DATA_621_HW5

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4/10/2022

```
train_df <- read.csv("wine-training-data.csv",fileEncoding="UTF-8-BOM")
test_df <- read.csv("wine-evaluation-data.csv",fileEncoding="UTF-8-BOM")

train_df$INDEX <- NULL
test_df$IN <- NULL
```

DATA EXPLORATION

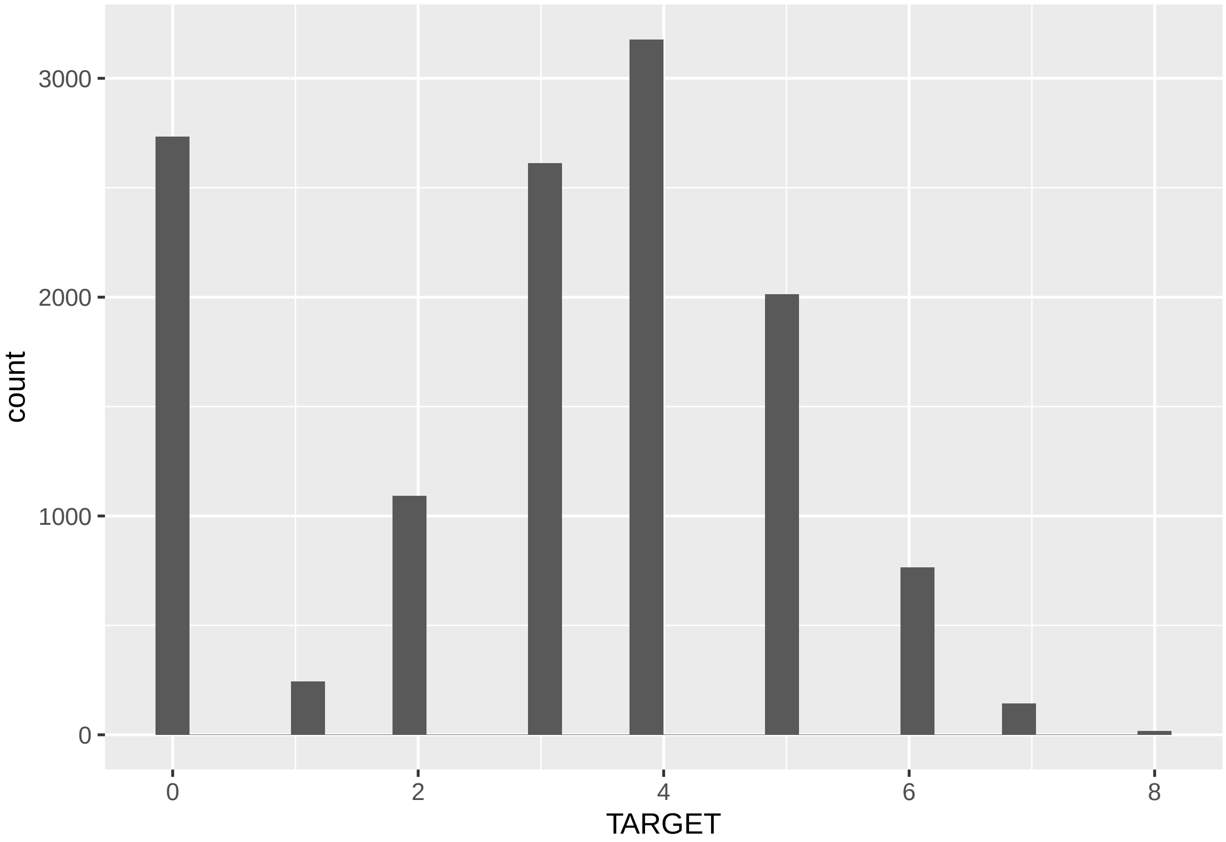
Data Summary

```
summary(train_df)
```

```
##      TARGET       FixedAcidity     VolatileAcidity     CitricAcid
##  Min.   :0.000   Min.   :-18.100   Min.   :-2.7900   Min.   :-3.2400
##  1st Qu.:2.000   1st Qu.:  5.200   1st Qu.: 0.1300   1st Qu.: 0.0300
##  Median :3.000   Median :  6.900   Median : 0.2800   Median : 0.3100
##  Mean   :3.029   Mean   :  7.076   Mean   : 0.3241   Mean   : 0.3084
##  3rd Qu.:4.000   3rd Qu.:  9.500   3rd Qu.: 0.6400   3rd Qu.: 0.5800
##  Max.   :8.000   Max.   : 34.400   Max.   : 3.6800   Max.   : 3.8600
##
##  ResidualSugar        Chlorides       FreeSulfurDioxide TotalSulfurDioxide
##  Min.   :-127.800   Min.   :-1.1710   Min.   :-555.00   Min.   :-823.0
##  1st Qu.:  -2.000   1st Qu.:-0.0310   1st Qu.:   0.00   1st Qu.:  27.0
##  Median :   3.900   Median : 0.0460   Median :  30.00   Median : 123.0
##  Mean   :   5.419   Mean   : 0.0548   Mean   :  30.85   Mean   : 120.7
##  3rd Qu.:  15.900   3rd Qu.: 0.1530   3rd Qu.:  70.00   3rd Qu.: 208.0
##  Max.   : 141.150   Max.   : 1.3510   Max.   : 623.00   Max.   :1057.0
##  NA’s   :616        NA’s   :638       NA’s   :647       NA’s   :682
##     Density             pH          Sulphates          Alcohol
##  Min.   :0.8881   Min.   :0.480   Min.   :-3.1300   Min.   :-4.70
##  1st Qu.:0.9877   1st Qu.:2.960   1st Qu.: 0.2800   1st Qu.: 9.00
##  Median :0.9945   Median :3.200   Median : 0.5000   Median :10.40
##  Mean   :0.9942   Mean   :3.208   Mean   : 0.5271   Mean   :10.49
##  3rd Qu.:1.0005   3rd Qu.:3.470   3rd Qu.: 0.8600   3rd Qu.:12.40
##  Max.   :1.0992   Max.   :6.130   Max.   : 4.2400   Max.   :26.50
##                   NA’s   :395     NA’s   :1210      NA’s   :653
##   LabelAppeal          AcidIndex          STARS
##  Min.   :-2.000000   Min.   : 4.000   Min.   :1.000
##  1st Qu.:-1.000000   1st Qu.: 7.000   1st Qu.:1.000
##  Median : 0.000000   Median : 8.000   Median :2.000
##  Mean   :-0.009066   Mean   : 7.773   Mean   :2.042
##  3rd Qu.: 1.000000   3rd Qu.: 8.000   3rd Qu.:3.000
##  Max.   : 2.000000   Max.   :17.000   Max.   :4.000
##                                       NA's   :3359
```

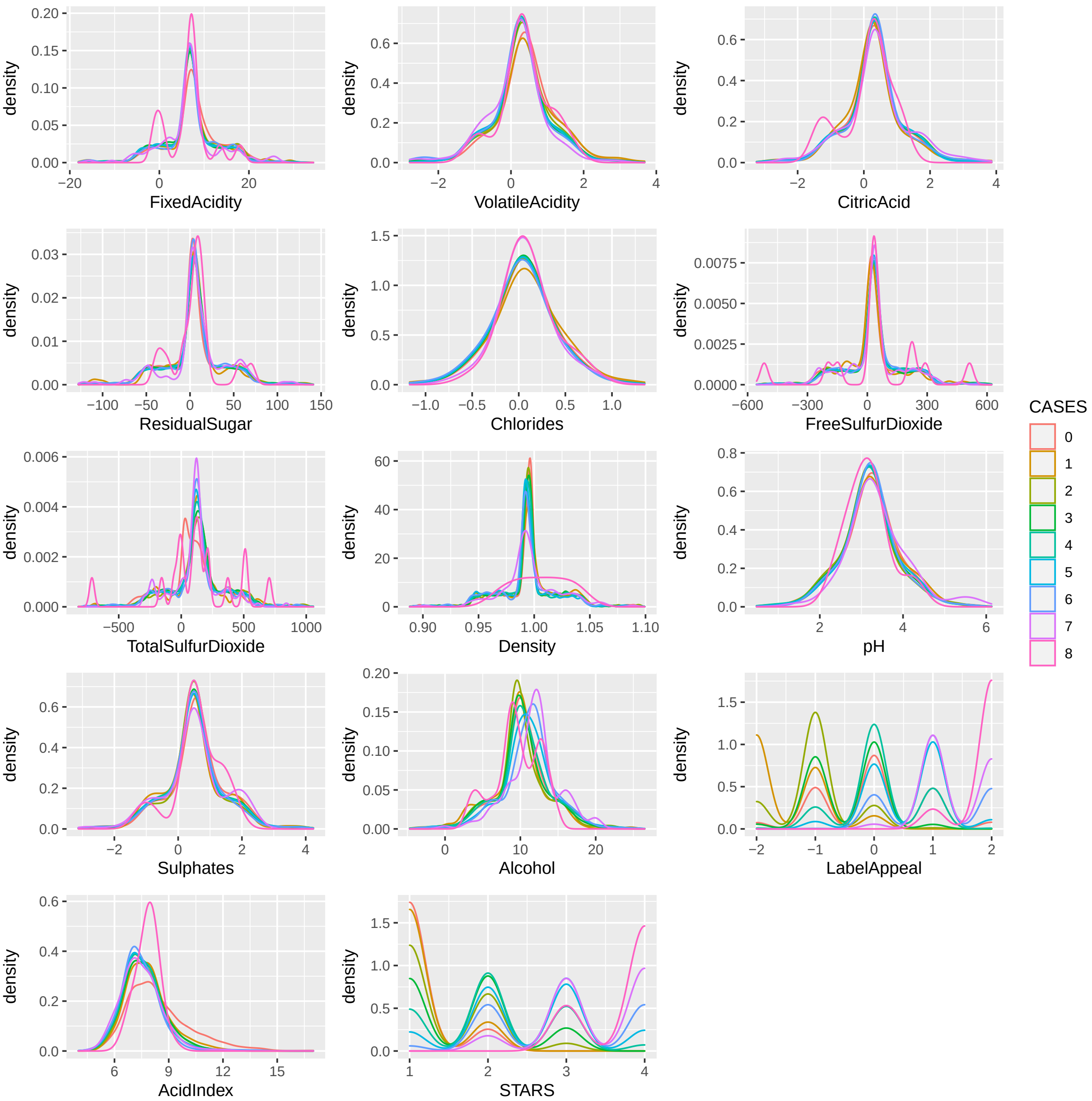
Distribution plots

```
ggplot(train_df, aes(x=TARGET)) + geom_histogram(na.rm =TRUE)
```



```
CASES <- as.factor(train_df$TARGET)

plot_FixedAcidity <- ggplot(train_df, aes(x=FixedAcidity, color=CASES)) + geom_density(na.rm =TRUE, bw=
plot_VolatileAcidity <- ggplot(train_df, aes(x=VolatileAcidity, color=CASES)) + geom_density(na.rm =TRU
plot_CitricAcid <- ggplot(train_df, aes(x=CitricAcid, color=CASES)) + geom_density(na.rm =TRUE, bw=0.3)
plot_ResidualSugar <- ggplot(train_df, aes(x=ResidualSugar, color=CASES)) + geom_density(na.rm =TRUE, b
plot_Chlorides <- ggplot(train_df, aes(x=Chlorides, color=CASES)) + geom_density(na.rm =TRUE, bw=0.2)
plot_FreeSulfurDioxide <- ggplot(train_df, aes(x=FreeSulfurDioxide, color=CASES)) + geom_density(na.rm =
plot_TotalSulfurDioxide <- ggplot(train_df, aes(x=TotalSulfurDioxide, color=CASES)) + geom_density(na.r
plot_Density <- ggplot(train_df, aes(x=Density, color=CASES)) + geom_density(na.rm =TRUE)
plot_pH <- ggplot(train_df, aes(x=pH, color=CASES)) + geom_density(na.rm =TRUE, bw=0.3)
plot_Sulphates <- ggplot(train_df, aes(x=Sulphates, color=CASES)) + geom_density(na.rm =TRUE, bw=0.3)
```

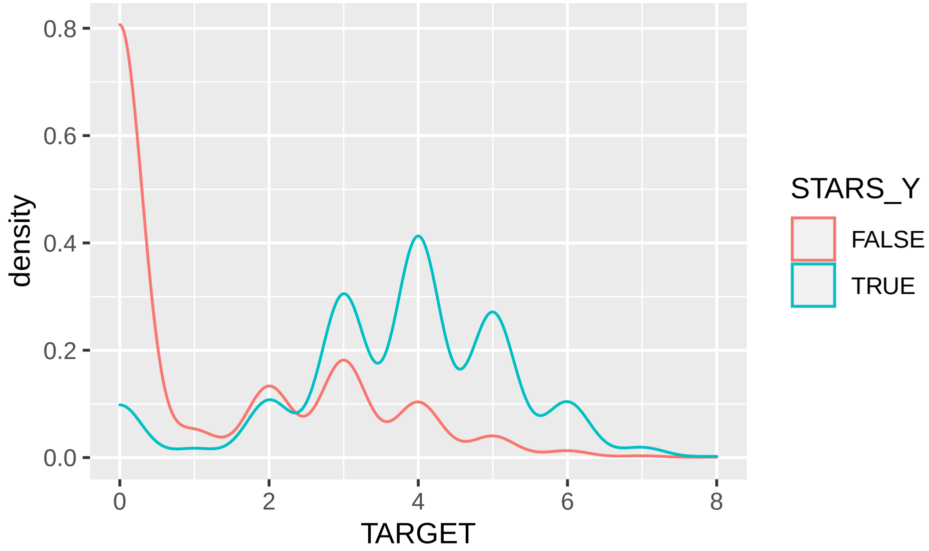
```
plot_Alcohol <- ggplot(train_df, aes(x=Alcohol, color=CASES)) + geom_density(na.rm =TRUE, bw=0.8)
plots_LabelAppeal <- ggplot(train_df, aes(x=LabelAppeal, color=CASES)) + geom_density(na.rm =TRUE, bw=0
plots_AcidIndex <- ggplot(train_df, aes(x=AcidIndex, color=CASES)) + geom_density(na.rm =TRUE, bw=0.5)
plots_STARS <- ggplot(train_df, aes(x=STARS, color=CASES)) + geom_density(na.rm =TRUE, bw=0.2)

plot_FixedAcidity+plot_VolatileAcidity+plot_CitricAcid+plot_ResidualSugar+plot_Chlorides+
  plot_FreeSulfurDioxide+plot_TotalSulfurDioxide+plot_Density+plot_pH+plot_Sulphates+
  plot_Alcohol+plots_LabelAppeal+plots_AcidIndex+plots_STARS+
  plot_layout(ncol = 3, guides = "collect")
```



```
ResidualSugar_Y <- !is.na(train_df$ResidualSugar)
Chlorides_Y <- !is.na(train_df$Chlorides)
FreeSulfurDioxide_Y <- !is.na(train_df$FreeSulfurDioxide)
```

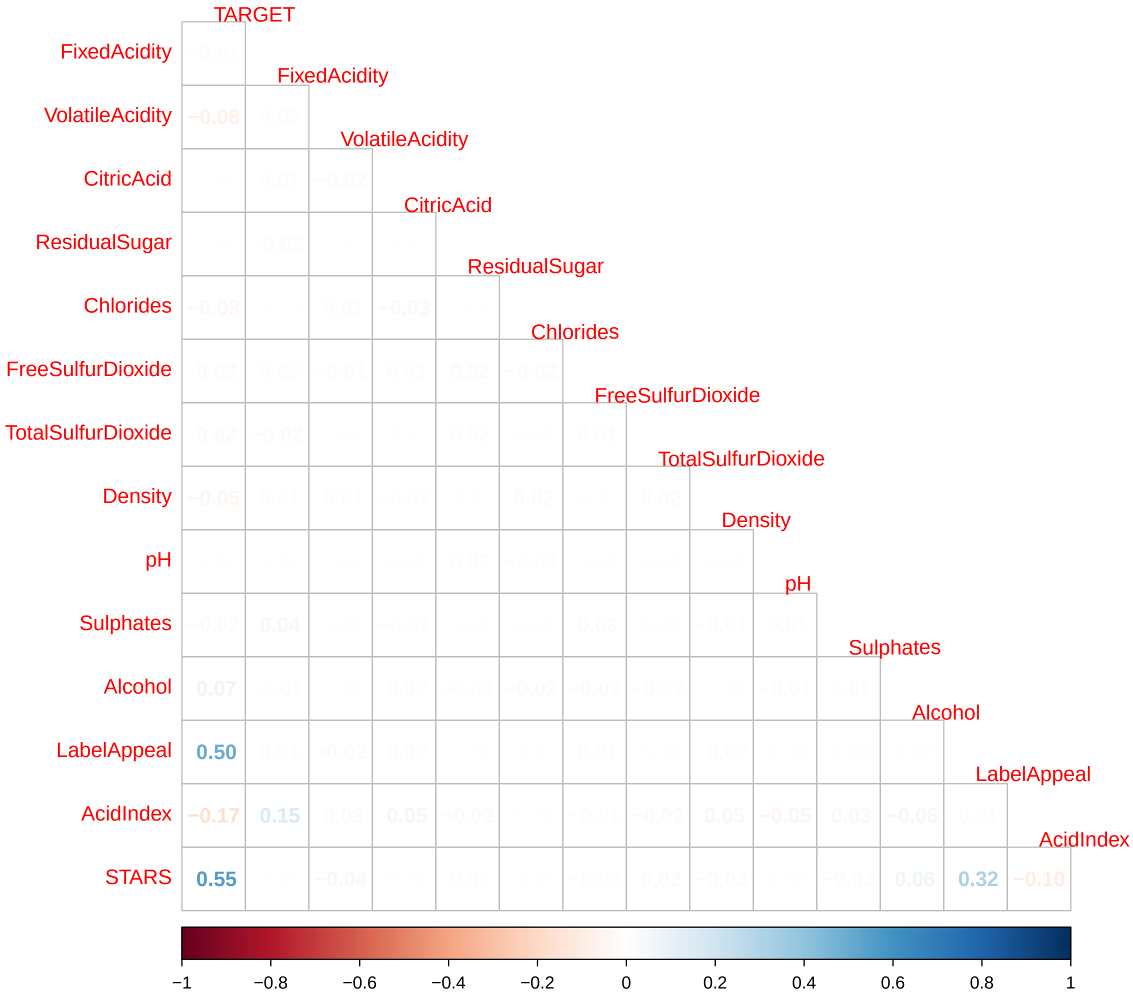
```
TotalSulfurDioxide_Y <- !is.na(train_df$TotalSulfurDioxide)
pH_Y <- !is.na(train_df$pH)
Sulphates_Y <- !is.na(train_df$Sulphates)
Alcohol_Y <- !is.na(train_df$Alcohol)
STARS_Y <- !is.na(train_df$STARS)
```

```
ggplot(train_df, aes(x=TARGET, color=STARS_Y)) + geom_density(na.rm =TRUE, bw=0.3)
```



Correlations

```
corrplot::corrplot(cor(train_df, use = "na.or.complete"),
                   method = 'number', type = 'lower', diag = FALSE, tl.srt = 0.1)
```



DATA PREPARATION

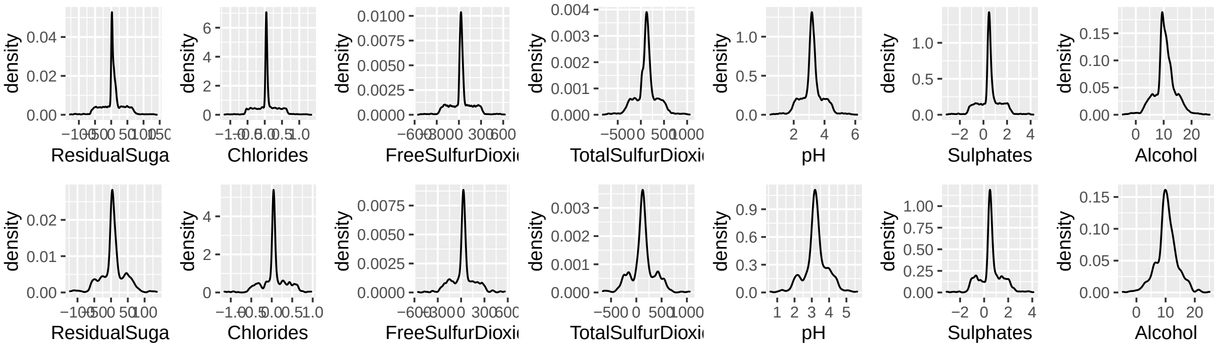
Data Imputation

```
#temporary exclude TARGET, LabelAppeal, and STARS in our imputation
TARGET <- train_df$TARGET
LabelAppeal <- train_df$LabelAppeal
STARS <- train_df$STARS

train_df$TARGET <- NULL
train_df$LabelAppeal <- NULL
```

```
train_df$STARS <- NULL

#save the imputation models to impute the test data set later
mickey <- parlmice(train_df, maxit = 5, m = 1, printFlag = FALSE, seed = 2022, cluster.seed = 2022)

#save the imputation result
train_df <- complete(mickey,1)

#Add TARGET, LabelAppeal, and STARS back to our dataframe
train_df$TARGET <- TARGET
train_df$LabelAppeal <- LabelAppeal
train_df$STARS <- STARS

TARGET <- NULL
LabelAppeal <- NULL
STARS <- NULL

#write.csv(train_df,"train_df.csv", row.names = FALSE)
```

```
#train_df <- read.csv("train_df.csv", stringsAsFactors = TRUE)
```

```
plot_ResidualSugar <- ggplot(train_df[ResidualSugar_Y,], aes(x=ResidualSugar, color=TARGET)) + geom_dens
plot_Chlorides <- ggplot(train_df[Chlorides_Y,], aes(x=Chlorides, color=TARGET)) + geom_density(na.rm =T
plot_FreeSulfurDioxide <- ggplot(train_df[FreeSulfurDioxide_Y,], aes(x=FreeSulfurDioxide, color=TARGET)
plot_TotalSulfurDioxide <- ggplot(train_df[TotalSulfurDioxide_Y,], aes(x=TotalSulfurDioxide, color=TARG
plot_pH <- ggplot(train_df[pH_Y,], aes(x=pH, color=TARGET)) + geom_density(na.rm =TRUE)
plot_Sulphates <- ggplot(train_df[Sulphates_Y,], aes(x=Sulphates, color=TARGET)) + geom_density(na.rm =T
plot_Alcohol <- ggplot(train_df[Alcohol_Y,], aes(x=Alcohol, color=TARGET)) + geom_density(na.rm =TRUE)

plot_ResidualSugar2 <- ggplot(train_df[!ResidualSugar_Y,], aes(x=ResidualSugar, color=TARGET)) + geom_de
plot_Chlorides2 <- ggplot(train_df[!Chlorides_Y,], aes(x=Chlorides, color=TARGET)) + geom_density(na.rm
plot_FreeSulfurDioxide2 <- ggplot(train_df[!FreeSulfurDioxide_Y,], aes(x=FreeSulfurDioxide, color=TARGE
plot_TotalSulfurDioxide2 <- ggplot(train_df[!TotalSulfurDioxide_Y,], aes(x=TotalSulfurDioxide, color=TA
plot_pH2 <- ggplot(train_df[!pH_Y,], aes(x=pH, color=TARGET)) + geom_density(na.rm =TRUE)
plot_Sulphates2 <- ggplot(train_df[!Sulphates_Y,], aes(x=Sulphates, color=TARGET)) + geom_density(na.rm
plot_Alcohol2 <- ggplot(train_df[!Alcohol_Y,], aes(x=Alcohol, color=TARGET)) + geom_density(na.rm =TRUE

plot_ResidualSugar+plot_Chlorides+plot_FreeSulfurDioxide+plot_TotalSulfurDioxide+
  plot_pH+plot_Sulphates+plot_Alcohol+
  plot_ResidualSugar2+plot_Chlorides2+plot_FreeSulfurDioxide2+plot_TotalSulfurDioxide2+
  plot_pH2+plot_Sulphates2+plot_Alcohol2+
  plot_layout(ncol = 7, guides = "collect")
```



Data Transformation

```
train_df$STARS[!STARS_Y] <- 0
train_df$STARS <- as.factor(train_df$STARS)
train_df$LabelAppeal <- as.factor(train_df$LabelAppeal)
```

BUILD MODELS

Poisson models

```
poisson_full <- glm(TARGET ~ ., data=train_df, family=poisson)
summary(poisson_full)
```

```
##
## Call:
## glm(formula = TARGET ~ ., family = poisson, data = train_df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.2252  -0.6543  -0.0040   0.4508   3.7773
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)        6.972e-01  1.990e-01   3.504 0.000458 ***
## FixedAcidity       2.626e-05  8.200e-04   0.032 0.974453
## VolatileAcidity   -3.051e-02  6.529e-03  -4.673 2.96e-06 ***
## CitricAcid         5.119e-03  5.897e-03   0.868 0.385411
## ResidualSugar      3.821e-05  1.503e-04   0.254 0.799361
## Chlorides         -3.924e-02  1.611e-02  -2.435 0.014894 *
## FreeSulfurDioxide  7.974e-05  3.425e-05   2.328 0.019896 *
## TotalSulfurDioxide 7.190e-05  2.210e-05   3.254 0.001139 **
## Density           -2.571e-01  1.918e-01  -1.341 0.179995
## pH                -1.381e-02  7.529e-03  -1.835 0.066577 .
## Sulphates         -1.084e-02  5.477e-03  -1.980 0.047752 *
## Alcohol            3.543e-03  1.376e-03   2.575 0.010014 *
## AcidIndex         -7.989e-02  4.572e-03 -17.474  < 2e-16 ***
## LabelAppeal-1       2.353e-01  3.799e-02   6.193 5.89e-10 ***
## LabelAppeal0        4.254e-01  3.705e-02  11.480  < 2e-16 ***
## LabelAppeal1        5.577e-01  3.769e-02  14.794  < 2e-16 ***
## LabelAppeal2        6.958e-01  4.244e-02  16.395  < 2e-16 ***
## STARS1              7.663e-01  1.954e-02  39.214  < 2e-16 ***
## STARS2              1.085e+00  1.824e-02  59.500  < 2e-16 ***
## STARS3              1.205e+00  1.920e-02  62.753  < 2e-16 ***
## STARS4              1.325e+00  2.431e-02  54.490  < 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: 13639  on 12774  degrees of freedom
## AIC: 45623
##
## Number of Fisher Scoring iterations: 6
```

Backward Elimination by AIC

```
poisson_AIC <- step(poisson_full,trace=0)
summary(poisson_AIC)
```

```
##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + Chlorides + FreeSulfurDioxide +
##     TotalSulfurDioxide + pH + Sulphates + Alcohol + AcidIndex +
##     LabelAppeal + STARS, family = poisson, data = train_df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.2282  -0.6537  -0.0040   0.4485   3.7686
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)          4.428e-01  6.105e-02   7.253 4.08e-13 ***
## VolatileAcidity     -3.071e-02  6.528e-03  -4.705 2.54e-06 ***
## Chlorides           -3.981e-02  1.611e-02  -2.471  0.01347 *
## FreeSulfurDioxide    7.976e-05  3.423e-05   2.330  0.01982 *
## TotalSulfurDioxide   7.142e-05  2.209e-05   3.234  0.00122 **
## pH                  -1.379e-02  7.527e-03  -1.832  0.06697 .
## Sulphates           -1.083e-02  5.475e-03  -1.978  0.04789 *
## Alcohol              3.576e-03  1.375e-03   2.600  0.00931 **
## AcidIndex           -7.987e-02  4.514e-03 -17.695  < 2e-16 ***
## LabelAppeal-1        2.351e-01  3.799e-02   6.190 6.03e-10 ***
## LabelAppeal0         4.254e-01  3.705e-02  11.481  < 2e-16 ***
## LabelAppeal1         5.579e-01  3.769e-02  14.800  < 2e-16 ***
## LabelAppeal2         6.954e-01  4.244e-02  16.388  < 2e-16 ***
## STARS1               7.665e-01  1.954e-02  39.229  < 2e-16 ***
## STARS2               1.086e+00  1.823e-02  59.550  < 2e-16 ***
## STARS3               1.206e+00  1.920e-02  62.789  < 2e-16 ***
## STARS4              1.325e+00  2.431e-02  54.523  < 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: 13642  on 12778  degrees of freedom
## AIC: 45618
##
## Number of Fisher Scoring iterations: 6
```

Backward Elimination by BIC

```
poisson_BIC <- step(poisson_full,trace=0, k=log(nrow(train_df)))
summary(poisson_BIC)
```

```
##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + TotalSulfurDioxide +
##     AcidIndex + LabelAppeal + STARS, family = poisson, data = train_df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.2430  -0.6534  -0.0061   0.4548   3.8100
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)          4.337e-01  5.236e-02   8.283  < 2e-16 ***
## VolatileAcidity     -3.090e-02  6.529e-03  -4.732 2.22e-06 ***
## TotalSulfurDioxide   7.142e-05  2.207e-05   3.235  0.00122 **
## AcidIndex           -8.049e-02  4.496e-03 -17.901  < 2e-16 ***
## LabelAppeal-1        2.350e-01  3.798e-02   6.187 6.12e-10 ***
## LabelAppeal0         4.253e-01  3.705e-02  11.479  < 2e-16 ***
## LabelAppeal1         5.569e-01  3.768e-02  14.778  < 2e-16 ***
## LabelAppeal2         6.951e-01  4.243e-02  16.384  < 2e-16 ***
## STARS1               7.689e-01  1.953e-02  39.362  < 2e-16 ***
## STARS2               1.089e+00  1.823e-02  59.727  < 2e-16 ***
## STARS3               1.210e+00  1.917e-02  63.136  < 2e-16 ***
## STARS4               1.330e+00  2.427e-02  54.812  < 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: 13667  on 12783  degrees of freedom
## AIC: 45633
##
## Number of Fisher Scoring iterations: 6
```

Negative Binomial models

```
nb_full <- glm(TARGET ~ ., data=train_df,negative.binomial(1))
summary(nb_full)
```

```
##
## Call:
## glm(formula = TARGET ~ ., family = negative.binomial(1), data = train_df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.90250  -0.34154  -0.01238   0.21600   2.02600
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        1.0743616  0.2382782   4.509 6.58e-06 ***
## FixedAcidity      -0.0001696  0.0009888  -0.171  0.86384
## VolatileAcidity   -0.0419826  0.0078679  -5.336 9.67e-08 ***
## CitricAcid         0.0065673  0.0071404   0.920  0.35773
## ResidualSugar      0.0001077  0.0001815   0.593  0.55306
## Chlorides         -0.0568091  0.0194292  -2.924  0.00346 **
## FreeSulfurDioxide  0.0001182  0.0000414   2.855  0.00431 **
## TotalSulfurDioxide 0.0001229  0.0000266   4.620 3.87e-06 ***
## Density           -0.2809959  0.2317799  -1.212  0.22541
## pH                -0.0276481  0.0090722  -3.048  0.00231 **
## Sulphates         -0.0183074  0.0066113  -2.769  0.00563 **
## Alcohol            0.0021878  0.0016561   1.321  0.18651
## AcidIndex         -0.1134576  0.0051465 -22.046  < 2e-16 ***
## LabelAppeal-1      0.2216406  0.0365876   6.058 1.42e-09 ***
## LabelAppeal0       0.3896430  0.0356763  10.922  < 2e-16 ***
## LabelAppeal1       0.4900872  0.0369138  13.277  < 2e-16 ***
## LabelAppeal2       0.6309517  0.0461819  13.662  < 2e-16 ***
## STARS1             0.7581734  0.0187883  40.353  < 2e-16 ***
## STARS2             1.0885802  0.0179498  60.646  < 2e-16 ***
## STARS3             1.2172280  0.0201044  60.545  < 2e-16 ***
## STARS4             1.3490347  0.0301766  44.705  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for Negative Binomial(1) family taken to be 0.3428193)
##
##     Null deviance: 9042.5  on 12794  degrees of freedom
## Residual deviance: 6474.6  on 12774  degrees of freedom
## AIC: 55248
##
## Number of Fisher Scoring iterations: 5
```

Backward Elimination by AIC

```
nb_AIC <- step(nb_full,trace=0)
summary(nb_AIC)
```

```
##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + Chlorides + FreeSulfurDioxide +
##     TotalSulfurDioxide + pH + Sulphates + AcidIndex + LabelAppeal +
##     STARS, family = negative.binomial(1), data = train_df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.90425  -0.34172  -0.01118   0.21688   2.02832
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)         8.229e-01  6.248e-02  13.171  < 2e-16 ***
## VolatileAcidity    -4.229e-02  7.868e-03  -5.375 7.78e-08 ***
## Chlorides          -5.825e-02  1.942e-02  -2.999  0.00271 **
## FreeSulfurDioxide   1.174e-04  4.139e-05   2.837  0.00456 **
## TotalSulfurDioxide  1.224e-04  2.659e-05   4.603 4.21e-06 ***
## pH                 -2.772e-02  9.071e-03  -3.056  0.00225 **
## Sulphates          -1.827e-02  6.609e-03  -2.764  0.00572 **
## AcidIndex          -1.139e-01  5.066e-03 -22.472  < 2e-16 ***
## LabelAppeal-1       2.209e-01  3.659e-02   6.037 1.62e-09 ***
## LabelAppeal0        3.888e-01  3.568e-02  10.899  < 2e-16 ***
## LabelAppeal1        4.892e-01  3.691e-02  13.253  < 2e-16 ***
## LabelAppeal2        6.298e-01  4.619e-02  13.635  < 2e-16 ***
## STARS1              7.585e-01  1.879e-02  40.367  < 2e-16 ***
## STARS2              1.090e+00  1.794e-02  60.744  < 2e-16 ***
## STARS3              1.219e+00  2.008e-02  60.704  < 2e-16 ***
## STARS4              1.352e+00  3.014e-02  44.849  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1) family taken to be 0.3429827)
##
##     Null deviance: 9042.5  on 12794  degrees of freedom
## Residual deviance: 6476.1  on 12779  degrees of freedom
## AIC: 55239
##
## Number of Fisher Scoring iterations: 5
```

Backward Elimination by BIC

```r
nb_BIC <- step(nb_full,trace=0, k=log(nrow(train_df)))
summary(nb_BIC)
```

```
##
## Call:
## glm(formula = TARGET ~ VolatileAcidity + TotalSulfurDioxide +
##     AcidIndex + LabelAppeal + STARS, family = negative.binomial(1),
##     data = train_df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.91436  -0.34141  -0.01335   0.21564   2.06009
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)         7.226e-01  5.375e-02  13.443  < 2e-16 ***
## VolatileAcidity    -4.243e-02  7.869e-03  -5.392 7.10e-08 ***
## TotalSulfurDioxide  1.237e-04  2.659e-05   4.652 3.32e-06 ***
## AcidIndex          -1.137e-01  5.050e-03 -22.520  < 2e-16 ***
## LabelAppeal-1       2.213e-01  3.659e-02   6.050 1.49e-09 ***
## LabelAppeal0        3.892e-01  3.568e-02  10.909  < 2e-16 ***
## LabelAppeal1        4.896e-01  3.691e-02  13.266  < 2e-16 ***
## LabelAppeal2        6.282e-01  4.618e-02  13.602  < 2e-16 ***
## STARS1              7.608e-01  1.878e-02  40.512  < 2e-16 ***
## STARS2              1.091e+00  1.793e-02  60.839  < 2e-16 ***
## STARS3              1.222e+00  2.007e-02  60.868  < 2e-16 ***
## STARS4              1.352e+00  3.014e-02  44.853  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for Negative Binomial(1) family taken to be 0.3431495)
##
##     Null deviance: 9042.5  on 12794  degrees of freedom
## Residual deviance: 6487.7  on 12783  degrees of freedom
## AIC: 55243
##
## Number of Fisher Scoring iterations: 5
```

Multiple Linear Regression Models

```
lm_full <- lm(TARGET ~ ., data=train_df)
summary(lm_full)
```

```
##
## Call:
## lm(formula = TARGET ~ ., data = train_df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.9597 -0.8612  0.0221  0.8418  6.1818
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)         2.865e+00  4.465e-01   6.416 1.45e-10 ***
## FixedAcidity        5.594e-04  1.859e-03   0.301 0.763526
## VolatileAcidity    -9.474e-02  1.478e-02  -6.411 1.50e-10 ***
## CitricAcid          1.711e-02  1.344e-02   1.273 0.202920
## ResidualSugar       1.295e-04  3.415e-04   0.379 0.704491
## Chlorides          -1.245e-01  3.646e-02  -3.414 0.000643 ***
## FreeSulfurDioxide   2.378e-04  7.798e-05   3.049 0.002299 **
## TotalSulfurDioxide  2.052e-04  4.994e-05   4.109 4.01e-05 ***
## Density            -7.945e-01  4.359e-01  -1.823 0.068381 .
## pH                 -3.598e-02  1.704e-02  -2.111 0.034753 *
## Sulphates          -2.914e-02  1.241e-02  -2.347 0.018917 *  
## Alcohol             1.204e-02  3.114e-03   3.867 0.000111 ***
## AcidIndex          -2.005e-01  9.098e-03 -22.033  < 2e-16 ***
## LabelAppeal-1       3.609e-01  6.286e-02   5.741 9.62e-09 ***
## LabelAppeal0        8.278e-01  6.130e-02  13.503  < 2e-16 ***
## LabelAppeal1        1.292e+00  6.403e-02  20.177  < 2e-16 ***
## LabelAppeal2        1.882e+00  8.436e-02  22.309  < 2e-16 ***
## STARS1              1.363e+00  3.292e-02  41.411  < 2e-16 ***
## STARS2              2.398e+00  3.202e-02  74.910  < 2e-16 ***
## STARS3              2.965e+00  3.707e-02  79.982  < 2e-16 ***
## STARS4              3.650e+00  5.925e-02  61.597  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
## 
## Residual standard error: 1.306 on 12774 degrees of freedom
## Multiple R-squared:  0.5411, Adjusted R-squared:  0.5404 
## F-statistic: 753.1 on 20 and 12774 DF,  p-value: < 2.2e-16
```

Backward Elimination by AIC

```
lm_AIC <- step(lm_full,trace=0)
summary(lm_AIC)
```

```
## 
## Call:
## lm(formula = TARGET ~ VolatileAcidity + Chlorides + FreeSulfurDioxide + 
##     TotalSulfurDioxide + Density + pH + Sulphates + Alcohol + 
##     AcidIndex + LabelAppeal + STARS, data = train_df)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -4.9600 -0.8616  0.0237  0.8388  6.1758 
## 
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)    
## (Intercept)         2.873e+00  4.465e-01   6.436 1.27e-10 ***
## VolatileAcidity    -9.509e-02  1.477e-02  -6.436 1.27e-10 ***
## Chlorides          -1.249e-01  3.645e-02  -3.426 0.000614 ***
## FreeSulfurDioxide   2.394e-04  7.796e-05   3.071 0.002140 ** 
## TotalSulfurDioxide  2.058e-04  4.992e-05   4.123 3.77e-05 ***
## Density            -8.031e-01  4.358e-01  -1.843 0.065388 .  
## pH                 -3.596e-02  1.704e-02  -2.111 0.034798 *  
## Sulphates          -2.937e-02  1.241e-02  -2.367 0.017942 *  
## Alcohol             1.208e-02  3.112e-03   3.882 0.000104 ***
## AcidIndex          -1.992e-01  8.940e-03 -22.282  < 2e-16 ***
## LabelAppeal-1       3.605e-01  6.286e-02   5.735 9.96e-09 ***
## LabelAppeal0        8.274e-01  6.130e-02  13.498  < 2e-16 ***
## LabelAppeal1        1.292e+00  6.402e-02  20.173  < 2e-16 ***
## LabelAppeal2        1.882e+00  8.435e-02  22.312  < 2e-16 ***
## STARS1              1.364e+00  3.292e-02  41.428  < 2e-16 ***
## STARS2              2.399e+00  3.200e-02  74.976  < 2e-16 ***
## STARS3              2.965e+00  3.706e-02  80.007  < 2e-16 ***
## STARS4              3.651e+00  5.924e-02  61.623  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Residual standard error: 1.306 on 12777 degrees of freedom
## Multiple R-squared:  0.541,  Adjusted R-squared:  0.5404
## F-statistic:   886 on 17 and 12777 DF,  p-value: < 2.2e-16
```

Backward Elimination by BIC

```
lm_BIC <- step(lm_full,trace=0, k=log(nrow(train_df)))
summary(lm_BIC)
```

```
##
## Call:
## lm(formula = TARGET ~ VolatileAcidity + Chlorides + TotalSulfurDioxide +
##     Alcohol + AcidIndex + LabelAppeal + STARS, data = train_df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.0103 -0.8631  0.0264  0.8393  6.2004
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)         1.956e+00  1.001e-01  19.540  < 2e-16 ***
## VolatileAcidity    -9.587e-02  1.478e-02  -6.486 9.17e-11 ***
## Chlorides          -1.262e-01  3.646e-02  -3.460 0.000541 ***
## TotalSulfurDioxide  2.074e-04  4.995e-05   4.152 3.32e-05 ***
## Alcohol             1.195e-02  3.113e-03   3.840 0.000124 ***
## AcidIndex          -2.003e-01  8.912e-03 -22.477  < 2e-16 ***
## LabelAppeal-1       3.615e-01  6.290e-02   5.748 9.26e-09 ***
## LabelAppeal0        8.301e-01  6.134e-02  13.534  < 2e-16 ***
## LabelAppeal1        1.294e+00  6.407e-02  20.198  < 2e-16 ***
## LabelAppeal2        1.882e+00  8.440e-02  22.294  < 2e-16 ***
## STARS1              1.368e+00  3.293e-02  41.544  < 2e-16 ***
## STARS2              2.404e+00  3.201e-02  75.117  < 2e-16 ***
## STARS3              2.971e+00  3.706e-02  80.167  < 2e-16 ***
## STARS4              3.653e+00  5.927e-02  61.639  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Residual standard error: 1.307 on 12781 degrees of freedom
## Multiple R-squared:  0.5402, Adjusted R-squared:  0.5398
## F-statistic:  1155 on 13 and 12781 DF,  p-value: < 2.2e-16
```

Model Coefficients Comparison

```
poisson_full_coef <- data.frame(poisson_full=poisson_full$coefficients)
poisson_AIC_coef <- data.frame(poisson_AIC=round(poisson_AIC$coefficients,4))
poisson_BIC_coef <- data.frame(poisson_BIC=round(poisson_BIC$coefficients,4))
```

```r
nb_AIC_coef <- data.frame(nb_AIC=round(nb_AIC$coefficients,4))
nb_BIC_coef <- data.frame(nb_BIC=round(nb_BIC$coefficients,4))
lm_AIC_coef <- data.frame(lm_AIC=round(lm_AIC$coefficients,4))
lm_BIC_coef <- data.frame(lm_BIC=round(lm_BIC$coefficients,4))
```

```r
summary_table <- merge(x=poisson_full_coef, y=poisson_AIC_coef, by="row.names", all=TRUE)
summary_table <- merge(x=summary_table, y=poisson_BIC_coef, by.x="Row.names", by.y = "row.names", all=TR
summary_table <- merge(x=summary_table, y=nb_AIC_coef, by.x="Row.names", by.y="row.names", all=TRUE)
summary_table <- merge(x=summary_table, y=nb_BIC_coef, by.x="Row.names", by.y="row.names", all=TRUE)
summary_table <- merge(x=summary_table, y=lm_AIC_coef, by.x="Row.names", by.y="row.names", all=TRUE)
summary_table <- merge(x=summary_table, y=lm_BIC_coef, by.x="Row.names", by.y="row.names", all=TRUE)
summary_table$poisson_full <- NULL
summary_table
```

```
##             Row.names poisson_AIC poisson_BIC  nb_AIC  nb_BIC  lm_AIC  lm_BIC
## 1         (Intercept)      0.4428      0.4337  0.8229  0.7226  2.8732  1.9558
## 2           AcidIndex     -0.0799     -0.0805 -0.1139 -0.1137 -0.1992 -0.2003
## 3             Alcohol      0.0036          NA      NA      NA  0.0121  0.0120
## 4           Chlorides     -0.0398          NA -0.0583      NA -0.1249 -0.1262
## 5          CitricAcid          NA          NA      NA      NA      NA      NA
## 6             Density          NA          NA      NA      NA -0.8031      NA
## 7        FixedAcidity          NA          NA      NA      NA      NA      NA
## 8   FreeSulfurDioxide      0.0001          NA  0.0001      NA  0.0002      NA
## 9        LabelAppeal-1      0.2351      0.2350  0.2209  0.2213  0.3605  0.3615
## 10        LabelAppeal0      0.4254      0.4253  0.3888  0.3892  0.8274  0.8301
## 11        LabelAppeal1      0.5579      0.5569  0.4892  0.4896  1.2916  1.2940
## 12        LabelAppeal2      0.6954      0.6951  0.6298  0.6282  1.8820  1.8816
## 13                  pH     -0.0138          NA -0.0277      NA -0.0360      NA
## 14       ResidualSugar          NA          NA      NA      NA      NA      NA
## 15              STARS1      0.7665      0.7689  0.7585  0.7608  1.3637  1.3680
## 16              STARS2      1.0859      1.0886  1.0899  1.0911  2.3993  2.4042
## 17              STARS3      1.2056      1.2105  1.2191  1.2215  2.9652  2.9712
## 18              STARS4      1.3253      1.3301  1.3518  1.3518  3.6505  3.6534
## 19           Sulphates     -0.0108          NA -0.0183      NA -0.0294      NA
## 20 TotalSulfurDioxide      0.0001      0.0001  0.0001  0.0001  0.0002  0.0002
## 21     VolatileAcidity     -0.0307     -0.0309 -0.0423 -0.0424 -0.0951 -0.0959
```

Hurdle Model

```r
mod_hurdle <- hurdle(TARGET~.-FixedAcidity-Density-CitricAcid-ResidualSugar-Chlorides, data=train_df)
summary(mod_hurdle)
```

```
## 
## Call:
## hurdle(formula = TARGET ~ . - FixedAcidity - Density - CitricAcid - ResidualSugar - 
##     Chlorides, data = train_df)
## 
## Pearson residuals:
##       Min        1Q    Median        3Q       Max 
## -2.099818 -0.442467 -0.002774  0.395516  4.566516 
```

```
##
## Count model coefficients (truncated poisson with log link):
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)         3.626e-01  7.045e-02   5.146 2.66e-07 ***
## VolatileAcidity    -1.057e-02  6.912e-03  -1.529 0.126222
## FreeSulfurDioxide   1.696e-05  3.556e-05   0.477 0.633501
## TotalSulfurDioxide -2.848e-05  2.260e-05  -1.260 0.207632
## pH                  7.395e-03  7.941e-03   0.931 0.351693
## Sulphates           1.532e-03  5.780e-03   0.265 0.790903
## Alcohol             7.332e-03  1.444e-03   5.077 3.84e-07 ***
## AcidIndex          -1.655e-02  4.934e-03  -3.354 0.000796 ***
## LabelAppeal-1       5.392e-01  4.973e-02  10.842  < 2e-16 ***
## LabelAppeal0        8.427e-01  4.881e-02  17.267  < 2e-16 ***
## LabelAppeal1        1.040e+00  4.937e-02  21.071  < 2e-16 ***
## LabelAppeal2        1.201e+00  5.319e-02  22.576  < 2e-16 ***
## STARS1              4.931e-02  2.142e-02   2.302 0.021317 *
## STARS2              1.635e-01  1.997e-02   8.189 2.63e-16 ***
## STARS3              2.545e-01  2.092e-02  12.164  < 2e-16 ***
## STARS4              3.576e-01  2.588e-02  13.819  < 2e-16 ***
## Zero hurdle model coefficients (binomial with logit link):
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)         4.358e+00  2.757e-01  15.808  < 2e-16 ***
## VolatileAcidity    -1.841e-01  3.645e-02  -5.052 4.37e-07 ***
## FreeSulfurDioxide   5.546e-04  1.953e-04   2.841  0.00450 **
## TotalSulfurDioxide  8.095e-04  1.235e-04   6.555 5.57e-11 ***
## pH                 -1.914e-01  4.192e-02  -4.565 4.99e-06 ***
## Sulphates          -9.504e-02  3.060e-02  -3.106  0.00190 **
## Alcohol            -2.072e-02  7.697e-03  -2.692  0.00710 **
## AcidIndex          -3.898e-01  2.141e-02 -18.206  < 2e-16 ***
## LabelAppeal-1      -4.803e-01  1.371e-01  -3.503  0.00046 ***
## LabelAppeal0       -9.002e-01  1.339e-01  -6.724 1.76e-11 ***
## LabelAppeal1       -1.445e+00  1.434e-01 -10.074  < 2e-16 ***
## LabelAppeal2       -1.814e+00  2.219e-01  -8.175 2.95e-16 ***
## STARS1              1.830e+00  6.140e-02  29.797  < 2e-16 ***
## STARS2              4.266e+00  1.171e-01  36.426  < 2e-16 ***
## STARS3              2.024e+01  3.634e+02   0.056  0.95558
## STARS4              2.039e+01  6.942e+02   0.029  0.97657
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Number of iterations in BFGS optimization: 23
## Log-likelihood: -2.03e+04 on 32 Df
```

Zero Inflation Model

```
mod_zeroinfl <- zeroinfl(TARGET~.-FixedAcidity-Density-CitricAcid-ResidualSugar-Chlorides, data=train_d
summary(mod_zeroinfl)
```

```
##
## Call:
## zeroinfl(formula = TARGET ~ . - FixedAcidity - Density - CitricAcid -
##     ResidualSugar - Chlorides, data = train_df)
```

```
##
## Pearson residuals:
##       Min        1Q    Median        3Q       Max
## -2.262008 -0.428094  0.001613  0.381012  5.354279
##
## Count model coefficients (poisson with log link):
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)         4.991e-01  6.402e-02   7.796 6.41e-15 ***
## VolatileAcidity    -1.231e-02  6.706e-03  -1.836  0.06631 .
## FreeSulfurDioxide   1.528e-05  3.453e-05   0.443  0.65804
## TotalSulfurDioxide -1.753e-05  2.194e-05  -0.799  0.42435
## pH                  4.774e-03  7.708e-03   0.619  0.53567
## Sulphates           1.619e-03  5.614e-03   0.288  0.77303
## Alcohol             6.907e-03  1.401e-03   4.931 8.18e-07 ***
## AcidIndex          -1.921e-02  4.832e-03  -3.975 7.02e-05 ***
## LabelAppeal-1       4.401e-01  4.134e-02  10.647  < 2e-16 ***
## LabelAppeal0        7.284e-01  4.041e-02  18.024  < 2e-16 ***
## LabelAppeal1        9.185e-01  4.108e-02  22.358  < 2e-16 ***
## LabelAppeal2        1.076e+00  4.559e-02  23.601  < 2e-16 ***
## STARS1              6.121e-02  2.113e-02   2.897  0.00377 **
## STARS2              1.823e-01  1.975e-02   9.229  < 2e-16 ***
## STARS3              2.803e-01  2.068e-02  13.556  < 2e-16 ***
## STARS4              3.785e-01  2.561e-02  14.778  < 2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)        -6.245e+00  4.481e-01 -13.937  < 2e-16 ***
## VolatileAcidity     1.865e-01  4.348e-02   4.289 1.80e-05 ***
## FreeSulfurDioxide  -7.064e-04  2.351e-04  -3.005 0.002659 **
## TotalSulfurDioxide -9.075e-04  1.471e-04  -6.168 6.92e-10 ***
## pH                  2.225e-01  5.007e-02   4.443 8.88e-06 ***
## Sulphates           1.240e-01  3.658e-02   3.390 0.000699 ***
## Alcohol             2.833e-02  9.232e-03   3.068 0.002152 **
## AcidIndex           4.318e-01  2.569e-02  16.810  < 2e-16 ***
## LabelAppeal-1       1.503e+00  3.325e-01   4.520 6.19e-06 ***
## LabelAppeal0        2.262e+00  3.300e-01   6.853 7.25e-12 ***
## LabelAppeal1        2.970e+00  3.355e-01   8.855  < 2e-16 ***
## LabelAppeal2        3.418e+00  3.866e-01   8.841  < 2e-16 ***
## STARS1             -2.089e+00  7.622e-02 -27.406  < 2e-16 ***
## STARS2             -5.747e+00  3.291e-01 -17.462  < 2e-16 ***
## STARS3             -2.024e+01  3.401e+02  -0.060 0.952541
## STARS4             -2.039e+01  6.405e+02  -0.032 0.974601
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Number of iterations in BFGS optimization: 38
## Log-likelihood: -2.034e+04 on 32 Df
```

SELECT MODELS

Root Mean Squared Error

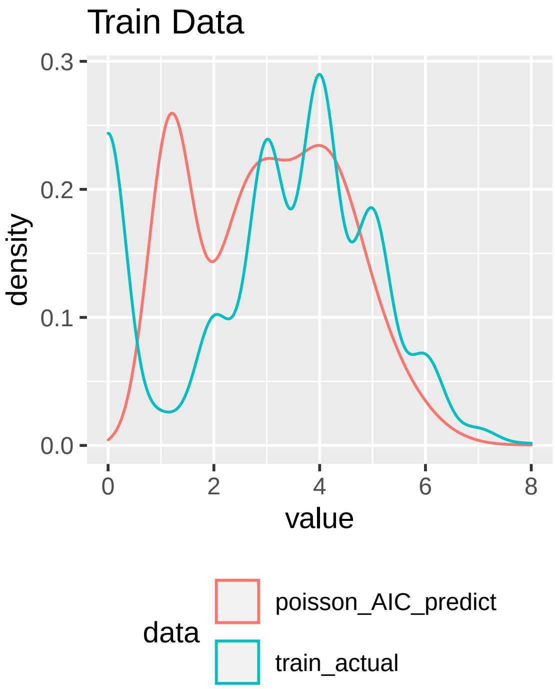
```
data.frame(poisson_AIC=sqrt(mean(residuals(poisson_AIC, type="response")^2)),
           poisson_BIC=sqrt(mean(residuals(poisson_BIC, type="response")^2)),
           nb_AIC=sqrt(mean(residuals(nb_AIC, type="response")^2)),
           nb_BIC=sqrt(mean(residuals(nb_BIC, type="response")^2)),
           lm_AIC=sqrt(mean(residuals(lm_AIC, type="response")^2)),
           lm_BIC=sqrt(mean(residuals(lm_BIC, type="response")^2)),
           mod_hurdle=sqrt(mean(residuals(mod_hurdle, type="response")^2)),
           mod_zeroinfl=sqrt(mean(residuals(mod_zeroinfl, type="response")^2)))
```

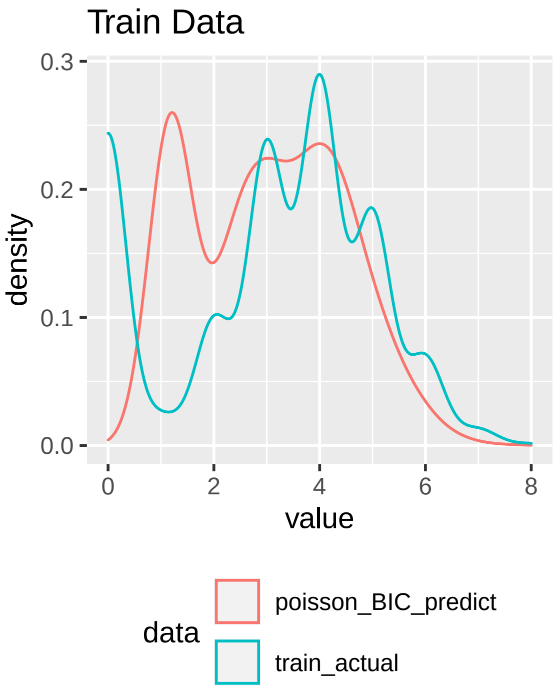
```
##   poisson_AIC poisson_BIC   nb_AIC   nb_BIC   lm_AIC   lm_BIC mod_hurdle
## 1    1.300983    1.302231 1.327142 1.324879 1.305009 1.306158   1.262333
##   mod_zeroinfl
## 1     1.263992
```

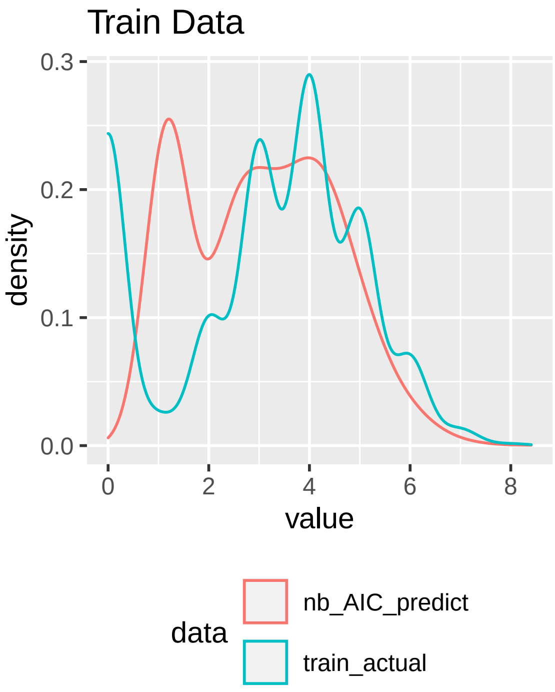
Distribution of Predicted Values (train data)

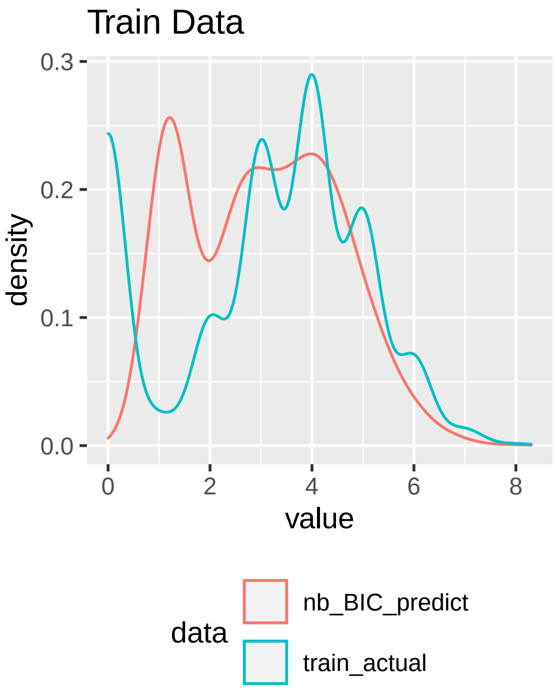
```
train_actual <- train_df$TARGET
poisson_AIC_predict <- predict(poisson_AIC,type="response")
poisson_BIC_predict <- predict(poisson_BIC,type="response")
nb_AIC_predict <- predict(nb_AIC,type="response")
nb_BIC_predict <- predict(nb_BIC,type="response")
lm_AIC_predict <- predict(lm_AIC,type="response")
lm_BIC_predict <- predict(lm_BIC,type="response")
mod_hurdle_predict <- predict(mod_hurdle,type="response")
mod_zeroinfl_predict <- predict(mod_zeroinfl,type="response")

dist_df <- data.frame(rbind(
      cbind(train_actual,"train_actual"),
      cbind(poisson_AIC_predict,"poisson_AIC_predict"),
      cbind(poisson_BIC_predict,"poisson_BIC_predict"),
      cbind(nb_AIC_predict,"nb_AIC_predict"),
      cbind(nb_BIC_predict,"nb_BIC_predict"),
      cbind(lm_AIC_predict,"lm_AIC_predict"),
      cbind(lm_BIC_predict,"lm_BIC_predict"),
      cbind(mod_hurdle_predict,"mod_hurdle_predict"),
      cbind(mod_zeroinfl_predict,"mod_zeroinfl_predict")
      ),stringsAsFactors=FALSE)
colnames(dist_df) <- c("value","data")
dist_df$value <- as.numeric(dist_df$value)
```

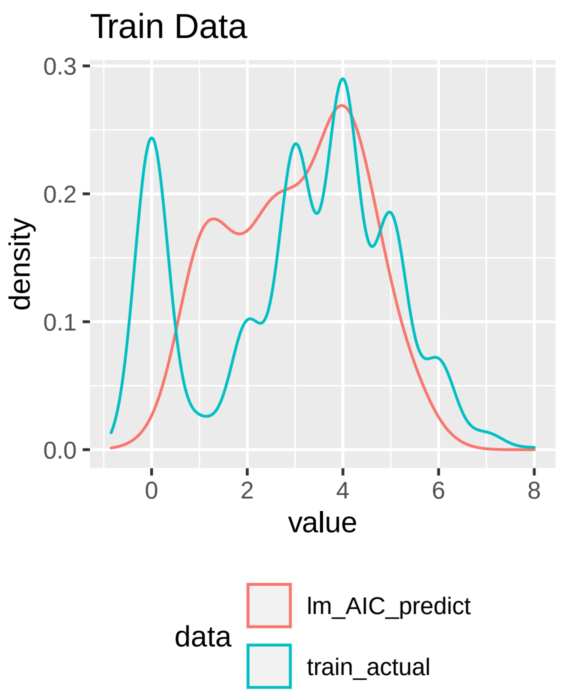
```
models <- unique(dist_df$data)[-1]
for (model in models) {
    plot<-ggplot(dist_df[dist_df$data=="train_actual" | dist_df$data==model,],
           aes(x=value, color=data))+ggtitle("Train Data")+geom_density(bw=0.35)+
           theme(legend.position="bottom")+
           guides(color=guide_legend(nrow=2, byrow=TRUE))
    print(plot)
}
```

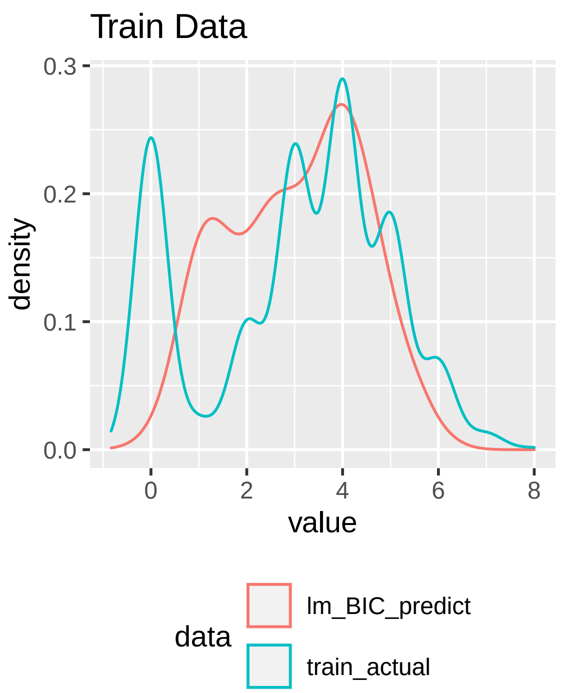

Train Data
0.3
0.2
0.1
0.0
density
0
2
4
6
8
value
data
poisson_AIC_predict
train_actual

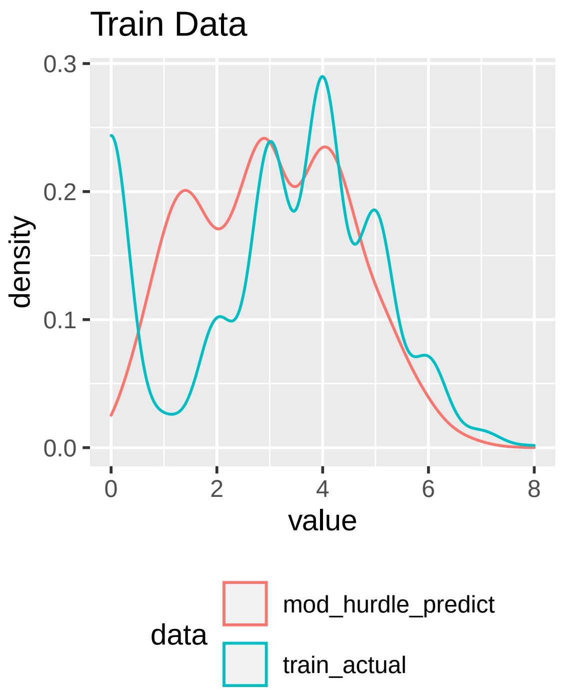

Train Data
0.3
0.2
0.1
0.0
density
0
2
4
6
8
value
data
poisson_BIC_predict
train_actual

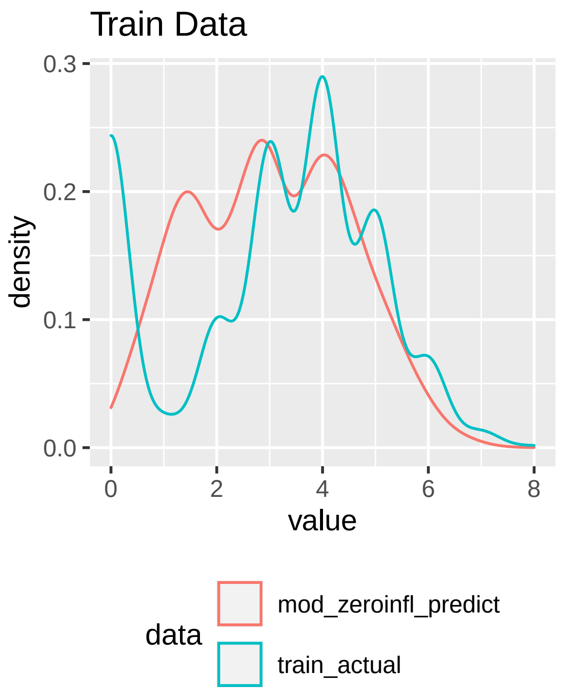

Train Data
0.3
0.2
0.1
0.0
density
0
2
4
6
8
value
data
nb_AIC_predict
train_actual


Train Data
0.3
0.2
0.1
0.0
density
0
2
4
6
8
value
data
nb_BIC_predict
train_actual


Train Data


Train Data


Train Data

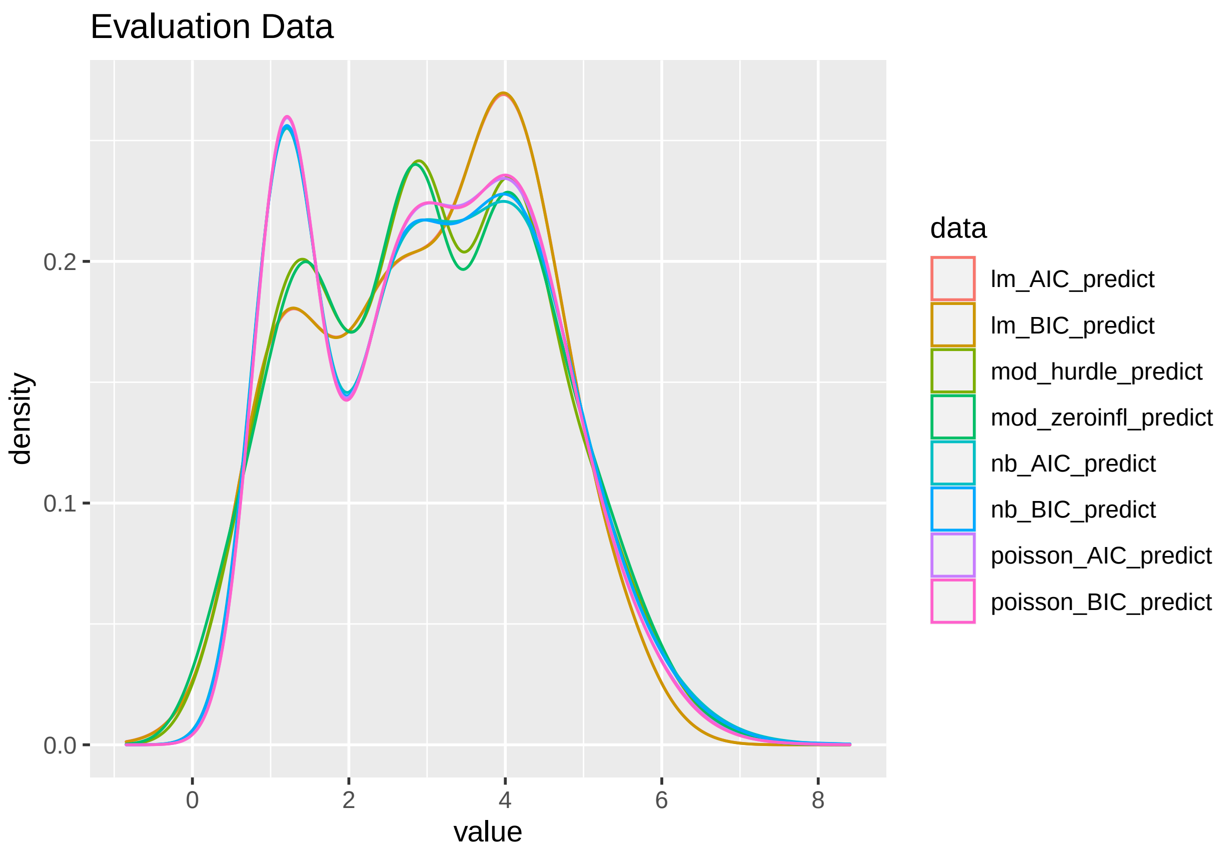

Train Data

Distribution of Predicted Values (test data)

```r
#temporary exclude LabelAppeal and STARS in our imputation
LabelAppeal <- test_df$LabelAppeal
STARS <- test_df$STARS
```

```r
test_df$TARGET <- NULL
test_df$LabelAppeal <- NULL
test_df$STARS <- NULL

test_df <- mice.reuse(mickey, test_df, maxit = 5, printFlag = FALSE, seed = 2022)[[1]]

test_df$LabelAppeal <- LabelAppeal
test_df$STARS <- STARS

LabelAppeal <- NULL
STARS <- NULL

STARS_Y <- !is.na(test_df$STARS)
test_df$STARS[!STARS_Y] <- 0
test_df$STARS <- as.factor(test_df$STARS)
test_df$LabelAppeal <- as.factor(test_df$LabelAppeal)
```

```r
poisson_AIC_predict <- predict(poisson_AIC,type="response",data=test_df)
poisson_BIC_predict <- predict(poisson_BIC,type="response",data=test_df)
nb_AIC_predict <- predict(nb_AIC,type="response",data=test_df)
nb_BIC_predict <- predict(nb_BIC,type="response",data=test_df)
lm_AIC_predict <- predict(lm_AIC,type="response",data=test_df)
lm_BIC_predict <- predict(lm_BIC,type="response",data=test_df)
mod_hurdle_predict <- predict(mod_hurdle,type="response",data=test_df)
mod_zeroinfl_predict <- predict(mod_zeroinfl,type="response",data=test_df)

dist_df <- data.frame(rbind(
      cbind(poisson_AIC_predict,"poisson_AIC_predict"),
      cbind(poisson_BIC_predict,"poisson_BIC_predict"),
      cbind(nb_AIC_predict,"nb_AIC_predict"),
      cbind(nb_BIC_predict,"nb_BIC_predict"),
      cbind(lm_AIC_predict,"lm_AIC_predict"),
      cbind(lm_BIC_predict,"lm_BIC_predict"),
      cbind(mod_hurdle_predict,"mod_hurdle_predict"),
      cbind(mod_zeroinfl_predict,"mod_zeroinfl_predict")
      ),stringsAsFactors=FALSE)
colnames(dist_df) <- c("value","data")
dist_df$value <- as.numeric(dist_df$value)

ggplot(dist_df, aes(x=value, color=data))+
  ggtitle("Evaluation Data")+geom_density(bw=0.35)
```


Evaluation Data
density
0.0
0.1
0.2
0
2
4
6
8
value
data
lm_AIC_predict
lm_BIC_predict
mod_hurdle_predict
mod_zeroinfl_predict
nb_AIC_predict
nb_BIC_predict
poisson_AIC_predict
poisson_BIC_predict