

In [41]: *#loading library*

```
library(boot)
library(caret)
library(tidyverse)
library(ISLR2)
library(glmnet)
library(tidyverse)
library(ISLR2)
library(caret)
library(e1071)
library(neuralnet)
library(dplyr)
library(ggplot2)
library(Hmisc)
library(corrplot)
library(DescTools)
library(kernlab)
library(xgboost)
```

In [42]: *#controlling the size of plot outputs*

```
fig <- function(width, height){
  options(repr.plot.width = width, repr.plot.height = height)
}
fig(18,10)
```

In [43]: *#loading data and naming default set*

```
defaults <- read.csv("data.csv")

#checking for nas
sum(is.na(defaults))
```

0

In [44]: *#in this block we look at the types of data in the our data set, there are only 2 factor variables, one integer and*

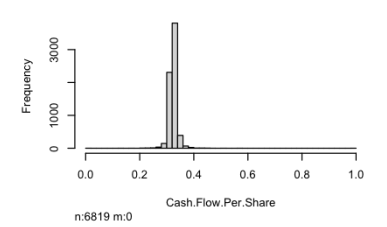
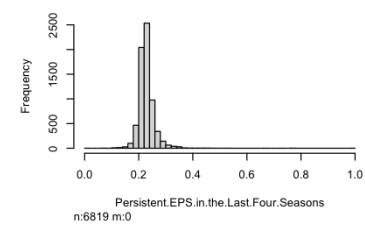
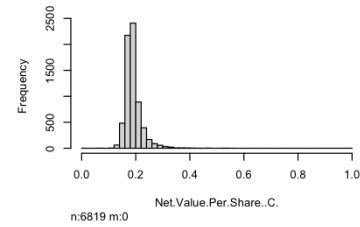
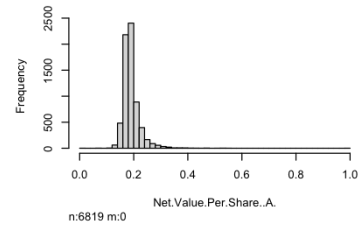
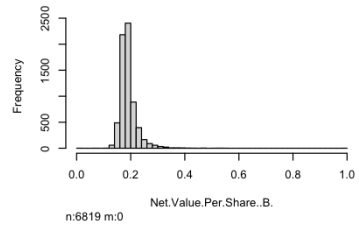
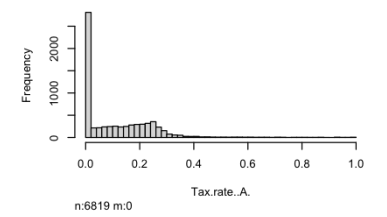
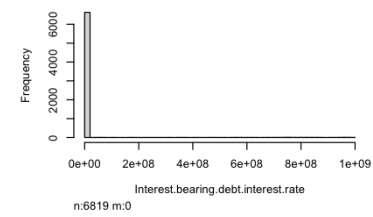
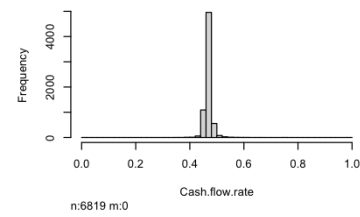
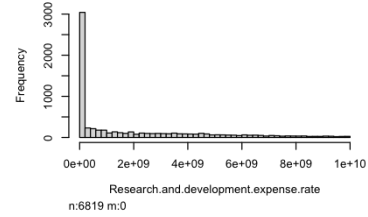
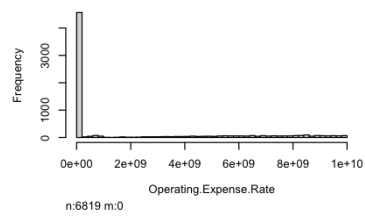
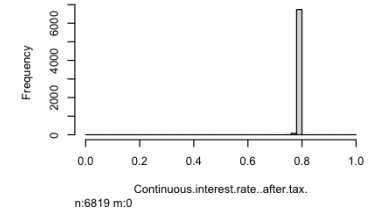
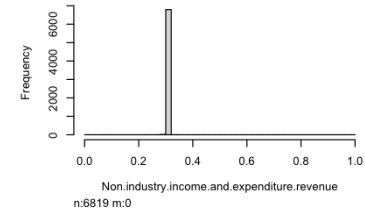
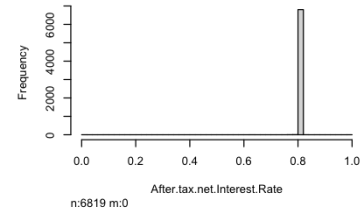
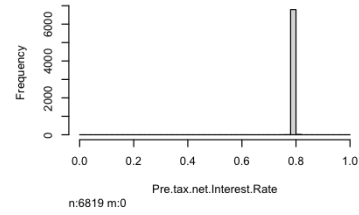
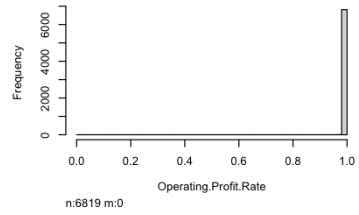
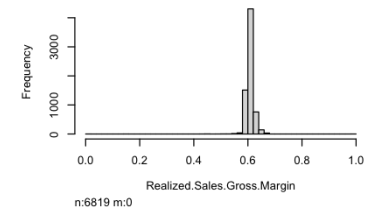
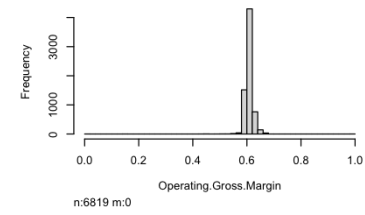
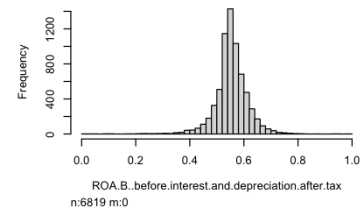
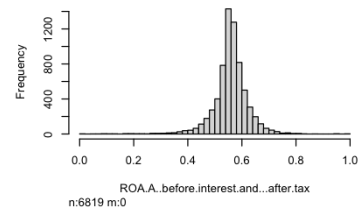
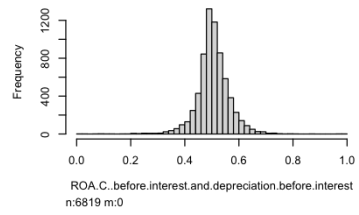
```
table(sapply(defaults,class))
```

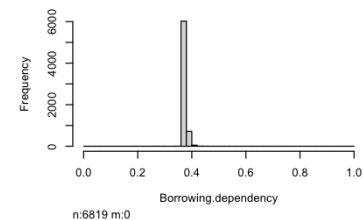
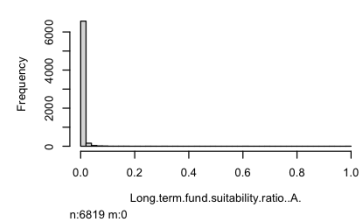
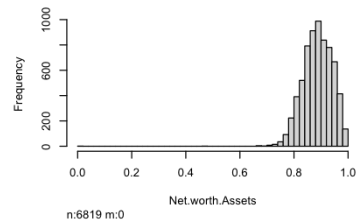
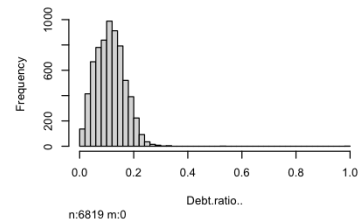
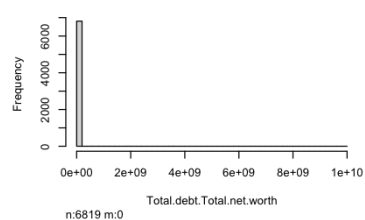
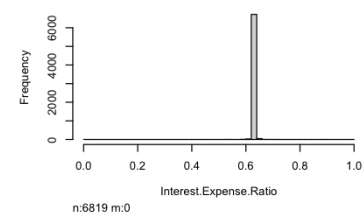
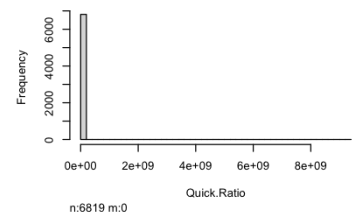
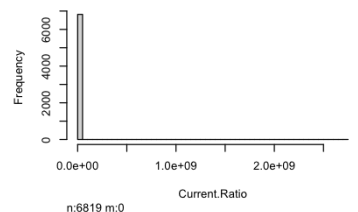
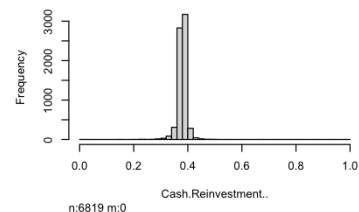
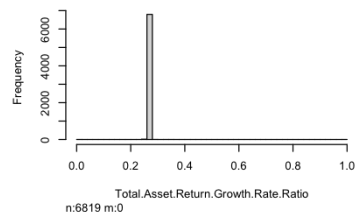
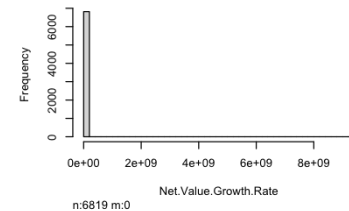
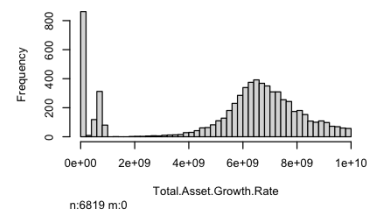
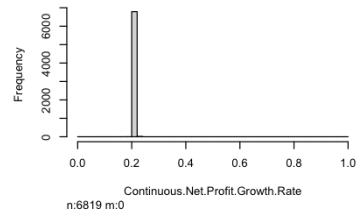
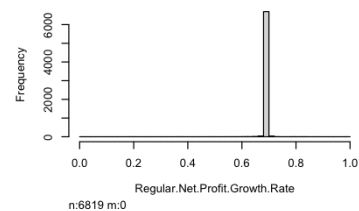
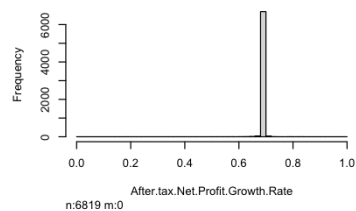
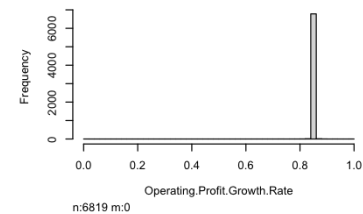
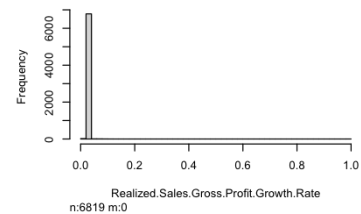
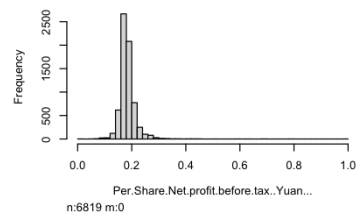
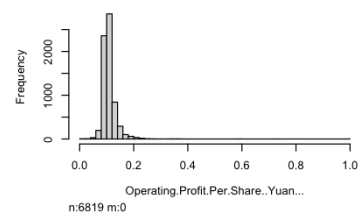
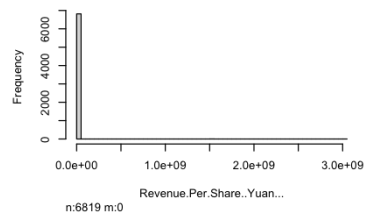
```
integer numeric
      3      93
```

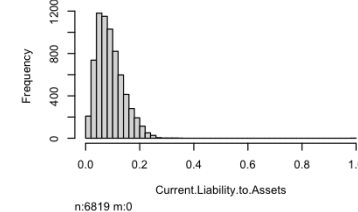
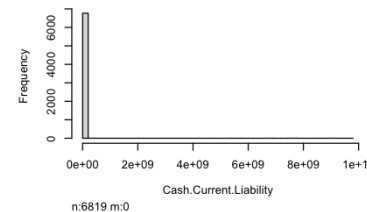
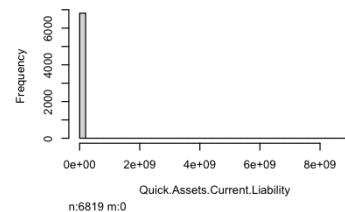
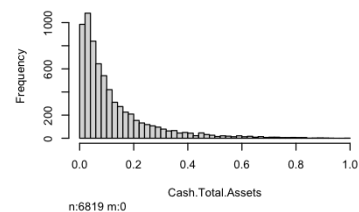
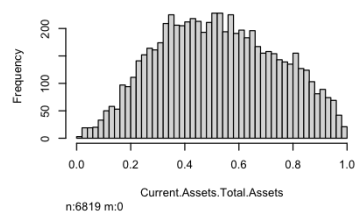
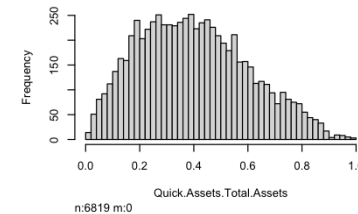
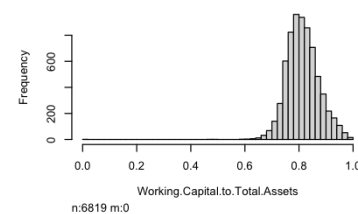
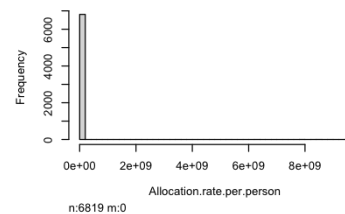
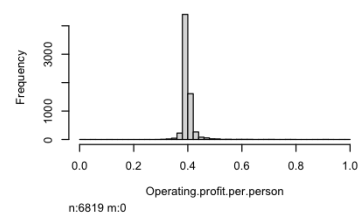
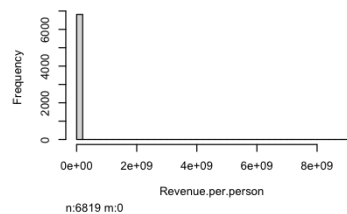
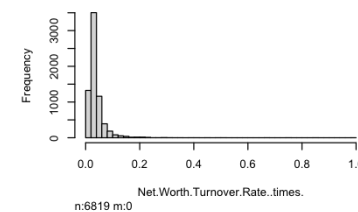
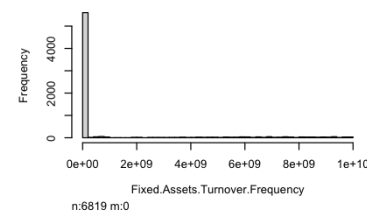
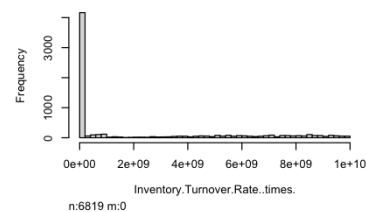
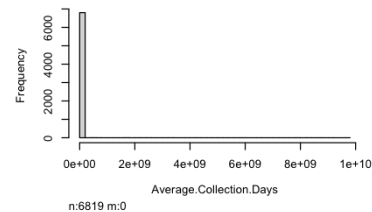
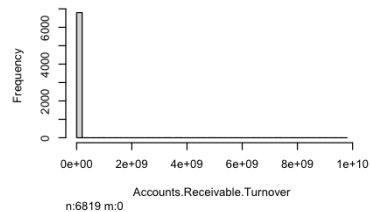
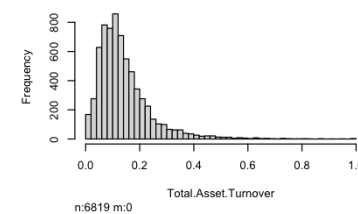
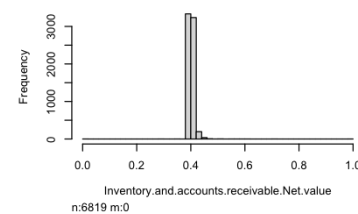
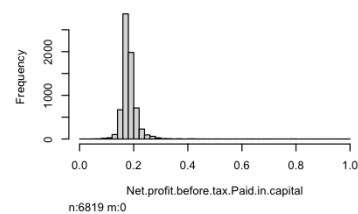
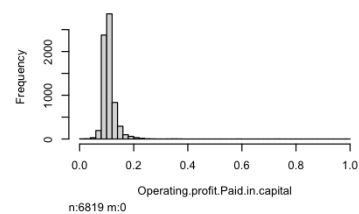
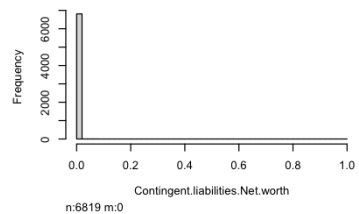
```
In [45]: #redefining factor variables
defaults$Bankrupt. <- as.factor(defaults$Bankrupt.)
defaults$Liability.Assets.Flag <- as.factor(defaults$Liability.Assets.Flag)

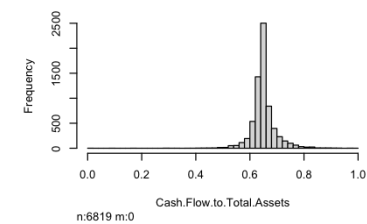
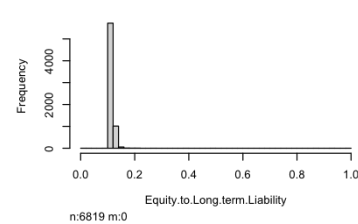
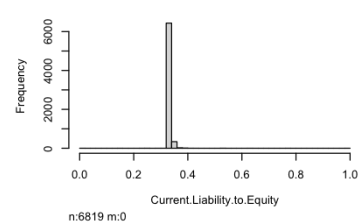
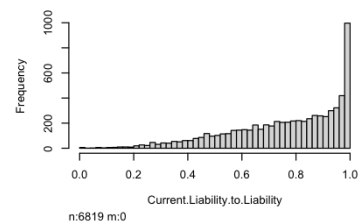
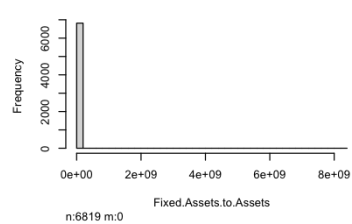
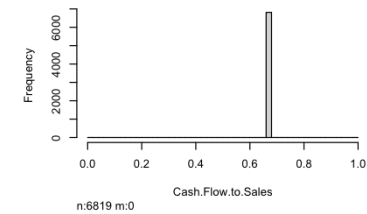
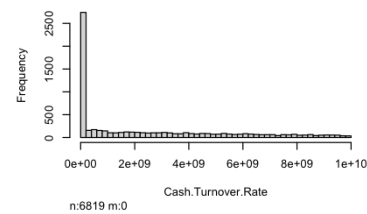
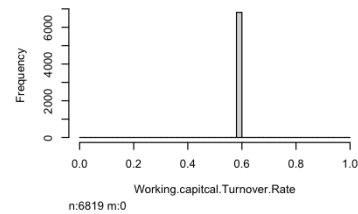
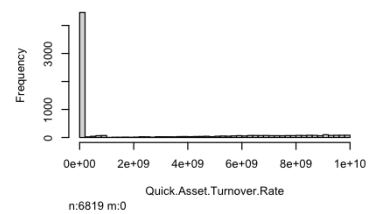
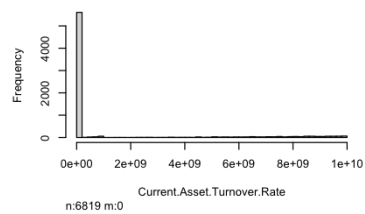
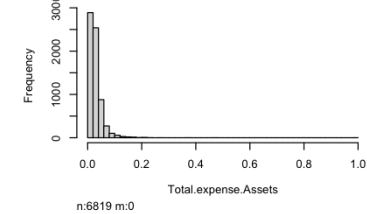
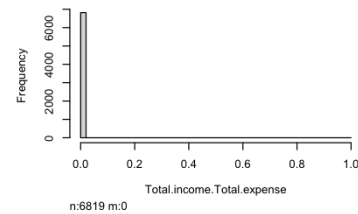
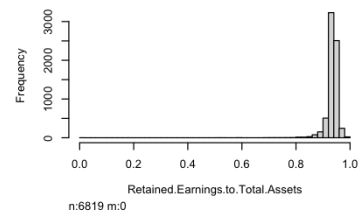
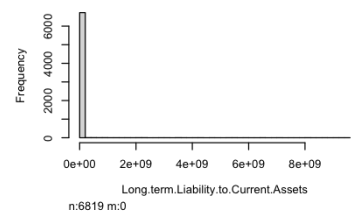
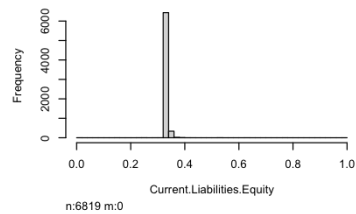
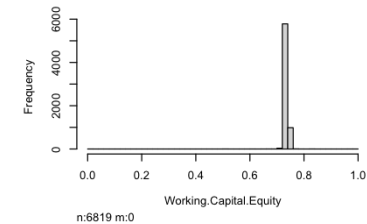
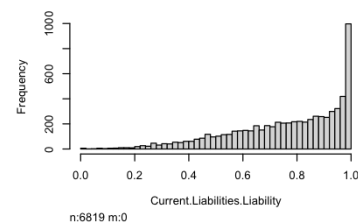
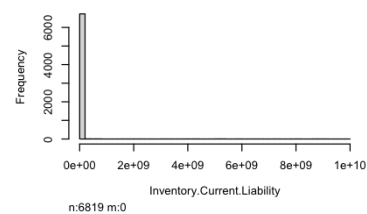
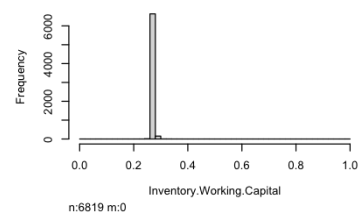
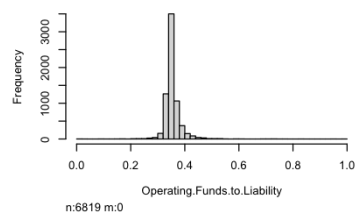
#removing this column because it has zero variance i.e all the values are the same. this means no new information
defaults$Net.Income.Flag <- NULL
```

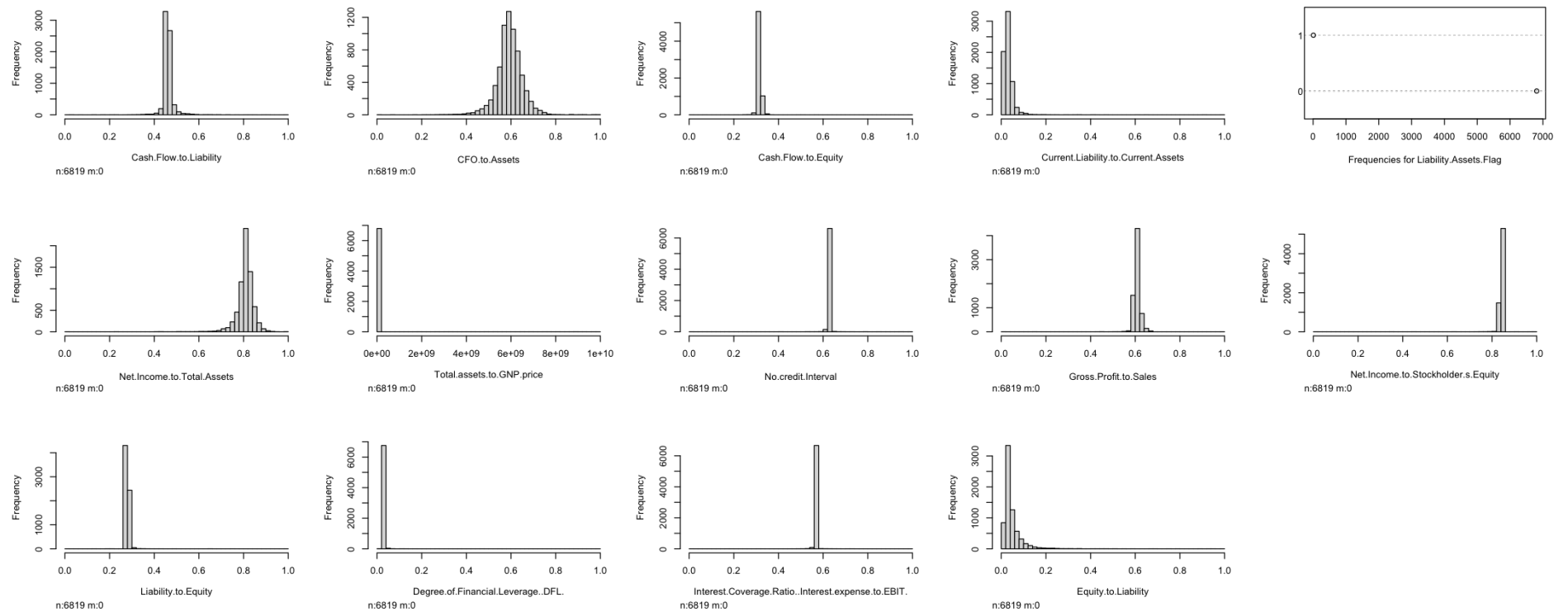
```
In [48]: #examining the distribution of each feature in the dataset
hist.data.frame(defaults[-1]) #generates histogram of each feature in model to examine their distributions
```







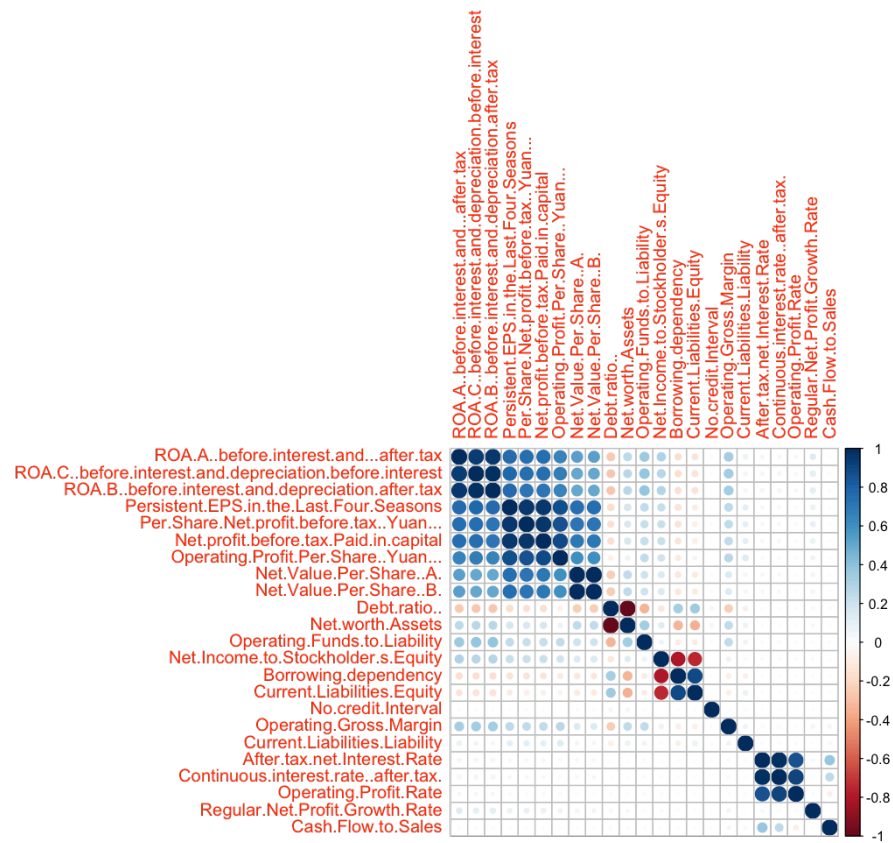




```
In [47]: #finding highly correlated variables
de.cor <- cor(select_if(defaults,is.numeric)) #selects only numeric columns since cor object doesn't like factors

#finding highly correlated variables at specified threshold and then getting index of those variables
cor.indx <- findCorrelation(de.cor, cutoff = 0.8, verbose = FALSE )

#visualising on the combinations with correlations above 0.8 due to the high number of features
corrplot(cor(defaults[-1][cor.indx]), method = 'circle')
```





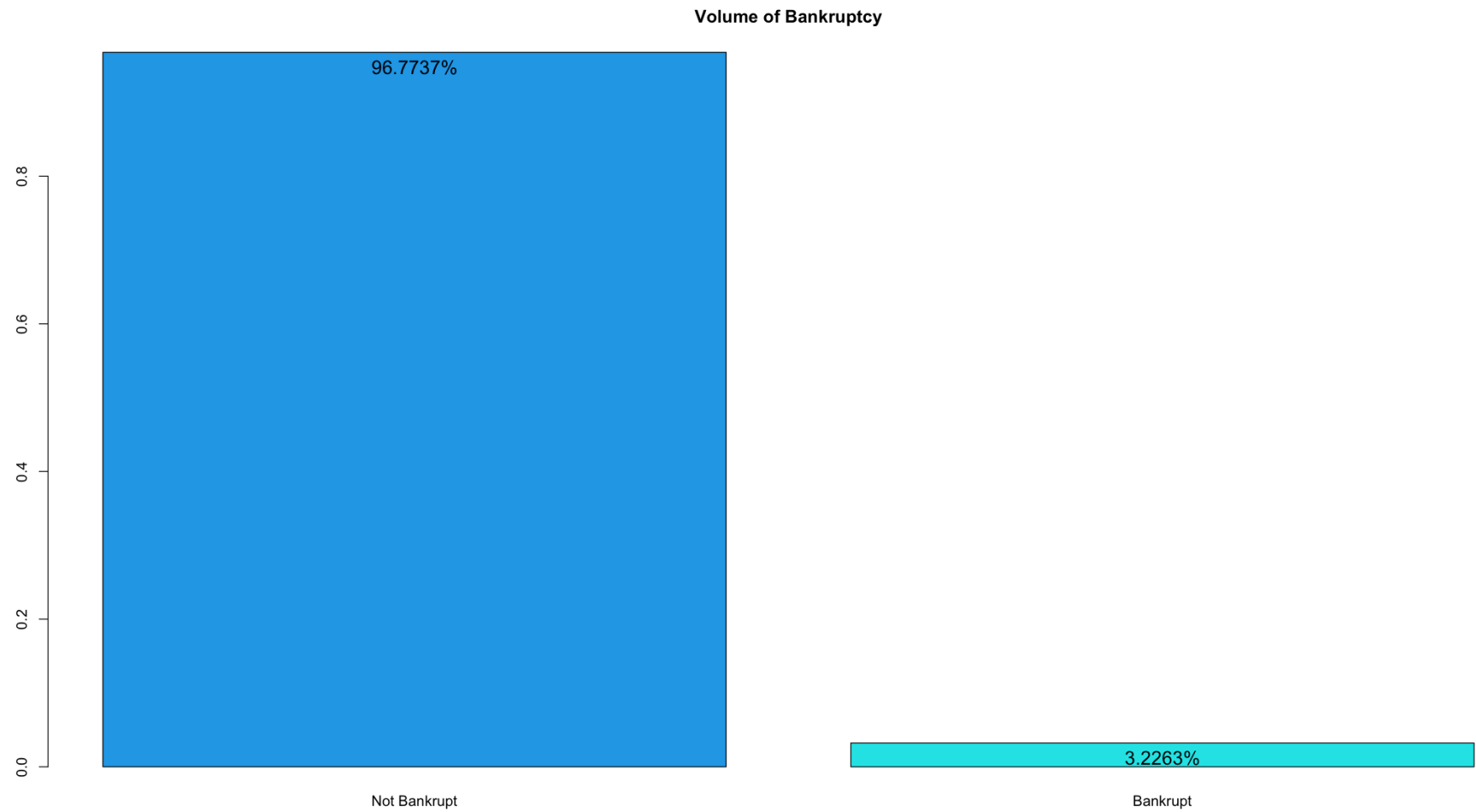
```
In [ ]: # creating new data set without highly correlated features
defaults.clean <- defaults[, !names(defaults) %in% #removes all column names in below list from dataframe
  c("ROA.B..before.interest.and.depreciation.after.tax",
    "ROA.C..before.interest.and.depreciation.before.interest",
    "Persistent.EPS.in.the.Last.Four.Seasons",
    "Operating.Profit.Per.Share..Yuan...",
    "Current.Liabilities.Equity",
    "Current.Liability.to.Equity",
    "Operating.Gross.Margin",
    "Pre.tax.net.Interest.Rate",
    "Operating.Profit.Rate",
    "Net.Value.Per.Share..A.",
    "Net.Value.Per.Share..B.",
    "Net.Value.Per.Share..C.")
  ]
```

```
In [49]: #visualizing bankruptcy classes
bankrupt <- sum(defaults$Bankrupt.== 1)/length(defaults$Bankrupt.) #counting number of bankrupt companies as fraction
not.bankrupt <- 1-bankrupt #counting no bankrupt cases

# bankrupt #percent of defaulters
# not.bankrupt*100 #percent of non-defaulters

#visualizing data as a bar plot
bar <- barplot( c(not.bankrupt,bankrupt),
  names.arg = c("Not Bankrupt", "Bankrupt"), #naming bars
  col = 4:5, #assigning color to each bar
  main = "Volume of Bankruptcy", #title of plot
)

text(x=bar, #since by default, barplot gets midpoint of each bar, so using this sets the text placement
  y = c(not.bankrupt,bankrupt)-.02, # sets vertical height of text. i adjusted it downwards
  labels=c("96.7737%", "3.2263%"), #sets labels
  cex = 1.3 #sets font size
)
```



## Methodology

Data Preparation - Splitting Train and Validation Sets and scaling data

```
In [50]: set.seed(1000)

splitSample <- sample(1:2, size=nrow(defaults.clean), prob=c(0.9,0.1), replace = TRUE)

train_set <- defaults.clean[splitSample==1,]
valid_set <- defaults.clean[splitSample==2,]
```

```
In [51]: #Standardize sets
count = 2
check = 0
while(count < length(defaults.clean[3,]) && check == 0){
  count = count + 1
  if(colnames(defaults.clean[1,])[count] == "Liability.Assets.Flag"){
    check = 1
  }
}
```

```
In [52]: for (i in 2:length(defaults.clean[3,])){
  if(i != count){
    means = mean(train_set[,i])
    sds = sd(train_set[,i])
    valid_set[,i] = (valid_set[,i]-means)/sds
  }
}
```

```

In [53]: train_liability <- train_set[,count]

total_col <- length(defaults.clean[3,])-1

train_set[,count] <- NULL

train_set[,2:total_col] <- scale(train_set[,2:total_col])

train_set[,total_col+1] <- train_liability

valid_liability <- valid_set[,count]
valid_set[,count] <- NULL
valid_set[,total_col+1] <- valid_liability

colnames(train_set)[total_col+1] <- "Liability.Assets.Flag"
colnames(valid_set)[total_col+1] <- "Liability.Assets.Flag"

```

## Model Cross Validation

```

In [ ]: #defining cross entropy loss function for random forest

crossEntropyLoss <- function(data, lev = NULL, model = NULL) {
  predictions <- predict(model, data, type = "prob")
  actual <- as.numeric(data$target) - 1
  loss <- -sum(actual * log(predictions[, 2]) + (1 - actual) * log(predictions[, 1])) / nrow(data)
  return(list(metric = loss, classProbs = predictions))
}

```

```

In [62]: #setting parameters for k-fold cross validation
control.base <- trainControl(method="cv", number=10)

```

```

In [56]: #Logistic Regression
fit.glm <- caret::train(Bankrupt. ~ .,
                        data = train_set,
                        method = "glm",
                        family = "binomial",
                        trControl = control.base)

```

```
Warning message:
"glm.fit: algorithm did not converge"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
"glm.fit: algorithm did not converge"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
"glm.fit: algorithm did not converge"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
"glm.fit: algorithm did not converge"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
"glm.fit: algorithm did not converge"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
```

```
"glm.fit: algorithm did not converge"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
"glm.fit: algorithm did not converge"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
"prediction from a rank-deficient fit may be misleading"
Warning message:
"glm.fit: algorithm did not converge"
Warning message:
"glm.fit: fitted probabilities numerically 0 or 1 occurred"
```

```
In [57]: #Random Forest
#defining grid for cross validation, due to size of feature space, we use the root of number of features. standar

#setting parameters for cross validation
ctrl.rf <- trainControl(method="cv", number=10)

tunegrid <- expand.grid(.mtry=sqrt(dim(train_set)[2])) #changes loss function to cross entropy

fit.rf<- caret::train(Bankrupt.~.,
                      data=train_set,
                      method = 'rf',
                      metric = 'Accuracy',
                      type = "class",
                      tuneGrid = tunegrid,
                      trControl = ctrl.rf)
```

In [59]: `#xgboosted tree`

```
#setting parameters for cross validation
ctrl.xgboost <- trainControl(method="cv", number=10)

# Define grid of parameter combinations to tune over. Here everything is at default value except for the number of
xgboost.grid <- expand.grid(
  nrounds = c(100, 500, 1000),
  max_depth = 6,
  eta = 0.3,
  gamma = 0.1,
  colsample_bytree = 1,
  min_child_weight = 1,
  subsample = 1
)

# Define cross-validation scheme
ctrl <- trainControl(
  method = "repeatedcv",
  number = 10,
  repeats = 1,
  verboseIter = FALSE,
  allowParallel = TRUE
  # numberParallel = 4
)

# Train the model using cross-validation
xgb_model <- train(
  Bankrupt. ~ .,
  data = train_set,
  method = "xgbTree",
  trControl = ctrl,
  tuneGrid = xgboost.grid,
  nthread = 5
)
```

```
[12:34:30] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:34:30] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:35:07] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:35:07] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:35:43] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:35:43] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:36:25] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:36:25] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:37:09] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:37:09] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:37:49] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:37:49] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:38:25] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:38:25] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:39:08] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:39:08] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:39:53] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:39:53] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:40:35] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
[12:40:35] WARNING: src/c_api/c_api.cc:935: `ntree_limit` is deprecated, use `iteration_range` instead.
```



In [64]: *#SVM*

```
#creating grid of parameters for to search through during tuning
tuneGrid.linear <- expand.grid(C = c(0.001,0.1,1,10,100))

#we benchmark the less computationally intense SVM w/linear kernel against the more expensive radial kernel

cv.svm.linear <- train(Bankrupt.~.,
                      data = train_set,
                      method="svmLinear", #defining kernel
                      tuneGrid = tuneGrid.linear,
                      trControl=control.base)

cv.svm.radial <- train(Bankrupt.~.,
                     data = train_set,
                     method="svmRadial",
                     trControl=control.base)

linear.svm.param <- cv.svm.linear$bestTune #best tuning for linear svm
# linear.svm.param
radial.svm.param <- cv.svm.radial$bestTune #best tuning for radial svm
# radial.svm.param
```

In [65]: *#SVM Sigmoid*

```
cost <- c(0.001, 0.01, 0.1, 1, 10, 1/dim(train_set))
gamma <- c(0.01, 0.1, 0.25, 0.5, 1)
sigmoid_svms_accu_mean <- data.frame(
  cost = 0,
  gamma = 0,
  accuracy = 0
)

j = 1
for(c in cost){
  for (g in gamma){
    sigmoid_svms_accu <- c()
    for (i in length(10)){

      splitSample <- sample(1:2, size=nrow(train_set), prob=c(0.9,0.1), replace = TRUE)
      train <- train_set[splitSample==1,]
```

```

    test <- train_set[splitSample==2,]
    sigmoid_svms <- svm(Bankrupt. ~., data = train, kernel = "sigmoid", cost = c, gamma = g)
    predict_svms <- predict(sigmoid_svms, test)
    cm_svms <- confusionMatrix(predict_svms, test$Bankrupt.)
    sigmoid_svms_accu[i] <- cm_svms$overall['Accuracy']
  }
  new_row = list(cost = c, gamma = g, accuracy = mean(sigmoid_svms_accu))
  sigmoid_svms_accu_mean = rbind(sigmoid_svms_accu_mean, new_row)
  j = j + 1
}
}

max_accuracy = 0
index = 1
j = 1
for(i in sigmoid_svms_accu_mean$accuracy){
  if(i > max_accuracy){
    max_accuracy = i
    index = j
  }
  j = j+1
}

#sigmoid_svms_accu_mean[which.max(sigmoid_svms_accu_mean$accuracy),]
#which.max(sigmoid_svms_accu_mean$accuracy)

```

```

In [66]: cv.svm.sigmoid <- svm(Bankrupt. ~., data = train_set,
                               kernel = "sigmoid",
                               cost = sigmoid_svms_accu_mean[index,1],
                               gamma = sigmoid_svms_accu_mean[index,2],
                               classProbs = TRUE)

```

```
In [68]: #kNN

#tunning to find optimal number of neighbors for this dataset
cv.knn <- train(Bankrupt.~.,
                data=train_set,
                method="knn",
                trControl=control.base)

#optimal number of neighbors
# knn.param <- cv.knn$bestTune
```

### Cross Validation Summary

```
In [84]: data.frame(Models = c("Logistic Regression", "Random Forest", "XGBoosted Tree",
                             "Linear SVM", "Radial SVM", "Sigmoidal SVM", "kNN"),
              Cross.Validated.Accuracy = c(fit.glm$results$Accuracy,
              fit.rf$results$Accuracy,
              xgb_model$results$Accuracy[1],
              cv.svm.linear$results[1,2],
              cv.svm.radial$results[1,3],
              sigmoid_svms_accu_mean[which.max(sigmoid_svms_accu_mean$accuracy),3],
              cv.knn$results[2,2]
              )
)
```

A data.frame: 7 × 2

| Models              | Cross.Validated.Accuracy |
|---------------------|--------------------------|
| <chr>               | <dbl>                    |
| Logistic Regression | 0.9539564                |
| Random Forest       | 0.9706550                |
| XGBoosted Tree      | 0.9685478                |
| Linear SVM          | 0.9683852                |
| Radial SVM          | 0.9678992                |
| Sigmoidal SVM       | 0.9819079                |
| kNN                 | 0.9698462                |

## Model Validation

```
In [85]: Results <- data.frame(Metric = c("Accuracy", "Sensitivity", "Specifity")) #generating dataframe to view collective
Models <- list(fit.glm, fit.rf, xgb_model, cv.svm.linear, cv.svm.radial, cv.svm.sigmoid, cv.knn) #storing models in
Model.Names <- c("Logistic Regression", "Random Forest", "XGBoosted Tree", "Linear SVM", "Radial SVM", "Sigmoidal
#the intuition behind the loop is to pass through the list of models, generate predictions and obtain the test st
for (i in 1:length(Models)){ #iterating through the list of models to calculate and visualize their performance
  temp <- confusionMatrix( #creating confusion matrix
    predict(Models[[i]], valid_set), #nesting prediction function inside confusion matrix
    valid_set$Bankrupt.
  )
  # print(i)
  Results[Model.Names[[i]]] <- c(temp$overall['Accuracy'], temp$byClass['Sensitivity'], temp$byClass['Specifity'])
  temp <- NULL #clearing temp variable
}
```

Results

Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :  
"prediction from a rank-deficient fit may be misleading"

A data.frame: 3 × 8

| Metric      | Logistic Regression | Random Forest | XGBoosted Tree | Linear SVM | Radial SVM | Sigmoidal SVM | kNN       |
|-------------|---------------------|---------------|----------------|------------|------------|---------------|-----------|
| <chr>       | <dbl>               | <dbl>         | <dbl>          | <dbl>      | <dbl>      | <dbl>         | <dbl>     |
| Accuracy    | 0.96774194          | 0.9708141     | 0.9723502      | 0.9662058  | 0.9662058  | 0.9662058     | 0.9723502 |
| Sensitivity | 0.99841017          | 0.9984102     | 0.9952305      | 1.0000000  | 1.0000000  | 1.0000000     | 0.9984102 |
| Specifity   | 0.09090909          | 0.1818182     | 0.3181818      | 0.0000000  | 0.0000000  | 0.0000000     | 0.2272727 |