Xkong_HW2

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1. Read data

score_class<- read.csv("https://raw.githubusercontent.com/xkong100/data-621/master/HW2/classification-or head(score_class)

```
pregnant glucose diastolic skinfold insulin bmi pedigree age class
##
## 1
            7
                   124
                              70
                                        33
                                                215 25.5
                                                            0.161
                                                                    37
            2
                   122
                                                200 35.9
                                                            0.483
## 2
                              76
                                        27
                                                                    26
                                                                           0
## 3
            3
                   107
                              62
                                        13
                                                 48 22.9
                                                            0.678
                                                                    23
                                                                           1
## 4
            1
                    91
                              64
                                                 0 29.2
                                                            0.192
                                                                           0
                                        24
                                                                    21
## 5
                    83
                              86
                                                 0 29.3
                                                            0.317
                                        19
                                                                    34
                                                                           0
## 6
            1
                   100
                              74
                                        12
                                                 46 19.5
                                                            0.149
                                                                    28
                                                                           0
     scored.class scored.probability
##
## 1
                 0
                           0.32845226
## 2
                 0
                           0.27319044
## 3
                 0
                           0.10966039
## 4
                 0
                           0.05599835
## 5
                 0
                           0.10049072
## 6
                           0.05515460
```

2. confusion Matrix

```
t <- table(score_class$class, score_class$scored.class)
colnames(t) <- c("Real Negative", "Real Positive")
rownames(t) <- c("Model Negative", "Model Positive")
t</pre>
```

```
##
## Real Negative Real Positive
## Model Negative 119 5
## Model Positive 30 27
```

The columns represent for Scored.Class which represent the predicted classes, The rows represents for the class which represent the predicted classes. "1=positive", "0=negative"

3. Accuracy

```
accuracy <- function(data){
    t <- table(data$class, data$scored.class)
    tn<-t[1,1]
    tp<-t[2,2]
    fn<-t[2,1]
    fp<-t[1,2]
acc <- (tp+tn)/ (tp+fp+tn+fn)

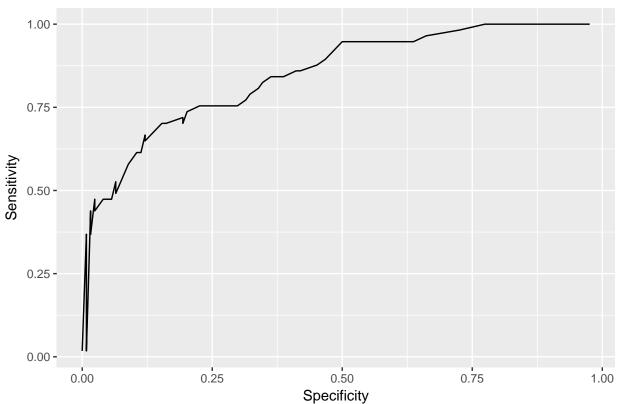
return (acc)
}
a<-accuracy(score_class)
a</pre>
```

```
## [1] 0.8066298
  4. Classification Error Rate
error_rate <- function(data){</pre>
  t <- table(data$class, data$scored.class)
  tn < -t[1,1]
  tp<-t[2,2]
  fn<-t[2,1]
  fp<-t[1,2]
error <- (fp+fn)/ (tp+fp+tn+fn)
return (error)
e<-error_rate(score_class)
## [1] 0.1933702
sum<-accuracy(score_class)+error_rate(score_class)</pre>
## [1] 1
  5. Precision
precision <- function(data){</pre>
  t <- table(data$class, data$scored.class)
  tn < -t[1,1]
  tp < -t[2,2]
  fn<-t[2,1]
  fp<-t[1,2]
pre <- (tp)/ (tp+fp)</pre>
return (pre)
pre<-precision(score_class)</pre>
pre
## [1] 0.84375
  6. Sensitivity
sensitivity <- function(data){</pre>
  t <- as.data.frame(table(Actual=data$class, Predicted= data$scored.class))
return(t$Freq[4]/(t$Freq[4]+t$Freq[2]))
}
sen<-sensitivity(score_class)</pre>
sen
## [1] 0.4736842
  7. Specificity
specificity <- function(data){</pre>
  t <- as.data.frame(table(Actual=data$class, Predicted= data$scored.class))
return(t$Freq[1]/(t$Freq[1]+t$Freq[3]))
```

```
sp<-specificity(score_class)</pre>
## [1] 0.9596774
  8. F1 Score
F1 Score <- function(data){
   t <- table(data$class, data$scored.class)</pre>
  tn<-t[1,1]
  tp < -t[2,2]
  fn<-t[2,1]
  fp<-t[1,2]
  pre <- (tp)/ (tp+fp)</pre>
  sen \leftarrow (tp)/(tp+fn)
  F1 <- (2*pre*sen)/(pre+sen)
  return(F1)
}
F1<- F1_Score(score_class)
## [1] 0.6067416
  9. Let P = Precision, S = Sensitivity, Since 0  and <math>0 < s < 1, we know that p(s - 1) < s < 1
     0 and s(p-1) < 0. In this case, we can find that ps < p, sp < s. ps + sp , <math>2ps , <math>\frac{2ps}{p+s} < 1.
     Since p > 0, s > 0, \frac{2ps}{p+s} > 0.
In conclusion, 0 < F1Score < 1.
 10. ROC Curve and AUC curve
library(ggplot2)
ROC <- function(data)</pre>
{
  data1 = data
  thresholds \leftarrow seq(0,1,0.01)
  Y \leftarrow c()
  X \leftarrow c()
  for (threshod in thresholds) {
    data1$scored.class <- ifelse(data1$scored.probability > threshod,1,0)
    X <- append(X,1-specificity(data1))</pre>
    Y <- append(Y,sensitivity(data1))
  df <- data.frame(X=X,Y=Y)</pre>
  df <- na.omit(df)</pre>
  g <- ggplot(df,aes(X,Y)) + geom_line() + ggtitle('ROC Curve') +
    xlab('Specificity') + ylab('Sensitivity')
  height = (df\$Y[-1]+df\$Y[-length(df\$Y)])/2
  width = -diff(df$X)
  area = sum(height*width)
  return(list(Plot =g,AUC = area))
r <-ROC(score_class)
```

\$Plot



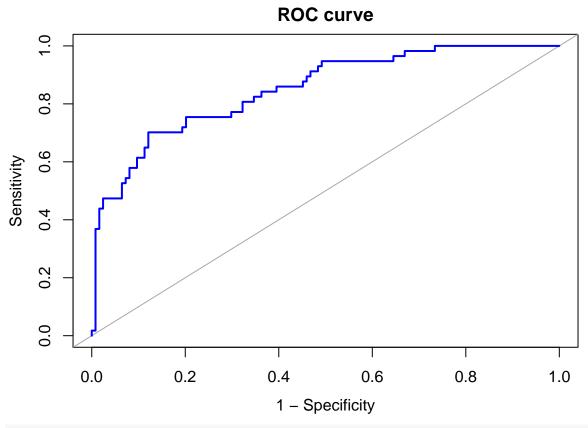


11. Matrix

list(accuracy=a, error_rate=e, precision=pre, sensitivity=sen, specificity=sp, F1=F1, Auc= r\$AUC)

```
## $accuracy
## [1] 0.8066298
##
## $error_rate
## [1] 0.1933702
## $precision
## [1] 0.84375
##
## $sensitivity
## [1] 0.4736842
##
## $specificity
## [1] 0.9596774
##
## $F1
## [1] 0.6067416
## $Auc
```

```
## [1] 0.8247029
 12. Investigate the "Caret" package
library(caret)
## Loading required package: lattice
##
## Attaching package: 'caret'
## The following objects are masked _by_ '.GlobalEnv':
##
##
       precision, sensitivity, specificity
confusionMatrix(as.factor(score_class$scored.class), as.factor(score_class$class), positive = "1")
## Confusion Matrix and Statistics
##
##
             Reference
## Prediction
               0
                  1
            0 119 30
##
##
               5 27
##
##
                  Accuracy : 0.8066
                    95% CI : (0.7415, 0.8615)
##
       No Information Rate : 0.6851
##
##
       P-Value [Acc > NIR] : 0.0001712
##
##
                     Kappa: 0.4916
   Mcnemar's Test P-Value: 4.976e-05
##
##
##
               Sensitivity: 0.4737
##
               Specificity: 0.9597
##
            Pos Pred Value: 0.8438
##
            Neg Pred Value: 0.7987
##
                Prevalence: 0.3149
##
            Detection Rate: 0.1492
##
      Detection Prevalence: 0.1768
##
         Balanced Accuracy: 0.7167
##
##
          'Positive' Class : 1
 13. Investigate the "pROC" package
library(pROC)
## Type 'citation("pROC")' for a citation.
##
## Attaching package: 'pROC'
## The following objects are masked from 'package:stats':
##
##
       cov, smooth, var
roc <- roc(score_class$class, score_class$scored.probability, plot=T, asp=NA, legacy.axes=T, main="ROC
```



roc["auc"]

\$auc

Area under the curve: 0.8503