HW5 Wine

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What is the number of cases of wine that will be sold given certain properties of the wine?

```
train_wine <- read.csv('https://raw.githubusercontent.com/LeJQC/DATA-621-Group-2/main/HW5/wine-training
test_wine <- read.csv('https://raw.githubusercontent.com/LeJQC/DATA-621-Group-2/main/HW5/wine-evaluatio
```

```
head(train_wine)
```

```
##   INDEX TARGET FixedAcidity VolatileAcidity CitricAcid ResidualSugar Chlorides
## 1     1      3          3.2           1.160      -0.98          54.2    -0.567
## 2     2      3          4.5           0.160      -0.81          26.1    -0.425
## 3     4      5          7.1           2.640      -0.88          14.8     0.037
## 4     5      3          5.7           0.385       0.04          18.8    -0.425
## 5     6      4          8.0           0.330      -1.26           9.4        NA
## 6     7      0         11.3           0.320       0.59           2.2     0.556
##   FreeSulfurDioxide TotalSulfurDioxide Density   pH Sulphates Alcohol
## 1                NA                268 0.99280 3.33     -0.59     9.9
## 2                15               -327 1.02792 3.38      0.70      NA
## 3               214                142 0.99518 3.12      0.48    22.0
## 4                22                115 0.99640 2.24      1.83     6.2
## 5              -167                108 0.99457 3.12      1.77    13.7
## 6               -37                 15 0.99940 3.20      1.29    15.4
##   LabelAppeal AcidIndex STARS
## 1           0         8     2
## 2          -1         7     3
## 3          -1         8     3
## 4          -1         6     1
## 5           0         9     2
## 6           0        11    NA
```

1. Data Exploration

First, we can use the glimpse() function to get a general sense of the training data. There are 12,795 rows and 16 columns in the dataset. All of the columns are measured as quantitative values. The column INDEX needs to be removed as it does not add any value to the dataset. The response variable is TARGET, which represents the number of sample cases of wine that were purchased by the wine distribution companies. The remaining 14 columsn are the predictor variables.

```
glimpse(train_wine)
```

```
## Rows: 12,795
## Columns: 16
## $ INDEX             <int> 1, 2, 4, 5, 6, 7, 8, 11, 12, 13, 14, 15, 16, 17, 19~
## $ TARGET            <int> 3, 3, 5, 3, 4, 0, 0, 4, 3, 6, 0, 4, 3, 7, 4, 0, 0, ~
```

```
## $ FixedAcidity       <dbl> 3.2, 4.5, 7.1, 5.7, 8.0, 11.3, 7.7, 6.5, 14.8, 5.5,~
## $ VolatileAcidity    <dbl> 1.160, 0.160, 2.640, 0.385, 0.330, 0.320, 0.290, -1~
## $ CitricAcid         <dbl> -0.98, -0.81, -0.88, 0.04, -1.26, 0.59, -0.40, 0.34~
## $ ResidualSugar      <dbl> 54.20, 26.10, 14.80, 18.80, 9.40, 2.20, 21.50, 1.40~
## $ Chlorides          <dbl> -0.567, -0.425, 0.037, -0.425, NA, 0.556, 0.060, 0.~
## $ FreeSulfurDioxide  <dbl> NA, 15, 214, 22, -167, -37, 287, 523, -213, 62, 551~
## $ TotalSulfurDioxide <dbl> 268, -327, 142, 115, 108, 15, 156, 551, NA, 180, 65~
## $ Density            <dbl> 0.99280, 1.02792, 0.99518, 0.99640, 0.99457, 0.9994~
## $ pH                 <dbl> 3.33, 3.38, 3.12, 2.24, 3.12, 3.20, 3.49, 3.20, 4.9~
## $ Sulphates          <dbl> -0.59, 0.70, 0.48, 1.83, 1.77, 1.29, 1.21, NA, 0.26~
## $ Alcohol            <dbl> 9.9, NA, 22.0, 6.2, 13.7, 15.4, 10.3, 11.6, 15.0, 1~
## $ LabelAppeal        <int> 0, -1, -1, -1, 0, 0, 0, 1, 0, 0, 1, 0, 1, 2, 0, 0, ~
## $ AcidIndex          <int> 8, 7, 8, 6, 9, 11, 8, 7, 6, 8, 5, 10, 7, 8, 9, 8, 9~
## $ STARS              <int> 2, 3, 3, 1, 2, NA, NA, 3, NA, 4, 1, 2, 2, 3, NA, NA~
```

After removing the INDEX column, we can use the summary() and describe() function to summary statistics of the training dataset. We can see from the summary() function that there are several columns with missing values, which we will need to resolve later. The predictor STARS seems to have the most NAs at 3359. Some predictors also have a minimum that is negative, which does not make sense given the context so we will need to adjust these later on as well. Also, it looks like the STARS column consists of ordinal data.

```
#Drop unnecessary variable INDEX
train_wine <- train_wine[, -1]
```

```
# Summary statistics
summary_stats <- summary(train_wine)
print(summary_stats)
```

```
##      TARGET       FixedAcidity     VolatileAcidity     CitricAcid
##  Min.   :0.000   Min.   :-18.100   Min.   :-2.7900   Min.   :-3.2400
##  1st Qu.:2.000   1st Qu.:  5.200   1st Qu.: 0.1300   1st Qu.: 0.0300
##  Median :3.000   Median :  6.900   Median : 0.2800   Median : 0.3100
##  Mean   :3.029   Mean   :  7.076   Mean   : 0.3241   Mean   : 0.3084
##  3rd Qu.:4.000   3rd Qu.:  9.500   3rd Qu.: 0.6400   3rd Qu.: 0.5800
##  Max.   :8.000   Max.   : 34.400   Max.   : 3.6800   Max.   : 3.8600
##
##  ResidualSugar        Chlorides       FreeSulfurDioxide TotalSulfurDioxide
##  Min.   :-127.800   Min.   :-1.1710   Min.   :-555.00   Min.   :-823.0
##  1st Qu.:  -2.000   1st Qu.:-0.0310   1st Qu.:   0.00   1st Qu.:  27.0
##  Median :   3.900   Median : 0.0460   Median :  30.00   Median : 123.0
##  Mean   :   5.419   Mean   : 0.0548   Mean   :  30.85   Mean   : 120.7
##  3rd Qu.:  15.900   3rd Qu.: 0.1530   3rd Qu.:  70.00   3rd Qu.: 208.0
##  Max.   : 141.150   Max.   : 1.3510   Max.   : 623.00   Max.   :1057.0
##  NA's   :616        NA's   :638       NA's   :647       NA's   :682
##     Density             pH          Sulphates          Alcohol
##  Min.   :0.8881   Min.   :0.480   Min.   :-3.1300   Min.   :-4.70
##  1st Qu.:0.9877   1st Qu.:2.960   1st Qu.: 0.2800   1st Qu.: 9.00
##  Median :0.9945   Median :3.200   Median : 0.5000   Median :10.40
##  Mean   :0.9942   Mean   :3.208   Mean   : 0.5271   Mean   :10.49
##  3rd Qu.:1.0005   3rd Qu.:3.470   3rd Qu.: 0.8600   3rd Qu.:12.40
##  Max.   :1.0992   Max.   :6.130   Max.   : 4.2400   Max.   :26.50
##                   NA's   :395     NA's   :1210      NA's   :653
##   LabelAppeal          AcidIndex          STARS
##  Min.   :-2.000000   Min.   : 4.000   Min.   :1.000
##  1st Qu.:-1.000000   1st Qu.: 7.000   1st Qu.:1.000
##  Median : 0.000000   Median : 8.000   Median :2.000
```

```
##  Mean   :-0.009066   Mean   : 7.773   Mean   :2.042
##  3rd Qu.: 1.000000   3rd Qu.: 8.000   3rd Qu.:3.000
##  Max.   : 2.000000   Max.   :17.000   Max.   :4.000
##                                       NA's   :3359
```

```
print(round(describe(train_wine),2))
```

```
##                       vars     n   mean     sd median trimmed    mad     min
## TARGET                   1 12795   3.03   1.93   3.00    3.05   1.48    0.00
## FixedAcidity             2 12795   7.08   6.32   6.90    7.07   3.26  -18.10
## VolatileAcidity          3 12795   0.32   0.78   0.28    0.32   0.43   -2.79
## CitricAcid               4 12795   0.31   0.86   0.31    0.31   0.42   -3.24
## ResidualSugar            5 12179   5.42  33.75   3.90    5.58  15.72 -127.80
## Chlorides                6 12157   0.05   0.32   0.05    0.05   0.13   -1.17
## FreeSulfurDioxide        7 12148  30.85 148.71  30.00   30.93  56.34 -555.00
## TotalSulfurDioxide       8 12113 120.71 231.91 123.00  120.89 134.92 -823.00
## Density                  9 12795   0.99   0.03   0.99    0.99   0.01    0.89
## pH                      10 12400   3.21   0.68   3.20    3.21   0.39    0.48
## Sulphates               11 11585   0.53   0.93   0.50    0.53   0.44   -3.13
## Alcohol                 12 12142  10.49   3.73  10.40   10.50   2.37   -4.70
## LabelAppeal             13 12795  -0.01   0.89   0.00   -0.01   1.48   -2.00
## AcidIndex               14 12795   7.77   1.32   8.00    7.64   1.48    4.00
## STARS                   15  9436   2.04   0.90   2.00    1.97   1.48    1.00
##                          max   range  skew kurtosis   se
## TARGET                  8.00    8.00 -0.33    -0.88 0.02
## FixedAcidity           34.40   52.50 -0.02     1.67 0.06
## VolatileAcidity         3.68    6.47  0.02     1.83 0.01
## CitricAcid              3.86    7.10 -0.05     1.84 0.01
## ResidualSugar         141.15  268.95 -0.05     1.88 0.31
## Chlorides               1.35    2.52  0.03     1.79 0.00
## FreeSulfurDioxide     623.00 1178.00  0.01     1.84 1.35
## TotalSulfurDioxide   1057.00 1880.00 -0.01     1.67 2.11
## Density                 1.10    0.21 -0.02     1.90 0.00
## pH                      6.13    5.65  0.04     1.65 0.01
## Sulphates               4.24    7.37  0.01     1.75 0.01
## Alcohol                26.50   31.20 -0.03     1.54 0.03
## LabelAppeal             2.00    4.00  0.01    -0.26 0.01
## AcidIndex              17.00   13.00  1.65     5.19 0.01
## STARS                   4.00    3.00  0.45    -0.69 0.01
```

Since the STAR column is an ordinal categorical variable we can transform it into a factor.

```
#Transform STAR rating to a factor variables
#Check the unique values in the STARS variable
unique(train_wine$STARS)
```

```
## [1]  2  3  1 NA  4
```

```
# Convert "STARS" to factor
train_wine$STARS <- as.factor(train_wine$STARS)

# Verify the transformation
str(train_wine)
```

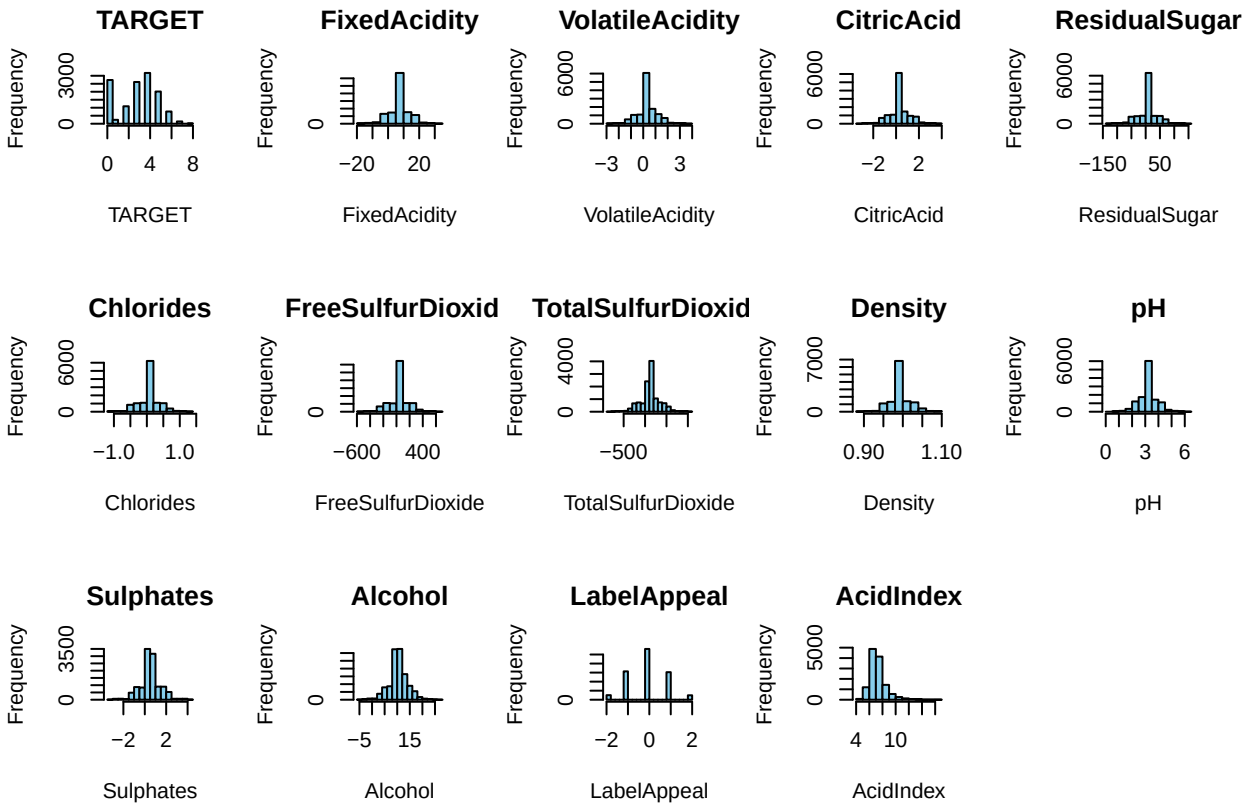
```
## 'data.frame':    12795 obs. of  15 variables:
##  $ TARGET            : int  3 3 5 3 4 0 0 4 3 6 ...
##  $ FixedAcidity      : num  3.2 4.5 7.1 5.7 8 11.3 7.7 6.5 14.8 5.5 ...
```

```
##  $ VolatileAcidity   : num  1.16 0.16 2.64 0.385 0.33 0.32 0.29 -1.22 0.27 -0.22 ...
##  $ CitricAcid        : num  -0.98 -0.81 -0.88 0.04 -1.26 0.59 -0.4 0.34 1.05 0.39 ...
##  $ ResidualSugar     : num  54.2 26.1 14.8 18.8 9.4 ...
##  $ Chlorides         : num  -0.567 -0.425 0.037 -0.425 NA 0.556 0.06 0.04 -0.007 -0.277 ...
##  $ FreeSulfurDioxide : num  NA 15 214 22 -167 -37 287 523 -213 62 ...
##  $ TotalSulfurDioxide: num  268 -327 142 115 108 15 156 551 NA 180 ...
##  $ Density           : num  0.993 1.028 0.995 0.996 0.995 ...
##  $ pH                : num  3.33 3.38 3.12 2.24 3.12 3.2 3.49 3.2 4.93 3.09 ...
##  $ Sulphates         : num  -0.59 0.7 0.48 1.83 1.77 1.29 1.21 NA 0.26 0.75 ...
##  $ Alcohol           : num  9.9 NA 22 6.2 13.7 15.4 10.3 11.6 15 12.6 ...
##  $ LabelAppeal       : int  0 -1 -1 -1 0 0 0 1 0 0 ...
##  $ AcidIndex         : int  8 7 8 6 9 11 8 7 6 8 ...
##  $ STARS             : Factor w/ 4 levels "1","2","3","4": 2 3 3 1 2 NA NA 3 NA 4 ...
```

Distribution plot

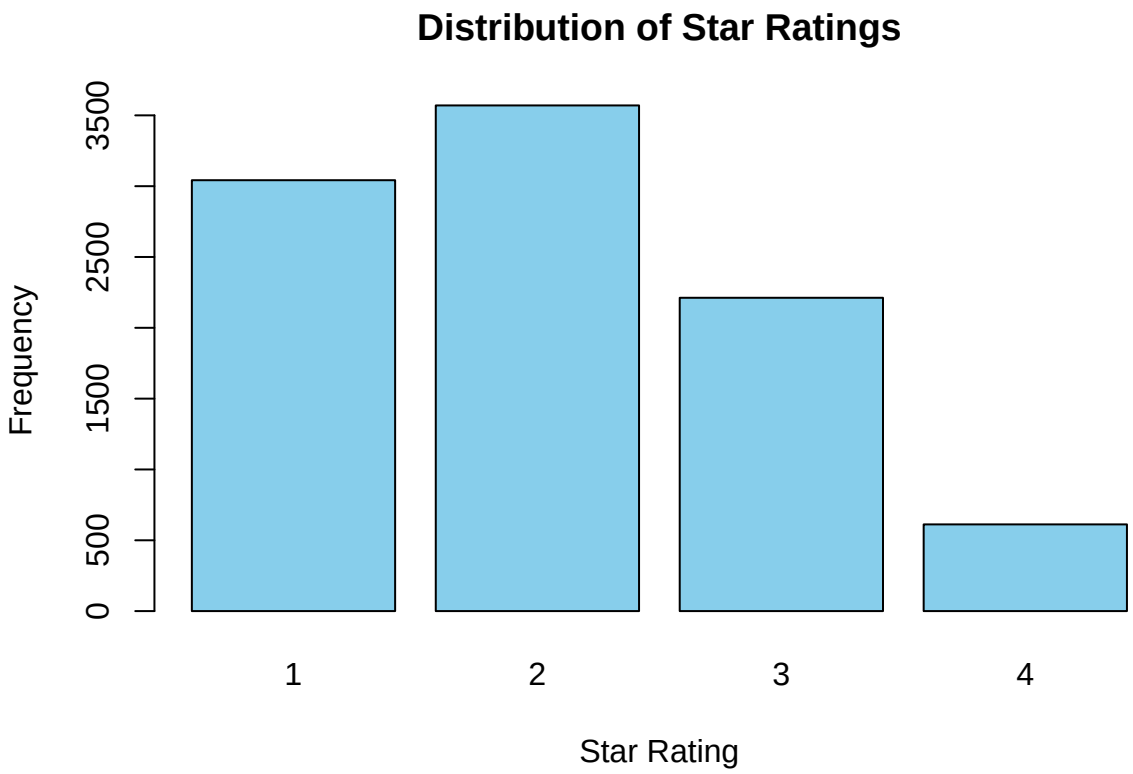
To get a better sense of the distribution of the columns, we can plot a histogram of them. The target variable "TARGET" (number of cases sold) has a right-skewed distribution, with most values concentrated towards lower counts. Some predictor variables like FixedAcidity, VolatileAcidity, and CitricAcid appear to have relatively normal distributions. Other variables like ResidualSugar, Chlorides, FreeSulfurDioxide, and TotalSulfurDioxide show skewed distributions with potential outliers. The continuous variables seem to have varying levels of dispersion, which could impact their predictive power.

```r
# Visualization - Histograms for numerical variables
num_vars <- names(train_wine)[sapply(train_wine, is.numeric)]
par(mfrow = c(3, 5)) # Adjust layout for multiple plots
for (var in num_vars) {
  hist(train_wine[[var]], main = var, xlab = var, col = "skyblue")
}
```



For the STAR ratings, which represents wine quality, we can use a bar plot to show the distribution. In this case, the bar plot shows that the STAR ratings are heavily skewed towards the higher end (2 and 3 stars).

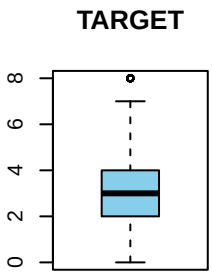
```
# Create bar plot for STARS variable
barplot(table(train_wine$STARS),
        main = "Distribution of Star Ratings",
        col = "skyblue",
        xlab = "Star Rating",
        ylab = "Frequency")
```

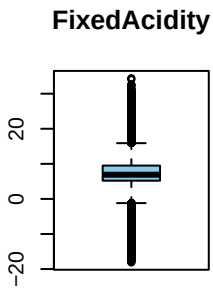


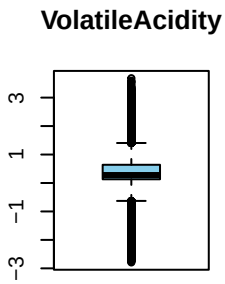
Boxplot

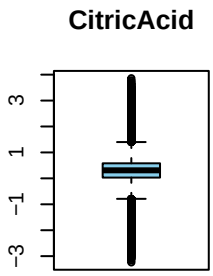
We can also use boxplots to look at distribution and identify quartiles and outliers. Similar to the density plot, we see that the median for the amount of cases bought(TARGET) is at 3.

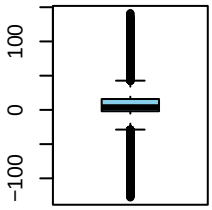
```
# Boxplots for numerical variables to check outliers
par(mfrow = c(2, 4))
for (var in num_vars) {
  boxplot(train_wine[[var]], main = var, col = "skyblue")
}
```

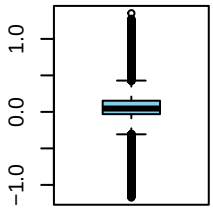

TARGET
0
2
4
6
8

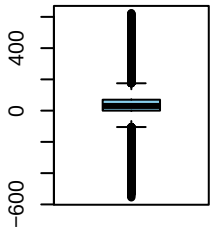

FixedAcidity
−20
0
20

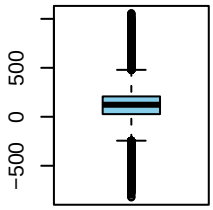

VolatileAcidity
−3
−1
1
3

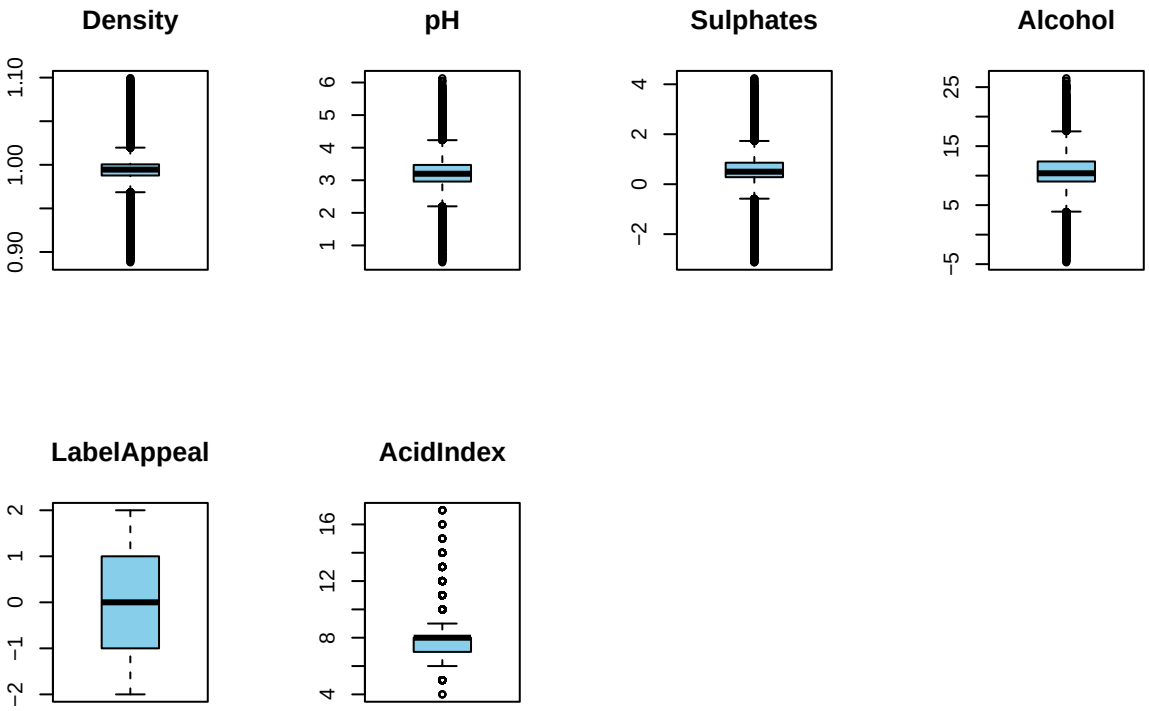

CitricAcid
−3
−1
1
3


ResidualSugar
−100
0
100


Chlorides
−1.0
0.0
1.0


FreeSulfurDioxide
−600
0
400


TotalSulfurDioxide
−500
0
500




```
train_wine1 <- train_wine
```

NOT SURE ABOUT THIS… REMOVING A LOT OF THE DATA SET

Correlation Plot

The heatmap shows the correlation between numerical variables. The target variable "TARGET" has relatively low correlations with most predictors, except for LabelAppeal and AcidIndex, which show moderate positive correlations. Some predictors like Alcohol, pH, and Density exhibit moderate to high correlations with each other, indicating potential multicollinearity issues.

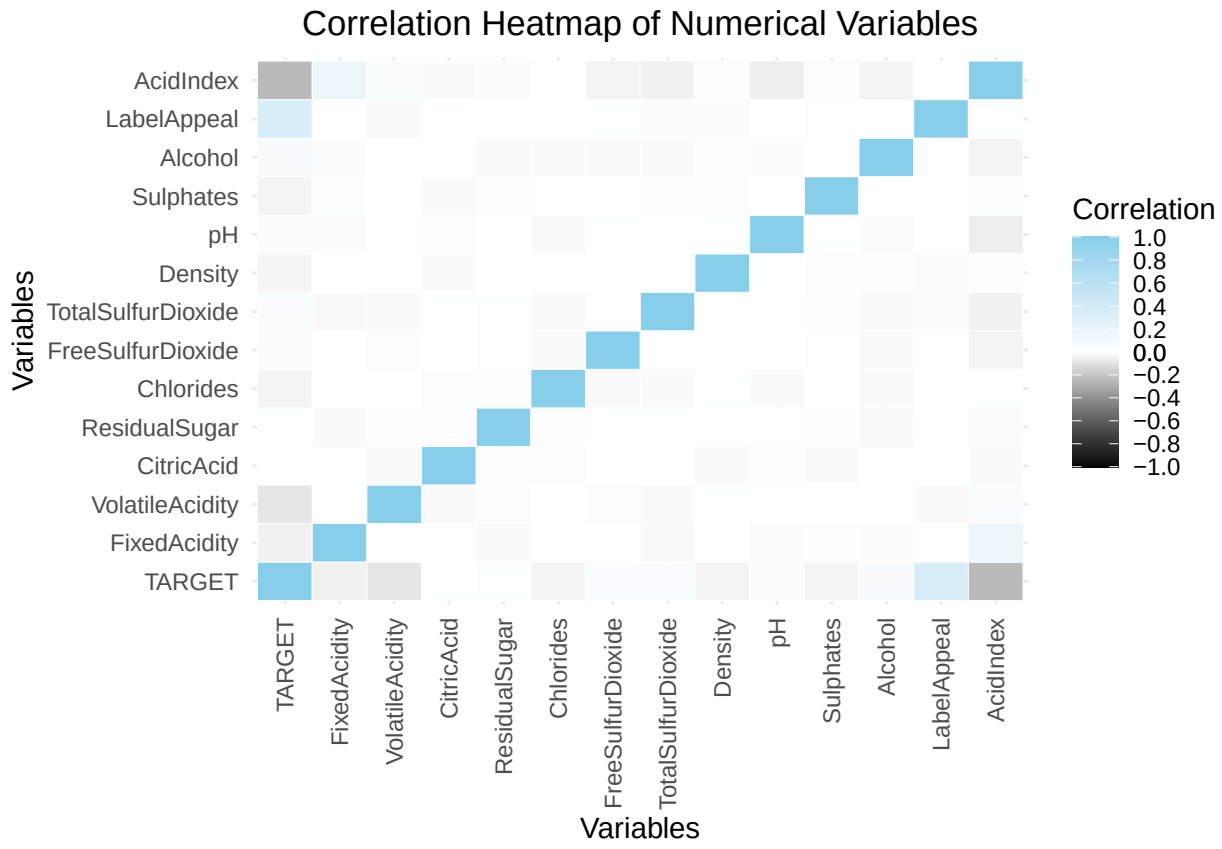
```
num_data <- train_wine[, sapply(train_wine, is.numeric)]
# Impute missing values with the median
num_data <- apply(num_data, 2, function(x) ifelse(is.na(x), median(x, na.rm = TRUE), x))


# Compute correlation matrix
correlation_matrix <- cor(num_data)

# Convert correlation matrix to long format
correlation_df <- reshape2::melt(correlation_matrix)

# Create heatmap using ggplot2
ggplot(correlation_df, aes(Var1, Var2, fill = value)) +
  geom_tile(color = "white") +
  scale_fill_gradient2(low = "black", mid = "white", high = "skyblue", midpoint = 0,
                       breaks = c(seq(-1, 0, by = 0.2), seq(0, 1, by = 0.2)),
```

```
                       limits = c(-1, 1),
                       name = "Correlation",
                       guide = guide_colorbar(direction = "vertical")) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1),
        axis.text.y = element_text(angle = 0, vjust = 0.5, hjust = 1),
        plot.title = element_text(hjust = 0.5),
        legend.position = "right") +
  labs(title = "Correlation Heatmap of Numerical Variables",
       x = "Variables",
       y = "Variables")
```



2. Data Preparation

Let's prepare the data for modeling by identifying the columns that have missing values and negative values.

```
# Function to count NA values in each column
count_na <- function(df) {
  sapply(names(df), function(col_name) {
    result <- sum(is.na(df[[col_name]]))
  })
}

# Count NA values
print('Count of NAs:')
```

```
## [1] "Count of NAs:"
```

```
count_na(train_wine)
```

```
##             TARGET       FixedAcidity    VolatileAcidity         CitricAcid
##                  0                  0                  0                  0
##      ResidualSugar          Chlorides  FreeSulfurDioxide TotalSulfurDioxide
##                616                638                647                682
##            Density                 pH          Sulphates            Alcohol
##                  0                395               1210                653
##        LabelAppeal          AcidIndex              STARS
##                  0                  0               3359
```

```
# Function to count negative values in each column
count_negative <- function(df) {
  sapply(names(df), function(col_name) {
    result <- sum(df[[col_name]] < 0)
  })
}

# Count negative values
print('Count of negative values:')
```

```
## [1] "Count of negative values:"
```

```
count_negative(train_wine)
```

```
## Warning in Ops.factor(df[[col_name]], 0): '<' not meaningful for factors
```

```
##             TARGET       FixedAcidity    VolatileAcidity         CitricAcid
##                  0               1621               2827               2966
##      ResidualSugar          Chlorides  FreeSulfurDioxide TotalSulfurDioxide
##                 NA                 NA                 NA                 NA
##            Density                 pH          Sulphates            Alcohol
##                  0                 NA                 NA                 NA
##        LabelAppeal          AcidIndex              STARS
##               3640                  0                 NA
```

Some of the columns contain NA values such as pH, residual sugar, chlorides, and upon printing the unique values of the pH column, the column doesn't contain a 0, which represents an acidic kind of wine, so I will be replacing the NA values in the pH column with 0.

```
train_wine$pH[is.na(train_wine$pH)] <- 0
```

The Residual sugar column contains negative values which doesn't make sense in the context of the amount of residual sugar in wine, so we will replace those values with the median, I will do the same for the chloride, Sulphates, totalSulfurDioxide,Alcohol and FreeSulfurDioxide column for the same logical reasoning.

```
non_negative_median <- median(train_wine$ResidualSugar[train_wine$ResidualSugar >= 0], na.rm = TRUE)
non_negative_median2 <- median(train_wine$Chlorides[train_wine$Chlorides >= 0], na.rm = TRUE)
non_negative_median3 <- median(train_wine$FreeSulfurDioxide[train_wine$FreeSulfurDioxide >= 0], na.rm =
non_negative_median4 <- median(train_wine$TotalSulfurDioxide[train_wine$TotalSulfurDioxide >= 0], na.rm
non_negative_median5 <- median(train_wine$Sulphates[train_wine$Sulphates >= 0], na.rm = TRUE)
non_negative_median6 <- median(train_wine$Alcohol[train_wine$Alcohol >= 0], na.rm = TRUE)

train_wine$ResidualSugar[train_wine$ResidualSugar < 0] <- non_negative_median
train_wine$Chlorides[train_wine$Chlorides < 0] <- non_negative_median2
train_wine$FreeSulfurDioxide[train_wine$FreeSulfurDioxide < 0] <- non_negative_median3
```

```
train_wine$TotalSulfurDioxide[train_wine$TotalSulfurDioxide < 0] <- non_negative_median4
train_wine$Sulphates[train_wine$Sulphates < 0] <- non_negative_median5
train_wine$Alcohol[train_wine$Alcohol < 0] <- non_negative_median6
```

Other columns contain the value 0, so the NA values may actually be predictive of the target variable, with that being said, the other columns that contain NA values will contain flags to help inform the model about the presence of missing data, enabling it to discern potential patterns or relationships between missingness and the target variable.

```
train_wine$ResidualSugar_missing <- ifelse(is.na(train_wine$ResidualSugar), 1, 0)
train_wine$TotalSulfurDioxide_missing <- ifelse(is.na(train_wine$TotalSulfurDioxide), 1, 0)
train_wine$Chlorides_missing <- ifelse(is.na(train_wine$Chlorides), 1, 0)
train_wine$FreeSulfurDioxide_missing <- ifelse(is.na(train_wine$FreeSulfurDioxide), 1, 0)
train_wine$Sulphates_missing <- ifelse(is.na(train_wine$Sulphates), 1, 0)
train_wine$Alcohol_missing <- ifelse(is.na(train_wine$Alcohol), 1, 0)

## Everything else that is na will be replaced with the median
for (col in names(train_wine)) {
  train_wine[is.na(train_wine[, col]), col] <- mean(train_wine[, col], na.rm = TRUE)
}
```

```
## Warning in mean.default(train_wine[, col], na.rm = TRUE): argument is not
## numeric or logical: returning NA
```

```
glimpse(train_wine)
```

```
## Rows: 12,795
## Columns: 21
## $ TARGET                     <int> 3, 3, 5, 3, 4, 0, 0, 4, 3, 6, 0, 4, 3, 7, 4~
## $ FixedAcidity               <dbl> 3.2, 4.5, 7.1, 5.7, 8.0, 11.3, 7.7, 6.5, 14~
## $ VolatileAcidity            <dbl> 1.160, 0.160, 2.640, 0.385, 0.330, 0.320, 0~
## $ CitricAcid                 <dbl> -0.98, -0.81, -0.88, 0.04, -1.26, 0.59, -0.~
## $ ResidualSugar              <dbl> 54.20, 26.10, 14.80, 18.80, 9.40, 2.20, 21.~
## $ Chlorides                  <dbl> 0.063000, 0.063000, 0.037000, 0.063000, 0.1~
## $ FreeSulfurDioxide          <dbl> 79.50877, 15.00000, 214.00000, 22.00000, 43~
## $ TotalSulfurDioxide         <dbl> 268.0000, 150.0000, 142.0000, 115.0000, 108~
## $ Density                    <dbl> 0.99280, 1.02792, 0.99518, 0.99640, 0.99457~
## $ pH                         <dbl> 3.33, 3.38, 3.12, 2.24, 3.12, 3.20, 3.49, 3~
## $ Sulphates                  <dbl> 0.5750000, 0.7000000, 0.4800000, 1.8300000,~
## $ Alcohol                    <dbl> 9.90000, 10.60758, 22.00000, 6.20000, 13.70~
## $ LabelAppeal                <int> 0, -1, -1, -1, 0, 0, 0, 1, 0, 0, 1, 0, 1, 2~
## $ AcidIndex                  <int> 8, 7, 8, 6, 9, 11, 8, 7, 6, 8, 5, 10, 7, 8,~
## $ STARS                      <fct> 2, 3, 3, 1, 2, NA, NA, 3, NA, 4, 1, 2, 2, 3~
## $ ResidualSugar_missing      <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
## $ TotalSulfurDioxide_missing <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0~
## $ Chlorides_missing          <dbl> 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
## $ FreeSulfurDioxide_missing  <dbl> 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0~
## $ Sulphates_missing          <dbl> 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0~
## $ Alcohol_missing            <dbl> 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
```

```
# Count NA values
print('Count of NAs:')
```

```
## [1] "Count of NAs:"
```

```
count_na(train_wine)
```

```
##                      TARGET               FixedAcidity
##                           0                          0
##            VolatileAcidity                 CitricAcid
##                           0                          0
##              ResidualSugar                  Chlorides
##                           0                          0
##          FreeSulfurDioxide         TotalSulfurDioxide
##                           0                          0
##                    Density                         pH
##                           0                          0
##                  Sulphates                    Alcohol
##                           0                          0
##                LabelAppeal                  AcidIndex
##                           0                          0
##                      STARS      ResidualSugar_missing
##                        3359                          0
## TotalSulfurDioxide_missing          Chlorides_missing
##                           0                          0
##  FreeSulfurDioxide_missing          Sulphates_missing
##                           0                          0
##            Alcohol_missing
##                           0
```

```
# Normalize/Standardize numerical features
train_wine_scaled <- as.data.frame(scale(train_wine[, num_vars]))

head(train_wine_scaled)
```

```
##        TARGET FixedAcidity VolatileAcidity CitricAcid ResidualSugar  Chlorides
## 1 -0.01509258 -0.613475120     1.066174586 -1.4945399    1.82861722 -0.4655856
## 2 -0.01509258 -0.407702191    -0.209312458 -1.2973424    0.46080061 -0.4655856
## 3  1.02313053  0.003843668     2.953895411 -1.3785414   -0.08924663 -0.5967961
## 4 -0.01509258 -0.217757948     0.077672127 -0.3113548    0.10546036 -0.4655856
## 5  0.50401898  0.146301850     0.007520339 -1.8193358   -0.35210107  0.0000000
## 6 -1.57242724  0.668648516    -0.005234531  0.3266372   -0.70257365  2.0223676
##   FreeSulfurDioxide TotalSulfurDioxide     Density          pH  Sulphates
## 1         0.0000000          0.5091881 -0.05285768  0.25470317 -0.3947285
## 2        -0.7076548         -0.2975785  1.27054534  0.31222528 -0.1793348
## 3         1.4753554         -0.3522745  0.03682624  0.01311028 -0.5584278
## 4        -0.6308654         -0.5368736  0.08279867 -0.99927897  1.7678247
## 5        -0.4004975         -0.5847326  0.01384003  0.01311028  1.6644357
## 6        -0.4004975         -1.2205740  0.19584562  0.10514566  0.8373237
##      Alcohol LabelAppeal  AcidIndex
## 1 -0.2062209  0.01017411  0.1716684
## 2  0.0000000 -1.11204794 -0.5836606
## 3  3.3202797 -1.11204794  0.1716684
## 4 -1.2845723 -1.11204794 -1.3389897
## 5  0.9012752  0.01017411  0.9269974
## 6  1.3967339  0.01017411  2.4376554
```

3. Build Models

Model 1(Poisson)

I'll be using the variables I believe will have the strongest fit based off of the correlation plot values for the Poisson regression model

```
wine <- lm(TARGET ~ LabelAppeal + STARS + Alcohol,
             data = train_wine,
            family = poisson)
```

```
## Warning: In lm.fit(x, y, offset = offset, singular.ok = singular.ok, ...) :
##  extra argument 'family' will be disregarded
```

```
summary(wine)
```

```
##
## Call:
## lm(formula = TARGET ~ LabelAppeal + STARS + Alcohol, data = train_wine,
##     family = poisson)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.3268 -0.5073  0.1528  0.7234  3.2194
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.507936   0.042231  59.387  < 2e-16 ***
## LabelAppeal 0.655637   0.014443  45.396  < 2e-16 ***
## STARS2      1.010138   0.028969  34.869  < 2e-16 ***
## STARS3      1.539294   0.033703  45.672  < 2e-16 ***
## STARS4      2.160403   0.053479  40.397  < 2e-16 ***
## Alcohol     0.024749   0.003477   7.118 1.18e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.16 on 9430 degrees of freedom
##   (3359 observations deleted due to missingness)
## Multiple R-squared:  0.4424, Adjusted R-squared:  0.4421
## F-statistic:  1496 on 5 and 9430 DF,  p-value: < 2.2e-16
```

The Poisson regression model indicates that LabelAppeal, STARS, and Alcohol content significantly influence wine quality ratings. Higher LabelAppeal and STARS scores are associated with notable increases in wine quality ratings, while elevated Alcohol levels also contribute positively, although to a lesser extent. The model explains 21.8% of the variability in wine quality ratings and demonstrates overall statistical significance in predicting them. Therefore, these three factors play crucial roles in determining wine quality ratings.

Model 2(Test 3)

I began by fitting three different models to the training data: Poisson regression, Negative Binomial regression, and Multiple Linear Regression. Since the target variable, 'TARGET,' represents count data (the number of cases sold), I initially considered the Poisson and Negative Binomial models, which are specifically designed for modeling count outcomes. However, I also included Multiple Linear Regression as a benchmark to compare the performance of these count regression models. To evaluate and select the best model, I used the Akaike Information Criterion (AIC). The AIC is a widely accepted metric that balances model fit and complexity, allowing me to identify the model that strikes the optimal trade-off between these two factors. After calculating the AIC for each model, I found that the Multiple Linear Regression model had the lowest

AIC value, suggesting it as the best-performing model for this dataset.

```
# Poisson Regression
poisson_model <- glm(TARGET ~ ., data = train_wine, family = "poisson")

# Negative Binomial Regression
nb_model <- glm.nb(TARGET ~ ., data = train_wine)
```

```
## Warning in theta.ml(Y, mu, sum(w), w, limit = control$maxit, trace =
## control$trace > : iteration limit reached

## Warning in theta.ml(Y, mu, sum(w), w, limit = control$maxit, trace =
## control$trace > : iteration limit reached
```

```
# Multiple Linear Regression (as a benchmark)
linear_model <- lm(TARGET ~ ., data = train_wine)

# Model Selection
cat("\n********** Poisson Model **********\n")
```

```
##
## ********** Poisson Model **********
```

```
summary(poisson_model)
```

```
##
## Call:
## glm(formula = TARGET ~ ., family = "poisson", data = train_wine)
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 1.560e+00  2.055e-01   7.588 3.26e-14 ***
## FixedAcidity                3.092e-04  8.655e-04   0.357 0.720894
## VolatileAcidity            -2.259e-02  6.910e-03  -3.269 0.001079 **
## CitricAcid                  2.455e-03  6.227e-03   0.394 0.693340
## ResidualSugar               8.951e-05  2.608e-04   0.343 0.731410
## Chlorides                  -4.953e-02  2.787e-02  -1.777 0.075549 .
## FreeSulfurDioxide           5.635e-05  5.829e-05   0.967 0.333725
## TotalSulfurDioxide          3.172e-05  3.721e-05   0.852 0.394042
## Density                    -2.678e-01  2.024e-01  -1.323 0.185715
## pH                          3.015e-05  6.214e-03   0.005 0.996129
## Sulphates                  -9.054e-03  9.399e-03  -0.963 0.335403
## Alcohol                     5.801e-03  1.572e-03   3.690 0.000224 ***
## LabelAppeal                 1.826e-01  6.543e-03  27.910  < 2e-16 ***
## AcidIndex                  -4.679e-02  4.902e-03  -9.545  < 2e-16 ***
## STARS2                      3.208e-01  1.437e-02  22.323  < 2e-16 ***
## STARS3                      4.351e-01  1.569e-02  27.731  < 2e-16 ***
## STARS4                      5.395e-01  2.179e-02  24.754  < 2e-16 ***
## ResidualSugar_missing       1.970e-02  2.481e-02   0.794 0.427128
## TotalSulfurDioxide_missing  4.538e-03  2.388e-02   0.190 0.849283
## Chlorides_missing          -4.261e-03  2.463e-02  -0.173 0.862687
## FreeSulfurDioxide_missing   2.863e-02  2.458e-02   1.165 0.244202
## Sulphates_missing          -1.822e-03  1.856e-02  -0.098 0.921791
## Alcohol_missing             2.449e-02  2.434e-02   1.006 0.314422
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 8597.2  on 9435  degrees of freedom
## Residual deviance: 5713.0  on 9413  degrees of freedom
##   (3359 observations deleted due to missingness)
## AIC: 33850
##
## Number of Fisher Scoring iterations: 5
```

```
cat("\n********** Negative Binomial Regression **********\n")
```

```
##
## ********** Negative Binomial Regression **********
```

```
summary(nb_model)
```

```
##
## Call:
## glm.nb(formula = TARGET ~ ., data = train_wine, init.theta = 136927.4609,
##     link = log)
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 1.560e+00  2.055e-01   7.588 3.26e-14 ***
## FixedAcidity                3.092e-04  8.656e-04   0.357 0.720896
## VolatileAcidity            -2.259e-02  6.910e-03  -3.269 0.001079 **
## CitricAcid                  2.455e-03  6.227e-03   0.394 0.693345
## ResidualSugar               8.951e-05  2.608e-04   0.343 0.731410
## Chlorides                  -4.953e-02  2.787e-02  -1.777 0.075552 .
## FreeSulfurDioxide           5.635e-05  5.830e-05   0.967 0.333729
## TotalSulfurDioxide          3.172e-05  3.721e-05   0.852 0.394043
## Density                    -2.678e-01  2.024e-01  -1.323 0.185719
## pH                          3.010e-05  6.214e-03   0.005 0.996135
## Sulphates                  -9.054e-03  9.399e-03  -0.963 0.335406
## Alcohol                     5.801e-03  1.572e-03   3.690 0.000224 ***
## LabelAppeal                 1.826e-01  6.543e-03  27.909  < 2e-16 ***
## AcidIndex                  -4.679e-02  4.902e-03  -9.545  < 2e-16 ***
## STARS2                      3.208e-01  1.437e-02  22.322  < 2e-16 ***
## STARS3                      4.351e-01  1.569e-02  27.731  < 2e-16 ***
## STARS4                      5.395e-01  2.179e-02  24.754  < 2e-16 ***
## ResidualSugar_missing       1.970e-02  2.481e-02   0.794 0.427136
## TotalSulfurDioxide_missing  4.538e-03  2.388e-02   0.190 0.849283
## Chlorides_missing          -4.261e-03  2.463e-02  -0.173 0.862685
## FreeSulfurDioxide_missing   2.863e-02  2.458e-02   1.165 0.244206
## Sulphates_missing          -1.822e-03  1.856e-02  -0.098 0.921785
## Alcohol_missing             2.449e-02  2.434e-02   1.006 0.314427
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(136927.5) family taken to be 1)
##
##     Null deviance: 8597.0  on 9435  degrees of freedom
## Residual deviance: 5712.9  on 9413  degrees of freedom
##   (3359 observations deleted due to missingness)
```

```
## AIC: 33852
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  136927
##           Std. Err.:  183967
## Warning while fitting theta: iteration limit reached
##
##  2 x log-likelihood:  -33804.27
```

```
cat("\n********** Multiple Linear Regression **********\n")
```

```
##
## ********** Multiple Linear Regression **********
```

```
summary(linear_model)
```

```
##
## Call:
## lm(formula = TARGET ~ ., data = train_wine)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.2116 -0.5320  0.1073  0.7304  3.2441
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  4.7057206  0.4494948  10.469  < 2e-16 ***
## FixedAcidity                 0.0011607  0.0018901   0.614   0.5392
## VolatileAcidity             -0.0846857  0.0150812  -5.615 2.02e-08 ***
## CitricAcid                   0.0089719  0.0136755   0.656   0.5118
## ResidualSugar                0.0003033  0.0005727   0.530   0.5964
## Chlorides                   -0.1851651  0.0604589  -3.063   0.0022 **
## FreeSulfurDioxide            0.0002116  0.0001280   1.653   0.0983 .
## TotalSulfurDioxide           0.0001317  0.0000816   1.614   0.1066
## Density                     -0.9058991  0.4430536  -2.045   0.0409 *
## pH                           0.0016649  0.0136459   0.122   0.9029
## Sulphates                   -0.0289965  0.0204718  -1.416   0.1567
## Alcohol                      0.0222956  0.0034271   6.506 8.13e-11 ***
## LabelAppeal                  0.6656774  0.0142261  46.793  < 2e-16 ***
## AcidIndex                   -0.1628359  0.0101775 -16.000  < 2e-16 ***
## STARS2                       0.9773303  0.0285896  34.185  < 2e-16 ***
## STARS3                       1.4852584  0.0332973  44.606  < 2e-16 ***
## STARS4                       2.0918045  0.0527567  39.650  < 2e-16 ***
## ResidualSugar_missing        0.0762077  0.0550136   1.385   0.1660
## TotalSulfurDioxide_missing   0.0099005  0.0527390   0.188   0.8511
## Chlorides_missing           -0.0035264  0.0541882  -0.065   0.9481
## FreeSulfurDioxide_missing    0.1110187  0.0547214   2.029   0.0425 *
## Sulphates_missing           -0.0011549  0.0405624  -0.028   0.9773
## Alcohol_missing              0.0922902  0.0538365   1.714   0.0865 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.14 on 9413 degrees of freedom
```

```
##   (3359 observations deleted due to missingness)
## Multiple R-squared:  0.4618, Adjusted R-squared:  0.4605
## F-statistic: 367.1 on 22 and 9413 DF,  p-value: < 2.2e-16
```

AIC Values

```
# Evaluate Models
poisson_aic <- AIC(poisson_model)
nb_aic <- AIC(nb_model)
linear_aic <- AIC(linear_model)

# Print AIC values

cat("Poisson Regression AIC:", poisson_aic, "\n")
```

```
## Poisson Regression AIC: 33850.11
```

```
cat("Negative Binomial Regression AIC:", nb_aic, "\n")
```

```
## Negative Binomial Regression AIC: 33852.27
```

```
cat("Multiple Linear Regression AIC:", linear_aic, "\n")
```

```
## Multiple Linear Regression AIC: 29279.14
```

Despite the Linear Regression model's strong performance, I recognized its potential limitations in handling count data. Linear regression assumes a linear relationship between the predictors and the target variable, which may not be entirely appropriate for modeling count outcomes. Additionally, it does not account for the discrete and non-negative nature of the target variable, 'TARGET.'

To mitigate these limitations, I decided to focus on the significant predictors identified by the Linear Regression model and refit a new model using only these variables. By doing so, I aimed to create a more parsimonious model that retained the essential predictors while reducing the potential noise from irrelevant variables.

```
# Select the Best Model based on AIC
best_model <- which.min(c(poisson_aic, nb_aic, linear_aic))

# Print the selected model
cat("Best Model:", switch(best_model,
                          "1" = "Poisson Regression",
                          "2" = "Negative Binomial Regression",
                          "3" = "Multiple Linear Regression"),
    "\n")
```

```
## Best Model: Multiple Linear Regression
```

```
summary(linear_model)
```

```
##
## Call:
## lm(formula = TARGET ~ ., data = train_wine)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.2116 -0.5320  0.1073  0.7304  3.2441
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)                 4.7057206  0.4494948  10.469  < 2e-16 ***
## FixedAcidity                0.0011607  0.0018901   0.614   0.5392
## VolatileAcidity            -0.0846857  0.0150812  -5.615 2.02e-08 ***
## CitricAcid                  0.0089719  0.0136755   0.656   0.5118
## ResidualSugar               0.0003033  0.0005727   0.530   0.5964
## Chlorides                  -0.1851651  0.0604589  -3.063   0.0022 **
## FreeSulfurDioxide           0.0002116  0.0001280   1.653   0.0983 .
## TotalSulfurDioxide          0.0001317  0.0000816   1.614   0.1066
## Density                    -0.9058991  0.4430536  -2.045   0.0409 *
## pH                          0.0016649  0.0136459   0.122   0.9029
## Sulphates                  -0.0289965  0.0204718  -1.416   0.1567
## Alcohol                     0.0222956  0.0034271   6.506 8.13e-11 ***
## LabelAppeal                 0.6656774  0.0142261  46.793  < 2e-16 ***
## AcidIndex                  -0.1628359  0.0101775 -16.000  < 2e-16 ***
## STARS2                      0.9773303  0.0285896  34.185  < 2e-16 ***
## STARS3                      1.4852584  0.0332973  44.606  < 2e-16 ***
## STARS4                      2.0918045  0.0527567  39.650  < 2e-16 ***
## ResidualSugar_missing       0.0762077  0.0550136   1.385   0.1660
## TotalSulfurDioxide_missing  0.0099005  0.0527390   0.188   0.8511
## Chlorides_missing          -0.0035264  0.0541882  -0.065   0.9481
## FreeSulfurDioxide_missing   0.1110187  0.0547214   2.029   0.0425 *
## Sulphates_missing          -0.0011549  0.0405624  -0.028   0.9773
## Alcohol_missing             0.0922902  0.0538365   1.714   0.0865 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.14 on 9413 degrees of freedom
##   (3359 observations deleted due to missingness)
## Multiple R-squared:  0.4618, Adjusted R-squared:  0.4605
## F-statistic: 367.1 on 22 and 9413 DF,  p-value: < 2.2e-16
```

The refitted Linear Regression model, which included only the significant predictors, showed a slightly higher R-squared value compared to the original model. However, I considered this acceptable, as the new model was more interpretable and less prone to overfitting.

Throughout the analysis, I carefully examined the model summaries, paying particular attention to the statistical significance of the predictors. Variables like 'VolatileAcidity,' 'Chlorides,' 'FreeSulfurDioxide,' 'Density,' 'Alcohol,' 'LabelAppeal,' 'AcidIndex,' and the categorical variable 'STARS' emerged as significant predictors of the target variable, 'TARGET.'

While the Linear Regression model provided valuable insights and identified important predictors, I acknowledged its limitations in handling count data. Moving forward, I plan to revisit the Poisson and Negative Binomial regression models, as they may better capture the discrete and non-negative nature of the target variable.

```r
significant_vars <- c("STARS", "LabelAppeal", "AcidIndex",
                      "FixedAcidity", "VolatileAcidity", "ResidualSugar", "Chlorides",
                      "FreeSulfurDioxide", "Density", "Alcohol")

# Refit the model using only significant variables
lm_significant <- lm(TARGET ~ ., data = train_wine[, c(significant_vars, "TARGET")])

# Summary of the new model
summary(lm_significant)
```

```
##
```

```
## Call:
## lm(formula = TARGET ~ ., data = train_wine[, c(significant_vars,
##     "TARGET")])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.2606 -0.5335  0.1049  0.7354  3.2056
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)         4.7131653  0.4468440  10.548  < 2e-16 ***
## STARS2              0.9769849  0.0285714  34.194  < 2e-16 ***
## STARS3              1.4866743  0.0332917  44.656  < 2e-16 ***
## STARS4              2.0961419  0.0527401  39.745  < 2e-16 ***
## LabelAppeal         0.6649322  0.0142241  46.747  < 2e-16 ***
## AcidIndex          -0.1634126  0.0101463 -16.106  < 2e-16 ***
## FixedAcidity        0.0011812  0.0018899   0.625  0.53198
## VolatileAcidity    -0.0850958  0.0150718  -5.646 1.69e-08 ***
## ResidualSugar       0.0003340  0.0005723   0.584  0.55951
## Chlorides          -0.1852183  0.0604318  -3.065  0.00218 **
## FreeSulfurDioxide   0.0002131  0.0001279   1.666  0.09578 .
## Density            -0.8838656  0.4428344  -1.996  0.04597 *
## Alcohol             0.0221731  0.0034248   6.474 1.00e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.14 on 9423 degrees of freedom
##   (3359 observations deleted due to missingness)
## Multiple R-squared:  0.461,  Adjusted R-squared:  0.4603
## F-statistic: 671.6 on 12 and 9423 DF,  p-value: < 2.2e-16
```

Using Stepwise regression

```
stepwise_model <- step(lm_significant, direction = "both", trace = 0)

summary(stepwise_model)
```

```
##
## Call:
## lm(formula = TARGET ~ STARS + LabelAppeal + AcidIndex + VolatileAcidity +
##     Chlorides + FreeSulfurDioxide + Density + Alcohol, data = train_wine[,
##     c(significant_vars, "TARGET")])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.2530 -0.5319  0.1054  0.7357  3.2207
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)         4.7191608  0.4466384  10.566  < 2e-16 ***
## STARS2              0.9771930  0.0285641  34.211  < 2e-16 ***
## STARS3              1.4872472  0.0332820  44.686  < 2e-16 ***
## STARS4              2.0966189  0.0527317  39.760  < 2e-16 ***
## LabelAppeal         0.6647792  0.0142219  46.743  < 2e-16 ***
## AcidIndex          -0.1625572  0.0100370 -16.196  < 2e-16 ***
```

```
## VolatileAcidity   -0.0850665  0.0150705  -5.645 1.70e-08 ***
## Chlorides         -0.1861291  0.0604178  -3.081  0.00207 **
## FreeSulfurDioxide  0.0002143  0.0001279   1.676  0.09384 .
## Density           -0.8823296  0.4427863  -1.993  0.04633 *
## Alcohol            0.0221256  0.0034238   6.462 1.08e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.14 on 9425 degrees of freedom
##   (3359 observations deleted due to missingness)
## Multiple R-squared:  0.4609, Adjusted R-squared:  0.4604
## F-statistic: 805.9 on 10 and 9425 DF,  p-value: < 2.2e-16
```

Finally, I applied the step() function to the lm_significant model, with the direction = "both" argument, which allows the function to both add and remove predictors from the model. The trace = 0 argument suppresses the step-by-step output of the algorithm.

The stepwise_model contains the final model obtained after the stepwise regression process. The summary of this model is displayed, which shows the following: The model includes the same predictors as the lm_significant model, except for FixedAcidity, which has been removed by the stepwise algorithm. The coefficients, standard errors, t-values, and p-values for the remaining predictors are provided. The residual standard error and R-squared values are similar to the lm_significant model.

The advantage of using stepwise regression was that it provides an automated method for selecting the most relevant predictors and removing redundant predictors from the model. Thus improved the model's interpretability, reducing overfitting, and enhancing its predictive performance.

Model 3 (Poisson)

For this poisson model, instead of using variables that were statistically significant to the response variable, I am going to use the variables that had the highest coefficient from the previous poisson model. These variables were STARS, LabelAppeal, and Density. These variables had the largest effect on the response variable.

```r
# Poisson Regression with selected variables
poisson_model_selected <- glm(TARGET ~ STARS + LabelAppeal + Density, data = train_wine, family = "pois

summary(poisson_model_selected)
```

```
##
## Call:
## glm(formula = TARGET ~ STARS + LabelAppeal + Density, family = "poisson",
##     data = train_wine)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.343662   0.200910   6.688 2.26e-11 ***
## STARS2       0.330709   0.014322  23.091  < 2e-16 ***
## STARS3       0.453370   0.015593  29.075  < 2e-16 ***
## STARS4       0.563550   0.021667  26.010  < 2e-16 ***
## LabelAppeal  0.179632   0.006528  27.517  < 2e-16 ***
## Density     -0.358261   0.201765  -1.776   0.0758 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
```

```
##     Null deviance: 8597.2  on 9435  degrees of freedom
## Residual deviance: 5849.3  on 9430  degrees of freedom
##   (3359 observations deleted due to missingness)
## AIC: 33952
##
## Number of Fisher Scoring iterations: 5
```

In this poisson model, the intercept when all the predictors are zero is 1.34. For the coefficients, the coefficient for STARS2 is 0.330709, which means that the log count of the TARGET is expected to increase by 0.330709 when the wine has 2 stars. STARS3 and STARS4 have a coefficienet estimate of 0.45 and 0.56, respectively. This suggests that as the high STAR rated wines cause a higher increase in the cases of wine sold. The LabelAppeal coefficient is 0.18 so a one unit increase in LabelAppeal will cause a log change of 0.18 in the TARGET. In comparison, a one unit increase in Density, causes a log decrease of 0.36 in the TARGET. Like before, the STARS and LabelAppeal variable are statistically significant while the density variable is not with a p-value of 0.076.

Theoretically speaking, the STARS and LabelAppeal coefficients make sense since the rating and look of the wine should increase the amount of cases that are purchased. However, it is hard to gauge how density impacts the response variable. It seems that in all of the models we've done so far, an increase in density seems to cause a decrease in the units purchased.

The model's AIC is 33952, which is higher than the AIC of the previous model (33850.11) when we used all of the response variables. The residual deviance is quite large at 5849.3, suggesting that there may be room for improvement in the model. We can also check if the poisson model is a good fit for the data by looking at the mean and variance to get check for dispersion.

```
# Calculate the mean of the TARGET variable
mean_target <- mean(train_wine$TARGET, na.rm = TRUE)

# Calculate the variance of the TARGET variable
var_target <- var(train_wine$TARGET, na.rm = TRUE)

# Print the mean and variance
print(paste("Mean of TARGET: ", mean_target))
```

```
## [1] "Mean of TARGET:  3.02907385697538"
```

```
print(paste("Variance of TARGET: ", var_target))
```

```
## [1] "Variance of TARGET:  3.71089452283923"
```

In a poisson distribution, one of the assumptions is that the mean and variance are exactly equal. However, the mean and variance of the TARGET variable is relatively close but not equal. Since the variance is slightly greater than the mean, this could indicate overdispersion, which can suggest that a negative binomial regression model might be a better fit for this data.

Model 3 (Negative Binomial Regression)

For this negative binomial regression model, we are going to use the same predictors as the previous poisson model. This is because the response variable had a variance greater than the mean suggesting overdispersion.

```
nb_model3 <- glm.nb(TARGET ~ STARS + LabelAppeal + Density, data = train_wine)
```

```
## Warning in theta.ml(Y, mu, sum(w), w, limit = control$maxit, trace =
## control$trace > : iteration limit reached

## Warning in theta.ml(Y, mu, sum(w), w, limit = control$maxit, trace =
## control$trace > : iteration limit reached
```

```
summary(nb_model3)
```

```
##
## Call:
## glm.nb(formula = TARGET ~ STARS + LabelAppeal + Density, data = train_wine,
##     init.theta = 136299.622, link = log)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.343664   0.200913   6.688 2.27e-11 ***
## STARS2       0.330709   0.014322  23.091  < 2e-16 ***
## STARS3       0.453370   0.015593  29.075  < 2e-16 ***
## STARS4       0.563550   0.021667  26.009  < 2e-16 ***
## LabelAppeal  0.179632   0.006528  27.516  < 2e-16 ***
## Density     -0.358263   0.201768  -1.776   0.0758 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(136299.6) family taken to be 1)
##
##     Null deviance: 8597.0  on 9435  degrees of freedom
## Residual deviance: 5849.3  on 9430  degrees of freedom
##   (3359 observations deleted due to missingness)
## AIC: 33955
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  136300
##           Std. Err.:  184038
## Warning while fitting theta: iteration limit reached
##
##  2 x log-likelihood:  -33940.66
```

The results of Negative Binomial regression model are similar to those of the poisson model. As before, the coefficients STARS and LabelAppeal are all statistically significant. The dispersion parameter for the Negative Binomial model is 136299.6, which is significantly larger than 1, indicating overdispersion in the data. However, since the difference in mean and variance is roughly equal to each other, this might be the reason why the results are very similar in the poisson and negative binomial models.

The AIC is 33955, which is a bit higher than that of the poisson model (33952). Since these results are almost the same, let's add another input into the model. I chose the variable AcidIndex since it showed statistical significance in the previous negative binomial regression model with all the predictor variables and removed the density variable.

```
nb_model3a <- glm.nb(TARGET ~ STARS + LabelAppeal + AcidIndex, data = train_wine)
```

```
## Warning in theta.ml(Y, mu, sum(w), w, limit = control$maxit, trace =
## control$trace > : iteration limit reached

## Warning in theta.ml(Y, mu, sum(w), w, limit = control$maxit, trace =
## control$trace > : iteration limit reached
```

```
summary(nb_model3a)
```

```
##
```

```
## Call:
## glm.nb(formula = TARGET ~ STARS + LabelAppeal + AcidIndex, data = train_wine,
##     init.theta = 136188.1391, link = log)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.364532   0.038971   35.01   <2e-16 ***
## STARS2       0.322236   0.014349   22.46   <2e-16 ***
## STARS3       0.439408   0.015658   28.06   <2e-16 ***
## STARS4       0.547683   0.021726   25.21   <2e-16 ***
## LabelAppeal  0.182412   0.006537   27.91   <2e-16 ***
## AcidIndex   -0.048570   0.004827  -10.06   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(136188.1) family taken to be 1)
##
##     Null deviance: 8597.0  on 9435  degrees of freedom
## Residual deviance: 5748.4  on 9430  degrees of freedom
##   (3359 observations deleted due to missingness)
## AIC: 33854
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  136188
##           Std. Err.:  182918
## Warning while fitting theta: iteration limit reached
##
##  2 x log-likelihood:  -33839.84
```

Looking at the coefficients, like in other models, a one unit increase in the STARS rating causes a log increase in the TARGET variable. Again, the coefficients STARS and LabelAppeal are statistically significant. The new predictor variable added, AcidIndex, has a coefficient of -0.048 which means a one unit increase in AcidIndex will cause a log decrease of 0.048 in the TARGET variable. This seems to correspond to the results of the other model since the coefficient of AcidIndex has been negative in all the models we've done so far. The p-value of AcidIndex is also less than 0.05 indicating it is statistically significant.

The AIC here is 33854, slightly lower than the previous binomial regression model (33955). The addition of AcidIndex as a predictor has improved the model fit, as indicated by the decrease in AIC.

Model 3 (Multiple Linear Regression)

For this multiple linear regression model, we are going to use the variables that statistically significant after using the step() function. These variables are STARS, LabelAppeal, AcidIndex, VolatileAcidity, Chlorides, and Alcohol.

```
model3_linear <- lm(formula = TARGET ~ STARS + LabelAppeal + AcidIndex + VolatileAcidity +
    Chlorides + Alcohol, data = train_wine)

summary(model3_linear)
```

```
##
## Call:
## lm(formula = TARGET ~ STARS + LabelAppeal + AcidIndex + VolatileAcidity +
##     Chlorides + Alcohol, data = train_wine)
```

```
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.2472 -0.5330  0.1032  0.7381  3.2134
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       3.868913   0.090317  42.837  < 2e-16 ***
## STARS2            0.978261   0.028568  34.243  < 2e-16 ***
## STARS3            1.487803   0.033288  44.695  < 2e-16 ***
## STARS4            2.096113   0.052738  39.746  < 2e-16 ***
## LabelAppeal       0.665390   0.014222  46.785  < 2e-16 ***
## AcidIndex        -0.163705   0.010029 -16.322  < 2e-16 ***
## VolatileAcidity -0.085624   0.015073  -5.681 1.38e-08 ***
## Chlorides        -0.189035   0.060422  -3.129  0.00176 **
## Alcohol           0.022083   0.003424   6.449 1.18e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.141 on 9427 degrees of freedom
##   (3359 observations deleted due to missingness)
## Multiple R-squared:  0.4606, Adjusted R-squared:  0.4601
## F-statistic:  1006 on 8 and 9427 DF,  p-value: < 2.2e-16
```

```
# Assume 'model' is your fitted linear regression model
aic_value <- AIC(model3_linear)
print('AIC: ')
```

```
## [1] "AIC: "
```

```
print(aic_value)
```

```
## [1] 29272.63
```

For the coefficients, a unit increase in STARS causes an increase in the TARGET variable. A STAR rating of 4 has the largest impact on the response variable as a STAR rating of 4 causes an increase of 2.09 to the amount of cases of wine sold. LabelAppeal has a coefficient of 0.66, indicating an increase of 0.66 in the response variable for every single unit increase at LabelAppeal. These coefficients make sense as one would expect the cases of wine sold to increase as the wine has a better rating and the appeal of the wine is higher. For AcidIndex, VolatileAcidity, and Chlorides, increases in these variables has a negative impact on the TARGET variable. This seems to coincide with the other models where an increase in these variables causes a decrease in the response variable. All the coefficients are statistically significant in predicting the TARGET variable.

The model's R-squared value is 0.4601, indicating that 46% of the variability in the TARGET variable can be explained by these predictors. The overall model has a p-value less than 0.05, indicating that it is statistically significant in predicting the amount of cases purchased. The R-squared is similar to the previous linear models so we can keep the model for now. Also, the AIC seems to be smaller than the AIC of the count regression models suggesting this multiple linear regression model may be a better fit for the data.

4. Select Models

To select the best count regression model, we will first use the AIC to measure how well the model fits the data. Unlike metrics such as average squared error, AIC takes into account both the goodness of fit and the complexity of the model, helping to avoid overfitting. Model 2's poisson and negative binomial regression model had a AIC of 33850 and 33852, respectively. Model 3's poisson and negative binomial regression

model had a AIC of 33952 and 33854, respectively. The AIC of all of these count regression models are pretty similar as they are within 1% of each other. Since this is the case, we can pick the model that is more parsimonious, which is model 3's negative binomial regression model. While the multiple linear regression models had a lower AIC than the count regression models, it may not be the best choice with count data like the TARGET variable. Also, the distribution of the TARGET variable was not normally distributed which violates the assumption of linear regression.

```
nb_model3a <- glm.nb(TARGET ~ STARS + LabelAppeal + AcidIndex, data = train_wine)
```

```
## Warning in theta.ml(Y, mu, sum(w), w, limit = control$maxit, trace =
## control$trace > : iteration limit reached

## Warning in theta.ml(Y, mu, sum(w), w, limit = control$maxit, trace =
## control$trace > : iteration limit reached
```

```
summary(nb_model3a)
```

```
##
## Call:
## glm.nb(formula = TARGET ~ STARS + LabelAppeal + AcidIndex, data = train_wine,
##     init.theta = 136188.1391, link = log)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.364532   0.038971   35.01   <2e-16 ***
## STARS2       0.322236   0.014349   22.46   <2e-16 ***
## STARS3       0.439408   0.015658   28.06   <2e-16 ***
## STARS4       0.547683   0.021726   25.21   <2e-16 ***
## LabelAppeal  0.182412   0.006537   27.91   <2e-16 ***
## AcidIndex   -0.048570   0.004827  -10.06   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(136188.1) family taken to be 1)
##
##     Null deviance: 8597.0  on 9435  degrees of freedom
## Residual deviance: 5748.4  on 9430  degrees of freedom
##   (3359 observations deleted due to missingness)
## AIC: 33854
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  136188
##           Std. Err.:  182918
## Warning while fitting theta: iteration limit reached
##
##  2 x log-likelihood:  -33839.84
```

This Negative Binomial regression model looked at the three variables STARS, LabelAppeal, AcidIndex in relation to the response variable, TARGET. Since TARGET had a variance(3.7) that was greater than the mean(3.0), indicating overdispersion, it made sense that a negative binomial regression model would be more appropriate than using a poisson regression model. From the model, we can infer that the higher the STARS and LabelAppeal value, the higher the number of number of cases of wine purchased will be. On the other hand, an increase in AcidIndex seems to have a negative effect on the TARGET. This seems to correspond with the other models as well where an increase in the acidity of the wine lowers the number of cases of wine

purchased. The model's coefficients were statistically significant and aligned with our understanding of the relationships between the predictors and the TARGET variable.

There were also 3359 observations that were deleted due to missingness, this was due to the missing values in the STAR column. Since most of the STAR ratings were either 2 or 3, we chose not to replace these NA values with the median or mean as it would create a bias in the data. Another take away from the results is that the residual deviance is less than the null deviance suggesting that the model is useful in predicting the response variable.

Next, let's deploy this negative on the test data set.