CIA LAB EXAM

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4/30/2021

Problem Description

The DublinTest is the provided Binary Classification dataset, where we have to classify the Target label 'Outcome' using other 7 variables namely BloodPressure, RBS, FBS, Serum.Insulin, BMI, BUN, and Age. Initailly we have to do neccessary Exploratory data analysis work to sort messy data and furture proceeding with feature seletions to get appropriate features to classify our dataset.

Dataset Understanding

The DublinTest dataset has 8 variables with 680 observations, considered to be an Binary Classification dataset sicne it's consists of 1 Target column and 7 Regresses.

Blood Pressure: This records the systolic blood pressure in the arteries when the heartbeats.

RBS: Random Blood Sugar testing measures the levels of glucose in the blood at any given point in the day.

FBS: Fasting Blood sugar measures your blood sugar after an overnight fast.

Serum Insulin: Insulin test, used to measure the amount of insulin in the body.

BMI: Body Mass Index is a reliable indicator of body fatness.

BUN: Blood Urea Nitrogen level of the person.

Age: Age of the patient.

Outcome: class variable

1. Import the DublinTest Dataset and load the necessary packages.

```
library(RColorBrewer)  # color
library(funModeling)   # histogram
```

```
## Loading required package: Hmisc
```

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

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

```
## Loading required package: Formula
```

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

```
##
## Attaching package: 'Hmisc'

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

## funModeling v.1.9.4 :)
## Examples and tutorials at livebook.datascienceheroes.com
##  / Now in Spanish: librovivodecienciadedatos.ai

library(Amelia)        # missmap

## Loading required package: Rcpp

## ##
## ## Amelia II: Multiple Imputation
## ## (Version 1.7.6, built: 2019-11-24)
## ## Copyright (C) 2005-2021 James Honaker, Gary King and Matthew Blackwell
## ## Refer to http://gking.harvard.edu/amelia/ for more information
## ##

library(tidyverse)     # duplicate values

## ── Attaching packages
──────────────────────────────────────────────────────────────────────
──────────────────────────────────────────────────────────────────────
──────── tidyverse 1.3.0 ──

## ✓ tibble  3.0.3     ✓ dplyr   1.0.4
## ✓ tidyr   1.1.1     ✓ stringr 1.4.0
## ✓ readr   1.4.0     ✓ forcats 0.5.1
## ✓ purrr   0.3.4

## ── Conflicts
──────────────────────────────────────────────────────────────────────
──────────────────────────────────────────────────────────────────────
─────────── tidyverse_conflicts() ──
## x dplyr::filter()    masks stats::filter()
## x dplyr::lag()       masks stats::lag()
## x dplyr::src()       masks Hmisc::src()
## x dplyr::summarize() masks Hmisc::summarize()

library(mice)          # impute missing values

##
## Attaching package: 'mice'

## The following object is masked from 'package:stats':
##
##     filter
```

```
## The following objects are masked from 'package:base':
##
##     cbind, rbind

library(caret)         # Classification and regression

##
## Attaching package: 'caret'

## The following object is masked from 'package:purrr':
##
##     lift

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

library(randomForest)  # Random forest

## randomForest 4.6-14

## Type rfNews() to see new features/changes/bug fixes.

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:dplyr':
##
##     combine

## The following object is masked from 'package:ggplot2':
##
##     margin

library(dplyr)         # Remove duplicate rows
library(e1071)

##
## Attaching package: 'e1071'

## The following object is masked from 'package:Hmisc':
##
##     impute

dataset <- read.csv("DublinTest dataset.csv")
head(dataset)

##   BloodPressure RBS FBS Serum.Insulin  BMI   BUN Age Outcome
## 1           117  92   0             0 34.1 0.337  38       0
## 2           109  75  26             0 36.0 0.546  60       0
## 3           158  76  36           245 31.6 0.851  28       1
## 4            88  58  11            54 24.8 0.267  22       0
```

```
## 5            92  92   0              0 19.9 0.188  28       0
## 6           122  78  31              0 27.6 0.512  45       0
```

2.Explore the Descriptive Analysis and visualize the data using plots

```
# Dimension of dataset

dim(dataset)

## [1] 681   8
```

Insights

```
  - The DublinTest dataset has 8 variables with 680 observations
  - All the 8 variables are numberical in nature.
```

```
# Check data structure

str(dataset)

## 'data.frame':    681 obs. of  8 variables:
##  $ BloodPressure: int  117 109 158 88 92 122 103 138 102 90 ...
##  $ RBS          : int  92 75 76 58 92 78 60 76 76 68 ...
##  $ FBS          : int  0 26 36 11 0 31 33 0 37 42 ...
##  $ Serum.Insulin: int  0 0 245 54 0 0 192 0 0 0 ...
##  $ BMI          : num  34.1 36 31.6 24.8 19.9 27.6 24 33.2 32.9 38.2 ...
##  $ BUN          : num  0.337 0.546 0.851 0.267 0.188 0.512 0.966 0.42
0.665 0.503 ...
##  $ Age          : int  38 60 28 22 28 45 33 35 46 27 ...
##  $ Outcome      : int  0 0 1 0 0 0 0 0 1 1 ...
```

Insights

```
  - BloodPressure,  RBS,    FBS,    Serum, Insulin, Age, and    Outcome are
Numberic and Discrite in nature.
  - BMI and BUN are Numberic and countinuous in nature.
  - Clearnly, Outcome is our Target classification variable
```

```
# Check data structure

summary(dataset)

##  BloodPressure        RBS              FBS        Serum.Insulin
##  Min.   :  0.0   Min.   :  0.0   Min.   : 0.00   Min.   :  0.00
##  1st Qu.: 99.0   1st Qu.: 64.0   1st Qu.: 0.00   1st Qu.:  0.00
##  Median :117.0   Median : 72.0   Median :23.00   Median : 30.50
##  Mean   :120.9   Mean   : 69.1   Mean   :20.64   Mean   : 80.05
##  3rd Qu.:141.0   3rd Qu.: 80.0   3rd Qu.:32.25   3rd Qu.:125.00
##  Max.   :198.0   Max.   :122.0   Max.   :99.00   Max.   :846.00
##  NA's   :1       NA's   :1       NA's   :1       NA's   :1
##       BMI             BUN              Age           Outcome
##  Min.   : 0.00   Min.   :0.0780   Min.   :21.00   Min.   :0.0000
##  1st Qu.:27.30   1st Qu.:0.2487   1st Qu.:24.00   1st Qu.:0.0000
##  Median :32.00   Median :0.3815   Median :30.00   Median :0.0000
```

```
##  Mean   :32.05   Mean   :0.4782   Mean   :33.59   Mean   :0.3632
##  3rd Qu.:36.60   3rd Qu.:0.6275   3rd Qu.:41.00   3rd Qu.:1.0000
##  Max.   :67.10   Max.   :2.4200   Max.   :81.00   Max.   :1.0000
##  NA's   :1       NA's   :1        NA's   :1       NA's   :1
```

Insights

- Summary is used to get basic stastistical report for all the 8 variables.
- BloodPressure has the 0.0 value as minimum, and 198 value as maximum.
- RBS has the 0.0 value as minimum, and 122 value as maximum.
- FBS has the 0.0 value as minimum, and 99 value as maximum.
- Serum.Insulin has the 0.0 value as minimum, and 846 value as maximum.
- BMI has the 0.0 value as minimum, and 67 value as maximum.
- BUN has the 0.0780 value as minimum, and 2.4200 value as maximum.
- Age has the 21.0 value as lowest, and 81 value as maximum.
- Outcome has 0 and 1 as class label value.

```
# Total missing count

colSums(is.na(dataset))
```

```
## BloodPressure           RBS           FBS Serum.Insulin           BMI
##             1             1             1             1             1
##           BUN           Age       Outcome
##             1             1             1
```

Insights

- All the variables having 1 NULL values in the DublinTest dataset.

```
dataset = na.omit(dataset)

# Total missing count

colSums(is.na(dataset))
```

```
## BloodPressure           RBS           FBS Serum.Insulin           BMI
##             0             0             0             0             0
##           BUN           Age       Outcome
##             0             0             0
```

```
#Checking for Empty Values

colSums(dataset=='')
```

```
## BloodPressure           RBS           FBS Serum.Insulin           BMI
##             0             0             0             0             0
##           BUN           Age       Outcome
##             0             0             0
```

Insights

```
  - Zero Empty Values values in the DublinTest dataset.


#Checking for Duplicate values

duplicated(dataset)
```

```
##   [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
##  [13] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
##  [25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
##  [37] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
##  [49] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
##  [61] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
##  [73] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
##  [85] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [433] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [445] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [457] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [469] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [481] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [493] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [505] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [517] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [577] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [589] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [601] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [613] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [625] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
```

```
## [637] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
FALSE
## [649] FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
TRUE
## [661]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
TRUE
## [673]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
```

Insights

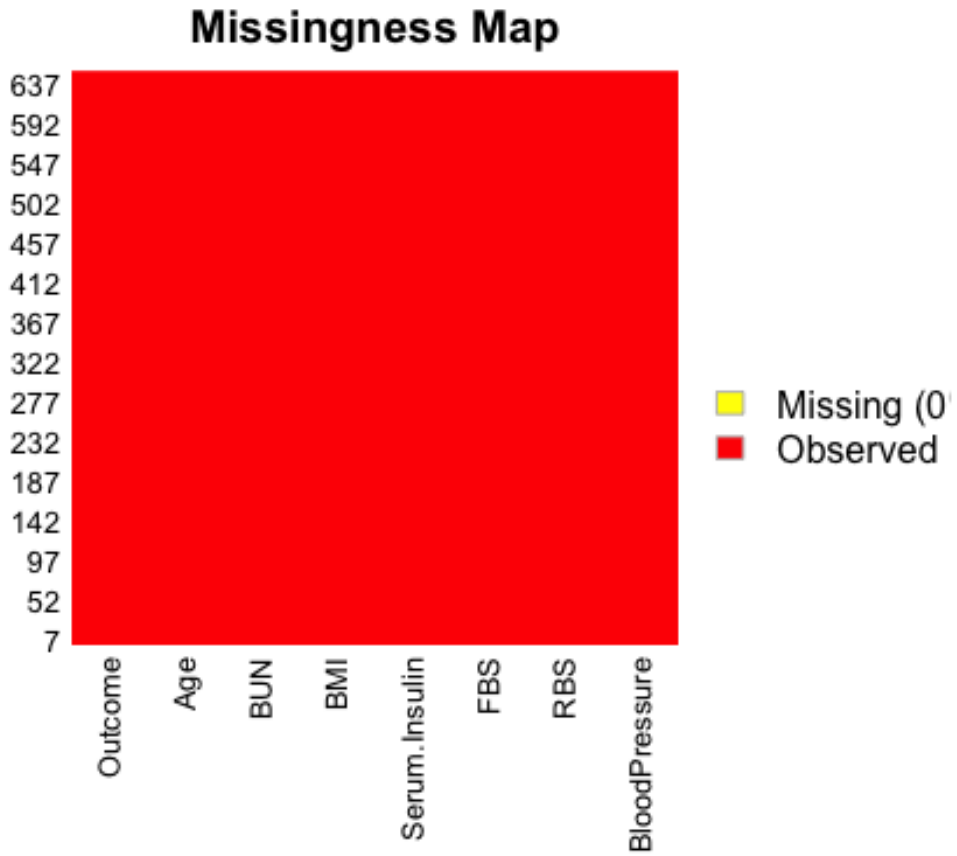
```
  - Clearly, we found 28 duplicated instance in the DublinTest dataset.
```

```
dataset = unique(dataset)
```

Insights

```
  - dplyr library is used to remove duplicate in the dataset.
  - To extract unique elements from the data frames: unique(datadet) is used.
```

```
# Missing value imputation

missmap(dataset,col=c("yellow","red"))
```



Insights

```
  - From the above chart it's clear that we don't have any missing values in
the DublinTest dataset
```

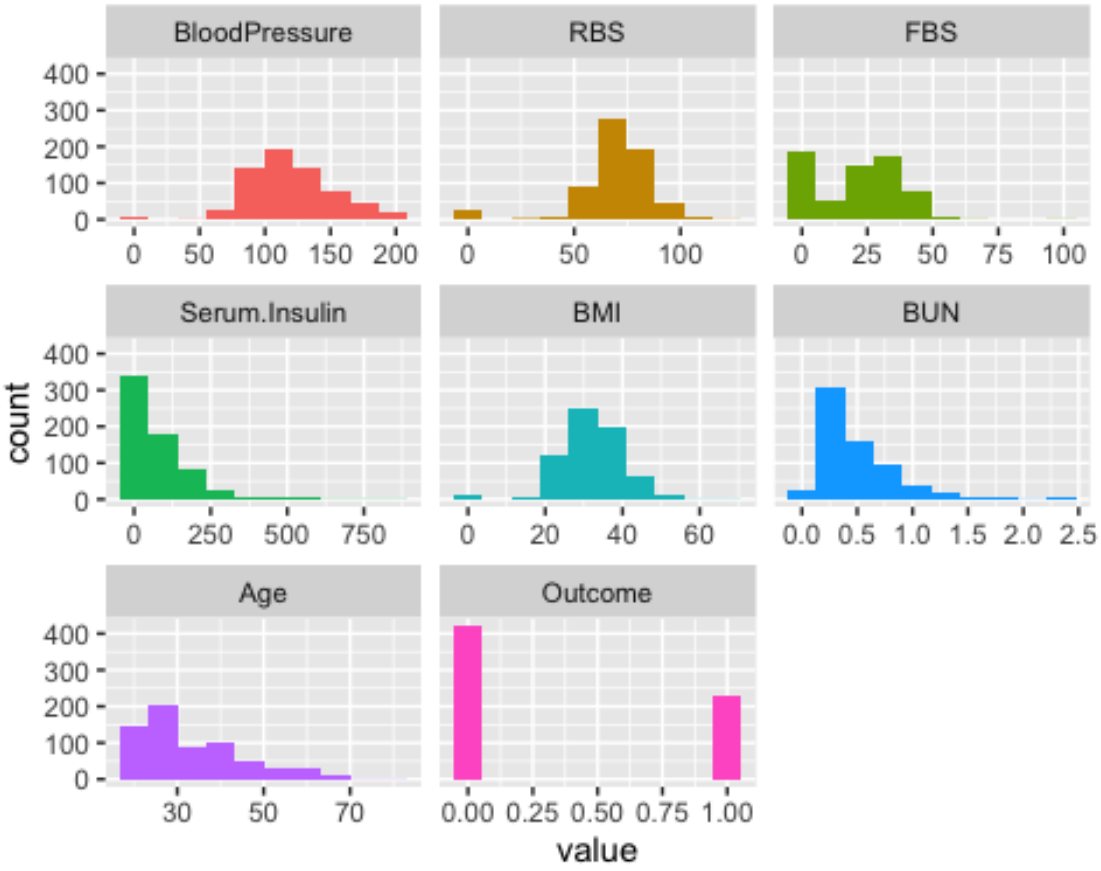
```
# To find the unique values in each column.

apply(dataset,2,function(x) length(unique(x)))
```

```
## BloodPressure           RBS           FBS Serum.Insulin           BMI
##           133            44            51           171           237
##           BUN           Age       Outcome
##           461            50             2
```

Insights

- From the above stastistical table we can find the unique values in each column.
- We can convert the Outcome class label column to factor since it's having only 2 distinct value

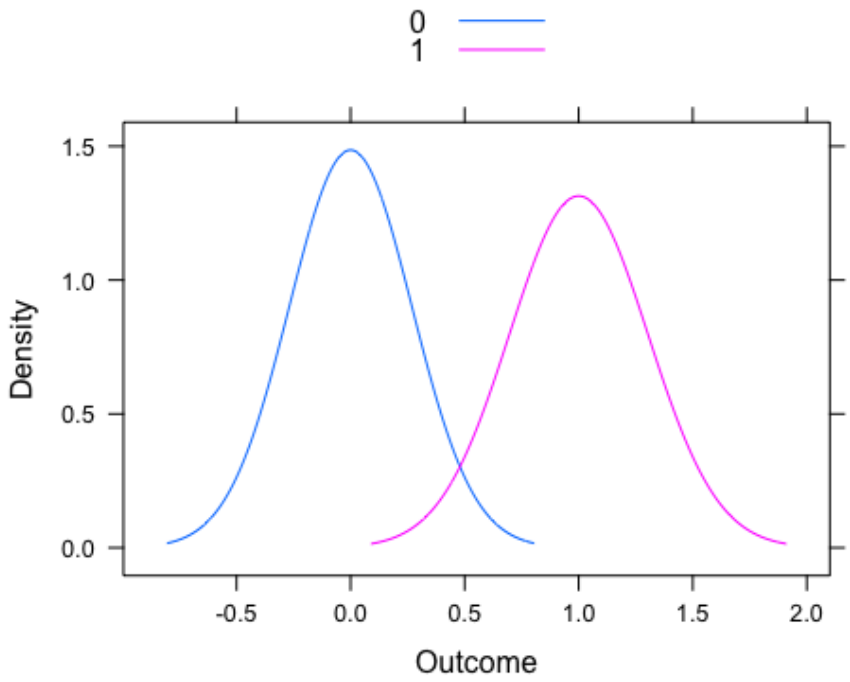
```
# Distribution of all the variables

plot_num(dataset)
```



Insights

- Blood Pressure is normally distributed.
- Serum Insulin, BUN, and Age is rightly skewed and showing possitive

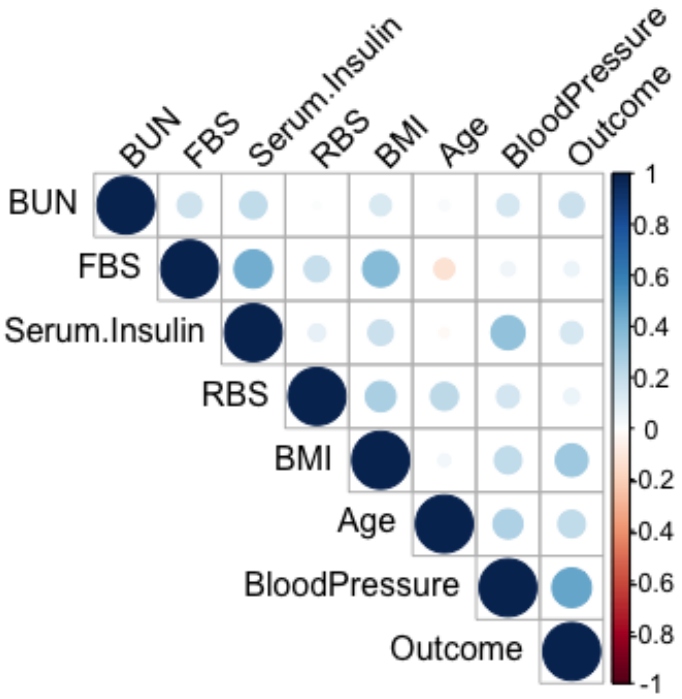
```
intent.
  - BMI, RBS, FBS are not normally distributed.

densityplot(~ Outcome, data =dataset,
            plot.points = FALSE,
            groups = Outcome,
            auto.key = TRUE)
```



Insights

```
  - Both the outomes are normally distributed.


# Compute correlation matrix
library(corrplot)

## corrplot 0.84 loaded

library(ggplot2)
library(reshape2)

##
## Attaching package: 'reshape2'

## The following object is masked from 'package:tidyr':
##
##     smiths
```

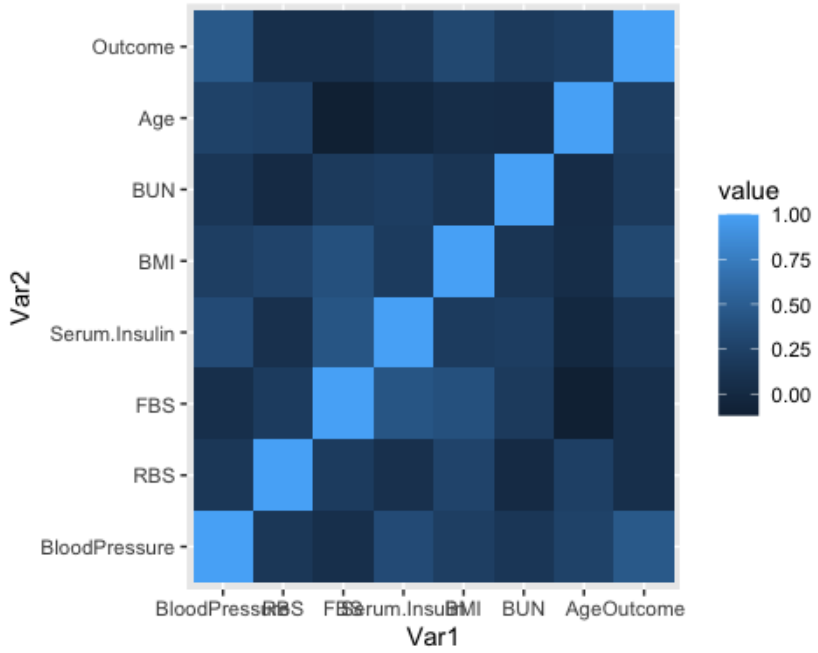
```
res <- cor(dataset)
corrplot(res, type = "upper", order = "hclust", tl.col = "black", tl.srt =
45)
```



Insights

```
  - BloodPressure and BMI having strong correlation value towards Outcome.
  - FBS and RBS having less correlation strenght while comparing with other
values.

library(GGally)

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

##
## Attaching package: 'GGally'

## The following object is masked from 'package:funModeling':
##
##     range01

ggcorr(dataset,label=T)
```


```
#Correlation Heat Map

cormat <- round(cor(dataset),2)
melted_cormat <- melt(cormat)
ggplot(data = melted_cormat, aes(x=Var1, y=Var2, fill=value)) + geom_tile()
```



Insights

```
  - Most of the columns were seems to be similar in shardings, so multi-
collinearity needs to validated.
```

Feature Selection

Checking for multi-collinearity using variance inflation factor

```
library(car)
```

```
## Loading required package: carData
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
##     recode
```

```
## The following object is masked from 'package:purrr':
##     some
```

```
lrm <- lm(dataset$Outcome~.,data=dataset)
vif(lrm)
```

```
## BloodPressure           RBS           FBS Serum.Insulin           BMI
##      1.299704      1.167541      1.496838      1.435367      1.285522
##           BUN           Age
##      1.072691      1.161110
```

Insights

```
  - Since all the variance inflation factor are less than 5, we can conclude
that there exist no Multi-Collinearity
```

```
dataset = subset(dataset, select = -c( RBS, FBS) )
head(dataset)
```

```
##   BloodPressure Serum.Insulin  BMI   BUN Age Outcome
## 1           117             0 34.1 0.337  38       0
## 2           109             0 36.0 0.546  60       0
## 3           158           245 31.6 0.851  28       1
## 4            88            54 24.8 0.267  22       0
## 5            92             0 19.9 0.188  28       0
## 6           122             0 27.6 0.512  45       0
```

```
# Converting Class label to Factor

dataset$Outcome=as.factor(dataset$Outcome)
```

3. Split your data set into training and test data

```
# Data Splitting

set.seed(52)

index <- createDataPartition(dataset$Outcome, p=0.80, list=FALSE)
train <- dataset[index,]      #Train data : 80%
test<- dataset[-index,]       #Test data : 20%
```

Insights

```
  - Here, our dataset is splitted into 8:2 ratio.
  - 80 % of Training data
  - 20 % of Testing data
```

4. Use any two machine learning algorithms to build your model

Decision tree

Decision tree works with both regression and classification problem. Since in dataset target variable has two values 0 and 1 that is its binary classification problem. A Decision tree is nothing but the graphical representation of solutions based on the certain conditions.One disadvantage of using this model is that its generally overfilling.

```
# Implementing Decision Tree

model_rpart<-train(Outcome~.,
                   test,
                   method='rpart')
prediction=predict.train(model_rpart,
                         test,
                         type="raw")
confusionMatrix(table(predict(model_rpart,test),
                      test$Outcome))

## Confusion Matrix and Statistics
##
##      0  1
##   0 81 31
##   1  3 14
##
##                Accuracy : 0.7364
##                  95% CI : (0.6516, 0.8101)
##     No Information Rate : 0.6512
##     P-Value [Acc > NIR] : 0.02437
##
##                   Kappa : 0.3219
##
##  Mcnemar's Test P-Value : 3.649e-06
##
##             Sensitivity : 0.9643
##             Specificity : 0.3111
```

```
##          Pos Pred Value : 0.7232
##          Neg Pred Value : 0.8235
##              Prevalence : 0.6512
##          Detection Rate : 0.6279
##    Detection Prevalence : 0.8682
##       Balanced Accuracy : 0.6377
##
##        'Positive' Class : 0
##
```

Insights

```
  - Accuracy : 0.7364*
```

```
# Using another evaluation error metrics ROC curve.
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
```

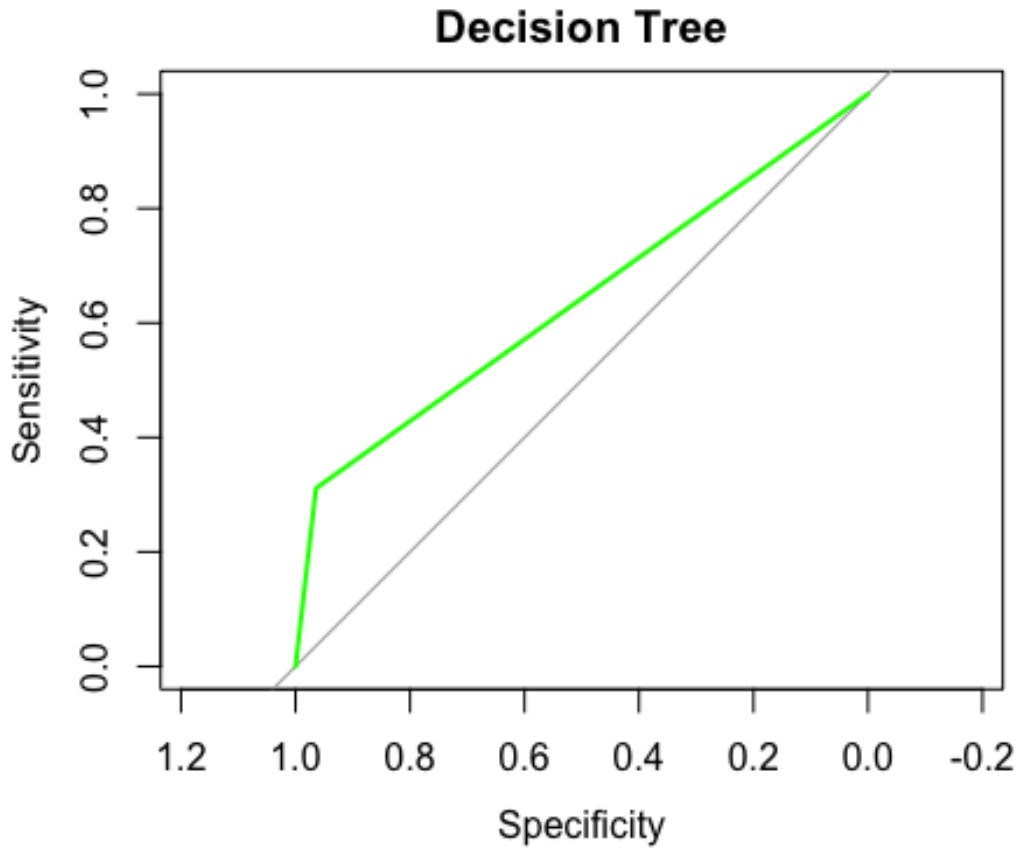
```
##
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
for_auc=predict(model_rpart,
                test,
                type="prob")

plot(roc(test$Outcome,for_auc[,2]),
     main="Decision Tree",
     col="green")
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```



SVM

Support vector machine(SVM) are supervised learning models with associated learning algorithms that analyze data used for classification and regression analysis. It is mostly used in classification problems. In this algorithm, each data item is plotted as a point in n-dimensional space (where n is number of features), with the value of each feature being the value of a particular coordinate. Then, classification is performed by finding the hyper-plane that best differentiates the two classes.

```
train[["Outcome"]] = factor(train[["Outcome"]])
trctrl <- trainControl(method = "repeatedcv", number = 10, repeats = 3)

#Building the model
svm_Linear <- train(Outcome ~., data = train, method = "svmLinear",
trControl=trctrl,
preProcess = c("center", "scale"),
tuneLength = 10)

#Model Summary
svm_Linear
```

```
## Support Vector Machines with Linear Kernel
##
## 523 samples
##   5 predictor
##   2 classes: '0', '1'
##
## Pre-processing: centered (5), scaled (5)
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 471, 471, 470, 471, 471, 470, ...
## Resampling results:
##
##   Accuracy   Kappa
##   0.7859223  0.4989604
##
## Tuning parameter 'C' was held constant at a value of 1
```

Insights

```
  - Accuracy : 0.7859223
```

Random Forest Model

```
  Random Forest also works with both Regression and Classification problems.
It builds a number of the Decision tree and adds them together to get a more
effective result. It can also be used for variable importance estimation.
Random Forest is a good choice if the model is suffering from the High
Variance problem.


#  Implementing random Forest.

set.seed(52)

model_rf<-train(Outcome~.,
                train,
                method='rf')
prediction=predict.train(model_rf,
                         train,
                         type="raw")
confusionMatrix(table(predict(model_rf,train),
                      train$Outcome))

## Confusion Matrix and Statistics
##
##
##       0   1
##   0 339   0
##   1   0 184
##
##                Accuracy : 1
##                  95% CI : (0.993, 1)
##     No Information Rate : 0.6482
```

```
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 1
##
##  Mcnemar's Test P-Value : NA
##
##             Sensitivity : 1.0000
##             Specificity : 1.0000
##          Pos Pred Value : 1.0000
##          Neg Pred Value : 1.0000
##              Prevalence : 0.6482
##          Detection Rate : 0.6482
##    Detection Prevalence : 0.6482
##       Balanced Accuracy : 1.0000
##
##        'Positive' Class : 0
##
```

Insights

```
  - Accuracy : 1
```

CONCLUSION

```
  - After doing the neccessary pre-processing work and modeling. Results
clearly show that Random Forest performs better than a Decision Tree. Also
pre-processing help us in avoiding errors. There are other packages also
those help R users for data wrangling and statistical analysis without doing
complex coding, but by studying caret package came to know that this one
package is enough to building machine learning system.
  - We got, 73 % of accuracy score from Decision Tree, where as Random Forest
provided almost 99 % of accuracy score.
  - Even through Random forest giving good result, its overfitting.
```