

Data 621 Homework 5: Wine

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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.

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	

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TotalSulfurDioxide	Total Sulfur Dioxide of Wine
VolatileAcidity	Volatile Acid content of wine
pH	pH of wine

DATA EXPLORATION

Data Summary

With over 12,000 observations in our sample, we must look into the data and explore key summary statistics. We also calculate the counts for NA's, 0, negative, and unique values.

```
##      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

vars
n
mean
sd
median
trimmed
mad
min
max
range
skew
kurtosis
se
na_count
neg_count
zero_count
unique_count
TARGET
1
12795
3.0290739
1.9263682
3.00000
3.0538244
1.4826000
0.00000
8.00000
8.00000
-0.3263010
-0.8772457
0.0170302
0

```

0
2734
9
FixedAcidity

2
12795
7.0757171
6.3176435
6.90000
7.0736739
3.2617200
-18.10000
34.40000
52.50000
-0.0225860
1.6749987
0.0558515

0
1621
548
470

VolatileAcidity
3
12795
0.3241039
0.7840142
0.28000
0.3243890
0.4299540
-2.79000
3.68000
6.47000
0.0203800
1.8322106
0.0069311
0

2827
9982
815
CitricAcid
4
12795
0.3084127
0.8620798
0.31000
0.3102520
0.4151280
-3.24000
3.86000
7.10000
-0.0503070
1.8379401
0.0076213
0
2966
9686
602
ResidualSugar
5
12179
5.4187331
33.7493790
3.90000
5.5800410
15.7155600
-127.80000
141.15000
268.95000
-0.0531229
1.8846917
0.3058158
616

NA
NA
2078
Chlorides
6
12157
0.0548225
0.3184673
0.04600
0.0540159
0.1349166
-1.17100
1.35100
2.52200
0.0304272
1.7886044
0.0028884
638
NA
NA
1664
FreeSulfurDioxide
7
12148
30.8455713
148.7145577
30.00000
30.9334877
56.3388000
-555.00000
623.00000
1178.00000
0.0063930
1.8364966
1.3492769
647

NA
NA
1000
TotalSulfurDioxide
8
12113
120.7142326
231.9132105
123.00000
120.8895367
134.9166000
-823.00000
1057.00000
1880.00000
-0.0071794
1.6746665
2.1071703
682
NA
NA
1371
Density
9
12795
0.9942027
0.0265376
0.99449
0.9942130
0.0093552
0.88809
1.09924
0.21115
-0.0186938
1.8999592
0.0002346
0

0
9492
5933
pH
10
12400
3.2076282
0.6796871
3.20000
3.2055706
0.3854760
0.48000
6.13000
5.65000
0.0442880
1.6462681
0.0061038
395
NA
NA
498
Sulphates
11
11585
0.5271118
0.9321293
0.50000
0.5271453
0.4447800
-3.13000
4.24000
7.37000
0.0059119
1.7525655
0.0086602
1210

NA

NA

631

Alcohol

12

12142

10.4892363

3.7278190

10.40000

10.5018255

2.3721600

-4.70000

26.50000

31.20000

-0.0307158

1.5394949

0.0338306

653

NA

NA

402

LabelAppeal

13

12795

-0.0090660

0.8910892

0.00000

-0.0099639

1.4826000

-2.00000

2.00000

4.00000

0.0084295

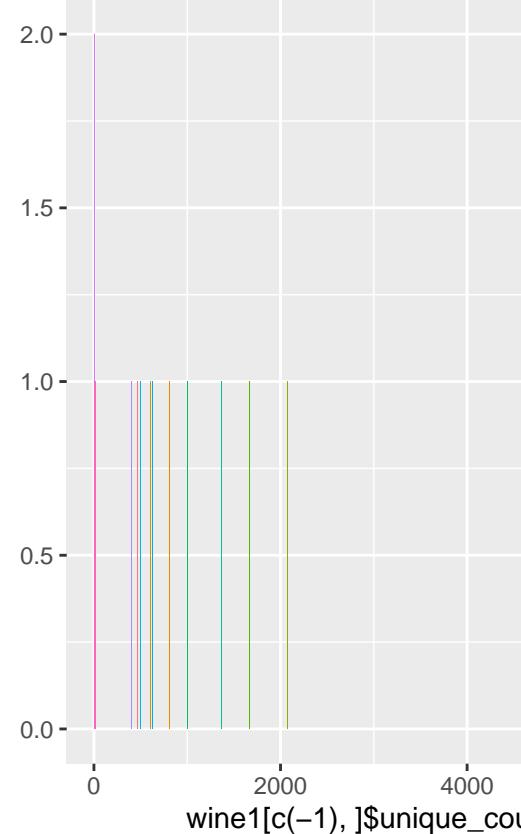
-0.2622916

0.0078777

0

3640
5617
5
AcidIndex
14
12795
7.7727237
1.3239264
8.00000
7.6431572
1.4826000
4.00000
17.00000
13.00000
1.6484959
5.1900925
0.0117043
0
0
0
14
STARS
15
9436
2.0417550
0.9025400
2.00000
1.9711258
1.4826000
1.00000
4.00000
3.00000
0.4472353
-0.6925343
0.0092912
3359

```
NA  
NA  
5
```



We visualize these counts per variable and then explore solutions further below.

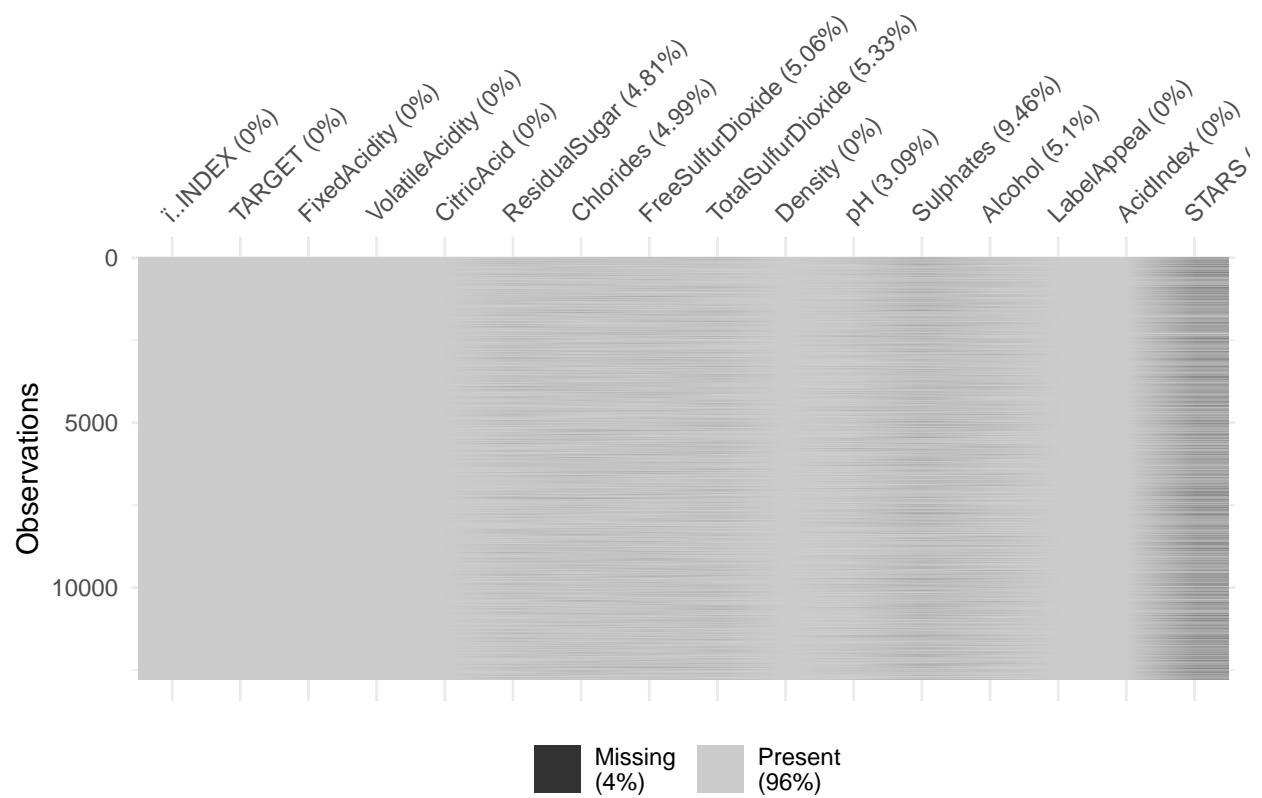
The dataset consists of two data files: training and evaluation. The training dataset contains 16 columns, and the evaluation dataset also contains 16 columns.

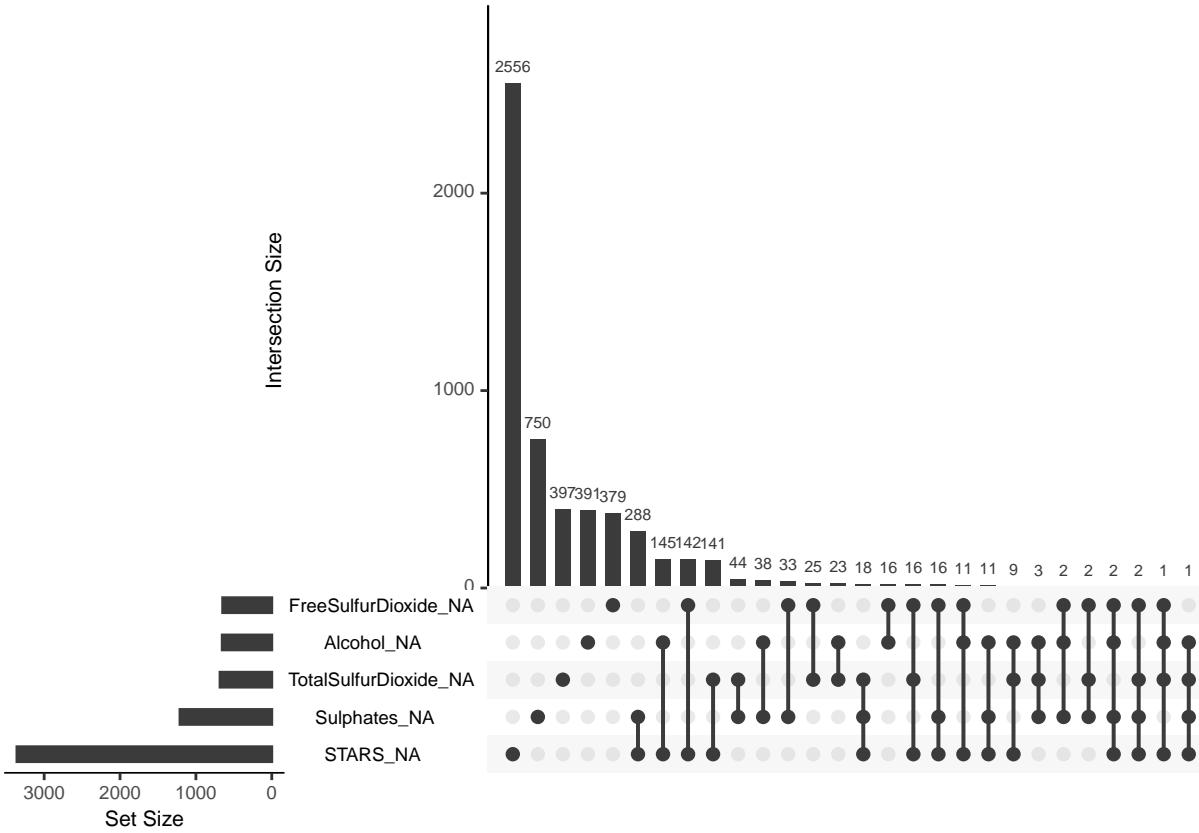
Missing Data

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. If we eliminate all non-complete rows and keep only rows with data for all the predictors in the dataset, our new dataset will result in 50% of the total dataset. We create a subset of data with complete cases if needed later in our analysis.

```

## Observations: 6,436
## Variables: 16
## $ .i..INDEX      <int> 4, 5, 13, 14, 16, 23, 24, 25, 26, 27, 28, 32, 34...
## $ TARGET          <int> 5, 3, 6, 0, 3, 4, 5, 4, 3, 2, 3, 4, 4, 3, 4, 3, ...
## $ FixedAcidity    <dbl> 7.1, 5.7, 5.5, -17.2, 6.0, -1.3, 10.0, 6.8, 5.8, ...
## $ VolatileAcidity <dbl> 2.640, 0.385, -0.220, 0.520, 0.330, 0.220, 0.230...
## $ CitricAcid      <dbl> -0.88, 0.04, 0.39, 0.15, -1.06, 2.95, 0.27, -0.2...
## $ ResidualSugar   <dbl> 14.80, 18.80, 1.80, -33.80, 3.00, -53.00, 14.10, ...
## $ Chlorides        <dbl> 0.037, -0.425, -0.277, -0.022, 0.518, 0.541, 0.0...
## $ FreeSulfurDioxide <dbl> 214, 22, 62, 551, 5, -85, -188, -88, 87, 15, 32, ...
## $ TotalSulfurDioxide <dbl> 142, 115, 180, 65, 378, -266, 229, 508, -283, 60...
## $ Density          <dbl> 0.99518, 0.99640, 0.94724, 0.99340, 0.96643, 0.9...
## $ pH               <dbl> 3.12, 2.24, 3.09, 4.31, 3.55, 3.61, 3.14, 3.23, ...
## $ Sulphates        <dbl> 0.48, 1.83, 0.75, 0.56, -0.86, 0.82, 0.88, 0.35, ...
## $ Alcohol           <dbl> 22.0, 6.2, 12.6, 13.1, 3.9, 10.0, 11.0, 18.3, 11...
## $ LabelAppeal      <int> -1, -1, 0, 1, 1, 0, 1, -1, -1, 0, 0, 1, -1, ...
## $ AcidIndex         <int> 8, 6, 8, 5, 7, 8, 11, 8, 6, 7, 8, 7, 8, 6, 9, ...
## $ STARS            <int> 3, 1, 4, 1, 2, 3, 2, 2, 1, 1, 2, 2, 1, 3, 1, ...

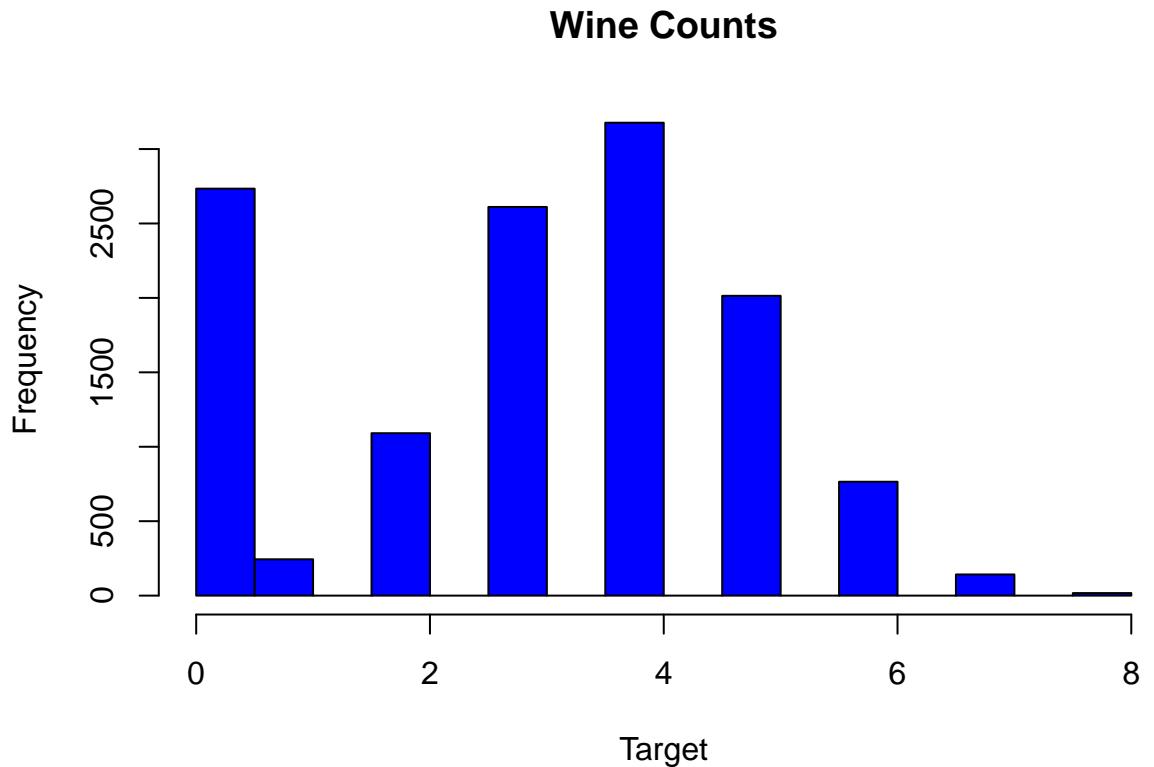
```

Visualization

We consider each variable

Target Variable

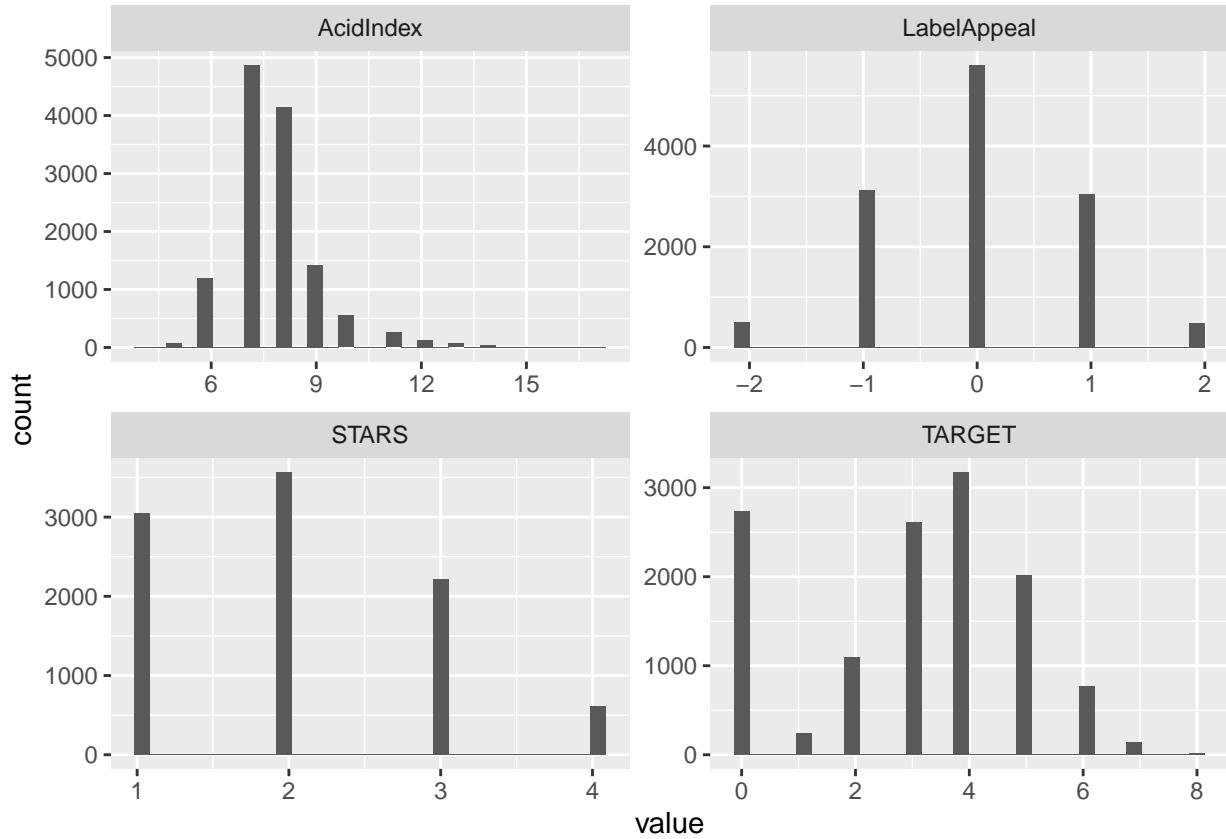
The distribution of our target variable is normal with the exception of many 0 Wine count entries. At such a high percentage, the zero scores likely reflect lack of popularity rather than error, especially if they get low human ratings.



Histogram

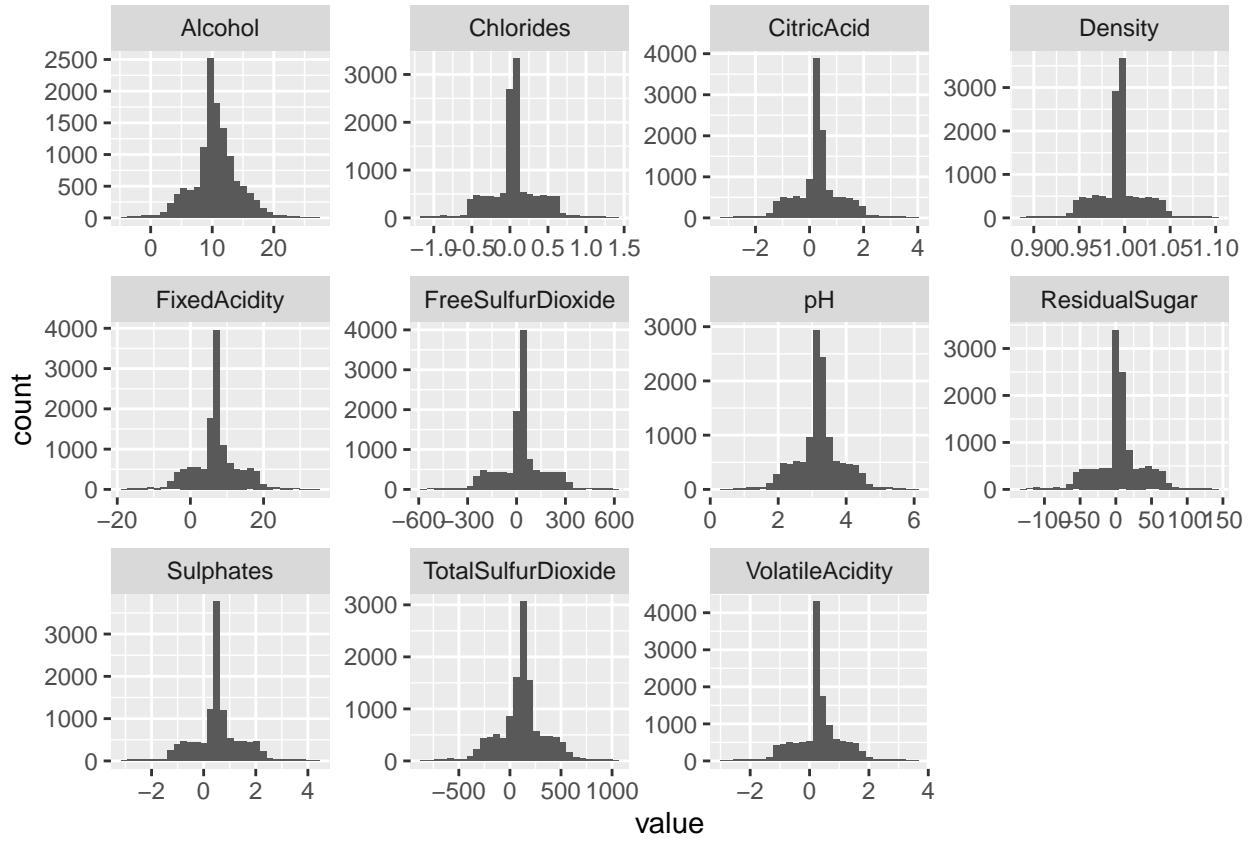
Integers The integer variables have a small range and look normal, similar to TARGET. Stars has the least number of values and has many 0 entries. We will treat these as meaningful due to the percentage of NA's. Decision makers who buy wine are similar to the population who creates the integer variables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

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



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.

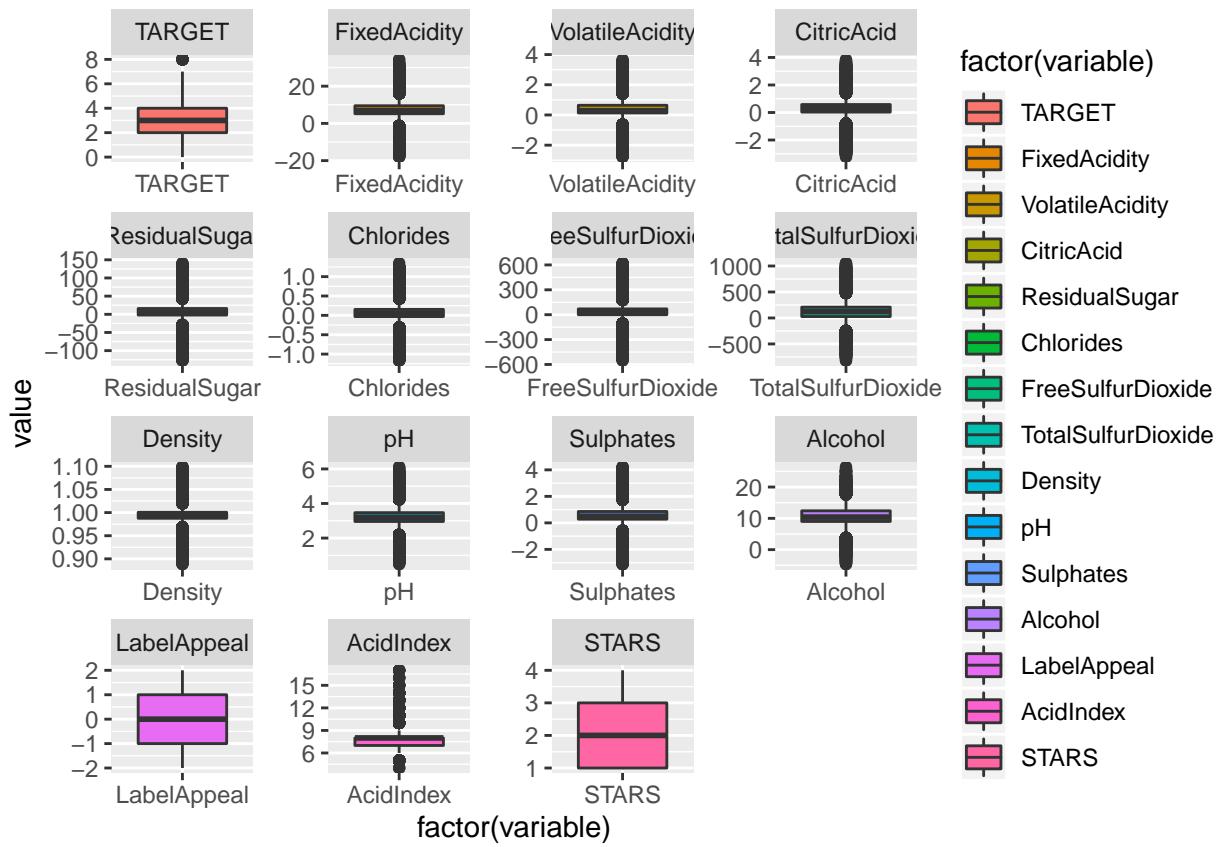
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Outliers

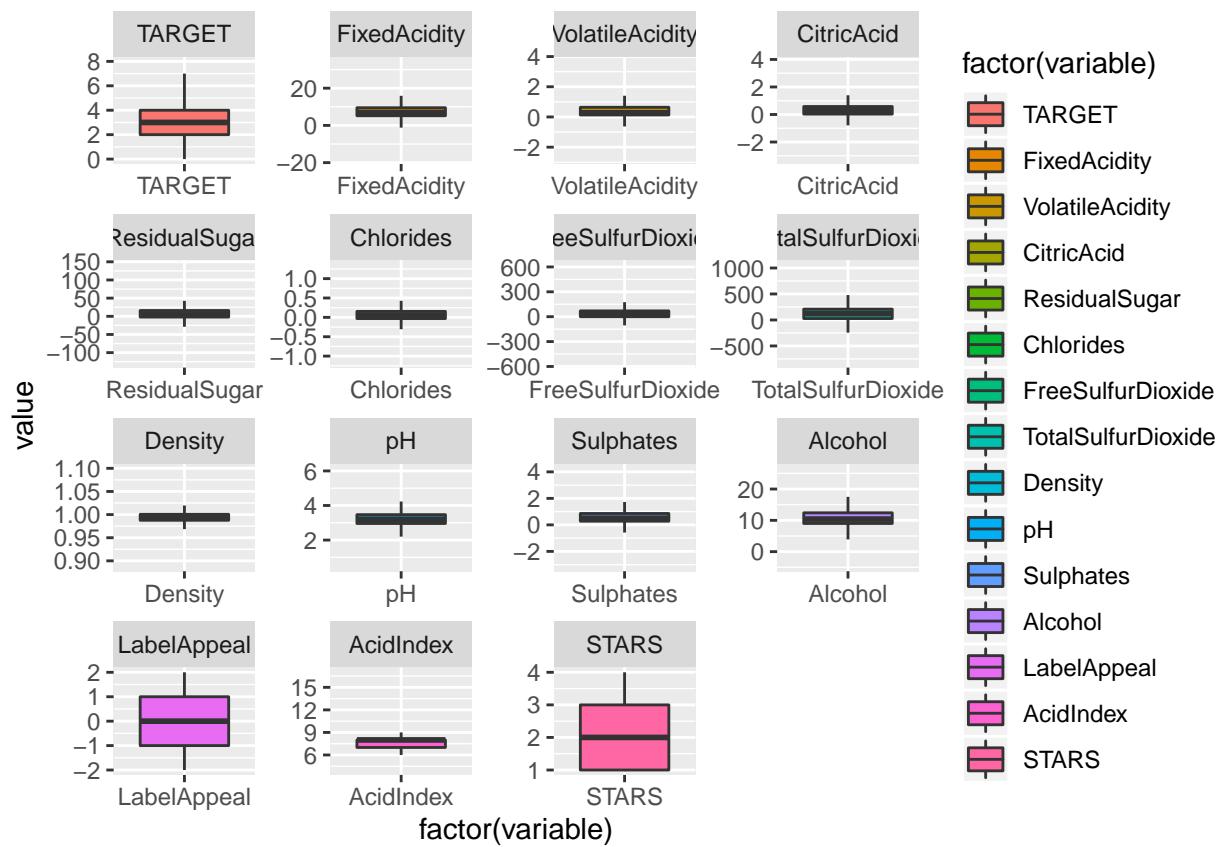
Boxplot

```
## No id variables; using all as measure variables
```

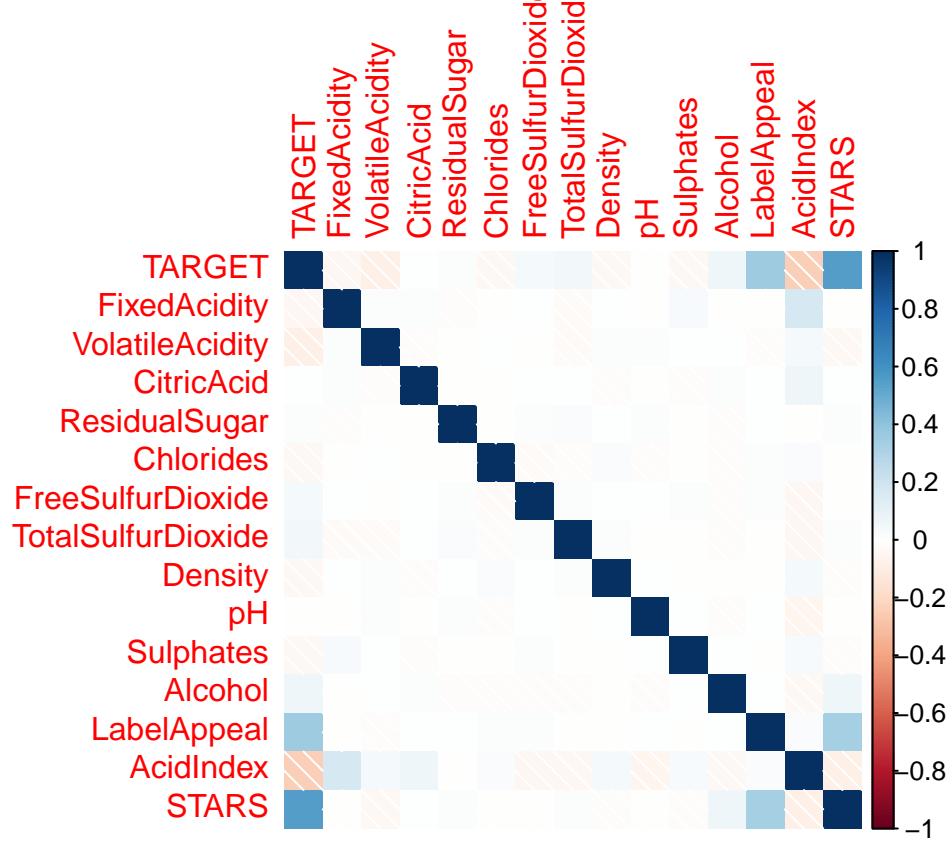


```
#### Boxplot Without outliers
```

```
## No id variables; using all as measure variables
```



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



DATA PREPERATION

	na_count	neg_count	zero_count	unique_count
## TARGET	0	0	2734	9
## 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

We recall that STARS has a high correlation with TARGET and we see that it has $r(\text{wine1}["\text{STARS}"], \text{"na_count"}) / \text{nrow}(\text{WineT})$ NA's and no zero's. We change NA to 0.

	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
## TARGET                     0       0      2734      9
## 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

```

The remaining NA counts include continuous variables which we will impute.

We can normalize the negative counts, through BoxCox, since one of them has some correlation and is based on human ratings. While the negative ratings make the data irregular to work with, it is unlikely that so many people ($r(wine1["STARS", "neg_count"] / nrow(WineTrain)) * 100\%$) did not mean to give a negative rating. We can do this to the continuous variables as well rather than delete them, since they also have high counts.

```

##                               na_count neg_count zero_count unique_count
## LabelAppeal                  0       3640     5617      5
## CitricAcid                  0       2966     9686     602
## VolatileAcidity              0       2827     9982     815
## FixedAcidity                 0       1621     548      470
## TARGET                      0       0      2734      9
## Density                      0       0      9492     5933
## AcidIndex                     0       0       0      14
## ResidualSugar                616      NA      NA      2078
## Chlorides                     638      NA      NA      1664
## FreeSulfurDioxide             647      NA      NA      1000
## TotalSulfurDioxide            682      NA      NA      1371
## pH                           395      NA      NA      498
## Sulphates                    1210      NA      NA      631
## Alcohol                      653      NA      NA      402
## STARS                       3359      NA      NA      5

```

By the same logic we will leave the zero counts alone until normalization. We can exclude the TARGET variable unless we will be normalizing it specifically for our later work.

```

##                               na_count neg_count zero_count unique_count
## VolatileAcidity              0       2827     9982     815
## CitricAcid                  0       2966     9686     602
## Density                      0       0      9492     5933
## LabelAppeal                  0       3640     5617      5
## TARGET                      0       0      2734      9
## FixedAcidity                 0       1621     548      470
## AcidIndex                     0       0       0      14
## ResidualSugar                616      NA      NA      2078
## Chlorides                     638      NA      NA      1664
## FreeSulfurDioxide             647      NA      NA      1000
## TotalSulfurDioxide            682      NA      NA      1371
## pH                           395      NA      NA      498
## Sulphates                    1210      NA      NA      631

```

```

## Alcohol           653      NA      NA      402
## STARS            3359     NA      NA       5

```

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 can exclude TARGET until we analyze our feature transformation decisions. We see that AcidIndex is a proprietary weighted method for measuring Acid. We do not need to impute this, given its complexity and relative influence, and the risk or changing our results over very small ranges.

	na_count	neg_count	zero_count	unique_count
## LabelAppeal	0	3640	5617	5
## STARS	3359	NA	NA	5
## TARGET	0	0	2734	9
## AcidIndex	0	0	0	14
## Alcohol	653	NA	NA	402
## FixedAcidity	0	1621	548	470
## pH	395	NA	NA	498
## CitricAcid	0	2966	9686	602
## Sulphates	1210	NA	NA	631
## VolatileAcidity	0	2827	9982	815
## FreeSulfurDioxide	647	NA	NA	1000
## TotalSulfurDioxide	682	NA	NA	1371
## Chlorides	638	NA	NA	1664
## ResidualSugar	616	NA	NA	2078
## Density	0	0	9492	5933

TODO: Diagnostic

BUILD MODEL

Model 1: Poisson Regression (all predictors)

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

```

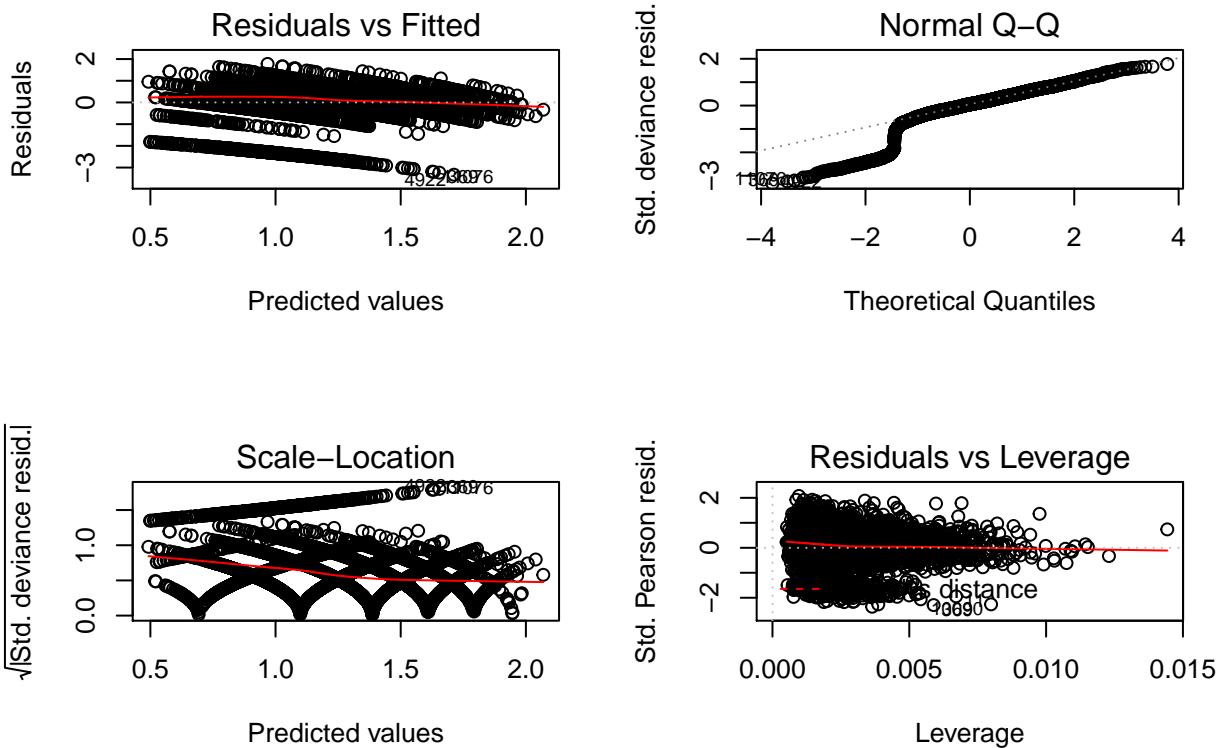
## 
## Call:
## glm(formula = TARGET ~ . - INDEX, family = poisson, data = WineTrain)
## 
## Deviance Residuals:
##      Min        1Q     Median        3Q       Max
## -3.3301  -0.2799   0.0536   0.3861   1.7744
## 
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)          1.688e+00  2.503e-01  6.742  1.56e-11 ***
## FixedAcidity         4.868e-04  1.053e-03  0.462   0.6438
## VolatileAcidity     -2.481e-02  8.362e-03 -2.968   0.0030 **
## CitricAcid          -1.614e-03  7.578e-03 -0.213   0.8313
## ResidualSugar       -6.875e-05  1.939e-04 -0.355   0.7229
## Chlorides           -3.327e-02  2.053e-02 -1.621   0.1050
## FreeSulfurDioxide   6.032e-05  4.399e-05  1.371   0.1703
## TotalSulfurDioxide  2.141e-05  2.854e-05  0.750   0.4531
## Density             -3.695e-01  2.462e-01 -1.501   0.1334
## pH                  -2.547e-03  9.608e-03 -0.265   0.7909
## Sulphates           -6.672e-03  7.051e-03 -0.946   0.3440
## Alcohol              4.443e-03  1.772e-03  2.507   0.0122 *

```

```

## LabelAppeal      1.783e-01  7.958e-03  22.403 < 2e-16 ***
## AcidIndex       -4.762e-02 5.911e-03  -8.056 7.88e-16 ***
## STARS2          3.232e-01  1.740e-02   18.574 < 2e-16 ***
## STARS3          4.387e-01  1.896e-02   23.134 < 2e-16 ***
## STARS4          5.509e-01  2.688e-02   20.491 < 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: 3928.8 on 6419 degrees of freedom
## (6359 observations deleted due to missingness)
## AIC: 23095
##
## Number of Fisher Scoring iterations: 5

```



Model 2: Poisson Regression (reduced predictors)

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

```

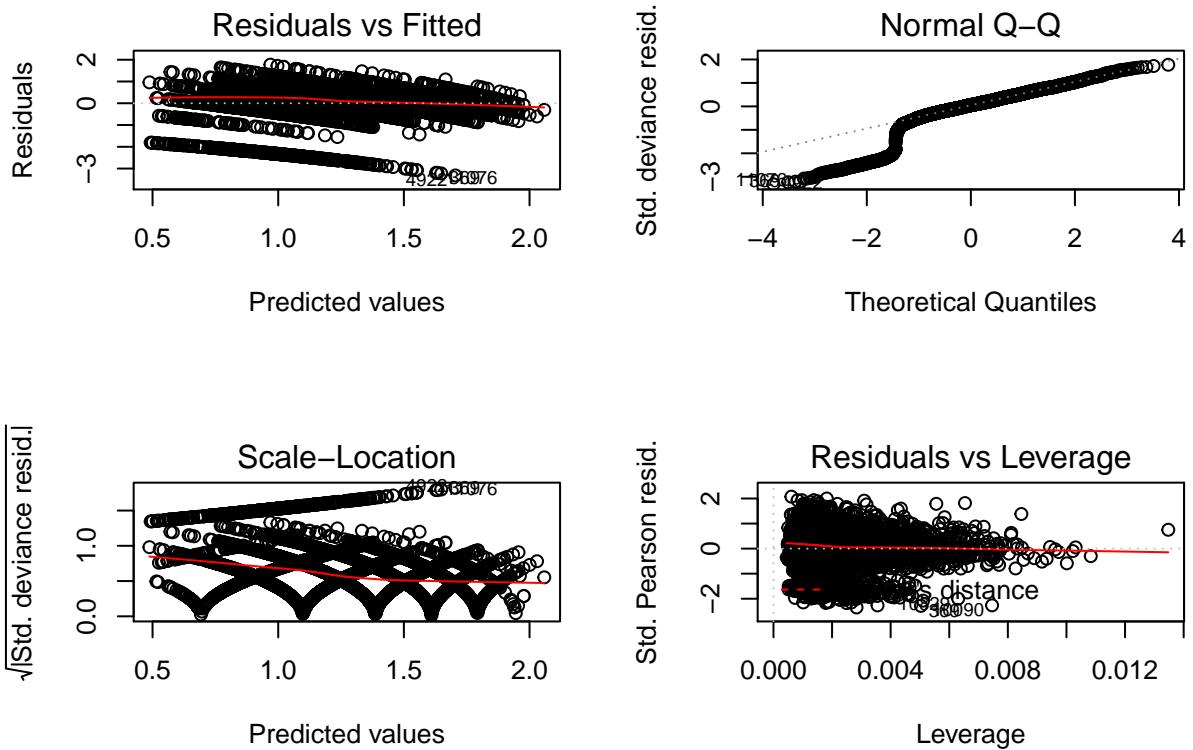
##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + CitricAcid + Chlorides +
##     FreeSulfurDioxide + TotalSulfurDioxide + Density + pH + Sulphates +
##     Alcohol + LabelAppeal + AcidIndex + STARS, family = poisson,
##     data = WineTrain)

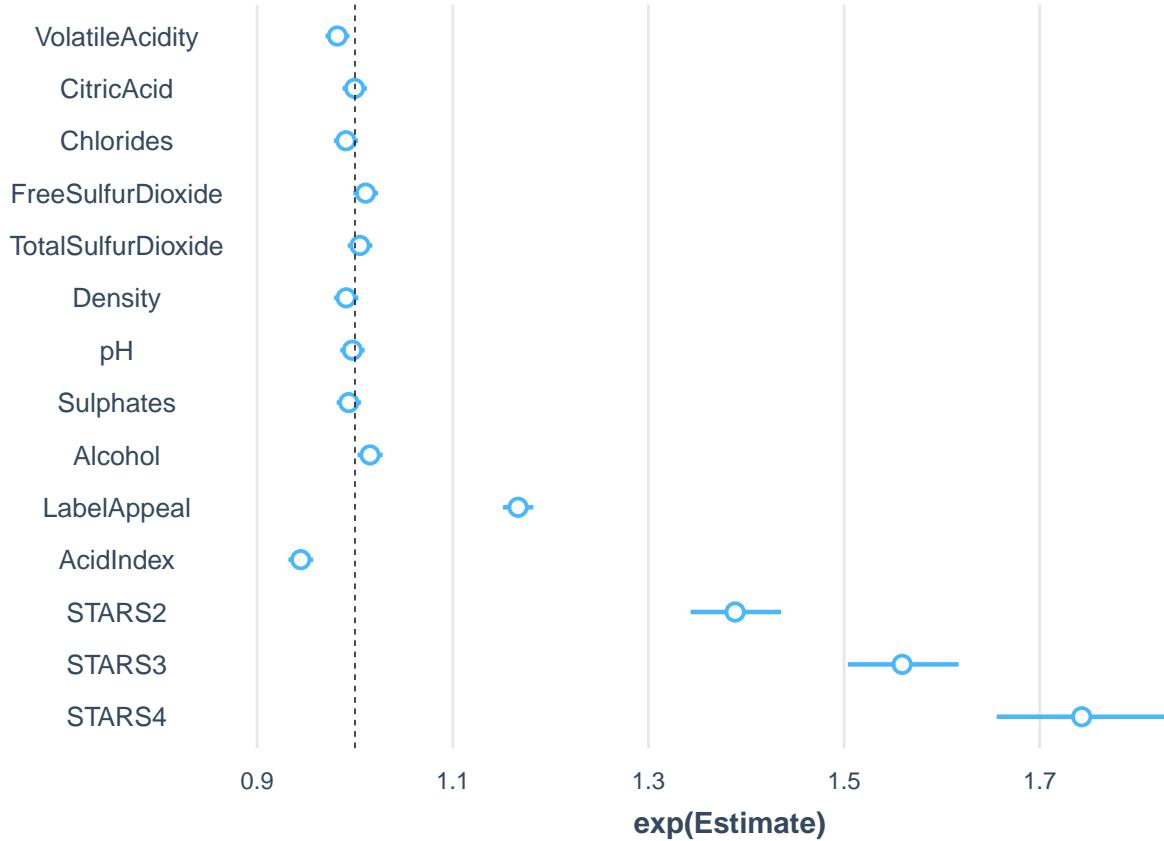
```

```

## 
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -3.3170 -0.2829  0.0543  0.3858  1.7731
## 
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)           1.669e+00 2.442e-01 6.832 8.37e-12 ***
## VolatileAcidity     -2.319e-02 8.142e-03 -2.849  0.00439 **
## CitricAcid          -4.347e-04 7.395e-03 -0.059  0.95313
## Chlorides           -2.918e-02 2.000e-02 -1.459  0.14447
## FreeSulfurDioxide   7.263e-05 4.282e-05  1.696  0.08987 .
## TotalSulfurDioxide  2.206e-05 2.785e-05  0.792  0.42828
## Density            -3.417e-01 2.402e-01 -1.422  0.15491
## pH                 -3.949e-03 9.411e-03 -0.420  0.67478
## Sulphates          -6.911e-03 6.869e-03 -1.006  0.31437
## Alcohol            4.113e-03 1.730e-03  2.377  0.01743 *
## LabelAppeal        1.766e-01 7.744e-03 22.801 < 2e-16 ***
## AcidIndex          -4.784e-02 5.720e-03 -8.363 < 2e-16 ***
## STARS2             3.283e-01 1.700e-02 19.307 < 2e-16 ***
## STARS3             4.443e-01 1.852e-02 23.996 < 2e-16 ***
## STARS4             5.556e-01 2.611e-02 21.280 < 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: 6145.7 on 6746 degrees of freedom
## Residual deviance: 4123.6 on 6732 degrees of freedom
## (6048 observations deleted due to missingness)
## AIC: 24216
## 
## Number of Fisher Scoring iterations: 5

```





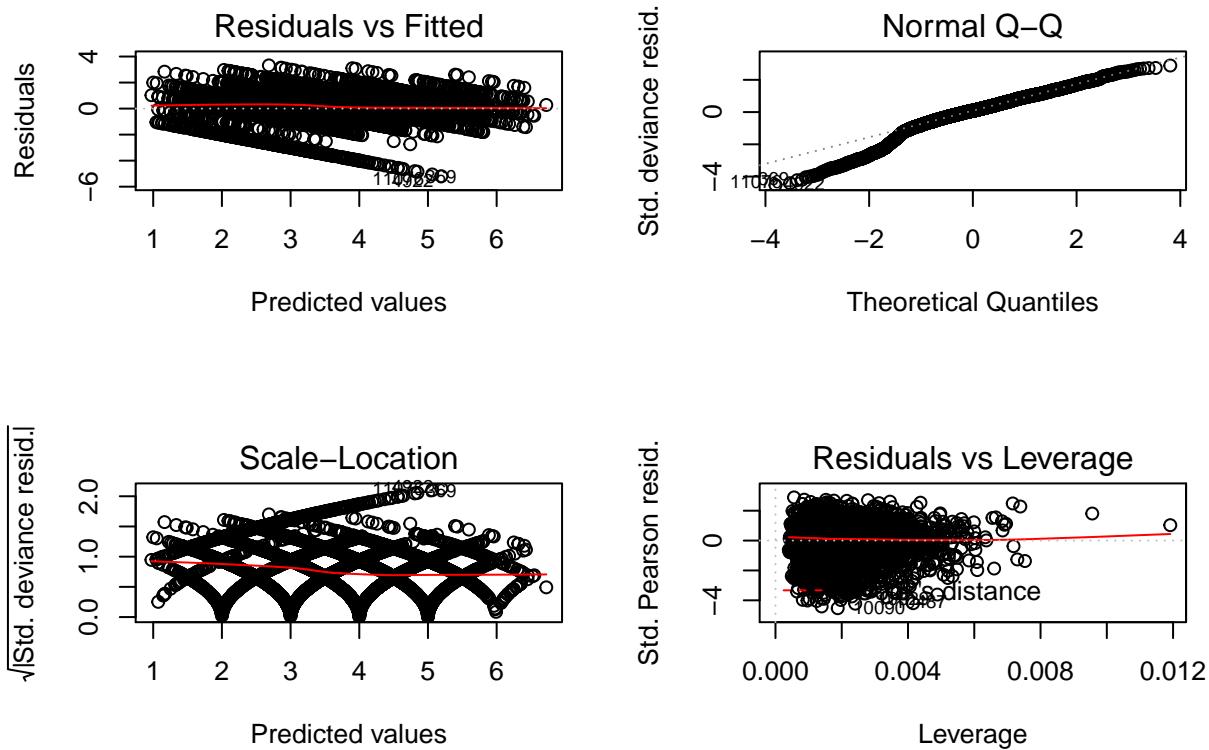
Model 3: Gaussian Regression (significant predictors)

```
##
## 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 
## -5.1949 -0.5359  0.0996  0.7405  3.3160 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 5.331e+00  5.229e-01 10.194 < 2e-16 ***
## VolatileAcidity -8.491e-02 1.740e-02 -4.881 1.08e-06 ***
## FreeSulfurDioxide 2.752e-04 9.243e-05 2.978  0.00291 ** 
## TotalSulfurDioxide 7.090e-05 5.952e-05 1.191  0.23358  
## Chlorides      -1.158e-01 4.293e-02 -2.697  0.00701 ** 
## Density        -1.300e+00 5.169e-01 -2.516  0.01191 *  
## pH             -1.875e-03 2.020e-02 -0.093  0.92607  
## Sulphates      -2.413e-02 1.471e-02 -1.641  0.10092  
## LabelAppeal    6.411e-01 1.649e-02 38.878 < 2e-16 ***
## AcidIndex      -1.611e-01 1.153e-02 -13.966 < 2e-16 ***
## STARS2         1.005e+00 3.313e-02 30.326 < 2e-16 ***
## STARS3         1.513e+00 3.839e-02 39.411 < 2e-16 ***
```

```

## STARS4          2.151e+00  6.199e-02  34.701  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.319364)
##
## Null deviance: 17036.4 on 7102 degrees of freedom
## Residual deviance: 9354.3 on 7090 degrees of freedom
## (5692 observations deleted due to missingness)
## AIC: 22141
##
## Number of Fisher Scoring iterations: 2

```



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

Model 4: Negative Binomial Regression

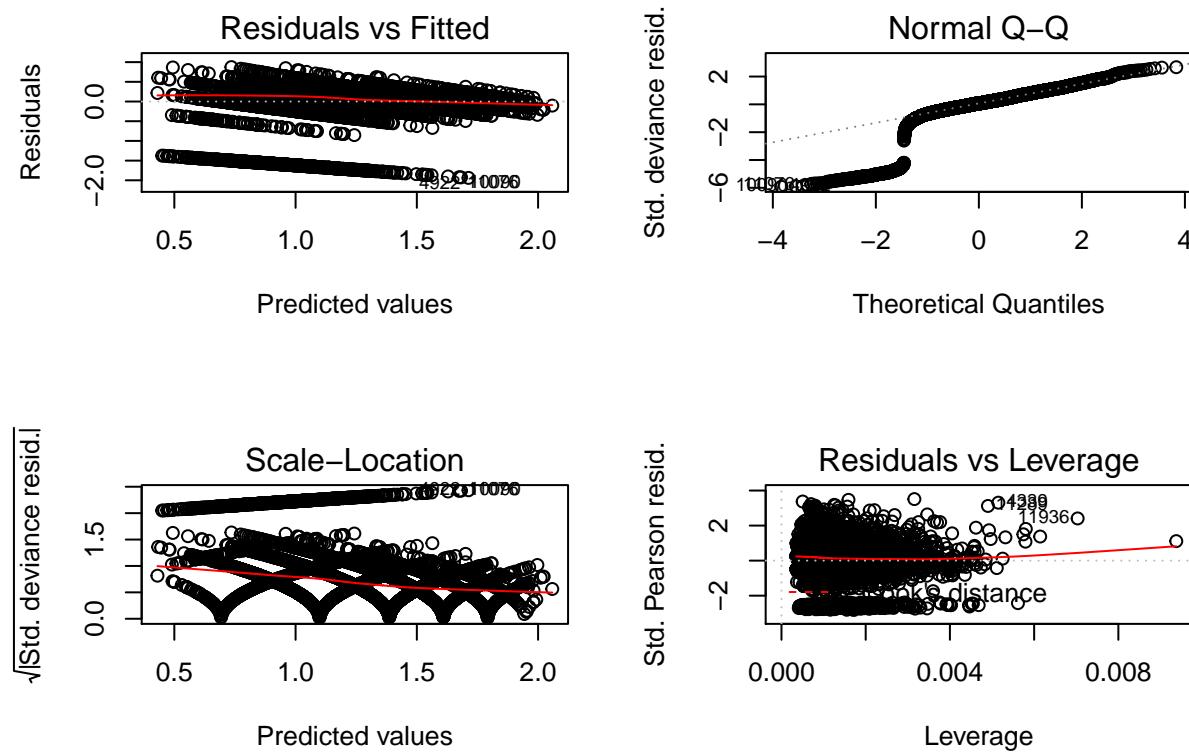
```

##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + TotalSulfurDioxide +
##      pH + Sulphates + LabelAppeal + AcidIndex + STARS, family = negative.binomial(1),
##      data = WineTrain)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.93848   -0.13164   0.02425   0.17731   0.87362
## 
```

```

## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.443e+00 3.642e-02 39.613 < 2e-16 ***
## VolatileAcidity     -2.766e-02 5.397e-03 -5.125 3.04e-07 ***
## TotalSulfurDioxide  2.430e-05 1.823e-05  1.333  0.1827
## pH                  -3.613e-03 6.190e-03 -0.584  0.5595
## Sulphates            -8.920e-03 4.527e-03 -1.970  0.0488 *
## LabelAppeal          1.862e-01 5.081e-03 36.649 < 2e-16 ***
## AcidIndex            -5.607e-02 3.622e-03 -15.480 < 2e-16 ***
## STARS2              3.232e-01 1.037e-02 31.160 < 2e-16 ***
## STARS3              4.375e-01 1.185e-02 36.914 < 2e-16 ***
## STARS4              5.464e-01 1.839e-02 29.716 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1) family taken to be 0.1073286)
##
## Null deviance: 2393.6 on 7878 degrees of freedom
## Residual deviance: 1870.2 on 7869 degrees of freedom
## (4916 observations deleted due to missingness)
## AIC: 37774
##
## Number of Fisher Scoring iterations: 5

```



SELECT MODEL

Pick the best regression model

	Model 1	Model 2	Model 3	Model 4
AIC	23095.3698167386	24216.2765273715	22141.0249335269	37774.0980469856
BIC	23210.4540793765	24318.5293259809	22237.1807486529	37843.8176096981

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

#CONCLUSION

TODO plot predictions

APPENDIX

Code used in analysis

```

kable(wine1, "html", escape = F, booktab = T) %>%
  kable_styling("striped", full_width = T, position = "float_left", font_size = 7) %>%
  column_spec(1, bold = T) %>%
  scroll_box(width = "100%", height = "700px")

# geom_point(data = wine1, color = "red", shape = 15, size = 5)

qplot(wine1[c(-1)], unique_count,
      geom="bar",
      fill=as_factor(rownames(wine1[c(-1)])))

colsTrain<-ncol(WineTrain)
colsEval<-ncol(WineEval)
missingCol<-colnames(WineTrain)[!(colnames(WineTrain) %in% colnames(WineEval))]
cc<-summary(complete.cases(WineTrain))
cWineTrain<-subset(WineTrain, complete.cases(WineTrain))
cc
vis_miss(WineTrain)
gg_miss_upset(WineTrain)
glimpse(cWineTrain)
WineTrain1$INDEX <- NULL
hist(WineTrain1$TARGET, col = "blue", xlab = " Target ", main = "Wine Counts")
WineTrain1[-1] %>%
  keep(is.integer) %>%
  gather() %>%
  ggplot(aes(value), main="") +
  facet_wrap(~ key, scales = "free") +
  geom_histogram()
WineTrain1 %>%
  keep(is.double) %>%
  gather() %>%
  ggplot(aes(value)) +
  facet_wrap(~ key, scales = "free") +
  geom_histogram()
ggplot(melt(WineTrain[-1]), aes(x=factor(variable), y=value, fill=factor(variable))) + facet_wrap(~variable)
ggplot(melt(WineTrain[-1]), aes(x=factor(variable), y=value, fill=factor(variable))) + facet_wrap(~variable)
corrplot(as.matrix(cor(WineTrain[-1], use = "pairwise.complete")), method = "shade")
print(wine1[,14:17])
print(wine1[order(-wine1$na_count),14:17])
#WineTrain$STARS <- sapply(WineTrain$STARS, function(x) ifelse(is.na(x), 0, x))
#WineTrain<-as.factor(WineTrain)
#wine1 <- var_stats(WineTrain)
#mice imputation
#print(wine1[order(-wine1$na_count),14:17])
print(wine1[order(-wine1$neg_count),14:17])



print(wine1[order(-wine1$zero_count),14:17])
print(wine1[order(wine1$unique_count),14:17])

WineTrain$STARS<-as.factor(WineTrain$STARS)
WineEval$STARS<-as.factor(WineEval$STARS)

```

```

#WineTest
m1 <- glm(TARGET ~ .-INDEX , 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)
library(jtools)
plot_summs(m2, scale = TRUE, exp = TRUE)
m3 <- glm(TARGET ~ VolatileAcidity + FreeSulfurDioxide + TotalSulfurDioxide + Chlorides + Density + pH +
           Sulphates + LabelAppeal + AcidIndex + STARS, family = negative.binomial(1),
           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")

```