DATA 621 HW2

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```
if (!require('ggplot2')) (install.packages('ggplot2'))
if (!require('caret')) (install.packages('caret'))
if (!require('pROC')) (install.packages('pROC'))
```

1. Download the classification output data set (attached in Blackboard to the assignment).

```
my_data <- read.csv('classification-output-data.csv', header=T)
head(my_data)
```

```
##   pregnant glucose diastolic skinfold insulin  bmi pedigree age class
## 1        7     124        70       33     215 25.5    0.161  37     0
## 2        2     122        76       27     200 35.9    0.483  26     0
## 3        3     107        62       13      48 22.9    0.678  23     1
## 4        1      91        64       24       0 29.2    0.192  21     0
## 5        4      83        86       19       0 29.3    0.317  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         0.05515460
```

2. The data set has three key columns we will use:

- class: the actual class for the observation
- scored.class: the predicted class for the observation (based on a threshold of 0.5)
- scored.probability: the predicted probability of success for the observation

Use the table() function to get the raw confusion matrix for this scored dataset. Make sure you understand the output. In particular, do the rows represent the actual or predicted class? The columns?

```
t <- table(my_data$scored.class, my_data$class)
knitr::kable(t)
```

	0	1
0	119	30
1	5	27

The rows represent the predicted class and the columns represent the actual class.

3. Write a function that takes the data set as a dataframe, with actual and predicted classifications identified, and returns the accuracy of the predictions.

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN}$$

Accuracy

```
a_fun <- function(df){
  df <- as.data.frame(table(my_data$scored.class, my_data$class))
  tp <- df$Freq[4]; fp <- df$Freq[2]; fn <- df$Freq[3]; tn <- df$Freq[1]
  accuracy <- ((tp + tn)/(tp + fp + tn + fn))
  return (accuracy)
}
a_fun(df)
```

```
## [1] 0.8066298
```

4. Write a function that takes the data set as a dataframe, with actual and predicted classifications identified, and returns the classification error rate of the predictions.

$$\text{Classification Error Rate} = \frac{FP + FN}{TP + FP + TN + FN}$$

Verify that you get an accuracy and an error rate that sums to one.

Classification Error Rate

```
err_fun <- function(df){
  df <- as.data.frame(table(my_data$scored.class, my_data$class))
  tp <- df$Freq[4]; fp <- df$Freq[2]; fn <- df$Freq[3]; tn <- df$Freq[1]
  error <- ((fp + fn)/(tp + fp + tn + fn))
  return (error)
}
err_fun(df)
```

```
## [1] 0.1933702
```

Varify

Accuracy + Classification Error Rate = 1

5. Write a function that takes the data set as a dataframe, with actual and predicted classifications identified, and returns the precision of the predictions.

$$Precision = \frac{TP}{TP + FP}$$

Precision

```
prec_fun <- function(df){
  df <- as.data.frame(table(my_data$scored.class, my_data$class))
  tp <- df$Freq[4]; fp <- df$Freq[2]
  prec <- tp/(tp + fp)
  return (prec)
}
prec_fun(df)
```

```
## [1] 0.84375
```

6. Write a function that takes the data set as a dataframe, with actual and predicted classifications identified, and returns the sensitivity of the predictions. Sensitivity is also known as recall.

$$Sensitivity = \frac{TP}{TP + FN}$$

Sensitivity

```
sen_fun <- function(df){
  df <- as.data.frame(table(my_data$scored.class, my_data$class))
  tp <- df$Freq[4]; fn <- df$Freq[3]
  sen <- tp/(tp + fn)
  return (sen)
}
sen_fun(df)
```

```
## [1] 0.4736842
```

7. Write a function that takes the data set as a dataframe, with actual and predicted classifications identified, and returns the specificity of the predictions.

$$Specificity = \frac{TN}{TN + FP}$$

Specificity

```
spec_fun <- function(df){
  df <- as.data.frame(table(my_data$scored.class, my_data$class))
  fp <- df$Freq[2]; tn <- df$Freq[1]
  spec <- tn/(tn + fp)
  return (spec)
}
spec_fun(df)
```

```
## [1] 0.9596774
```

8. Write a function that takes the data set as a dataframe, with actual and predicted classifications identified, and returns the F1 score of the predictions.

$$F1\ Score = \frac{2 \times Precision \times Sensitivity}{Precision + Sensitivity}$$

F1 Score

```
f1_fun <- function(df){
  df <- as.data.frame(table(my_data$scored.class, my_data$class))
  tp <- df$Freq[4]; fp <- df$Freq[2]; fn <- df$Freq[3]
  prec <- tp/(tp + fp); sen <- tp/(tp + fn)
  f1 <- (2 * prec * sen) / (prec + sen)
  return (f1)
}
f1_fun(df)
```

```
## [1] 0.6067416
```

9. Before we move on, let's consider a question that was asked: What are the bounds on the F1 score? Show that the F1 score will always be between 0 and 1. (Hint: If 0 < a < 1 and 0 < b < 1 then ab < a).

Since F1 score is a function of precision and sensitivity which are themselves bounded between 0 and 1, the solution to equation, $F1\ Score = \frac{2 \times Precision \times Sensitivity}{Precision + Sensitivity}$ will always be between 0 and 1.

e.g.

```r
set.seed(1023)
prec <- runif(50, 0, 1)
sen <- runif(50, 0, 1)
f1 <- (2 * prec * sen) / (prec + sen)
result <- summary(f1)
c(result[1], result[6])
```

```
##    Min.    Max.
## 0.03142 0.92510
```

10. Write a function that generates an ROC curve from a data set with a true classification column (class in our example) and a probability column (scored.probability in our example). Your function should return a list that includes the plot of the ROC curve and a vector that contains the calculated area under the curve (AUC). Note that I recommend using a sequence of thresholds ranging from 0 to 1 at 0.01 intervals.

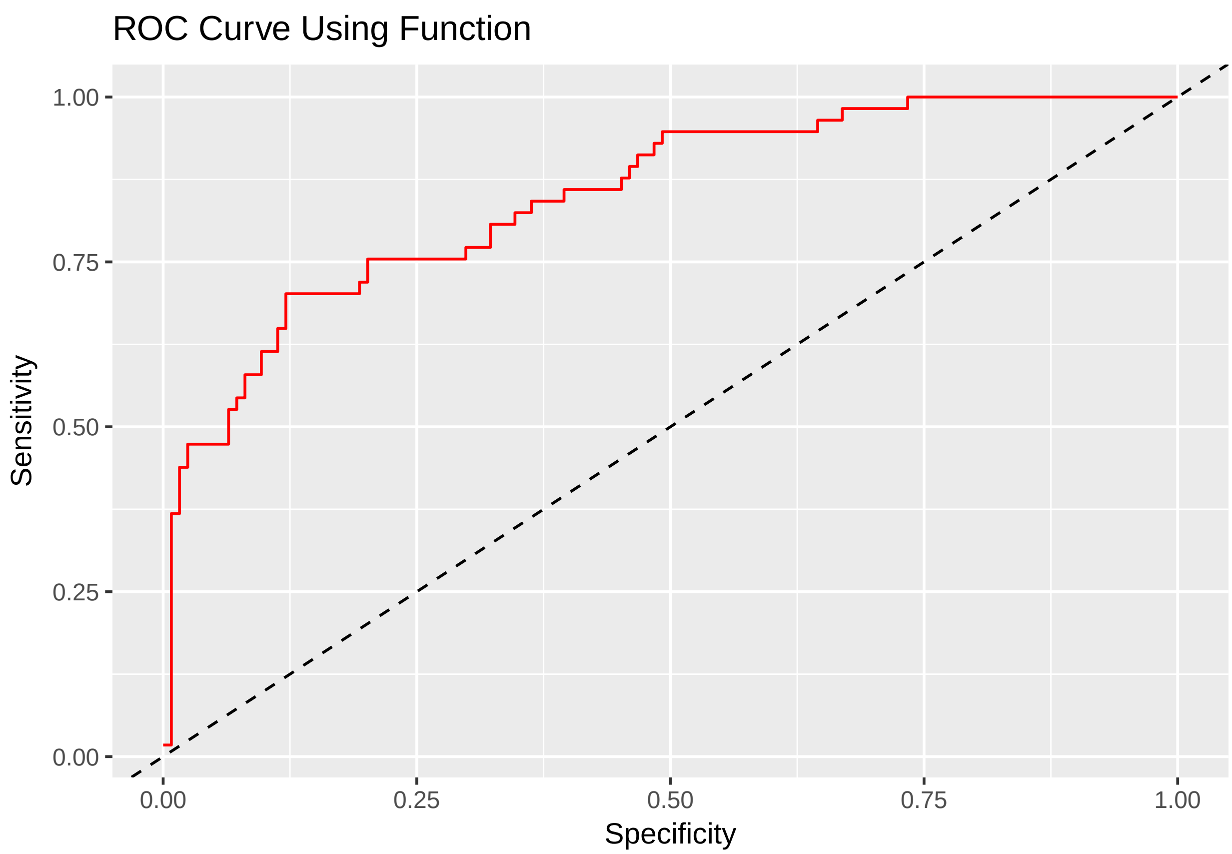
```r
my_roc <- function(class, results){
  class <- class[order(results, decreasing=TRUE)]
  df <- data.frame(TPR=(cumsum(class)/sum(class)), FPR=(cumsum(!class)/sum(!class)), class)

  dFPR <- c(diff(df$FPR), 0)
  dTPR <- c(diff(df$TPR), 0)
  AUC <- sum(df$TPR * dFPR) + sum(dTPR * dFPR) / 2

  results <- list(df, AUC)
  return(results)
}

my_roc_auc <- my_roc(my_data$class, my_data$scored.probability)
my_roc_results <- my_roc_auc[[1]]
auc <- my_roc_auc[[2]]

ggplot(my_roc_results, aes(FPR, TPR)) +
  geom_line(color='red') +
  labs(title = "ROC Curve Using Function" , x = "Specificity", y = "Sensitivity") +
  geom_abline(linetype=2)
```




```
auc
```

```
## [1] 0.8503113
```

```
# reference: http://blog.revolutionanalytics.com/2016/08/roc-curves-in-two-lines-of-code.html
           # http://blog.revolutionanalytics.com/2016/11/calculating-auc.html
```

11. Use your **created R functions** and the provided classification output data set to produce all of the classification metrics discussed above.

```
Classification <- c('Accuracy','Classification Error Rate', 'Precision',
                    'Sensitivity','Specificity', 'F1 Score')
Results <- round(c(a_fun(df), err_fun(data), prec_fun(df), sen_fun(df),
                   spec_fun(df), f1_fun(df)),4)
df1 <- as.data.frame(cbind(Classification, Results))
knitr::kable(df1)
```

Classification	Results
Accuracy	0.8066
Classification Error Rate	0.1934
Precision	0.8438
Sensitivity	0.4737
Specificity	0.9597
F1 Score	0.6067

12. Investigate the **caret** package. In particular, consider the functions confusionMatrix, sensitivity, and specificity. Apply the functions to the data set. How do the results compare with your own functions?

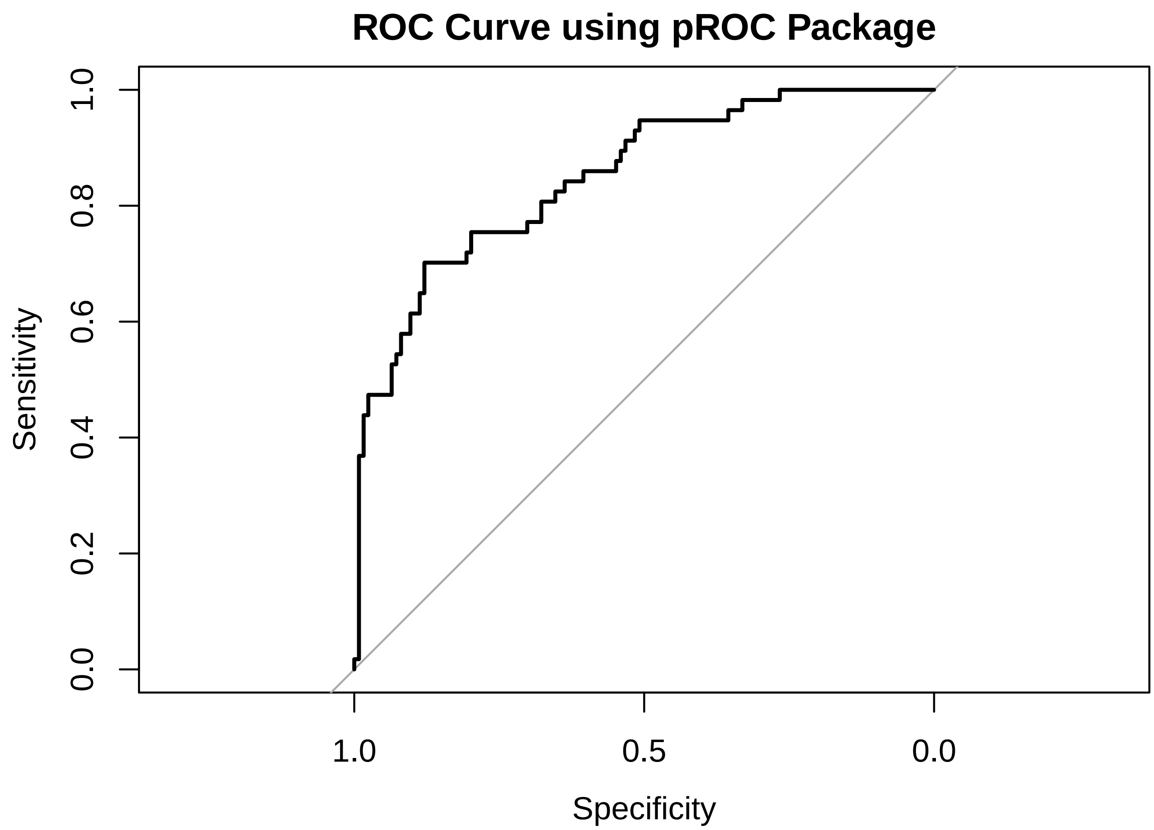
```r
confusionMatrix(my_data$scored.class, my_data$class, positive="1")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 119  30
##          1   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
##
```

The caret package result and my results are the same.

13. Investigate the **pROC** package. Use it to generate an ROC curve for the data set. How do the results compare with your own functions?

```r
r_curve <- roc(my_data$class~my_data$scored.probability)
plot(r_curve, main= "ROC Curve using pROC Package")
```




```r
auc(roc(my_data$class, my_data$scored.probability))
```

```
## Area under the curve: 0.8503
```

The results are exact match with my functions.