Exercise01

Immanuel Klein

```r
library("tidyverse")
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.3     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.4.4     v tibble    3.2.1
v lubridate 1.9.3     v tidyr     1.3.1
v purrr     1.0.2
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

```r
library("ggplot2")
```

1 Sample statistics

Data set

Exercise (a)

Reading the data into R:

```r
#Reading the whole data set
winequality.white <- read.csv("wine+quality/winequality-white.csv", sep = ";")

#Using only volatile.acidity and residual.sugar and adding binary variable good which is 1 i
working.df <- winequality.white %>%
  mutate(good = ifelse(quality > 5, 1, 0)) %>%
  select(volatile.acidity, residual.sugar, good)

head(working.df)
```

```
  volatile.acidity residual.sugar good
1             0.27           20.7    1
2             0.30            1.6    1
3             0.28            6.9    1
4             0.23            8.5    1
5             0.23            8.5    1
6             0.28            6.9    1
```

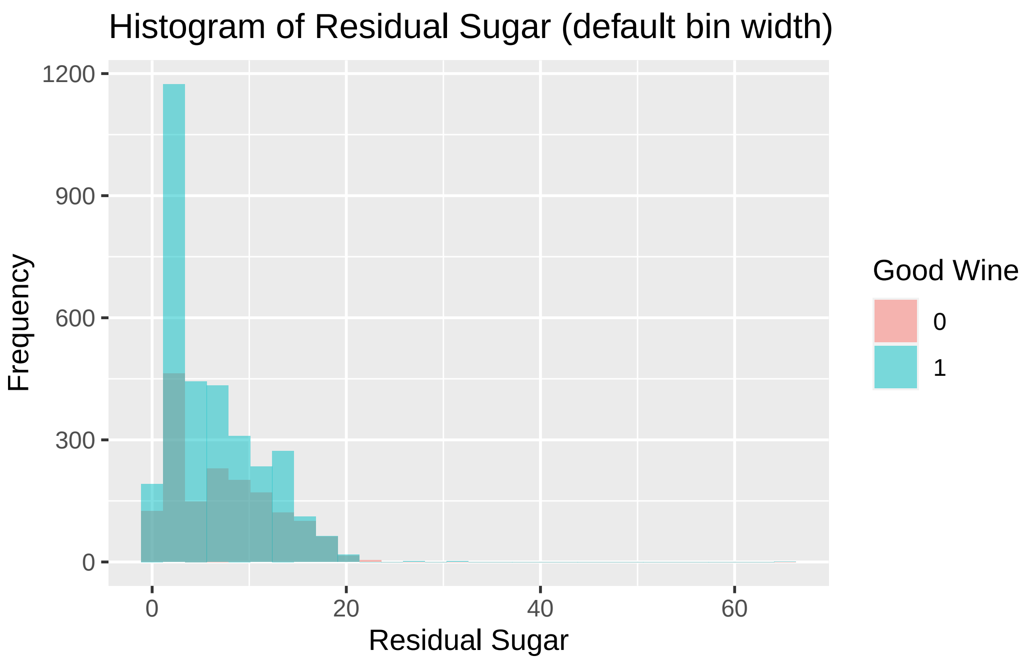
Exercise (b)

Histograms

Plotting histograms of residual.sugar for good and bad wines using different methods available in R to choose the bin width.

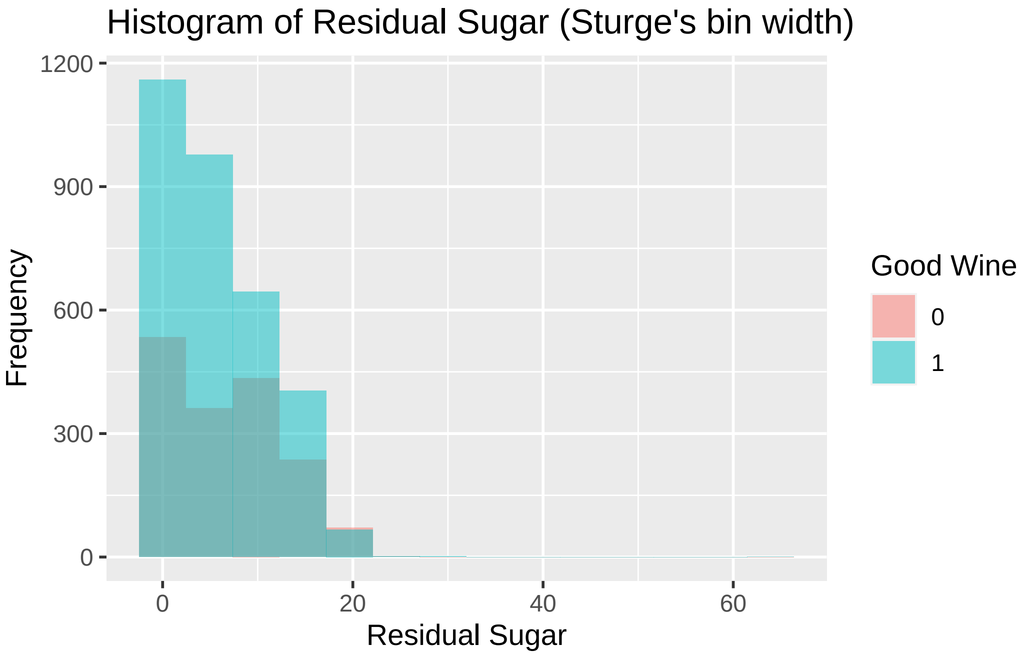
Default

```
#Plotting the histogram with the default bin width
ggplot(working.df) +
  aes(x = residual.sugar, fill = factor(good)) +
  geom_histogram(position = "identity", alpha = 0.5, bins = 30) +
  labs(title = "Histogram of Residual Sugar (default bin width)",
       x = "Residual Sugar",
       y = "Frequency",
       fill = "Good Wine")
```



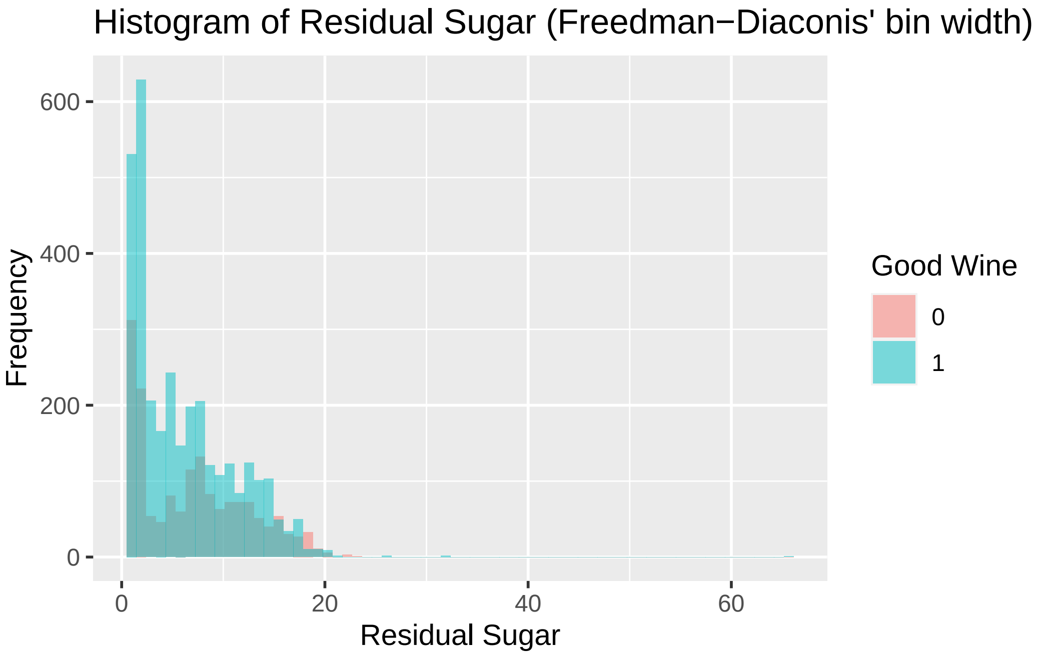
Sturge's Choice

```
#Plotting the histogram and calculating Sturge's bin width
ggplot(working.df) +
  aes(x = residual.sugar, fill = factor(good)) +
  geom_histogram(position = "identity", alpha = 0.5,
                 binwidth = diff(range(working.df$residual.sugar)) /
                              (1 + log2(length(working.df$residual.sugar)))) +
  labs(title = "Histogram of Residual Sugar (Sturge's bin width)",
       x = "Residual Sugar",
       y = "Frequency",
       fill = "Good Wine")
```



Freedman-Diaconis' Choice

```
#Plotting the histogram and calculating Freedman-Diaconis' bin width
ggplot(working.df) +
  aes(x = residual.sugar, fill = factor(good)) +
  geom_histogram(position = "identity", alpha = 0.5,
                 binwidth = 2 * IQR(working.df$residual.sugar) /
                              (length(working.df$residual.sugar)^(1/3))) +
  labs(title = "Histogram of Residual Sugar (Freedman-Diaconis' bin width)",
       x = "Residual Sugar",
       y = "Frequency",
       fill = "Good Wine")
```



Analysis

As residual sugar levels increase, the number of both good and bad wines decreases. This trend might be due to underrepresentation of wines with high residual sugar in the dataset, or it could be a general thing that such wines are less represented in the population. Additionally, there is a noticeable increase in the number of bad wines with moderate levels of residual sugar. If we disregard the low residual sugar range - where both good and bad wines are most common - we observe that many bad wines have moderate residual sugar content.

Summary Statistics

```
summary_stats <- working.df %>%
  group_by(good) %>%
  summarise(
    "Mean" = mean(residual.sugar, na.rm = TRUE),
    "Median" = median(residual.sugar, na.rm = TRUE),
    "Standard Deviation" = sd(residual.sugar, na.rm = TRUE),
    "IQR" = IQR(residual.sugar, na.rm = TRUE),
    "min" = min(residual.sugar, na.rm = TRUE),
    "max" = max(residual.sugar, na.rm = TRUE)
  )
```

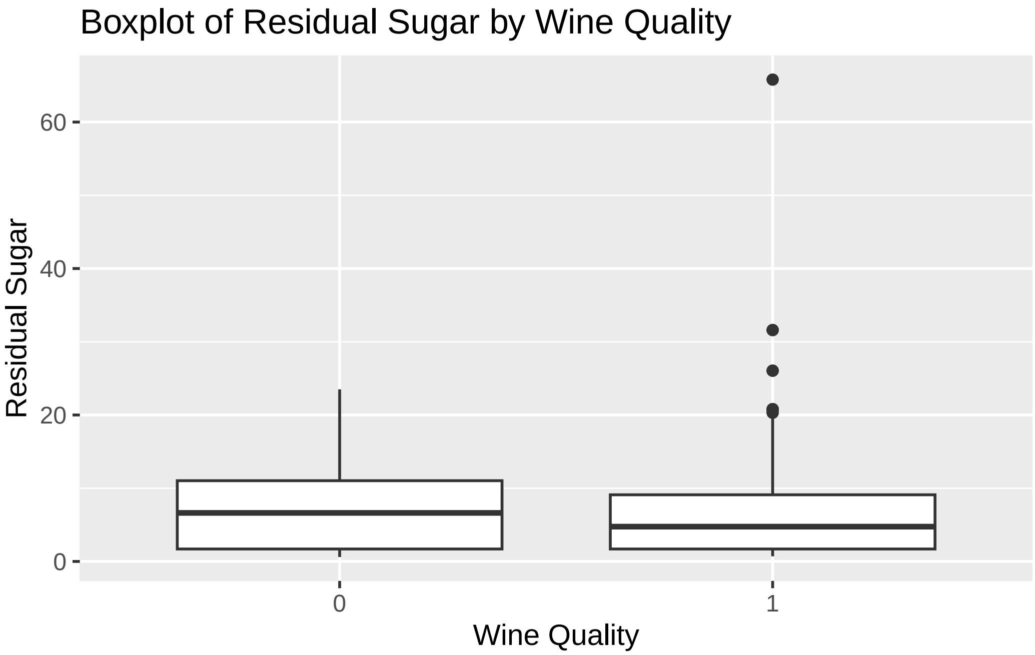
```
summary_stats
```

```
# A tibble: 2 x 7
   good  Mean Median `Standard Deviation`   IQR   min   max
  <dbl> <dbl>  <dbl>                <dbl> <dbl> <dbl> <dbl>
1     0  7.05   6.62                 5.28  9.33   0.6  23.5
2     1  6.06   4.75                 4.93  7.4    0.7  65.8
```

- The mean residual sugar is higher for bad wines (7.05) compared to good wines (6.06).
- The median residual sugar is also higher for bad wines (6.625) compared to good wines (4.75). On average, bad wines seem to have slightly higher residual sugar content than good wines.
- The standard deviation is slightly higher for bad wines (5.28) compared to good wines (4.93), so there is more variability in the residual sugar content among bad wines.
- The IQR is also higher for bad wines (9.325) compared to good wines (7.4). This suggests that bad wines have a wider spread in their residual sugar in the central portion of the data.
- The minimum value of residual sugar is very similar for both categories (0.6 for bad wines and 0.7 for good wines).
- The maximum value of residual sugar is much higher for good wines (65.8) compared to bad wines (23.5). This difference indicates that some good wines have extremely high levels of residual sugar (outliers).

Boxplots

```
boxplot <- ggplot(working.df) +
  aes(x = factor(good), y = residual.sugar) +
  geom_boxplot() +
  labs(title = "Boxplot of Residual Sugar by Wine Quality",
       x = "Wine Quality",
       y = "Residual Sugar")

boxplot
```

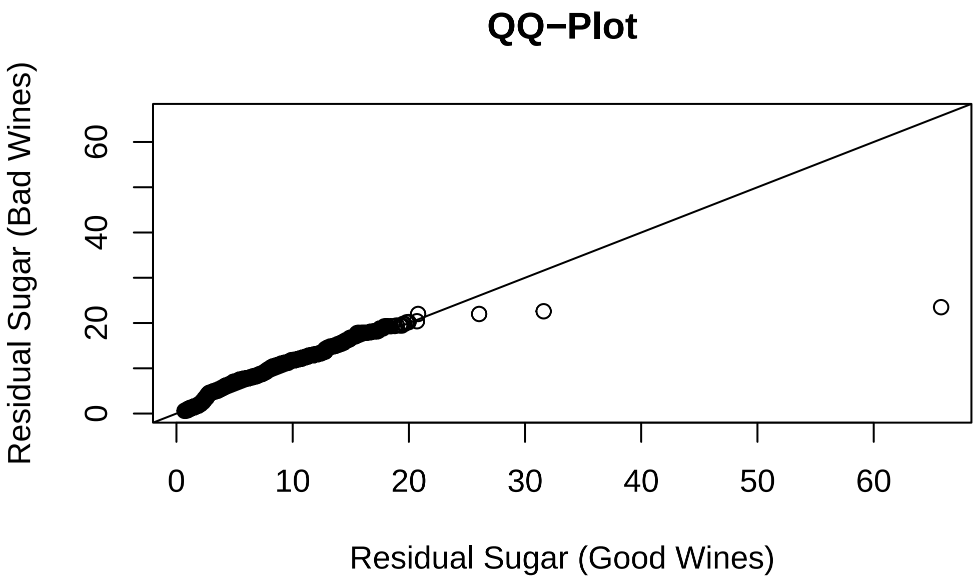


The box plot visualization reveals several key points consistent with the summary statistics:

- Good wines show a wider overall range and more outliers compared to bad wines.
- Bad wines have a higher IQR, indicating greater variability in the middle 50% of their residual sugar content.
- The range of bad wines is entirely contained within the whiskers, showing fewer extreme values beyond the central data points.

QQ-Plot

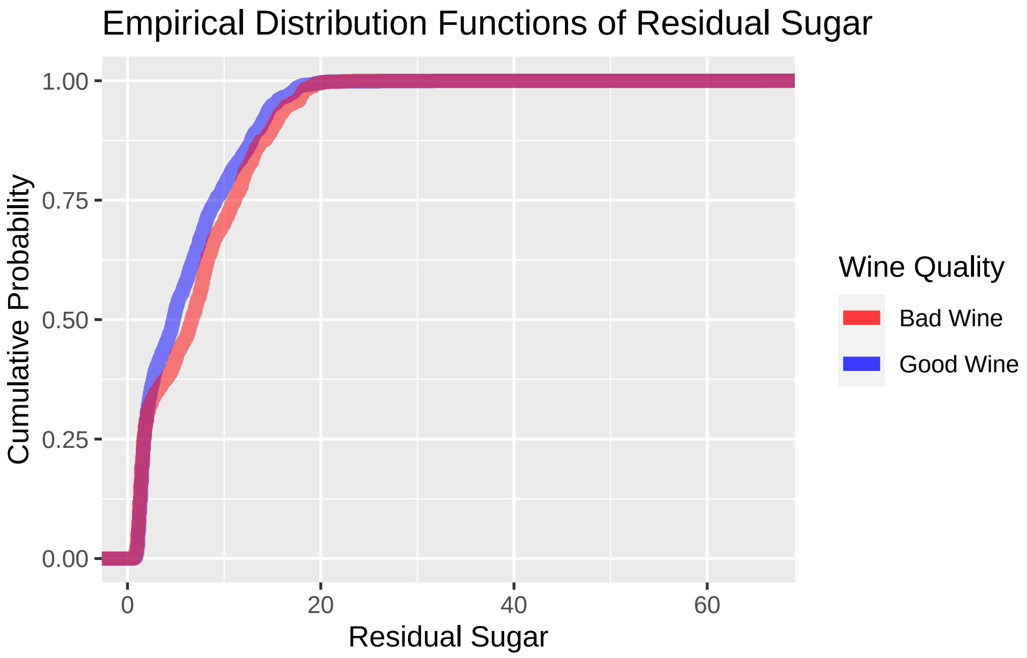
```r
residual.sugar.good <- working.df %>% filter(good == 1) %>% pull(residual.sugar)
residual.sugar.bad <- working.df %>% filter(good == 0) %>% pull(residual.sugar)

xlim.range <- range(residual.sugar.good, residual.sugar.bad)
ylim.range <- range(residual.sugar.good, residual.sugar.bad)

# Create QQ-plot
qqplot(residual.sugar.good, residual.sugar.bad,
       xlab = "Residual Sugar (Good Wines)",
       ylab = "Residual Sugar (Bad Wines)",
       main = "QQ-Plot",
       xlim = xlim.range,
       ylim = ylim.range)
abline(0, 1)
```



- If the distributions were identical, the points would fall on the 45-degree line. Here, we can see a smaller deviation from this line in the middle part and a strong deviation in the tails.
- Almost exclusively, points fall slightly above the line (indicating higher residual sugar for bad wines).
- The outliers of good wines are apparent.

Empirical Distribution

```
working.good <- working.df %>% filter(good == 1)
working.bad <- working.df %>% filter(good == 0)

ggplot() +
  stat_ecdf(data = working.good, aes(x = residual.sugar, color = "Good Wine"), geom = "step"
  stat_ecdf(data = working.bad, aes(x = residual.sugar, color = "Bad Wine"), geom = "step", 
  scale_color_manual(values = c("Good Wine" = "blue", "Bad Wine" = "red")) +
  labs(title = "Empirical Distribution Functions of Residual Sugar",
       x = "Residual Sugar",
       y = "Cumulative Probability",
       color = "Wine Quality")
```



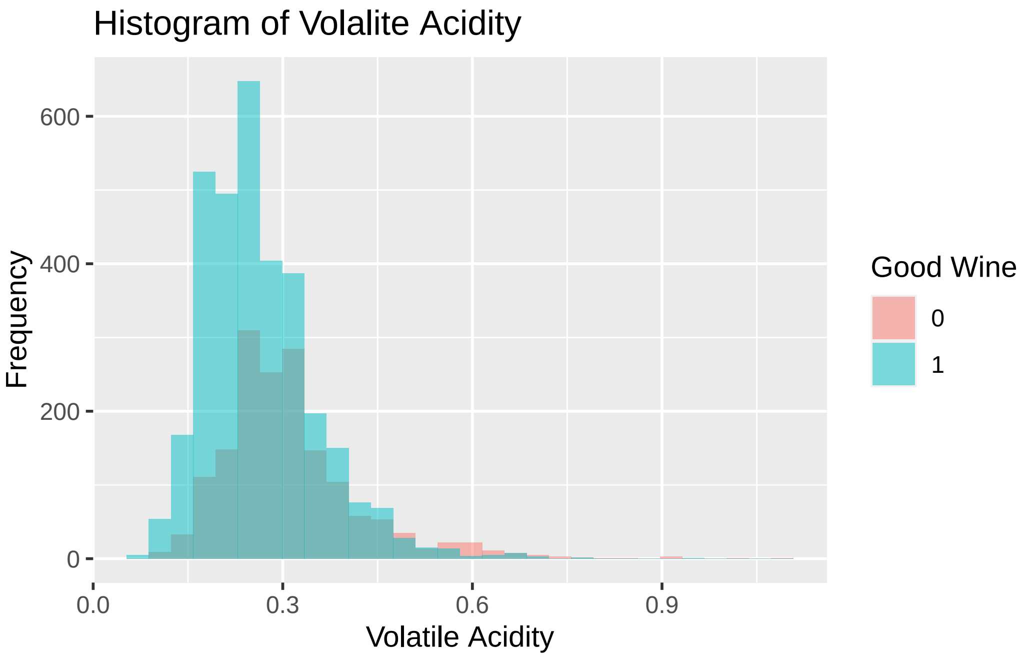
- Since the median residual sugar content of good wines is lower, the curve rises more steeply initially, indicating that a higher proportion of good wines have lower residual sugar content.
- Given the higher median residual sugar content of bad wines, the slope is less steep in the middle part compared to good wines, indicating that a lower proportion of bad wines have lower residual sugar content.

Exercise (c)

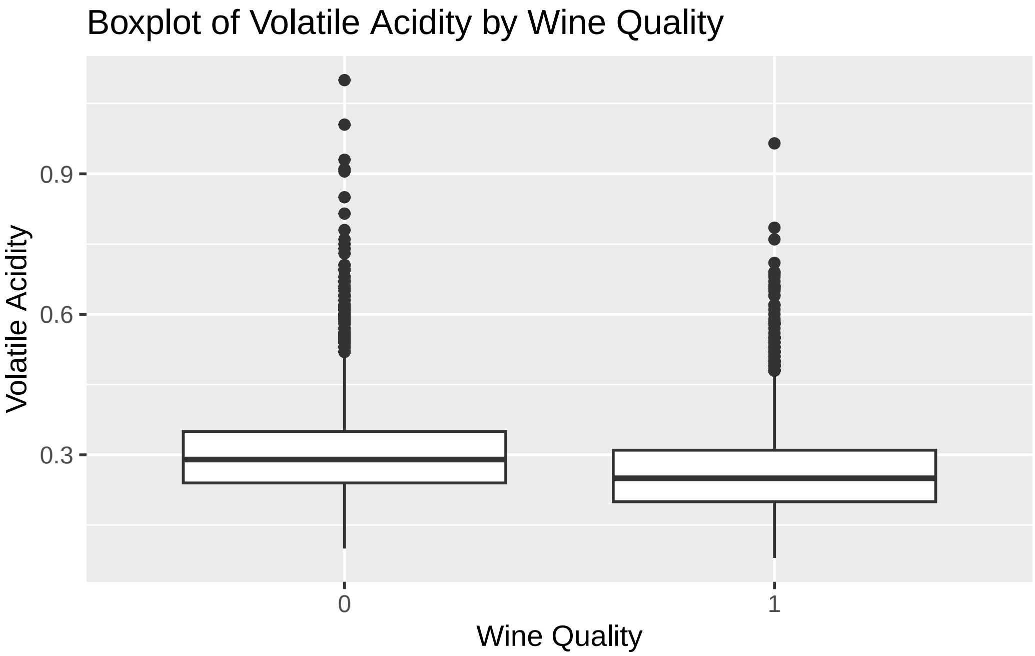
```
# Summary statistics
summary_stats <- working.df %>%
  group_by(good) %>%
  summarise(
    "Mean" = mean(volatile.acidity, na.rm = TRUE),
    "Median" = median(volatile.acidity, na.rm = TRUE),
    "Standard Deviation" = sd(volatile.acidity, na.rm = TRUE),
    "IQR" = IQR(volatile.acidity, na.rm = TRUE),
    "min" = min(volatile.acidity, na.rm = TRUE),
    "max" = max(volatile.acidity, na.rm = TRUE)
  )

summary_stats
```

```
# A tibble: 2 x 7
   good  Mean Median `Standard Deviation`   IQR   min   max
  <dbl> <dbl>  <dbl>                <dbl> <dbl> <dbl> <dbl>
1     0 0.310   0.29               0.113   0.11  0.1  1.1
2     1 0.262   0.25               0.0901  0.11  0.08 0.965
```

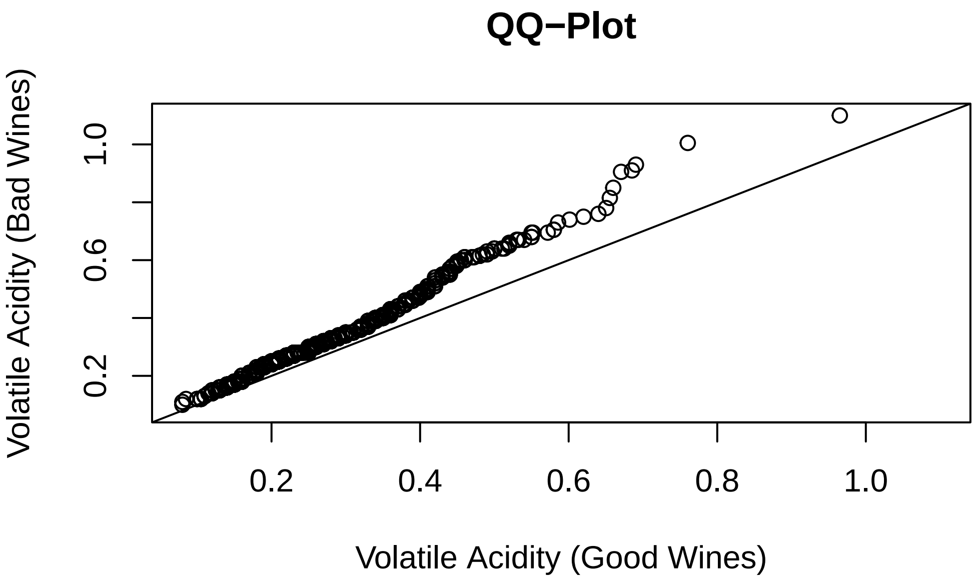
```
# Creating a histogram
ggplot(working.df) +
  aes(x = volatile.acidity, fill = factor(good)) +
  geom_histogram(position = "identity", alpha = 0.5, bins = 30) +
  labs(title = "Histogram of Volalite Acidity",
       x = "Volatile Acidity",
       y = "Frequency",
       fill = "Good Wine")
```



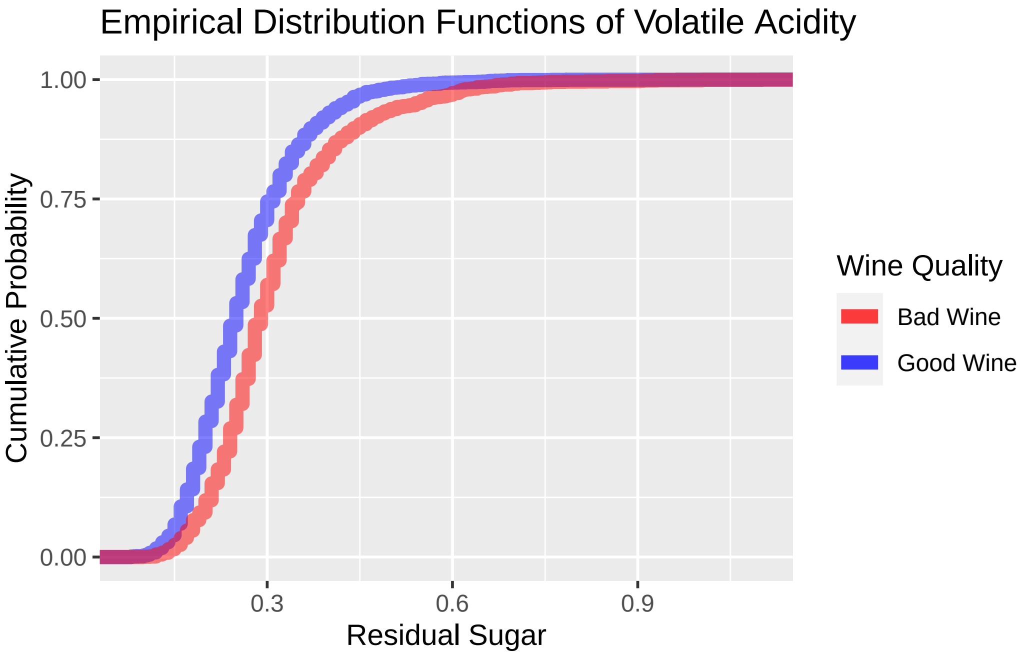
```
# Creating box plots
boxplot <- ggplot(working.df) +
  aes(x = factor(good), y = volatile.acidity) +
  geom_boxplot() +
  labs(title = "Boxplot of Volatile Acidity by Wine Quality",
       x = "Wine Quality",
       y = "Volatile Acidity")

boxplot
```



```
# Creating a QQ plot
volatile.acidity.good <- working.df %>% filter(good == 1) %>% pull(volatile.acidity)
volatile.acidity.bad <- working.df %>% filter(good == 0) %>% pull(volatile.acidity)

xlim.range <- range(volatile.acidity.good, volatile.acidity.bad)
ylim.range <- range(volatile.acidity.good, volatile.acidity.bad)

qqplot(volatile.acidity.good, volatile.acidity.bad,
       xlab = "Volatile Acidity (Good Wines)",
       ylab = "Volatile Acidity (Bad Wines)",
       main = "QQ-Plot",
       xlim = xlim.range,
       ylim = ylim.range)
abline(0, 1)
```



```
# Creating an ECDF plot
working.good <- working.df %>% filter(good == 1)
working.bad <- working.df %>% filter(good == 0)

ggplot() +
  stat_ecdf(data = working.good, aes(x = volatile.acidity, color = "Good Wine"), geom = "ste
  stat_ecdf(data = working.bad, aes(x = volatile.acidity, color = "Bad Wine"), geom = "step"
  scale_color_manual(values = c("Good Wine" = "blue", "Bad Wine" = "red")) +
  labs(title = "Empirical Distribution Functions of Volatile Acidity",
       x = "Residual Sugar",
       y = "Cumulative Probability",
       color = "Wine Quality")
```



The summary statistics suggest that good wines have lower volatile acidity on average, with less variability and fewer extreme values compared to bad wines. This reflects in the histograms, boxplots, QQ plots, and ECDFs as follows:

- **Histograms:** Good wines have a sharper peak and a little bit of a narrower spread.
- **Boxplots:** Good wines have lower medians and a somewhat lesser spread with fewer “extreme” outliers compared to bad wines.
- **QQ Plots:** Good wines shows consistently lower values compared to bad wines for the same quantiles resulting in all points being above the diagonal.
- **ECDFs:** Good wines’ ECDF start to rise at a lower value.

Lower volatile acidity seems to be associated with higher quality wines, as could have been expected.