

# Count Regression Model

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5/22/2021

## Introduction

The goal of this assignment is to explore, analyze and model a dataset containing information on approximately 12,000 commercially available wines. The dataset 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. 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. The target variable, cases of wine sold, is count data and therefore will be modeled using appropriate techniques such as Poisson and Negative Binomial regressions.

## Data Exploration

```
## Rows: 12,795
## Columns: 16
## $ i..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~
```

All the variable in this dataset are numeric and continuous except for AcidIndex, STARS and LabelAppeal which are discrete. The target variable TARGET is also discrete. There are a number of missing observations for certain chemical composition variables as well as a large number of wines with no STARS rating. The distribution of the continuous variables appear well centered.

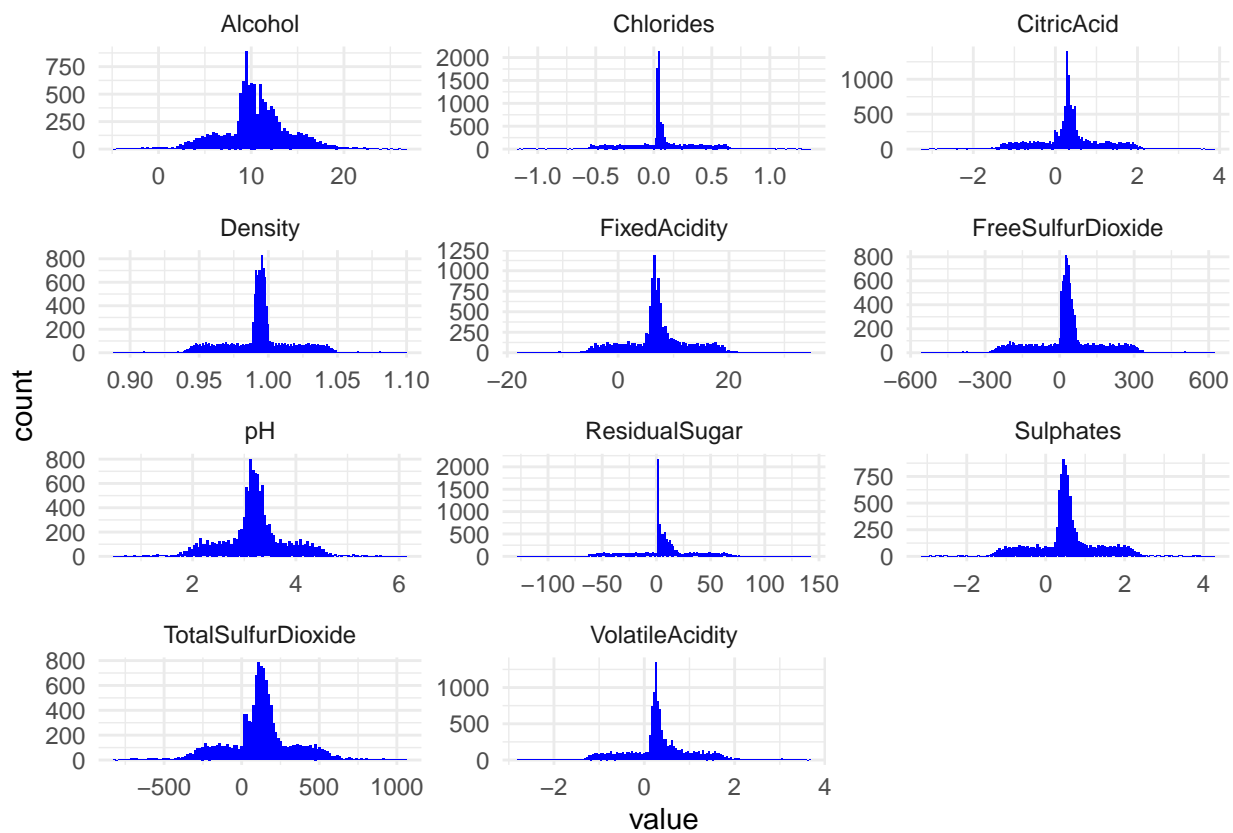
```

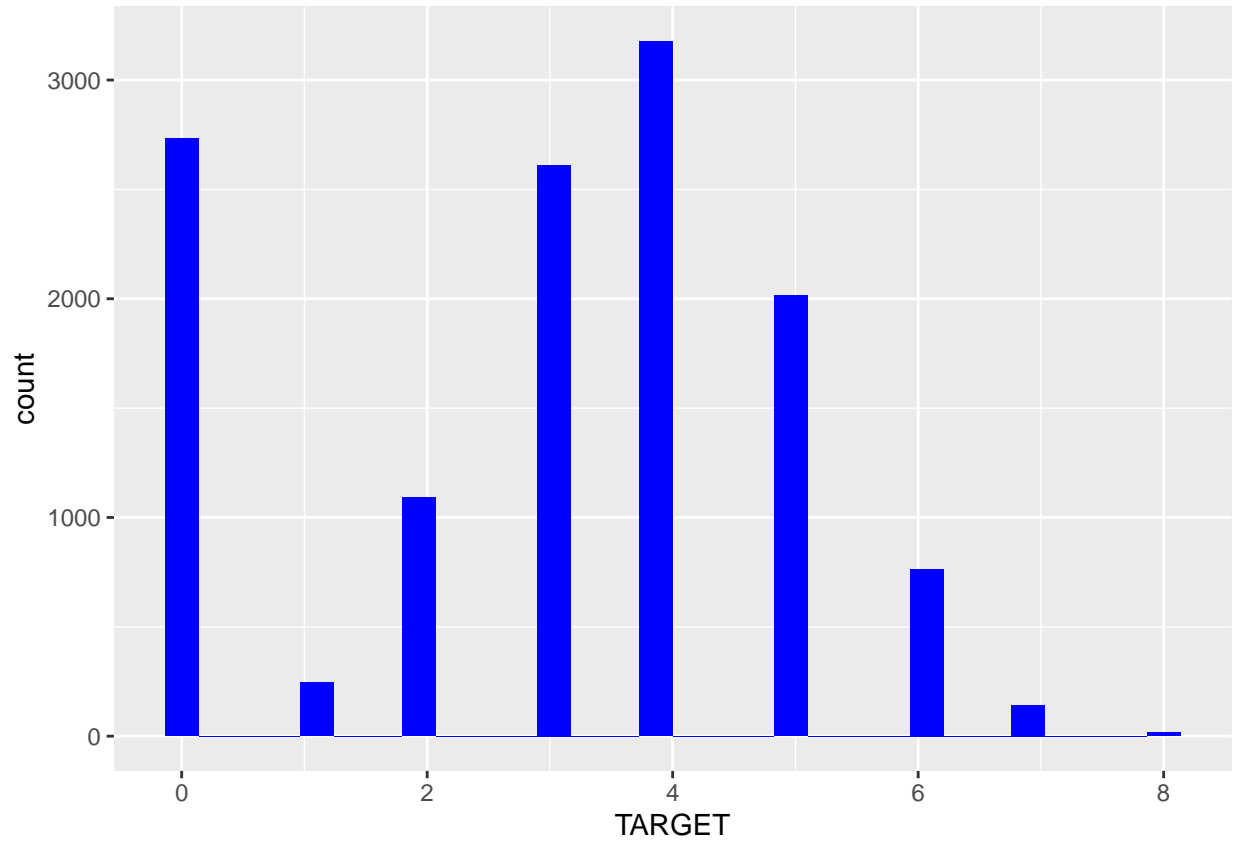
##      i..INDEX      TARGET      FixedAcidity      VolatileAcidity
##  Min.      :    1  Min.      :0.000  Min.      : -18.100  Min.      : -2.7900
## 1st Qu.: 4038 1st Qu.:2.000 1st Qu.:  5.200 1st Qu.: 0.1300
## Median : 8110 Median :3.000 Median :  6.900 Median : 0.2800
## Mean   : 8070 Mean  :3.029 Mean   :  7.076 Mean   : 0.3241
## 3rd Qu.:12106 3rd Qu.:4.000 3rd Qu.:  9.500 3rd Qu.: 0.6400
## Max.    :16129 Max.    :8.000 Max.    : 34.400 Max.    : 3.6800
##
##      CitricAcid      ResidualSugar      Chlorides      FreeSulfurDioxide
##  Min.      : -3.2400  Min.      : -127.800  Min.      : -1.1710  Min.      : -555.00
## 1st Qu.:  0.0300 1st Qu.:  -2.000 1st Qu.: -0.0310 1st Qu.:  0.00
## Median :  0.3100 Median :   3.900 Median :  0.0460 Median :  30.00
## Mean   :  0.3084 Mean   :   5.419 Mean   :  0.0548 Mean   :  30.85
## 3rd Qu.:  0.5800 3rd Qu.:  15.900 3rd Qu.:  0.1530 3rd Qu.:  70.00
## Max.    :  3.8600 Max.    : 141.150 Max.    :  1.3510 Max.    : 623.00
## NA's      :616 NA's      :638 NA's      :647
## 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.: 0.2800
## Median : 123.0 Median :0.9945 Median :3.200 Median : 0.5000
## Mean   : 120.7 Mean   :0.9942 Mean   :3.208 Mean   : 0.5271
## 3rd Qu.: 208.0 3rd Qu.:1.0005 3rd Qu.:3.470 3rd Qu.: 0.8600
## Max.    :1057.0 Max.    :1.0992 Max.    :6.130 Max.    : 4.2400
## NA's      :682 NA's      :395 NA's      :1210
##      Alcohol      LabelAppeal      AcidIndex      STARS
##  Min.      : -4.70  Min.      : -2.000000  Min.      : 4.000  Min.      :1.000
## 1st Qu.:  9.00 1st Qu.: -1.000000 1st Qu.: 7.000 1st Qu.:1.000
## Median :10.40 Median : 0.000000 Median : 8.000 Median :2.000
## Mean   :10.49 Mean   : -0.009066 Mean   : 7.773 Mean   :2.042
## 3rd Qu.:12.40 3rd Qu.: 1.000000 3rd Qu.: 8.000 3rd Qu.:3.000
## Max.    :26.50 Max.    : 2.000000 Max.    :17.000 Max.    :4.000
## NA's      :653 NA's      :3359

```

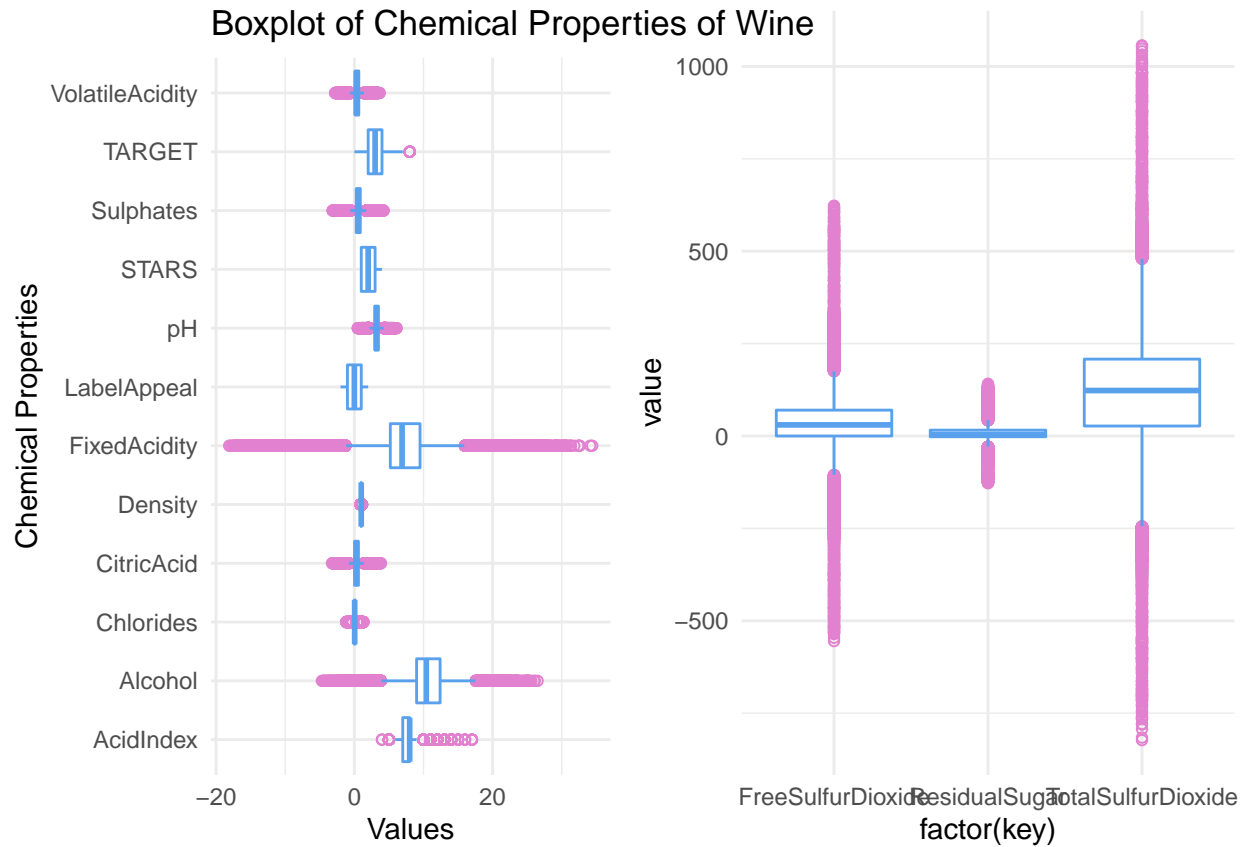
## Visualization

To take a look at the distributions of the dataset, we plot some histograms and can see that all continuous variables are centered and close to normally distributed. We also note that some variables are centered around zero and take negative values which is unexpected and will be investigated further and transformed for our analysis. The distribution of the TARGET variable looks like it could be well described by the poisson distribution which has equal mean and variance but the high number of zero values justifies the use of a zero-inflated model as well. The mean and variance of TARGET are 3.02 and 3.71 respectively, which is close enough to satisfy the equal mean-variance assumption of the poisson distribution.





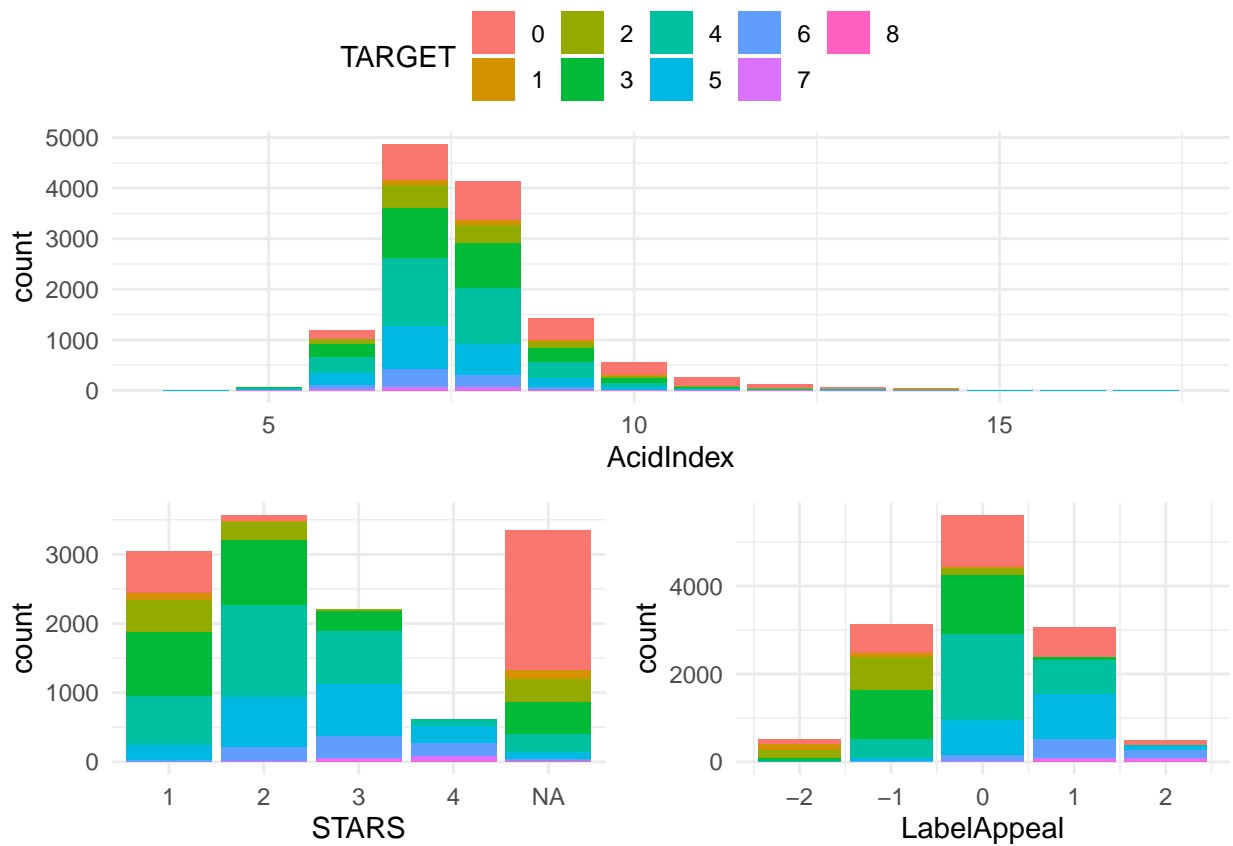
below box plot shows several variables in to two panels. Some variables such as TotalSulfurDioxide, FreeSulfurDioxide, and ResidualSugar have large ranges compared to other variables. Therefore, we separated those variables in to a different panel to view their distribution. From both panel, we can tell a high number of variables have numerous outliers.



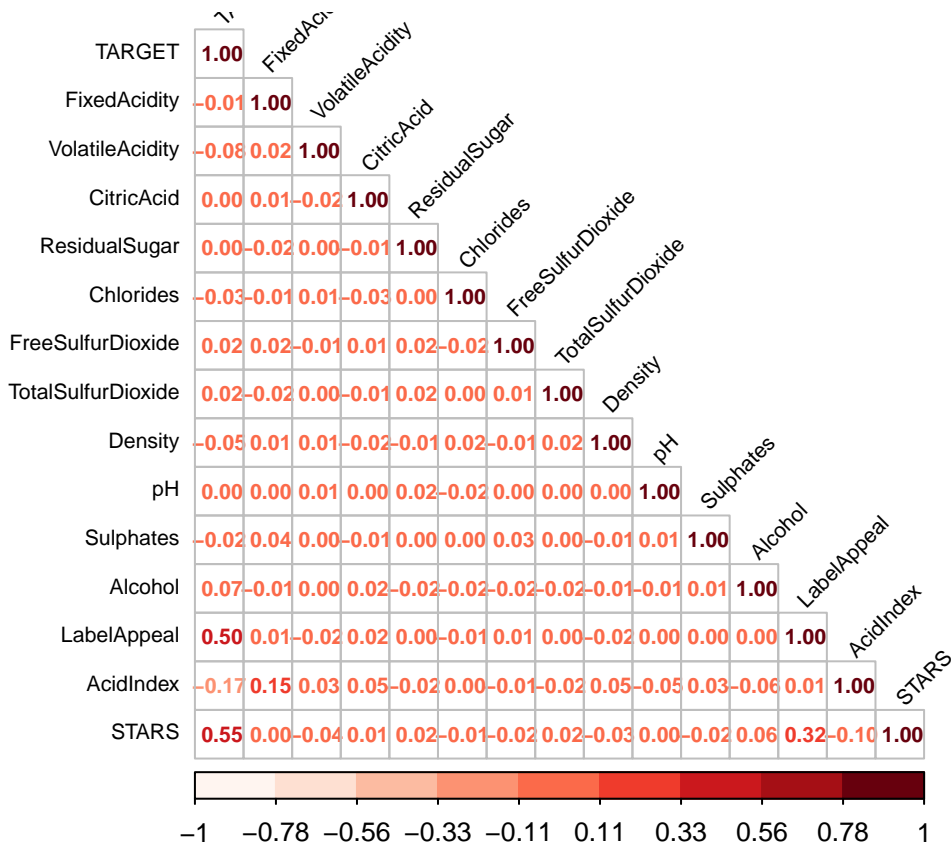
by taking a look at the bar char below, we can conclude the following point:

- AcidIndex tells us that large quantity of wine were sold with the index number 7 and 8.
- LabelAppeal tells us generic labeled wine sells the most;
- However, better label does yield higher number of wine samples per order.
- STARS tells us excellent quality does not result in high wine orders. It could be due to high star wine bottle's high price tag.

	Correlation
TARGET	1.0000000
STARS	0.5546857
LabelAppeal	0.4979465
Alcohol	0.0737771
FreeSulfurDioxide	0.0226398
TotalSulfurDioxide	0.0216021
ResidualSugar	0.0035196
CitricAcid	0.0023450
pH	0.0002199
FixedAcidity	-0.0125381
Sulphates	-0.0212204
Chlorides	-0.0304301
Density	-0.0475989
VolatileAcidity	-0.0759979
AcidIndex	-0.1676431



The plot below represent the correlation table and plot, and we can see that STARS and LabelAppeal are most positively correlated variables with the response variable. We expected this because our variable description mentions these variable's theoretical affect are higher than other variables. Also, we some mild negative correlation between the response variable and AcidIndex variable.



## Data Preparation

To explore the missing variables we Used the `aggr` function from `VIM` package, from the plot we see several variables have missing values. According to UCI Machine Learning, who published this dataset, all wine contain some natural sulfites. Therefore, to avoid creating problems while analyzing our data we will impute the missing values for sulfite chemical properties. Also We will impute values of wines with less than 1 gram/liter of sugar. Matter of fact, since all missing values are missing at random, we will impute all the missing values using the `mice` package and random forest method. `Mice` package uses multivariate imputations to estimate the missing values. Using multiple imputations helps in resolving the uncertainty for the missing values. Our target variable will be removed as a predictor variable but still will be imputed. Our response variables will be removed as predictor variables but still will be imputed.

```
##
## iter imp variable
## 1 1 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 1 2 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 1 3 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 1 4 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 1 5 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 2 1 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 2 2 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 2 3 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 2 4 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 2 5 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
## 3 1 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol STARS
```

##	3	2	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	3	3	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	3	4	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	3	5	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	1	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	2	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	3	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	4	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	5	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	1	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	2	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	3	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	4	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	5	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST

```
## [1] "Missing value after imputation: 0"
```

### Model 1: Poisson (Raw data)



```

## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.2158  -0.2734   0.0616   0.3732   1.6830
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.593e+00  2.506e-01   6.359 2.03e-10 ***
## FixedAcidity    3.293e-04  1.053e-03   0.313  0.75447
## VolatileAcidity -2.560e-02  8.353e-03  -3.065  0.00218 **
## CitricAcid      -7.259e-04  7.575e-03  -0.096  0.92365
## ResidualSugar   -6.141e-05  1.941e-04  -0.316  0.75165
## Chlorides       -3.007e-02  2.056e-02  -1.463  0.14346
## FreeSulfurDioxide 6.734e-05  4.404e-05   1.529  0.12620
## TotalSulfurDioxide 2.081e-05  2.855e-05   0.729  0.46618
## Density         -3.725e-01  2.462e-01  -1.513  0.13026
## pH              -4.661e-03  9.598e-03  -0.486  0.62722
## Sulphates       -5.164e-03  7.051e-03  -0.732  0.46398
## Alcohol         3.948e-03  1.771e-03   2.229  0.02579 *
## LabelAppeal     1.771e-01  7.954e-03  22.271 < 2e-16 ***
## AcidIndex       -4.870e-02  5.903e-03  -8.251 < 2e-16 ***
## STARS           1.871e-01  7.487e-03  24.993 < 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: 5844.1  on 6435  degrees of freedom
## Residual deviance: 4009.1  on 6421  degrees of freedom
##      (6359 observations deleted due to missingness)
## AIC: 23172
##
## Number of Fisher Scoring iterations: 5

## [1] "Goodness of Fit Test:"

##      res.deviance  df p
## [1,]      4009.142 6421 1

```

From the output we can say that the deviance residuals is quite symmetrical. This means that the predicted points are close to actual observed points. As can be seen in our correlation table, this is as predicted. STARS, LabelAppeal and AcidIndex are significant variables. And the variation in standard error is low. The goodness of fit test has a high p value which indicates that the model fits the data well.

## Model 2: Poisson (Imputed Data)

```

##
## Call:
## glm(formula = TARGET ~ ., family = poisson, data = train_data_imputed)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.8387  -0.5031   0.2162   0.6282   2.6384
##

```

```
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.131e+00  1.956e-01  10.898 < 2e-16 ***
## FixedAcidity   -2.187e-04  8.196e-04  -0.267 0.789613
## VolatileAcidity -5.200e-02  6.480e-03  -8.024 1.03e-15 ***
## CitricAcid      1.371e-02  5.893e-03   2.326 0.020010 *
## ResidualSugar   1.253e-04  1.504e-04   0.833 0.404695
## Chlorides       -5.865e-02  1.601e-02  -3.663 0.000250 ***
## FreeSulfurDioxide 1.510e-04  3.425e-05   4.407 1.05e-05 ***
## TotalSulfurDioxide 1.178e-04  2.206e-05   5.337 9.46e-08 ***
## Density        -4.318e-01  1.921e-01  -2.247 0.024623 *
## pH             -2.156e-02  7.524e-03  -2.865 0.004169 **
## Sulphates       -1.920e-02  5.455e-03  -3.519 0.000433 ***
## Alcohol         5.684e-03  1.376e-03   4.131 3.62e-05 ***
## LabelAppeal     2.001e-01  6.087e-03  32.868 < 2e-16 ***
## AcidIndex       -1.240e-01  4.453e-03 -27.851 < 2e-16 ***
## STARS           1.665e-01  5.822e-03  28.598 < 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: 18736  on 12780  degrees of freedom
## AIC: 50708
##
## Number of Fisher Scoring iterations: 5

## [1] "Goodness of Fit Test:"

##      res.deviance    df          p
## [1,]      18735.63 12780 2.506431e-234
```

The deviance residuals are the same as before. Imputation, on the other hand, introduces more important variables into the model. Furthermore, the AIC score increased significantly from 23172 to 50384. In addition, the deviance residuals fell from 40,000 to 18,412. The goodness of fit measure, on the other hand, has a very low p value, indicating that this model does not fit the data well. Since the residual deviance is greater than the degrees of freedom, then some over-dispersion exists.

Given what we observed when looking at the distribution of TARGET, we should expect the inflated count of zeros to affect the model and bias results. For this reason, we move to a zero-inflated model to reflect this.

### Model 3: Quasipoisson Model

We try a quasipoisson model to account for any overdispersion and to see if the results change significantly. As seen in the summary below, the models are nearly identical.

```
##
## Call:
## glm(formula = TARGET ~ ., family = quasipoisson(link = "log"),
##      data = train_data_imputed)
##
## Deviance Residuals:
```

```

##      Min      1Q   Median      3Q      Max
## -3.8387 -0.5031  0.2162   0.6282   2.6384
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.131e+00  1.923e-01  11.081 < 2e-16 ***
## FixedAcidity   -2.187e-04  8.061e-04  -0.271 0.786171
## VolatileAcidity -5.200e-02  6.373e-03  -8.159 3.71e-16 ***
## CitricAcid      1.371e-02  5.796e-03   2.365 0.018034 *
## ResidualSugar    1.253e-04  1.479e-04   0.847 0.396869
## Chlorides       -5.865e-02  1.575e-02  -3.724 0.000197 ***
## FreeSulfurDioxide 1.510e-04  3.369e-05   4.481 7.48e-06 ***
## TotalSulfurDioxide 1.178e-04  2.170e-05   5.426 5.86e-08 ***
## Density         -4.318e-01  1.890e-01  -2.285 0.022330 *
## pH              -2.156e-02  7.400e-03  -2.913 0.003584 **
## Sulphates       -1.920e-02  5.365e-03  -3.578 0.000347 ***
## Alcohol         5.684e-03  1.353e-03   4.200 2.69e-05 ***
## LabelAppeal     2.001e-01  5.986e-03  33.419 < 2e-16 ***
## AcidIndex       -1.240e-01  4.379e-03 -28.318 < 2e-16 ***
## STARS           1.665e-01  5.726e-03  29.078 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 0.9672522)
##
##      Null deviance: 22861  on 12794  degrees of freedom
## Residual deviance: 18736  on 12780  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5

## [1] "Goodness of Fit Test:"

##      res.deviance    df          p
## [1,]      18735.63 12780 2.506431e-234

```

#### Model 4: Zero Inflated

We saw earlier that the dependent variable had an excess number of zeros which skewed the distribution from a typical poisson. The zero inflated model generates coefficients for the zero count part of the model as well as for the count part.

```

##
## Call:
## zeroinfl(formula = TARGET ~ ., data = train_data_imputed, dist = "poisson")
##
## Pearson residuals:
##      Min      1Q   Median      3Q      Max
## -2.2647 -0.3637  0.1660   0.5024   4.5568
##
## Count model coefficients (poisson with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.436e+00  2.064e-01   6.957 3.48e-12 ***

```

```

## FixedAcidity      2.761e-04  8.583e-04  0.322  0.74772
## VolatileAcidity   -1.340e-02  6.869e-03 -1.950  0.05113 .
## CitricAcid        1.665e-06  6.141e-03  0.000  0.99978
## ResidualSugar     -8.537e-05  1.574e-04 -0.542  0.58768
## Chlorides         -1.864e-02  1.689e-02 -1.103  0.26983
## FreeSulfurDioxide  3.421e-05  3.517e-05  0.973  0.33071
## TotalSulfurDioxide -2.484e-05  2.242e-05 -1.108  0.26781
## Density           -3.173e-01  2.025e-01 -1.567  0.11715
## pH                7.552e-03  7.929e-03  0.952  0.34089
## Sulphates         -4.784e-04  5.758e-03 -0.083  0.93378
## Alcohol           7.454e-03  1.431e-03  5.208  1.90e-07 ***
## LabelAppeal       2.490e-01  6.413e-03 38.830 < 2e-16 ***
## AcidIndex         -1.632e-02  4.985e-03 -3.274  0.00106 **
## STARS             9.228e-02  6.282e-03 14.690 < 2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -6.0101503  1.0351369 -5.806 6.39e-09 ***
## FixedAcidity    0.0022671  0.0043130  0.526  0.59913
## VolatileAcidity  0.2410929  0.0346521  6.958 3.46e-12 ***
## CitricAcid     -0.0808575  0.0313726 -2.577  0.00996 **
## ResidualSugar  -0.0012063  0.0007978 -1.512  0.13049
## Chlorides       0.2513384  0.0847036  2.967  0.00300 **
## FreeSulfurDioxide -0.0007432  0.0001806 -4.115 3.86e-05 ***
## TotalSulfurDioxide -0.0008516  0.0001157 -7.359 1.85e-13 ***
## Density         0.8678799  1.0174164  0.853  0.39365
## pH              0.1862523  0.0400600  4.649 3.33e-06 ***
## Sulphates       0.1201562  0.0291157  4.127 3.68e-05 ***
## Alcohol         0.0086516  0.0072511  1.193  0.23282
## LabelAppeal     0.3177151  0.0331974  9.570 < 2e-16 ***
## AcidIndex       0.4798872  0.0196945 24.366 < 2e-16 ***
## STARS          -0.4876110  0.0340780 -14.309 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 36
## Log-likelihood: -2.257e+04 on 30 Df

##
## Call:
## zeroinfl(formula = TARGET ~ . - FixedAcidity - Density, data = train_data_imputed,
##   dist = "poisson")
##
## Pearson residuals:
##      Min      1Q  Median      3Q      Max
## -2.2637 -0.3611  0.1657  0.5028  4.2429
##
## Count model coefficients (poisson with log link):
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.123e+00  5.218e-02 21.528 < 2e-16 ***
## VolatileAcidity -1.348e-02  6.869e-03 -1.963  0.04966 *
## CitricAcid      8.106e-05  6.141e-03  0.013  0.98947
## ResidualSugar   -8.645e-05  1.574e-04 -0.549  0.58294
## Chlorides       -1.934e-02  1.688e-02 -1.145  0.25207

```

```
## FreeSulfurDioxide 3.317e-05 3.515e-05 0.944 0.34541
## TotalSulfurDioxide -2.555e-05 2.241e-05 -1.140 0.25422
## pH 7.531e-03 7.930e-03 0.950 0.34229
## Sulphates -3.744e-04 5.756e-03 -0.065 0.94814
## Alcohol 7.471e-03 1.431e-03 5.221 1.78e-07 ***
## LabelAppeal 2.490e-01 6.412e-03 38.831 < 2e-16 ***
## AcidIndex -1.647e-02 4.939e-03 -3.336 0.00085 ***
## STARS 9.240e-02 6.282e-03 14.709 < 2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -5.1500574 0.2384962 -21.594 < 2e-16 ***
## VolatileAcidity 0.2418331 0.0346319 6.983 2.89e-12 ***
## CitricAcid -0.0813522 0.0313463 -2.595 0.00945 **
## ResidualSugar -0.0012059 0.0007977 -1.512 0.13057
## Chlorides 0.2517730 0.0846799 2.973 0.00295 **
## FreeSulfurDioxide -0.0007424 0.0001806 -4.111 3.94e-05 ***
## TotalSulfurDioxide -0.0008507 0.0001157 -7.353 1.93e-13 ***
## pH 0.1864564 0.0400542 4.655 3.24e-06 ***
## Sulphates 0.1203503 0.0291009 4.136 3.54e-05 ***
## Alcohol 0.0086686 0.0072495 1.196 0.23180
## LabelAppeal 0.3170975 0.0331851 9.555 < 2e-16 ***
## AcidIndex 0.4822325 0.0193585 24.911 < 2e-16 ***
## STARS -0.4876789 0.0340664 -14.316 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 31
## Log-likelihood: -2.257e+04 on 26 Df
```

## Model 5: Linear Model

Let build a multiple linear regression

```
##
## Call:
## lm(formula = TARGET ~ ., data = train_data_imputed)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.8273 -0.6997  0.3798  1.1196  4.3471
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.755e+00  5.610e-01  10.259 < 2e-16 ***
## FixedAcidity -3.077e-04  2.356e-03  -0.131 0.896082
## VolatileAcidity -1.571e-01  1.871e-02  -8.399 < 2e-16 ***
## CitricAcid  3.931e-02  1.703e-02   2.308 0.020999 *
## ResidualSugar  4.399e-04  4.331e-04   1.016 0.309780
## Chlorides -1.893e-01  4.598e-02  -4.118 3.85e-05 ***
## FreeSulfurDioxide  4.574e-04  9.873e-05   4.633 3.64e-06 ***
## TotalSulfurDioxide  3.422e-04  6.322e-05   5.413 6.32e-08 ***
## Density -1.262e+00  5.524e-01  -2.285 0.022323 *
```

```
## pH -5.770e-02 2.161e-02 -2.671 0.007575 **
## Sulphates -5.632e-02 1.571e-02 -3.585 0.000339 ***
## Alcohol 1.951e-02 3.948e-03 4.941 7.86e-07 ***
## LabelAppeal 6.035e-01 1.740e-02 34.687 < 2e-16 ***
## AcidIndex -3.285e-01 1.138e-02 -28.858 < 2e-16 ***
## STARS 5.410e-01 1.736e-02 31.171 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.655 on 12780 degrees of freedom
## Multiple R-squared: 0.2623, Adjusted R-squared: 0.2615
## F-statistic: 324.5 on 14 and 12780 DF, p-value: < 2.2e-16
```

## Model 6: Negative Binomial

```
##
## Call:
## glm.nb(formula = TARGET ~ ., data = train_data_imputed, link = "log",
##       init.theta = 33879.1139)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.8385  -0.5031   0.2162   0.6281   2.6383
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.131e+00  1.956e-01  10.898 < 2e-16 ***
## FixedAcidity   -2.187e-04  8.197e-04  -0.267 0.789597
## VolatileAcidity -5.200e-02  6.481e-03  -8.023 1.03e-15 ***
## CitricAcid      1.371e-02  5.893e-03   2.326 0.020017 *
## ResidualSugar   1.253e-04  1.504e-04   0.833 0.404699
## Chlorides      -5.865e-02  1.601e-02  -3.663 0.000250 ***
## FreeSulfurDioxide 1.510e-04  3.426e-05   4.407 1.05e-05 ***
## TotalSulfurDioxide 1.178e-04  2.206e-05   5.337 9.47e-08 ***
## Density       -4.318e-01  1.921e-01  -2.247 0.024628 *
## pH            -2.156e-02  7.524e-03  -2.865 0.004170 **
## Sulphates     -1.920e-02  5.456e-03  -3.519 0.000433 ***
## Alcohol        5.684e-03  1.376e-03   4.130 3.62e-05 ***
## LabelAppeal    2.001e-01  6.087e-03  32.866 < 2e-16 ***
## AcidIndex     -1.240e-01  4.453e-03 -27.850 < 2e-16 ***
## STARS          1.665e-01  5.823e-03  28.596 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(33879.11) family taken to be 1)
##
##      Null deviance: 22859  on 12794  degrees of freedom
## Residual deviance: 18735  on 12780  degrees of freedom
## AIC: 50710
##
## Number of Fisher Scoring iterations: 1
##
##
```

```
##          Theta: 33879
##          Std. Err.: 59308
## Warning while fitting theta: iteration limit reached
##
## 2 x log-likelihood: -50677.75
```

## Model Selection

Based on the models tested, we select the Zero Inflated model due to the highest accuracy compared to other models. Also, Zero Inflation model corrects many zeros which are dominated in poisson distributions especially in this case where there are many zeros normally distributed.

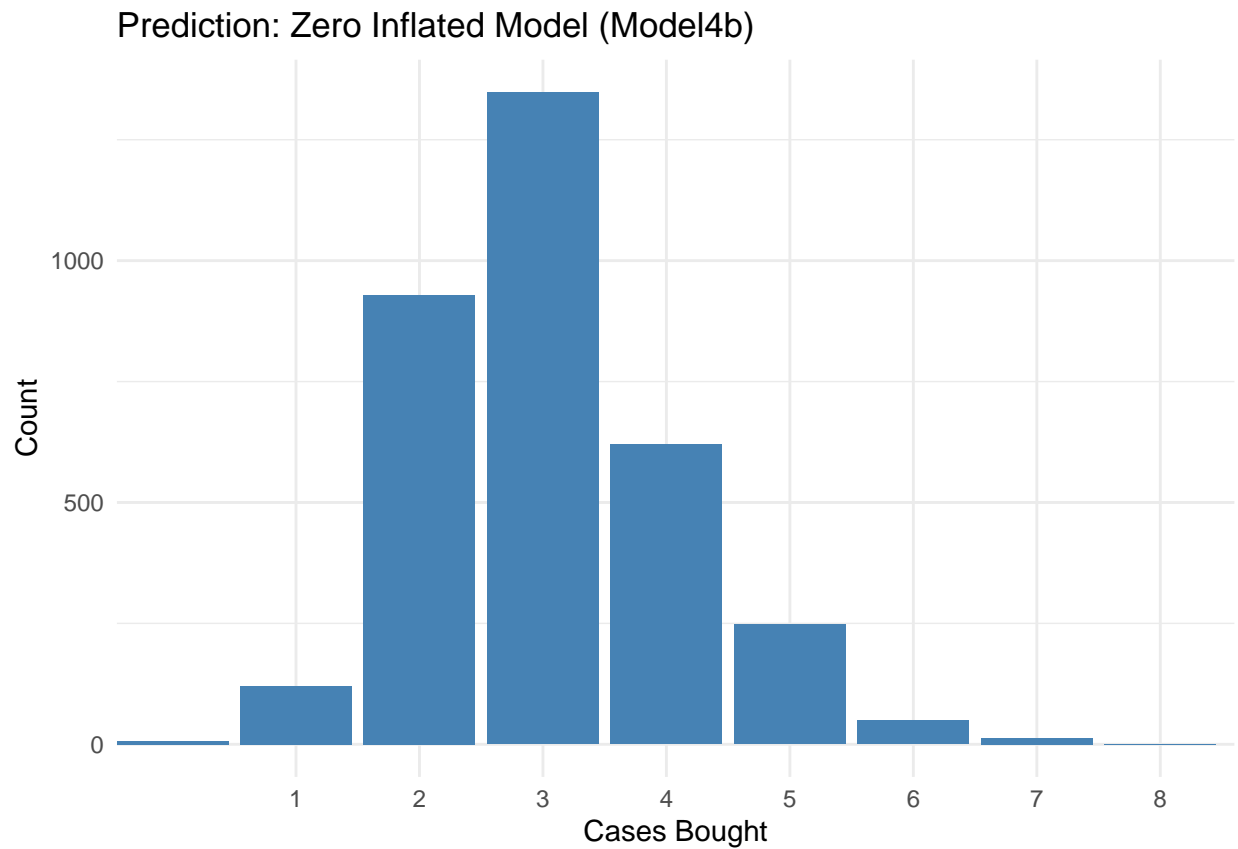
	Poisson (Imputed)	Quasipoisson Model	Zero Inflated
## Accuracy	0.24	0.24	0.26
## Kappa	0.10	0.10	0.12
## AccuracyLower	0.24	0.24	0.26
## AccuracyUpper	0.25	0.25	0.27
## AccuracyNull	0.25	0.25	0.25
## AccuracyPValue	0.83	0.83	0.00
## McNemarPValue	NaN	NaN	NaN

```
##
## iter imp variable
## 1 1 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 1 2 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 1 3 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 1 4 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 1 5 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 2 1 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 2 2 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 2 3 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 2 4 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 2 5 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 3 1 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 3 2 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 3 3 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 3 4 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 3 5 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 4 1 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 4 2 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 4 3 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 4 4 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 4 5 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 5 1 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 5 2 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 5 3 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 5 4 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
## 5 5 ResidualSugar Chlorides FreeSulfurDioxide TotalSulfurDioxide pH Sulphates Alcohol ST
```

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

##	1	2	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	1	3	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	1	4	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	1	5	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	2	1	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	2	2	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	2	3	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	2	4	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	2	5	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	3	1	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	3	2	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	3	3	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	3	4	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	3	5	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	1	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	2	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	3	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	4	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	4	5	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	1	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	2	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	3	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	4	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST
##	5	5	ResidualSugar	Chlorides	FreeSulfurDioxide	TotalSulfurDioxide	pH	Sulphates	Alcohol	ST

## [1] "Missing value after imputation: 3335"





## Appendix

```
library(corrplot)
library(tidyverse)
library(Hmisc)
library(PerformanceAnalytics)
library(mice)
library(gt)
library(caret)
library(bnstruct)
library(VIM)
library(corr)
library(kableExtra)
library(rpart)
library(gtsummary)
library(reshape)
library(pROC)
library(randomForest)
library(pscl)
library(skimr)
## Data Exploration
train_data <- read.csv("./data/wine-training-data.csv", header = TRUE)
test_data <- read.csv("./data/wine-evaluation-data.csv", header = TRUE)
glimpse(train_data)
skim(train_data)
# remove index column as it is not needed
train_data <- train_data %>%
  dplyr::select(-"i..INDEX")
data_test <- test_data %>%
  dplyr::select(-"IN")
## Visualization
# histogram
train_data %>%
  dplyr::select(-c("AcidIndex", "STARS", "TARGET", "LabelAppeal")) %>%
  gather() %>%
  ggplot(aes(value)) +
  facet_wrap(~key, scale = "free", ncol = 3) +
  geom_histogram(binwidth = function(x) 2 * IQR(x) / (length(x)^(1/3)), fill="blue") +
  theme_minimal()
train_data %>%
  ggplot(aes(x=TARGET)) +
  geom_histogram(fill='blue')
# boxplot
p1 <- train_data %>%
  dplyr::select(-c("TotalSulfurDioxide", "FreeSulfurDioxide", "ResidualSugar")) %>%
  gather(na.rm = TRUE) %>%
  ggplot(aes(factor(key), value)) +
  geom_boxplot(outlier.colour = "#e281cf", outlier.shape = 1, color = "#5aa1ed") +
  coord_flip() +
  labs(title = "Boxplot of Chemical Properties of Wine", x = "Chemical Properties", y = "Values") +
  theme_minimal()
p2 <- train_data %>%
  dplyr::select(c("TotalSulfurDioxide", "FreeSulfurDioxide", "ResidualSugar")) %>%
  gather(na.rm = TRUE) %>%
```

```

  ggplot(aes(factor(key), value)) +
  geom_boxplot(outlier.colour = "#e281cf", outlier.shape = 1, color = "#5aa1ed") +
  #labs(title = "Boxplot of Chemical Properties of Wine", x = "Chemical Properties", y = "Values") +
  theme_minimal()
ggarrange(p1, p2)
# barchart
p3 <- train_data %>%
  dplyr::select(TARGET, STARS) %>%
  mutate(STARS = as.factor(STARS),
         TARGET = as.factor(TARGET)) %>%
  ggplot(aes(STARS)) +
  geom_bar(aes(fill = TARGET)) +
  theme_minimal()
p4 <- train_data %>%
  dplyr::select(TARGET, LabelAppeal) %>%
  mutate(STARS = as.factor(LabelAppeal),
         TARGET = as.factor(TARGET)) %>%
  ggplot(aes(LabelAppeal)) +
  geom_bar(aes(fill = TARGET)) +
  theme_minimal()
p5 <- train_data %>%
  dplyr::select(TARGET, AcidIndex) %>%
  mutate(STARS = as.factor(AcidIndex),
         TARGET = as.factor(TARGET)) %>%
  ggplot(aes(AcidIndex)) +
  geom_bar(aes(fill = TARGET)) +
  theme_minimal()
ggarrange(p5, ggarrange(p3, p4, ncol = 2, nrow = 1, legend = "none"), nrow = 2, common.legend = TRUE)
# top correlation
wine_train_corr <- train_data %>%
  drop_na() %>%
  cor()
kable(sort(wine_train_corr[,1], decreasing = T), col.names = c("Correlation")) %>%
  kable_styling(full_width = F)
# correlation plot
corrplot(wine_train_corr,
         method = "number",
         type = "lower",
         col = brewer.pal(n = 15, name = "Reds"),
         number.cex = .7, tl.cex = .7,
         tl.col = "black", tl.srt = 45)
# missing value columns
aggr(train_data,
     sortVars=TRUE,
     labels=names(train_data),
     cex.axis=.5,
     bars = FALSE,
     col = c("white", "#E46726"),
     combined = TRUE,
     #border = NA,
     ylab = "Missing Values")
# imputating train data
init <- mice(train_data)
meth <- init$method

```

```

predM <- init$predictorMatrix
predM[, c("TARGET")] <- 0 #this code will remove the variable as a predictor but still will be imputed
train_data_impute <- mice(train_data, method = 'rf', predictorMatrix=predM)
train_data_imputed <-mice:: complete(train_data_impute)
print(paste0("Missing value after imputation: ", sum(is.na(train_data_imputed))))
## Model Building
### Model 1: Poisson (Raw data)
# poisson model with the missing values
model1 <- glm(TARGET ~ ., family = poisson, train_data)
summary(model1)
print('Goodness of Fit Test:')
with(model1, cbind(res.deviance = deviance, df = df.residual, p = pchisq(deviance, df.residual, lower.t
### Model 2: Poisson (Imputed Data)
# poisson model with the imputed values
model2 <- glm(TARGET ~ ., family = poisson, train_data_imputed)
summary(model2)
print('Goodness of Fit Test:')
with(model2, cbind(res.deviance = deviance, df = df.residual, p = pchisq(deviance, df.residual, lower.t
### Model 3: Quasipoisson Model
# poisson model with the imputed values
model3 <- glm(TARGET ~ ., family = quasipoisson(link='log'), train_data_imputed)
summary(model3)
print('Goodness of Fit Test:')
with(model3, cbind(res.deviance = deviance, df = df.residual, p = pchisq(deviance, df.residual, lower.t
### Model 4: Zero Inflated
model4 <- zeroinfl(TARGET ~., train_data_imputed, dist = 'poisson')
summary(model4)
model4b <- zeroinfl(TARGET ~ . - FixedAcidity - Density, train_data_imputed, dist = 'poisson')
summary(model4b)
## Model Selection
pred_train <- data.frame(TARGET=train_data_imputed$TARGET,
                        model2=model2$fitted.values,
                        model3=model3$fitted.values,
                        model4b=model4b$fitted.values)
pred_train <- round(pred_train, 0)
colnames(pred_train) <- c("TARGET","Poisson (Imputed)", "Quasipoisson Model", "Zero Inflated")
pred_train %>%
  gather() %>%
  ggplot(aes(value)) +
  facet_wrap(~key, scale = "free", ncol = 4) +
  geom_bar(fill="blue") +
  theme_minimal() + labs(x="Cases Bought", y = "Count", title = "Prediction Histogram")
model2_fitted.values <- factor(round(model2$fitted.values),levels=rev(0:9))
model3_fitted.values <- factor(round(model3$fitted.values),levels=rev(0:9))
model4b_fitted.values <- factor(round(model4b$fitted.values),levels=rev(0:9))
m2_cfm <- confusionMatrix(model2_fitted.values, factor(train_data_imputed$TARGET,levels=rev(0:9)))
m3_cfm <- confusionMatrix(model3_fitted.values, factor(train_data_imputed$TARGET,levels=rev(0:9)))
m4_cfm <- confusionMatrix(model4b_fitted.values, factor(train_data_imputed$TARGET,levels=rev(0:9)))
models_sum <- data.frame(m2_cfm$overall, m3_cfm$overall, m4_cfm$overall)
colnames(models_sum) <- c("Poisson (Imputed)", "Quasipoisson Model", "Zero Inflated")
round(models_sum, 2)
init <- mice(data_test)
meth <- init$method
predM <- init$predictorMatrix

```

```

predM[, c("TARGET")] <- 0 #this code will remove the variable as a predictor but still will be imputed
data_test_impute <- mice(data_test, method = 'rf', predictorMatrix=predM)
data_test_imputed <- mice::complete(data_test_impute)
print(paste0("Missing value after imputation: ", sum(is.na(data_test_imputed))))
test_predict <- predict(model4b, newdata=data_test_imputed)
test_predict <- round(test_predict,0)
data_pred <- data.frame(TARGET=test_predict)
ggplot(data_pred, aes(x=TARGET)) + geom_bar(fill="steelblue") + theme_minimal() +
  labs(y="Count", title = "Prediction: Zero Inflated Model (Model4b)") +
  scale_x_discrete(name = "Cases Bought", limits=c("1","2","3","4", "5", "6", "7", "8"))
write.csv(test_predict, "WinePredictions.csv")

```