

Quality of Wine

Introduction

How much of volatile acidity, citric acid, residual sugar, chlorides, free sulfur dioxide, total sulfur dioxide, density, pH, sulphates, and alcohol help explain the quality of wine? A linear regression will estimate the quality of wine based on these 11 predictors. The following series of tests will filter out the best model to get the most accurate results for this question.

Downloading Wine Quality Data Set

```
Wine_Quality<- read.csv("~/Downloads/WineQT.csv")
View(Wine_Quality)
```

Histograms

In histograms 1 (fixed acidity), 2 (volatile acidity), 4 (residual sugar), 5 (chlorides), 6 (free sulfur dioxide), 7 (total sulfur dioxide), 10 (sulphates), and 11 (alcohol) the models are right-skewed, meaning there is a positive distribution. Histograms 8 (pH) and 9 (density) have a normal distribution.

```
library(MASS)
hist(Wine_Quality$alcohol, prob = TRUE, xlab = "Alcohol", ylab = "Frequency", main = "Histogram of Alcohol")
fit1<-fitdistr(Wine_Quality$alcohol, densfun="logistic")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

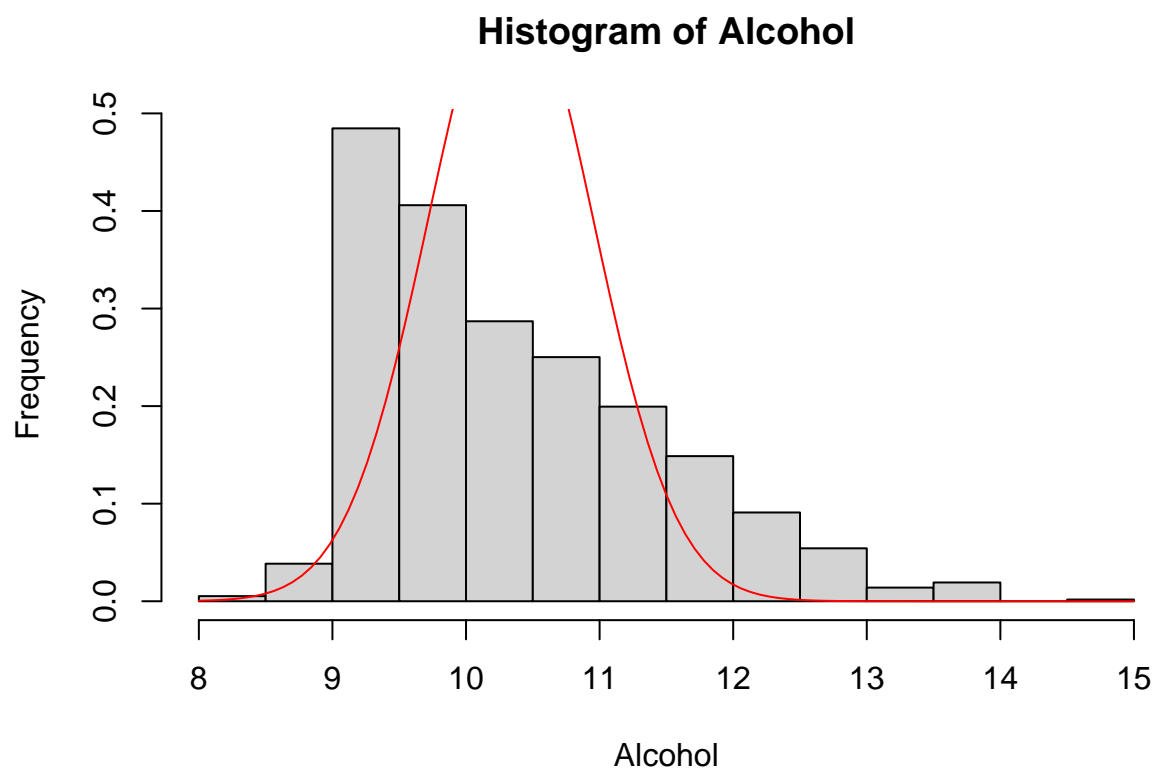
```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```



```
hist(Wine_Quality$fixed.acidity, prob = TRUE, xlab = "Fixed Acidity", ylab = "Frequency", main = "Histogram of Fixed Acidity")
fit1<-fitdistr(Wine_Quality$fixed.acidity, densfun="logistic")
```

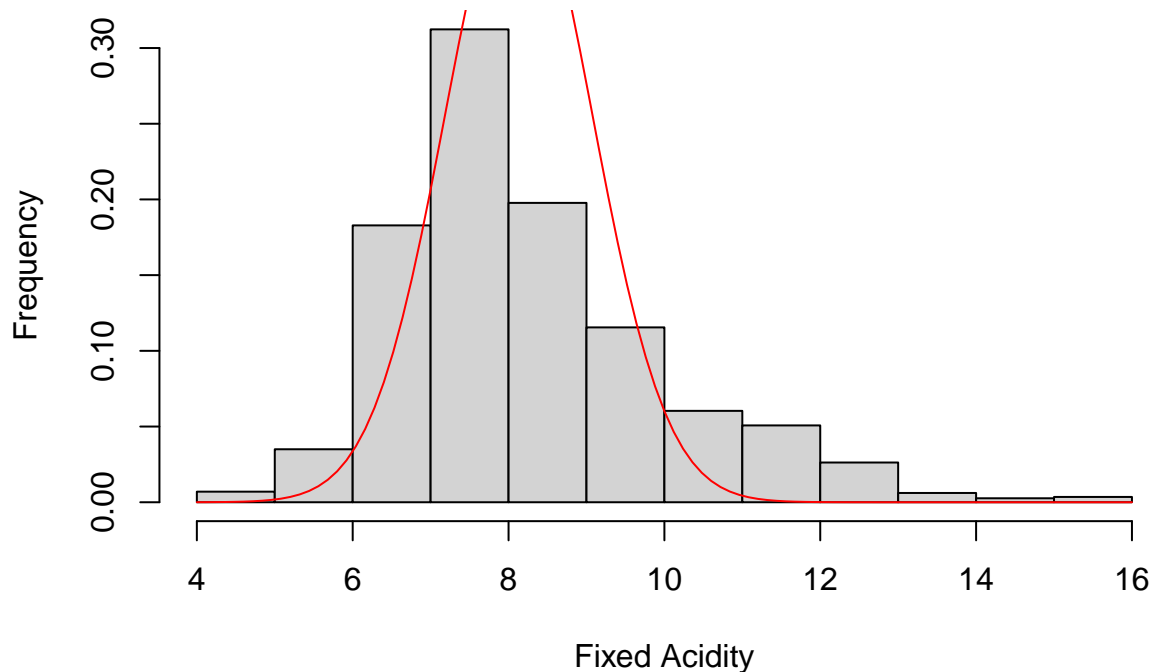
```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```

Histogram of Fixed Acidity



```
hist(Wine_Quality$volatile.acidity, prob = TRUE, xlab = "Volatile Acidity", ylab = "Frequency", main =  
fit1<-fitdistr(Wine_Quality$volatile.acidity, densfun="logistic")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

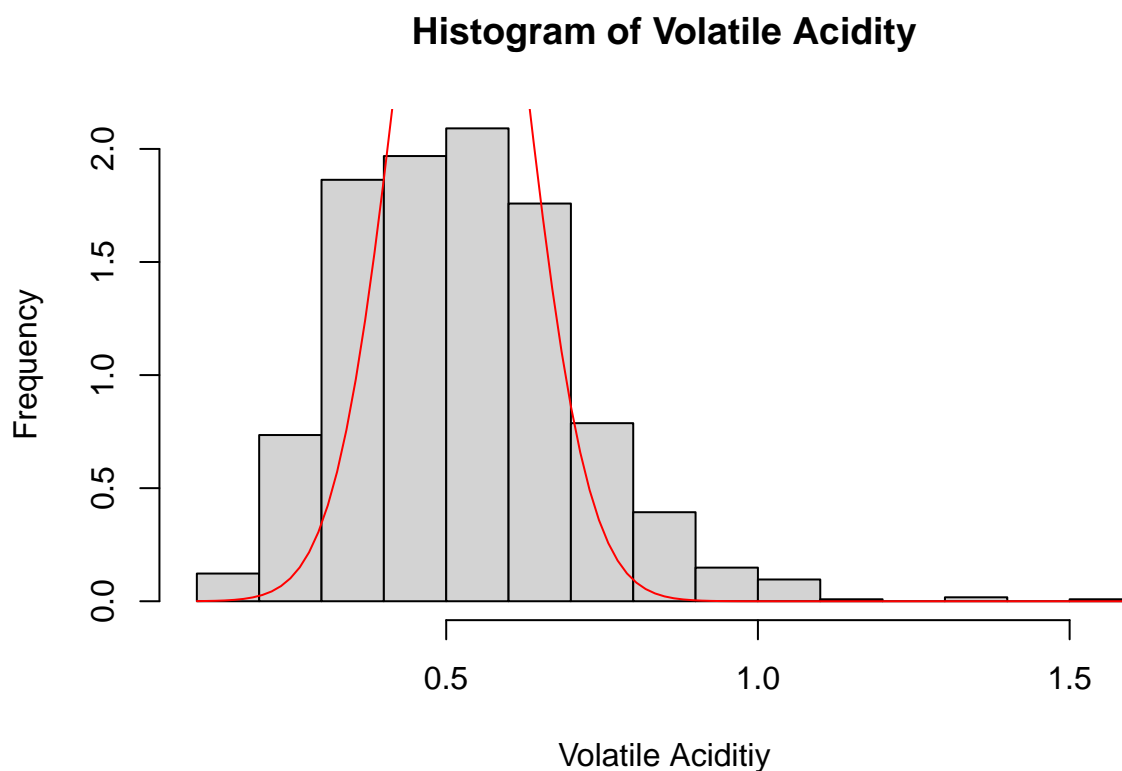
```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
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```

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```

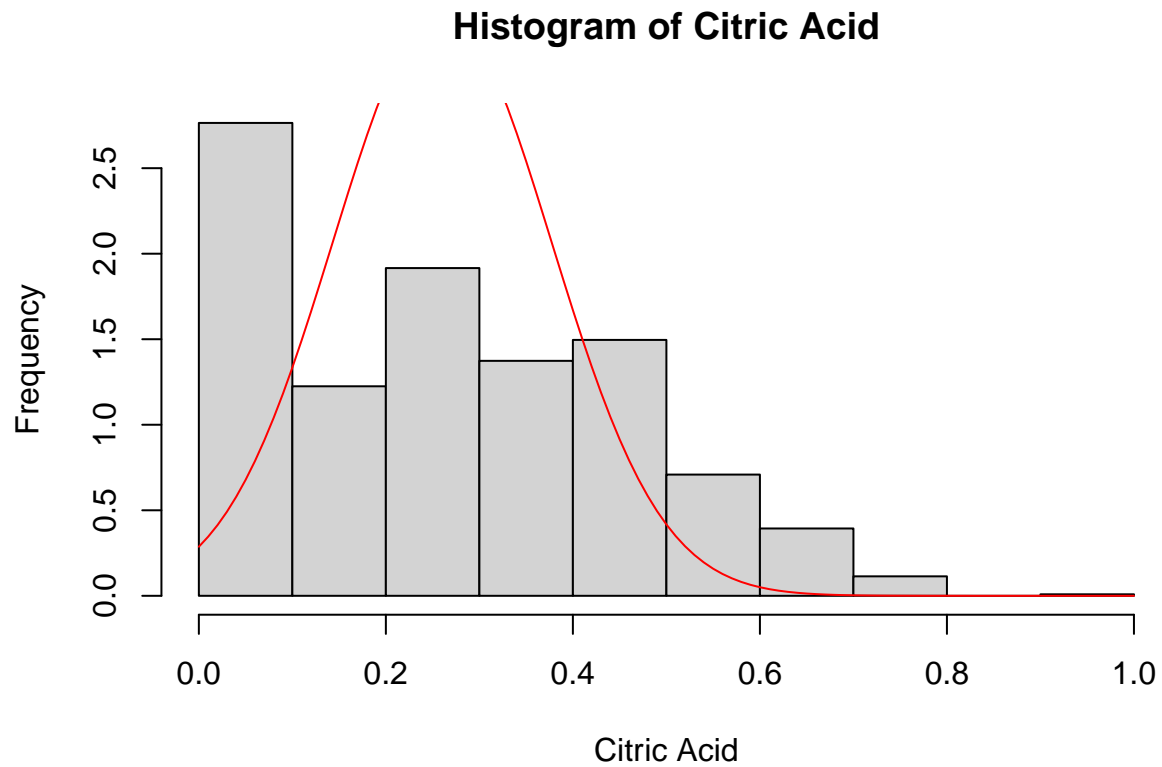
```
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```



```
hist(Wine_Quality$citric.acid, prob = TRUE, xlab = "Citric Acid", ylab = "Frequency", main = "Histogram
fit1<-fitdistr(Wine_Quality$citric.acid, densfun="logistic")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
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```

```
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```



```
hist(Wine_Quality$residual.sugar, prob = TRUE, xlab = "Residual Sugar", ylab = "Frequency", main = "Histogram of Residual Sugar")
fit1<-fitdistr(Wine_Quality$residual.sugar, densfun="logistic")
```

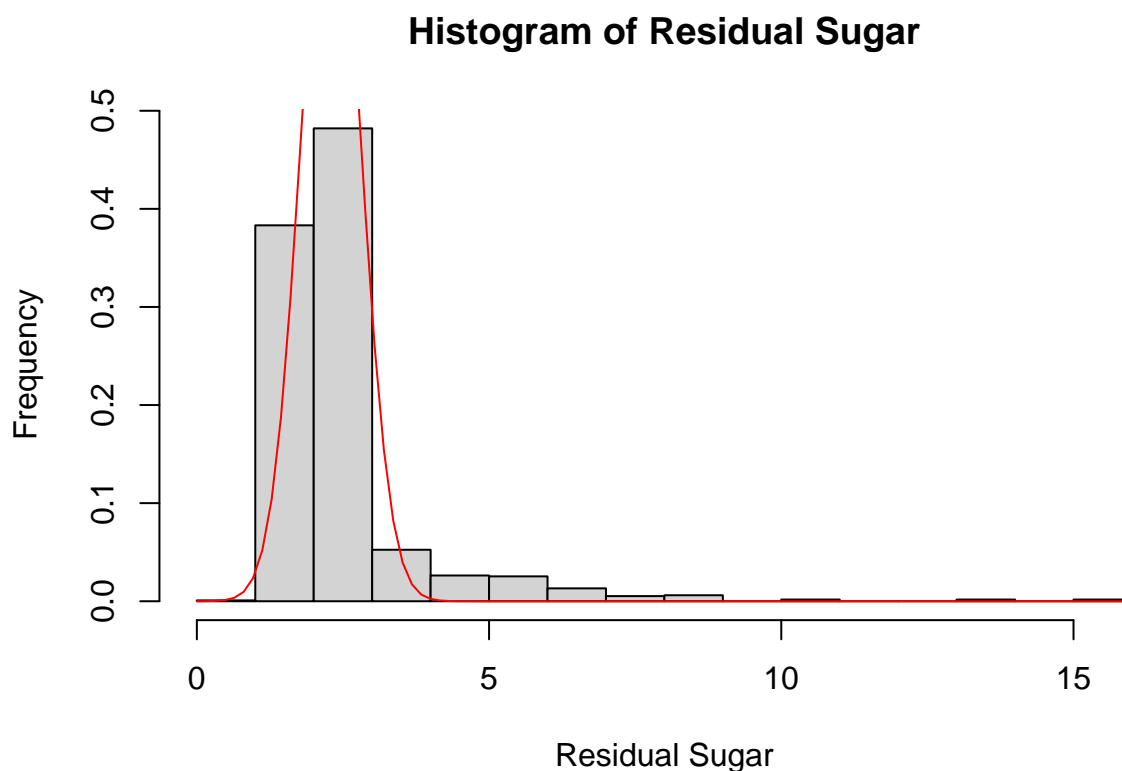
```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
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```

```
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```

```
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```

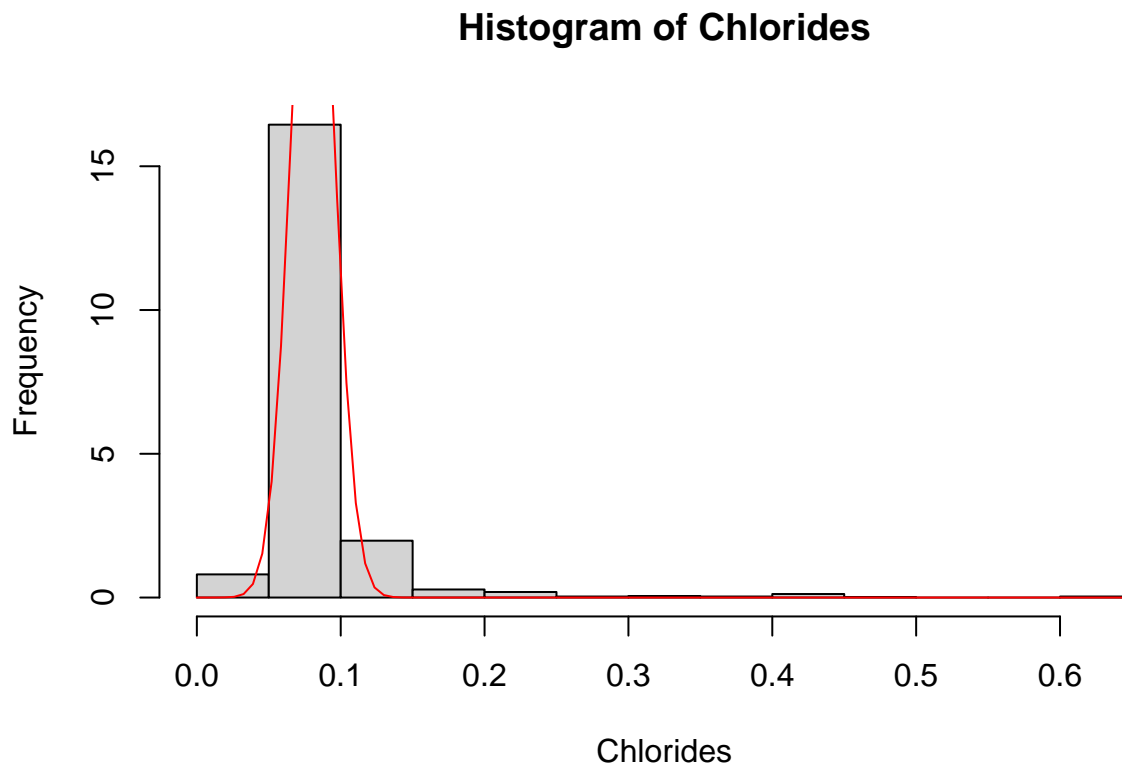


```
hist(Wine_Quality$chlorides, prob = TRUE, xlab = "Chlorides", ylab = "Frequency", main = "Histogram of Chlorides")
fit1<-fitdistr(Wine_Quality$chlorides, densfun="logistic")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
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## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced

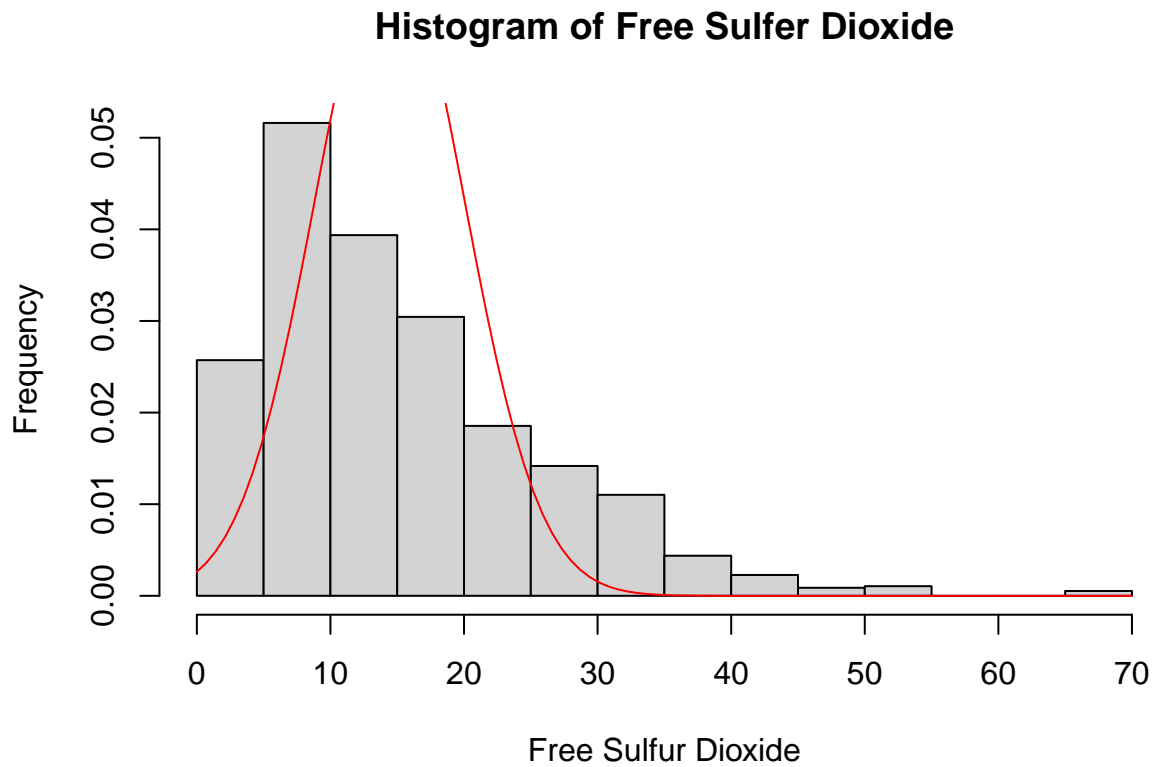
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```



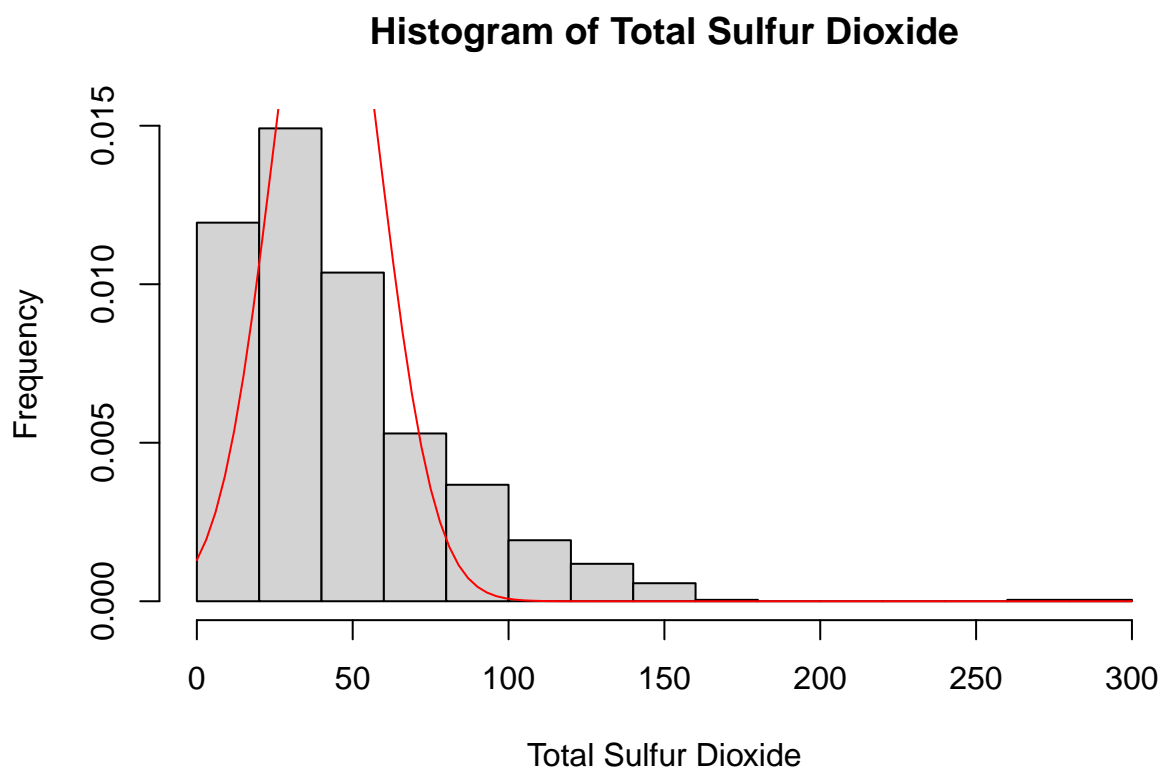
```
hist(Wine_Quality$free.sulfur.dioxide, prob = TRUE, xlab = "Free Sulfur Dioxide", ylab = "Frequency", main = "Histogram of Free Sulfur Dioxide")
fit1<-fitdistr(Wine_Quality$free.sulfur.dioxide, densfun="logistic")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```



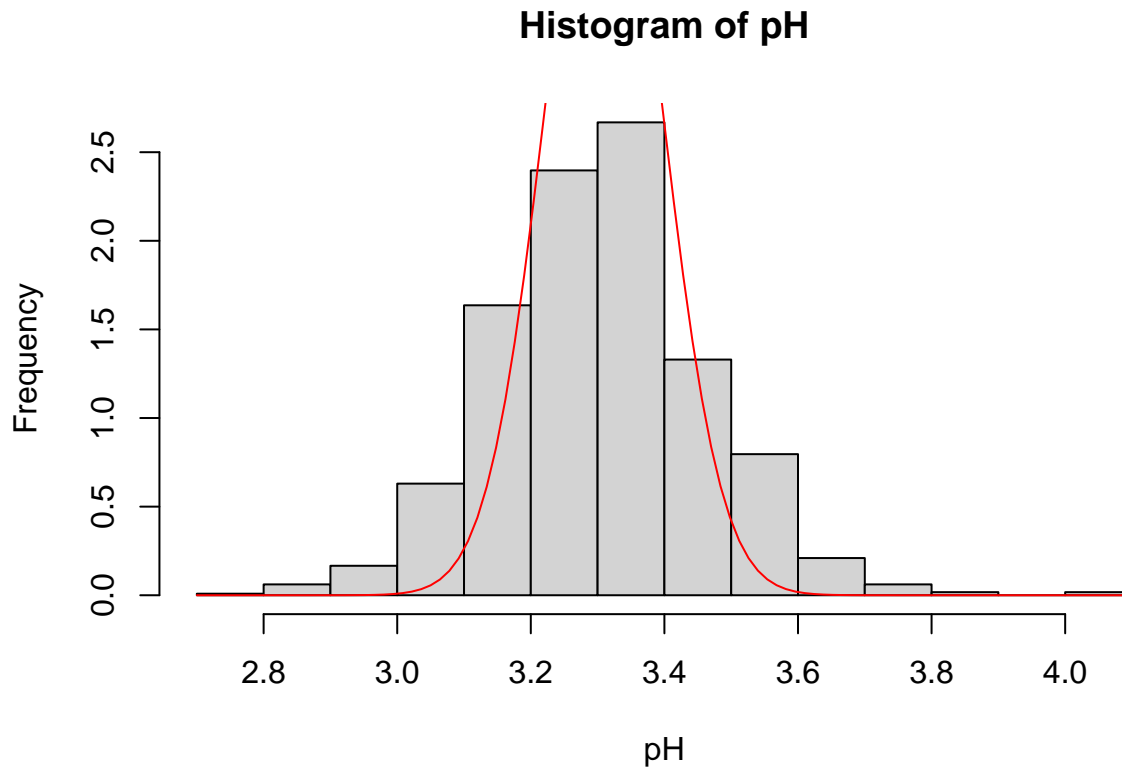
```
hist(Wine_Quality$total.sulfur.dioxide, prob = TRUE, xlab = "Total Sulfur Dioxide", ylab = "Frequency",
fit1<-fitdistr(Wine_Quality$total.sulfur.dioxide, densfun="logistic")
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```

```
hist(Wine_Quality$pH, prob = TRUE, xlab = "pH", ylab = "Frequency", main = "Histogram of pH")
fit1<-fitdistr(Wine_Quality$pH, densfun="logistic")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
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## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```

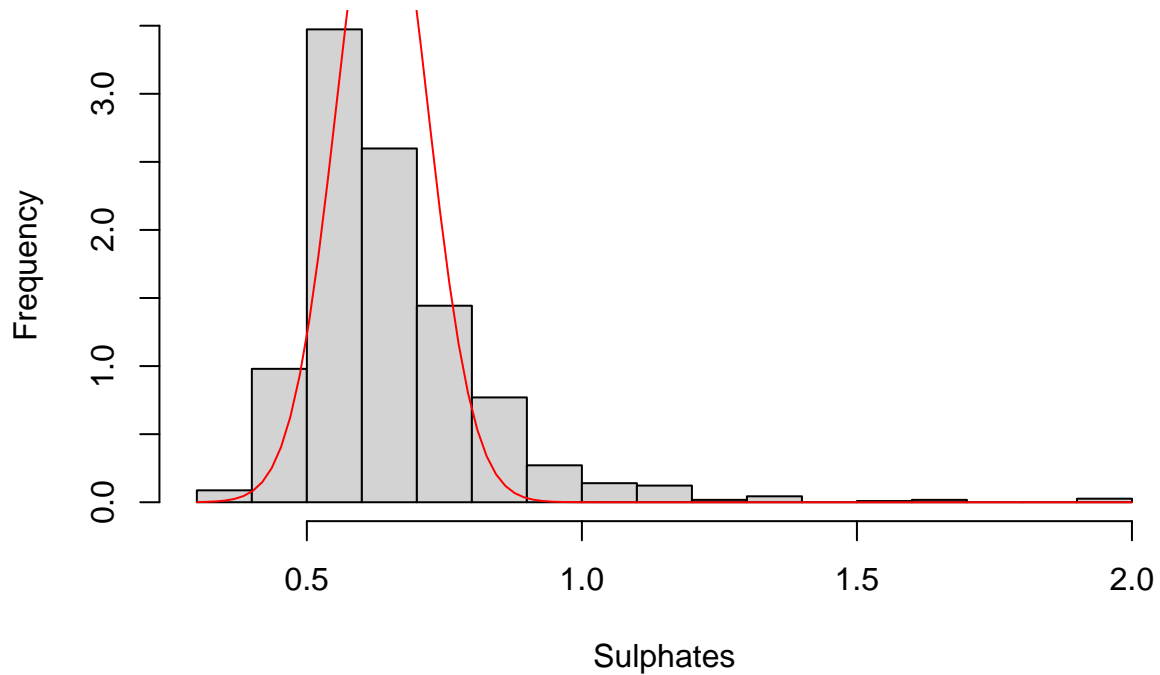


```
hist(Wine_Quality$sulphates, prob = TRUE, xlab = "Sulphates", ylab = "Frequency", main = "Histogram of Sulphates")
fit1<-fitdistr(Wine_Quality$sulphates, densfun="logistic")
```

```
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
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## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
```

```
curve(dnorm(x,fit1$estimate[1], fit1$estimate[2]), col="red", add=T)
```

Histogram of Sulphates



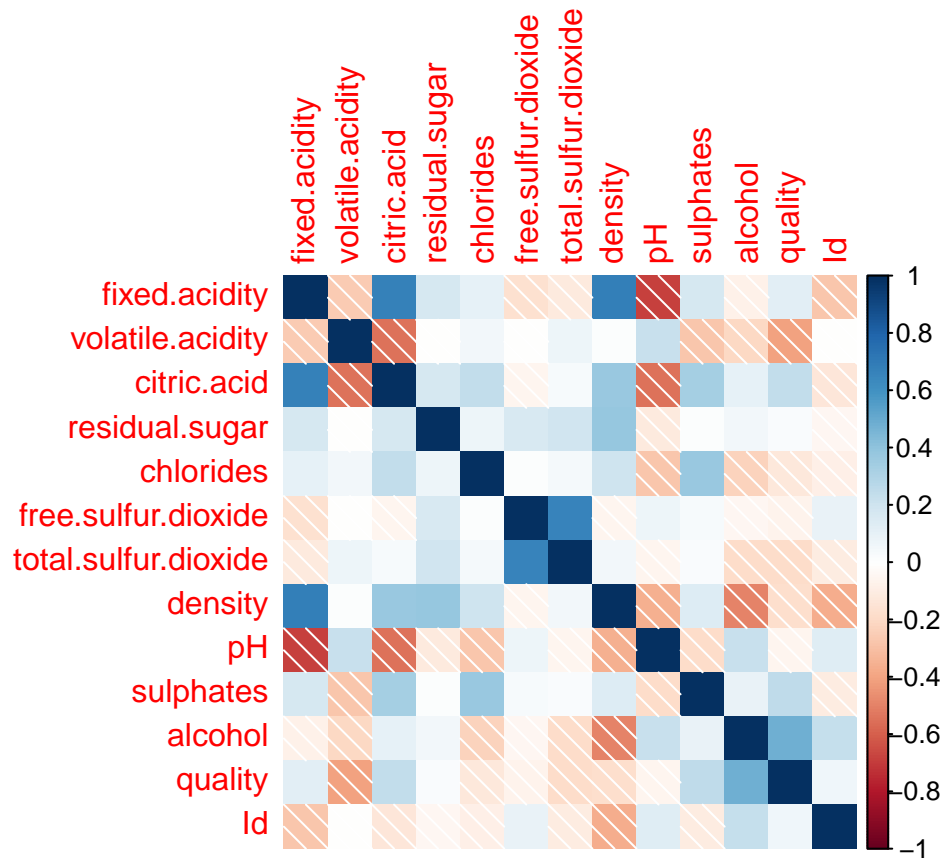
Correlation Plot

Based on the correlation plot above, there is a positive correlation between the quality of wine and alcohol, sulphates, citric acid, and fixed acidity. However, there is a negative correlation between wine quality and volatile acidity, chlorides, free sulfur dioxide, total sulfur dioxide, density, and pH.

```
library(corrplot)
```

```
## corrplot 0.92 loaded
```

```
M = cor(Wine_Quality)
corrplot(M, method = 'shade')
```

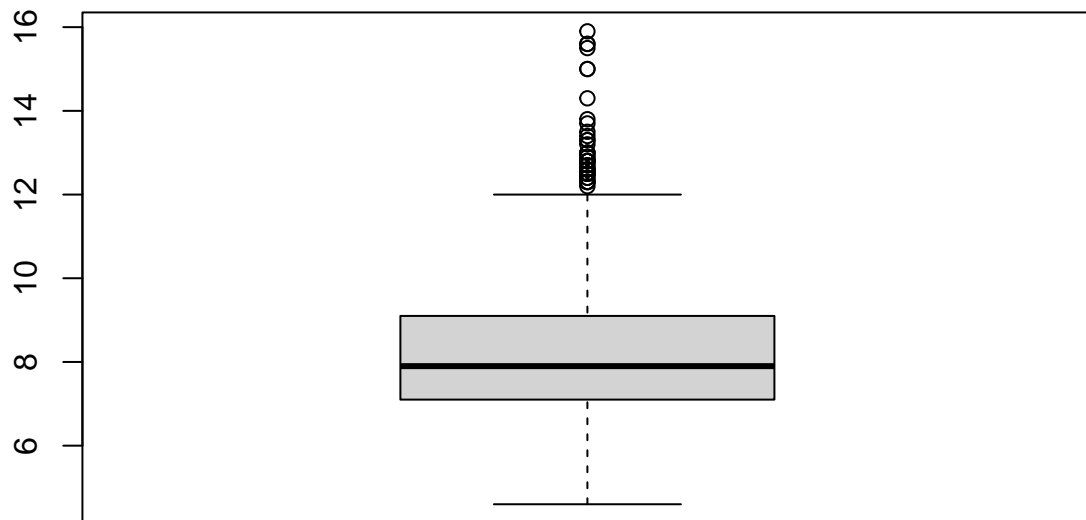


Box Plot

It is evident by the models above that the data is moderately concentrated with the predictor variable citric acid having the largest spread and chlorides having the smallest spread. It is important to note when there are many outliers, as it may skew results.

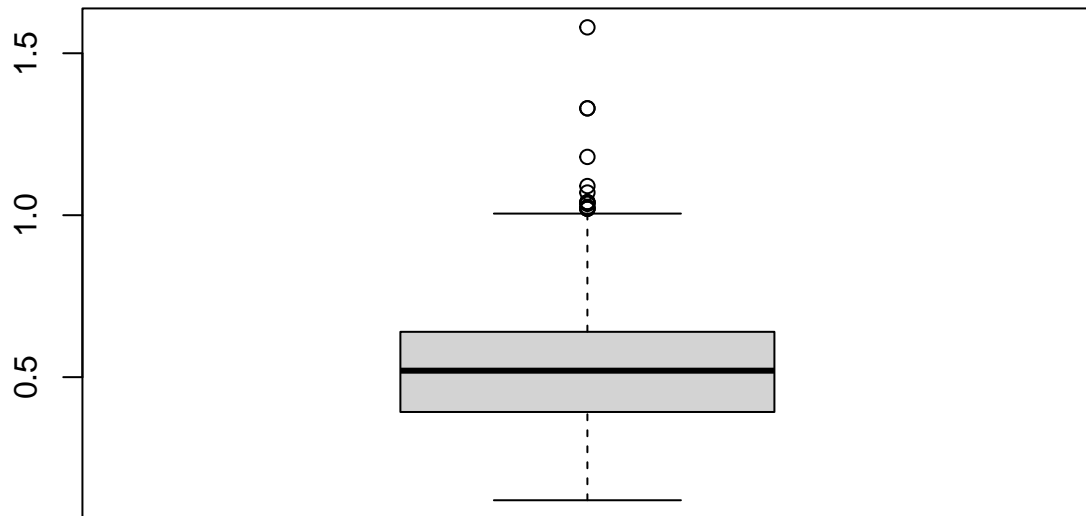
```
boxplot(Wine_Quality$fixed.acidity, main = "Fixed Acidity")
```

Fixed Acidity



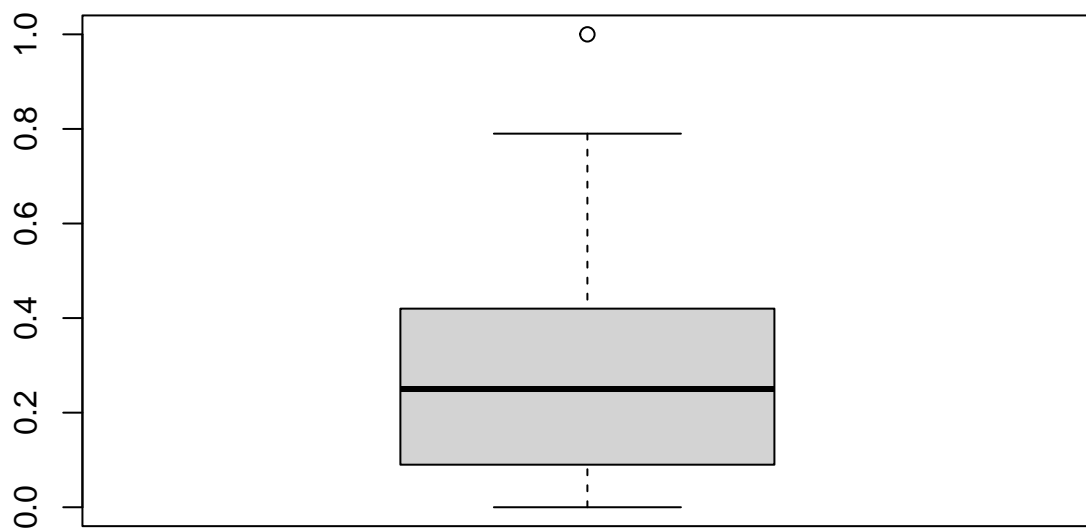
```
boxplot(Wine_Quality$volatile.acidity, main = "Volatile Acidity")
```

Volatile Acidity



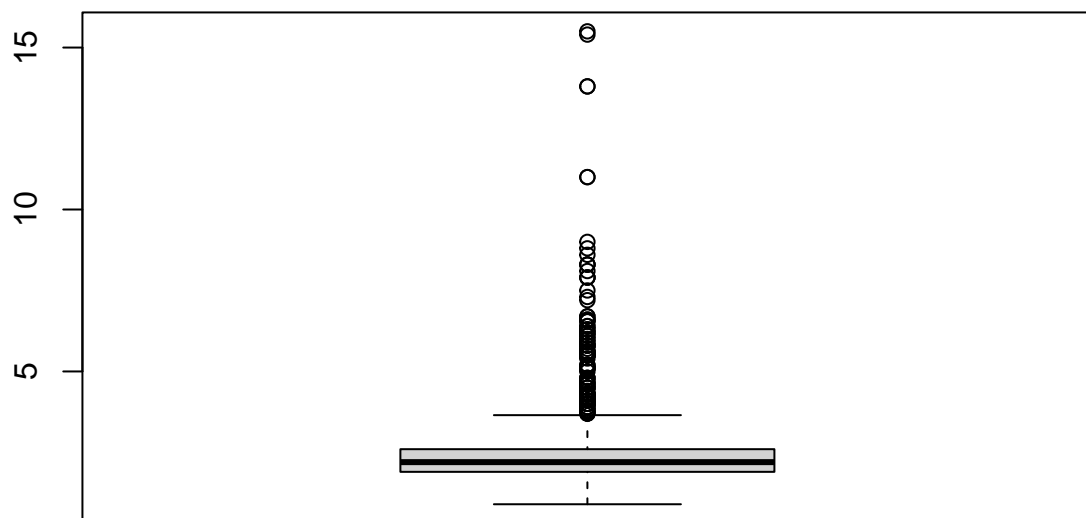
```
boxplot(Wine_Quality$citric.acid, main = "Citric Acid")
```

Citric Acid



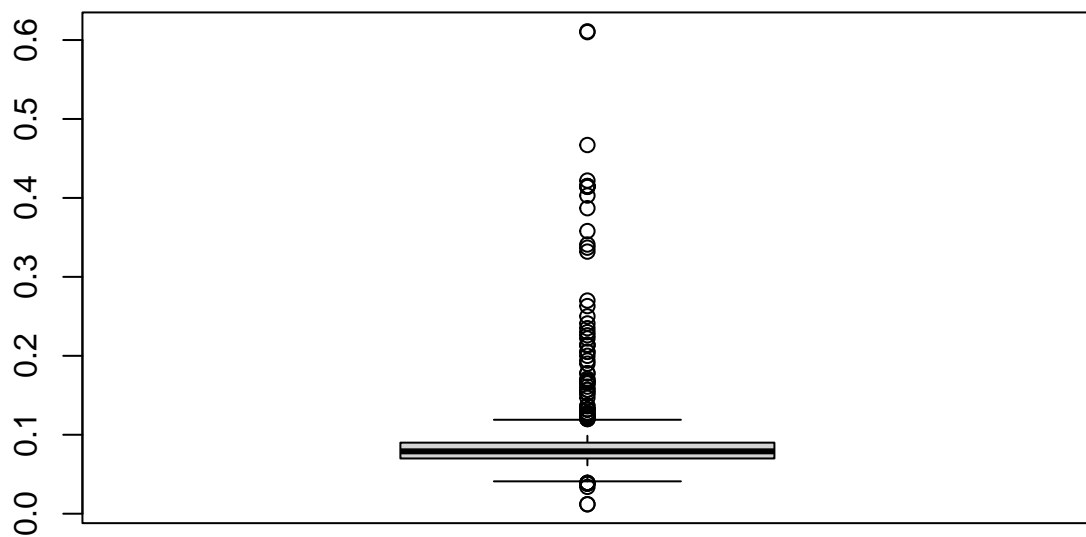
```
boxplot(Wine_Quality$residual.sugar, main = "Residual Sugar")
```

Residual Sugar



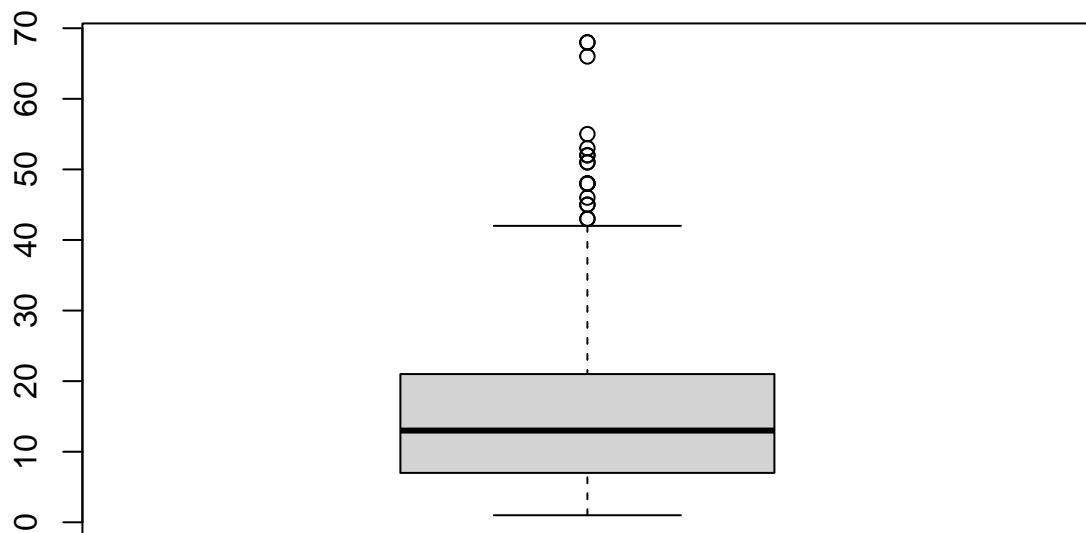
```
boxplot(Wine_Quality$chlorides, main = "Chlorides")
```


Chlorides

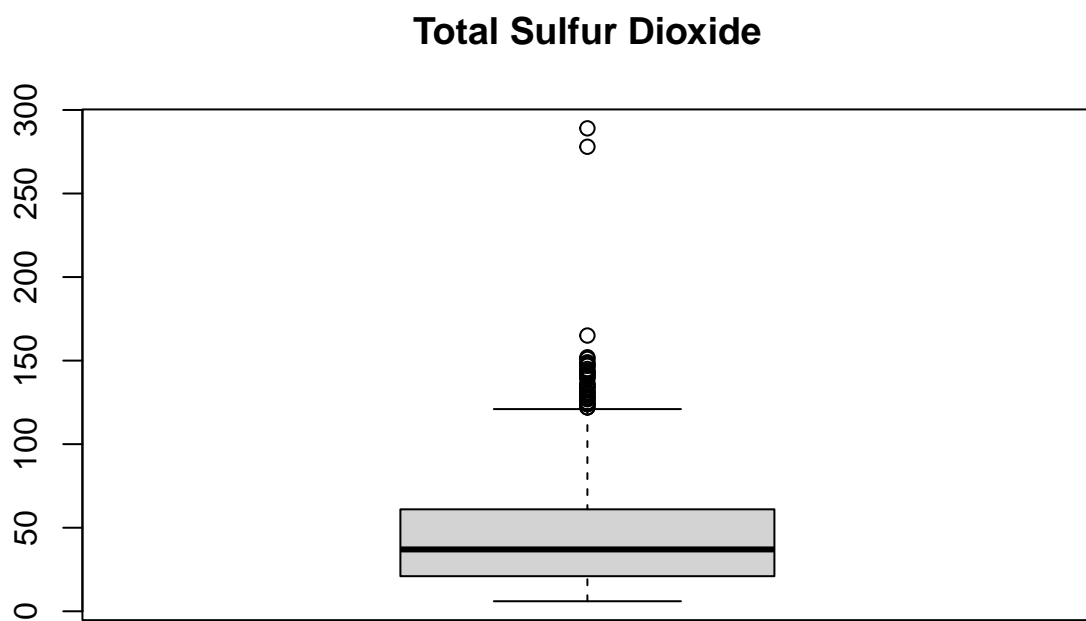


```
boxplot(Wine_Quality$free.sulfur.dioxide, main = "Free Sulfur Dioxide")
```

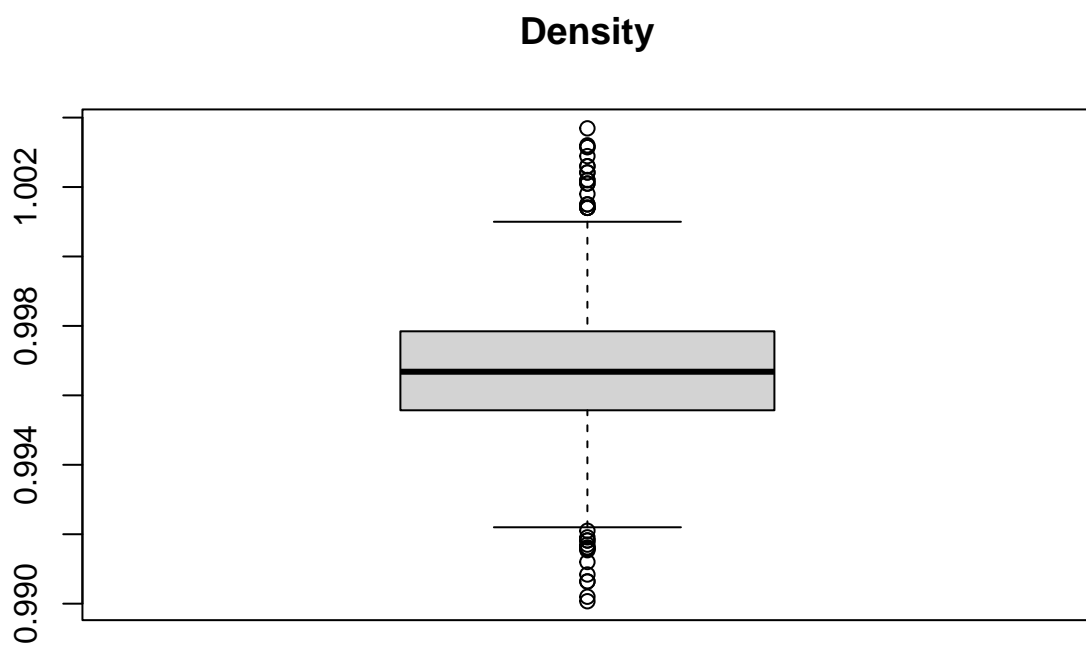
Free Sulfur Dioxide



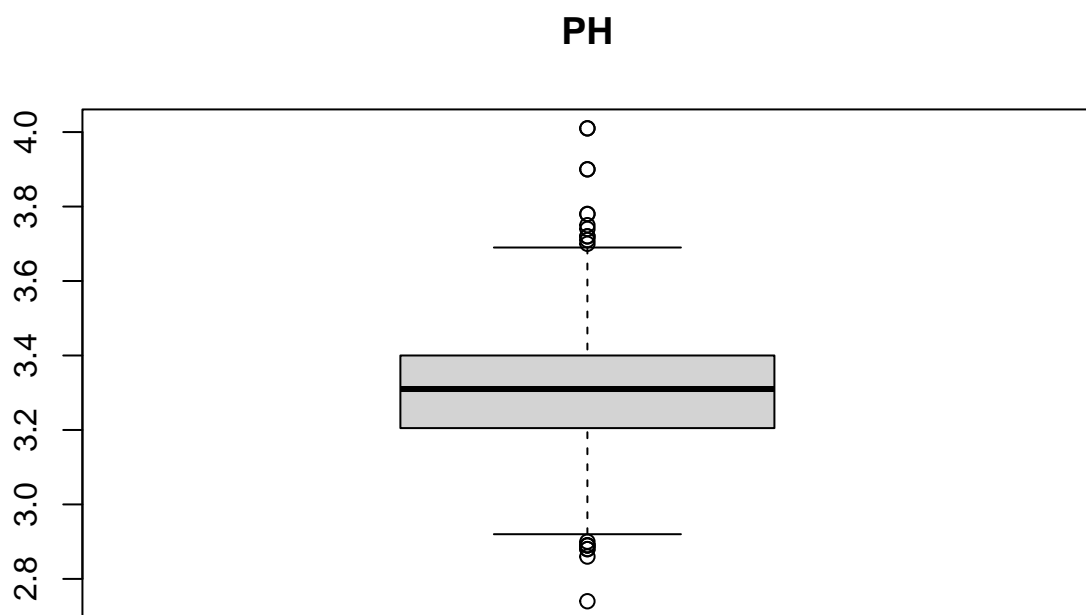
```
boxplot(Wine_Quality$total.sulfur.dioxide, main = "Total Sulfur Dioxide")
```



```
boxplot(Wine_Quality$density, main = "Density")
```

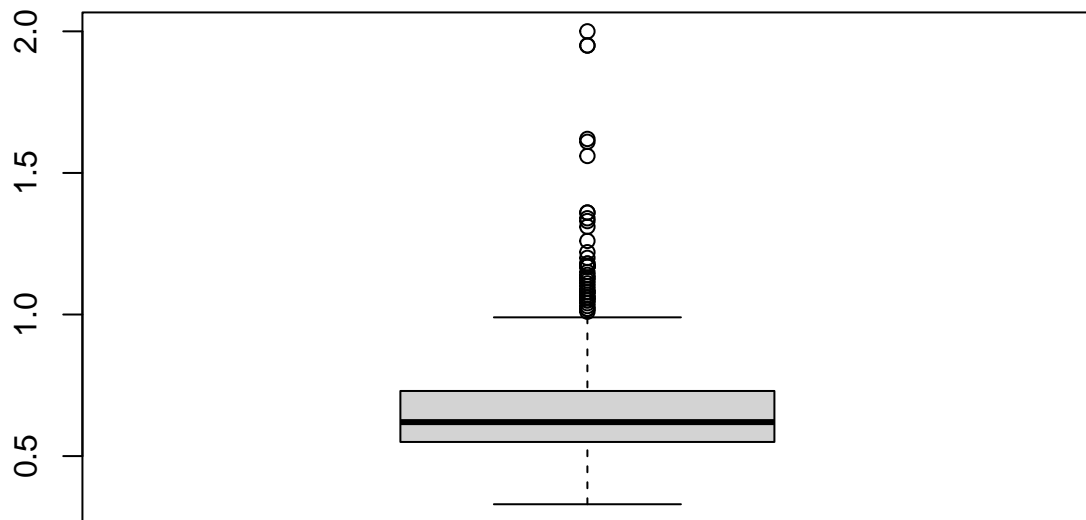


```
boxplot(Wine_Quality$pH, main = "PH")
```

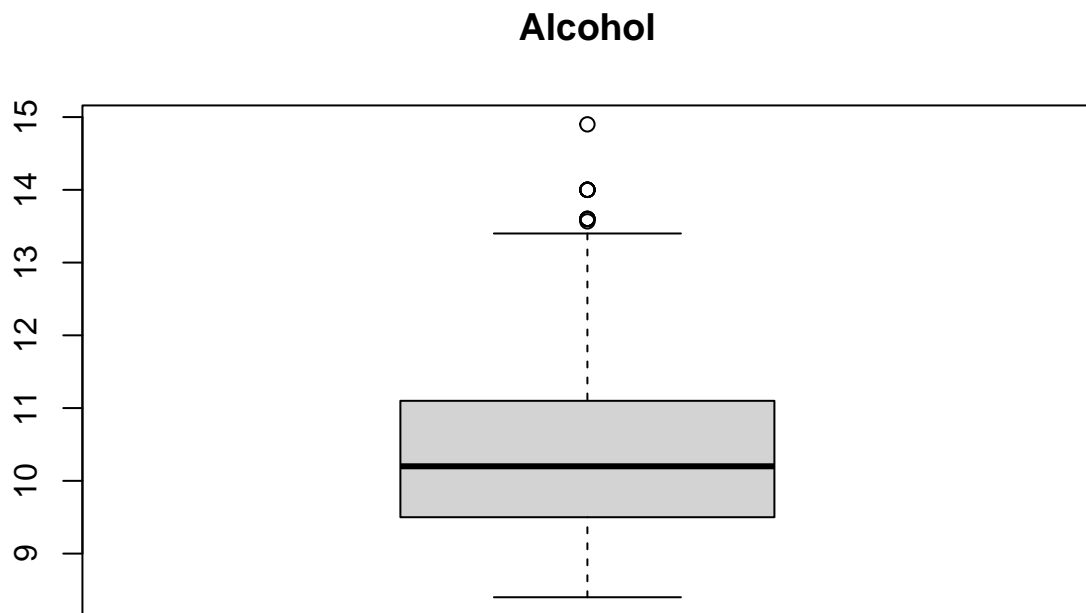


```
boxplot(Wine_Quality$sulphates, main = "Sulphates")
```

Sulphates



```
boxplot(Wine_Quality$alcohol, main = "Alcohol")
```

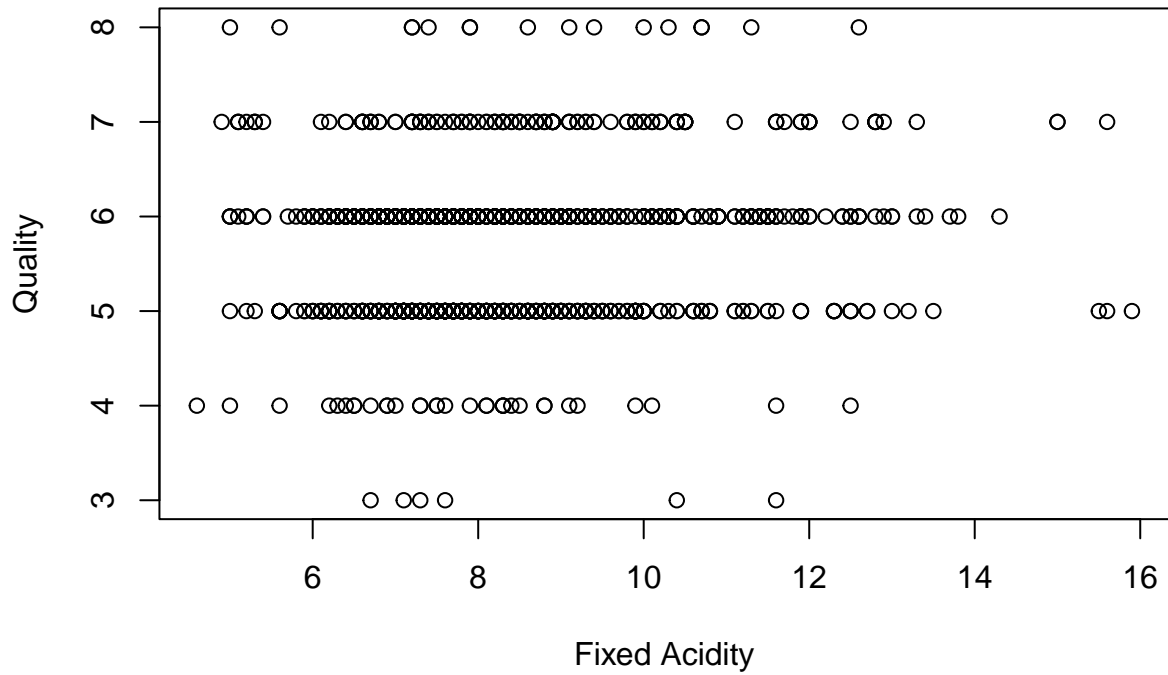


Scatter Plot

A scatterplot shows the relationship between two variables. In this data set, it's a visual of the relationship between the quality of wine and fixed acidity, pH, alcohol, etc... Variables with a strong relationship will have clusters of data points while variables with weak relationships will have data points that are spread out. From the scatter plots, it can be said there is a strong relationship between wine quality and the other variables as of now.

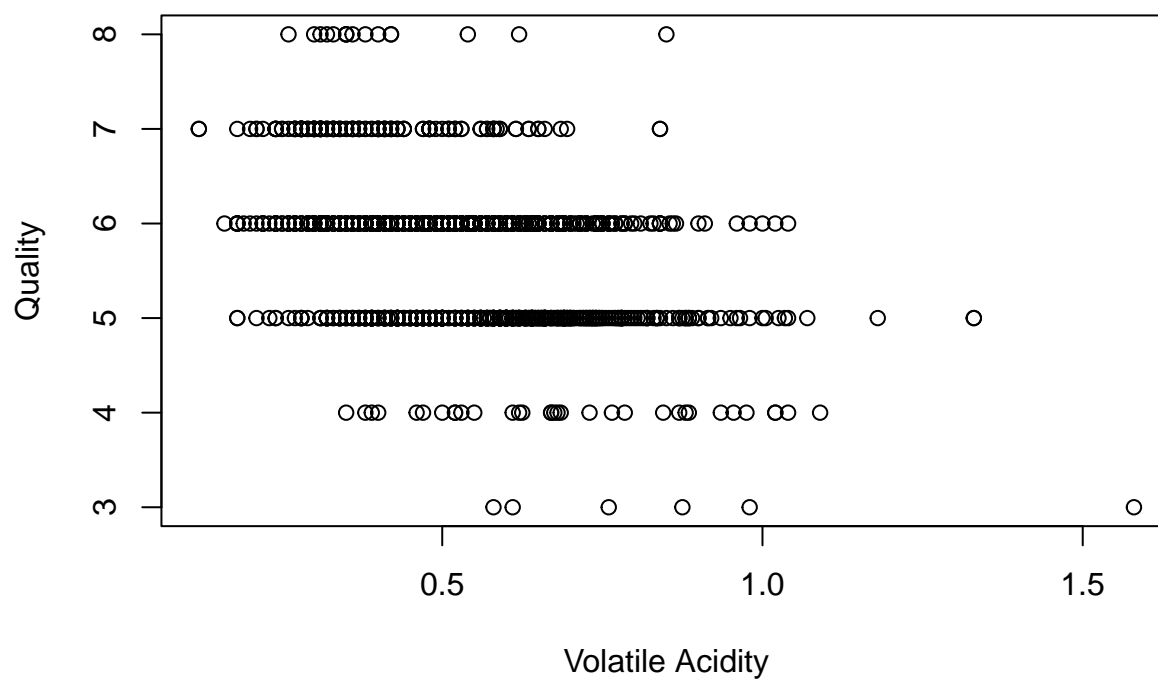
```
plot(Wine_Quality$fixed.acidity, Wine_Quality$quality, xlab="Fixed Acidity", ylab="Quality", main = "Scatter Plot of Fixed Acidity vs Quality")
```

Scatterplot of Fixed Acidity and Quality



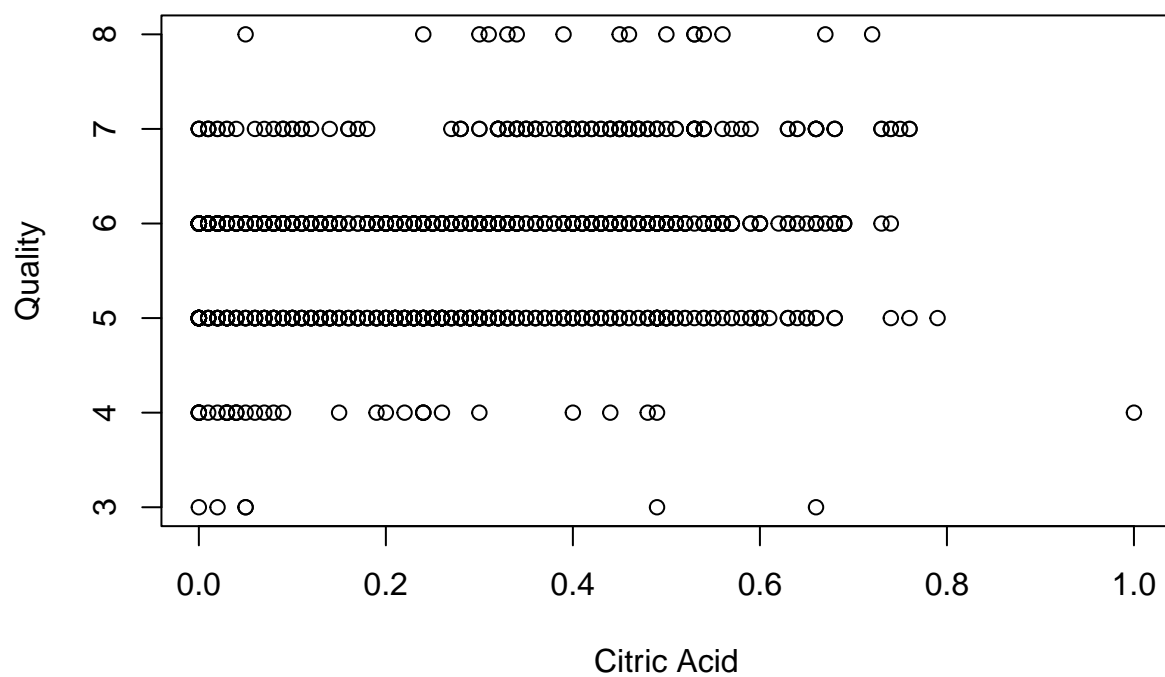
```
plot(Wine_Quality$volatile.acidity, Wine_Quality$quality, xlab="Volatile Acidity", ylab="Quality", main
```


Scatterplot of Volatile Acidity and Quality



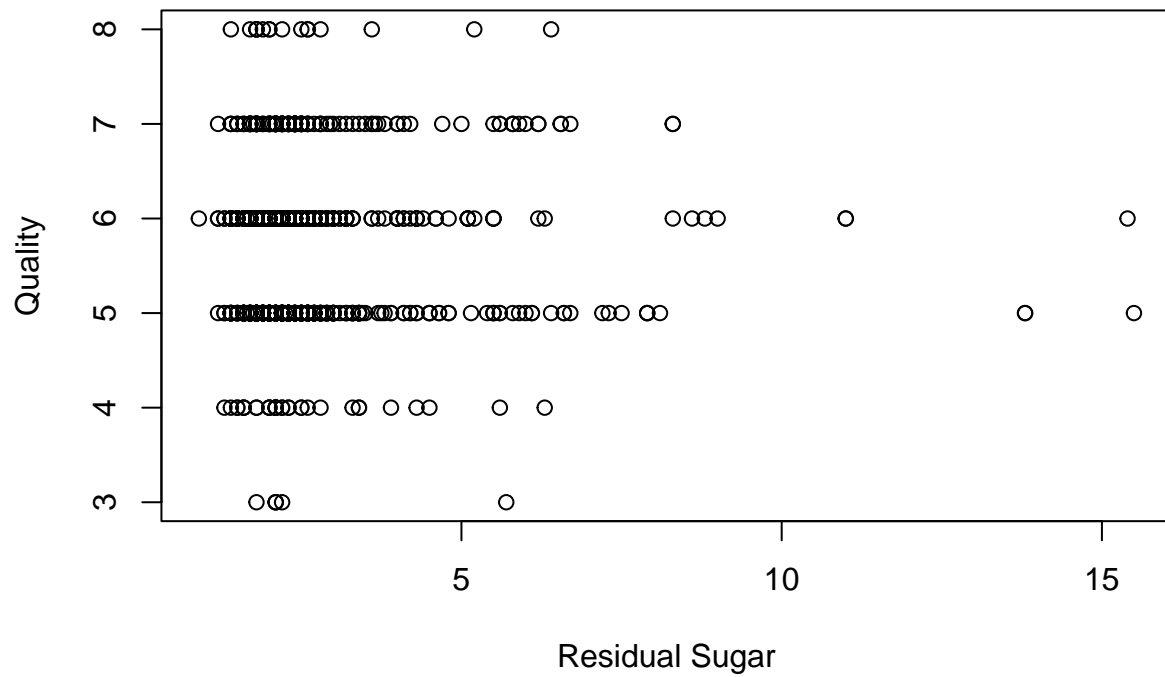
```
plot(Wine_Quality$citric.acid, Wine_Quality$quality, xlab="Citric Acid", ylab="Quality", main = "Scatterplot of Volatile Acidity and Quality")
```

Scatterplot of Citric Acid and Quality



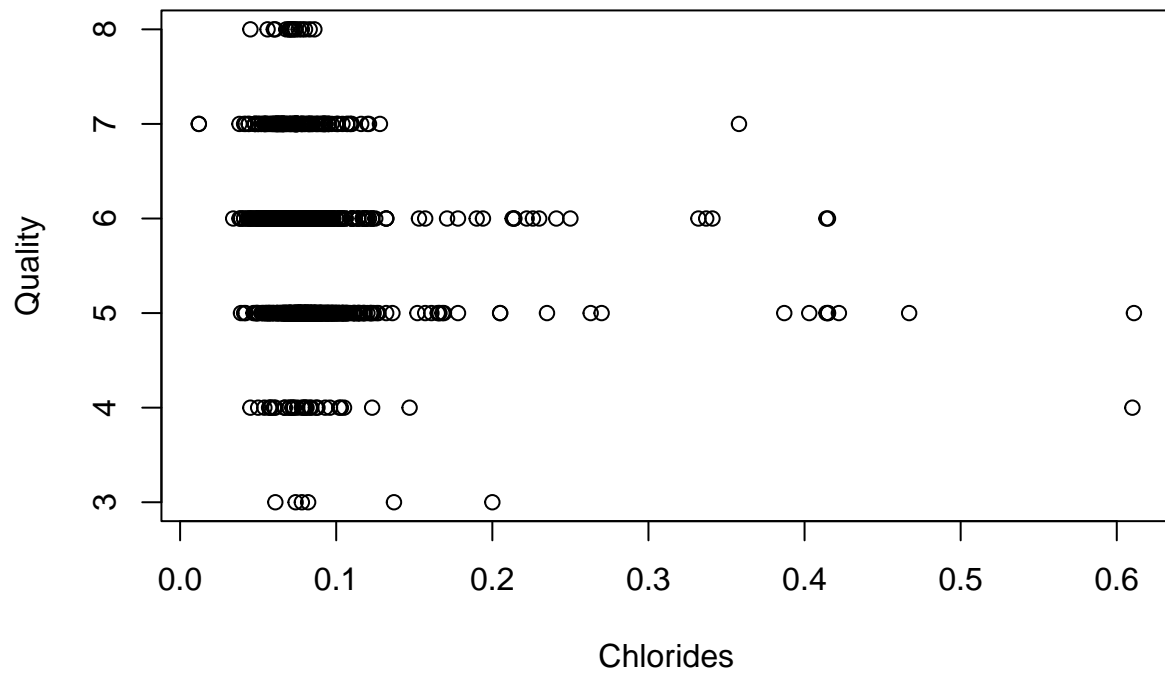
```
plot(Wine_Quality$residual.sugar, Wine_Quality$quality, xlab="Residual Sugar", ylab="Quality", main = "Residual Sugar vs Quality")
```

Scatterplot of Residual Sugar and Quality



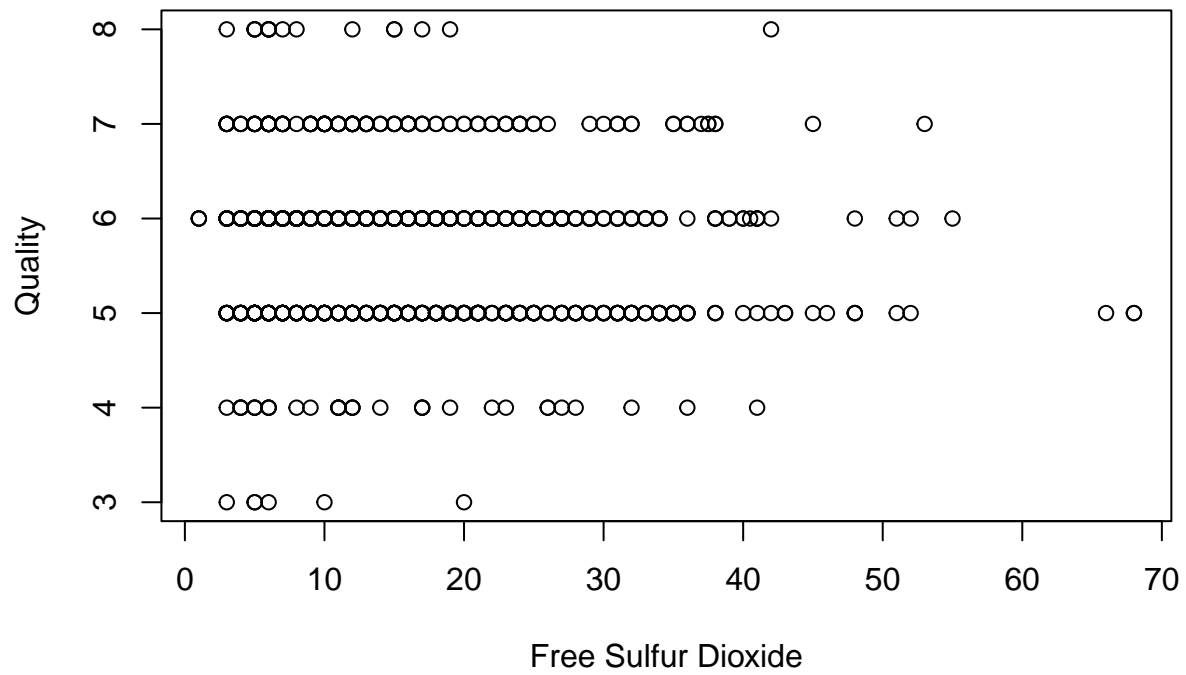
```
plot(Wine_Quality$chlorides, Wine_Quality$quality, xlab="Chlorides", ylab="Quality", main = "Scatterplot")
```

Scatterplot of Chlorides and Quality



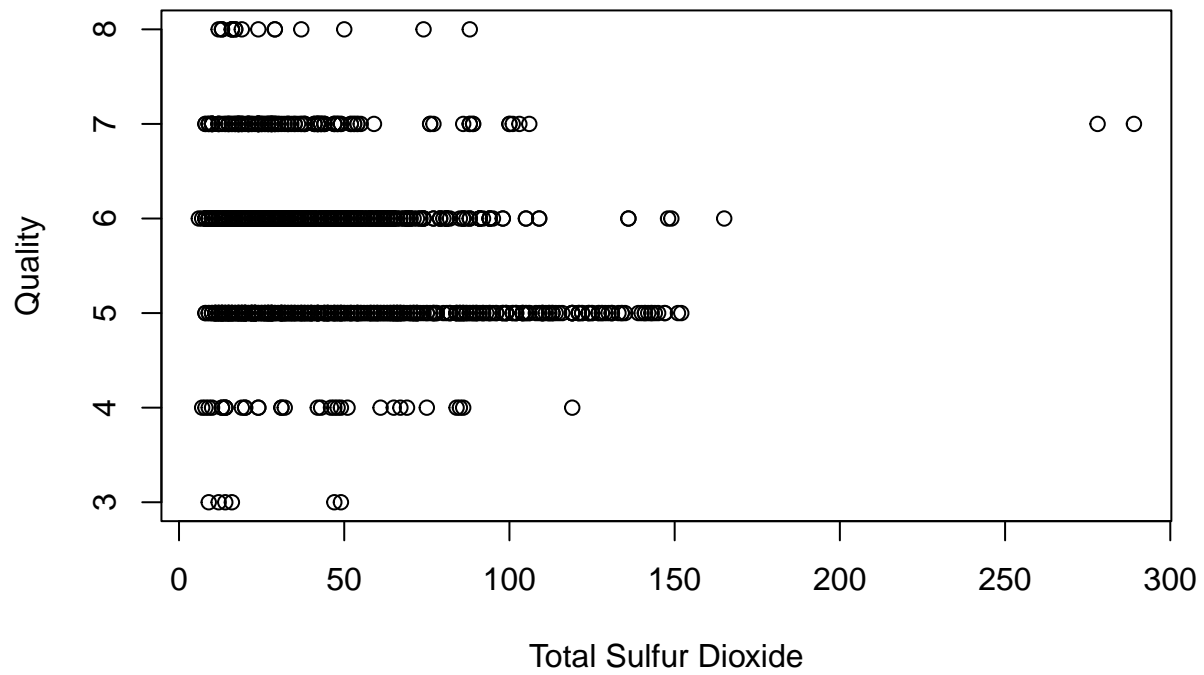
```
plot(Wine_Quality$free.sulfur.dioxide, Wine_Quality$quality, xlab="Free Sulfur Dioxide", ylab="Quality")
```

Scatterplot of Free Sulfur Dioxide and Quality



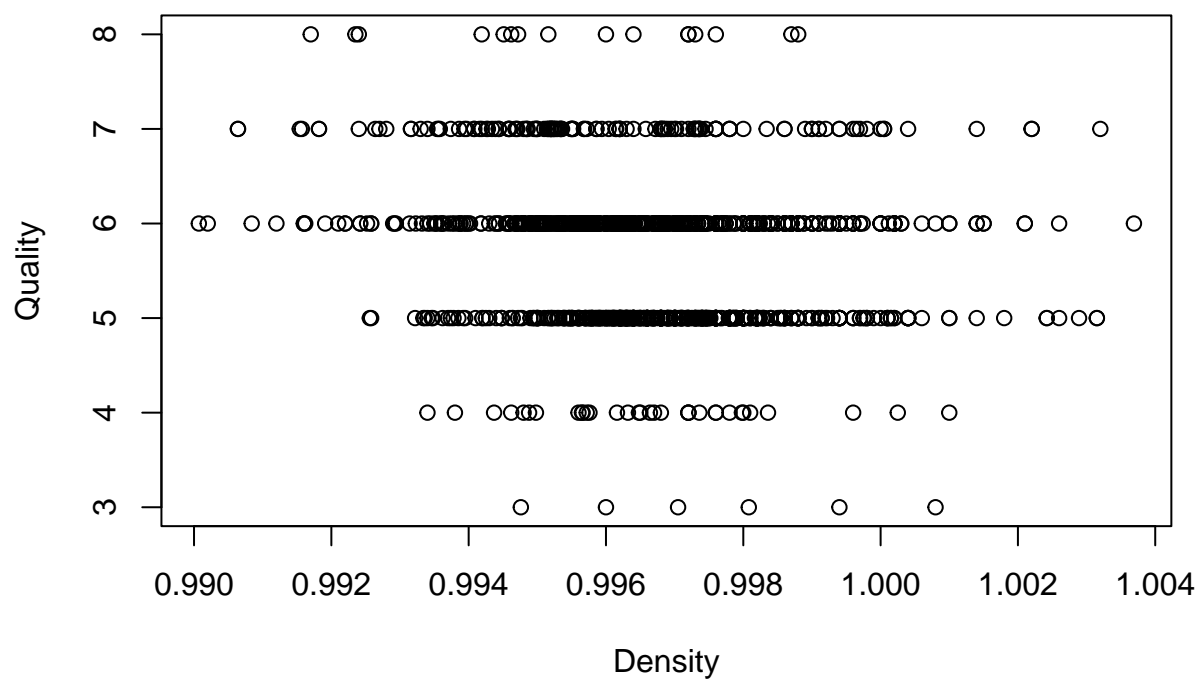
```
plot(Wine_Quality$total.sulfur.dioxide, Wine_Quality$quality, xlab="Total Sulfur Dioxide", ylab="Quality")
```

Scatterplot of Total Sulfur Dioxide and Quality

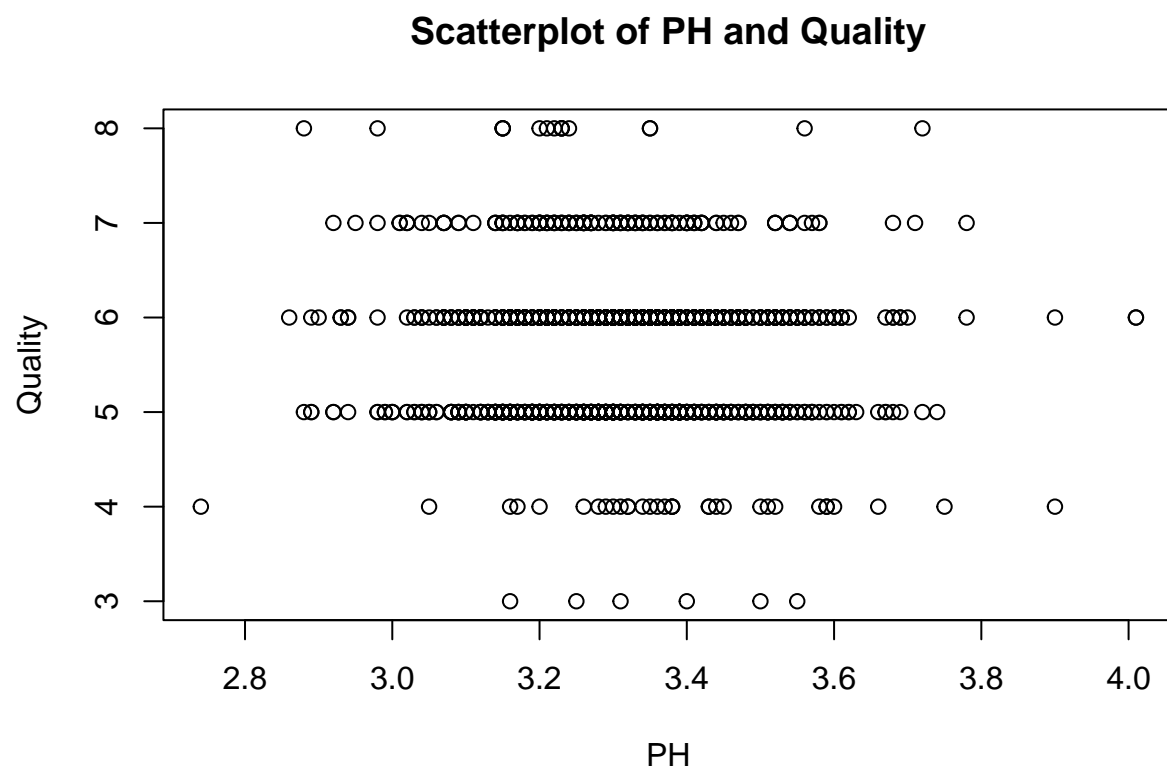


```
plot(Wine_Quality$density, Wine_Quality$quality, xlab="Density", ylab="Quality", main = "Scatterplot of
```

Scatterplot of Density and Quality

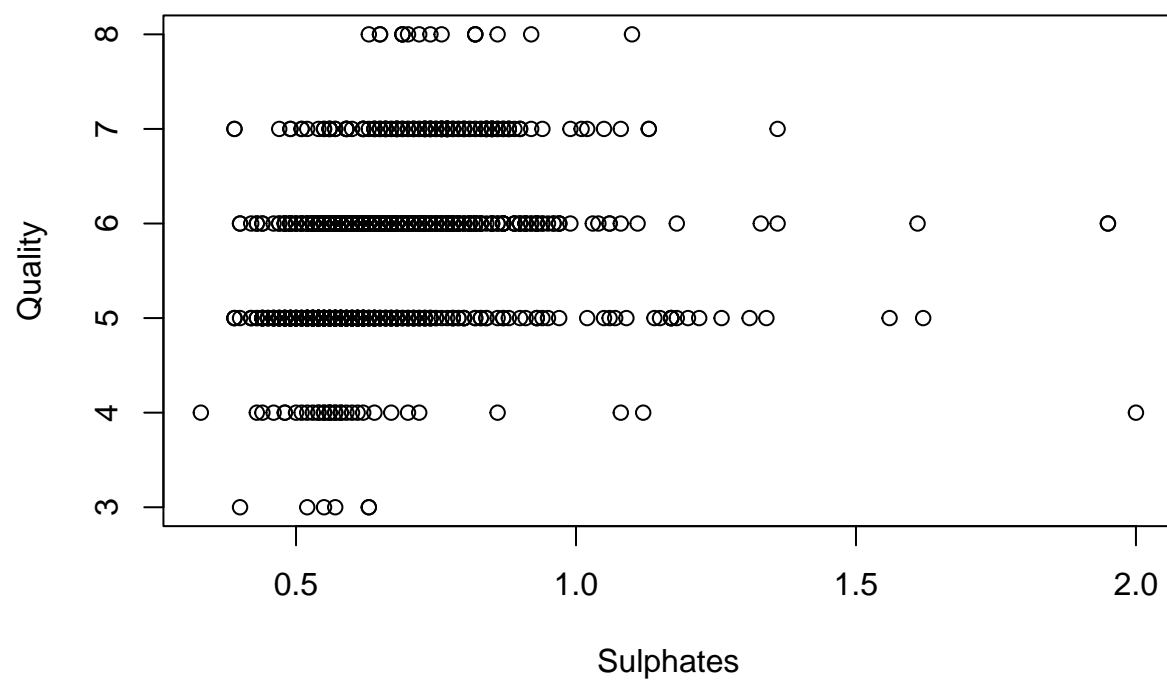


```
plot(Wine_Quality$pH, Wine_Quality$quality, xlab="PH", ylab="Quality", main = "Scatterplot of PH and Quality")
```



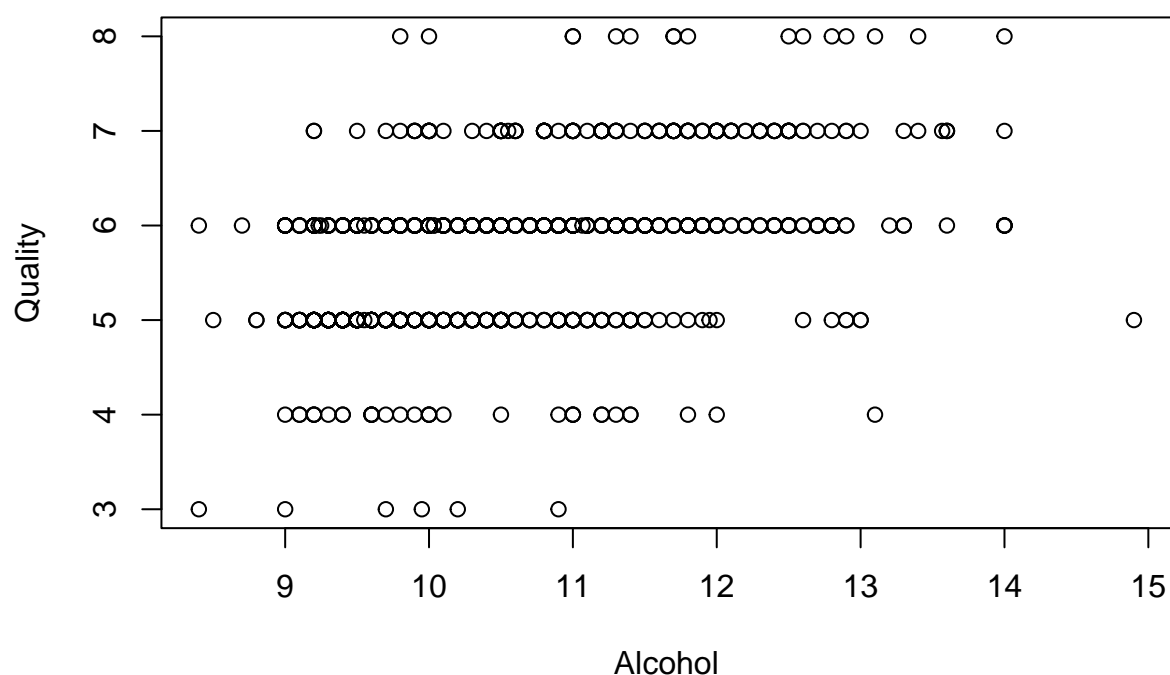
```
plot(Wine_Quality$sulphates, Wine_Quality$quality, xlab="Sulphates", ylab="Quality", main = "Scatterplot")
```


Scatterplot of Sulphates and Quality



```
plot(Wine_Quality$alcohol, Wine_Quality$quality, xlab="Alcohol", ylab="Quality", main = "Scatterplot of
```

Scatterplot of Alcohol and Quality



Statistical Summary

```
summary(Wine_Quality)
```

```
## fixed.acidity    volatile.acidity    citric.acid    residual.sugar
## Min.   : 4.600    Min.   :0.1200    Min.   :0.0000    Min.   : 0.900
## 1st Qu.: 7.100    1st Qu.:0.3925    1st Qu.:0.0900    1st Qu.: 1.900
## Median : 7.900    Median :0.5200    Median :0.2500    Median : 2.200
## Mean   : 8.311    Mean   :0.5313    Mean   :0.2684    Mean   : 2.532
## 3rd Qu.: 9.100    3rd Qu.:0.6400    3rd Qu.:0.4200    3rd Qu.: 2.600
## Max.   :15.900    Max.   :1.5800    Max.   :1.0000    Max.   :15.500
## chlorides      free.sulfur.dioxide    total.sulfur.dioxide    density
## Min.   :0.01200    Min.   : 1.00      Min.   : 6.00      Min.   :0.9901
## 1st Qu.:0.07000    1st Qu.: 7.00      1st Qu.: 21.00     1st Qu.:0.9956
## Median :0.07900    Median :13.00      Median : 37.00     Median :0.9967
## Mean   :0.08693    Mean   :15.62      Mean   : 45.91     Mean   :0.9967
## 3rd Qu.:0.09000    3rd Qu.:21.00      3rd Qu.: 61.00     3rd Qu.:0.9978
## Max.   :0.61100    Max.   :68.00      Max.   :289.00     Max.   :1.0037
## pH            sulphates            alcohol            quality
## Min.   :2.740    Min.   :0.3300    Min.   : 8.40     Min.   :3.000
## 1st Qu.:3.205    1st Qu.:0.5500    1st Qu.: 9.50     1st Qu.:5.000
## Median :3.310    Median :0.6200    Median :10.20     Median :6.000
## Mean   :3.311    Mean   :0.6577    Mean   :10.44     Mean   :5.657
## 3rd Qu.:3.400    3rd Qu.:0.7300    3rd Qu.:11.10     3rd Qu.:6.000
```

```
## Max. :4.010 Max. :2.0000 Max. :14.90 Max. :8.000
## Id
## Min. : 0
## 1st Qu.: 411
## Median : 794
## Mean : 805
## 3rd Qu.:1210
## Max. :1597
```

Question 2

Multiple Linear Regression Model

```
wineq <- lm(quality ~ fixed.acidity + volatile.acidity + citric.acid + residual.sugar + chlorides + free.sulfur.dioxide + total.sulfur.dioxide + density + pH + sulphates + alcohol, data = Wine_Quality)
summary(wineq)
```

```
##
## Call:
## lm(formula = quality ~ fixed.acidity + volatile.acidity + citric.acid +
##     residual.sugar + chlorides + free.sulfur.dioxide + total.sulfur.dioxide +
##     density + pH + sulphates + alcohol, data = Wine_Quality)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.49977 -0.36903 -0.04658  0.43956  2.00117
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.155e+01  2.477e+01   0.870  0.384551
## fixed.acidity    2.297e-02  3.025e-02   0.759  0.447770
## volatile.acidity -1.129e+00  1.407e-01  -8.023  2.56e-15 ***
## citric.acid     -1.319e-01  1.730e-01  -0.762  0.446105
## residual.sugar    1.351e-02  1.846e-02   0.732  0.464278
## chlorides       -1.708e+00  4.974e-01  -3.434  0.000616 ***
## free.sulfur.dioxide  2.369e-03  2.553e-03   0.928  0.353547
## total.sulfur.dioxide -2.785e-03  8.386e-04  -3.321  0.000926 ***
## density         -1.745e+01  2.529e+01  -0.690  0.490284
## pH              -4.082e-01  2.229e-01  -1.832  0.067280 .
## sulphates        8.752e-01  1.335e-01   6.555  8.44e-11 ***
## alcohol          2.801e-01  3.126e-02   8.963  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6405 on 1131 degrees of freedom
## Multiple R-squared:  0.3742, Adjusted R-squared:  0.3682
## F-statistic: 61.49 on 11 and 1131 DF, p-value: < 2.2e-16
```

Outlier, High Leverage, and New Model

It is evident that there are outliers and high leverage observations by the values outputted by the boxplot.stats() and hats() codes. The values derived by performing these tests confirm the outcomes of the

histogram, boxplot, scatterplot, and summary functions. These values are important because they are capable of altering the model's best-fit line.

```
# Outlier  
# uses boxplot.stats() with $out to capture outliers  
boxplot.stats(Wine_Quality$fixed.acidity)$out
```

```
## [1] 12.8 12.8 15.0 15.0 12.5 13.3 13.4 12.5 13.8 13.5 12.6 12.5 12.8 12.8 13.7  
## [16] 12.2 12.5 12.8 12.3 12.3 12.6 15.6 12.5 13.0 12.5 13.3 12.5 12.9 14.3 12.4  
## [31] 15.5 15.6 13.0 12.7 13.0 12.7 12.3 12.3 12.4 13.2 15.9 12.9 12.6 12.6
```

```
boxplot.stats(Wine_Quality$volatile.acidity)$out
```

```
## [1] 1.020 1.070 1.330 1.330 1.040 1.090 1.040 1.020 1.035 1.025 1.020 1.580  
## [13] 1.180 1.040
```

```
boxplot.stats(Wine_Quality$citric.acid)$out
```

```
## [1] 1
```

```
boxplot.stats(Wine_Quality$residual.sugar)$out
```

```
## [1] 5.50 5.90 4.65 4.65 5.50 5.50 5.50 7.30 7.20 5.60 4.00 4.00  
## [13] 4.00 4.00 6.40 5.60 5.60 11.00 11.00 4.50 4.80 5.80 5.80 6.20  
## [25] 4.20 7.90 7.90 4.50 6.70 6.60 3.70 5.20 15.50 8.30 6.55 6.55  
## [37] 6.10 4.30 5.80 5.15 6.30 4.20 4.60 4.20 4.30 4.30 7.90 5.10  
## [49] 5.60 8.60 7.50 6.00 3.90 4.20 4.00 6.60 6.00 3.80 9.00 8.80  
## [61] 5.00 3.80 4.10 5.90 4.10 6.20 4.00 3.90 4.00 8.10 6.40 8.30  
## [73] 8.30 4.70 5.50 5.50 4.30 5.50 3.70 6.20 5.60 4.60 5.80 4.10  
## [85] 4.30 4.80 6.30 4.50 4.50 4.30 3.80 5.40 6.10 5.10 5.10 3.90  
## [97] 15.40 4.80 5.20 3.75 13.80 13.80 5.70 4.30 4.10 4.10 4.40 3.70  
## [109] 6.70 5.10
```

```
boxplot.stats(Wine_Quality$chlorides)$out
```

```
## [1] 0.341 0.332 0.467 0.178 0.610 0.270 0.039 0.337 0.263 0.611 0.358 0.213  
## [13] 0.214 0.121 0.128 0.120 0.122 0.122 0.121 0.127 0.152 0.125 0.122 0.200  
## [25] 0.226 0.250 0.124 0.222 0.039 0.157 0.422 0.034 0.387 0.415 0.157 0.241  
## [37] 0.190 0.132 0.126 0.038 0.165 0.147 0.012 0.012 0.194 0.132 0.161 0.120  
## [49] 0.120 0.123 0.123 0.414 0.171 0.178 0.166 0.136 0.132 0.132 0.123 0.123  
## [61] 0.403 0.137 0.414 0.166 0.168 0.415 0.153 0.415 0.123 0.214 0.169 0.205  
## [73] 0.205 0.039 0.235 0.230 0.038
```

```
boxplot.stats(Wine_Quality$free.sulfur.dioxide)$out
```

```
## [1] 68 68 43 46 45 53 52 51 45 48 48 43 51 52 55 48 48 66
```

```
boxplot.stats(Wine_Quality$total.sulfur.dioxide)$out
```

```
## [1] 136 125 140 136 134 141 128 129 128 143 127 135 165 124 124 122 134 124 151
## [20] 142 149 147 145 148 152 122 125 127 139 143 144 130 278 289 141 133 147 131
## [39] 131 131
```

```
boxplot.stats(Wine_Quality$density)$out
```

```
## [1] 0.99160 0.99160 1.00140 1.00150 1.00150 1.00180 0.99120 1.00220 1.00220
## [10] 1.00140 1.00140 1.00320 1.00260 1.00140 1.00315 1.00315 1.00210 1.00210
## [19] 0.99170 1.00260 0.99210 0.99154 0.99064 0.99064 1.00289 0.99162 0.99007
## [28] 0.99020 0.99157 0.99084 0.99191 1.00369 1.00242 0.99182 1.00242 0.99182
```

```
boxplot.stats(Wine_Quality$pH)$out
```

```
## [1] 3.90 3.75 2.74 2.88 2.86 3.74 3.72 2.89 2.89 3.90 3.71 2.89 3.78 3.70 3.78
## [16] 4.01 2.90 4.01 2.88 3.72
```

```
boxplot.stats(Wine_Quality$sulphates)$out
```

```
## [1] 1.56 1.08 1.20 1.12 1.95 1.22 1.95 1.31 2.00 1.08 1.02 1.61 1.09 1.26 1.08
## [16] 1.36 1.13 1.04 1.11 1.13 1.07 1.06 1.06 1.05 1.02 1.14 1.36 1.05 1.17 1.62
## [31] 1.06 1.18 1.34 1.15 1.17 1.17 1.33 1.18 1.17 1.03 1.17 1.10 1.01
```

```
boxplot.stats(Wine_Quality$alcohol)$out
```

```
## [1] 14.00000 14.00000 14.00000 14.00000 14.90000 14.00000 13.60000 13.60000
## [9] 13.60000 14.00000 13.56667 13.60000
```

```
# High Leverage
# creates a dataframe named hats
# uses hatvalues to be able to see high leverage
hats <- as.data.frame(hatvalues(wineq))
hats
```

```
##      hatvalues(wineq)
## 1      0.005079901
## 2      0.008111271
## 3      0.004023940
## 4      0.007623793
## 5      0.005079901
## 6      0.005195357
## 7      0.004376642
## 8      0.006281831
## 9      0.004199146
## 10     0.004587509
## 11     0.007865355
## 12     0.039475498
## 13     0.009102351
```

## 14	0.031016001
## 15	0.007029088
## 16	0.006842187
## 17	0.007758928
## 18	0.004464620
## 19	0.006623544
## 20	0.004968706
## 21	0.003894204
## 22	0.004424527
## 23	0.004086631
## 24	0.010734583
## 25	0.012192743
## 26	0.011429170
## 27	0.005009245
## 28	0.004019111
## 29	0.013214273
## 30	0.003247586
## 31	0.033958794
## 32	0.018021960
## 33	0.023179000
## 34	0.017739270
## 35	0.006858603
## 36	0.005920293
## 37	0.006436876
## 38	0.007741004
## 39	0.006880550
## 40	0.011403010
## 41	0.002198632
## 42	0.006725434
## 43	0.007631385
## 44	0.012291719
## 45	0.002939521
## 46	0.008984319
## 47	0.008984319
## 48	0.005352136
## 49	0.009143397
## 50	0.005917860
## 51	0.003420589
## 52	0.014484615
## 53	0.005104983
## 54	0.005348206
## 55	0.018567518
## 56	0.007867479
## 57	0.008761552
## 58	0.010479424
## 59	0.002094741
## 60	0.081831903
## 61	0.003620478
## 62	0.017934258
## 63	0.005626477
## 64	0.011034703
## 65	0.081831903
## 66	0.003620478
## 67	0.026058577

## 68	0.004965231
## 69	0.006924950
## 70	0.003190962
## 71	0.002627188
## 72	0.003190962
## 73	0.004031028
## 74	0.005401992
## 75	0.004031028
## 76	0.062431247
## 77	0.009445839
## 78	0.006613036
## 79	0.013188200
## 80	0.005808918
## 81	0.006613036
## 82	0.005807121
## 83	0.002636436
## 84	0.017216599
## 85	0.010090365
## 86	0.006487944
## 87	0.009381146
## 88	0.025899899
## 89	0.025814195
## 90	0.008154838
## 91	0.017073414
## 92	0.016196634
## 93	0.011667638
## 94	0.006802741
## 95	0.007359562
## 96	0.006802741
## 97	0.019198679
## 98	0.007868277
## 99	0.019198679
## 100	0.016013518
## 101	0.008720091
## 102	0.002624015
## 103	0.008817519
## 104	0.133177620
## 105	0.009118347
## 106	0.009118347
## 107	0.012727589
## 108	0.012756503
## 109	0.012727589
## 110	0.004855619
## 111	0.009480488
## 112	0.009656767
## 113	0.018813497
## 114	0.003852312
## 115	0.018054168
## 116	0.017540038
## 117	0.010572574
## 118	0.006444366
## 119	0.006811906
## 120	0.003491123
## 121	0.008754605

## 122	0.004811525
## 123	0.006578860
## 124	0.005091483
## 125	0.005738819
## 126	0.009100582
## 127	0.005299619
## 128	0.003903896
## 129	0.003903896
## 130	0.019719613
## 131	0.003667121
## 132	0.006932116
## 133	0.007178859
## 134	0.008580822
## 135	0.008959370
## 136	0.016851147
## 137	0.008874103
## 138	0.008743930
## 139	0.003114941
## 140	0.003114941
## 141	0.003397219
## 142	0.010101226
## 143	0.014083877
## 144	0.005132741
## 145	0.006620674
## 146	0.010819629
## 147	0.010819629
## 148	0.005353649
## 149	0.012565433
## 150	0.003784830
## 151	0.004905335
## 152	0.005009256
## 153	0.015115312
## 154	0.006786415
## 155	0.006552290
## 156	0.004272601
## 157	0.005587752
## 158	0.005362801
## 159	0.006347747
## 160	0.003965990
## 161	0.003260961
## 162	0.047373878
## 163	0.013709180
## 164	0.008068169
## 165	0.004527924
## 166	0.012228389
## 167	0.004337255
## 168	0.020350076
## 169	0.006367275
## 170	0.012445977
## 171	0.038927348
## 172	0.038927348
## 173	0.013354946
## 174	0.002880585
## 175	0.013354946

## 176	0.005447317
## 177	0.004486328
## 178	0.005743384
## 179	0.013168467
## 180	0.009846312
## 181	0.005307292
## 182	0.005441965
## 183	0.118854325
## 184	0.006671231
## 185	0.004892508
## 186	0.009623948
## 187	0.005224927
## 188	0.004748625
## 189	0.010272145
## 190	0.013920363
## 191	0.015867654
## 192	0.016450816
## 193	0.015948092
## 194	0.005741738
## 195	0.005741738
## 196	0.016450816
## 197	0.015948092
## 198	0.014611609
## 199	0.008730115
## 200	0.013429971
## 201	0.039029734
## 202	0.008730115
## 203	0.012499295
## 204	0.012499295
## 205	0.008724965
## 206	0.005379783
## 207	0.006233517
## 208	0.012040431
## 209	0.006233517
## 210	0.006000866
## 211	0.005537018
## 212	0.010874625
## 213	0.008722790
## 214	0.009601031
## 215	0.010585386
## 216	0.013886143
## 217	0.003703577
## 218	0.010377901
## 219	0.007113945
## 220	0.014361988
## 221	0.005800270
## 222	0.013157968
## 223	0.012623822
## 224	0.008455737
## 225	0.006137896
## 226	0.009964636
## 227	0.004332168
## 228	0.007314865
## 229	0.007856334

## 230	0.006368845
## 231	0.045802556
## 232	0.045802556
## 233	0.008834126
## 234	0.006942294
## 235	0.014390546
## 236	0.009720319
## 237	0.007599918
## 238	0.012673264
## 239	0.006153202
## 240	0.005348831
## 241	0.026551003
## 242	0.009479648
## 243	0.009479648
## 244	0.009438034
## 245	0.015746980
## 246	0.005781693
## 247	0.009408379
## 248	0.006095757
## 249	0.028558323
## 250	0.026248601
## 251	0.011641691
## 252	0.010141486
## 253	0.006726683
## 254	0.006654301
## 255	0.008701215
## 256	0.005024658
## 257	0.004753529
## 258	0.009562148
## 259	0.010455555
## 260	0.013921791
## 261	0.013921791
## 262	0.011758921
## 263	0.011547039
## 264	0.013992321
## 265	0.010405945
## 266	0.012926691
## 267	0.011547039
## 268	0.023843261
## 269	0.006974247
## 270	0.004847490
## 271	0.005092769
## 272	0.020007777
## 273	0.010750765
## 274	0.006550467
## 275	0.023650110
## 276	0.039783183
## 277	0.006765622
## 278	0.007956123
## 279	0.039783183
## 280	0.007861485
## 281	0.005216551
## 282	0.005167776
## 283	0.003596048

## 284	0.006890454
## 285	0.021423679
## 286	0.005482052
## 287	0.004727162
## 288	0.013054666
## 289	0.007306184
## 290	0.023402575
## 291	0.007871348
## 292	0.010072335
## 293	0.007953246
## 294	0.011574141
## 295	0.012706800
## 296	0.010430451
## 297	0.006622259
## 298	0.012706800
## 299	0.003944442
## 300	0.008553293
## 301	0.003698456
## 302	0.017075068
## 303	0.006622259
## 304	0.005273926
## 305	0.010108172
## 306	0.007040437
## 307	0.010108172
## 308	0.011261060
## 309	0.009360822
## 310	0.011490732
## 311	0.011537910
## 312	0.025358646
## 313	0.010417620
## 314	0.010046370
## 315	0.004379162
## 316	0.003219880
## 317	0.008076105
## 318	0.008076105
## 319	0.004270310
## 320	0.011048877
## 321	0.007651280
## 322	0.019567842
## 323	0.005388295
## 324	0.004917417
## 325	0.013032216
## 326	0.005976044
## 327	0.004078504
## 328	0.007996837
## 329	0.008754485
## 330	0.012433077
## 331	0.009526742
## 332	0.016791331
## 333	0.008973606
## 334	0.004982638
## 335	0.009640338
## 336	0.007973323
## 337	0.004951452

## 338	0.009118691
## 339	0.006120230
## 340	0.106565971
## 341	0.007306222
## 342	0.009940647
## 343	0.006553434
## 344	0.006943406
## 345	0.003293674
## 346	0.008400204
## 347	0.010253720
## 348	0.020589839
## 349	0.024727263
## 350	0.004409090
## 351	0.004947392
## 352	0.013087617
## 353	0.004409090
## 354	0.020589839
## 355	0.004947392
## 356	0.020551793
## 357	0.020551793
## 358	0.009875256
## 359	0.009846301
## 360	0.008868427
## 361	0.009615620
## 362	0.012181753
## 363	0.008574148
## 364	0.004609210
## 365	0.009893982
## 366	0.009893982
## 367	0.025941965
## 368	0.013859403
## 369	0.011810765
## 370	0.010962999
## 371	0.012043933
## 372	0.007779451
## 373	0.010138358
## 374	0.005522090
## 375	0.013897454
## 376	0.007779723
## 377	0.007779723
## 378	0.014623105
## 379	0.008180976
## 380	0.013897454
## 381	0.005522090
## 382	0.007608308
## 383	0.019157753
## 384	0.012549933
## 385	0.002669846
## 386	0.012289740
## 387	0.005982028
## 388	0.012811628
## 389	0.018746333
## 390	0.011146179
## 391	0.005947660

## 392	0.005432180
## 393	0.009596262
## 394	0.005086123
## 395	0.003389547
## 396	0.004417586
## 397	0.030825023
## 398	0.025866299
## 399	0.019690144
## 400	0.026132260
## 401	0.029248156
## 402	0.010039624
## 403	0.012731858
## 404	0.007694591
## 405	0.029248156
## 406	0.010039624
## 407	0.013477930
## 408	0.017124899
## 409	0.006930447
## 410	0.009566124
## 411	0.004912524
## 412	0.006744248
## 413	0.008704061
## 414	0.008420771
## 415	0.006231876
## 416	0.010115137
## 417	0.010115137
## 418	0.009559295
## 419	0.006806976
## 420	0.015828703
## 421	0.005841226
## 422	0.025544368
## 423	0.005841226
## 424	0.009191441
## 425	0.018638090
## 426	0.008576398
## 427	0.003954989
## 428	0.006229862
## 429	0.006010567
## 430	0.005674210
## 431	0.019888309
## 432	0.013569976
## 433	0.011202074
## 434	0.010302514
## 435	0.003932326
## 436	0.013615173
## 437	0.008909637
## 438	0.007270941
## 439	0.008210024
## 440	0.007443318
## 441	0.004748573
## 442	0.015410233
## 443	0.005628613
## 444	0.005628613
## 445	0.002867840

## 446	0.004271219
## 447	0.002867840
## 448	0.007069472
## 449	0.004140436
## 450	0.023923626
## 451	0.012181585
## 452	0.012794476
## 453	0.016363669
## 454	0.015786810
## 455	0.022727770
## 456	0.007195552
## 457	0.007195552
## 458	0.007195552
## 459	0.006907687
## 460	0.001791692
## 461	0.037970561
## 462	0.013166343
## 463	0.064431145
## 464	0.017399250
## 465	0.013168482
## 466	0.012250051
## 467	0.013166343
## 468	0.012702911
## 469	0.008022115
## 470	0.008022115
## 471	0.006411230
## 472	0.004665163
## 473	0.007553608
## 474	0.014709885
## 475	0.008890054
## 476	0.008890054
## 477	0.006281198
## 478	0.006281198
## 479	0.005332526
## 480	0.004426889
## 481	0.013874626
## 482	0.011200291
## 483	0.004629409
## 484	0.006649564
## 485	0.006866976
## 486	0.021461370
## 487	0.006866976
## 488	0.006273689
## 489	0.010854356
## 490	0.014800555
## 491	0.047290280
## 492	0.009511356
## 493	0.009359931
## 494	0.021617918
## 495	0.004578662
## 496	0.006762835
## 497	0.005876937
## 498	0.018529768
## 499	0.004578662

## 500	0.004729266
## 501	0.007112874
## 502	0.005939253
## 503	0.015524387
## 504	0.004577662
## 505	0.002813320
## 506	0.004385304
## 507	0.018084401
## 508	0.011204375
## 509	0.005966568
## 510	0.006388212
## 511	0.007729637
## 512	0.005196377
## 513	0.007729637
## 514	0.009955767
## 515	0.062110237
## 516	0.003325647
## 517	0.014533859
## 518	0.006651515
## 519	0.006651515
## 520	0.012517657
## 521	0.046096151
## 522	0.014948332
## 523	0.004961432
## 524	0.008680905
## 525	0.005776592
## 526	0.008964746
## 527	0.012297773
## 528	0.006784455
## 529	0.008975675
## 530	0.011444870
## 531	0.010515204
## 532	0.005503159
## 533	0.007021380
## 534	0.005101395
## 535	0.005503159
## 536	0.003212240
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## Warning in xtfrm.data.frame(x): cannot xtfrm data frames

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## [313] 0.005517165 0.005519616 0.005522090 0.005522090 0.005529905 0.005537018
## [319] 0.005537560 0.005545873 0.005546230 0.005558538 0.005562992 0.005562992

```

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 ## [625] 0.008242147 0.008266779 0.008319370 0.008340855 0.008340855 0.008351917
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 ## [637] 0.008455737 0.008471542 0.008493557 0.008498004 0.008553293 0.008564196
 ## [643] 0.008564196 0.008572701 0.008574148 0.008576398 0.008580822 0.008599023

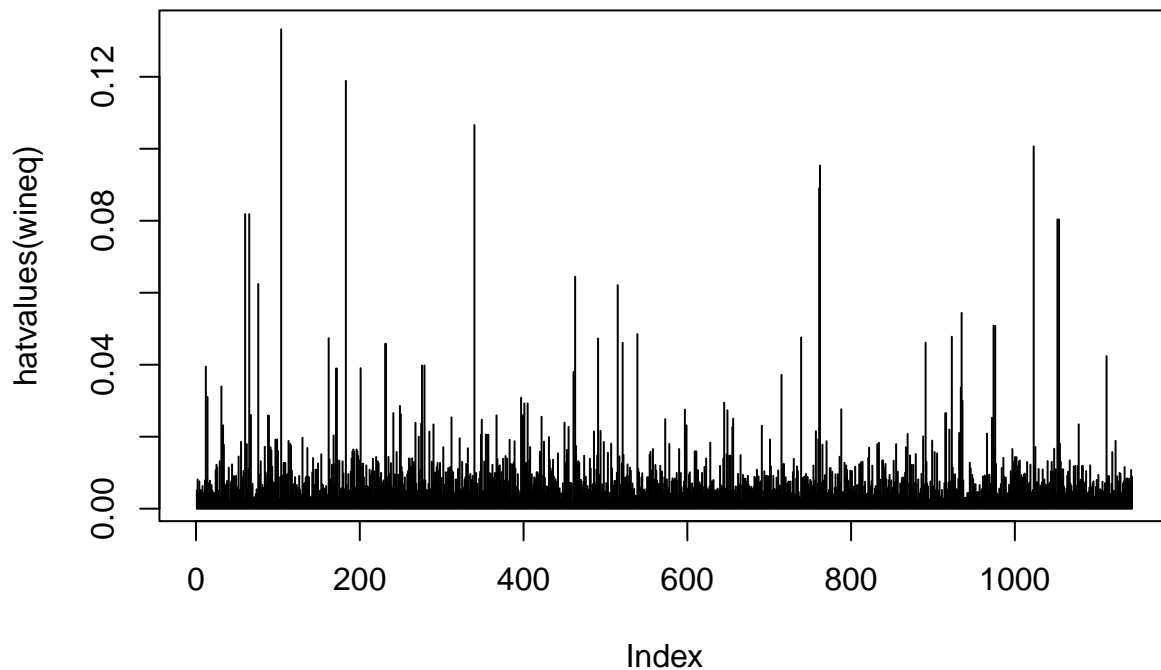
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## [967] 0.014153490 0.014296550 0.014300420 0.014300420 0.014336139 0.014361988

```

```
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## [1111] 0.037970561 0.038927348 0.038927348 0.039029734 0.039475498 0.039783183
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## [1123] 0.047290280 0.047373878 0.047571012 0.047768638 0.048494966 0.050782777
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## [1135] 0.080368069 0.081831903 0.081831903 0.089029480 0.095333756 0.100657718
## [1141] 0.106565971 0.118854325 0.133177620
```

```
plot(hatvalues(wineq), type = 'h')
```



New Regression Model

```
wineq2 <- lm(quality ~ volatile.acidity + chlorides + free.sulfur.dioxide + total.sulfur.dioxide + pH +
summary(wineq2)
```

```
##
## Call:
## lm(formula = quality ~ volatile.acidity + chlorides + free.sulfur.dioxide +
##     total.sulfur.dioxide + pH + sulphates + alcohol, data = Wine_Quality)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.39463 -0.36932 -0.04649  0.44290  2.00640
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.466534   0.461804   9.672 < 2e-16 ***
## volatile.acidity -1.082354   0.117570  -9.206 < 2e-16 ***
## chlorides      -1.837430   0.465909  -3.944 8.51e-05 ***
## free.sulfur.dioxide  0.002845   0.002510   1.134 0.257199
## total.sulfur.dioxide -0.002937   0.000796  -3.689 0.000236 ***
## pH              -0.485507   0.135380  -3.586 0.000350 ***
## sulphates       0.845081   0.128332   6.585 6.93e-11 ***
## alcohol         0.293758   0.019382  15.156 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 0.6398 on 1135 degrees of freedom
## Multiple R-squared:  0.3736, Adjusted R-squared:  0.3697
## F-statistic: 96.69 on 7 and 1135 DF,  p-value: < 2.2e-16
```

Boruta Algorithm, Mallows CP

First, the Boruta Algorithm is applied to filter out which response variables were insignificant before also conducting the Mallows CP test. The Boruta Algorithm shows alcohol is the best variable, as it had the highest importance. Also, this test allows the report “rejected” on some variables which means they are insignificant and they can be eliminated. Next, with the results of the significant variables from the Boruta algorithm, the Mallows CP test is run. Here, the smaller the value, the better the model. Evidently, the best model had the predictors volatile acidity, chlorides, total sulfur dioxide, sulphates, and alcohol. The models to the right of the model are higher and therefore, insignificant.

```
library(Boruta)
Bor.res <- Boruta(quality ~ volatile.acidity + chlorides + free.sulfur.dioxide + total.sulfur.dioxide +

## 1. run of importance source...

## 2. run of importance source...

## 3. run of importance source...

## 4. run of importance source...

## 5. run of importance source...

## 6. run of importance source...

## 7. run of importance source...

## 8. run of importance source...

## 9. run of importance source...

## 10. run of importance source...

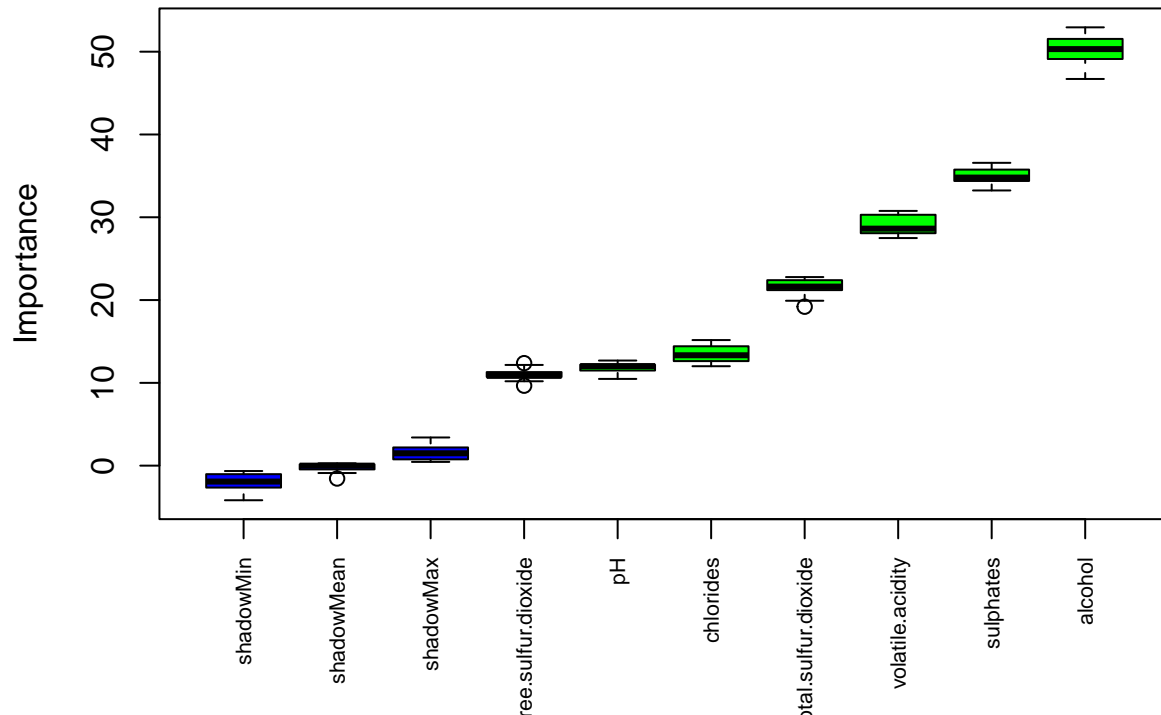
## After 10 iterations, +9.3 secs:

## confirmed 7 attributes: alcohol, chlorides, free.sulfur.dioxide, pH, sulphates and 2 more;

## no more attributes left.

plot(Bor.res, xlab = "", xaxt = "n", main="Boruta Algorithm")
Lz <- lapply(1:ncol(Bor.res$ImpHistory),function(i) Bor.res$ImpHistory[is.finite(Bor.res$ImpHistory[,i]),
names(Lz) <- colnames(Bor.res$ImpHistory)
Labels <- sort(sapply(Lz,median))
axis(side = 1,las=2,labels = names(Labels),
at = 1:ncol(Bor.res$ImpHistory), cex.axis = 0.7)
```


Boruta Algorithm



```
boruta_signif <- names(Bor.res$finalDecision[Bor.res$finalDecision %in% c("Confirmed", "Tentative")])
boruta_signif_Conf <- names(Bor.res$finalDecision[Bor.res$finalDecision %in% c("Confirmed")])
boruta_signif_Tent <- names(Bor.res$finalDecision[Bor.res$finalDecision %in% c("Tentative")])
boruta_signif_Reject <- names(Bor.res$finalDecision[Bor.res$finalDecision %in% c("Rejected")])
print(boruta_signif_Conf)
```

```
## [1] "alcohol"          "sulphates"        "pH"
## [4] "total.sulfur.dioxide" "free.sulfur.dioxide" "chlorides"
## [7] "volatile.acidity"
```

```
attStats(Bor.res)
```

```
##           meanImp medianImp   minImp   maxImp normHits decision
## alcohol      50.21424  50.31270 46.704855 52.94055         1 Confirmed
## sulphates    34.90733  34.79388 33.239216 36.57690         1 Confirmed
## pH           11.81983  12.02327 10.476230 12.69449         1 Confirmed
## total.sulfur.dioxide 21.49372  21.62699 19.198927 22.77689         1 Confirmed
## free.sulfur.dioxide 11.00015  10.84284  9.656997 12.37755         1 Confirmed
## chlorides     13.48343  13.33111 12.009345 15.16746         1 Confirmed
## volatile.acidity  29.03553  28.62633 27.489466 30.76679         1 Confirmed
```

```
sorted_vars = attStats(Bor.res)[order(-attStats(Bor.res)$meanImp),]
print(sorted_vars)
```

	meanImp	medianImp	minImp	maxImp	normHits	decision
alcohol	50.21424	50.31270	46.704855	52.94055	1	Confirmed
sulphates	34.90733	34.79388	33.239216	36.57690	1	Confirmed
volatile.acidity	29.03553	28.62633	27.489466	30.76679	1	Confirmed
total.sulfur.dioxide	21.49372	21.62699	19.198927	22.77689	1	Confirmed
chlorides	13.48343	13.33111	12.009345	15.16746	1	Confirmed
pH	11.81983	12.02327	10.476230	12.69449	1	Confirmed
free.sulfur.dioxide	11.00015	10.84284	9.656997	12.37755	1	Confirmed

```
#mallowscp
library(AER)
```

```
## Loading required package: car
```

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

```
## Loading required package: lmtest
```

```
## Loading required package: zoo
```

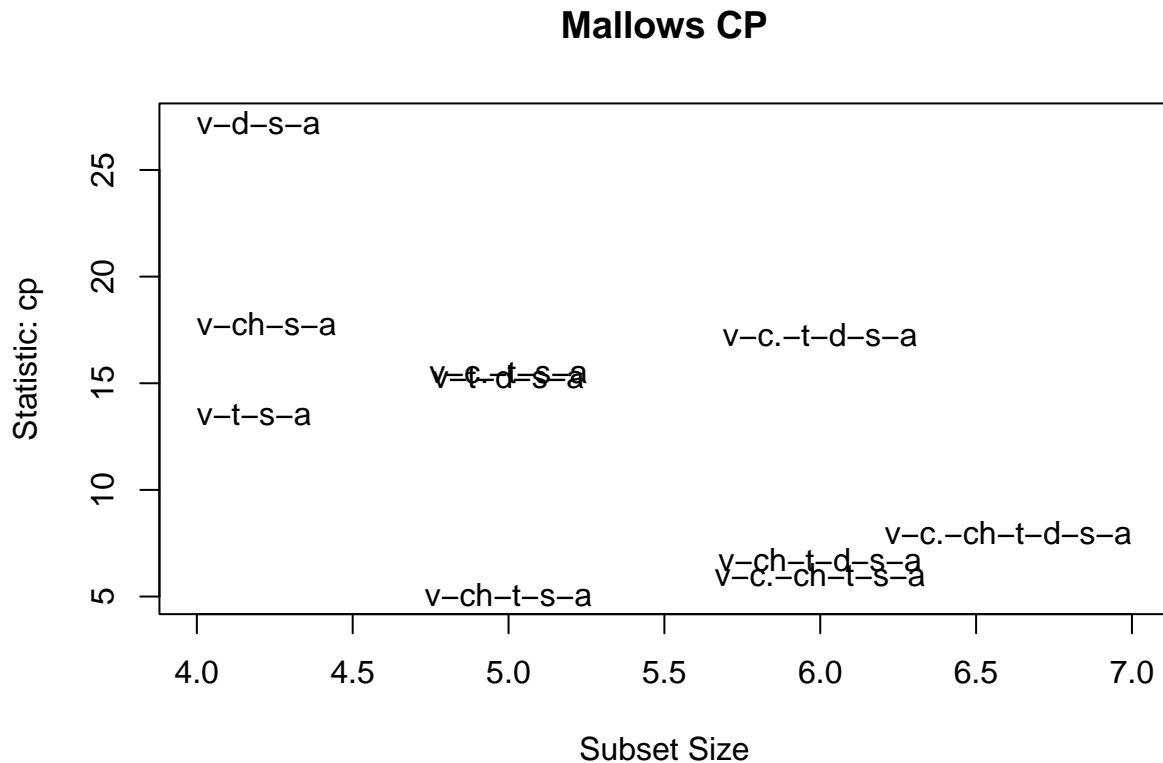
```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##   as.Date, as.Date.numeric
```

```
## Loading required package: sandwich
```

```
## Loading required package: survival
```

```
library(leaps)
mcp <- lm(quality ~ volatile.acidity + citric.acid + chlorides + total.sulfur.dioxide + density + sulphates)
ss =regsubsets(quality ~ volatile.acidity + citric.acid + chlorides + total.sulfur.dioxide + density + sulphates,
subsets(ss, statistic = "cp", legend =F , main = "Mallovs CP", col = "green", min.size = 4)
```



```
##                               Abbreviation
## volatile.acidity              v
## citric.acid                   c.
## chlorides                     ch
## total.sulfur.dioxide          t
## density                       d
## sulphates                     s
## alcohol                       a
```

Question 5

Multi Collinearity with VIF

With the output for the `vif()`, all of the predictor variables are in the range of $[1,2]$. This means there are no variables that are highly correlated with another. Therefore the model with the removed variables won't have significant issues with multicollinearity.

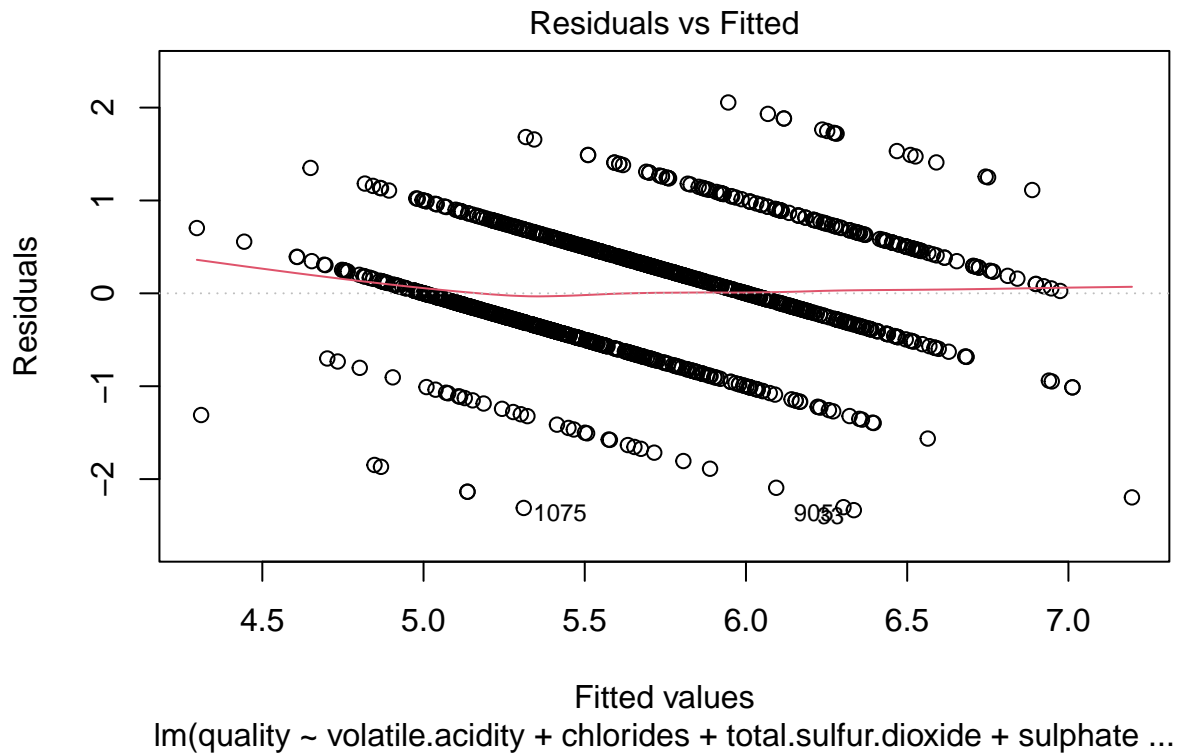
```
# Multi Collinearity
vifFunction<- lm(quality ~ volatile.acidity + chlorides + total.sulfur.dioxide + sulphates + alcohol,
vif(vifFunction))
```

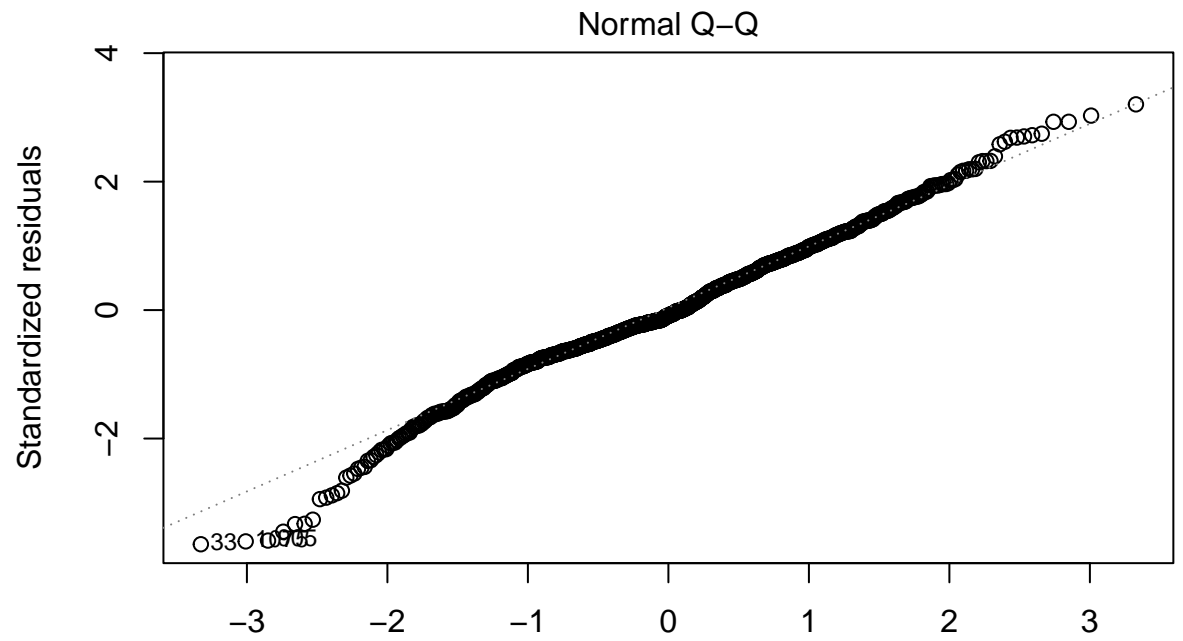
```
##      volatile.acidity      chlorides total.sulfur.dioxide
##           1.145466           1.291971           1.042551
##           sulphates           alcohol
##           1.331226           1.159650
```

Plotting The Respective Residuals

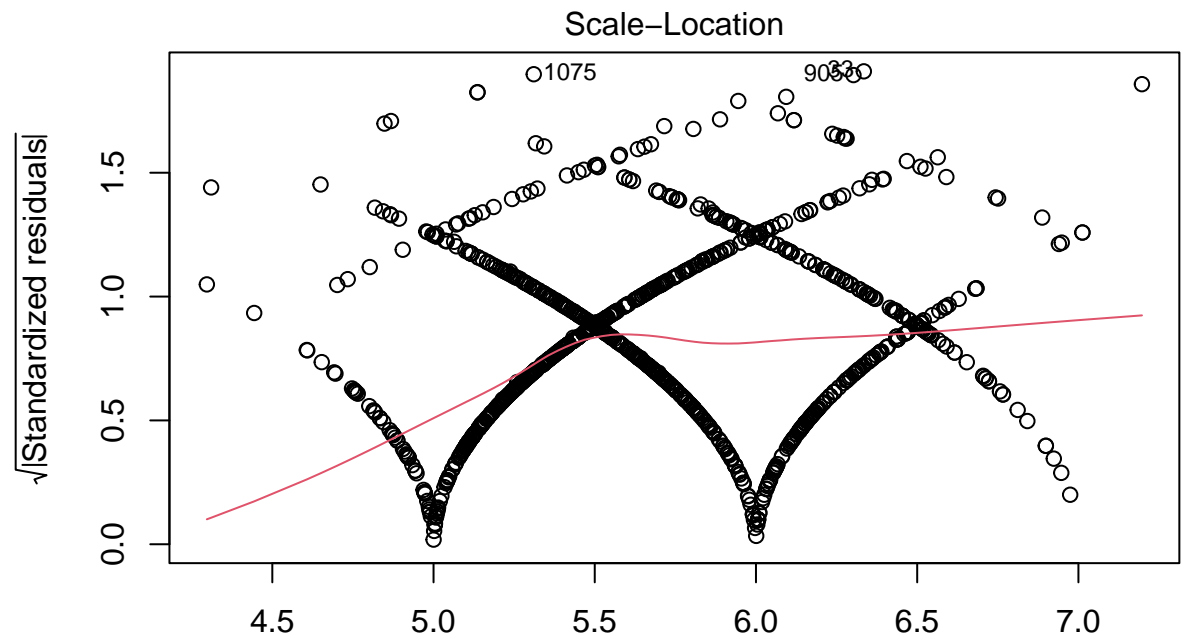
The graph with residuals versus fitted shows a red line that tries to capture all of the residuals. There are more values that are above the red line than below the red line. The residuals vs y-hat plot visualize whether heteroskedasticity is present. The results show that there is a spread in the variance, so it is present.

```
# Plotting Respective Residuals/VIF Function  
plot(vifFunction)
```

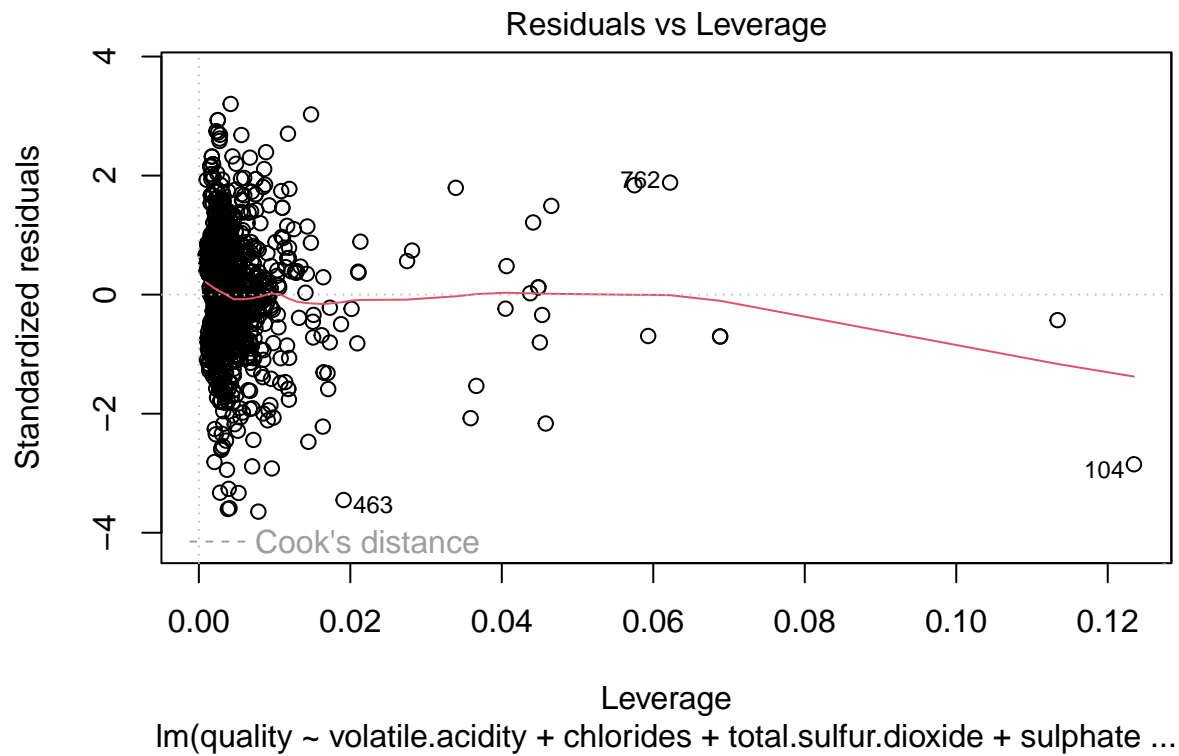




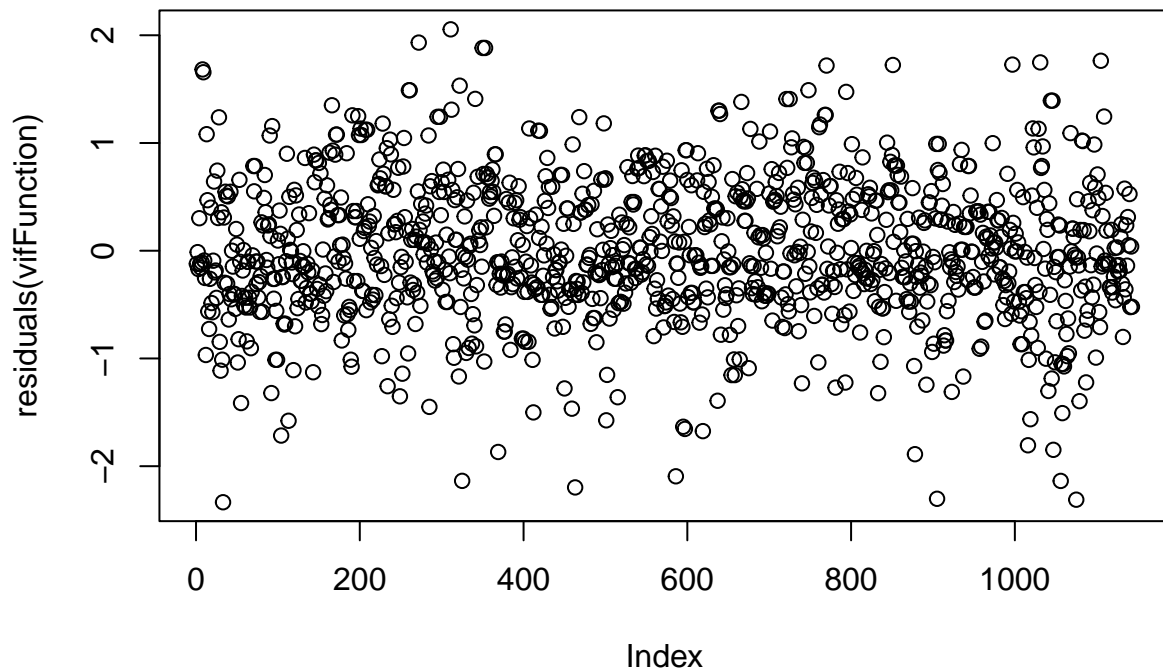
lm(quality ~ volatile.acidity + chlorides + total.sulfur.dioxide + sulphate ...



lm(quality ~ volatile.acidity + chlorides + total.sulfur.dioxide + sulphate ...



```
# Just to see more of the actual residuals  
plot(residuals(vifFunction))
```



Heteroskedasticity

Using the Breusch Pagan test, it is confirmed heteroskedasticity is present. The robust standard errors fix this. With this, all of the variables are significant and the standard errors decreased resulting in a better model.

```
reg.mod = lm(quality ~ volatile.acidity + chlorides + total.sulfur.dioxide + sulphates + alcohol, data = W)
# BP Test Short Way
bptest(reg.mod)
```

```
##
## studentized Breusch-Pagan test
##
## data: reg.mod
## BP = 35.162, df = 5, p-value = 1.397e-06
```

```
# BP Test Long Way
alpha <- 0.05
ressq <- resid(reg.mod)^2
modres <- lm(ressq~volatile.acidity + chlorides + total.sulfur.dioxide + sulphates + alcohol, data = W)
summary(modres)
```

```
##
## Call:
```



```
## lm(formula = ressq ~ volatile.acidity + chlorides + total.sulfur.dioxide +
##     sulphates + alcohol, data = Wine_Quality)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.7400 -0.3492 -0.2046  0.0790  4.8907
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.6402296   0.2461118   -2.601  0.00941 **
## volatile.acidity    0.1707468   0.1183714    1.442  0.14945
## chlorides       -0.2438618   0.4777576   -0.510  0.60985
## total.sulfur.dioxide -0.0014706   0.0006188   -2.377  0.01764 *
## sulphates        0.3664716   0.1345247    2.724  0.00654 **
## alcohol          0.0774116   0.0197697    3.916 9.55e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6714 on 1137 degrees of freedom
## Multiple R-squared:  0.03076,    Adjusted R-squared:  0.0265
## F-statistic: 7.217 on 5 and 1137 DF,  p-value: 1.156e-06
```

```
#Robust Standard Errors
cov1<-hccm(reg.mod, type="hc1")
coeftest(reg.mod, vcov.=cov1)
```

```
##
## t test of coefficients:
##
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3.03976345   0.27457600  11.0708 < 2.2e-16 ***
## volatile.acidity -1.20284003   0.12700674   -9.4707 < 2.2e-16 ***
## chlorides       -1.48112808   0.51586067   -2.8712 0.0041653 **
## total.sulfur.dioxide -0.00227580   0.00062456   -3.6439 0.0002807 ***
## sulphates        0.86674198   0.14302592    6.0600 1.848e-09 ***
## alcohol         0.27959699   0.02268052   12.3276 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

AIC/BIC Model

Visualizing the plot of the respective residuals and y-hats in question 6, it seemed that the best fit could be a log linear form. AIC/BIC helps test if this hypothesis is correct. The AIC/BIC test included different models with varying predictors, the best model found previously, and the best model in terms of log. From the results, the best model is still the best model but better as a log linear with the same predictors obtained from previous tests.

```
#AIC Model
# For the new model, it is in log linear form.
bestMOD<- lm(log(quality) ~ chlorides + total.sulfur.dioxide + sulphates + alcohol + volatile.acidity, data = Wine_Quality)
bestMOD2<- lm(quality ~ chlorides + total.sulfur.dioxide + sulphates + alcohol + volatile.acidity, data = Wine_Quality)
MOD_1 <- lm(log(quality) ~ sulphates + alcohol,data = Wine_Quality)
MOD_2 <- lm(log(quality) ~ pH + sulphates + alcohol,data = Wine_Quality)
```

```

MOD_3 <- lm(log(quality) ~ density + pH + sulphates + alcohol, data = Wine_Quality)
MOD_4 <- lm(log(quality) ~ total.sulfur.dioxide + density + pH + sulphates + alcohol, data = Wine_Quality)
MOD_5 <- lm(log(quality) ~ free.sulfur.dioxide + total.sulfur.dioxide + density + pH + sulphates + alcohol, data = Wine_Quality)
MOD_6 <- lm(log(quality) ~ chlorides + free.sulfur.dioxide + total.sulfur.dioxide + density + pH + sulphates + alcohol, data = Wine_Quality)
MOD_7 <- lm(log(quality) ~ residual.sugar + chlorides + free.sulfur.dioxide + total.sulfur.dioxide + density + pH + sulphates + alcohol, data = Wine_Quality)
MOD_8 <- lm(log(quality) ~ citric.acid + residual.sugar + chlorides + free.sulfur.dioxide + total.sulfur.dioxide + density + pH + sulphates + alcohol, data = Wine_Quality)
MOD_9 <- lm(log(quality) ~ volatile.acidity + citric.acid + residual.sugar + chlorides + free.sulfur.dioxide + total.sulfur.dioxide + density + pH + sulphates + alcohol, data = Wine_Quality)
MOD_10 <- lm(log(quality) ~ fixed.acidity + volatile.acidity + citric.acid + residual.sugar + chlorides + free.sulfur.dioxide + total.sulfur.dioxide + density + pH + sulphates + alcohol, data = Wine_Quality)
AIC(MOD_1, MOD_2, MOD_3, MOD_4, MOD_5, MOD_6, MOD_7, MOD_8, MOD_9, MOD_10, bestMOD, bestMOD2)

```

```

##          df          AIC
## MOD_1      4 -1526.656
## MOD_2      5 -1547.205
## MOD_3      6 -1545.221
## MOD_4      7 -1558.177
## MOD_5      8 -1559.779
## MOD_6      9 -1586.914
## MOD_7     10 -1584.923
## MOD_8     11 -1599.442
## MOD_9     12 -1670.418
## MOD_10    13 -1668.687
## bestMOD     7 -1667.423
## bestMOD2    7  2241.781

```

```

BIC(MOD_1, MOD_2, MOD_3, MOD_4, MOD_5, MOD_6, MOD_7, MOD_8, MOD_9, MOD_10, bestMOD, bestMOD2)

```

```

##          df          BIC
## MOD_1      4 -1506.491
## MOD_2      5 -1521.998
## MOD_3      6 -1514.973
## MOD_4      7 -1522.887
## MOD_5      8 -1519.448
## MOD_6      9 -1541.541
## MOD_7     10 -1534.509
## MOD_8     11 -1543.987
## MOD_9     12 -1609.921
## MOD_10    13 -1603.149
## bestMOD     7 -1632.133
## bestMOD2    7  2277.070

```

Cross-Validation

A 5-fold cross validation resulted in an RMSE of .11608. This means that on average the predicted value is off by .11608. In addition, splitting the data into testing/training to calculate the RMSE for both subsets and also got small numbers. Thus, the model is a good fit for the data and the results are accurate.

```

# train for training sample
# test for testing sample
set.seed(1)
row.number <- sample(1:nrow(Wine_Quality), 0.66*nrow(Wine_Quality))
train = Wine_Quality[row.number,]
test = Wine_Quality[-row.number,]

```

```
reg.mod=lm(log(quality) ~ volatile.acidity + chlorides + total.sulfur.dioxide + sulphates + alcohol,
#RMSE
sqrt(mean(log(test$quality)-predict(reg.mod,test))^2)
```

```
## [1] 0.009056762
```

```
sqrt(mean(log(train$quality)-predict(reg.mod,train))^2)
```

```
## [1] 1.582641e-15
```

```
# Cross Validation
library(lmvar)
fit= lm(log(quality) ~ volatile.acidity + chlorides + total.sulfur.dioxide + sulphates + alcohol,x = '
cv.lm(fit, k = 5)
```

```
## Mean absolute error      : 0.08922306
## Sample standard deviation : 0.007942391
##
## Mean squared error       : 0.01370225
## Sample standard deviation : 0.003211446
##
## Root mean squared error   : 0.1164704
## Sample standard deviation : 0.01308115
```