# Data 621 Homework 5: Wine

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## 0.1 OVERVIEW

In this homework assignment, we will explore, analyze and model a data set containing information on approximately 12,000 commercially available wines. The variables are mostly related to the chemical properties of the wine being sold. The response variable is the number of sample cases of wine that were purchased by wine distribution companies after sampling a wine. These cases would be used to provide tasting samples to restaurants and wine stores around the United States. The more sample cases purchased, the more likely is a wine to be sold at a high end restaurant. A large wine manufacturer is studying the data in order to predict the number of wine cases ordered based upon the wine characteristics. If the wine manufacturer can predict the number of cases, then that manufacturer will be able to adjust their wine offering to maximize sales.

## 0.2 Objective:

Our objective is to build a count regression model to predict the number of cases of wine that will be sold given certain properties of the wine. HINT: Sometimes, the fact that a variable is missing is actually predictive of the target. You can only use the variables given to you (or variables that you derive from the variables provided).

Below is a short description of the variables of interest in the data set:

| VARIABLE.NAME | DEFINITION | THEORETICAL.EFFECT |
|---|---|---|
| INDEX | Identification Variable (do not use) | None |
| TARGET | Number of Cases Purchased | None |
| | | |
| | | |
| AcidIndex | Proprietary method of testing total acidity of wine by using a weighted average, | |
| Alcohol | Alcohol Content | |
| Chlorides | Chloride content of wine | |
| CitricAcid | Citric Acid Content | |
| Density | Density of Wine | |
| FixedAcidity | Fixed Acidity of Wine | |
| FreeSulfurDioxide | Sulfur Dioxide content of wine | |
| LabelAppeal | Marketing Score indicating the appeal of label design for consumers. High numbers suggest customers like the label design. Negative numbers suggest customers don’t like the design | Many consumers purchase based on the visual appeal of the wine label design. Higher numbers suggest better sales. |
| ResidualSugar | Residual Sugar of wine | |
| STARS | Wine rating by a team of experts. 4 Stars = Excellent, 1 Star = Poor | A high number of stars suggests high sales |
| Sulphates | Sulfate content of wine | |
| TotalSulfurDioxide | Total Sulfur Dioxide of Wine | |
| VolatileAcidity | Volatile Acid content of wine | |
| pH | pH of wine | |

# 1 DATA EXPLORATION

## 1.1 Data Summary

With over 12,000 observations in our sample, we must look into the data and explore key summary statistics.

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

We also calculate the counts for NA's, 0, negative, and unique values.

```
##                    vars     n          mean          sd    median
## FixedAcidity          1 12795   7.075717077   6.31764346   6.90000
## VolatileAcidity       2 12795   0.324103947   0.78401424   0.28000
## CitricAcid            3 12795   0.308412661   0.86207979   0.31000
## ResidualSugar         4 12179   5.418733065  33.74937899   3.90000
## Chlorides             5 12157   0.054822489   0.31846729   0.04600
## FreeSulfurDioxide     6 12148  30.845571287 148.71455765  30.00000
## TotalSulfurDioxide    7 12113 120.714232643 231.91321051 123.00000
## Density               8 12795   0.994202718   0.02653765   0.99449
## pH                    9 12400   3.207628226   0.67968708   3.20000
## Sulphates            10 11585   0.527111782   0.93212926   0.50000
## Alcohol              11 12142  10.489236260   3.72781904  10.40000
## LabelAppeal          12 12795  -0.009066041   0.89108925   0.00000
## AcidIndex            13 12795   7.772723720   1.32392637   8.00000
## STARS                14  9436   2.041754981   0.90254005   2.00000
##                         trimmed          mad        min        max
## FixedAcidity         7.073673928 3.261720e+00  -18.10000   34.40000
## VolatileAcidity      0.324388981 4.299540e-01   -2.79000    3.68000
## CitricAcid           0.310252027 4.151280e-01   -3.24000    3.86000
## ResidualSugar        5.580041047 1.571556e+01 -127.80000  141.15000
## Chlorides            0.054015935 1.349166e-01   -1.17100    1.35100
## FreeSulfurDioxide   30.933487654 5.633880e+01 -555.00000  623.00000
## TotalSulfurDioxide 120.889536684 1.349166e+02 -823.00000 1057.00000
## Density              0.994213045 9.355206e-03    0.88809    1.09924
## pH                   3.205570565 3.854760e-01    0.48000    6.13000
## Sulphates            0.527145323 4.447800e-01   -3.13000    4.24000
## Alcohol             10.501825544 2.372160e+00   -4.70000   26.50000
## LabelAppeal         -0.009963857 1.482600e+00   -2.00000    2.00000
## AcidIndex            7.643157175 1.482600e+00    4.00000   17.00000
## STARS                1.971125828 1.482600e+00    1.00000    4.00000
##                        range         skew   kurtosis           se
## FixedAcidity         52.50000 -0.022585961  1.6749987 0.0558515162
## VolatileAcidity       6.47000  0.020379965  1.8322106 0.0069311262
## CitricAcid            7.10000 -0.050307040  1.8379401 0.0076212695
## ResidualSugar       268.95000 -0.053122905  1.8846917 0.3058158360
## Chlorides             2.52200  0.030427175  1.7886044 0.0028883621
## FreeSulfurDioxide  1178.00000  0.006393010  1.8364966 1.3492769213
## TotalSulfurDioxide 1880.00000 -0.007179351  1.6746665 2.1071702666
## Density               0.21115 -0.018693764  1.8999592 0.0002346077
## pH                    5.65000  0.044288014  1.6462681 0.0061037702
## Sulphates             7.37000  0.005911895  1.7525655 0.0086602040
## Alcohol              31.20000 -0.030715836  1.5394949 0.0338306006
## LabelAppeal           4.00000  0.008429457 -0.2622916 0.0078777294
## AcidIndex            13.00000  1.648495945  5.1900925 0.0117042526
## STARS                 3.00000  0.447235292 -0.6925343 0.0092912151
##                    na_count neg_count zero_count unique_count
## FixedAcidity              0      1621        548          470
## VolatileAcidity           0      2827       9982          815
## CitricAcid                0      2966       9686          602
## ResidualSugar           616        NA         NA         2078
## Chlorides               638        NA         NA         1664
## FreeSulfurDioxide       647        NA         NA         1000
## TotalSulfurDioxide      682        NA         NA         1371
## Density                   0         0       9492         5933
## pH                      395        NA         NA          498
## Sulphates              1210        NA         NA          631
## Alcohol                 653        NA         NA          402
## LabelAppeal               0      3640       5617            5
## AcidIndex                 0         0          0           14
## STARS                  3359        NA         NA            5
```

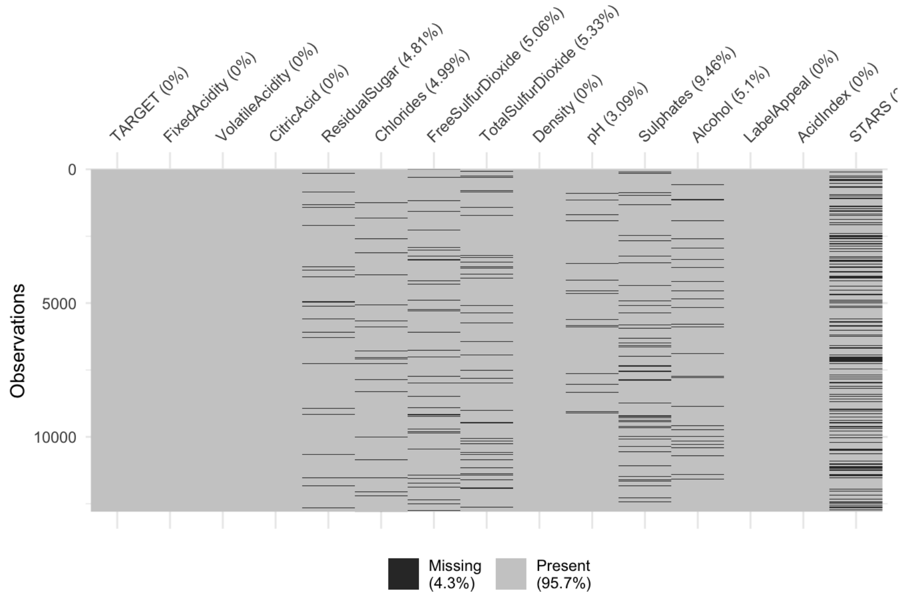
The dataset consists of two data files: training and evaluation. The training dataset contains 16 columns, and the evaluation dataset also contains 16 columns.

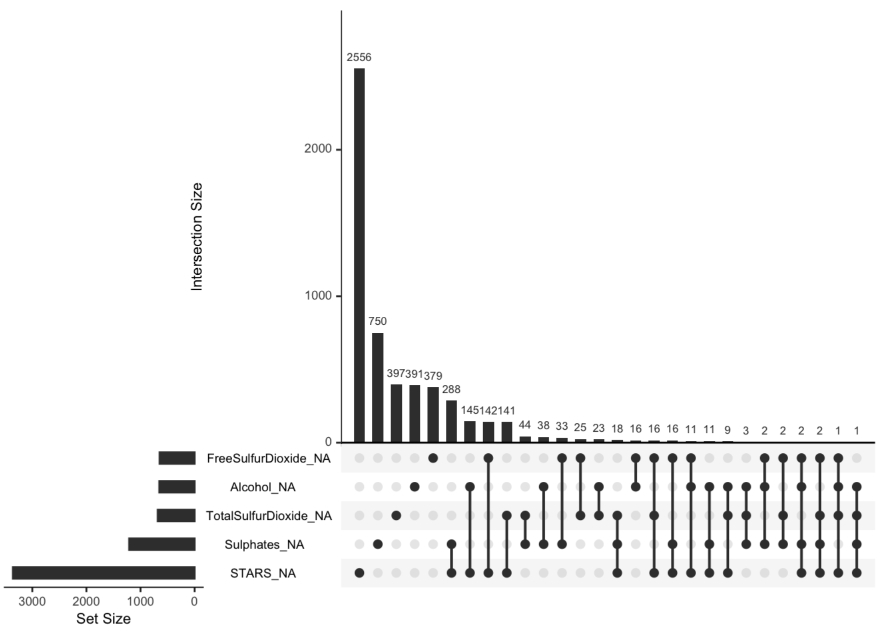
## 1.2 Missing Data

An important aspect of any dataset is to determine how much, if any, data is missing. We look at all the variables to see which if any have missing data. We look at the basic descriptive statistics as well as the missing data and percentages.

We start by looking at the dataset as a whole and determine how many complete rows, that is rows with data for all predictors we have.

```
##    Mode   FALSE    TRUE
## logical    6359    6436
```




With these results, if we remove all rows with incomplete rows, there will be a total of 6436 rows out of 12795, or 50% of the total dataset. We create a subset of data with complete cases if needed later in our analysis.

```
## Observations: 6,436
## Variables: 15
## $ TARGET             <int> 5, 3, 6, 0, 3, 4, 5, 4, 3, 2, 3, 4, 4, 3, 4, …
## $ FixedAcidity       <dbl> 7.1, 5.7, 5.5, -17.2, 6.0, -1.3, 10.0, 6.8, 5…
## $ VolatileAcidity    <dbl> 2.640, 0.385, -0.220, 0.520, 0.330, 0.220, 0.…
## $ CitricAcid         <dbl> -0.88, 0.04, 0.39, 0.15, -1.06, 2.95, 0.27, -…
## $ ResidualSugar      <dbl> 14.80, 18.80, 1.80, -33.80, 3.00, -53.00, 14.…
## $ Chlorides          <dbl> 0.037, -0.425, -0.277, -0.022, 0.518, 0.541, …
## $ FreeSulfurDioxide  <dbl> 214, 22, 62, 551, 5, -85, -188, -88, 87, 15, …
## $ TotalSulfurDioxide <dbl> 142, 115, 180, 65, 378, -266, 229, 508, -283,…
## $ Density            <dbl> 0.99518, 0.99640, 0.94724, 0.99340, 0.96643, …
## $ pH                 <dbl> 3.12, 2.24, 3.09, 4.31, 3.55, 3.61, 3.14, 3.2…
## $ Sulphates          <dbl> 0.48, 1.83, 0.75, 0.56, -0.86, 0.82, 0.88, 0.…
## $ Alcohol            <dbl> 22.0, 6.2, 12.6, 13.1, 3.9, 10.0, 11.0, 18.3,…
## $ LabelAppeal        <int> -1, -1, 0, 1, 1, 0, 1, -1, -1, -1, 0, 0, 1, -…
## $ AcidIndex          <int> 8, 6, 8, 5, 7, 8, 11, 8, 6, 7, 8, 7, 7, 8, 6,…
## $ STARS              <int> 3, 1, 4, 1, 2, 3, 2, 2, 1, 1, 1, 2, 2, 1, 3, …
```

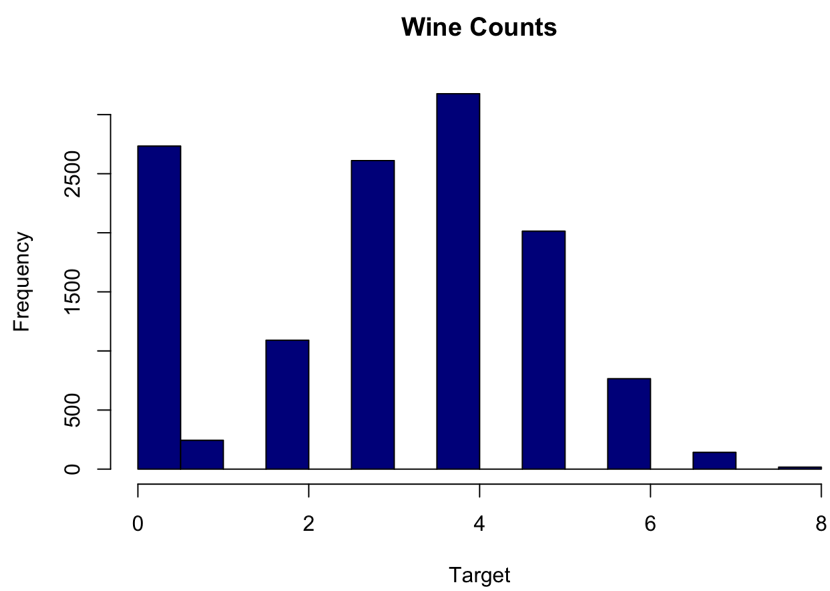
# 1.3 Visualization

We consider each variable

## 1.3.1 Target Variable

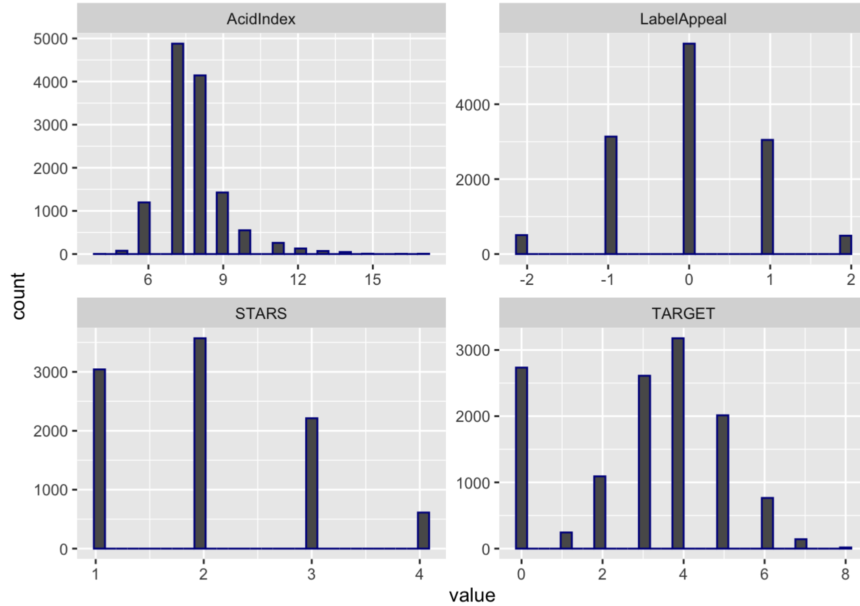
The distribution of our target variable is normal with the exception of many 0 Wine count entries. At such a high percentage, the zero scores likely reflect lack of popularity rather than error, especially if they get low human ratings.

### 1.3.1.1 Histogram



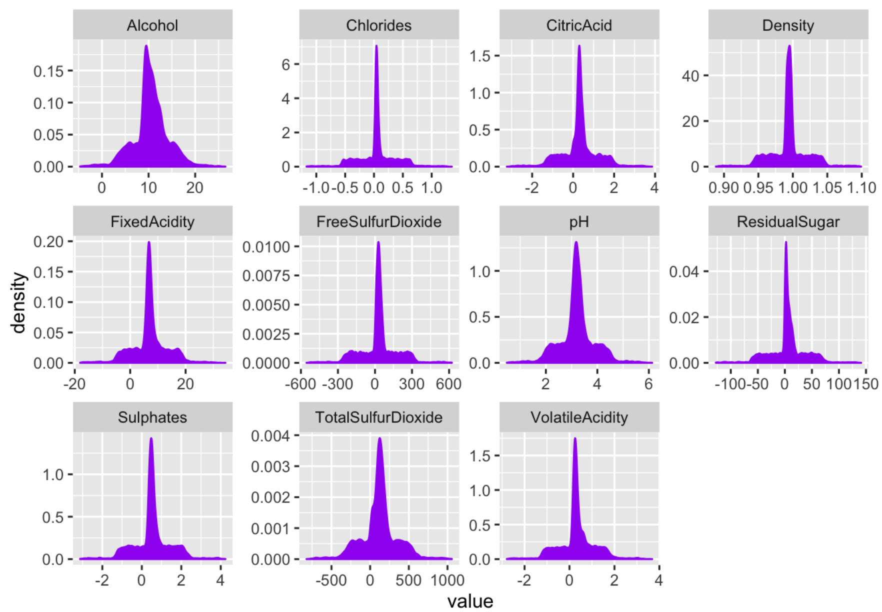

### 1.3.1.2 Integers

The integer variables have a small range and look normal, similar to TARGET. Stars has the least number of values and has many 0 entries. We will treat these as meaningful due to the percentage of NA’s. Decision makers who buy wine are similar to the population who creates the integer variables and the range of values is small, so we choose not to impute these.



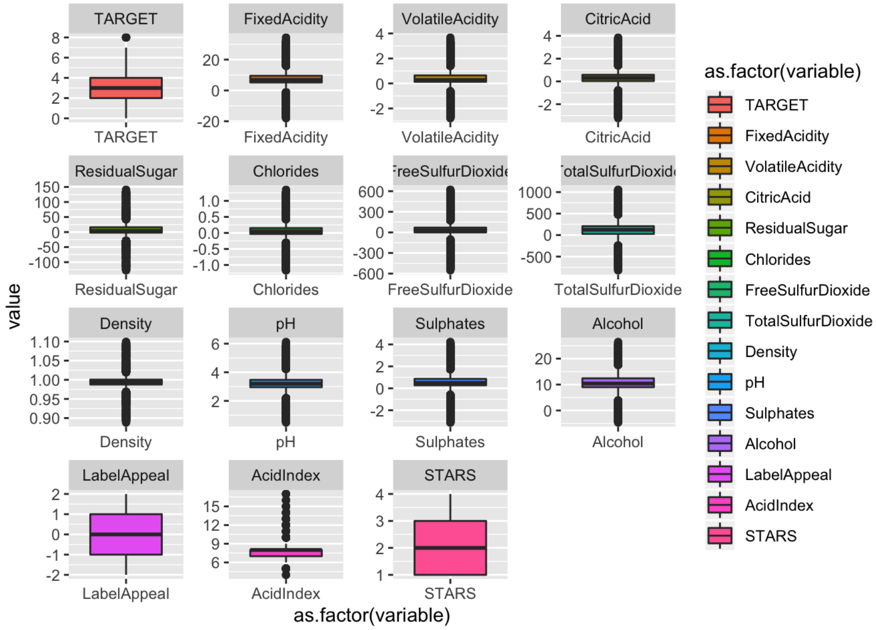

### 1.3.1.3 Doubles

The Double variable types look very similar to one another, and look somewhat normal. These look okay to impute after we've run our diagnostic plots.

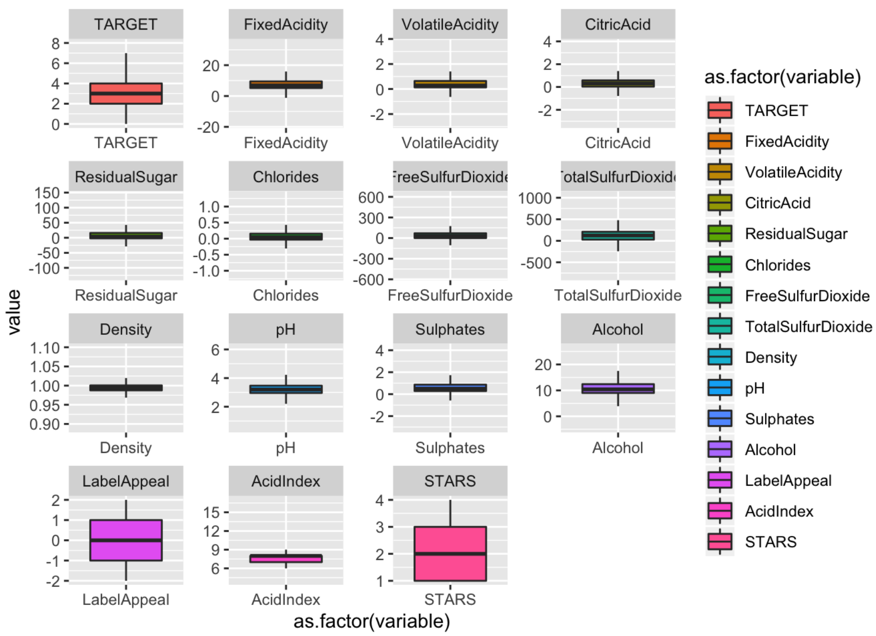



## 1.3.2 Outliers

### 1.3.2.1 Boxplot

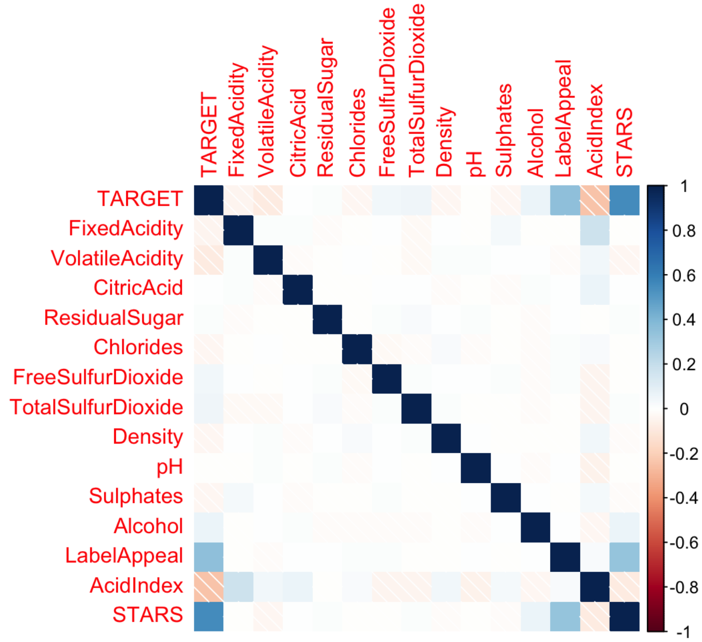



### 1.3.2.2 Boxplot Without outliers




### 1.3.2.3 Correlation

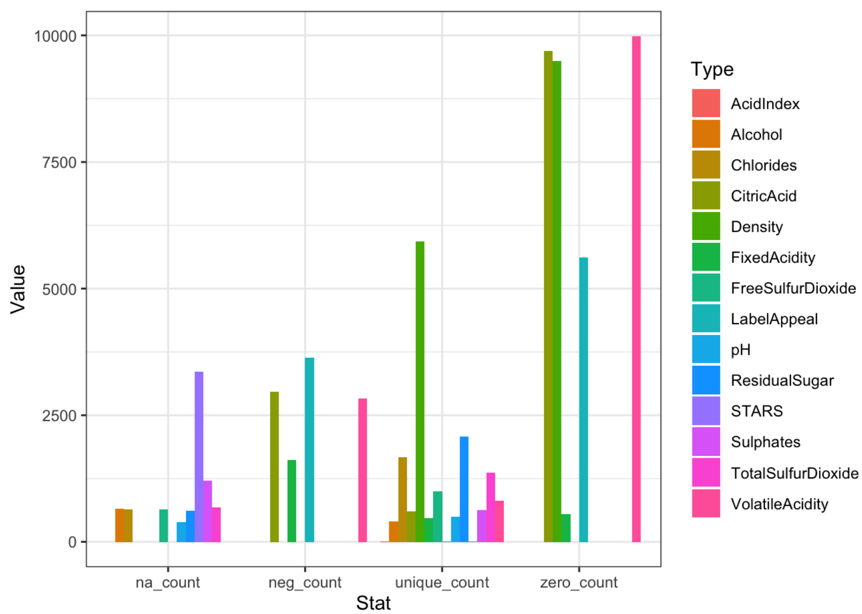
We note that the human ratings all have high correlations than do our chemical features.




### 1.3.2.4 Abnormal Data

Finally, we can visualize data abnormalities by visualizing our previously calculated vNA, Negative, Zero, and Unique counts.

```
ab_wine_desc <- wine_desc[,c(-1:-13)]
stat_chart_data <- ab_wine_desc %>% t() %>% as.data.frame() %>% mutate(.,Stat=rownames(.))
stat_chart_data %>%
  gather("Type", "Value", -Stat) %>%
  ggplot(aes(Stat, Value, fill = Type)) +
  geom_bar(position = "dodge", stat = "identity", na.rm=TRUE) +
  plot_layout(ncol = 1) +
  theme_bw()
```




# 2 DATA PREPERATION

To begin data preparation, we look at some of our abnormal data and consider transformations.

```
##                    na_count neg_count zero_count unique_count
## STARS                  3359        NA         NA            5
## Sulphates              1210        NA         NA          631
## TotalSulfurDioxide      682        NA         NA         1371
## Alcohol                 653        NA         NA          402
## FreeSulfurDioxide       647        NA         NA         1000
## Chlorides               638        NA         NA         1664
## ResidualSugar           616        NA         NA         2078
## pH                      395        NA         NA          498
## FixedAcidity              0      1621        548          470
## VolatileAcidity           0      2827       9982          815
## CitricAcid                0      2966       9686          602
## Density                   0         0       9492         5933
## LabelAppeal               0      3640       5617            5
## AcidIndex                 0         0          0           14
```

# 2.1 NAs

We recall that STARS has a high correlation with TARGET and we see that it has r `(wine1["STARS","na_count"]/nrow(WineTrain))*100` % NA's and no zero's. We change NA to 0 for STARS.

The remaining NA counts include continuous variables which we can impute via a statistical method.

```
## 
##  iter imp variable
##   1   1  ResidualSugar  Chlorides  FreeSulfurDioxide  TotalSulfurDioxide  pH  Sulphates  Alcohol
```

# 2.2 Negatives

While the negative ratings make the data irregular to work with, it is unlikely that so many people (r `(wine1["STARS","neg_count"]/nrow(WineTrain))*100` % ) accidentally used a negative rating. We can consider these for normalization only.

```
##                    na_count neg_count zero_count unique_count
## LabelAppeal               0      3640       5617            5
## Chlorides                 0      3378      12617         1663
## ResidualSugar             0      3289        142         2077
## FreeSulfurDioxide         0      3198         11          999
## CitricAcid                0      2966       9686          602
## VolatileAcidity           0      2827       9982          815
## TotalSulfurDioxide        0      2642          7         1370
## Sulphates                 0      2586       9213          630
## FixedAcidity              0      1621        548          470
## Alcohol                   0       124         77          401
## Density                   0         0       9492         5933
## pH                        0         0         55          497
## AcidIndex                 0         0          0           14
## STARS                     0         0       3359            5
```

# 2.3 Zeros

By the same logic we will leave the zero counts alone. We can exclude the TARGET variable unless we will be normalizing it specifically in our later analysis.

```
##                    na_count neg_count zero_count unique_count
## Chlorides                 0      3378      12617         1663
## VolatileAcidity           0      2827       9982          815
## CitricAcid                0      2966       9686          602
## Density                   0         0       9492         5933
## Sulphates                 0      2586       9213          630
## LabelAppeal               0      3640       5617            5
## STARS                     0         0       3359            5
## FixedAcidity              0      1621        548          470
## ResidualSugar             0      3289        142         2077
## Alcohol                   0       124         77          401
## pH                        0         0         55          497
## FreeSulfurDioxide         0      3198         11          999
## TotalSulfurDioxide        0      2642          7         1370
## AcidIndex                 0         0          0           14
```

## 2.4 Uniques

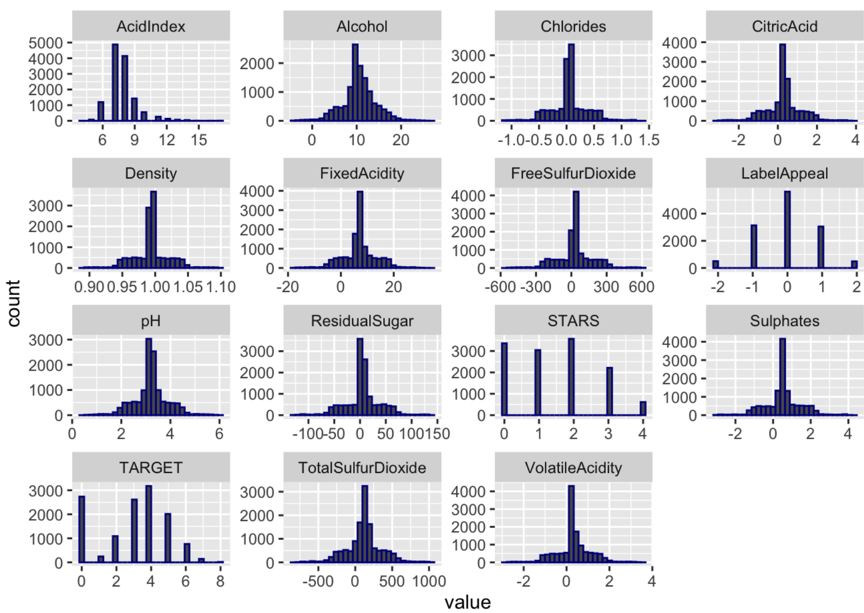
We want to take a look at the least unique counts next, and by a large margin LabelAppeal, STARS, and AcidIndex show low unique counts. We see that AcidIndex is a proprietary weighted method for measuring Acid, so we decide not to perform any transformation on AcidIndex.

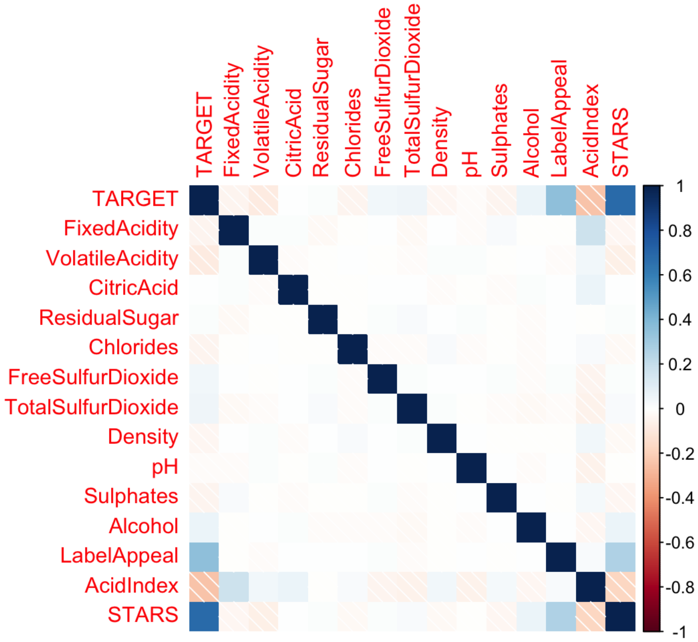
```
##                    na_count neg_count zero_count unique_count
## LabelAppeal               0      3640       5617            5
## STARS                     0         0       3359            5
## AcidIndex                 0         0          0           14
## Alcohol                   0       124         77          401
## FixedAcidity              0      1621        548          470
## pH                        0         0         55          497
## CitricAcid                0      2966       9686          602
## Sulphates                 0      2586       9213          630
## VolatileAcidity           0      2827       9982          815
## FreeSulfurDioxide         0      3198         11          999
## TotalSulfurDioxide        0      2642          7         1370
## Chlorides                 0      3378      12617         1663
## ResidualSugar             0      3289        142         2077
## Density                   0         0       9492         5933
```

## 2.5 Data Finalization

We've finalized our dataset for analysis.

```
##      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
##  Min.   :-127.800   Min.   :-1.17100   Min.   :-555.00
##  1st Qu.:  -2.000   1st Qu.:-0.03300   1st Qu.:   0.00
##  Median :   3.850   Median : 0.04600   Median :  30.00
##  Mean   :   5.422   Mean   : 0.05459   Mean   :  30.53
##  3rd Qu.:  15.800   3rd Qu.: 0.15200   3rd Qu.:  70.00
##  Max.   : 141.150   Max.   : 1.35100   Max.   : 623.00
##  TotalSulfurDioxide    Density              pH          Sulphates
##  Min.   :-823.0     Min.   :0.8881   Min.   :0.480   Min.   :-3.1300
##  1st Qu.:  27.0     1st Qu.:0.9877   1st Qu.:2.960   1st Qu.: 0.2900
##  Median : 124.0     Median :0.9945   Median :3.200   Median : 0.5000
##  Mean   : 120.8     Mean   :0.9942   Mean   :3.208   Mean   : 0.5304
##  3rd Qu.: 208.0     3rd Qu.:1.0005   3rd Qu.:3.470   3rd Qu.: 0.8700
##  Max.   :1057.0     Max.   :1.0992   Max.   :6.130   Max.   : 4.2400
##     Alcohol      LabelAppeal          AcidIndex          STARS
##  Min.   :-4.7   Min.   :-2.000000   Min.   : 4.000   Min.   :0.000
##  1st Qu.: 9.0   1st Qu.:-1.000000   1st Qu.: 7.000   1st Qu.:0.000
##  Median :10.4   Median : 0.000000   Median : 8.000   Median :1.000
##  Mean   :10.5   Mean   :-0.009066   Mean   : 7.773   Mean   :1.506
##  3rd Qu.:12.4   3rd Qu.: 1.000000   3rd Qu.: 8.000   3rd Qu.:2.000
##  Max.   :26.5   Max.   : 2.000000   Max.   :17.000   Max.   :4.000
```



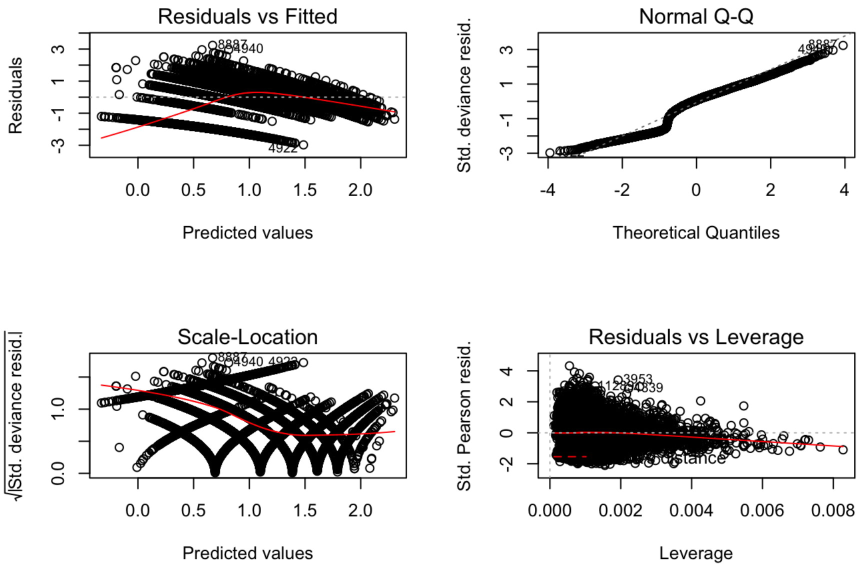



# 3 BUILD MODEL

## 3.1 Model 1: Poisson Regression (all predictors)

For the first model, we used the Poisson regression and all of the predictors.

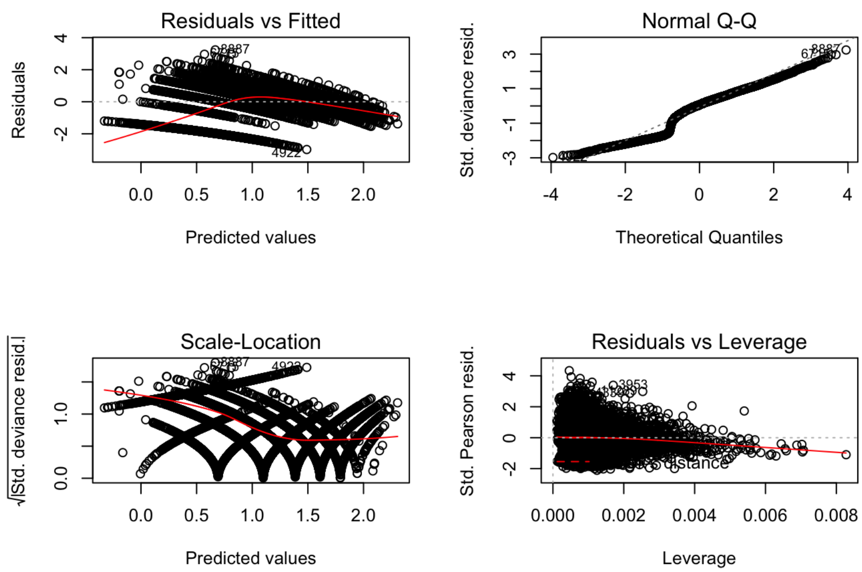
```
## 
## Call:
## glm(formula = TARGET ~ ., family = poisson, data = WineTrain)
## 
## Deviance Residuals: 
##     Min       1Q   Median       3Q      Max  
## -2.9733  -0.7218   0.0695   0.5768   3.2331  
## 
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)    
## (Intercept)         1.536e+00  1.953e-01   7.866 3.67e-15 ***
## FixedAcidity       -3.108e-04  8.205e-04  -0.379 0.704814    
## VolatileAcidity    -3.376e-02  6.517e-03  -5.181 2.20e-07 ***
## CitricAcid          7.871e-03  5.891e-03   1.336 0.181505    
## ResidualSugar       7.776e-05  1.507e-04   0.516 0.605963    
## Chlorides          -4.661e-02  1.595e-02  -2.922 0.003476 ** 
## FreeSulfurDioxide   1.285e-04  3.433e-05   3.743 0.000182 ***
## TotalSulfurDioxide  8.288e-05  2.215e-05   3.741 0.000183 ***
## Density            -2.840e-01  1.920e-01  -1.479 0.139027    
## pH                 -1.811e-02  7.513e-03  -2.410 0.015932 *  
## Sulphates          -1.200e-02  5.475e-03  -2.192 0.028405 *  
## Alcohol             2.116e-03  1.375e-03   1.538 0.123987    
## LabelAppeal         1.332e-01  6.063e-03  21.965  < 2e-16 ***
## AcidIndex          -8.705e-02  4.549e-03 -19.136  < 2e-16 ***
## STARS               3.112e-01  4.534e-03  68.633  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for poisson family taken to be 1)
## 
##     Null deviance: 22861  on 12794  degrees of freedom
## Residual deviance: 14723  on 12780  degrees of freedom
## AIC: 46695
## 
## Number of Fisher Scoring iterations: 5
```




# 3.2 Model 2: Poisson Regression (reduced predictors)

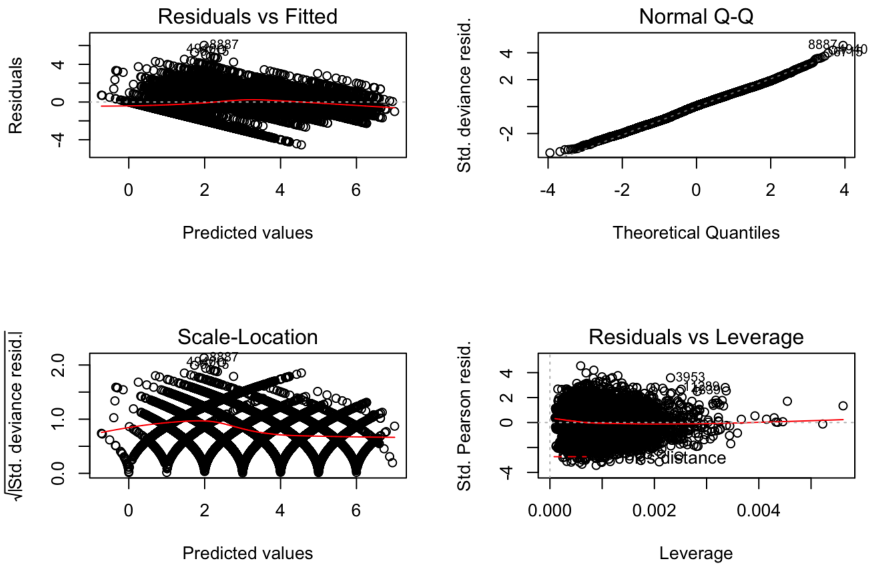
For the second model, based on model 1, we reduced the number of predictors.

```
## 
## Call:
## glm(formula = TARGET ~ VolatileAcidity + CitricAcid + Chlorides + 
##     FreeSulfurDioxide + TotalSulfurDioxide + Density + pH + Sulphates + 
##     Alcohol + LabelAppeal + AcidIndex + STARS, family = poisson, 
##     data = WineTrain)
## 
## Deviance Residuals: 
##     Min       1Q   Median       3Q      Max  
## -2.9785  -0.7233   0.0696   0.5767   3.2385  
## 
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)    
## (Intercept)         1.537e+00  1.953e-01   7.868 3.60e-15 ***
## VolatileAcidity    -3.380e-02  6.517e-03  -5.187 2.13e-07 ***
## CitricAcid          7.829e-03  5.891e-03   1.329 0.183856    
## Chlorides          -4.661e-02  1.595e-02  -2.922 0.003473 ** 
## FreeSulfurDioxide   1.285e-04  3.432e-05   3.743 0.000182 ***
## TotalSulfurDioxide  8.323e-05  2.215e-05   3.758 0.000171 ***
## Density            -2.844e-01  1.920e-01  -1.482 0.138462    
## pH                 -1.805e-02  7.512e-03  -2.403 0.016276 *  
## Sulphates          -1.206e-02  5.474e-03  -2.203 0.027623 *  
## Alcohol             2.100e-03  1.375e-03   1.527 0.126697    
## LabelAppeal         1.332e-01  6.063e-03  21.971  < 2e-16 ***
## AcidIndex          -8.729e-02  4.501e-03 -19.394  < 2e-16 ***
## STARS               3.112e-01  4.533e-03  68.647  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for poisson family taken to be 1)
## 
##     Null deviance: 22861  on 12794  degrees of freedom
## Residual deviance: 14723  on 12782  degrees of freedom
## AIC: 46691
## 
## Number of Fisher Scoring iterations: 5
```




## 3.3 Model 3: Gaussian Regression (significant predictors)

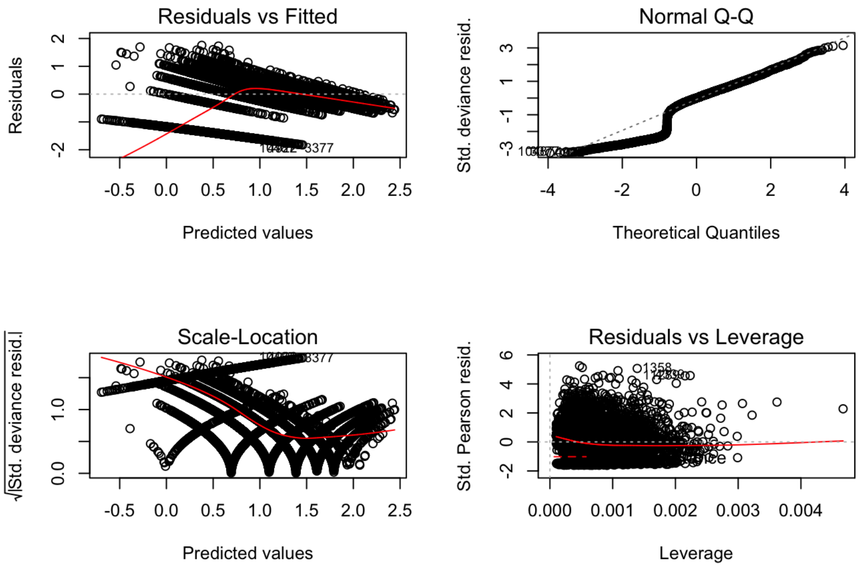
```
##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + FreeSulfurDioxide +
##     TotalSulfurDioxide + Chlorides + Density + pH + Sulphates +
##     LabelAppeal + AcidIndex + STARS, family = gaussian, data = WineTrain)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.5472  -0.9528   0.0617   0.9068   6.0152
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)         4.147e+00  4.470e-01   9.277  < 2e-16 ***
## VolatileAcidity    -1.000e-01  1.498e-02  -6.680 2.49e-11 ***
## FreeSulfurDioxide   3.202e-04  7.915e-05   4.045 5.27e-05 ***
## TotalSulfurDioxide  2.248e-04  5.061e-05   4.441 9.04e-06 ***
## Chlorides          -1.383e-01  3.667e-02  -3.772 0.000163 ***
## Density            -8.210e-01  4.419e-01  -1.858 0.063203 .
## pH                 -4.140e-02  1.725e-02  -2.401 0.016373 *
## Sulphates          -3.215e-02  1.257e-02  -2.558 0.010544 *
## LabelAppeal         4.321e-01  1.367e-02  31.615  < 2e-16 ***
## AcidIndex          -2.082e-01  9.050e-03 -23.000  < 2e-16 ***
## STARS               9.786e-01  1.044e-02  93.744  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.753742)
##
##     Null deviance: 47477  on 12794  degrees of freedom
## Residual deviance: 22420  on 12784  degrees of freedom
## AIC: 43511
##
## Number of Fisher Scoring iterations: 2
```




Model 3 shows a better Q-Q plot than the previous two models.

# 3.4 Model 4: Negative Binomial Regression

```
##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + TotalSulfurDioxide +
##     pH + Sulphates + LabelAppeal + AcidIndex + STARS, family = negative.binomial(1),
##     data = WineTrain)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.82623  -0.39491   0.00259   0.29971   1.75413
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)         1.454e+00  4.969e-02  29.267  < 2e-16 ***
## VolatileAcidity    -4.567e-02  7.454e-03  -6.127 9.21e-10 ***
## TotalSulfurDioxide  1.280e-04  2.521e-05   5.080 3.82e-07 ***
## pH                 -2.955e-02  8.581e-03  -3.444 0.000576 ***
## Sulphates          -1.758e-02  6.254e-03  -2.811 0.004950 **
## LabelAppeal         1.186e-01  6.837e-03  17.352  < 2e-16 ***
## AcidIndex          -1.175e-01  4.774e-03 -24.610  < 2e-16 ***
## STARS               3.659e-01  5.170e-03  70.773  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1) family taken to be 0.3104983)
##
##     Null deviance: 9042.5  on 12794  degrees of freedom
## Residual deviance: 6764.5  on 12787  degrees of freedom
## AIC: 55512
##
## Number of Fisher Scoring iterations: 6
```




# 4 SELECT MODEL

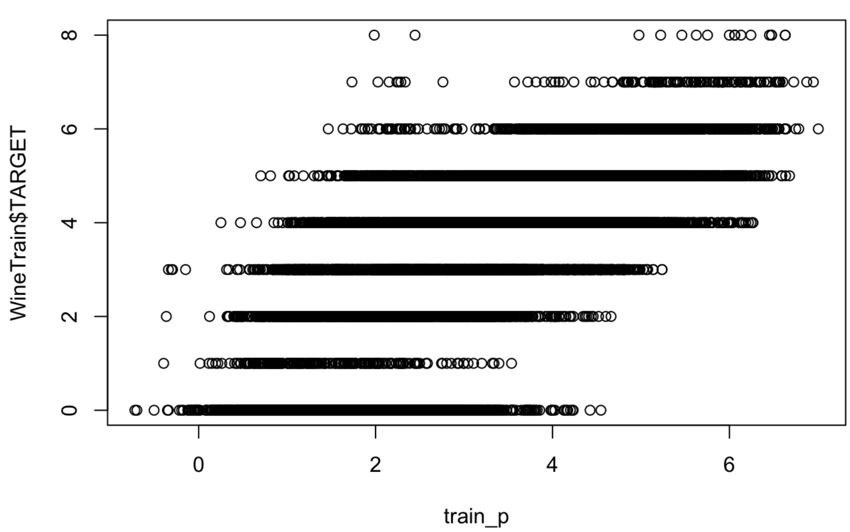
## 4.1 Pick the best regression model

| | Model 1 | Model 2 | Model 3 | Model 4 |
|---|---|---|---|---|
| AIC | 46694.5977996685 | 46691.0158133176 | 43511.2443254015 | 55511.7198722206 |
| BIC | 46806.4499458974 | 46787.9543400493 | 43600.7260423846 | 55571.3743502094 |

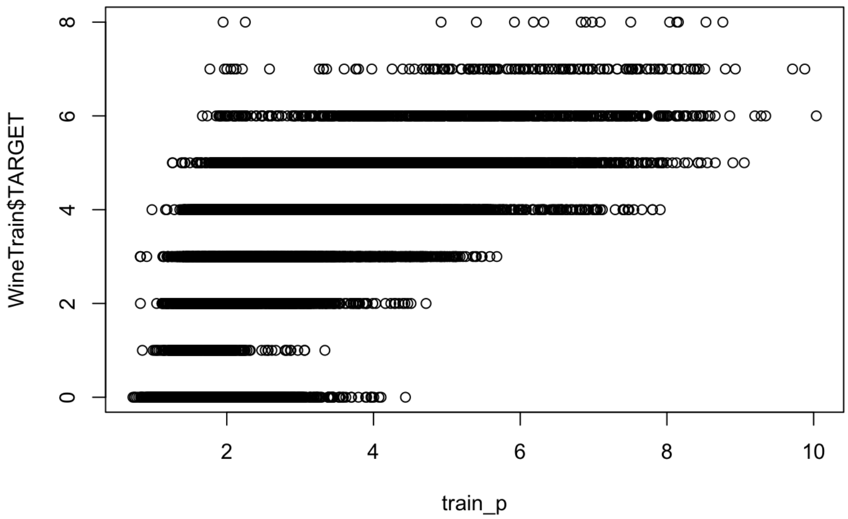
With 4 models computed, we select the model with the lowest combination of AIC and BIC. From the table, we can see the model to pick is model 3

# 5 CONCLUSION

Model 3 showed the best result. We can observe its performance by plotting the datasets TARGET values agaisnt the predicted values. One thing we observe is that the model doesn't predict a TARGET of 8.




Other models, although of worse performace according to our selection metric, do show results of TARGET 8, but as can be seen in the graph below, they do not corresponde to real TARGET 8 classifications.




# 6 APPENDIX

**Code used in analysis**

```
knitr::opts_chunk$set(echo = FALSE, warning = FALSE, fig.align='center')
require(knitr)
library(MASS)
library(psych)
library(kableExtra)
library(tidyverse)
library(faraway)
library(gridExtra)
library(reshape2)
library(leaps)
library(caret)
library(naniar)
library(pander)
library(pROC)
library(corrplot)
library(jtools)
library(mice)
#devtools::install_github("thomasp85/patchwork")
library(patchwork)
WineTrain <- read.csv("https://raw.githubusercontent.com/pkowalchuk/CUNY621-HW5/master/wine-training-data.csv",na.strings
="",header=TRUE)
WineTrain1 <- WineTrain
WineEval <- read.csv("wine-evaluation-data.csv",na.strings="",header=TRUE)
kable_styling(kable(textbook<-data.frame(VARIABLE.NAME=c("INDEX","TARGET","","","AcidIndex","Alcohol","Chlorides","Citric
Acid","Density"," FixedAcidity","FreeSulfurDioxide","LabelAppeal","ResidualSugar","STARS","Sulphates","TotalSulfurDioxid
e","VolatileAcidity","pH"),DEFINITION=c("Identification Variable (do not use)","Number of Cases Purchased","","","Proprie
tary method of testing total acidity of wine by using a weighted average,","Alcohol Content","Chloride content of wine",
"Citric Acid Content","Density of Wine ","Fixed Acidity of Wine","Sulfur Dioxide content of wine","Marketing Score indica
ting the appeal of label design for consumers. High numbers suggest customers like the label design. Negative numbers sug
gest customers don't like the design","Residual Sugar of wine","Wine rating by a team of experts. 4 Stars = Excellent, 1
 Star = Poor","Sulfate content of wine","Total Sulfur Dioxide of Wine","Volatile Acid content of wine","pH of wine"),THEO
RETICAL.EFFECT=c("None","None","","","","","","","","","","Many consumers purchase based on the visual appeal of the wine
label design. Higher numbers suggest better sales.","","A high number of stars suggests high sales","","","",""))), boots
trap_options = c("striped"))
#glimpse(WineTrain)
#colnames(WineTrain[-1])<-"INDEX"
WineTrainVars <- WineTrain[-1]
WineTrainFeatures <- WineTrain[-c(1:2)]
kable_styling(kable(summary(WineTrainVars)))

var_stats<- function(WineTrainVars){
  wt <- WineTrainVars
  wine1 <- describe(wt)
  wine1$na_count <- sapply(wt, function(y) sum(is.na(y)))
  wine1$neg_count <- sapply(wt, function(y) sum(y<0))
  wine1$zero_count <- sapply(wt, function(y) sum(as.integer(y)==0))
  wine1$unique_count <- sapply(wt, function(y) sum(n_distinct(y)))

  return(wine1)
}
wine_desc <- var_stats(WineTrainFeatures)

wine_desc %>% as.data.frame()

colsTrain<-ncol(WineTrain)
colsEval<-ncol(WineEval)
missingCol<-colnames(WineTrain)[!(colnames(WineTrain) %in% colnames(WineEval))]
#missingCol
cc<-summary(complete.cases(WineTrainVars))
cWineTrain<-subset(WineTrainVars, complete.cases(WineTrainVars))
cc
vis_miss(WineTrainVars)
gg_miss_upset(WineTrainVars)
glimpse(cWineTrain)
#WineTrain1$INDEX <- NULL
hist(WineTrainVars$TARGET, col='darkblue', xlab = " Target ", main = "Wine Counts")
```

```
WineTrainVars %>%
  keep(is.integer) %>%
  gather() %>%
  ggplot(aes(value), main="") +
  facet_wrap(~ key, scales = "free") +
  geom_histogram(color='darkblue') +
  plot_layout(ncol = 1)
WineTrainFeatures %>%
  keep(is.double) %>%
  gather() %>%
  ggplot(aes(value)) +
  facet_wrap(~ key, scales = "free") +
  geom_density(color='purple', fill='purple') +
  plot_layout(ncol = 1)
ggplot(melt(WineTrainVars), aes(x=as.factor(variable), y=value, fill=as.factor(variable))) + facet_wrap(~variable, scale=
"free") + geom_boxplot()
ggplot(melt(WineTrainVars), aes(x=as.factor(variable), y=value, fill=as.factor(variable))) + facet_wrap(~variable, scale=
"free") + geom_boxplot(outlier.shape=NA)
corrplot(as.matrix(cor(WineTrainVars, use = "pairwise.complete")),method = "shade")
ab_wine_desc <- wine_desc[,c(-1:-13)]
stat_chart_data <- ab_wine_desc %>% t() %>% as.data.frame() %>% mutate(.,Stat=rownames(.))
stat_chart_data %>%
  gather("Type", "Value", -Stat) %>%
  ggplot(aes(Stat, Value, fill = Type)) +
  geom_bar(position = "dodge", stat = "identity", na.rm=TRUE) +
  plot_layout(ncol = 1) +
  theme_bw()
WineTrainTrans <- WineTrain[-c(1)]
ab_wine_desc <- var_stats(WineTrainTrans)[-c(1),c(-1:-13)]
print(ab_wine_desc[order(-ab_wine_desc$na_count),])
WineTrainTrans$STARS <- sapply(WineTrainTrans$STARS,function(x) ifelse(is.na(x),0,x))
#WineTrain<-as.factor(WineTrain)
WineTrainTrans<-complete(mice(WineTrainTrans, m=1, maxit=1),1)

ab_wine_desc <- var_stats(WineTrainTrans)[-c(1),c(-1:-13)]
print(ab_wine_desc[order(-ab_wine_desc$neg_count),])
ab_wine_desc <- var_stats(WineTrainTrans)[-c(1),c(-1:-13)]
print(ab_wine_desc[order(-ab_wine_desc$zero_count),])
ab_wine_desc <- var_stats(WineTrainTrans)[-c(1),c(-1:-13)]
print(ab_wine_desc[order(ab_wine_desc$unique_count),])
#WineTrainTrans$STARS<-as.factor(WineTrainTrans$LabelAppeal)
#WineTrainTrans$STARS<-as.factor(WineTrainTrans$STARS)
#WineTrainTrans$STARS<-as.factor(WineTrainTrans$AcidIndex)
WineTrain<-WineTrainTrans
summary(WineTrain)


WineTrain %>%
  keep(is.numeric) %>%
  gather() %>%
  ggplot(aes(value), main="") +
  facet_wrap(~ key, scales = "free") +
  geom_histogram(color='darkblue') +
  plot_layout(ncol = 1)


corrplot(as.matrix(cor(WineTrain %>% keep(is.numeric), use = "pairwise.complete")),method = "shade")

m1 <- glm(TARGET ~ ., family = poisson, data = WineTrain)
#m1 <- glm(TARGET ~ ., family = poisson, data = WineTrain)
summary(m1)
par(mfrow = c(2,2))
plot(m1)
m2 <- glm(TARGET ~ VolatileAcidity + CitricAcid + Chlorides + FreeSulfurDioxide
                        + TotalSulfurDioxide + Density + pH + Sulphates + Alcohol + LabelAppeal
```

```
            + AcidIndex + STARS, family = poisson, data = WineTrain)
summary(m2)
par(mfrow = c(2,2))
plot(m2)
m3 <- glm(TARGET ~ VolatileAcidity + FreeSulfurDioxide + TotalSulfurDioxide + Chlorides + Density + pH + Sulphates + Labe
lAppeal + AcidIndex + STARS, family=gaussian, data = WineTrain)
summary(m3)
par(mfrow = c(2,2))
plot(m3)
m4 <- glm(TARGET ~ VolatileAcidity + TotalSulfurDioxide +
     pH + Sulphates + LabelAppeal + AcidIndex + STARS, family = negative.binomial(1),
     data = WineTrain)
summary(m4)
par(mfrow = c(2,2))
plot(m4)
m1AIC <- AIC(m1)
m1BIC <- BIC(m1)
m2AIC <- AIC(m2)
m2BIC <- BIC(m2)
m3AIC <- AIC(m3)
m3BIC <- BIC(m3)
m4AIC <- AIC(m4)
m4BIC <- BIC(m4)

AIC <- list(m1AIC, m2AIC, m3AIC, m4AIC)
BIC <- list(m1BIC, m2BIC, m3BIC, m4BIC)
kable(rbind(AIC, BIC), col.names = c("Model 1", "Model 2", "Model 3", "Model 4"))  %>%
  kable_styling(full_width = T)

eval_p<-predict(m3,WineEval, type = "response")
write.csv(eval_p,"predicted_eval_values.csv")
train_p<-predict(m3,WineTrain, type = "response")
plot(train_p,WineTrain$TARGET)
train_p<-predict(m2,WineTrain, type = "response")
plot(train_p,WineTrain$TARGET)
```