MINI PROJECT

PROJECT TOPIC : Prediction and Analysis on Diabetes Dataset

Project Description :

The system will allow us to predict if the patient has diabetes on the basis of certain diagnostic measures available in the dataset. The different steps involved in EDA include: 1.Data Collection, 2.Data Cleaning and 3.Data Visualization. This project first conducts Exploratory Data Analysis (EDA) and data visualization on the diabetes dataset and then predict the diabetes.

Exploratory Data Analysis (EDA)

1. Descriptive statistics

Attribute type, Class distribution, Mean, Standard Deviation, Median, Quartile, Skewness, Correlation

2. Data Visualization

Histogram plot

Density plot

Box and Whisker plot

Bar plot

Missing data map

Pair-wise correlation plot

Prediction on Diabetes

We compare the performance for the following classifiers:

1. Logistic Regression

   Logistic regression is basically a supervised classification algorithm. In a classification problem, the target variable(or output), y, can take only discrete values for given set of features(or inputs), X.

2. Support Vector Machine (SVM)

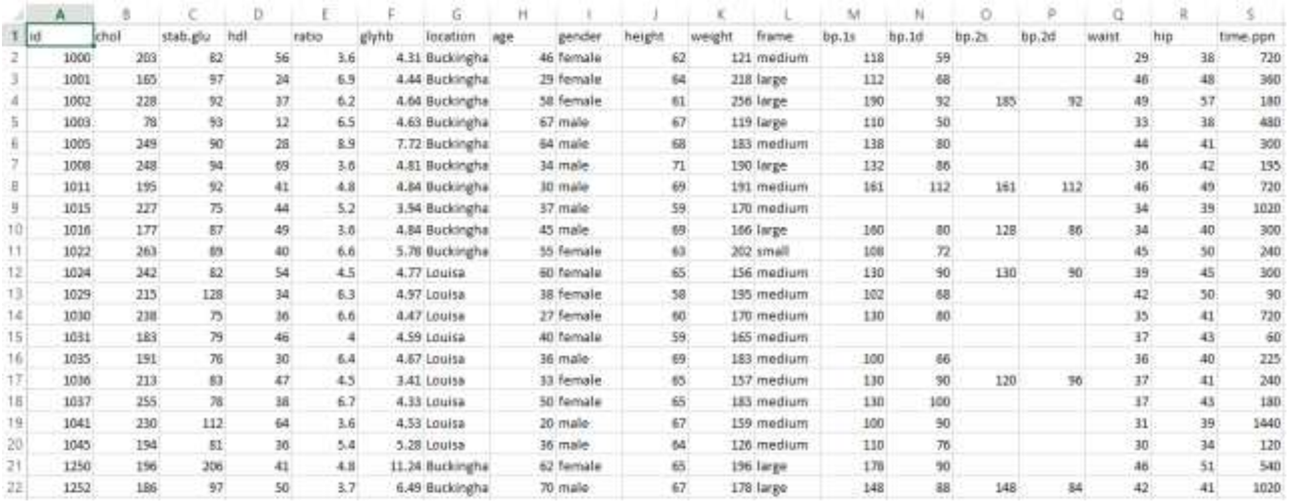
   “Support Vector Machine” (SVM) is a supervised machine learning algorithm which can be used for both classification or regression challenges. However, it is mostly used in classification problems. In the SVM algorithm, we plot each data item as a point in n-dimensional space (where n is number of features you have) with the value of each feature being the value of a particular coordinate. Then, we perform classification by finding the hyper-plane that differentiates the two classes very well

3. random Forest

The random forest algorithm works by aggregating the predictions made by multiple decision trees of varying depth. Every decision tree in the forest is trained on a subset of the dataset called the bootstrapped dataset.

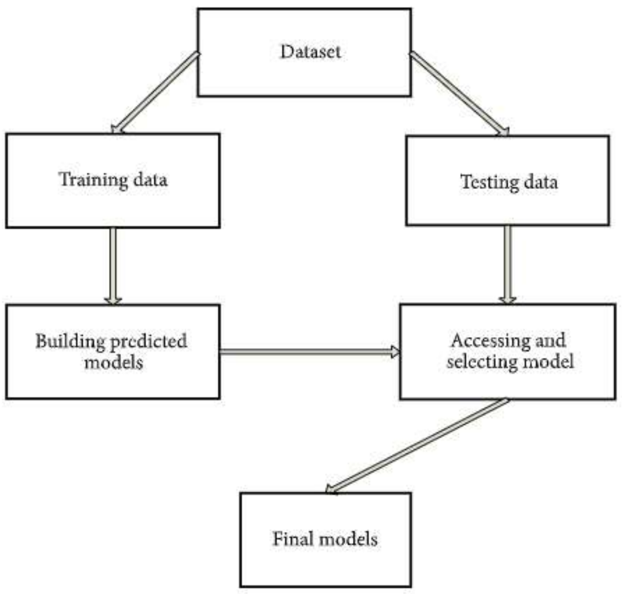
Dataset:

The dataset used in this study is downloaded from:
http://biostat.mc.vanderbilt.edu/wiki/Main/DataSets?CGISESSID=10713f6d891653ddcbb7ddbdd9cffb79



id	chol	stab.glu	hdl	ratio	glyhb	location	age	gender	height	weight	frame	bp.1s	bp.1d	bp.2s	bp.2d	waist	hip	time.ppn
1000	203	82	56	3.6	4.31	Buckingha	46	female	62	121	medium	118	59			29	38	720
1001	165	97	24	6.9	4.44	Buckingha	29	female	64	218	large	112	68			46	48	360
1002	228	92	37	6.2	4.64	Buckingha	58	female	61	256	large	190	92	185	92	49	57	180
1003	78	93	12	6.5	4.63	Buckingha	67	male	67	119	large	110	50			33	38	480
1005	249	90	28	8.9	7.72	Buckingha	64	male	68	183	medium	138	80			44	41	300
1008	248	94	69	3.6	4.81	Buckingha	34	male	71	190	large	132	86			36	42	195
1011	195	92	41	4.8	4.84	Buckingha	30	male	69	191	medium	161	112	161	112	46	49	720
1015	227	75	44	5.2	3.94	Buckingha	37	male	59	170	medium					34	39	1020
1016	177	87	49	3.6	4.84	Buckingha	45	male	69	166	large	160	80	128	86	34	40	300
1022	263	89	40	6.6	5.78	Buckingha	55	female	63	202	small	108	72			45	50	240
1024	242	82	54	4.5	4.77	Louisa	60	female	65	156	medium	130	90	130	90	39	45	300
1029	215	128	34	6.3	4.97	Louisa	38	female	58	195	medium	102	68			42	50	90
1030	238	75	36	6.6	4.47	Louisa	27	female	60	170	medium	130	80			35	41	720
1031	183	79	46	4	4.59	Louisa	40	female	59	165	medium					37	43	60
1035	191	76	30	6.4	4.67	Louisa	36	male	69	183	medium	100	66			36	40	225
1036	213	83	47	4.5	3.41	Louisa	33	female	65	157	medium	130	90	120	96	37	41	240
1037	255	78	38	6.7	4.33	Louisa	50	female	65	183	medium	130	100			37	43	180
1041	230	112	64	3.6	4.53	Louisa	20	male	67	159	medium	100	90			31	39	1440
1045	194	81	36	5.4	5.28	Louisa	36	male	64	126	medium	110	76			30	34	120
1250	196	206	41	4.8	11.24	Buckingha	62	female	65	196	large	178	90			46	51	540
1252	186	97	50	3.7	6.49	Buckingha	70	male	67	178	large	148	88	148	84	42	41	1020

Our research dataset is divided into two parts; two-thirds of the data is used as a training set, and one-third of the dataset is defined as a testing set to evaluate the performance of several classifiers. All classifiers were fitted to the same training and testing data. The specific process is: .



Liabraries:

- **randomforest**
  randomForest implements Breiman's random forest algorithm (based on Breiman and Cutler's original Fortran code) for classification and regression. It can also be used in unsupervised mode for assessing proximities among data points.

- **Caret**
  The caret package (short for Classification And REgression Training) is a set of functions that attempt to streamline the process for creating predictive models. The package contains tools for:
  - data splitting
  - pre-processing
  - feature selection
  - model tuning using resampling
  - variable importance estimation
  - as well as other functionality.
  -

For EDA and Visualization Steps performed:
1. Load libraries
2. Load the data
3. Clean the data
4. Delete columns 15 and 16 due to many missing values and column 1 (id), column 7 (location) because they contain no useful information
5. Remove the row with missing values
6. Encode the class label (column 5): Glycosolated hemoglobin > 7.0 is taken as a positive diagnosis of diabetes
7. Encode the categorical data (column-7 gender)
8. Encode the categorical data (column-10 frame)
9. Descriptive statistics
10. Display the first 20 rows
11. Display the dimensions of the dataset
12. List types for each attribute
13. Distribution of the class labels
14. Summarize the dataset
15. Standard Deviations for the non-categorical columns
16. Perrom other operations like: Skewness, Correlation, and Visualization Plots

Predcition and Classification Steps performed:
1. Load libraries
2. Load the data
3. Clean the data
4. Delete columns 15 and 16 due to many missing values and column 1 (id), column 7 (location) because they contain no useful information
5. Remove the row with missing values
6. Encode the class label (column 5): Glycosolated hemoglobin > 7.0 is taken as a positive diagnosis of diabetes
7. Encode the categorical data (column-7 gender)

8. Encode the categorical data (column-10 frame)
9. Split the data into training and validation sets
10. Comparison among different classifiers
    1. Logistic Regression
    2. Support Vector Machine
    3. random forest
    4. Parameter tunning via grid search for random forest
11. Make predictions on the validation sets
12. Confusion matrix
13. Save the final classifier model into disk
14. Load the model from the disk
15. Make predictions using the loaded model
15. Make predictions using the loaded model

Output:

# Load libraries
library(randomForest)
library(caret)

# load the data
```
> filename="C:\\Users\\Tejal Chaudhary\\Desktop\\Exploratory-Data-Analysis
-and-Prediction-on-Diabetes-Dataset-using-R-master\\diabetes_data.csv"
> datasetRaw = read.csv(filename)
> print(head(datasetRaw))
    id chol stab.glu hdl ratio glyhb   location age gender height weight
frame bp.1s bp.1d bp.2s bp.2d
1 1000  203       82  56   3.6  4.31 Buckingham  46 female     62    121 m
edium   118     59    NA    NA
2 1001  165       97  24   6.9  4.44 Buckingham  29 female     64    218
large   112     68    NA    NA
3 1002  228       92  37   6.2  4.64 Buckingham  58 female     61    256
large   190     92   185    92
4 1003   78       93  12   6.5  4.63 Buckingham  67   male     67    119
large   110     50    NA    NA
5 1005  249       90  28   8.9  7.72 Buckingham  64   male     68    183 m
edium   138     80    NA    NA
6 1008  248       94  69   3.6  4.81 Buckingham  34   male     71    190
large   132     86    NA    NA
  waist hip time.ppn
1    29  38      720
2    46  48      360
3    49  57      180
4    33  38      480
5    44  41      300
6    36  42      195
# clean the data
> numColumns = dim(datasetRaw)[2]
> vector_NAs = rep(0, numColumns)
> for (i in 1:numColumns) {
+   vector_NAs[i] = sum(is.na(datasetRaw[,i]))
+
+ }
> print("The missing values in each column:")
[1] "The missing values in each column:"
> print(vector_NAs)
 [1]   0   1   0   1   1  13   0   0   0   5   1   0   5   5 262 262   2
2   3
```

# delete columns 15 and 16 due to many missing values

# delete column 1 (id), column 7 (location) because they contain no useful information

```
> print(dim(dataset))
[1] 403  15
# remove the row with missing values
> row.has.na <- apply(dataset, 1, function(x){any(is.na(x))})
> dataset = dataset[!row.has.na,]
> print(dim(dataset))
[1] 375  15
> print(head(dataset))
  chol stab.glu hdl ratio glyhb age gender height weight  frame bp.1s bp.1
d waist hip time.ppn
1  203       82  56   3.6  4.31  46 female     62    121 medium   118    5
9    29  38      720
2  165       97  24   6.9  4.44  29 female     64    218  large   112    6
8    46  48      360
3  228       92  37   6.2  4.64  58 female     61    256  large   190    9
2    49  57      180
4   78       93  12   6.5  4.63  67   male     67    119  large   110    5
0    33  38      480
5  249       90  28   8.9  7.72  64   male     68    183 medium   138    8
0    44  41      300
6  248       94  69   3.6  4.81  34   male     71    190  large   132    8
6    36  42      195
# encode the class label (column 5): Glycosolated hemoglobin  > 7.0 is tak
en as a positive diagnosis of diabetes.
> dataset[,5] = ifelse(dataset[,5] >= 7.0, 1, 0)
> dataset[,5] = factor(dataset[,5])
# encode the categorical data (column-7 gender)
> dataset[,7] = ifelse(dataset[,7] == "female", 0, 1)
> dataset[,7] = factor(dataset[,7])
# encode the categorical data (column-10 frame)
> dataset[,10] = ifelse(dataset[,10] == "small", 0, ifelse(dataset[,10] ==
"medium", 1,2) )
> dataset[,10] = factor(dataset[,10])
# Descriptive statistics %%%%%%
# display the first 20 rows
> print(head(dataset, n=20))
   chol stab.glu hdl ratio glyhb age gender height weight frame bp.1s bp.1
d waist hip time.ppn
1   203       82  56   3.6     0  46      0     62    121     1   118    5
9    29  38      720
2   165       97  24   6.9     0  29      0     64    218     2   112    6
8    46  48      360
3   228       92  37   6.2     0  58      0     61    256     2   190    9
2    49  57      180
4    78       93  12   6.5     0  67      1     67    119     2   110    5
0    33  38      480
5   249       90  28   8.9     1  64      1     68    183     1   138    8
0    44  41      300
6   248       94  69   3.6     0  34      1     71    190     2   132    8
6    36  42      195
7   195       92  41   4.8     0  30      1     69    191     1   161   11
2    46  49      720
9   177       87  49   3.6     0  45      1     69    166     2   160    8
0    34  40      300
10  263       89  40   6.6     0  55      0     63    202     0   108    7
2    45  50      240
11  242       82  54   4.5     0  60      0     65    156     1   130    9
0    39  45      300
12  215      128  34   6.3     0  38      0     58    195     1   102    6
8    42  50       90
13  238       75  36   6.6     0  27      0     60    170     1   130    8
0    35  41      720
15  191       76  30   6.4     0  36      1     69    183     1   100    6
6    36  40      225
16  213       83  47   4.5     0  33      0     65    157     1   130    9
0    37  41      240
17  255       78  38   6.7     0  50      0     65    183     1   130   10
0    37  43      180
```

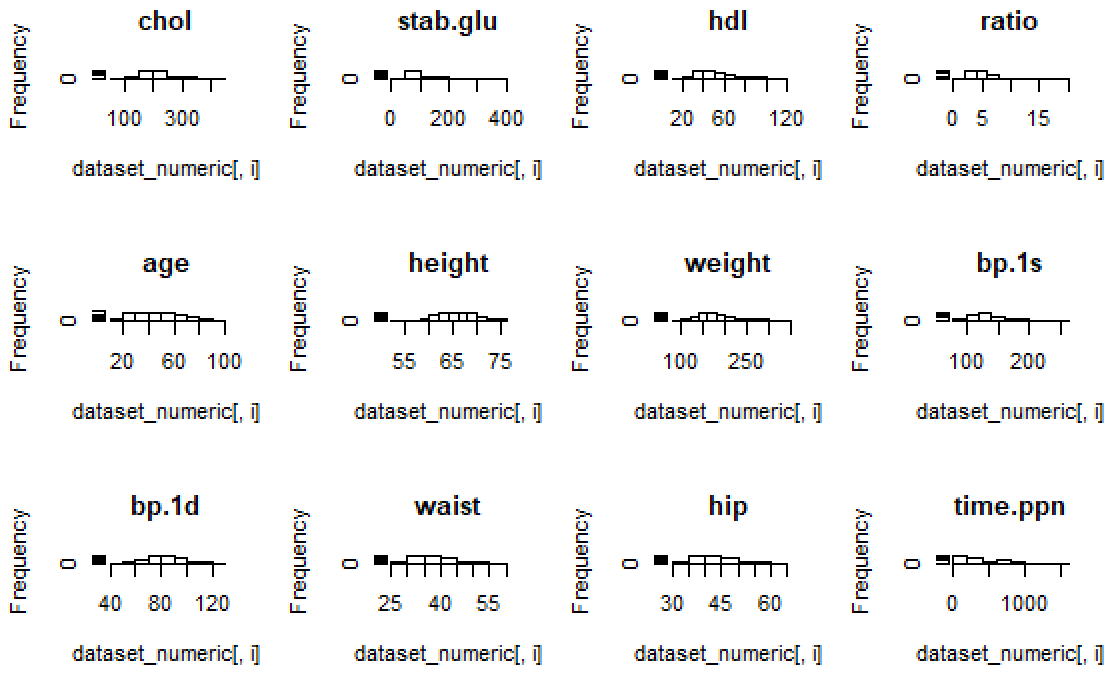
```
18  230       112  64   3.6      0  20        1      67     159      1   100     9
0    31  39      1440
19  194        81  36   5.4      0  36        1      64     126      1   110     7
6    30  34       120
20  196       206  41   4.8      1  62        0      65     196      2   178     9
0    46  51       540
21  186        97  50   3.7      0  70        1      67     178      2   148     8
8    42  41      1020
22  234        65  76   3.1      0  47        1      67     230      2   137    10
0    45  46       480

# display the dimensions of the dataset
> print(dim(dataset))
 [1] 375  15
> print(head(dataset))
  chol stab.glu hdl ratio glyhb age gender height weight  frame bp.1s bp.1
d waist hip time.ppn
1  203       82  56   3.6  4.31  46 female     62    121 medium   118     5
9    29  38       720
2  165       97  24   6.9  4.44  29 female     64    218  large   112     6
8    46  48       360
3  228       92  37   6.2  4.64  58 female     61    256  large   190     9
2    49  57       180
4   78       93  12   6.5  4.63  67   male     67    119  large   110     5
0    33  38       480
5  249       90  28   8.9  7.72  64   male     68    183 medium   138     8
0    44  41       300
6  248       94  69   3.6  4.81  34   male     71    190  large   132     8
6    36  42       195
> # encode the class label (column 5): Glycosolated hemoglobin  > 7.0 is t
aken as a positive diagnosis of diabetes.
> dataset[,5] = ifelse(dataset[,5] >= 7.0, 1, 0)
> dataset[,5] = factor(dataset[,5])
> # encode the categorical data (column-7 gender)
> dataset[,7] = ifelse(dataset[,7] == "female", 0, 1)
> dataset[,7] = factor(dataset[,7])
> # encode the categorical data (column-10 frame)
> dataset[,10] = ifelse(dataset[,10] == "small", 0, ifelse(dataset[,10] ==
"medium", 1,2) )
> dataset[,10] = factor(dataset[,10])
> # Descriptive statistics %%%%%%
> # display the first 20 rows
> print(head(dataset, n=20))
   chol stab.glu hdl ratio glyhb age gender height weight frame bp.1s bp.1
d waist hip time.ppn
1   203       82  56   3.6      0  46        0      62     121      1   118     5
9    29  38       720
2   165       97  24   6.9      0  29        0      64     218      2   112     6
8    46  48       360
3   228       92  37   6.2      0  58        0      61     256      2   190     9
2    49  57       180
4    78       93  12   6.5      0  67        1      67     119      2   110     5
0    33  38       480
5   249       90  28   8.9      1  64        1      68     183      1   138     8
0    44  41       300
6   248       94  69   3.6      0  34        1      71     190      2   132     8
6    36  42       195
7   195       92  41   4.8      0  30        1      69     191      1   161    11
2    46  49       720
9   177       87  49   3.6      0  45        1      69     166      2   160     8
0    34  40       300
10  263       89  40   6.6      0  55        0      63     202      0   108     7
2    45  50       240
11  242       82  54   4.5      0  60        0      65     156      1   130     9
0    39  45       300
12  215      128  34   6.3      0  38        0      58     195      1   102     6
8    42  50        90
13  238       75  36   6.6      0  27        0      60     170      1   130     8
0    35  41       720
```

```
15  191        76  30   6.4     0  36       1      69     183      1   100     6
6    36  40        225
16  213        83  47   4.5     0  33       0      65     157      1   130     9
0    37  41        240
17  255        78  38   6.7     0  50       0      65     183      1   130    10
0    37  43        180
18  230       112  64   3.6     0  20       1      67     159      1   100     9
0    31  39       1440
19  194        81  36   5.4     0  36       1      64     126      1   110     7
6    30  34        120
20  196       206  41   4.8     1  62       0      65     196      2   178     9
0    46  51        540
21  186        97  50   3.7     0  70       1      67     178      2   148     8
8    42  41       1020
22  234        65  76   3.1     0  47       1      67     230      2   137    10
0    45  46        480
> # display the dimensions of the dataset
> print(dim(dataset))
[1] 375  15
> # list types for each attribute
> print(sapply(dataset,class))
     chol  stab.glu       hdl      ratio      glyhb        age     gender     h
eight    weight     frame     bp.1s
"integer" "integer" "integer" "numeric"  "factor" "integer"  "factor" "int
eger" "integer"  "factor" "integer"
    bp.1d     waist       hip  time.ppn
"integer" "integer" "integer" "integer"
> # distribution of the class labels
> y = dataset$glyhb
> print(cbind(freq=table(y),percentage=prop.table(table(y))*100))
  freq percentage
0  317   84.53333
1   58   15.46667
> print(table(y))
y
  0   1
317  58
> print(table(y)/length(y))
y
        0         1
0.8453333 0.1546667
> # summarize the dataset
> print(summary(dataset))
      chol           stab.glu          hdl              ratio         glyhb
age          gender      height
 Min.   : 78.0   Min.   : 48.0   Min.   : 12.00   Min.   : 1.500   0:317
Min.   :19.00   0:220   Min.   :52
 1st Qu.:179.0   1st Qu.: 81.0   1st Qu.: 38.00   1st Qu.: 3.200   1: 58
1st Qu.:34.00   1:155   1st Qu.:63
 Median :204.0   Median : 90.0   Median : 46.00   Median : 4.200
Median :45.00           Median :66
 Mean   :207.6   Mean   :107.6   Mean   : 50.43   Mean   : 4.525
Mean   :46.98           Mean   :66
 3rd Qu.:229.5   3rd Qu.:108.5   3rd Qu.: 59.00   3rd Qu.: 5.400
3rd Qu.:60.00           3rd Qu.:69
 Max.   :443.0   Max.   :385.0   Max.   :120.00   Max.   :19.300
Max.   :92.00           Max.   :76
     weight      frame       bp.1s           bp.1d            waist
hip             time.ppn
 Min.   : 99.0   0: 98   Min.   : 90.0   Min.   : 48.00   Min.   :26.00
Min.   :30.00   Min.   :   5
 1st Qu.:151.0   1:172   1st Qu.:121.5   1st Qu.: 75.00   1st Qu.:33.00
1st Qu.:39.00   1st Qu.:  90
 Median :174.0   2:105   Median :136.0   Median : 82.00   Median :37.00
Median :42.00   Median : 240
 Mean   :177.9           Mean   :137.5   Mean   : 83.38   Mean   :37.95
Mean   :43.09   Mean   : 335
 3rd Qu.:200.0           3rd Qu.:148.0   3rd Qu.: 91.00   3rd Qu.:41.50
3rd Qu.:46.00   3rd Qu.: 480
```

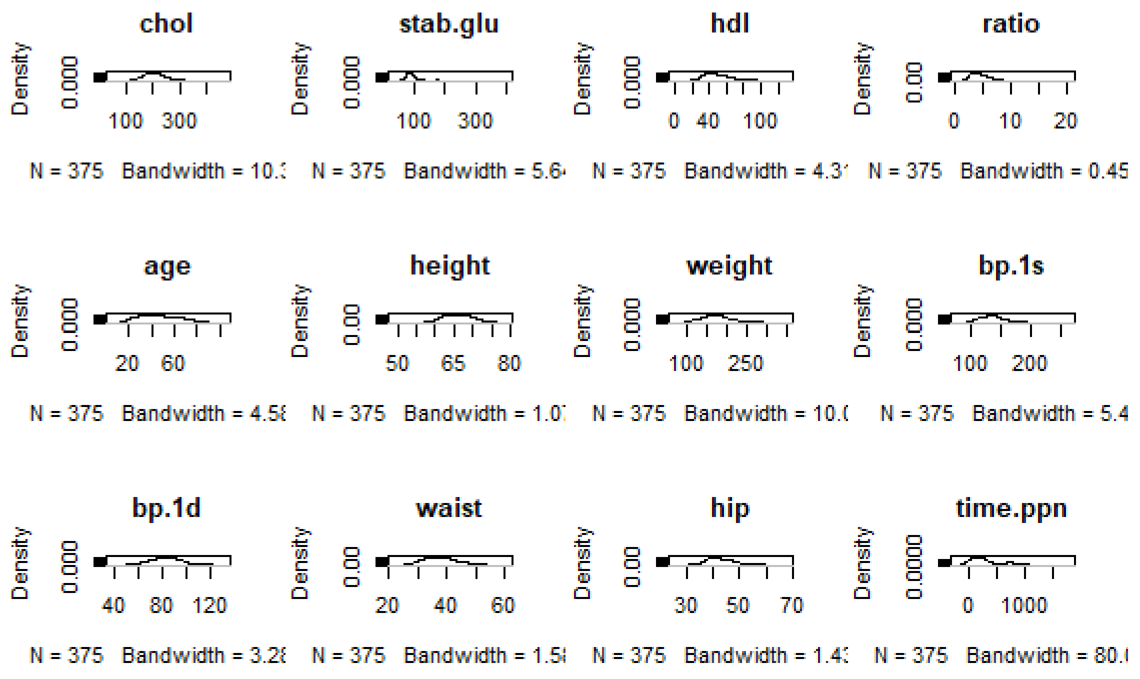
```
 Max.   :325.0           Max.   :250.0   Max.   :124.00   Max.   :56.00   
Max.   :64.00   Max.   :1560  
# Standard Deviations for the non-categorical columns
> std=sapply(dataset[,-c(5,7,10)],sd)
> print('The standard deviations are:')
[1] "The standard deviations are:"
> print(std)
chol   stab.glu   hdl       ratio      age      height     weight      bp.1s 
44.700780  54.082496  17.444346   1.755499  16.661203   3.915210  40.56894
0  23.178154 
     bp.1d      waist        hip   time.ppn 
 13.544167   5.777105   5.642679 309.056806 
# Skewness
#The further the distribution of the skew value from zero,
# the larger the skew to the left (negative skew value) or right (positive
skew value).
> library(e1071) # the library for skewness
> skew=apply(dataset[,-c(5,7,10)], 2, skewness)
> print(skew)
      chol   stab.glu        hdl      ratio        age     height     weig
ht      bp.1s 
0.97739823 2.69790949 1.21275829 2.24132546 0.30061280 0.02678693 0.748807
75 1.05634395 
     bp.1d      waist        hip   time.ppn 
0.23310577 0.47060516 0.80724954 1.28077802 
# Correlations
> correlations=cor(dataset[,-c(5,7,10)])
> print(correlations)
                  chol    stab.glu         hdl       ratio         age     
height
chol       1.0000000000  0.17605760  0.18918622  0.47685119  0.25807515 -0.
0726825795
stab.glu   0.1760576046  1.00000000 -0.15845068  0.29353513  0.28820616  0.
0864302351
hdl        0.1891862222 -0.15845068  1.00000000 -0.68325757  0.02624555 -0.
0901427069
ratio      0.4768511857  0.29353513 -0.68325757  1.00000000  0.16952389  0.
0782807237
age        0.2580751516  0.28820616  0.02624555  0.16952389  1.00000000 -0.
0953003330
height    -0.0726825795  0.08643024 -0.09014271  0.07828072 -0.09530033  1.
0000000000
weight     0.0545001654  0.17918946 -0.29760400  0.27690932 -0.06523800  0.
2460901156
bp.1s      0.2084006482  0.16181629  0.03436444  0.11090086  0.45236549 -0.
0470999583
bp.1d      0.1715635556  0.02867443  0.07630061  0.03904864  0.06562279  0.
0383903197
waist      0.1192740454  0.22720469 -0.28499211  0.30894469  0.15068806  0.
0450335672
hip        0.0732717715  0.13333204 -0.23280194  0.20246310 -0.00208207 -0.
1176291370
time.ppn   0.0009236077 -0.05010410  0.06822885 -0.05007620 -0.03962976 -0.
0001877958
               weight       bp.1s       bp.1d       waist         hip     
time.ppn
chol       0.05450017  0.20840065  0.17156356  0.11927405  0.07327177  0.00
09236077
stab.glu   0.17918946  0.16181629  0.02867443  0.22720469  0.13333204 -0.05
01040985
hdl       -0.29760400  0.03436444  0.07630061 -0.28499211 -0.23280194  0.06
82288499
ratio      0.27690932  0.11090086  0.03904864  0.30894469  0.20246310 -0.05
00762030
age       -0.06523800  0.45236549  0.06562279  0.15068806 -0.00208207 -0.03
96297574
height     0.24609012 -0.04709996  0.03839032  0.04503357 -0.11762914 -0.00
01877958
```

```
weight     1.00000000  0.08797282  0.17190112  0.85176414  0.82931024 -0.05
77287098
bp.1s      0.08797282  1.00000000  0.61104157  0.20342942  0.14425492 -0.08
14349347
bp.1d      0.17190112  0.61104157  1.00000000  0.17056560  0.15538918 -0.06
69496556
waist      0.85176414  0.20342942  0.17056560  1.00000000  0.83224050 -0.06
47235445
hip        0.82931024  0.14425492  0.15538918  0.83224050  1.00000000 -0.09
43397549
time.ppn -0.05772871 -0.08143493 -0.06694966 -0.06472354 -0.09433975  1.00
00000000
```

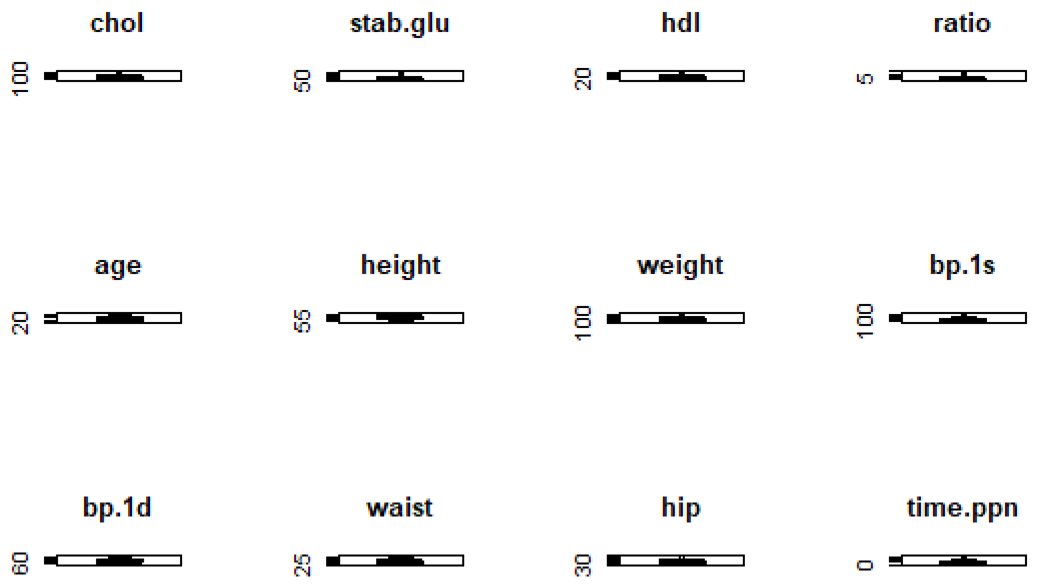
```
# Data visualizations
> dataset_numeric = dataset[,-c(5,7,10)]
> #Histograms
> par(mfrow=c(3,4)) # put four figures in a row (2*4)
> for (i in 1:12) {
+   hist(dataset_numeric[,i],main=names(dataset_numeric)[i])
+ }
```



```
#Density Plots
> par(mfrow=c(3,4))
> for(i in 1:12) {
+   plot(density(dataset_numeric[,i]), main=names(dataset_numeric)[i])
+ }
```

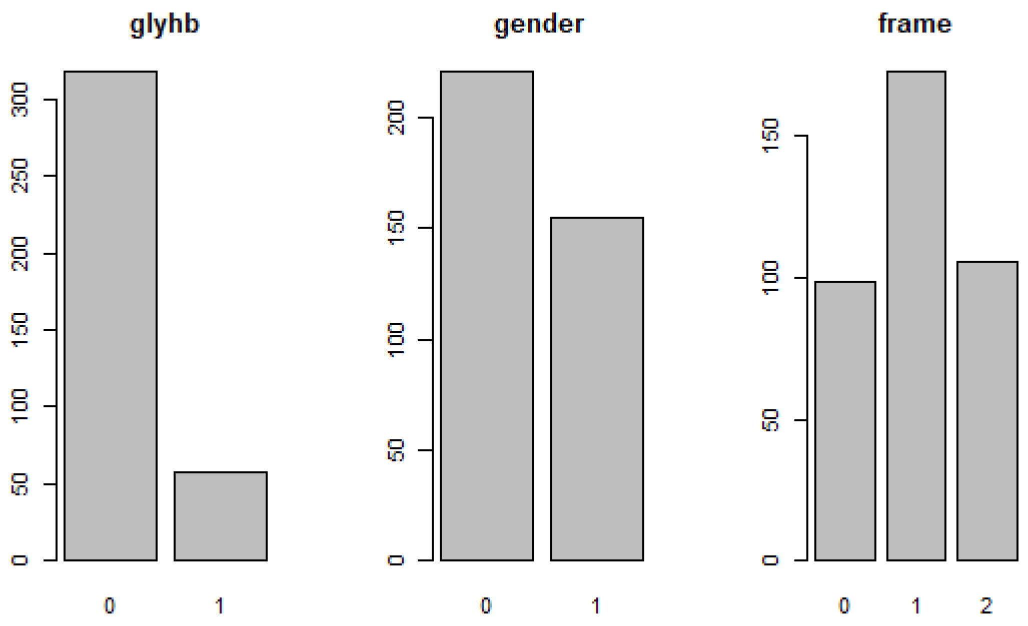


```
#Box And Whisker Plots
> par(mfrow=c(3,4))
> for(i in 1:12) {
+   boxplot(dataset_numeric[,i], main=names(dataset_numeric)[i])
+ }
```

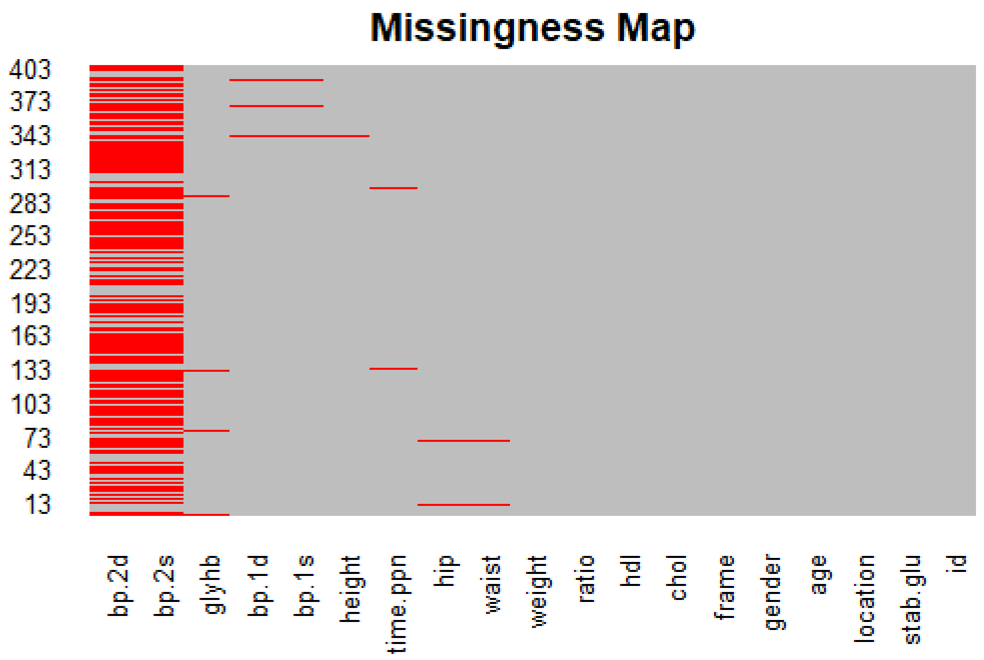


```
#Barplots, which is used to count the accurances for categorical attribute
s
> dataset_categorical = dataset[,c(5,7,10)]
> par(mfrow=c(1,3))
> for(i in 1:3) {
```

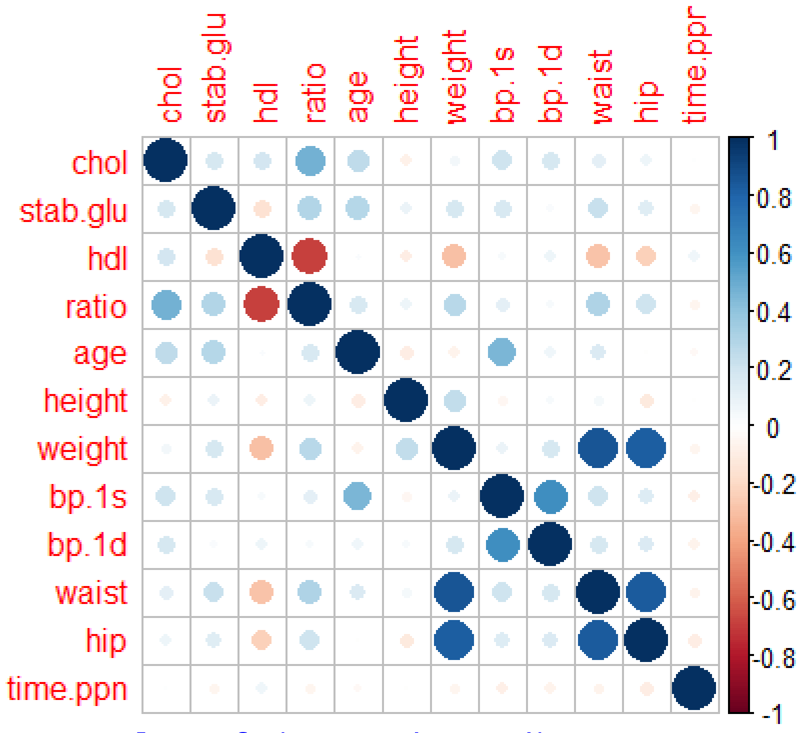
```
+   counts <- table(dataset_categorical[,i]) # get the count for each cate
gorical value
+   name <- names(dataset_categorical)[i]
+   barplot(counts, main=name)
+ }
#Missing data Plot
```



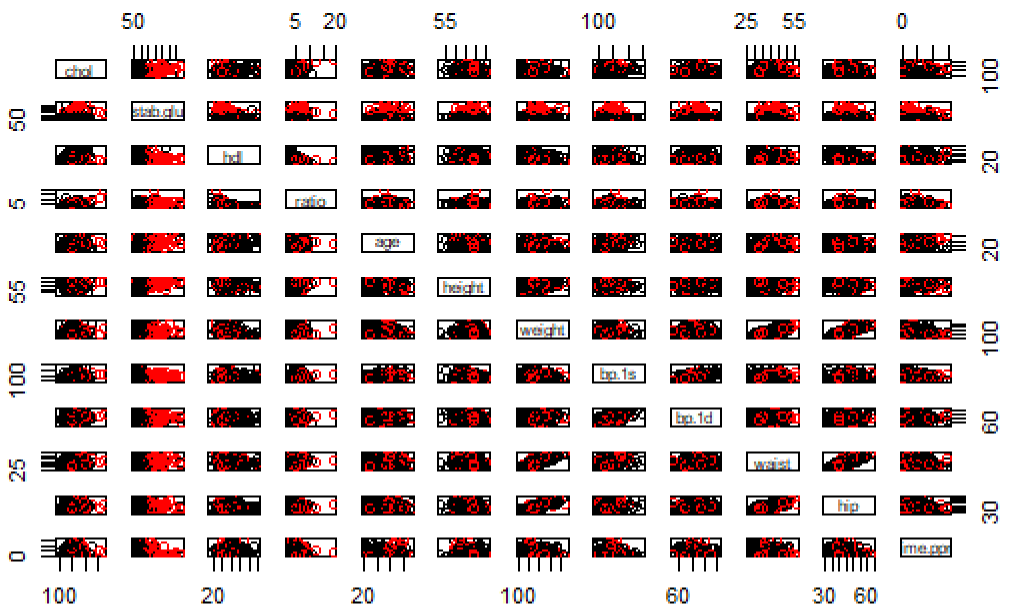
```
> library(Amelia) # library for the function missmap
> par(mfrow=c(1,1))
> missmap(datasetRaw, col=c("red", "grey"), legend=FALSE)
```



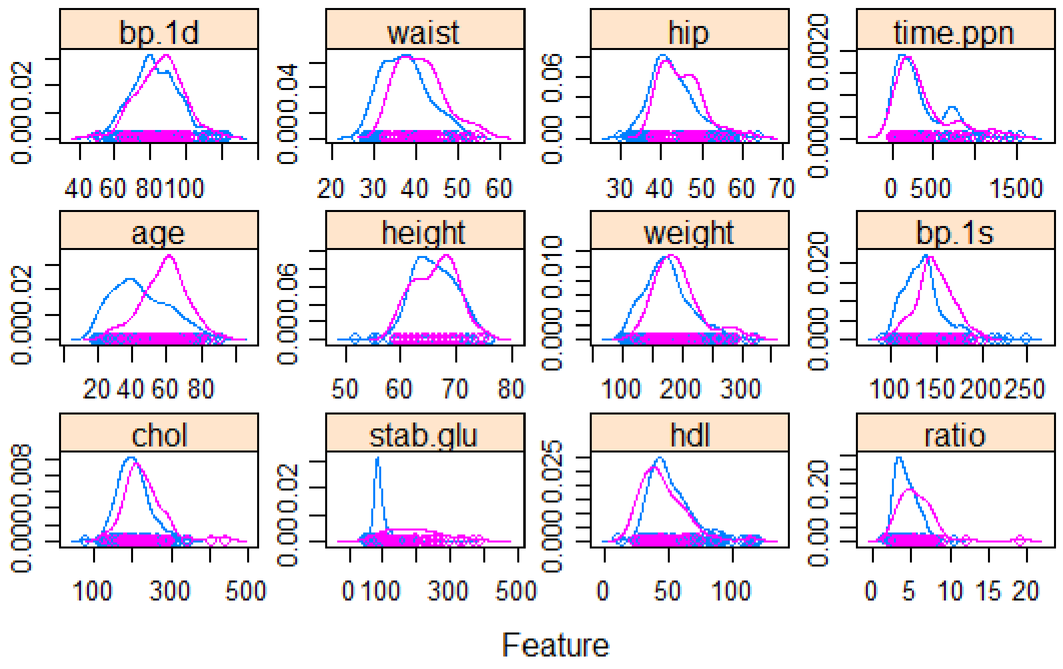
```
#Multivariate Visualization
> library(corrplot) # for function corrplot()
corrplot 0.84 loaded
> correlations1=cor(dataset_numeric)
> print(correlations1)
                  chol     stab.glu         hdl       ratio         age
height
chol      1.0000000000  0.17605760  0.18918622  0.47685119  0.25807515 -0.
0726825795
stab.glu  0.1760576046  1.00000000 -0.15845068  0.29353513  0.28820616  0.
0864302351
hdl       0.1891862222 -0.15845068  1.00000000 -0.68325757  0.02624555 -0.
0901427069
ratio     0.4768511857  0.29353513 -0.68325757  1.00000000  0.16952389  0.
0782807237
age       0.2580751516  0.28820616  0.02624555  0.16952389  1.00000000 -0.
0953003330
height   -0.0726825795  0.08643024 -0.09014271  0.07828072 -0.09530033  1.
0000000000
weight    0.0545001654  0.17918946 -0.29760400  0.27690932 -0.06523800  0.
2460901156
bp.1s     0.2084006482  0.16181629  0.03436444  0.11090086  0.45236549 -0.
0470999583
bp.1d     0.1715635556  0.02867443  0.07630061  0.03904864  0.06562279  0.
0383903197
waist     0.1192740454  0.22720469 -0.28499211  0.30894469  0.15068806  0.
0450335672
hip       0.0732717715  0.13333204 -0.23280194  0.20246310 -0.00208207 -0.
1176291370
time.ppn  0.0009236077 -0.05010410  0.06822885 -0.05007620 -0.03962976 -0.
0001877958
              weight       bp.1s       bp.1d       waist         hip
time.ppn
chol      0.05450017  0.20840065  0.17156356  0.11927405  0.07327177  0.00
09236077
stab.glu  0.17918946  0.16181629  0.02867443  0.22720469  0.13333204 -0.05
01040985
hdl      -0.29760400  0.03436444  0.07630061 -0.28499211 -0.23280194  0.06
82288499
ratio     0.27690932  0.11090086  0.03904864  0.30894469  0.20246310 -0.05
00762030
age      -0.06523800  0.45236549  0.06562279  0.15068806 -0.00208207 -0.03
96297574
height    0.24609012 -0.04709996  0.03839032  0.04503357 -0.11762914 -0.00
01877958
weight    1.00000000  0.08797282  0.17190112  0.85176414  0.82931024 -0.05
77287098
bp.1s     0.08797282  1.00000000  0.61104157  0.20342942  0.14425492 -0.08
14349347
bp.1d     0.17190112  0.61104157  1.00000000  0.17056560  0.15538918 -0.06
69496556
waist     0.85176414  0.20342942  0.17056560  1.00000000  0.83224050 -0.06
47235445
hip       0.82931024  0.14425492  0.15538918  0.83224050  1.00000000 -0.09
43397549
time.ppn -0.05772871 -0.08143493 -0.06694966 -0.06472354 -0.09433975  1.00
00000000
> par(mfrow=c(1,1))
> corrplot(correlations1, methods="circle")
```



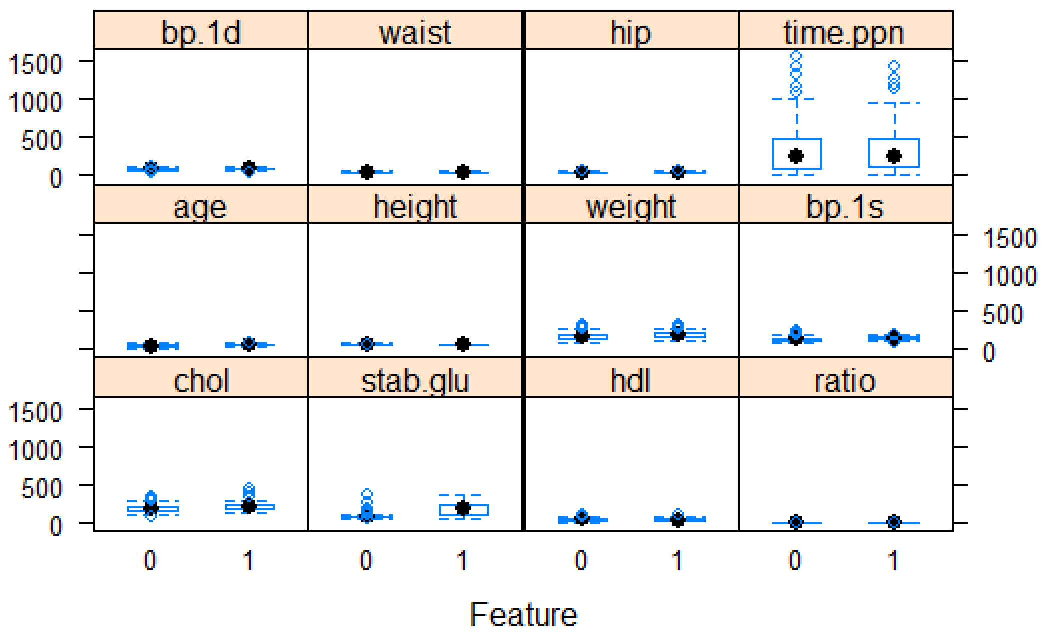
```
# pair-wise scatterplots of the numeric attributes
> par(mfrow=c(1,1))
pairs(dataset_numeric)
> #Scatterplot Matrix By Class (use different color to distinguish differe
nt class)
> par(mfrow=c(1,1))
> pairs(dataset_numeric, col=dataset[,5])
```



```
#Density By Class
> library(caret)
> # load the data
> data(iris)
> # density plots for each attribute by class value
> x <- dataset_numeric
> y <- dataset[,5]
> scales <- list(x=list(relation="free"), y=list(relation="free"))
> par(mfrow=c(1,1))
> featurePlot(x=dataset_numeric, y=dataset[,5], plot="density", scales=sca
les)
```



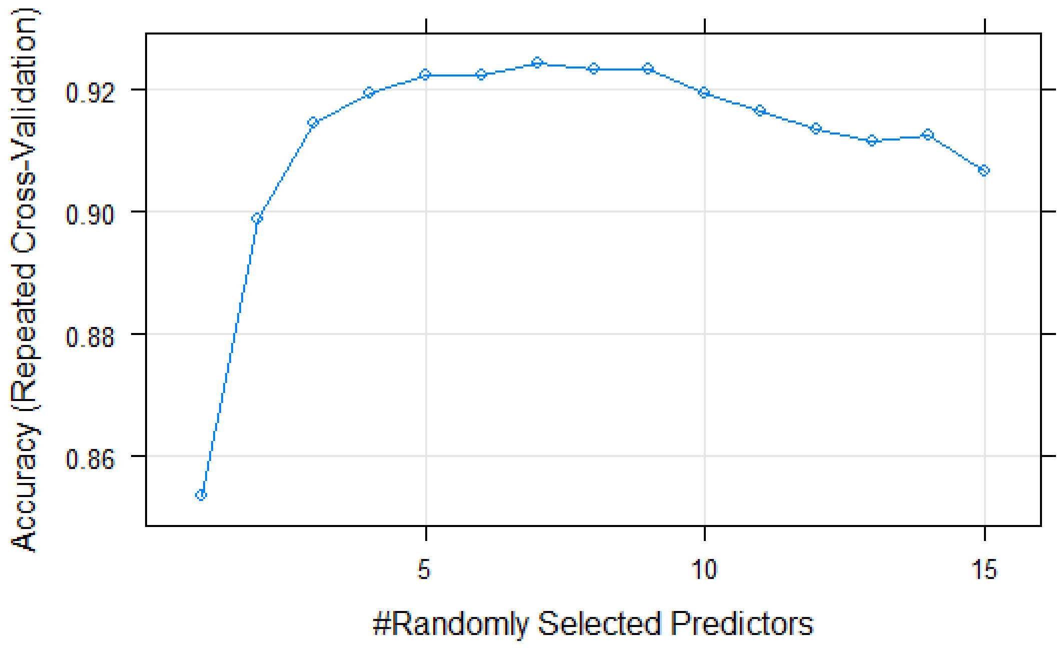
```
#Box And Whisker Plots By Class
> featurePlot(x=dataset_numeric, y=dataset[,5], plot="box")
```



```
# Load libraries
> library(randomForest)
> library(caret)

> # load the data
> filename="C:\Users\Tejal Chaudhary\Desktop\Exploratory-Data-Analysis-and
-Prediction-on-Diabetes-Dataset-using-R-master\diabetes_data.csv"
> datasetRaw = read.csv(filename)
> print(head(datasetRaw))
    id chol stab.glu hdl ratio glyhb   location age gender height weight
frame bp.1s
1 1000  203       82  56   3.6  4.31 Buckingham  46 female     62    121 m
edium   118
2 1001  165       97  24   6.9  4.44 Buckingham  29 female     64    218
large   112
3 1002  228       92  37   6.2  4.64 Buckingham  58 female     61    256
large   190
4 1003   78       93  12   6.5  4.63 Buckingham  67   male     67    119
large   110
5 1005  249       90  28   8.9  7.72 Buckingham  64   male     68    183 m
edium   138
6 1008  248       94  69   3.6  4.81 Buckingham  34   male     71    190
large   132
  bp.1d bp.2s bp.2d waist hip time.ppn
1    59    NA    NA    29  38      720
2    68    NA    NA    46  48      360
3    92   185    92    49  57      180
4    50    NA    NA    33  38      480
5    80    NA    NA    44  41      300
6    86    NA    NA    36  42      195

# clean the data
> numColumns = dim(datasetRaw)[2]
> vector_NAs = rep(0, numColumns)
> for (i in 1:numColumns) {
+   vector_NAs[i] = sum(is.na(datasetRaw[,i]))
+
+ }
> print("The missing values in each column:")
[1] "The missing values in each column:"
> print(vector_NAs)
 [1]   0   1   0   1   1  13   0   0   0   5   1   0   5   5 262 262   2
2   3

# delete columns 15 and 16 due to many missing values
> # delete column 1 (id), column 7 (location) because they contain no usef
ul information
> dataset = datasetRaw[,-c(1,7,15,16)]
> print(dim(dataset))
[1] 403  15

# remove the row with missing values
> row.has.na <- apply(dataset, 1, function(x){any(is.na(x))})
> dataset = dataset[!row.has.na,]
> print(dim(dataset))
[1] 375  15
> print(head(dataset))
  chol stab.glu hdl ratio glyhb age gender height weight  frame bp.1s bp.1
d waist hip
1  203       82  56   3.6  4.31  46 female     62    121 medium   118    5
9    29  38
2  165       97  24   6.9  4.44  29 female     64    218  large   112    6
8    46  48
3  228       92  37   6.2  4.64  58 female     61    256  large   190    9
2    49  57
4   78       93  12   6.5  4.63  67   male     67    119  large   110    5
0    33  38
```

```
5  249       90  28   8.9  7.72  64   male      68    183 medium   138    8
0    44  41
6  248       94  69   3.6  4.81  34   male      71    190  large   132    8
6    36  42
  time.ppn
1      720
2      360
3      180
4      480
5      300
6      195

# encode the class label (column 5): Glycosolated hemoglobin  > 7.0 is tak
en as a positive diagnosis of diabetes.
> dataset[,5] = ifelse(dataset[,5] >= 7.0, 1, 0)
> dataset[,5] = factor(dataset[,5])
> # encode the categorical data (column-7 gender)
> dataset[,7] = ifelse(dataset[,7] == "female", 0, 1)
> dataset[,7] = factor(dataset[,7])
> # encode the categorical data (column-10 frame)
> dataset[,10] = ifelse(dataset[,10] == "small", 0, ifelse(dataset[,10] ==
"medium", 1,2) )
> dataset[,10] = factor(dataset[,10])
> # split the data into training and validation sets
> set.seed(7)
> validation_index = createDataPartition(dataset$glyhb, p=0.90, list=FALSE
)
> validationData = dataset[-validation_index,]
> trainingData = dataset[validation_index,]
> # comparison among different classifiers
> #1. Logistic Regression
> set.seed(7)
> control.glm = trainControl(method = "cv", number = 5)
> fit.glm = train(glyhb~., data = trainingData, method = "glm", preProc =
c("center","scale"), trControl = control.glm)
> print(fit.glm$results)
  parameter  Accuracy     Kappa AccuracySD   KappaSD
1      none 0.9113696 0.6246138 0.03189889 0.1209417

#2. Support Vector Machine
> set.seed(7)
> control.svmRadial = trainControl(method="cv", number=5)
> fit.svmRadial <- train(glyhb~., data=trainingData, method="svmRadial", m
etric="Accuracy", preProc=c("center","scale"), trControl=control.svmRadial
)
> # summarize fit
> print(fit.svmRadial$results)
       sigma    C  Accuracy     Kappa AccuracySD   KappaSD
1 0.04419447 0.25 0.8672520 0.2457674 0.01803261 0.1117821
2 0.04419447 0.50 0.8996927 0.4850752 0.03357527 0.1936929
3 0.04419447 1.00 0.9026778 0.5334358 0.03377470 0.1934882
#3. random forest
> control.rf = trainControl(method="cv", number=5)
> set.seed(7)
> metric = "Accuracy"
> mtry = 7 # mtry=7 (number of variables to try)
> tunegrid <- expand.grid(.mtry=mtry)
> fit.rf_default <- train(glyhb~., data=trainingData, method="rf", metric=
metric, tuneGrid=tunegrid, preProc=c("center","scale"), trControl=control)
> print(fit.rf_default$results)
> #4. parameter tunning via grid search for random forest
> control.rf_search <- trainControl(method="repeatedcv", number=5, repeats
=3, search="grid")
> set.seed(7)
> tunegrid <- expand.grid(.mtry=c(1:15))
> fit.rf_gridsearch <- train(glyhb~., data=trainingData, method="rf", metr
ic=metric, tuneGrid=tunegrid, trControl=control.rf_search, ntree=1000)
> print(fit.rf_gridsearch) # accuracy = 0.9204355 when mtry = 12
Random Forest
```

```
339 samples
 14 predictor
  2 classes: '0', '1'

No pre-processing
Resampling: Cross-Validated (5 fold, repeated 3 times)
Summary of sample sizes: 271, 271, 272, 271, 271, 272, ...
Resampling results across tuning parameters:

  mtry  Accuracy   Kappa
   1    0.8535218  0.1258378
   2    0.8987098  0.5300869
   3    0.9144692  0.6339489
   4    0.9193858  0.6581317
   5    0.9222981  0.6750889
   6    0.9222835  0.6785513
   7    0.9242447  0.6863912
   8    0.9232643  0.6838630
   9    0.9232497  0.6832487
  10    0.9193277  0.6721862
  11    0.9163719  0.6622605
  12    0.9134449  0.6507448
  13    0.9114841  0.6445033
  14    0.9124495  0.6516127
  15    0.9065379  0.6273732

Accuracy was used to select the optimal model using the largest value.
The final value used for the model was mtry = 7.
> print(fit.rf_gridsearch$finalModel)

Call:
 randomForest(x = x, y = y, ntree = 1000, mtry = param$mtry)
               Type of random forest: classification
                     Number of trees: 1000
No. of variables tried at each split: 7

        OOB estimate of  error rate: 8.55%
Confusion matrix:
    0  1 class.error
0 274 12  0.04195804
1  17 36  0.32075472
> plot(fit.rf_gridsearch)
> # make predictions on the validation set
> set.seed(7)
> predictions = predict(fit.rf_gridsearch, newdata=validationData)
> confusionMatrix = confusionMatrix(predictions, validationData$glyhb)
> # confusion matrix
> print(confusionMatrix$table)
          Reference
Prediction  0  1
         0 29  3
         1  2  2
```



```
# save the final classifier model into disk
> saveRDS(fit.rf_gridsearch, "C:\\Users\\Tejal Chaudhary\\Desktop\\Explora
tory-Data-Analysis-and-Prediction-on-Diabetes-Dataset-using-R-master\\diab
etes_classification")

> # load the model from the disk
> final_model <- readRDS("C:\\Users\\Tejal Chaudhary\\Desktop\\Exploratory
-Data-Analysis-and-Prediction-on-Diabetes-Dataset-using-R-master\\diabetes
_classification")
> #final_model <- readRDS("C:\\data\\diabetes_classification")
> print(final_model)
Random Forest

339 samples
 14 predictor
  2 classes: '0', '1'

No pre-processing
Resampling: Cross-Validated (5 fold, repeated 3 times)
Summary of sample sizes: 271, 271, 272, 271, 271, 272, ...
Resampling results across tuning parameters:

  mtry  Accuracy   Kappa
   1    0.8535218  0.1258378
   2    0.8987098  0.5300869
   3    0.9144692  0.6339489
   4    0.9193858  0.6581317
   5    0.9222981  0.6750889
   6    0.9222835  0.6785513
   7    0.9242447  0.6863912
   8    0.9232643  0.6838630
   9    0.9232497  0.6832487
  10    0.9193277  0.6721862
  11    0.9163719  0.6622605
  12    0.9134449  0.6507448
  13    0.9114841  0.6445033
  14    0.9124495  0.6516127
  15    0.9065379  0.6273732

Accuracy was used to select the optimal model using the largest value.
The final value used for the model was mtry = 7.
```

```
# make predictions using the loaded model
> set.seed(7)
> predictions = predict(final_model, newdata=validationData)
> print(predictions)
 [1] 0 0 0 0 0 0 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0
0
Levels: 0 1
```