Quiz2

Xi Fang

6/25/2020

Q1

```
library(AppliedPredictiveModeling)
data(AlzheimerDisease)
library(caret)
```

```
## Loading required package: lattice
```

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

```
adData = data.frame(diagnosis,predictors)
trainIndex = createDataPartition(diagnosis, p = 0.50,list=FALSE)
training = adData[-trainIndex,]
testing = adData[trainIndex,]
```

Q2

```
library(AppliedPredictiveModeling)
data(concrete)
library(caret)
set.seed(1000)
inTrain <- createDataPartition(mixtures$CompressiveStrength, p = 3/4)[[1]]
training = mixtures[ inTrain,]
testing = mixtures[-inTrain,]

library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

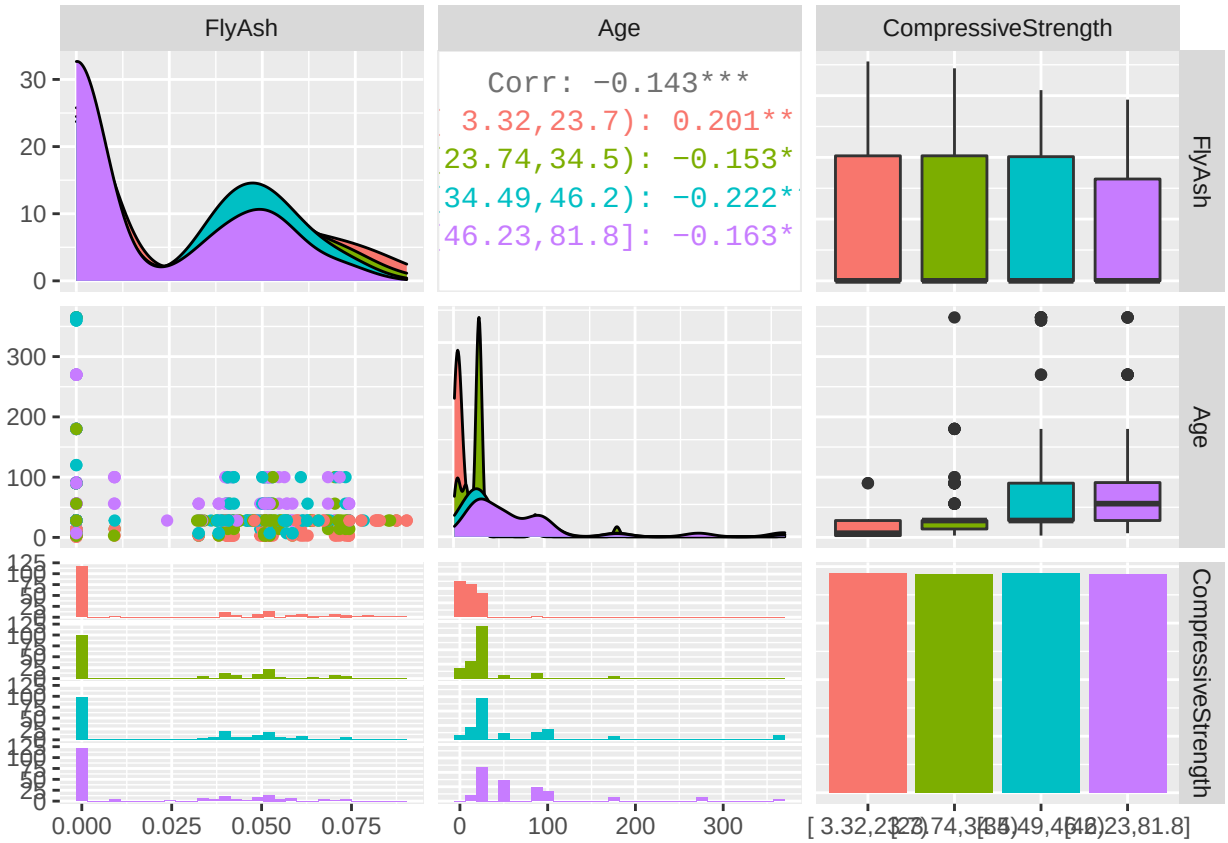
```
library(Hmisc)
```

```
## Loading required package: survival
```

```
##
## Attaching package: 'survival'

## The following object is masked from 'package:caret':
##
##     cluster

## Loading required package: Formula

##
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:base':
##
##     format.pval, units
```

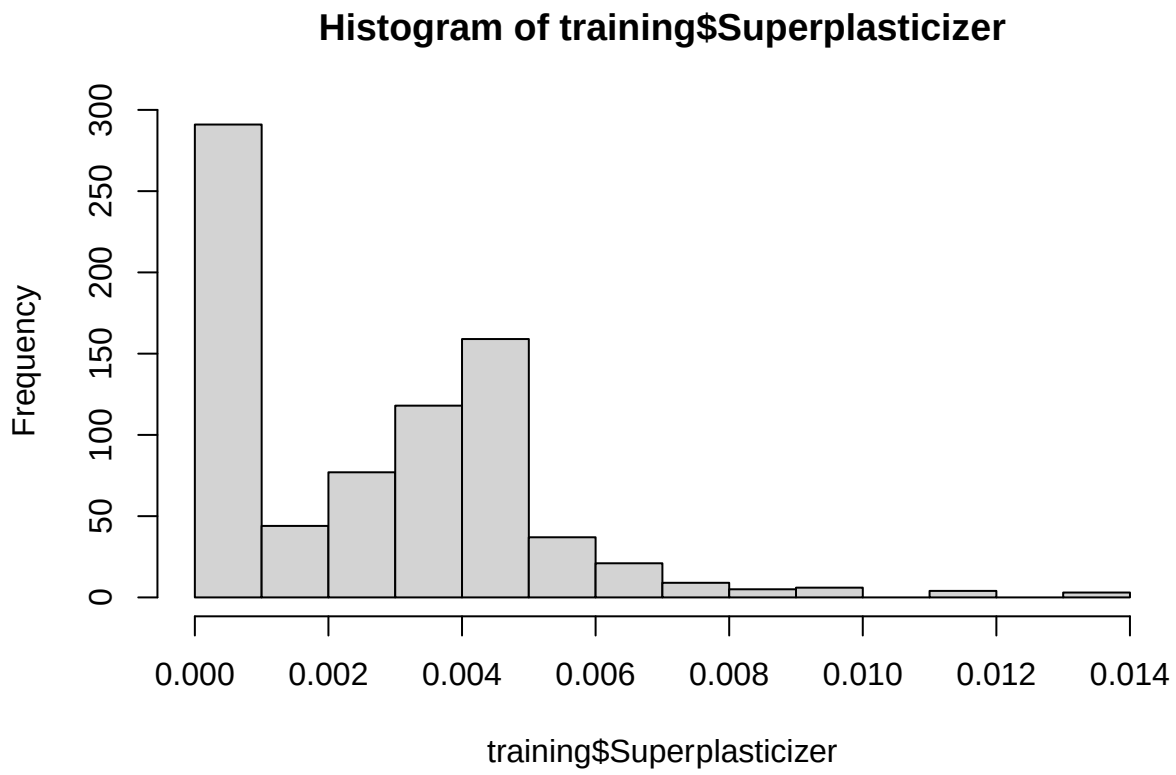
```
t2 <- training
t2$CompressiveStrength <-cut2(t2$CompressiveStrength, g=4)
ggpairs(data=t2, columns = c("FlyAsh","Age","CompressiveStrength"),
        mapping = ggplot2::aes(colour=CompressiveStrength))
```

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

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

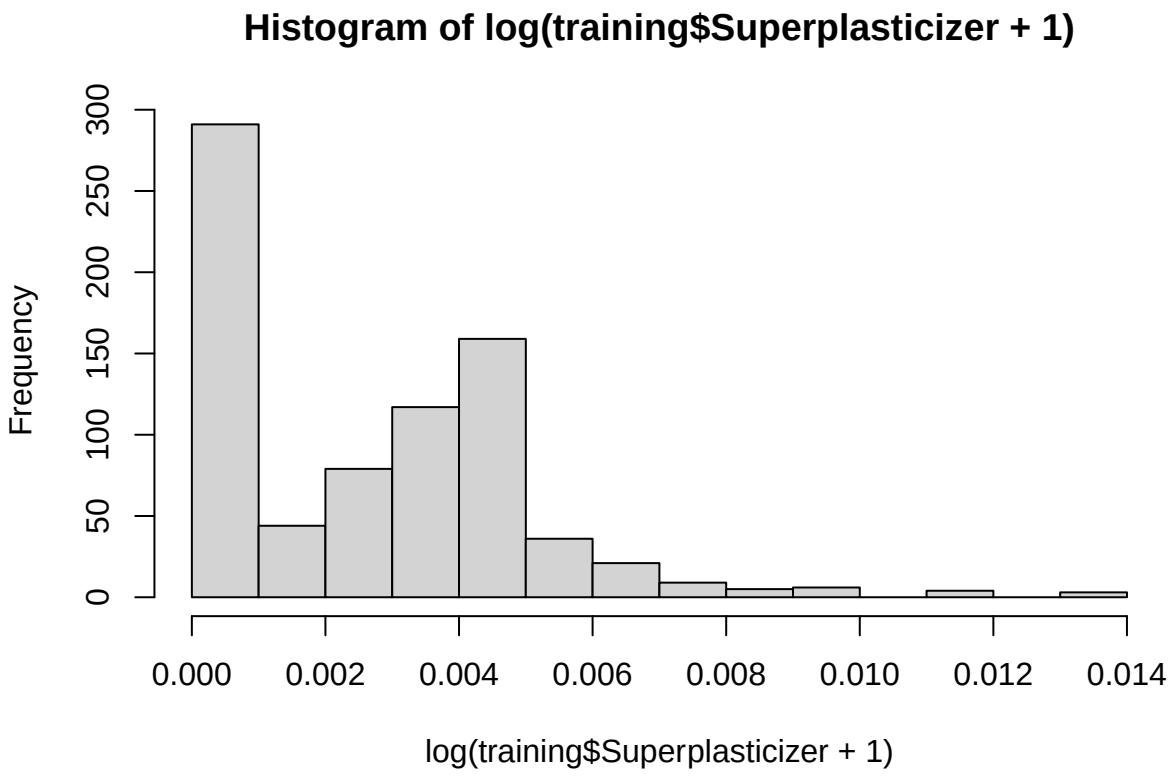


Q3

```
library(AppliedPredictiveModeling)
data(concrete)
library(caret)
set.seed(1000)
inTrain = createDataPartition(mixtures$CompressiveStrength, p = 3/4)[[1]]
training = mixtures[ inTrain,]
testing = mixtures[-inTrain,]
hist(training$Superplasticizer)
```




```
hist(log(training$Superplasticizer+1))
```



Q4

```
library(caret)
library(AppliedPredictiveModeling)
set.seed(3433)
data(AlzheimerDisease)
adData = data.frame(diagnosis,predictors)
inTrain = createDataPartition(adData$diagnosis, p = 3/4)[[1]]
training = adData[inTrain,]
testing = adData[-inTrain,]
# select out columes start with "IL"
b <- training[,grep("^IL", colnames((training)))]

preProcess(b, method="pca", thresh = 0.9)
```

```
## Created from 251 samples and 12 variables
##
## Pre-processing:
##   - centered (12)
##   - ignored (0)
##   - principal component signal extraction (12)
##   - scaled (12)
##
## PCA needed 9 components to capture 90 percent of the variance
```

```r
# below are additional code for exploring the data
c <- as.vector(names(b))
d <- as.formula(paste("diagnosis ~ ", paste(c, collapse="+")))
model <- train(d, method="glm",
               preProcess="pca", data=training)
confusionMatrix(testing$diagnosis, predict(model, testing))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Impaired Control
##   Impaired        2      20
##   Control         2      58
##
##                Accuracy : 0.7317
##                  95% CI : (0.6224, 0.8236)
##     No Information Rate : 0.9512
##     P-Value [Acc > NIR] : 1.0000000
##
##                   Kappa : 0.0777
##
##  Mcnemar's Test P-Value : 0.0002896
##
##             Sensitivity : 0.50000
##             Specificity : 0.74359
##          Pos Pred Value : 0.09091
##          Neg Pred Value : 0.96667
##              Prevalence : 0.04878
##          Detection Rate : 0.02439
##    Detection Prevalence : 0.26829
##       Balanced Accuracy : 0.62179
##
##        'Positive' Class : Impaired
##
```

Q5

```r
library(caret)
library(AppliedPredictiveModeling)
set.seed(3433)
data(AlzheimerDisease)
adData = data.frame(diagnosis,predictors)
inTrain = createDataPartition(adData$diagnosis, p = 3/4)[[1]]
training = adData[ inTrain,]
testing = adData[-inTrain,]

# select all columns start with "IL" in the training and testing set, and add diagnosis
trainingIL <- training[,grep("^IL|diagnosis", colnames(training))]
testingIL <- testing[,grep("^IL|diagnosis", colnames(testing))]

## model1 -- using all variables
```

```r
model1 <- train(diagnosis~., method="glm",
                data=trainingIL)
predict_model1 <- predict(model1, testingIL)
confusionMatrix(predict_model1, testingIL$diagnosis)$overall[1]
```

```
##  Accuracy
## 0.7560976
```

```r
## model2 --- using PCA 80%

model2 <- train(diagnosis ~., method="glm",
                data=trainingIL, preProcess="pca",
                trControl=trainControl(preProcOptions=list(thresh=0.8)))
confusionMatrix(testingIL$diagnosis, predict(model2, testingIL))$overall[1]
```

```
##  Accuracy
## 0.7195122
```