***
## SpeciesParkki      63.129     38.889   1.623    0.107
## SpeciesPerch      -23.941     21.745  -1.101    0.273
## SpeciesPike      -400.964     33.350 -12.023  < 2e-16 ***
## SpeciesRoach      -19.876     30.111  -0.660    0.510
## SpeciesSmelt      256.408     39.858   6.433 1.85e-09 ***
## SpeciesWhitefish  -14.971     42.063  -0.356    0.722
## Total.Length       40.775      1.181  34.527  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 94.86 on 140 degrees of freedom
## Multiple R-squared:  0.9353, Adjusted R-squared:  0.9321
## F-statistic: 289.1 on 7 and 140 DF,  p-value: < 2.2e-16
```

(b) Conduct a partial F-test comparing model3 with model2. What can you conclude using an α level of 0.01?

```
# Conduct Partial F-test
anova(model3, model2)
```

```
## Analysis of Variance Table
##
## Model 1: Weight ~ Species + Total.Length
## Model 2: Weight ~ Species + Body.Height + Total.Length + Diagonal.Length +
##     Height + Width
##   Res.Df     RSS Df Sum of Sq      F Pr(>F)
## 1    140 1259746
## 2    136 1197659  4     62087 1.7626   0.14
```

$H_0 : \alpha_{Body.Height} = \alpha_{Diagonal.Length} = \alpha_{Height} = \alpha_{Width} = 0$

H_A: At least one coefficient $\neq 0$

Using a α level of 0.01, since the pvalue $> \alpha_{0.01}$ we fail to reject the null hypothesis that the four additional coefficients equal zero. Thus the additional variables do not provide additional explanatory power to the

model that already includes Species and Total.Length.

Question 6: Reduced Model Residual Analysis and Multicollinearity Test [7 points]

(a) Conduct a multicollinearity test on model3. Comment on the multicollinearity in model3.

```
# VIF Threshold
cat("VIF Threshold:", max(10, 1/(1-summary(model3)$r.squared)), "\n")
```

```
## VIF Threshold: 15.45466
```

```
# Calculate VIF
vif(model3)
```

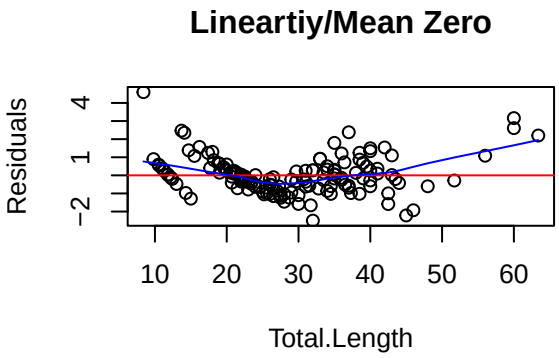
```
##                   GVIF Df GVIF^(1/(2*Df))
## Species      2.654472  6        1.084755
## Total.Length 2.654472  1        1.629255
```

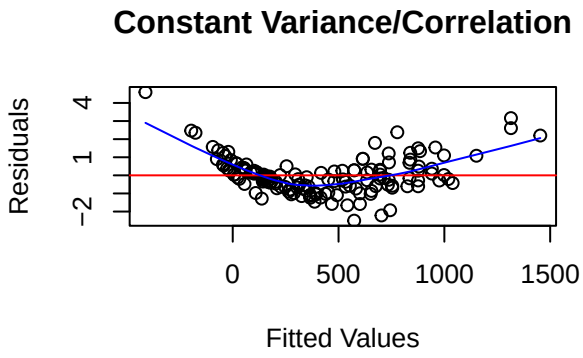
Since the predictors all have VIF < 15.45, the remaining multicollinearity is negligible in the model and should not affect our inferences.

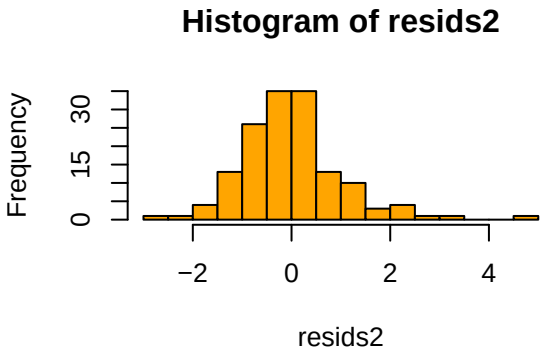
(b) Conduct residual analysis for model3 (similar to Q4). Comment on each assumption and whether they hold.

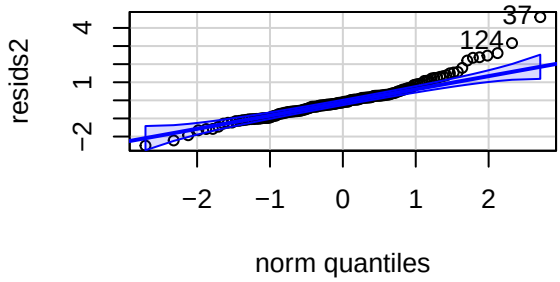
```
# Get standardized residuals
resids2 =rstandard(model3)

# Residual plots
par(mfrow=c(2,2))
plot(fish2$Total.Length, resids2 , main="Lineartiy/Mean Zero",
     xlab="Total.Length", ylab="Residuals")
abline(h=0, col="red")
lines(lowess(fish2$Total.Length, resids2), col='blue')
plot(model3$fitted.values, resids2 , main="Constant Variance/Correlation",
     xlab="Fitted Values", ylab="Residuals")
abline(h=0, col="red")
lines(lowess(model3$fitted.values, resids2), col='blue')
hist(resids2 , col="orange", nclass=15)
qqPlot(resids2)
```










```
##  37 124
##  36 123
```

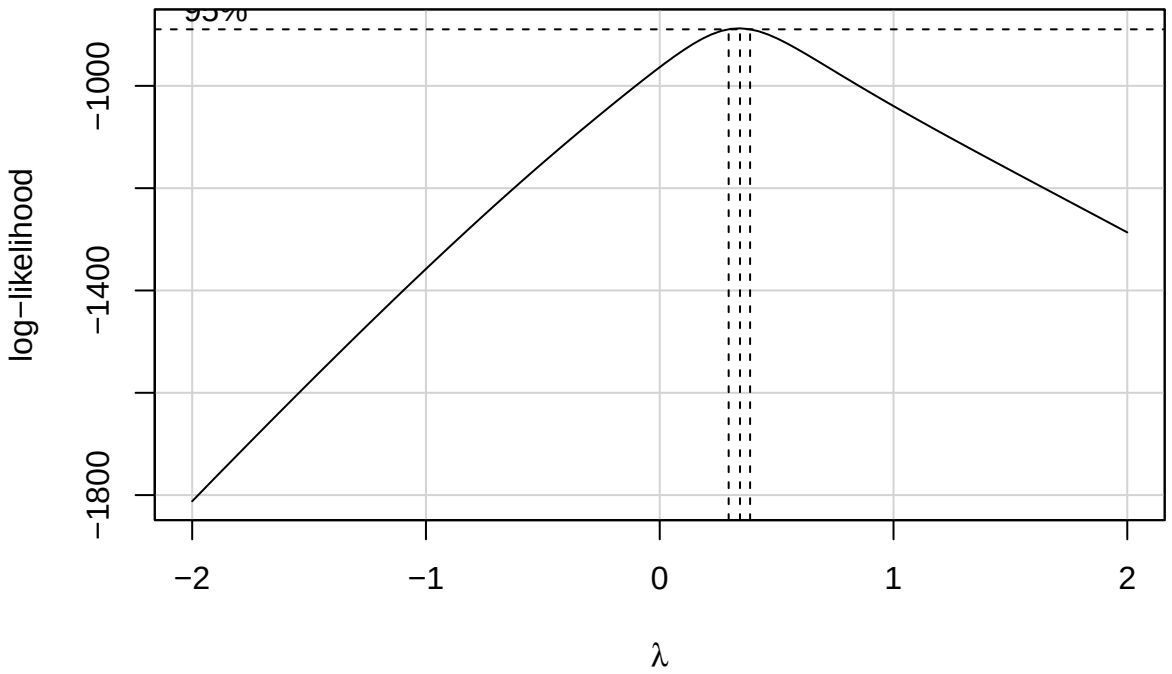
We have similar linearity/mean zero and constant variance violations as model2 with a u-shape in the residuals and increasing variance as fitted values increase.

The histogram and QQ plot both show a normal peak with a heavy right tail. Thus Normality does not hold either. A transformation of the response may help center up the residuals.

Question 7: Transformation [9 pts]

(a) Use model3 to find the optimal lambda, rounded to the nearest 0.5, for a Box-Cox transformation on model3. What transformation, if any, should be applied according to the lambda value? Please ensure you use model3

```
# Box-Cox transformation
bc<-boxCox(model3)
```




```
# Extract optimal lambda
opt.lambda<-bc$x[which.max(bc$y)]

# Rounded optimal lambda
cat("Optimal Lambda = ", round(opt.lambda/0.5)*0.5, end="\n")
```

```
## Optimal Lambda =  0.5
```

A lambda value = 0.5 equates to a square root transformation of the response variable.

(b) Based on the the results in (a), create model4 with the appropriate transformation. Display the summary.

```
model4<-lm(Weight^(1/2)~ Species + Total.Length, data=fish2)
summary(model4)
```

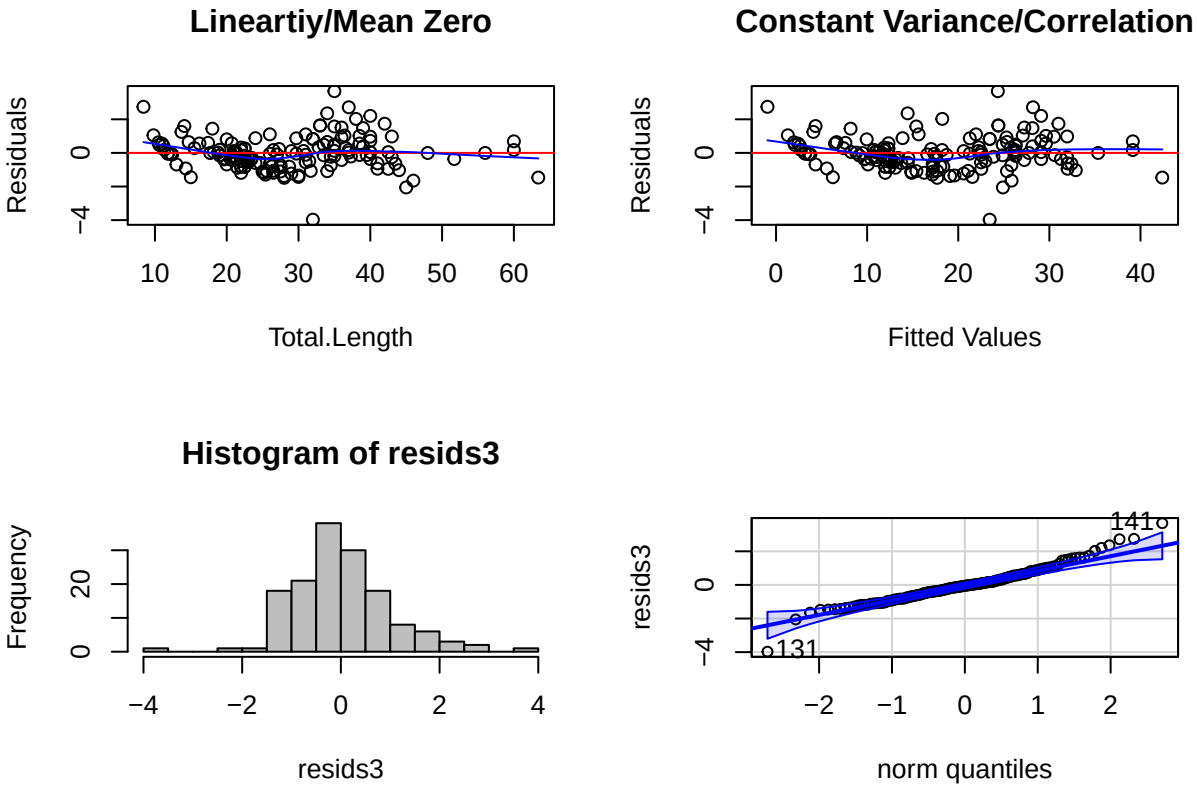
```
##
## Call:
## lm(formula = Weight^(1/2) ~ Species + Total.Length, data = fish2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.0111 -0.7687 -0.0579  0.6797  4.6383
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -6.96654    0.57278 -12.163  < 2e-16 ***
## SpeciesParkki     -0.36404    0.52476  -0.694   0.4890
## SpeciesPerch      -1.95734    0.29342  -6.671 5.46e-10 ***
## SpeciesPike      -10.90490    0.45001 -24.233  < 2e-16 ***
## SpeciesRoach      -2.09340    0.40630  -5.152 8.58e-07 ***
## SpeciesSmelt      -1.04994    0.53782  -1.952   0.0529 .
```

```
## SpeciesWhitefish  -0.55048    0.56758  -0.970   0.3338
## Total.Length       0.95052    0.01594  59.649  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.28 on 140 degrees of freedom
## Multiple R-squared:  0.9817, Adjusted R-squared:  0.9808
## F-statistic:  1074 on 7 and 140 DF,  p-value: < 2.2e-16
```

(c) Perform Residual Analysis on model4. Comment on each assumption. Was the transformation successful/unsuccessful?

```
# Get standardized residuals
resids3 =rstandard(model4)

# Residual plots
par(mfrow=c(2,2))
plot(fish2$Total.Length, resids3, main="Lineartiy/Mean Zero",
     xlab="Total.Length", ylab="Residuals")
abline(h=0, col="red")
lines(lowess(fish2$Total.Length, resids3), col='blue')
plot(model4$fitted.values, resids3, main="Constant Variance/Correlation",
     xlab="Fitted Values", ylab="Residuals")
abline(h=0, col="red")
lines(lowess(model4$fitted.values, resids3), col='blue')
hist(resids3, col="grey", nclass=15)
qqPlot(resids3)
```




```
## 131 141
## 130 140
```

In the Linearity/Mean Zero plot, the residuals are now scattered more evenly across the zero line. Linearity assumption seems to hold.

In the Constant Variance/Correlation plot, the spread of the residuals show no pattern or increasing/decreasing trend. Constant Variance and assumption seems to hold. Also, there does not appear to be any clear clustering in the residuals. This suggests that the errors are uncorrelated.

Lastly, the QQ plot shows that the majority of the residuals lines up considerably well with the normal line except for a slight tail and a few possible outliers. Overall, based on these plots, the normality assumption seems to hold.

Overall, the transformation was successful in improving everything from the weak linearity, to the constant variance, and the heavy left tail of the Histogram.

Question 8: Model Comparison [2 pts]

(a) Using each model summary, compare and discuss the R-squared and Adjusted R-squared of model2, model3, and model4.

Rsquared:

model2 = 0.9385

model3 = 0.9353

model4 = 0.9817

We expect the R-squared value of model3 to increase as we add more variables. Despite the results, we would not want to use R-squared to compare models with a different number of variables.

Adjusted Rsquared:

model2 = 0.9335

model3 = 0.9321

model4 = 0.9808

Since the Adjusted R-sqaured adjusts the R-squared for the number of predicting variables in the model, we would say model2 explains more of the variance in the model than model3. Yet, this difference is extremely minimal. The transformed model4 has a much higher adjusted r-squared than the other two models. Thus, we prefer model4 over the other two models using this criteria.

Question 9: Prediction [8 points]

(a) Predict Weight for the last 10 rows of data (fishtest) using both model3 and model4. Compare and discuss the mean squared prediction error (MSPE) of both models.

```
# Calculate estimates
pred3<-predict(model3, fishtest)
# Calculate MSPE
mse.model3<-mean((pred3-fishtest$Weight)^2)

# Calculate estimates in terms of the original data
pred4<-predict(model4, fishtest)^2
# Calculate MSPE
mse.model4<-mean((pred4-fishtest$Weight)^2)

cat("The MSPE of model3 is", mse.model3, "\n")
```

```
## The MSPE of model3 is 9392.25
```

```
cat("The MSPE of model4 is", mse.model4, "\n")
```

```
## The MSPE of model4 is 2442.998
```

Since the MSPE of model4 is smaller than model3, based on this prediction accuracy measurement, model4 is preferred for predicting the weight of fish.

(b) Suppose you have found a Perch fish with a Body.Height of 28 cm, and a Total.Length of 32 cm. Using model4, predict the weight on this fish with a 90% prediction interval. Provide an interpretation of the prediction interval.

```
# Create new data point
new.point<-data.frame(Species="Perch", Total.Length=32)
# Calulate prediction interval
predict(model4, new.point, interval="prediction", level=0.9)^2
```

```
##        fit      lwr      upr
## 1 461.9429 374.4536 558.6091
```

Model4 predicts the fish to weigh 461.94 grams with a 90% prediction interval of 374.45 to 558.61. We can be 90% confident that the expected weight of a fish with these specific characteristics will be between 374.45 to 558.61 grams.