CMTH642 Assignment 3

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Data Prep

Preparation: The dataset is related to white Portuguese "Vinh o Verde" wine. For more info: https://archive.ics.uci.edu/ml/datasets/Wine+Quality

Import to R the following file: http://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/winequality-white.csv

```
# Download remote content
# wine.df <- read.csv("http://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/winequalit
wine.df <- read.csv("winequality-white.csv", header=T, sep=";")
```

QUESTIONS

1. Check data characteristics. Is there missing data?

```
sum(is.na(wine.df)) #0
```

```
## [1] 0
```

```
str(wine.df)
```

```
## 'data.frame':    4898 obs. of  12 variables:
##  $ fixed.acidity       : num  7 6.3 8.1 7.2 7.2 8.1 6.2 7 6.3 8.1 ...
##  $ volatile.acidity    : num  0.27 0.3 0.28 0.23 0.23 0.28 0.32 0.27 0.3 0.22 ...
##  $ citric.acid         : num  0.36 0.34 0.4 0.32 0.32 0.4 0.16 0.36 0.34 0.43 ...
##  $ residual.sugar      : num  20.7 1.6 6.9 8.5 8.5 6.9 7 20.7 1.6 1.5 ...
##  $ chlorides           : num  0.045 0.049 0.05 0.058 0.058 0.05 0.045 0.045 0.049 0.044 ...
##  $ free.sulfur.dioxide : num  45 14 30 47 47 30 30 45 14 28 ...
##  $ total.sulfur.dioxide: num  170 132 97 186 186 97 136 170 132 129 ...
##  $ density             : num  1.001 0.994 0.995 0.996 0.996 ...
##  $ pH                  : num  3 3.3 3.26 3.19 3.19 3.26 3.18 3 3.3 3.22 ...
##  $ sulphates           : num  0.45 0.49 0.44 0.4 0.4 0.44 0.47 0.45 0.49 0.45 ...
##  $ alcohol             : num  8.8 9.5 10.1 9.9 9.9 10.1 9.6 8.8 9.5 11 ...
##  $ quality             : int  6 6 6 6 6 6 6 6 6 6 ...
```

```
sapply(wine.df, function(x) sum(is.na(x))) # 0 NAs
```

```
##        fixed.acidity     volatile.acidity          citric.acid
##                    0                    0                    0
##       residual.sugar            chlorides  free.sulfur.dioxide
##                    0                    0                    0
## total.sulfur.dioxide              density                   pH
##                    0                    0                    0
##            sulphates              alcohol              quality
##                    0                    0                    0
```

```
sapply(wine.df, function(x) sum(is.null(x))) # 0 NULLs
```

```
##        fixed.acidity     volatile.acidity          citric.acid
##                    0                    0                    0
##       residual.sugar            chlorides  free.sulfur.dioxide
##                    0                    0                    0
## total.sulfur.dioxide              density                   pH
##                    0                    0                    0
##            sulphates              alcohol              quality
##                    0                    0                    0
```

2. What is the correlation between the attributes other than wine quality?

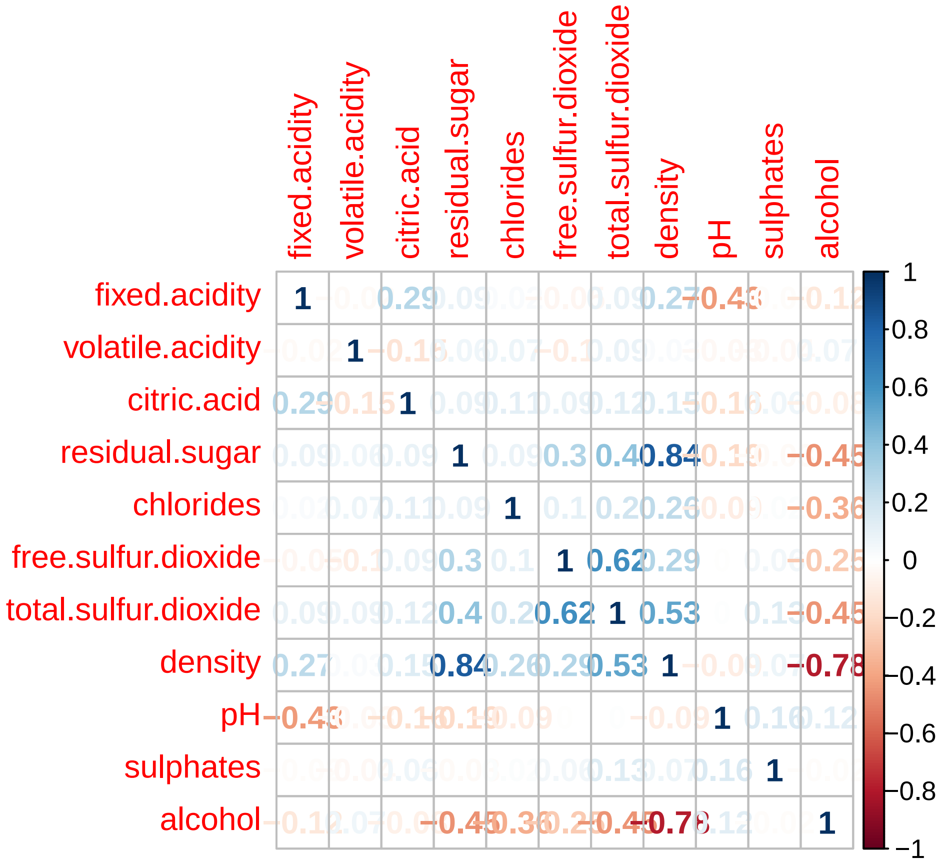
```
# For Visualizing Correlation:
# install.packages("corrplot")
library(corrplot)
```

```
## corrplot 0.84 loaded
```

```
(wine.cor <- cor(wine.df[,-12]))
```

```
##                      fixed.acidity volatile.acidity citric.acid
## fixed.acidity           1.00000000      -0.02269729  0.28918070
## volatile.acidity       -0.02269729       1.00000000 -0.14947181
## citric.acid             0.28918070      -0.14947181  1.00000000
## residual.sugar          0.08902070       0.06428606  0.09421162
## chlorides               0.02308564       0.07051157  0.11436445
## free.sulfur.dioxide    -0.04939586      -0.09701194  0.09407722
## total.sulfur.dioxide    0.09106976       0.08926050  0.12113080
## density                 0.26533101       0.02711385  0.14950257
## pH                     -0.42585829      -0.03191537 -0.16374821
## sulphates              -0.01714299      -0.03572815  0.06233094
## alcohol                -0.12088112       0.06771794 -0.07572873
##                      residual.sugar   chlorides free.sulfur.dioxide
## fixed.acidity            0.08902070  0.02308564       -0.0493958591
## volatile.acidity         0.06428606  0.07051157       -0.0970119393
## citric.acid              0.09421162  0.11436445        0.0940772210
## residual.sugar           1.00000000  0.08868454        0.2990983537
## chlorides                0.08868454  1.00000000        0.1013923521
## free.sulfur.dioxide      0.29909835  0.10139235        1.0000000000
## total.sulfur.dioxide     0.40143931  0.19891030        0.6155009650
## density                  0.83896645  0.25721132        0.2942104109
## pH                      -0.19413345 -0.09043946       -0.0006177961
## sulphates               -0.02666437  0.01676288        0.0592172458
## alcohol                 -0.45063122 -0.36018871       -0.2501039415
##                      total.sulfur.dioxide     density            pH
## fixed.acidity                 0.091069756  0.26533101 -0.4258582910
## volatile.acidity              0.089260504  0.02711385 -0.0319153683
## citric.acid                   0.121130798  0.14950257 -0.1637482114
## residual.sugar                0.401439311  0.83896645 -0.1941334540
## chlorides                     0.198910300  0.25721132 -0.0904394560
## free.sulfur.dioxide           0.615500965  0.29421041 -0.0006177961
## total.sulfur.dioxide          1.000000000  0.52988132  0.0023209718
## density                       0.529881324  1.00000000 -0.0935914935
## pH                            0.002320972 -0.09359149  1.0000000000
## sulphates                     0.134562367  0.07449315  0.1559514973
## alcohol                      -0.448892102 -0.78013762  0.1214320987
##                        sulphates     alcohol
## fixed.acidity        -0.01714299 -0.12088112
## volatile.acidity     -0.03572815  0.06771794
## citric.acid           0.06233094 -0.07572873
## residual.sugar       -0.02666437 -0.45063122
## chlorides             0.01676288 -0.36018871
## free.sulfur.dioxide   0.05921725 -0.25010394
## total.sulfur.dioxide  0.13456237 -0.44889210
## density               0.07449315 -0.78013762
## pH                    0.15595150  0.12143210
## sulphates             1.00000000 -0.01743277
## alcohol              -0.01743277  1.00000000
```

```
corrplot(wine.cor, method="number") # I did this because I appreciate the visual
```

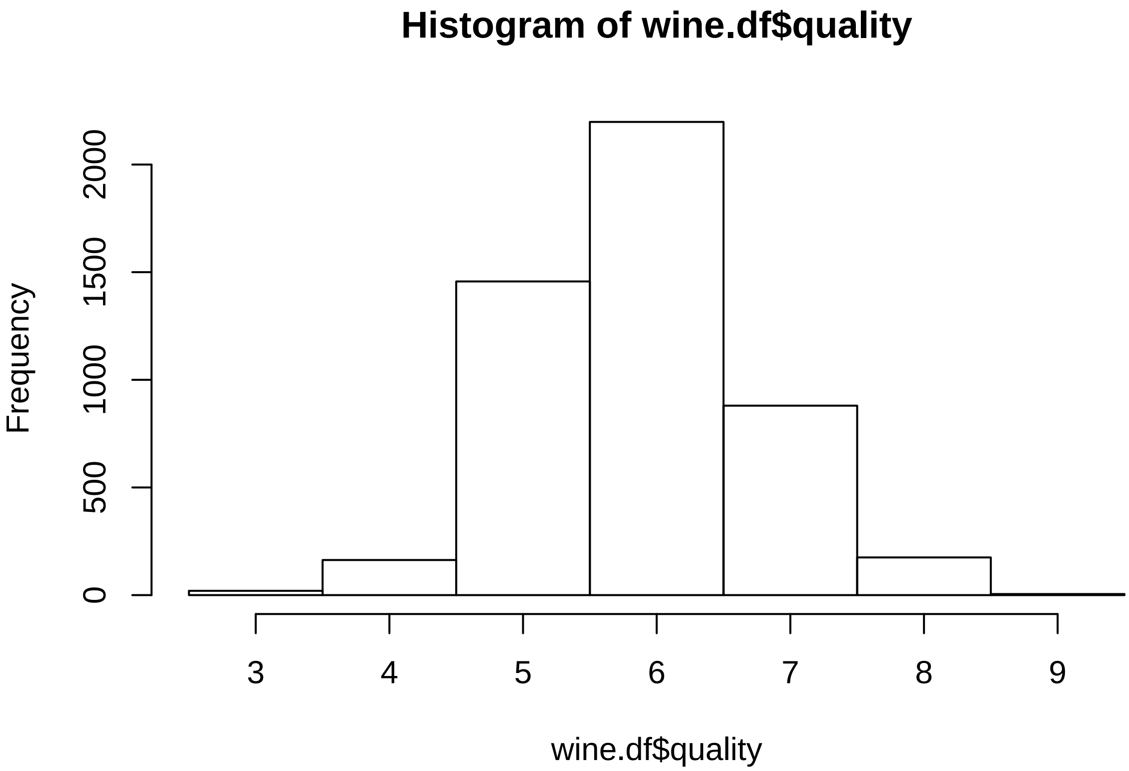


```
# highest correlation:
# density & residual.sugar: 0.84
# density & alcohol: -0.78

# I found a cool SO thread on how to do this programmatically:
# https://stackoverflow.com/questions/7074246/show-correlations-as-an-ordered-list-not-as-a-large-matri

# as.data.frame(as.table(wine.cor))

# install.packages("reshape")
library(reshape) # includes melt()

wine.cor.list <- wine.cor
wine.cor.list[wine.cor.list == 1] <- NA
wine.cor.list <- na.omit(melt(wine.cor.list))
wine.cor.list[order(-abs(wine.cor.list$value)),]
```

```
##                       X1                   X2         value
## 41               density       residual.sugar  0.8389664549
## 81        residual.sugar              density  0.8389664549
## 88               alcohol              density -0.7801376214
## 118              density              alcohol -0.7801376214
## 62  total.sulfur.dioxide  free.sulfur.dioxide  0.6155009650
## 72   free.sulfur.dioxide total.sulfur.dioxide  0.6155009650
## 74               density total.sulfur.dioxide  0.5298813239
## 84  total.sulfur.dioxide              density  0.5298813239
## 44               alcohol       residual.sugar -0.4506312220
## 114       residual.sugar              alcohol -0.4506312220
## 77               alcohol total.sulfur.dioxide -0.4488921021
## 117 total.sulfur.dioxide              alcohol -0.4488921021
## 9                     pH        fixed.acidity -0.4258582910
## 89         fixed.acidity                   pH -0.4258582910
## 40  total.sulfur.dioxide       residual.sugar  0.4014393112
## 70        residual.sugar total.sulfur.dioxide  0.4014393112
## 55               alcohol            chlorides -0.3601887121
## 115            chlorides              alcohol -0.3601887121
## 39   free.sulfur.dioxide       residual.sugar  0.2990983537
## 59        residual.sugar  free.sulfur.dioxide  0.2990983537
## 63               density  free.sulfur.dioxide  0.2942104109
## 83   free.sulfur.dioxide              density  0.2942104109
## 3            citric.acid        fixed.acidity  0.2891806977
## 23         fixed.acidity          citric.acid  0.2891806977
## 8                density        fixed.acidity  0.2653310138
## 78         fixed.acidity              density  0.2653310138
## 52               density            chlorides  0.2572113204
## 82             chlorides              density  0.2572113204
## 66               alcohol  free.sulfur.dioxide -0.2501039415
## 116  free.sulfur.dioxide              alcohol -0.2501039415
## 51  total.sulfur.dioxide            chlorides  0.1989102996
## 71             chlorides total.sulfur.dioxide  0.1989102996
## 42                    pH       residual.sugar -0.1941334540
## 92        residual.sugar                   pH -0.1941334540
## 31                    pH          citric.acid -0.1637482114
## 91           citric.acid                   pH -0.1637482114
## 98             sulphates                   pH  0.1559514973
## 108                   pH            sulphates  0.1559514973
## 30               density          citric.acid  0.1495025706
## 80           citric.acid              density  0.1495025706
## 14           citric.acid     volatile.acidity -0.1494718106
## 24      volatile.acidity          citric.acid -0.1494718106
## 76             sulphates total.sulfur.dioxide  0.1345623669
## 106 total.sulfur.dioxide            sulphates  0.1345623669
## 99               alcohol                   pH  0.1214320987
## 119                   pH              alcohol  0.1214320987
## 29  total.sulfur.dioxide          citric.acid  0.1211307977
## 69           citric.acid total.sulfur.dioxide  0.1211307977
## 11               alcohol        fixed.acidity -0.1208811232
## 111        fixed.acidity              alcohol -0.1208811232
## 27             chlorides          citric.acid  0.1143644484
## 47           citric.acid            chlorides  0.1143644484
## 50   free.sulfur.dioxide            chlorides  0.1013923521
## 60             chlorides  free.sulfur.dioxide  0.1013923521
## 17   free.sulfur.dioxide     volatile.acidity -0.0970119393
## 57      volatile.acidity  free.sulfur.dioxide -0.0970119393
## 26        residual.sugar          citric.acid  0.0942116243
## 36           citric.acid       residual.sugar  0.0942116243
## 28   free.sulfur.dioxide          citric.acid  0.0940772210
## 58           citric.acid  free.sulfur.dioxide  0.0940772210
## 86                    pH              density -0.0935914935
## 96               density                   pH -0.0935914935
## 7   total.sulfur.dioxide        fixed.acidity  0.0910697562
## 67         fixed.acidity total.sulfur.dioxide  0.0910697562
## 53                    pH            chlorides -0.0904394560
## 93             chlorides                   pH -0.0904394560
## 18  total.sulfur.dioxide     volatile.acidity  0.0892605036
## 68      volatile.acidity total.sulfur.dioxide  0.0892605036
## 4         residual.sugar        fixed.acidity  0.0890207014
## 34         fixed.acidity       residual.sugar  0.0890207014
## 38             chlorides       residual.sugar  0.0886845359
## 48        residual.sugar            chlorides  0.0886845359
## 33               alcohol          citric.acid -0.0757287301
## 113          citric.acid              alcohol -0.0757287301
## 87             sulphates              density  0.0744931485
## 107              density            sulphates  0.0744931485
## 16             chlorides     volatile.acidity  0.0705115715
## 46      volatile.acidity            chlorides  0.0705115715
## 22               alcohol     volatile.acidity  0.0677179428
## 112     volatile.acidity              alcohol  0.0677179428
## 15        residual.sugar     volatile.acidity  0.0642860601
## 35      volatile.acidity       residual.sugar  0.0642860601
## 32             sulphates          citric.acid  0.0623309403
## 102          citric.acid            sulphates  0.0623309403
## 65             sulphates  free.sulfur.dioxide  0.0592172458
## 105  free.sulfur.dioxide            sulphates  0.0592172458
## 6    free.sulfur.dioxide        fixed.acidity -0.0493958591
## 56         fixed.acidity  free.sulfur.dioxide -0.0493958591
## 21             sulphates     volatile.acidity -0.0357281469
## 101     volatile.acidity            sulphates -0.0357281469
## 20                    pH     volatile.acidity -0.0319153683
## 90      volatile.acidity                   pH -0.0319153683
## 19               density     volatile.acidity  0.0271138455
## 79      volatile.acidity              density  0.0271138455
## 43             sulphates       residual.sugar -0.0266643659
## 103       residual.sugar            sulphates -0.0266643659
## 5              chlorides        fixed.acidity  0.0230856437
## 45         fixed.acidity            chlorides  0.0230856437
## 2       volatile.acidity        fixed.acidity -0.0226972901
## 12         fixed.acidity     volatile.acidity -0.0226972901
## 110              alcohol            sulphates -0.0174327719
## 120            sulphates              alcohol -0.0174327719
## 10             sulphates        fixed.acidity -0.0171429850
## 100        fixed.acidity            sulphates -0.0171429850
## 54             sulphates            chlorides  0.0167628837
## 104            chlorides            sulphates  0.0167628837
## 75                    pH total.sulfur.dioxide  0.0023209718
## 95  total.sulfur.dioxide                   pH  0.0023209718
## 64                    pH  free.sulfur.dioxide -0.0006177961
## 94   free.sulfur.dioxide                   pH -0.0006177961
```

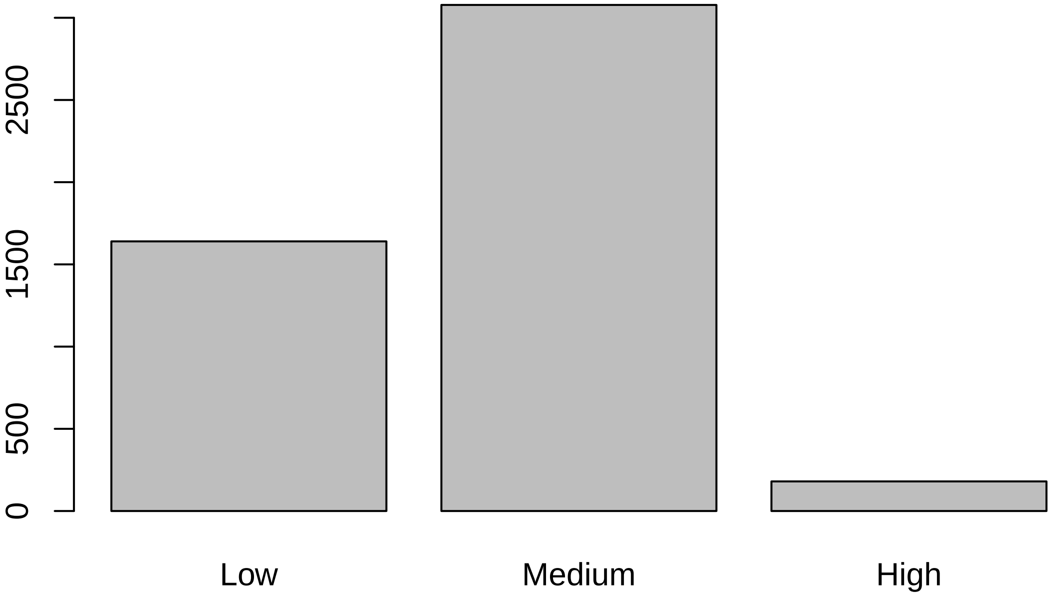
3. Graph the frequency distribution of wine quality .

```
hist(wine.df$quality, freq=T, breaks=seq(2.5,9.5,1))
```



4. Reduce the levels of rating for quality to three levels as high, medium and low.

```
wine.df$quality <- cut(wine.df$quality, 3, labels=c("Low","Medium","High"))
plot(wine.df$quality) # unequal distribution of class variables (potential class imbalance problem)
```



5. Normalize the data set.

```r
# scale() returns a matrix. Also requires numerical values (exclude class attribute (factor): column 12
wine.df.norm <- as.data.frame(scale(wine.df[,-12]))
wine.df.norm <- cbind(wine.df.norm, wine.df[,12]) # Re-add class attribute
names(wine.df.norm)[12] <- names(wine.df)[12] # Re-name the class attribute
```

6. Divide the data to training and testing groups.

```r
wine.train_index <- sample(1:nrow(wine.df.norm), 0.7*nrow(wine.df.norm))
wine.train <- wine.df.norm[wine.train_index,]
wine.test <- wine.df.norm[-wine.train_index,]
(nrow(wine.df) == (nrow(wine.train) + nrow(wine.test))) # Did we include all observations?
```

```
## [1] TRUE
```

7. Use the KNN algorithm to predict the quality of wine using its attributes.

```r
library(class) # needed for knn()
```

```
##
## Attaching package: 'class'

## The following object is masked from 'package:reshape':
##
##     condense
```

```r
# I chose to reference the test group directly in the following calls to knn().
# wine.train_labels <- wine.train$quality
# wine.test_labels <- wine.test$quality
```

```
#
# note the subsetting & removing the attribute quality (wine.test[,-12]): this
# was done because knn() doesn't accept numerical values and seems to react
# poorly to having the class attribute included in either train or test sets.

wine.knn <- list(k3=factor(),k5=factor(),k7=factor())
wine.knn$k3 <- knn(train=wine.train[,-12], test=wine.test[,-12], cl=wine.train$quality, k=3, prob=T)
wine.knn$k5 <- knn(train=wine.train[,-12], test=wine.test[,-12], cl=wine.train$quality, k=5)
wine.knn$k7 <- knn(train=wine.train[-12], test=wine.test[,-12], cl=wine.train$quality, k=7)
```

8. Evaluate the model performance .

```
library(gmodels) # Necessary for CrossTable()

# I prefer actual results along the top of the table: I find it easier to read
# This seems pretty standard, and is likewise on Wikipedia: https://en.wikipedia.org/wiki/Confusion_mat
CrossTable(x=wine.knn$k3, y=wine.test$quality, prop.chisq = F)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  1470
##
##
##              | wine.test$quality
##  wine.knn$k3 |       Low |    Medium |      High | Row Total |
## -------------|-----------|-----------|-----------|-----------|
##          Low |       278 |       149 |         1 |       428 |
##              |     0.650 |     0.348 |     0.002 |     0.291 |
##              |     0.566 |     0.160 |     0.020 |           |
##              |     0.189 |     0.101 |     0.001 |           |
## -------------|-----------|-----------|-----------|-----------|
##       Medium |       207 |       759 |        38 |      1004 |
##              |     0.206 |     0.756 |     0.038 |     0.683 |
##              |     0.422 |     0.816 |     0.776 |           |
##              |     0.141 |     0.516 |     0.026 |           |
## -------------|-----------|-----------|-----------|-----------|
##         High |         6 |        22 |        10 |        38 |
##              |     0.158 |     0.579 |     0.263 |     0.026 |
##              |     0.012 |     0.024 |     0.204 |           |
##              |     0.004 |     0.015 |     0.007 |           |
## -------------|-----------|-----------|-----------|-----------|
## Column Total |       491 |       930 |        49 |      1470 |
##              |     0.334 |     0.633 |     0.033 |           |
## -------------|-----------|-----------|-----------|-----------|
##
```

```
##
```

```
CrossTable(x=wine.knn$k5, y=wine.test$quality, prop.chisq = F)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  1470
##
##
##              | wine.test$quality
##  wine.knn$k5 |       Low |    Medium |      High | Row Total |
## -------------|-----------|-----------|-----------|-----------|
##          Low |       283 |       139 |         1 |       423 |
##              |     0.669 |     0.329 |     0.002 |     0.288 |
##              |     0.576 |     0.149 |     0.020 |           |
##              |     0.193 |     0.095 |     0.001 |           |
## -------------|-----------|-----------|-----------|-----------|
##       Medium |       206 |       782 |        44 |      1032 |
##              |     0.200 |     0.758 |     0.043 |     0.702 |
##              |     0.420 |     0.841 |     0.898 |           |
##              |     0.140 |     0.532 |     0.030 |           |
## -------------|-----------|-----------|-----------|-----------|
##         High |         2 |         9 |         4 |        15 |
##              |     0.133 |     0.600 |     0.267 |     0.010 |
##              |     0.004 |     0.010 |     0.082 |           |
##              |     0.001 |     0.006 |     0.003 |           |
## -------------|-----------|-----------|-----------|-----------|
## Column Total |       491 |       930 |        49 |      1470 |
##              |     0.334 |     0.633 |     0.033 |           |
## -------------|-----------|-----------|-----------|-----------|
##
##
```

```
CrossTable(x=wine.knn$k7, y=wine.test$quality, prop.chisq = F)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
```

```
## Total Observations in Table:  1470 
## 
##  
##              | wine.test$quality 
##  wine.knn$k7 |       Low |    Medium |      High | Row Total | 
## -------------|-----------|-----------|-----------|-----------|
##          Low |       279 |       132 |         0 |       411 | 
##              |     0.679 |     0.321 |     0.000 |     0.280 | 
##              |     0.568 |     0.142 |     0.000 |           | 
##              |     0.190 |     0.090 |     0.000 |           | 
## -------------|-----------|-----------|-----------|-----------|
##       Medium |       211 |       791 |        49 |      1051 | 
##              |     0.201 |     0.753 |     0.047 |     0.715 | 
##              |     0.430 |     0.851 |     1.000 |           | 
##              |     0.144 |     0.538 |     0.033 |           | 
## -------------|-----------|-----------|-----------|-----------|
##         High |         1 |         7 |         0 |         8 | 
##              |     0.125 |     0.875 |     0.000 |     0.005 | 
##              |     0.002 |     0.008 |     0.000 |           | 
##              |     0.001 |     0.005 |     0.000 |           | 
## -------------|-----------|-----------|-----------|-----------|
## Column Total |       491 |       930 |        49 |      1470 | 
##              |     0.334 |     0.633 |     0.033 |           | 
## -------------|-----------|-----------|-----------|-----------|
## 
## 
```

```
# Different values of k produce very similar results with the best being a toss up between k=3 & k=5
# I think that overall this model performed acceptably. It would be interesting to compare to other
# models (Naive Bayes, Decesion Tree, etc) and see how it compares in terms of accuracy.
#
# I think another important concept that wasn't included in this assignment is the concept of "research
# and "metrics of success". For example, below I listed the True Positive rates for the three levels: l
# medium and high. However, perhaps True Positives aren't the most important metrics for your research
# Maybe False Positives are a bigger issue, or False Negatives. This is context specific but extremely
# with these types of models. For example, look at the classification of High Quality wines: The highes
# is approximately 26%. That might not be considered very high depending on your research question.
#
#
#
# TP rates (k=3): 59.8%, 74.9%, 26.3% for Low, medium & high respectively
#
# Note above values are approximate and will change with each run of code unless pseudo-random number g
# is held constant with set.seed(). I chose not to do this as I was interested to see how different ite
# would affect the results.
```

Extra

Visualization

I tried to plot the KNN output of this assignment visually and ran into some trouble I still believe this to be a great exercise but perhaps not ideal for this particular assignment.

Some resources:

- https://cran.r-project.org/web/packages/ElemStatLearn/ElemStatLearn.pdf # pg 8: mixture.example examples
- https://stats.stackexchange.com/questions/21572/how-to-plot-decision-boundary-of-a-k-nearest-neighbor-classifier-from-21602#21602
- https://stackoverflow.com/questions/31234621/variation-on-how-to-plot-decision-boundary-of-a-k-nearest-neighbor-class

I adapted my code as much as possible from the examples and discussion on Stack Overflow but in the end had to settle for a relatively straightforward cluster plot based on kNN algorithm. I think this could be improved with dimensionality reduction: There are 12 dimenstions in this data set so reducing them to two or three principal components would perhaps make for a better visual and also contribute in general to the analysis. I chose to plot pH vs. free.sulfur.dioxide because these are the least correlated factors in the dataset.

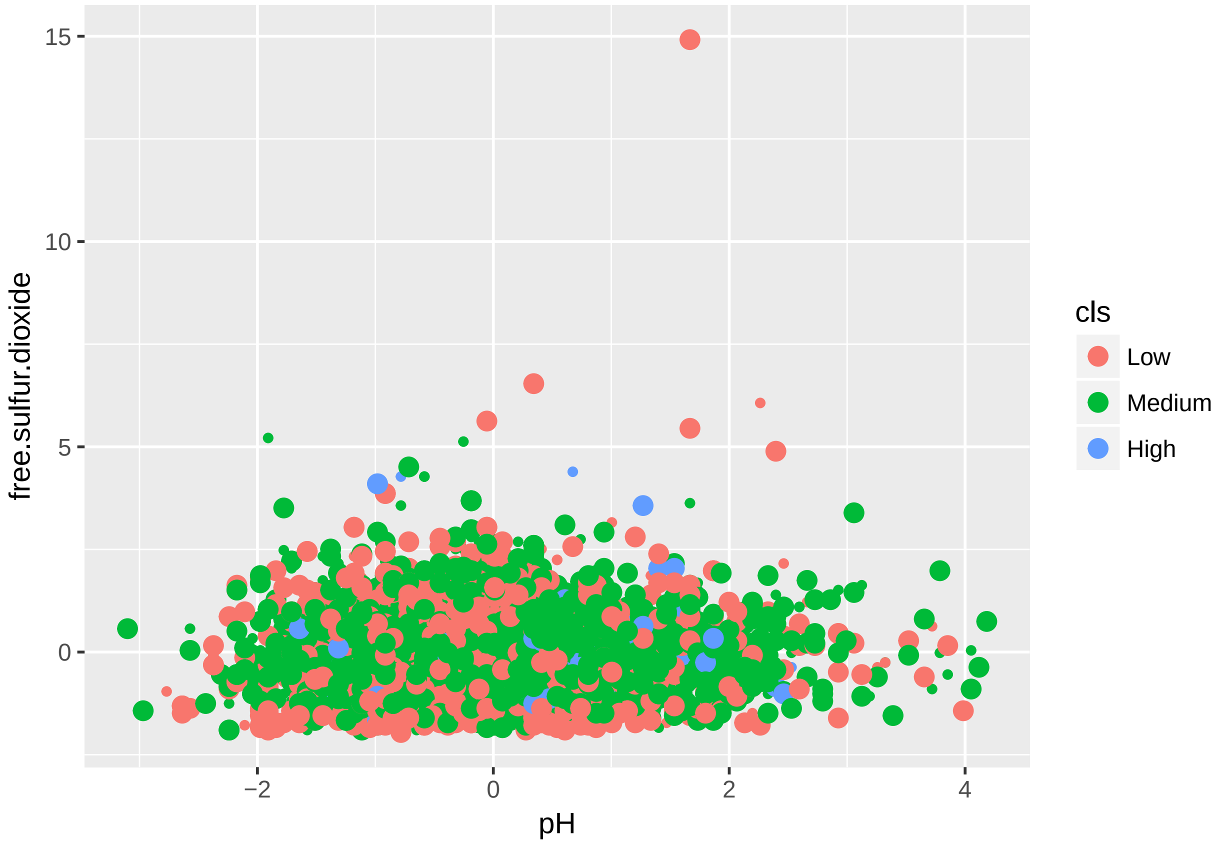
```
require(dplyr)
```

```
## Loading required package: dplyr

##
## Attaching package: 'dplyr'

## The following object is masked from 'package:reshape':
##
##     rename

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
classif <- wine.knn$k3
prob <- attr(classif, "prob")
wine.gf.df <- bind_rows(mutate(wine.test[,-12],
                               prob=prob,
                               cls="Low",
                               prob_cls=ifelse(classif==cls, 1, 0)),
                        mutate(wine.test[,-12],
                               prob=prob,
                               cls="Medium",
                               prob_cls=ifelse(classif==cls, 1, 0)),
                        mutate(wine.test[,-12],
                               prob=prob,
                               cls="High",
                               prob_cls=ifelse(classif==cls, 1, 0)))

# wine.gf.df.unq <- wine.gf.df[!duplicated(wine.gf.df[, c('pH', 'free.sulfur.dioxide')]), ]

require(ggplot2)
```

```
## Loading required package: ggplot2
```

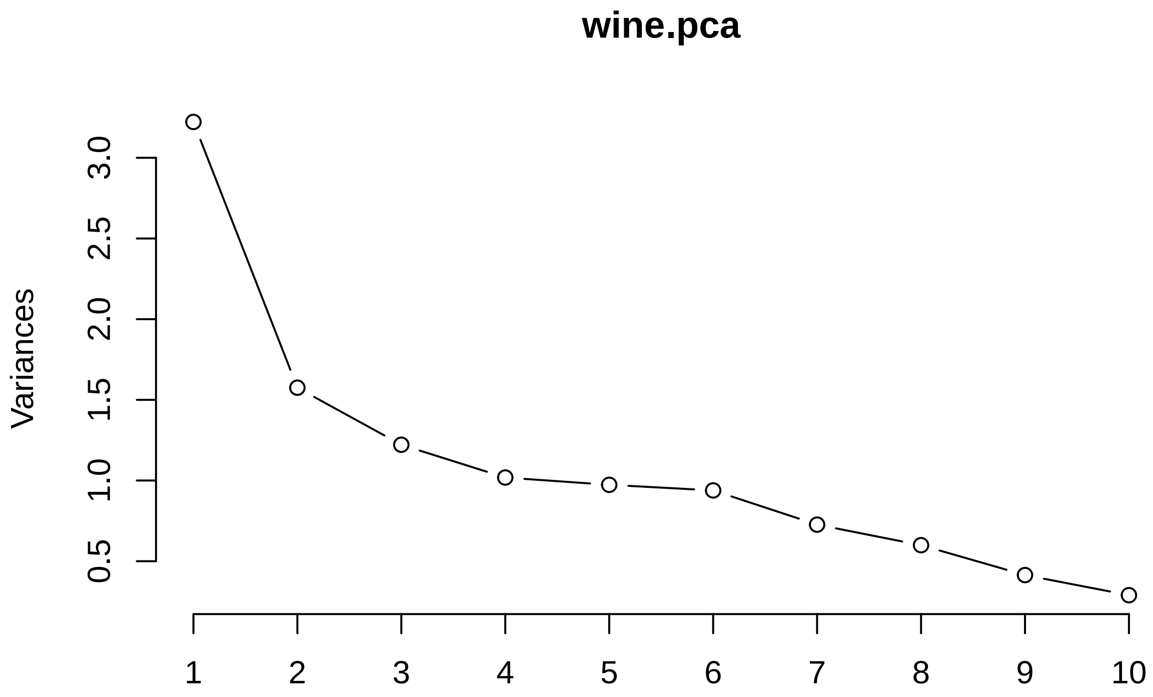
```
ggplot(wine.gf.df) +
  geom_point(aes(x=pH, y=free.sulfur.dioxide, col=cls),
             data=mutate(wine.test[,-12], cls=classif),
             size=1.2) +
  # geom_contour(aes(x=pH, y=free.sulfur.dioxide, z=prob_cls, group=cls, color=cols),
  #              bins=2,
  #              data=wine.gf.df.unq) +
  geom_point(aes(x=x, y=y, col=cls),
             size=3,
             data=data.frame(x=wine.train$pH, y=wine.train$free.sulfur.dioxide, cls=wine.train$quality)
```



PCA

I decided to spend some more time on this dataset and applied PCA. My goal was the same as above; to organize the data in such a way to be able to create an effective visual. I was unsuccesful in that regard but did notice that the model performs better, with regards to the TP Rate, than without doing PCA.

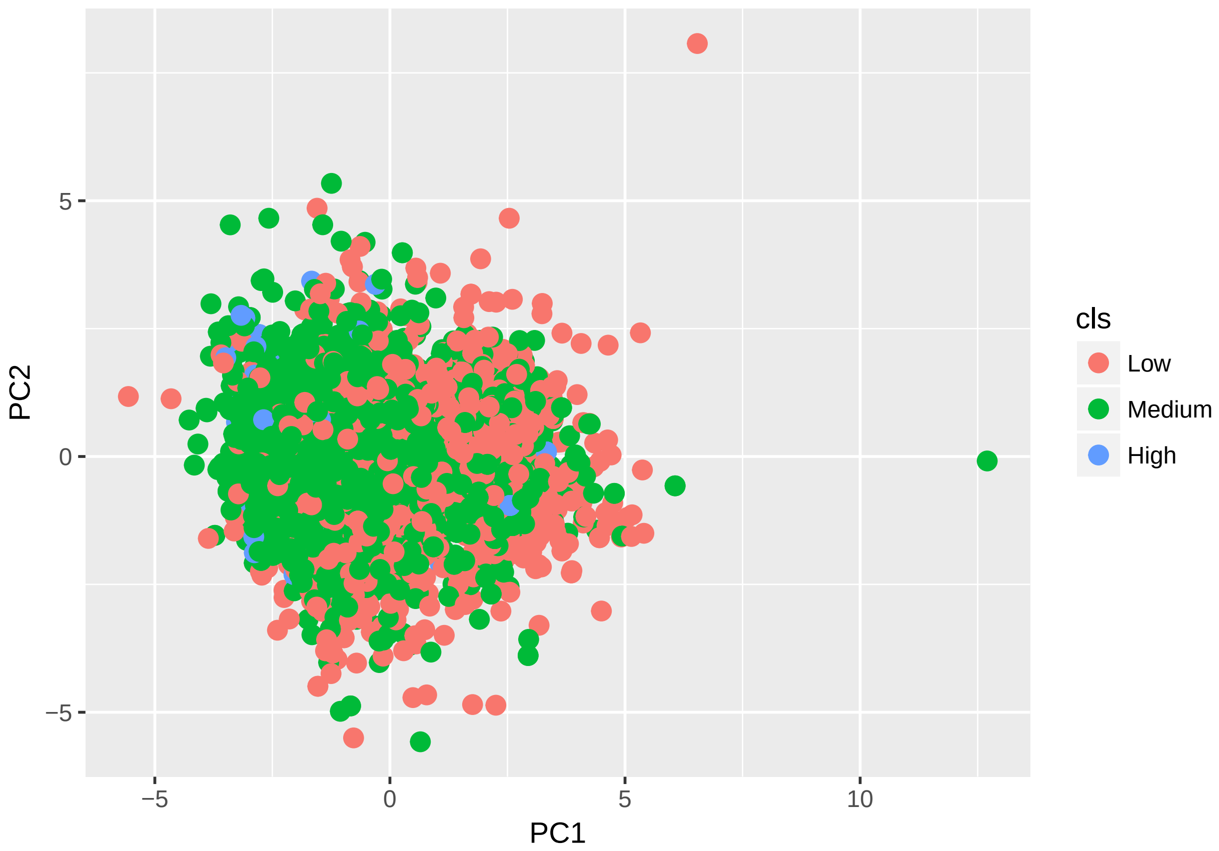
```
wine.pca <- prcomp(wine.df[,-12], scale. = T, center = T)
screeplot(wine.pca, type="lines")
```



```
wine.pca.knn <- knn(train=wine.pca$x[wine.train_index,], test=wine.pca$x[-wine.train_index,], cl=wine.d

CrossTable(x=wine.pca.knn, y=wine.df[-wine.train_index,'quality'], prop.chisq = F)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  1470
##
##
##              | wine.df[-wine.train_index, "quality"]
## wine.pca.knn |       Low |    Medium |      High | Row Total |
## -------------|-----------|-----------|-----------|-----------|
##          Low |       277 |       149 |         1 |       427 |
##              |     0.649 |     0.349 |     0.002 |     0.290 |
##              |     0.564 |     0.160 |     0.020 |           |
##              |     0.188 |     0.101 |     0.001 |           |
## -------------|-----------|-----------|-----------|-----------|
##       Medium |       209 |       760 |        38 |      1007 |
##              |     0.208 |     0.755 |     0.038 |     0.685 |
##              |     0.426 |     0.817 |     0.776 |           |
##              |     0.142 |     0.517 |     0.026 |           |
## -------------|-----------|-----------|-----------|-----------|
##         High |         5 |        21 |        10 |        36 |
##              |     0.139 |     0.583 |     0.278 |     0.024 |
##              |     0.010 |     0.023 |     0.204 |           |
##              |     0.003 |     0.014 |     0.007 |           |
## -------------|-----------|-----------|-----------|-----------|
## Column Total |       491 |       930 |        49 |      1470 |
##              |     0.334 |     0.633 |     0.033 |           |
## -------------|-----------|-----------|-----------|-----------|
##
##
```

```
prob <- attr(wine.pca.knn, "prob")
test <- as.data.frame(wine.pca$x)

wine.pca.gf.df <- bind_rows(mutate(test[-wine.train_index,],
                              prob=prob,
                              cls="Low",
                              prob_cls=ifelse(wine.pca.knn==cls, 1, 0)),
                       mutate(test[-wine.train_index,],
                              prob=prob,
                              cls="Medium",
                              prob_cls=ifelse(wine.pca.knn==cls, 1, 0)),
                       mutate(test[-wine.train_index,],
                              prob=prob,
                              cls="High",
                              prob_cls=ifelse(wine.pca.knn==cls, 1, 0)))


wine.pca.gf.df$cols <- vector(length=nrow(wine.pca.gf.df))
wine.pca.gf.df$cols[wine.pca.gf.df$cls == 'Low'] <- 'c'
wine.pca.gf.df$cols[wine.pca.gf.df$cls == 'Medium'] <- 's'
wine.pca.gf.df$cols[wine.pca.gf.df$cls == 'High'] <- 'v'

ggplot(wine.gf.df) +
  geom_point(aes(x=PC1, y=PC2, col=cls),
             data=mutate(test[-wine.train_index,], cls=wine.pca.knn),
             size=1.2) +
  # geom_contour(aes(x=PC1, y=PC2, z=prob_cls, group=cls, color=cols),
  #              bins=2,
  #              data=wine.pca.gf.df) +
  geom_point(aes(x=x, y=y, col=cls),
             size=3,
             data=data.frame(x=wine.pca$x[,1], y=wine.pca$x[,2], cls=wine.df$quality))
```



Save your R codes in an RMD file. Send your RMD and PDF files to the course shell.