Exercise 1

(a) To perform an analysis based on the given linear model on the dataset, one can run the following lines of code in the R console.

```
ModelLog <- lm(log(Mass) ~ Height + Width + Length, data = mussels)
summary(ModelLog)</pre>
```

From the summary, we obtain the estimates of the paramaters as follows

```
(Intercept) Height Width Length 3.135116758 0.009421034 0.014325594 0.002362504
```

(b) We provide 95% confidence interval for our parameter β_1 as shown below.

We can convince ourselves that $\beta_1 = 0$ lies in the rejected region, hence we choose to reject the hypothesis. This might suggests log(Mass) and Height are positively correlated to each other with $\beta_1 > 0$.

(c) To obtain the prediction on the specified input, we run the following code:

```
newdata < -data.frame(Height=100, Width=50, Length=200)
yhat <-predict(ModelLog,newdata)
yhat</pre>
```

This returns the value 5.266001.

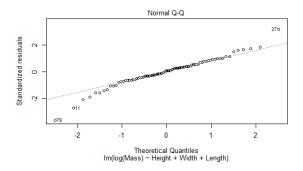
(d) Now, we use again the predict function, with some additional arguments as shown below, to obtain the prediction with 95% confidence interval.

```
ypred <-predict(ModelLog, newdata, interval="prediction", level=0.95)
ypred</pre>
```

This gives us

```
fit lwr upr
1 5.266001 5.099812 5.432189
```

(e) We run **plot(ModelLog)** to obtain the diagnostic plots of our linear model. The Scale-Location plot highlighted few potential outliers (points which standardised residuals above 1.5) that can be referred to the dataset. Plus, the Normal probability plot suggests a systematic error based on the deviation of the points at the tails, which might against our assumption on the distribution of the errors ε_i .



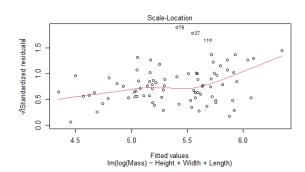


Figure 1: Two of the diagnostic plots of the model

```
log(Mass) Height
                             Width Length
         5.52069
11
                       135
                                 48
                                        260
                                        228
37
         5.75737
                       129
                                 46
79
         5.15149
                       112
                                 45
```

These values are very close to our **newdata** as defined in (c) hence might strongly influence our answers in (c) and (d)