Hw 5

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Exposition

Here we have a training set of about 12700 observations with the following features:

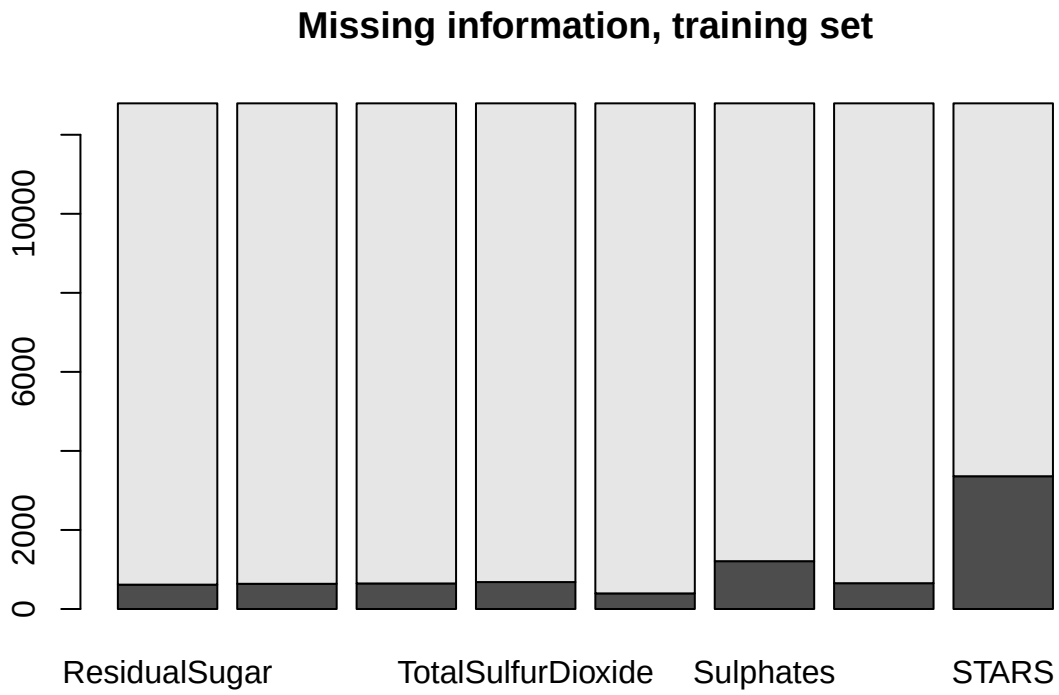
VARIABLE NAME	DEFINITION	THEORETICAL EFFECT
INDEX	Identification Variable (do not use)	None
TARGET	Number of Cases Purchased	None
AcidIndex	Proprietary method of testing total acidity of wine by using a weighted average	
Alcohol	Alcohol Content	
Chlorides	Chloride content of wine	
CitricAcid	Citric Acid 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 customes 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 conten of wine	
TotalSulfurDioxide	Total Sulfur Dioxide of Wine	
VolatileAcidity	Volatile Acid content of wine	
pH	pH of wine	

The variables are mostly related to the chemical properties of the wine being sold. The response variable is the number of cases of wine being sold. The response variable is the number of sample cases of wine that were purchased by wine distribution companies after sampling. These cases would be used to provide tasting samples to restaurants and wine stores around the united states.

A large manufacturer is studying the data in prder to predict the number of win cases ordered based upon the wine characteristics.

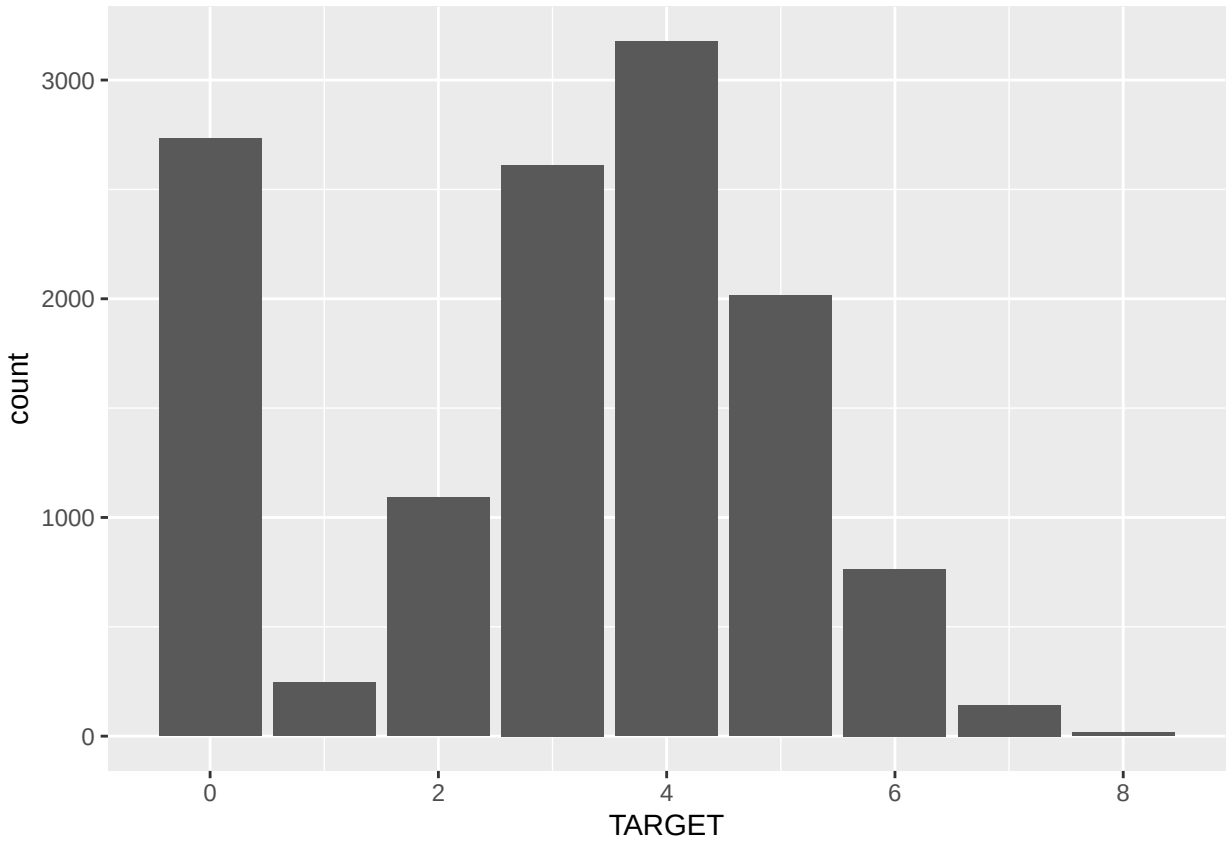
We must build a counr regression model to predict the number of cases of wine that will be sold, given certain properties.

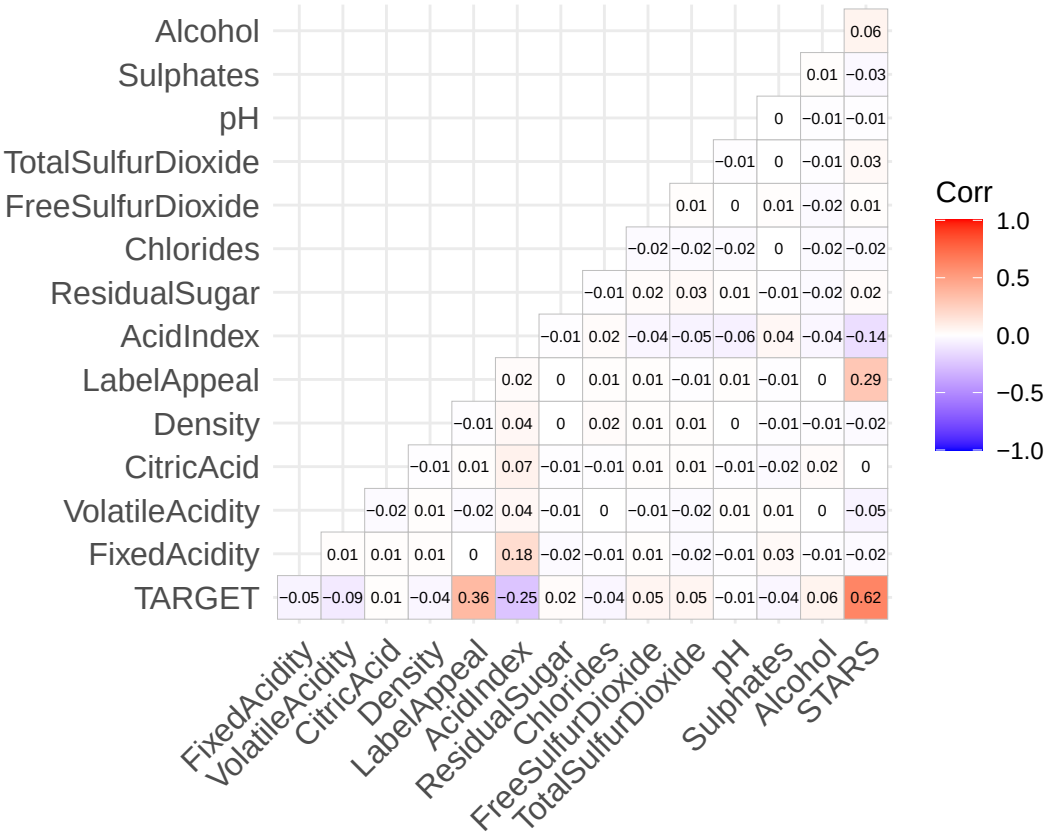
Data Exploration and Preparation



There is a small amount of missing information in just 8 columns. We can impute these values using a chained regression approach.

```
## Warning: Ignoring unknown parameters: binwidth, bins, pad
```


3000
2000
1000
0
count
0
2
4
6
8
TARGET



Wow. Apparently number of stars and label appeal are the only things that correlate strongly with the the target, and people are less likely to purchases cases of acidic wine.

```
mean(tr.f$TARGET)
```

[1] 3.029074

```
var(tr.f$TARGET)
```

[1] 3.710895 The mean and variance are nearly the same, so this is a good candidate for modeling based ona Poisson distrbution.

Build Models

We will build a model from the Poisson distribution with just the most meaningful variables listed above. Then we will use a bidirectional stepwise selection based on the default complete set of features for the second version.

Then we do the same process for the negative binomial distribution.

Since we are trying to predict the number of tasting cases purchased based on the chemistry of these bottles, we can consider each purchase a progressive success. It may be prudent to try to predict exactly how many "successes" there will be for each wine, or to try to predict how many "successes" will happen before a "failure", or an unsold case.

Select Models

Confusion Matrices

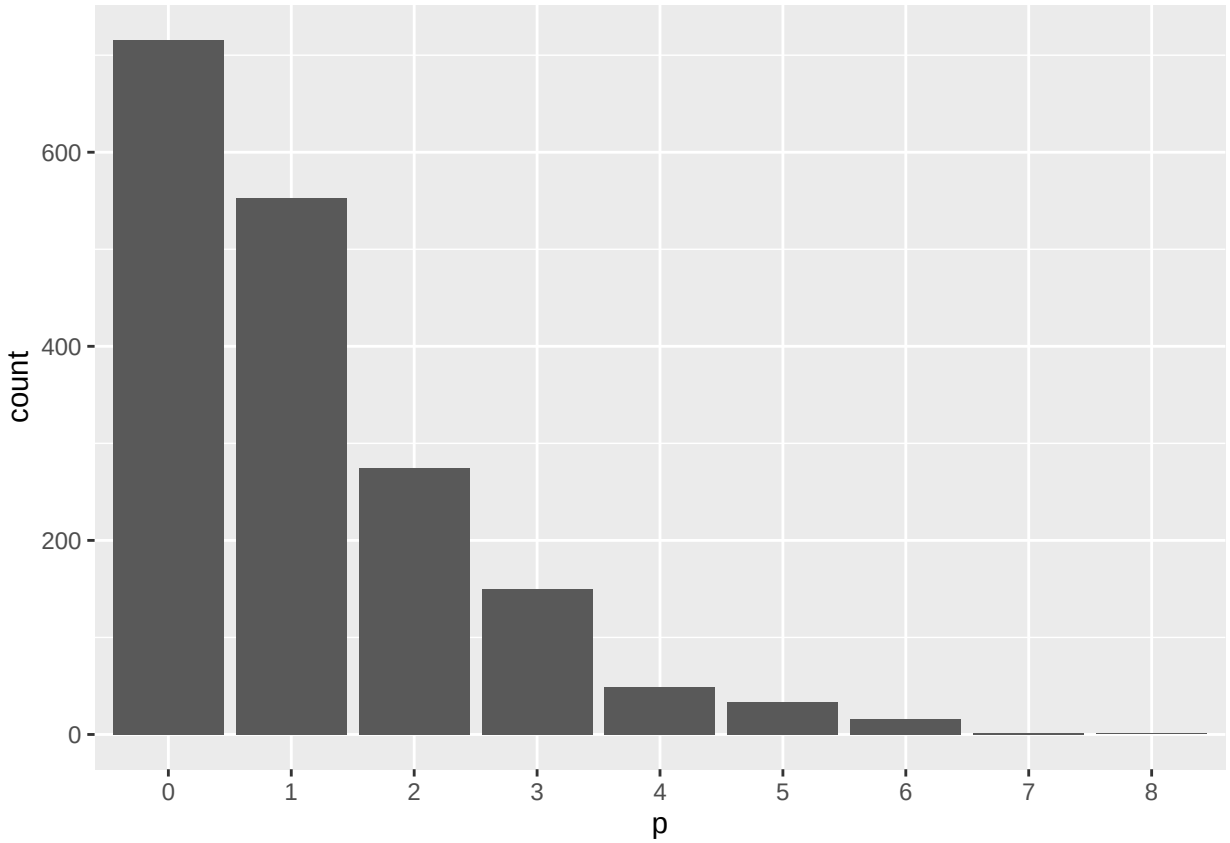
```
##
## p1    0   1   2   3   4   5   6   7
##   0 304  33  95 149  80  24   4   0
##   1  95   7  47 153 184  74   9   0
##   2   9   0   7  34 108  87  29   0
##   3   0   0   1   7  59  61  27   6
##   4   0   0   0   0   5  23  15   2
##   5   0   0   0   0   5  14  19   0
##   6   0   0   0   0   1   2   9   4
##   7   0   0   0   0   0   0   2   0
##   8   0   0   0   0   0   0   0   1

##
## p2    0   1   2   3   4   5   6   7
##   0 317  34 100 153  84  25   3   0
##   1  84   6  44 147 187  73  12   0
##   2   7   0   5  37 106  91  29   0
##   3   0   0   1   6  55  59  24   5
##   4   0   0   0   0   5  24  17   3
##   5   0   0   0   0   5   9  18   1
##   6   0   0   0   0   0   4   9   3
##   7   0   0   0   0   0   0   2   0
##   8   0   0   0   0   0   0   0   1

##
## p3    0   1   2   3   4   5   6   7
##   0 304  33  95 149  80  24   4   0
##   1  95   7  47 153 184  74   9   0
##   2   9   0   7  34 108  87  29   0
##   3   0   0   1   7  59  61  27   6
##   4   0   0   0   0   5  23  15   2
##   5   0   0   0   0   5  14  19   0
##   6   0   0   0   0   1   2   9   4
##   7   0   0   0   0   0   0   2   0
##   8   0   0   0   0   0   0   0   1

##
## p4    0   1   2   3   4   5   6   7
##   0 317  34 100 153  84  25   3   0
##   1  84   6  44 147 187  73  12   0
##   2   7   0   5  37 106  91  29   0
##   3   0   0   1   6  55  59  24   5
##   4   0   0   0   0   5  24  17   3
##   5   0   0   0   0   5   9  18   1
##   6   0   0   0   0   0   4   9   3
##   7   0   0   0   0   0   0   2   0
##   8   0   0   0   0   0   0   0   1
```

All of these models perform fairly similarly. They are based off of the same data, and the construction of their underlying models are equivalent in this type of situation.

There is a clear error that occurs with all of them. They are pretty good at telling which bottles will make no sales at all. They also don't tend to overshoot the sales of cases of wine across any of the case counts. A good way to use this model would be to estimate the minimum cases likely to be sold.

Export Predictions

```
## Warning: Ignoring unknown parameters: binwidth, bins, pad
```



So clearly, we have an issue. This distribution does come as expected, but the distribution which described the sales of cases in the training set is a normal distribution. My interpretation would be that these features can produce accurate predictions of minimum case sales, or tell which things just won't get sold. However, the major determining factor for the actual number of cases sold, given that the wine is bought, is drunken randomness!

Code Appendix

```
library(tidyverse)
library(mice)
library(MASS)
library(ggcorrplot)
library(caret)

tr <- read.csv('wine-training-data.csv')
```

```
ev <- read.csv('wine-evaluation-data.csv')

miss <- c(6, 7, 8, 9, 11, 12, 13, 16)

as.binMat <- function(df) {
  m <- c()
  for (i in colnames(df)) {
    x <- sum(is.na(df[,i]))
    m <- append(m, x)
    m <- append(m, nrow(df) - x)
  }

  a <- matrix(m, nrow = 2)
  rownames(a) <- c("Missing", "Present")
  colnames(a) <- colnames(df)

  return(a)
}

tr.binmat <- as.binMat(tr)
ev.binmat <- as.binMat(ev)

barplot(tr.binmat[,miss],
        main = "Missing information, training set")
colSums(is.na(tr))

fill.missing <- function(df, n) {
  imp <- miss - n
  x <- rbind(df)[,(n+1):16]
  y <- mice(x, maxit = 20)
  z <- complete(y, 1)

  compl <- cbind(x[,-imp], z[,imp])
  return(compl)
}

tr.f <- fill.missing(df = tr, n = 1)
ev.f <- fill.missing(df = ev, n = 2)

anyNA(ev.f)
anyNA(tr.f)

ggplot(tr, aes(x = TARGET)) +
  geom_histogram(stat = 'count')

model.matrix(~0+., data=tr.f) %>%
  cor(use="pairwise.complete.obs") %>%
  ggcorrplot(show.diag = F, type="lower", lab=TRUE, lab_size=2)

mean(tr.f$TARGET)
var(tr.f$TARGET)

tr.tr <- tr.f[1:11000,]
tr.ev <- tr.f[11001:12795,]
```

```
m1 <- glm(TARGET ~ FixedAcidity + VolatileAcidity + CitricAcid +
            LabelAppeal + AcidIndex + pH + STARS,
          tr.tr, family = 'poisson')

m2 <- glm(TARGET ~ ., tr.tr, family = 'poisson') %>%
  stepAIC(direction = 'both', keep = NULL)

m3 <- glm.nb(TARGET ~ FixedAcidity + VolatileAcidity + CitricAcid +
            LabelAppeal + AcidIndex + pH + STARS,
            tr.tr)

m4 <- glm.nb(TARGET ~ ., tr.tr) %>%
  stepAIC(direction = 'both', keep = NULL)

transform <- function(predictions) {
  p <- round(predictions - min(predictions))
  for (i in 1:length(predictions)) {
    if (p[i] != 0) {
      p[i] <- p[i] - 1
    }
  }
  return(as.factor(p))
}

p1 <- transform(predict(m1, tr.ev, type = 'response'))
p2 <- transform(predict(m2, tr.ev, type = 'response'))
p3 <- transform(predict(m3, tr.ev, type = 'response'))
p4 <- transform(predict(m4, tr.ev, type = 'response'))

table(p1,tr.ev[,1])
table(p2,tr.ev[,1])
table(p3,tr.ev[,1])
table(p4,tr.ev[,1])

p <- transform(predict(m4, tr.ev, type = 'response'))
write.csv(p, 'predictions.csv')

ggplot(data.frame(p), aes(x = p)) +
  geom_histogram(stat = 'count')
```