Midterm Project

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```
library(tidyverse)
library(readxl)
library(caret)
library(ModelMetrics)
library(glmnet)
library(gam)
library(mgcv)
library(splines)
library(pdp)
library(earth)
library(dplyr)
library(naniar)
library(bnstruct)
library(corrplot)
library(logisticPCA)
library(MASS)
library(e1071)
library(mlbench)
library(pROC)
library(AppliedPredictiveModeling)
```

Reading the Datasets. Adding the column names to the Breast_Cancer dataset.

```
Diagnosis =
read_csv('./data/Diagnosis.csv')
Prognosis =
  read_csv('./data/Prognosis.csv')
Breast_Cancer =
  read_csv(file = './data/Breast_Cancer.csv' ,col_names = c('id_number','Clump_thickness','Uniformity_o
```

Replacing the missing observations that are denoted by a ? with na and then using KNN imputation to impute the missing values.

```
Breast_Cancer = Breast_Cancer %>% replace_with_na_all(condition = ~.x == '?')
```

```
Breast_Cancer <- knn.impute(as.matrix(Breast_Cancer), k = 10, cat.var = 2:ncol(Breast_Cancer) - 2,
  to.impute = 1:nrow(Breast_Cancer), using = 1:nrow(Breast_Cancer))
```

Creating a data frame called Breast_Cancer.

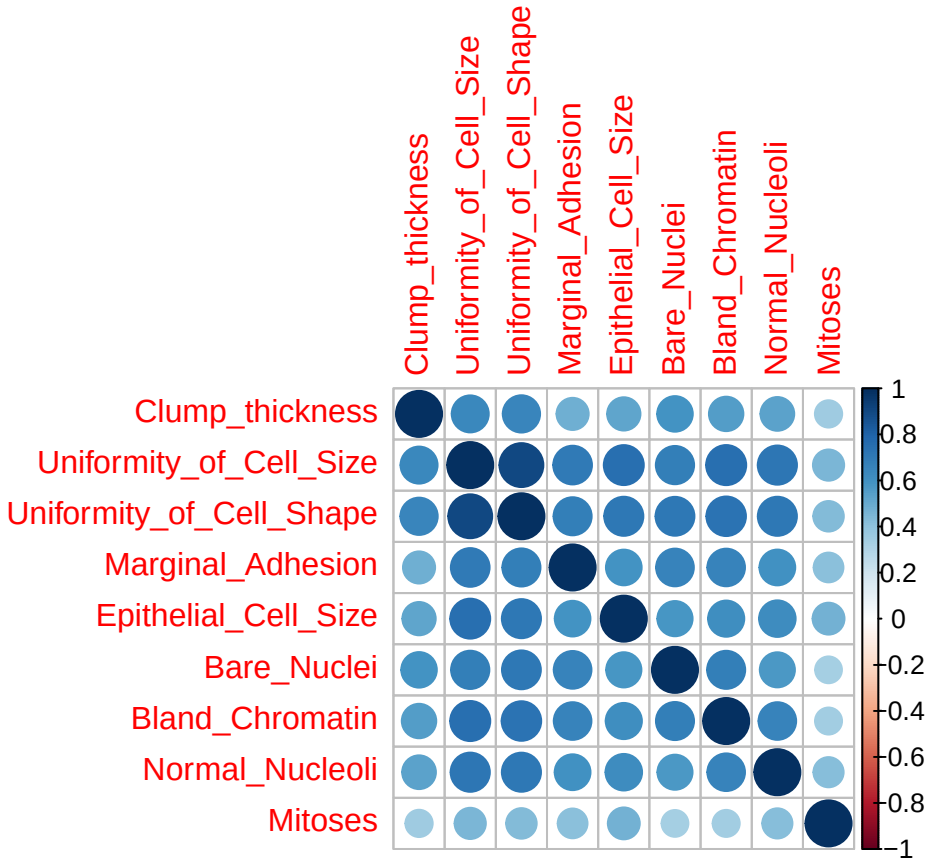
```
Breast_Cancer <- data.frame(Breast_Cancer)
```

Using ifelse on the column Class_cancer –> If Class_cancer = 4 then it's malignant, else its benign. Converted the Class_cancer into factors.

```
Breast_Cancer$Class_cancer = as.factor(ifelse(Breast_Cancer$Class_cancer == 4, 'mal','benign'))
Breast_Cancer = Breast_Cancer[,2:11]
```

Creating a correlation plot to check the correlation between the variables.

```
x = model.matrix(Class_cancer~., Breast_Cancer) [,-1]
corrplot(cor(x))
```



Here we are diving the data into training and test data.

```
set.seed(1)
rowTrain <- createDataPartition(y = Breast_Cancer$Class_cancer,
                                p = 2/3,
                                list = FALSE)
```

Logistic Regression:

```
glm.fit <- glm(Class_cancer~.,
               data = Breast_Cancer,
               subset = rowTrain,
               family = binomial)

contrasts(Breast_Cancer$Class_cancer)
```

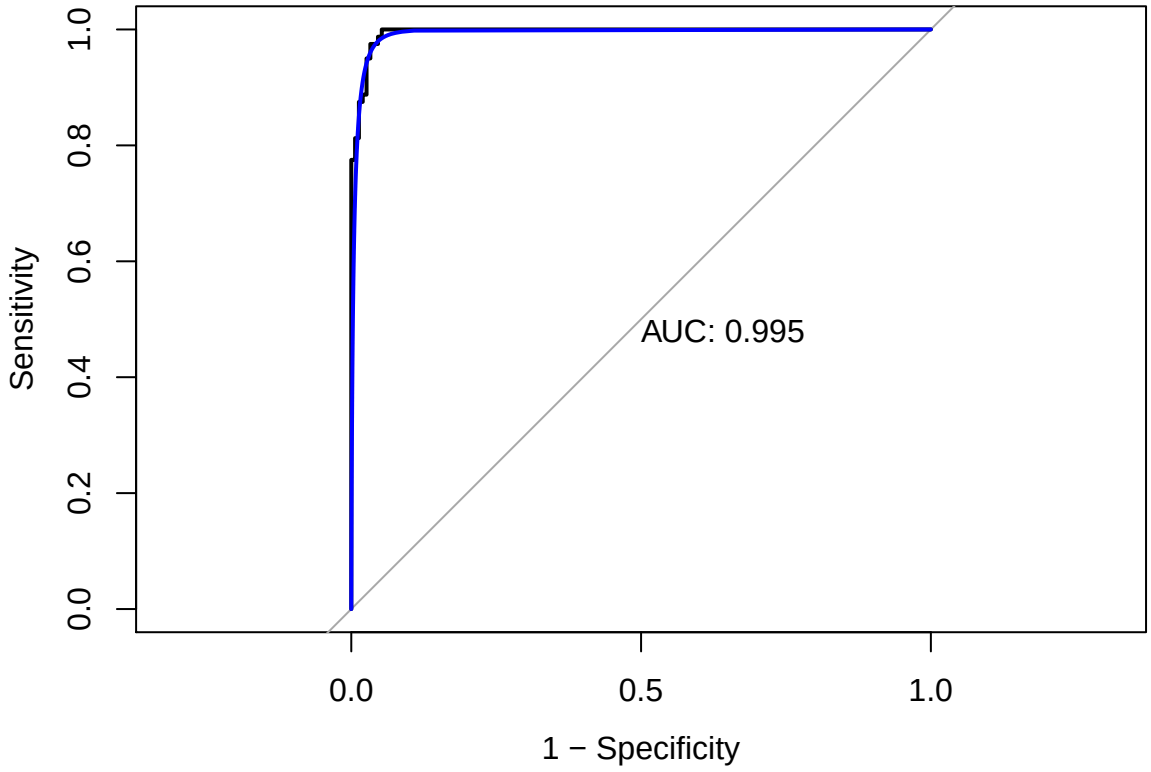
```
##        mal
```

```
## benign   0
## mal      1
```

We first consider the Bayes classifier (cutoff 0.5) and evaluate its performance on the test data and then plot the test ROC curve.

```
test.pred.prob  <- predict(glm.fit, newdata = Breast_Cancer[-rowTrain,1:9],
                           type = "response")
test.pred <- rep("benign", length(test.pred.prob))
test.pred[test.pred.prob > 0.5] <- "mal"

roc.glm <- roc(Breast_Cancer$Class_cancer[-rowTrain], test.pred.prob)
plot(roc.glm, legacy.axes = TRUE, print.auc = TRUE)
plot(smooth(roc.glm), col = 4, add = TRUE)
```



We can also fit a logistic regression using caret. This is to compare the cross-valiation performance with other models, rather than tuning the model.

```
ctrl <- trainControl(method = "repeatedcv",
                     repeats = 5,
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)
```

```
set.seed(1)
model.glm <- train(x = Breast_Cancer[rowTrain,1:9],
                   y = Breast_Cancer$Class_cancer[rowTrain],
                    method = "glm",
                    metric = "ROC",
                    trControl = ctrl)
```

```r
coef(glm.fit)
```

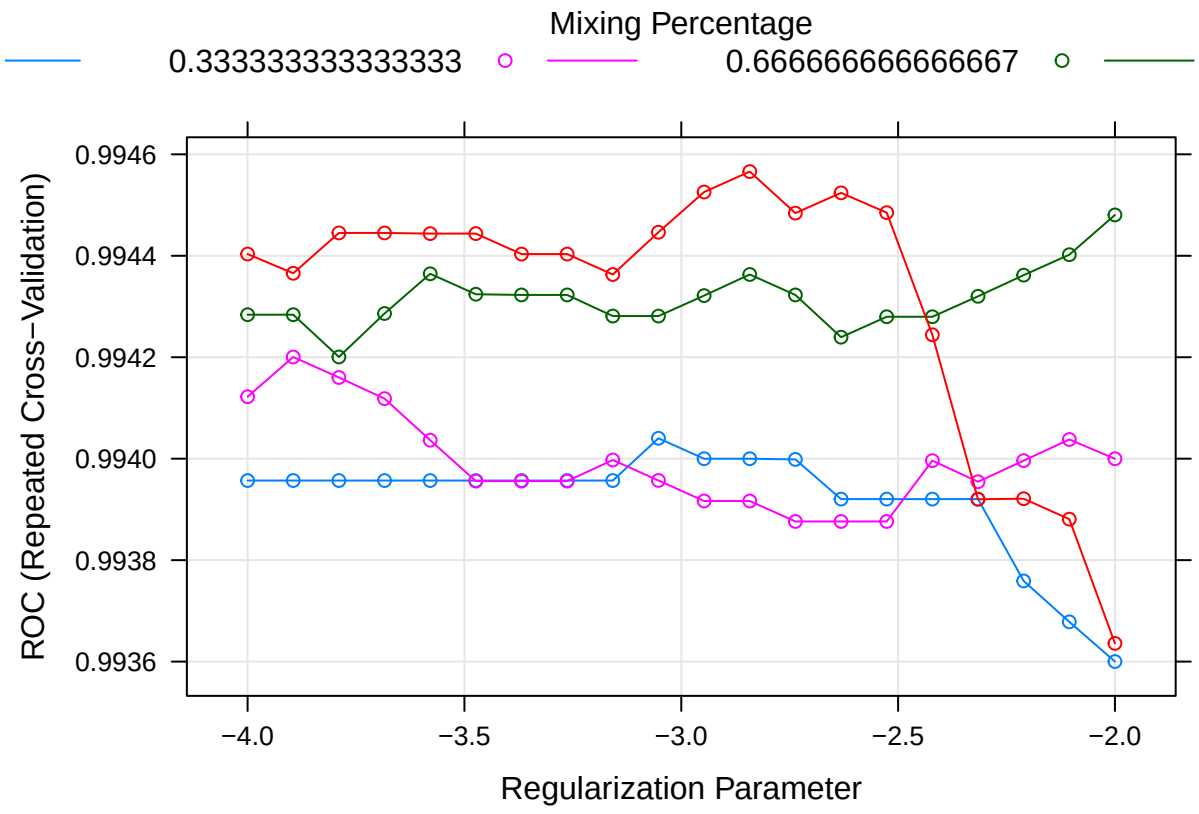
```
##              (Intercept)          Clump_thickness  Uniformity_of_Cell_Size
##               -9.0107637                0.4221055                0.1457212
## Uniformity_of_Cell_Shape        Marginal_Adhesion     Epithelial_Cell_Size
##                0.6370116                0.1479078               -0.2071035
##               Bare_Nuclei          Bland_Chromatin          Normal_Nucleoli
##                0.5172205                0.2023960                0.1863717
##                  Mitoses
##                0.6735681
```

Regularized logistic regression can be fitted using `glmnet'. We use the`train‘ function to select the optimal tuning parameters.

```r
glmnGrid <- expand.grid(.alpha = seq(0, 1, length = 4),
                        .lambda = exp(seq(-4, -2, length = 20)))


set.seed(1)
model.glmn <- train(x = Breast_Cancer[rowTrain,1:9],
                    y = Breast_Cancer$Class_cancer[rowTrain],
                    method = "glmnet",
                    tuneGrid = glmnGrid,
                    metric = "ROC",
                    trControl = ctrl)

plot(model.glmn, xTrans = function(x) log(x))
```



```
model.glmn$bestTune
```

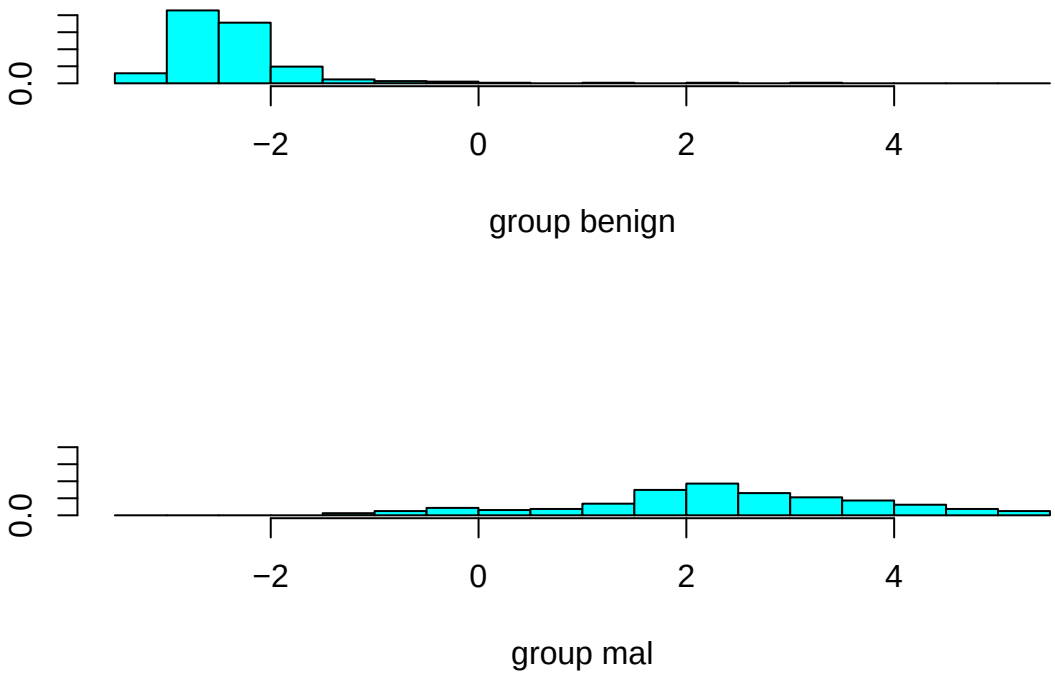
```
##    alpha     lambda
## 72     1 0.05830279
```

```
test.pred.prob  <- predict(model.glmn, x = Breast_Cancer[-rowTrain,1:9],
                      method = "glmnet")
```

Here we use the function `lda` in library `MASS` to conduct LDA.

```
library(MASS)

lda.fit <- lda(Class_cancer~., data = Breast_Cancer,
               subset = rowTrain)
plot(lda.fit)
```



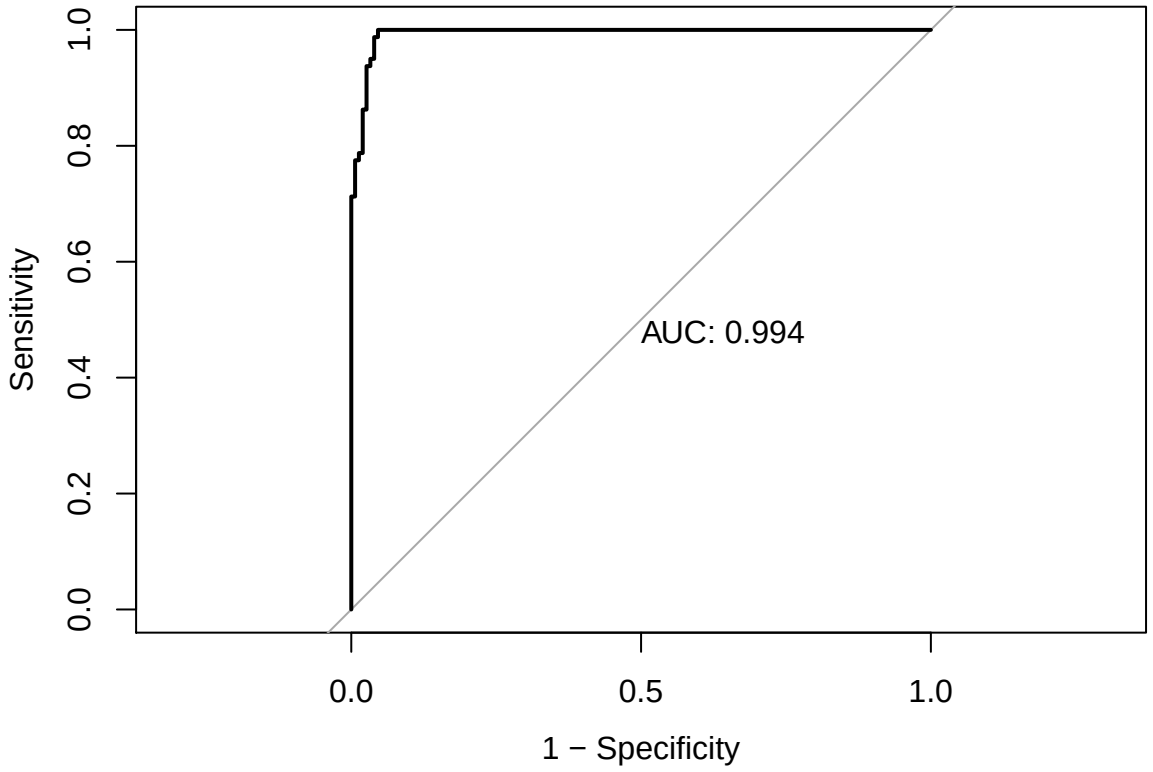
Here we are evaluating the test set performance using ROC.

```
lda.pred <- predict(lda.fit, newdata = Breast_Cancer[-rowTrain,])
head(lda.pred$posterior)
```

```
##       benign          mal
## 3 0.99998228 1.772454e-05
## 4 0.00875467 9.912453e-01
## 5 0.99998862 1.137890e-05
## 7 0.81869551 1.813045e-01
## 8 0.99999630 3.695724e-06
## 9 0.99999902 9.816974e-07
```

```
roc.lda <- roc(Breast_Cancer$Class_cancer[-rowTrain], lda.pred$posterior[,2],
               levels = c("benign", "mal"))

plot(roc.lda, legacy.axes = TRUE, print.auc = TRUE)
```



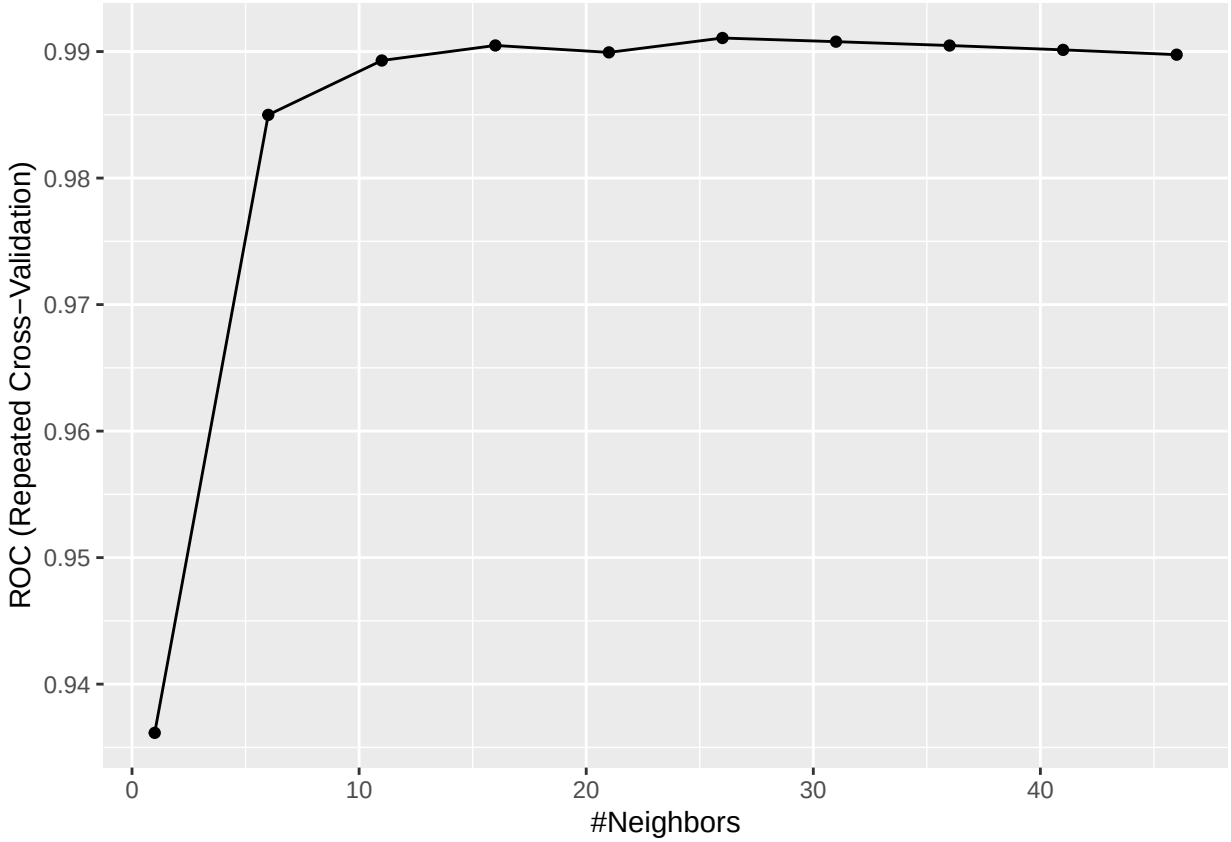
Using caret:

```
set.seed(1)
model.lda <- train(x = Breast_Cancer[rowTrain,1:9],
                   y = Breast_Cancer$Class_cancer[rowTrain],
                   method = "lda",
                   metric = "ROC",
                   trControl = ctrl)
```

Using KNN:

```
set.seed(1)
model.knn <- train(x = Breast_Cancer[rowTrain,1:9],
                   y = Breast_Cancer$Class_cancer[rowTrain],
                   method = "knn",
                   preProcess = c("center","scale"),
                   tuneGrid = data.frame(k = seq(1,50,by = 5)),
                   trControl = ctrl)

ggplot(model.knn)
```



GLM, Regularized GLM and LDA have relatively good performance.

```
res <- resamples(list(GLM = model.glm, GLMNET = model.glmn,
                      LDA = model.lda, KNN = model.knn))
summary(res)
```

```
##
## Call:
## summary.resamples(object = res)
##
## Models: GLM, GLMNET, LDA, KNN
## Number of resamples: 50
##
## ROC
##             Min.   1st Qu.    Median      Mean 3rd Qu. Max. NA's
## GLM    0.9556452 0.9883233 0.9979503 0.9935506       1    1    0
## GLMNET 0.9576613 0.9917339 0.9979839 0.9945660       1    1    0
## LDA    0.9556452 0.9905637 0.9979839 0.9941979       1    1    0
## KNN    0.9506048 0.9881048 0.9964767 0.9910701       1    1    0
##
## Sens
##             Min.   1st Qu.   Median      Mean 3rd Qu. Max. NA's
## GLM    0.9333333 0.9666667 0.983871 0.9777419       1    1    0
## GLMNET 0.9354839 0.9677419 1.000000 0.9875699       1    1    0
## LDA    0.9333333 0.9677419 1.000000 0.9855914       1    1    0
## KNN    0.9333333 0.9666667 0.983871 0.9803656       1    1    0
##
```

```
## Spec
##           Min.   1st Qu.    Median      Mean   3rd Qu. Max. NA's
## GLM    0.8125 0.8750000 0.9375000 0.9363235 1.0000000    1    0
## GLMNET 0.6875 0.8235294 0.8750000 0.8942647 0.9375000    1    0
## LDA    0.6875 0.8750000 0.8786765 0.9003676 0.9375000    1    0
## KNN    0.7500 0.8750000 0.9375000 0.9188971 0.9852941    1    0
```

Now looking at the test set performance.

```
lda.pred <- predict(model.lda, newdata = Breast_Cancer[-rowTrain,], type = "prob")[,2]
glm.pred <- predict(model.glm, newdata = Breast_Cancer[-rowTrain,], type = "prob")[,2]
glmn.pred <- predict(model.glmn, newdata = Breast_Cancer[-rowTrain,], type = "prob")[,2]
knn.pred <- predict(model.knn, newdata = Breast_Cancer[-rowTrain,], type = "prob")[,2]


roc.lda <- roc(Breast_Cancer$Class_cancer[-rowTrain], lda.pred)
roc.glm <- roc(Breast_Cancer$Class_cancer[-rowTrain], glm.pred)
roc.glmn <- roc(Breast_Cancer$Class_cancer[-rowTrain], glmn.pred)
roc.knn <- roc(Breast_Cancer$Class_cancer[-rowTrain], knn.pred)

auc <- c(roc.glm$auc[1], roc.glmn$auc[1], roc.lda$auc[1], roc.knn$auc[1])

plot(roc.glm, legacy.axes = TRUE)
plot(roc.glmn, col = 2, add = TRUE)
plot(roc.lda, col = 3, add = TRUE)
plot(roc.knn, col = 6, add = TRUE)
modelNames <- c("glm","glmn","lda","knn")
legend("bottomright", legend = paste0(modelNames, ": ", round(auc,3)),
       col = 1:6, lwd = 2)
```