```
#Importing Libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

```
#Reading the dataset & storing it in a variable

health_df=pd.read_csv("health care diabetes.csv")
health_df.head()
```

```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin
BMI  \
0            6      148             72             35        0  33.6

1            1       85             66             29        0  26.6

2            8      183             64              0        0  23.3

3            1       89             66             23       94  28.1

4            0      137             40             35      168  43.1


   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
2                     0.672   32        1
3                     0.167   21        0
4                     2.288   33        1
```

Project Task: Week 1

```
health_df.shape
```

```
(768, 9)
```

```
health_df.describe()
```

```
       Pregnancies     Glucose  BloodPressure  SkinThickness
Insulin  \
count   768.000000  768.000000     768.000000     768.000000
768.000000
mean      3.845052  120.894531      69.105469      20.536458
79.799479
std       3.369578   31.972618      19.355807      15.952218
115.244002
min       0.000000    0.000000       0.000000       0.000000
0.000000
25%       1.000000   99.000000      62.000000       0.000000
```

```
0.000000
50%       3.000000  117.000000      72.000000      23.000000
30.500000
75%       6.000000  140.250000      80.000000      32.000000
127.250000
max      17.000000  199.000000     122.000000      99.000000
846.000000

              BMI  DiabetesPedigreeFunction         Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
mean    31.992578                  0.471876   33.240885    0.348958
std      7.884160                  0.331329   11.760232    0.476951
min      0.000000                  0.078000   21.000000    0.000000
25%     27.300000                  0.243750   24.000000    0.000000
50%     32.000000                  0.372500   29.000000    0.000000
75%     36.600000                  0.626250   41.000000    1.000000
max     67.100000                  2.420000   81.000000    1.000000
```

Check for missing values & columns having no variance

```
health_df.isnull().any()

Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool

health_df.var()

Pregnancies                    11.354056
Glucose                      1022.248314
BloodPressure                 374.647271
SkinThickness                 254.473245
Insulin                     13281.180078
BMI                            62.159984
DiabetesPedigreeFunction        0.109779
Age                           138.303046
Outcome                         0.227483
dtype: float64

health_df['Glucose'].value_counts()

99     17
100    17
111    14
129    14
```

```
125    14
       ..
191     1
177     1
44      1
62      1
190     1
Name: Glucose, Length: 136, dtype: int64
```

```
health_df['BloodPressure'].value_counts()
```

```
70     57
74     52
78     45
68     45
72     44
64     43
80     40
76     39
60     37
0      35
62     34
66     30
82     30
88     25
84     23
90     22
86     21
58     21
50     13
56     12
52     11
54     11
75      8
92      8
65      7
85      6
94      6
48      5
96      4
44      4
100     3
106     3
98      3
110     3
55      2
108     2
104     2
46      2
30      2
122     1
```

```
95      1
102     1
61      1
24      1
38      1
40      1
114     1
Name: BloodPressure, dtype: int64
```

```
health_df['SkinThickness'].value_counts()
```

```
0     227
32     31
30     27
27     23
23     22
33     20
28     20
18     20
31     19
19     18
39     18
29     17
40     16
25     16
26     16
22     16
37     16
41     15
35     15
36     14
15     14
17     14
20     13
24     12
42     11
13     11
21     10
46      8
34      8
12      7
38      7
11      6
43      6
16      6
45      6
14      6
44      5
10      5
48      4
47      4
```

```
49      3
50      3
8       2
7       2
52      2
54      2
63      1
60      1
56      1
51      1
99      1
Name: SkinThickness, dtype: int64
```

```
health_df['Insulin'].value_counts()
```

```
0      374
105     11
130      9
140      9
120      8
      ...
73       1
171      1
255      1
52       1
112      1
Name: Insulin, Length: 186, dtype: int64
```

The dataset does not contain missing values(i.e. NaN) but presnce of 0 in features such as BP,Insulin,Glucose,etc. indicates the presence of Null values. So, here we will try to replace zero with np.Nan & later impute those null values.

```
health_df[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']]
=health_df[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']
].replace(0,np.nan)
```

```
health_df.isnull().any()
```

```
Pregnancies                 False
Glucose                      True
BloodPressure                True
SkinThickness                True
Insulin                      True
BMI                          True
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

Working with Missing Values & Imputation

```
health_df.sample(10)
```

```
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  
\
461            1     71.0           62.0            NaN      NaN  21.8   

364            4    147.0           74.0           25.0    293.0  34.9   

743            9    140.0           94.0            NaN      NaN  32.7   

632            2    111.0           60.0            NaN      NaN  26.2   

693            7    129.0           68.0           49.0    125.0  38.5   

681            0    162.0           76.0           36.0      NaN  49.6   

673            3    123.0          100.0           35.0    240.0  57.3   

584            8    124.0           76.0           24.0    600.0  28.7   

405            2    123.0           48.0           32.0    165.0  42.1   

465            0    124.0           56.0           13.0    105.0  21.8   


     DiabetesPedigreeFunction  Age  Outcome  
461                     0.416   26        0  
364                     0.385   30        0  
743                     0.734   45        1  
632                     0.343   23        0  
693                     0.439   43        1  
681                     0.364   26        1  
673                     0.880   22        0  
584                     0.687   52        1  
405                     0.520   26        0  
465                     0.452   21        0  
```

```
health_df['Glucose'].median()
```

```
117.0
```

```
health_df['BloodPressure'].median()
```

```
72.0
```

```
health_df['SkinThickness'].median()
```

```
29.0
```

```
health_df['Insulin'].median()
```

```
125.0
```

```
health_df['BMI'].median()
```

```
32.3
```

```
health_df['Glucose']=health_df['Glucose'].fillna(117)
health_df['BloodPressure']=health_df['BloodPressure'].fillna(72)
health_df['SkinThickness']=health_df['SkinThickness'].fillna(29)
health_df['Insulin']=health_df['Insulin'].fillna(125)
health_df['BMI']=health_df['BMI'].fillna(32)
```

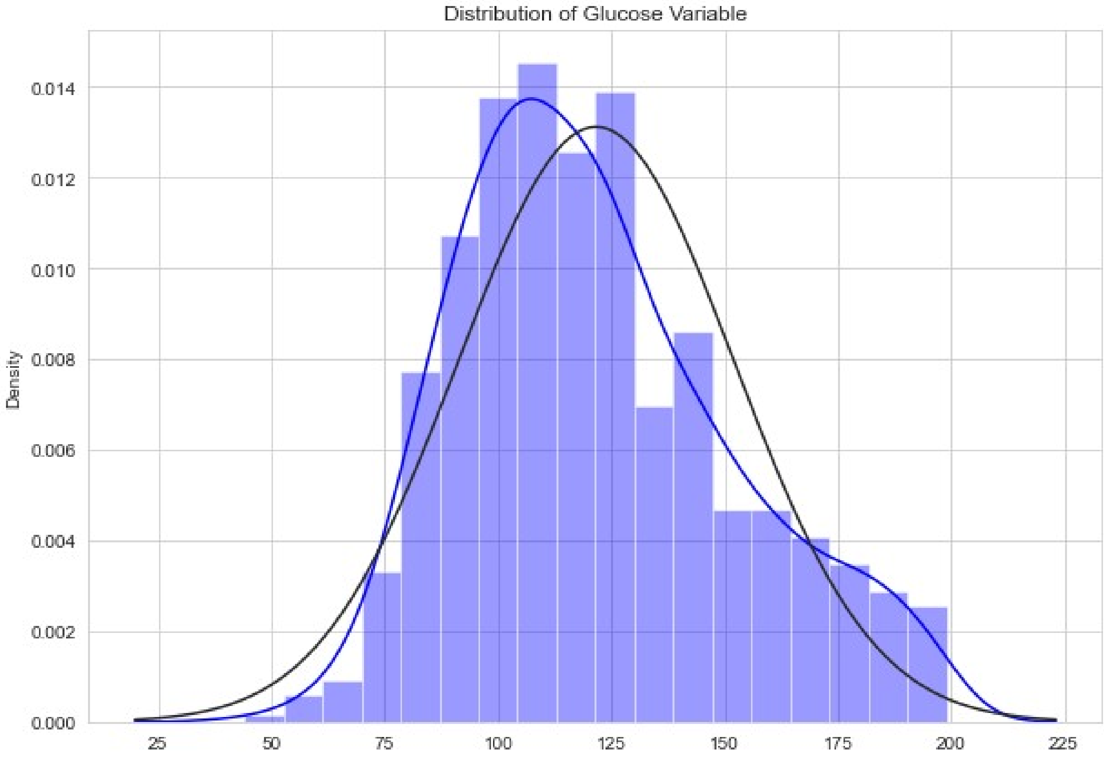
```
health_df.isnull().any()
```

```
Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

Visualization to depict distribution of Variables

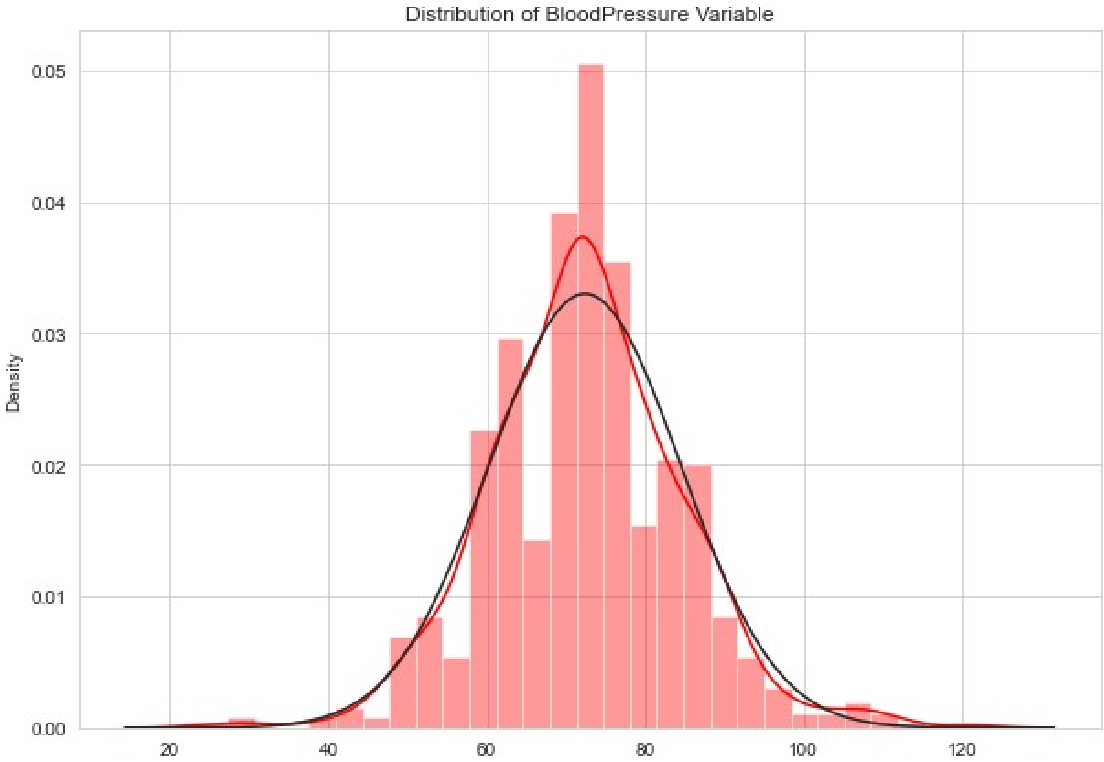
```
from scipy.stats import norm
plt.figure(figsize=(10,7))
sns.set_style('whitegrid')

sns.distplot(x=health_df['Glucose'],color='blue',fit=norm)
plt.title("Distribution of Glucose Variable")
plt.show()
```

```
C:\Users\faiza\Anaconda3\lib\site-packages\seaborn\
distributions.py:2619: FutureWarning: `distplot` is a deprecated
function and will be removed in a future version. Please adapt your
code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



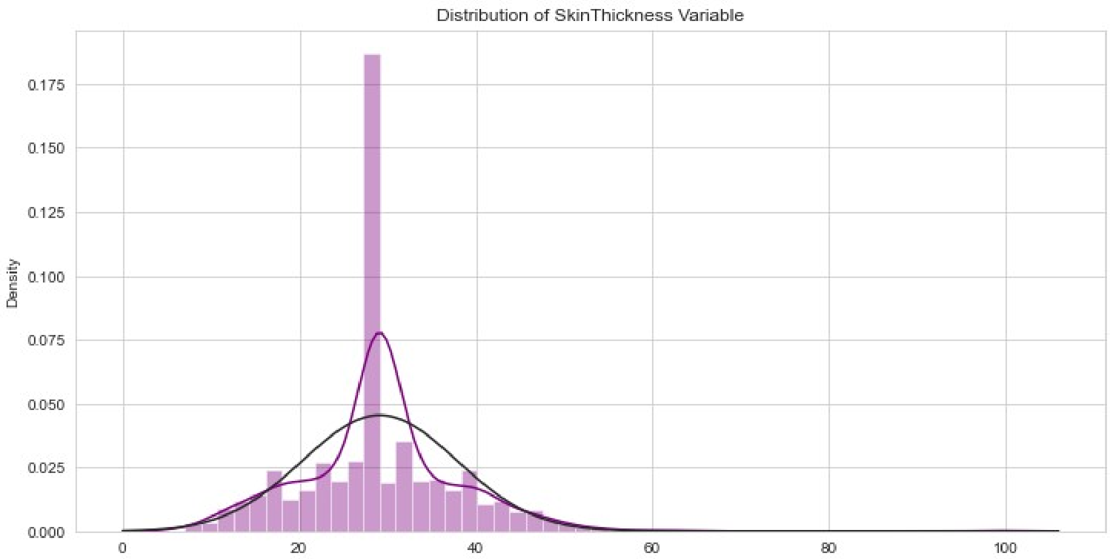
```
from scipy.stats import norm
plt.figure(figsize=(10,7))
sns.set_style('whitegrid')

sns.distplot(x=health_df['BloodPressure'],color='red',fit=norm)
plt.title("Distribution of BloodPressure Variable")
plt.show()
```

```
C:\Users\faiza\Anaconda3\lib\site-packages\seaborn\
distributions.py:2619: FutureWarning: `distplot` is a deprecated
function and will be removed in a future version. Please adapt your
code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



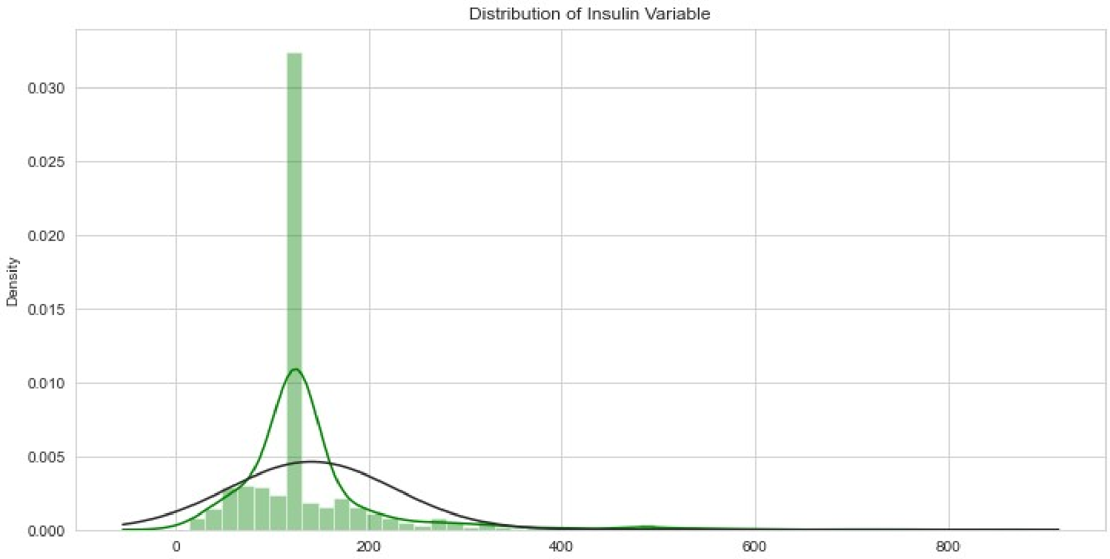
```
from scipy.stats import norm
plt.figure(figsize=(12,6))
sns.set_style('whitegrid')

sns.distplot(x=health_df['SkinThickness'],color='purple',fit=norm)
plt.title("Distribution of SkinThickness Variable")
plt.show()
```

```
C:\Users\faiza\Anaconda3\lib\site-packages\seaborn\
distributions.py:2619: FutureWarning: `distplot` is a deprecated
function and will be removed in a future version. Please adapt your
code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



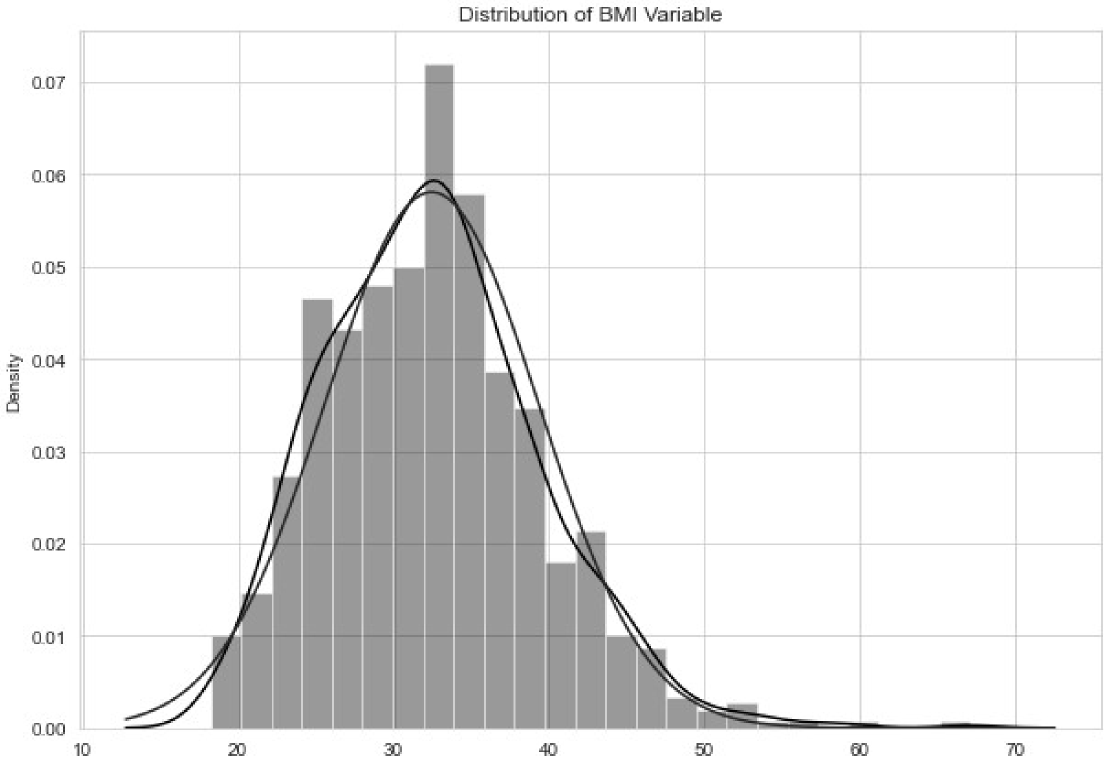
```
from scipy.stats import norm
plt.figure(figsize=(12,6))
sns.set_style('whitegrid')

sns.distplot(x=health_df['Insulin'],color='green',fit=norm)
plt.title("Distribution of Insulin Variable")
plt.show()
```

```
C:\Users\faiza\Anaconda3\lib\site-packages\seaborn\
distributions.py:2619: FutureWarning: `distplot` is a deprecated
function and will be removed in a future version. Please adapt your
code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



```
from scipy.stats import norm
plt.figure(figsize=(10,7))
sns.set_style('whitegrid')

sns.distplot(x=health_df['BMI'],color='black',fit=norm)
plt.title("Distribution of BMI Variable")
plt.show()
```

```
C:\Users\faiza\Anaconda3\lib\site-packages\seaborn\
distributions.py:2619: FutureWarning: `distplot` is a deprecated
function and will be removed in a future version. Please adapt your
code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

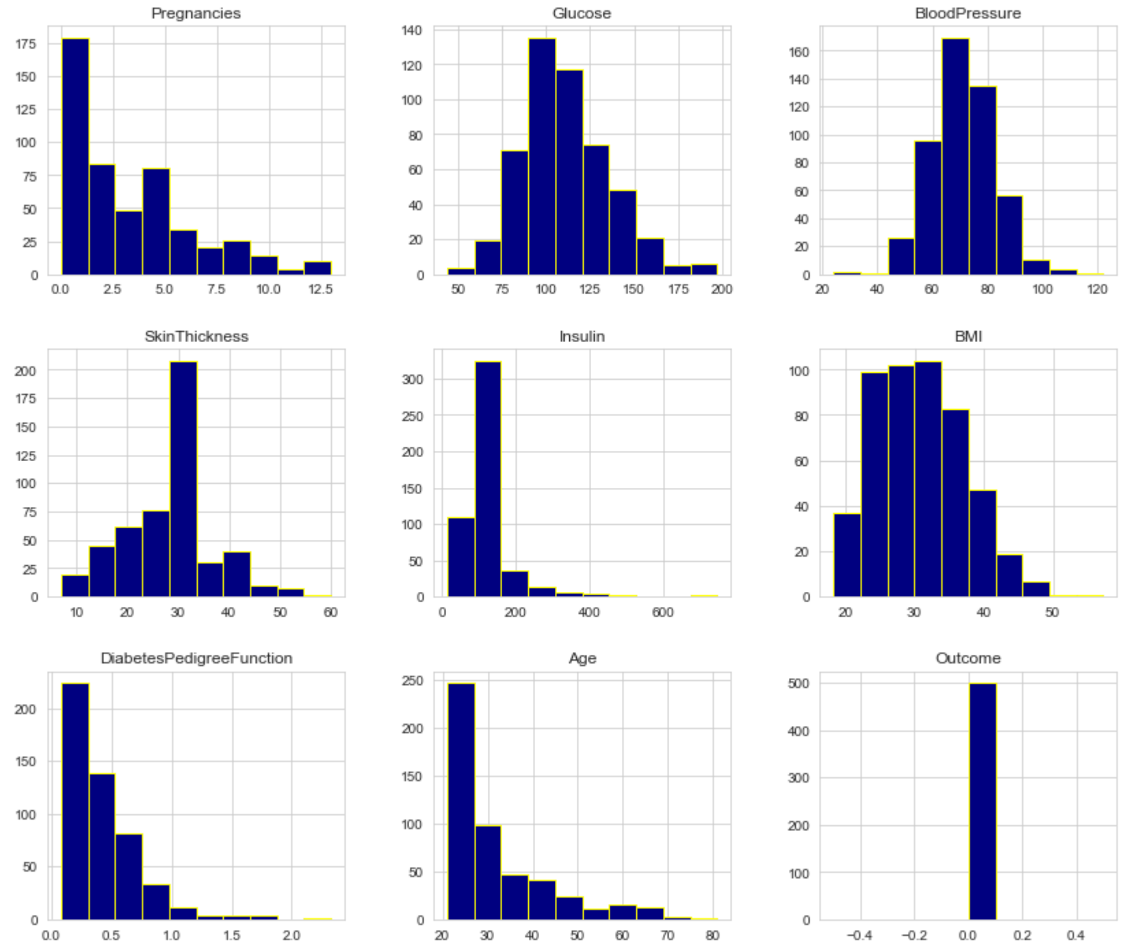


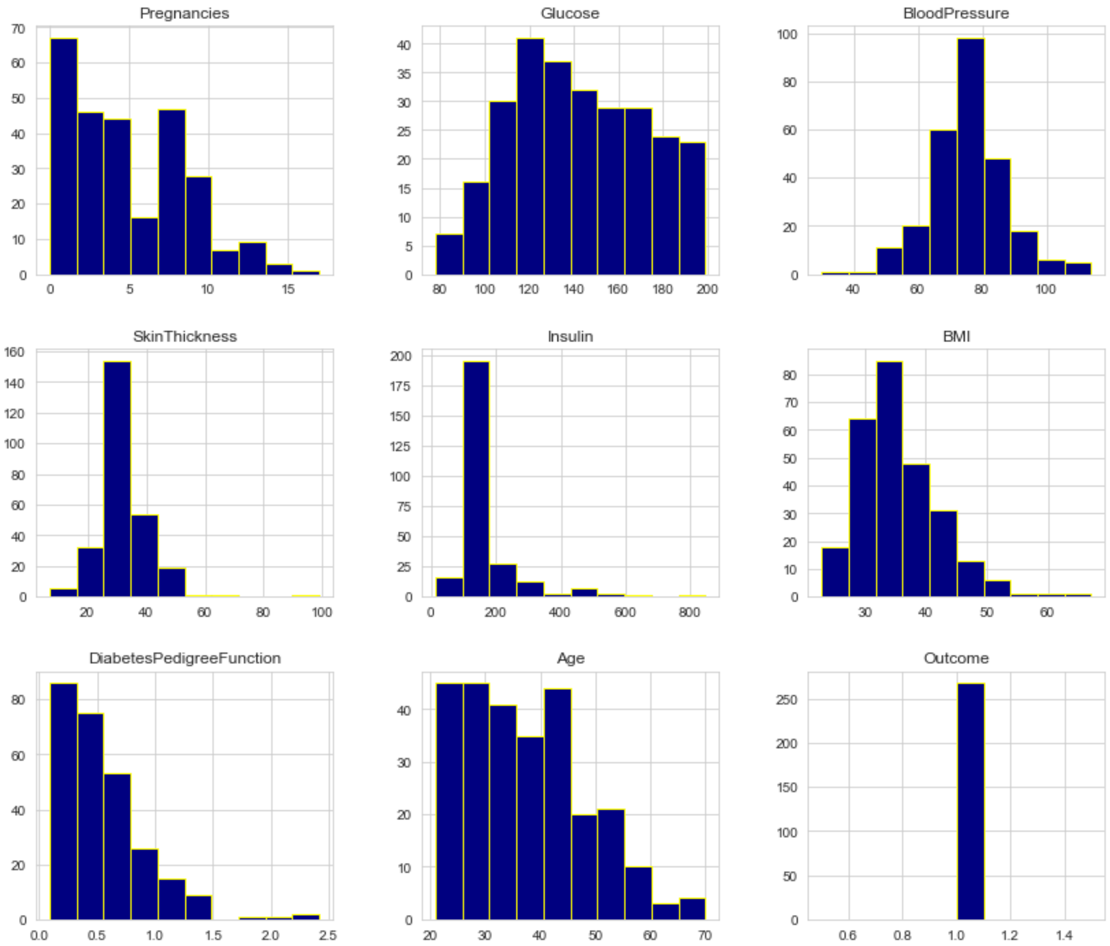
Above distplots show that there is slight deviation from Normal Distribution & data contains some Outliers.

Visual Exploration of Variables Using Histogram for possible values of Outcome(0,1)

```
health_df.groupby('Outcome').hist(figsize=(14,12),color='navy',edgecol
or='yellow')
```

```
Outcome
0    [[AxesSubplot(0.125,0.670278;0.215278x0.209722...
1    [[AxesSubplot(0.125,0.670278;0.215278x0.209722...
dtype: object
```


Pregnancies
0
25
50
75
100
125
150
175
0.0
2.5
5.0
7.5
10.0
12.5
Glucose
0
20
40
60
80
100
120
140
50
75
100
125
150
175
200
BloodPressure
0
20
40
60
80
100
120
140
160
20
40
60
80
100
120
SkinThickness
0
25
50
75
100
125
150
175
200
10
20
30
40
50
60
Insulin
0
50
100
150
200
250
300
0
200
400
600
BMI
0
20
40
60
80
100
20
30
40
50
DiabetesPedigreeFunction
0
50
100
150
200
0.0
0.5
1.0
1.5
2.0
Age
0
50
100
150
200
250
20
30
40
50
60
70
80
Outcome
0
100
200
300
400
500
−0.4
−0.2
0.0
0.2
0.4



Above code shows the frequency ditribution of all the variables in the dataset for the possible cases of Non-Diabetic(0) & Diabetic(1)

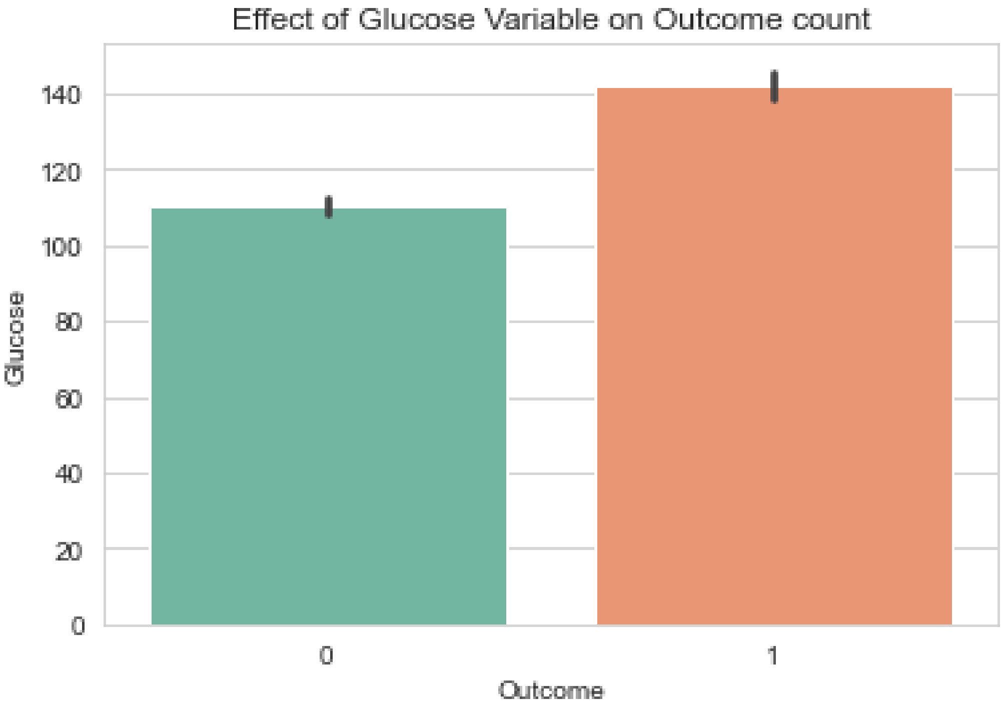
Dtypes of Variables & Outcome

```
for col,val in health_df.iteritems():
    if(val.dtype=='int64'):
        if(val.nunique()>5):
            print(col," "+'Integer_Type-Continuous')

        else:
            print(col," "+'Integer_Type-Discrete or Categorical')


    elif (val.dtype=='float64'):
        if(val.nunique()>5):
            print(col," "+'Float_Type-Continuous')

        else:
            print(col," "+'Float_Type but Discrete or Categorical')

    else:
        print(col," "+'Object_DType-Categorical')
```

```
Pregnancies  Integer_Type-Continuous
Glucose  Float_Type-Continuous
BloodPressure  Float_Type-Continuous
SkinThickness  Float_Type-Continuous
Insulin  Float_Type-Continuous
BMI  Float_Type-Continuous
DiabetesPedigreeFunction  Float_Type-Continuous
Age  Integer_Type-Continuous
Outcome  Integer_Type-Discrete or Categorical
```

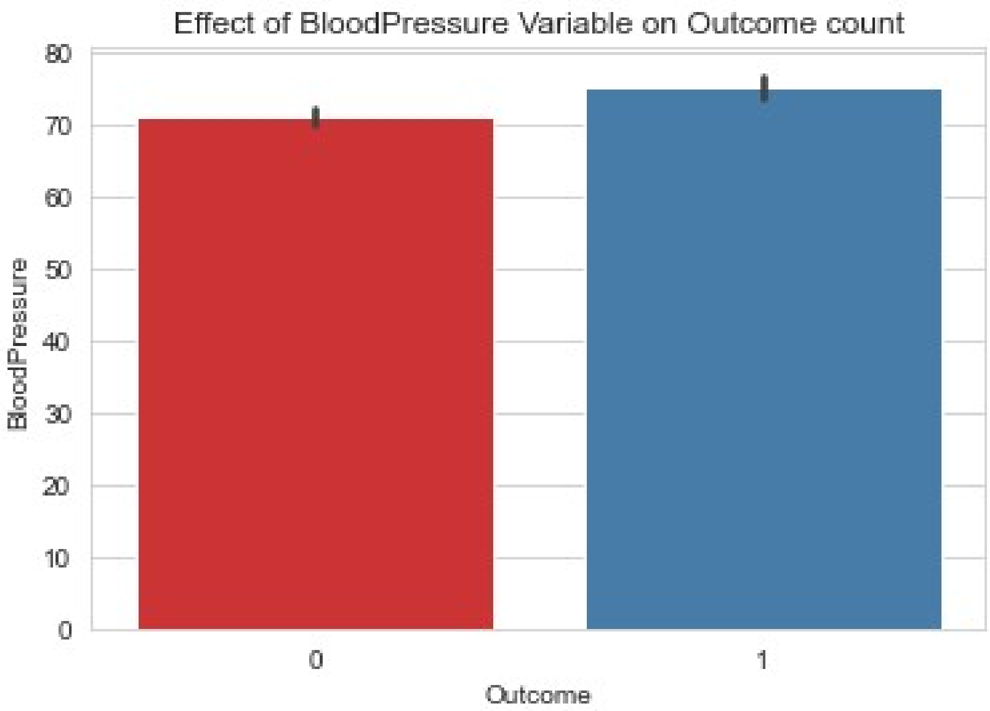
Count of variables for outcome classes

```
sns.barplot(x='Outcome',y="Glucose",data=health_df,palette='Set2')
plt.title("Effect of Glucose Variable on Outcome count")
plt.show()
```



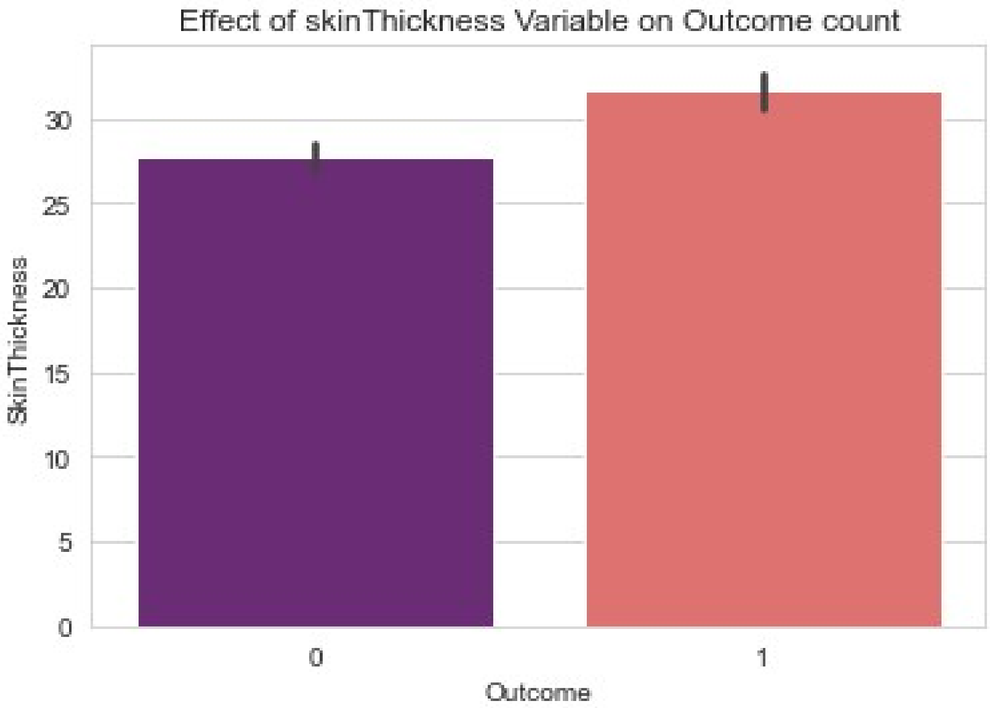
There seems to be a positive correlation between Glucose measure & Outcome.

```
sns.barplot(x='Outcome',y="BloodPressure",data=health_df,palette='Set1
')
plt.title("Effect of BloodPressure Variable on Outcome count")
plt.show()
```



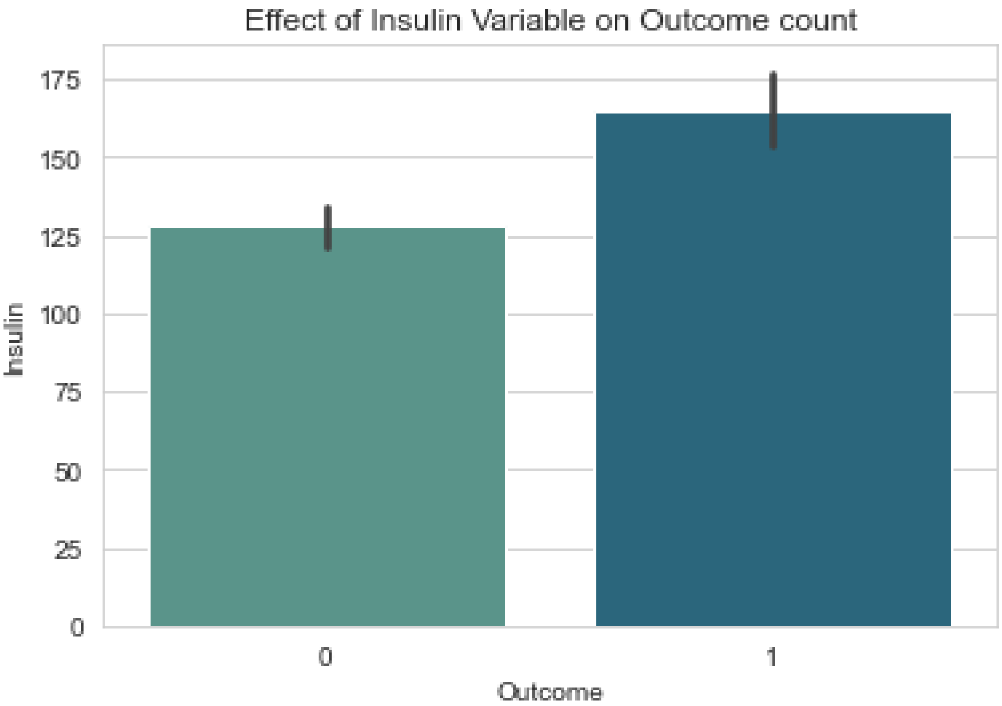
There seems to be a weak correlation between Glucose measure & Outcome.

```
sns.barplot(x='Outcome',y="SkinThickness",data=health_df,palette='magm
a')
plt.title("Effect of skinThickness Variable on Outcome count")
plt.show()
```



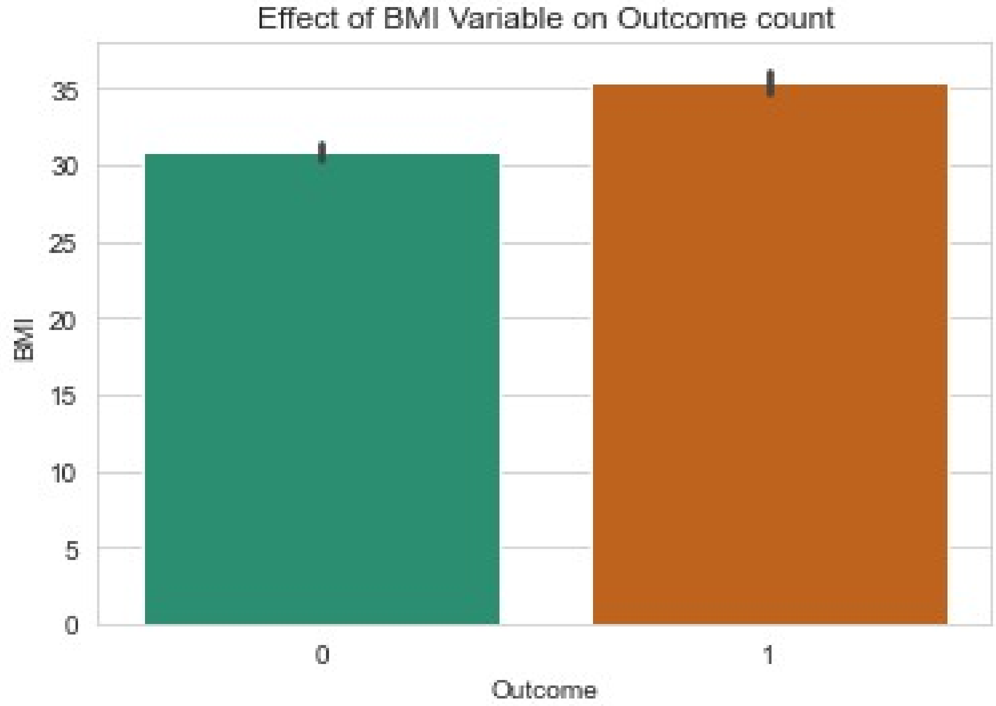
The correlation between skinThickness & Outcome doesn't seem to be significant.

```
sns.barplot(x='Outcome',y="Insulin",data=health_df,palette='crest')
plt.title("Effect of Insulin Variable on Outcome count")
plt.show()
```



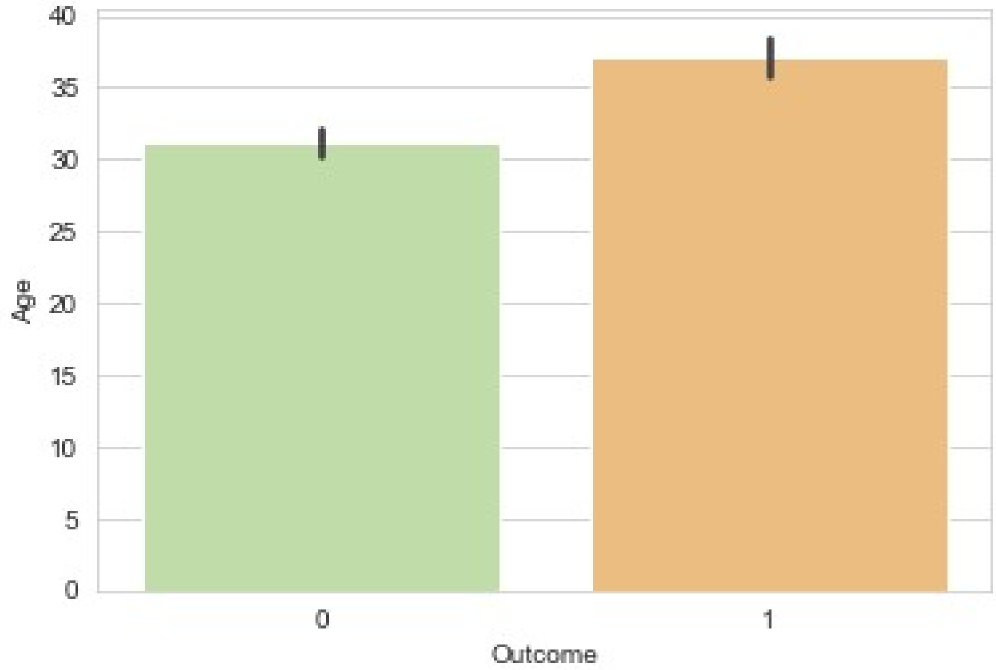
There correlation between Insulin & Outcome doesn't seem to be significant.

```
sns.barplot(x='Outcome',y="BMI",data=health_df,palette='Dark2')
plt.title("Effect of BMI Variable on Outcome count")
plt.show()
```



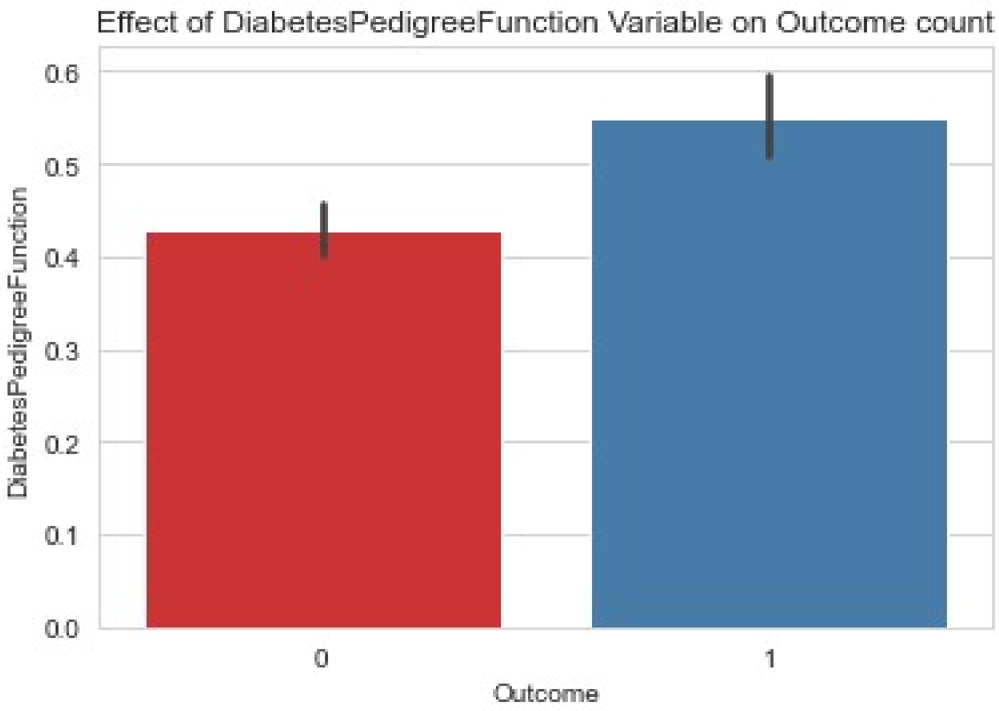
There seems to be a positive correlation between BMI measure & Outcome.

```
sns.barplot(x='Outcome',y="Age",data=health_df,palette='Spectral_r');
```



There seems to be a positive correlation between Age factor & Outcome.

```
sns.barplot(x='Outcome',y='DiabetesPedigreeFunction',data=health_df,pa
lette='Set1');
plt.title("Effect of DiabetesPedigreeFunction Variable on Outcome
count")
plt.show()
```

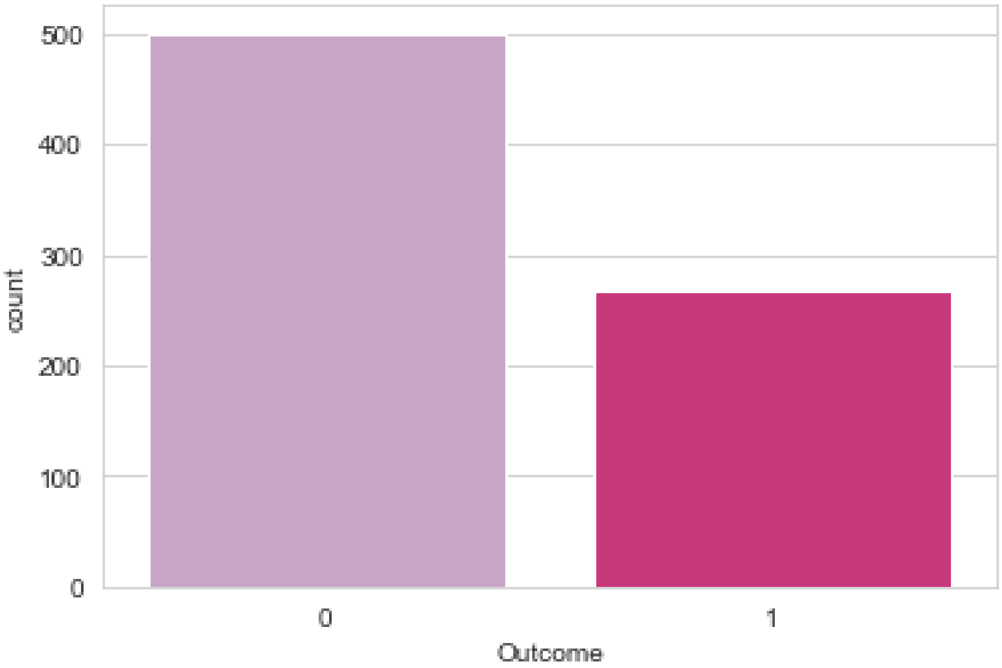


There seems to be a positive correlation between Glucose measure & Outcome.

Project Task: Week 2

Data Exploration

```
sns.countplot(x='Outcome',data=health_df,palette='PuRd');
```



```
health_df['Outcome'].value_counts()
```

```
0    500
1    268
Name: Outcome, dtype: int64
```

Here class is imbalanced ,where 65% data of Outcome Variable belongs to Class 1 & 35% data belongs to Class 0.

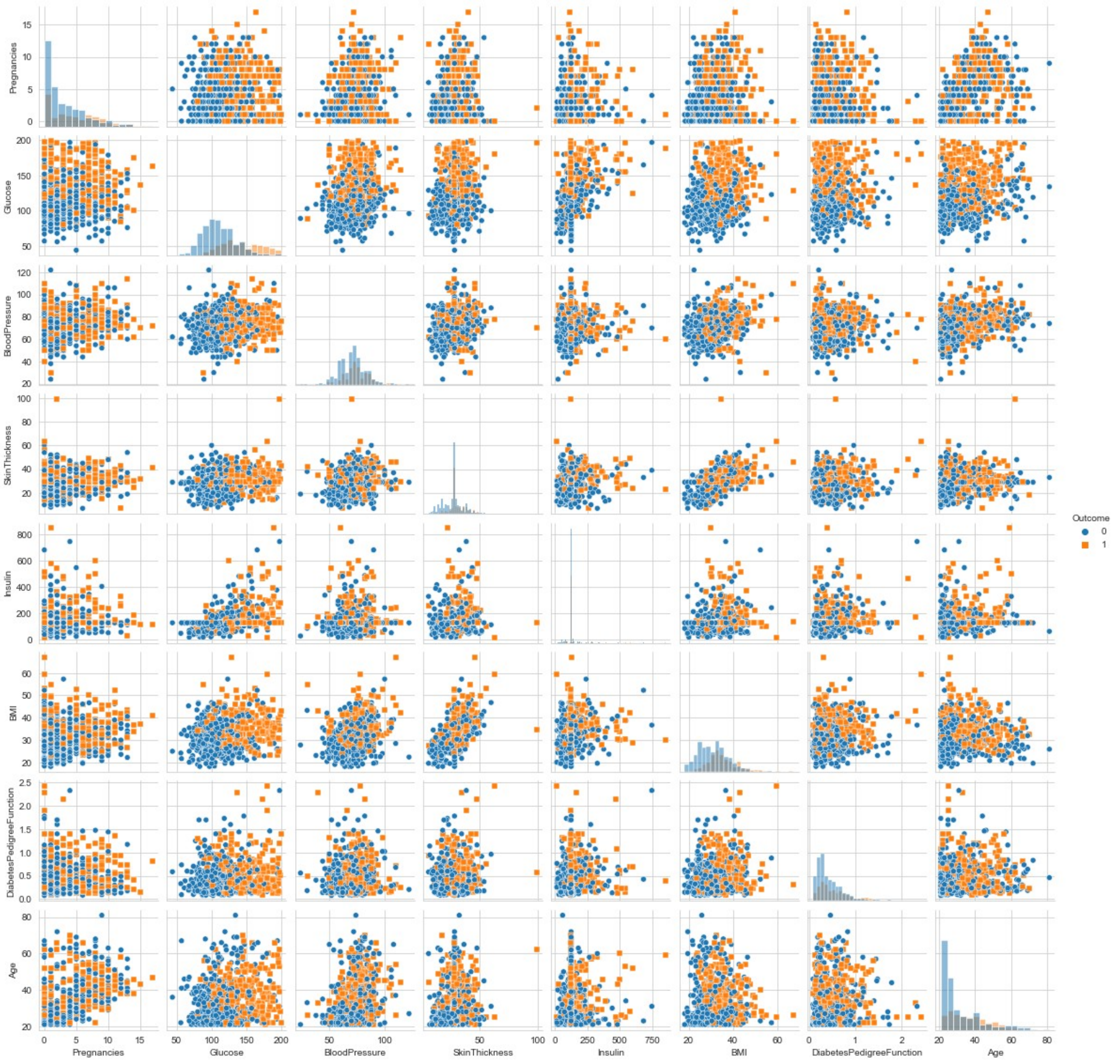
We will try to remove imbalance by Over-Sampling technique.

```
health_df.shape
```

```
(768, 9)
```

Relationship between different variables through Scatter plot employed using Pair plot

```
sns.pairplot(health_df,hue='Outcome',palette='tab10',height=2,diag_kin
d='hist',markers=['o','s']);
```



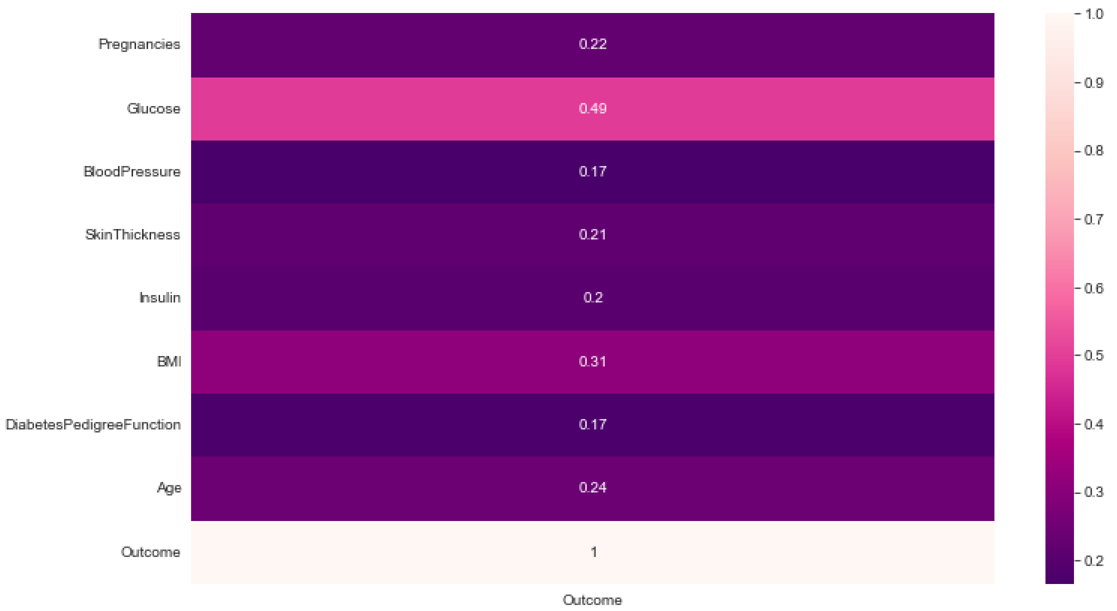
out of all the plots SkinThickness & BMI seems to have some correlation.

Correlation Analysis

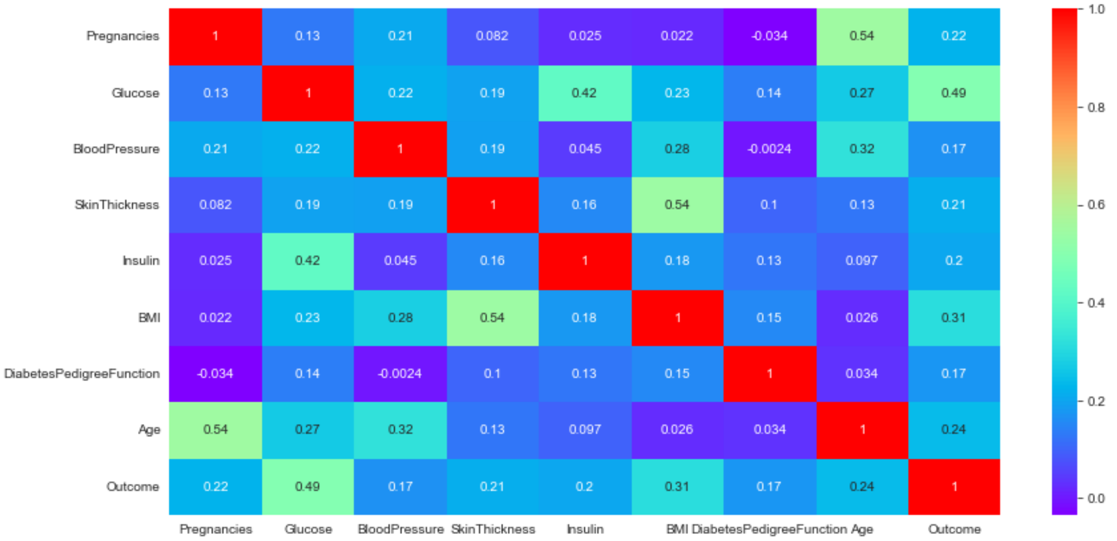
```
health_df.corr()

                          Pregnancies   Glucose  BloodPressure
SkinThickness  \
Pregnancies                  1.000000  0.128213       0.208615
0.081770
Glucose                      0.128213  1.000000       0.218937
0.192615
BloodPressure                0.208615  0.218937       1.000000
0.191892
SkinThickness                0.081770  0.192615       0.191892
1.000000
Insulin                      0.025047  0.419451       0.045363
0.155610
BMI                          0.021546  0.231400       0.281132
```

```
0.543275
DiabetesPedigreeFunction    -0.033523  0.137327      -0.002378
0.102188
Age                          0.544341  0.266909       0.324915
0.126107
Outcome                      0.221898  0.492782       0.165723
0.214873

                           Insulin       BMI  DiabetesPedigreeFunction
\
Pregnancies               0.025047  0.021546                 -0.033523

Glucose                   0.419451  0.231400                  0.137327

BloodPressure             0.045363  0.281132                 -0.002378

SkinThickness             0.155610  0.543275                  0.102188

Insulin                   1.000000  0.180373                  0.126503

BMI                       0.180373  1.000000                  0.153506

DiabetesPedigreeFunction  0.126503  0.153506                  1.000000

Age                       0.097101  0.025744                  0.033561

Outcome                   0.203790  0.312249                  0.173844


                               Age   Outcome
Pregnancies               0.544341  0.221898
Glucose                   0.266909  0.492782
BloodPressure             0.324915  0.165723
SkinThickness             0.126107  0.214873
Insulin                   0.097101  0.203790
BMI                       0.025744  0.312249
DiabetesPedigreeFunction  0.033561  0.173844
Age                       1.000000  0.238356
Outcome                   0.238356  1.000000
```

```
plt.figure(figsize=(12,7))
sns.heatmap(health_df.corr()[['Outcome']],annot=True, cmap='RdPu_r');
```



```
plt.figure(figsize=(14,7))
sns.heatmap(health_df.corr(),annot=True, cmap='rainbow');
```



Correlation analysis shows that there is no multi collinearity among the features.

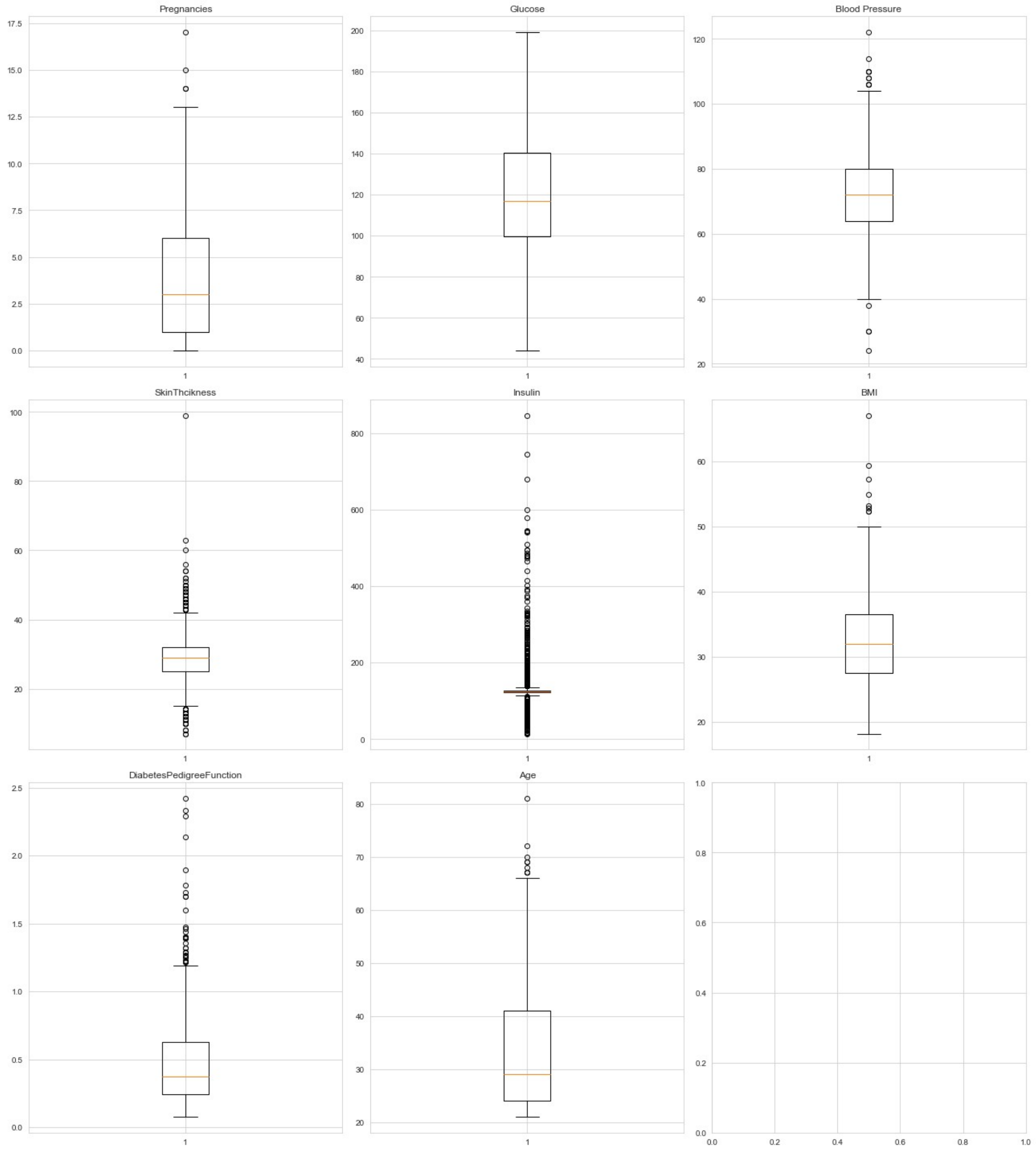
It also seems that some independent variables may be insignificant for modelling purpose.

Outlier Detection & Removal

```
health_df.columns
```

```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness',
'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

```python
fig,ax=plt.subplots(3,3,figsize=(18,20))
ax[0,0].boxplot(health_df['Pregnancies'])
ax[0,1].boxplot(health_df['Glucose'])
ax[0,2].boxplot(health_df['BloodPressure'])
ax[1,0].boxplot(health_df['SkinThickness'])
ax[1,1].boxplot(health_df['Insulin'])
ax[1,2].boxplot(health_df['BMI'])
ax[2,0].boxplot(health_df['DiabetesPedigreeFunction'])
ax[2,1].boxplot(health_df['Age'])


ax[0,0].set_title('Pregnancies')
ax[0,1].set_title('Glucose')
ax[0,2].set_title('Blood Pressure')
ax[1,0].set_title('SkinThcikness')
ax[1,1].set_title('Insulin')
ax[1,2].set_title('BMI')
ax[2,0].set_title('DiabetesPedigreeFunction')
ax[2,1].set_title('Age')

plt.tight_layout()
plt.show();
```



```
health_df.describe()

       Pregnancies     Glucose  BloodPressure  SkinThickness  
Insulin  \
count   768.000000  768.000000     768.000000     768.000000  
768.000000   
mean      3.845052  121.656250      72.386719      29.108073  
140.671875   
std       3.369578   30.438286      12.096642       8.791221   
86.383060   
min       0.000000   44.000000      24.000000       7.000000   
14.000000   
25%       1.000000   99.750000      64.000000      25.000000   
```

```
121.500000
50%       3.000000  117.000000      72.000000      29.000000
125.000000
75%       6.000000  140.250000      80.000000      32.000000
127.250000
max      17.000000  199.000000     122.000000      99.000000
846.000000

              BMI  DiabetesPedigreeFunction         Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
mean    32.450911                  0.471876   33.240885    0.348958
std      6.875366                  0.331329   11.760232    0.476951
min     18.200000                  0.078000   21.000000    0.000000
25%     27.500000                  0.243750   24.000000    0.000000
50%     32.000000                  0.372500   29.000000    0.000000
75%     36.600000                  0.626250   41.000000    1.000000
max     67.100000                  2.420000   81.000000    1.000000
```

```
#Creating a copy of Health_df

health=health_df.copy()
health.shape
```

```
(768, 9)
```

Project Task: Week 3

Check for significant features

```
import statsmodels.api as sm

features=health.drop(columns='Outcome')
target=health['Outcome']

sm_model=sm.OLS(target,features).fit()
sm_model
sm_model.summary()
```

```
<class 'statsmodels.iolib.summary.Summary'>
"""
                                 OLS Regression Results

======================================================================
=================
Dep. Variable:                Outcome   R-squared (uncentered):
0.502
Model:                            OLS   Adj. R-squared (uncentered):
0.496
Method:                 Least Squares   F-statistic:
95.66
Date:                Sat, 08 Oct 2022   Prob (F-statistic):
```

```
1.28e-109
Time:                        20:03:30   Log-Likelihood:
-417.96
No. Observations:                 768   AIC:
851.9
Df Residuals:                     760   BIC:
889.1
Df Model:                           8

Covariance Type:            nonrobust

======================================================================
======================
                               coef    std err          t      P>|t|
[0.025      0.975]
----------------------------------------------------------------------
----------------------
Pregnancies                  0.0247      0.005      4.613      0.000
0.014       0.035
Glucose                      0.0052      0.001      9.271      0.000
0.004       0.006
BloodPressure               -0.0084      0.001     -7.227      0.000
-0.011      -0.006
SkinThickness               -0.0009      0.002     -0.448      0.654
-0.005       0.003
Insulin                     -0.0001      0.000     -0.602      0.548
-0.001       0.000
BMI                          0.0072      0.003      2.724      0.007
0.002       0.012
DiabetesPedigreeFunction     0.0925      0.047      1.984      0.048
0.001       0.184
Age                          0.0004      0.002      0.225      0.822
-0.003       0.004
======================================================================
========
Omnibus:                      195.899   Durbin-Watson:
2.019
Prob(Omnibus):                  0.000   Jarque-Bera (JB):
66.733
Skew:                           0.519   Prob(JB):
3.23e-15
Kurtosis:                       1.995   Cond. No.
675.
======================================================================
========

Notes:
[1] R² is computed without centering (uncentered) since the model does
not contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is
```

```
correctly specified.
"""
```

```
health.corr()['Outcome']*100
```

```
Pregnancies                  22.189815
Glucose                      49.278240
BloodPressure                16.572291
SkinThickness                21.487322
Insulin                      20.379034
BMI                          31.224903
DiabetesPedigreeFunction     17.384407
Age                          23.835598
Outcome                     100.000000
Name: Outcome, dtype: float64
```

On analysing the p_value of features, we find that features like { Age,SkinThickness & Insulin) are statistically insignificant.

```
from sklearn.ensemble import ExtraTreesClassifier
model=ExtraTreesClassifier()
model.fit(features,target)
```

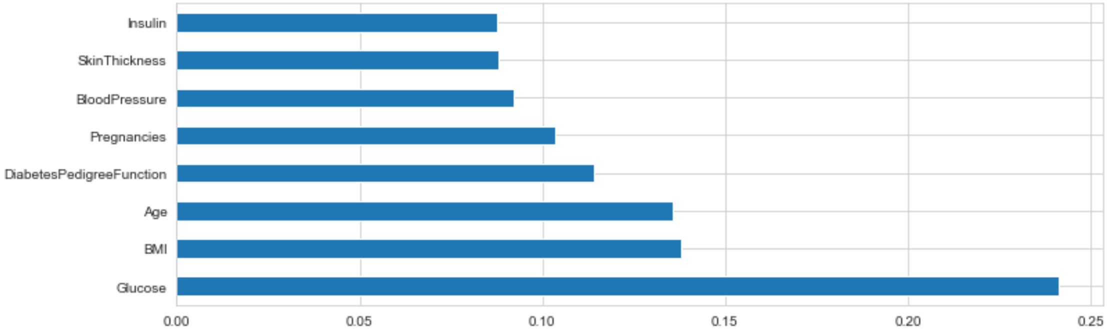
```
ExtraTreesClassifier()
```

```
print(model.feature_importances_)
```

```
[0.10344518 0.241295   0.09214672 0.08784809 0.08762691 0.13775837
 0.11420148 0.13567825]
```

```
plt.figure(figsize=(12,4))
ranked_features=pd.Series(model.feature_importances_,index=health.colu
mns[:-1])
ranked_features.nlargest(8).plot(kind='barh')
```

```
<AxesSubplot:>
```



```
health.corr()['Outcome'].sort_values(ascending=True)*100
```

```
BloodPressure                16.572291
DiabetesPedigreeFunction     17.384407
Insulin                      20.379034
```

```
SkinThickness                 21.487322
Pregnancies                   22.189815
Age                           23.835598
BMI                           31.224903
Glucose                       49.278240
Outcome                      100.000000
Name: Outcome, dtype: float64
```

On analysing 1)the p_value of features using OLS Statsmodels we find that features like { Age,SkinThickness & Insulin) are statistically insignificant where as 2)ExtraTreeClassifier predicts features like (BloodPressure,SkinThickness & Insulin) are leastsignificant whereas 3) Correlation matrix describes BloodPressure ,SkinThickness ,Pregnancies,Insulin to be amongst least correlated the outcome. So combining results from 1) & 2) and using correlation value,

We conclude that features like Insulin,SkinThickness are not significant.

Hence, we might not consider these features for model building.

```
features=features.drop(columns=['Insulin','SkinThickness'])
features.shape
```

```
(768, 6)
```

Outlier Detection & removal

```
q1=health_df['DiabetesPedigreeFunction'].quantile(0.25)
q3=health_df['DiabetesPedigreeFunction'].quantile(0.75)
iqr=q3-q1
max=1.5*iqr+ q3
min=q1-1.5*iqr
print(max,min)
```

```
1.2 -0.32999999999999996
```

```
np.where(health_df['DiabetesPedigreeFunction']>1.3)
```

```
(array([  4,  12,  39,  45,  58, 147, 187, 228, 243, 259, 308, 330, 
370,
        371, 395, 445, 593, 621, 622, 661], dtype=int64),)
```

```
np.where(health_df['DiabetesPedigreeFunction']<-0.32)
```

```
(array([], dtype=int64),)
```

```
np.where(health_df['Pregnancies']>13)
```

```
(array([ 88, 159, 298, 455], dtype=int64),)
```

```
np.where(health_df['BMI']>60)
```

```
(array([177], dtype=int64),)
```

```
np.where(health_df['BloodPressure']>110)
```

```
(array([106, 691], dtype=int64),)
```

```
np.where(health_df['BloodPressure']<30)
```

```
(array([597], dtype=int64),)
```

```
outliers={4,  12,  39,  45,  58, 147, 187, 228, 243, 259, 308, 330,
370,
        371, 395, 593, 621, 622, 661,88, 159, 298, 455}
outliers=list(outliers)
outliers
```

```
[259,
 4,
 455,
 330,
 395,
 12,
 593,
 147,
 661,
 88,
 159,
 228,
 39,
 298,
 45,
 621,
 622,
 370,
 243,
 308,
 371,
 58,
 187]
```

```
health=health.drop(outliers,axis=0)
health.shape
```

```
(745, 9)
```

Handling Class Imbalanced Data & Over_Sampling

```
health=health.drop(columns=['Insulin','SkinThickness'])
health.shape
```

```
(745, 7)
```

```
health['Outcome'].value_counts(normalize=True)*100
```

```
0    65.771812
1    34.228188
Name: Outcome, dtype: float64
```

```
health['Outcome'].value_counts()
```

```
0    490
1    255
Name: Outcome, dtype: int64
```

It is evident that Outcome has imbalanced data as 253 observations belong to Class 0 (i.e 34%)

while 489 observations belong to Class 1(i.e 66%)

Since the size of the Dataset is small, we can consider :

1)Over_Sampling Technique to balance the data

First we will divide the dataset into two parts, one for training & validation and other for testing. So, first we will use Train_test_split to divide the dataset & then use SKF for training & validation.

```
health.shape
```

```
(745, 7)
```

```
data=health.drop(columns='Outcome')
target=health['Outcome']
```

Splitting the dataset into 1)Train & Validation Set and 2)Test Set

```
from sklearn.model_selection import train_test_split
x, x_test, y, y_test = train_test_split(data, target, test_size = 0.2,
random_state = 1)
print(x.shape, x_test.shape, y.shape, y_test.shape)
```

```
(596, 6) (149, 6) (596,) (149,)
```

```
y.value_counts()
```

```
0    391
1    205
Name: Outcome, dtype: int64
```

Oversampling by SMOTE

```
from imblearn.over_sampling import SMOTE
smote=SMOTE(sampling_strategy='minority')
x_os,y_os=smote.fit_resample(x,y)
```

```
y_os.value_counts()
```

```
0    391
1    391
Name: Outcome, dtype: int64
```

Both classes have the same number of count after Over sampling ,hence the data is balanced.

Startified K-Fold CV

```
from sklearn.model_selection import StratifiedKFold
skf=StratifiedKFold(n_splits=5)
skf
```

```
StratifiedKFold(n_splits=5, random_state=None, shuffle=False)
```

```
from sklearn.neighbors import KNeighborsClassifier
model1=KNeighborsClassifier(n_neighbors=5, p=2,metric='minkowski')
```

```
from sklearn.linear_model import LogisticRegression
model2=LogisticRegression(solver = 'newton-cg', C = 1000,
penalty='l2')
```

```
from sklearn.ensemble import RandomForestClassifier
model3=RandomForestClassifier(n_estimators=50,max_depth=40)
```

```
from sklearn.svm import SVC
model4=SVC()
```

```
from sklearn.naive_bayes import GaussianNB
model5=GaussianNB(var_smoothing=1e-07)
```

```
from xgboost import XGBClassifier
model6=XGBClassifier(base_score=0.25, booster='gbtree',
             colsample_bylevel=1, colsample_bynode=1,
colsample_bytree=1,n_estimators=50)
```

```
from sklearn.model_selection import cross_val_score

def get_scores(model):
    score=cross_val_score(model,x_os,y_os,cv=skf)
    mean_score=np.mean(score)
    print('Model: ',model)
    return mean_score
```

```
get_scores(model1)
```

```
Model:  KNeighborsClassifier()

0.7763187979748489
```

```
get_scores(model2)
```

```
Model:  LogisticRegression(C=1000, solver='newton-cg')

0.7417034133594643
```

```
get_scores(model3)
```

```
Model:  RandomForestClassifier(max_depth=40, n_estimators=50)

0.826139147476727
```

```
get_scores(model4)

Model:  SVC()

0.7276171811203659

get_scores(model5)

Model:  GaussianNB(var_smoothing=1e-07)

0.7365997060264576

get_scores(model6)

Model:  XGBClassifier(base_score=0.25, booster='gbtree',
callbacks=None,
              colsample_bylevel=1, colsample_bynode=1,
colsample_bytree=1,
              early_stopping_rounds=None, enable_categorical=False,
              eval_metric=None, gamma=None, gpu_id=None,
grow_policy=None,
              importance_type=None, interaction_constraints=None,
              learning_rate=None, max_bin=None,
max_cat_to_onehot=None,
              max_delta_step=None, max_depth=None, max_leaves=None,
              min_child_weight=None, missing=nan,
monotone_constraints=None,
              n_estimators=50, n_jobs=None, num_parallel_tree=None,
              predictor=None, random_state=None, reg_alpha=None,
              reg_lambda=None, ...)

0.8094888126735261
```

Comparing the performance of KNN Algorithm with five other Algoritms using Stratified K-Fold CV score, KNN is 3rd ranked model in terms of accuracy while Random Forest gives the best result & Naive Bayes being the worst performer.

Project Task: Week 4

Model Building Using KNeighbours Classifier

```
from sklearn.neighbors import KNeighborsClassifier
model1=KNeighborsClassifier(n_neighbors=9, p=2,metric='minkowski')

model1.fit(x_os,y_os)

KNeighborsClassifier(n_neighbors=9)

model1.score(x_os,y_os)

0.8132992327365729

y_pred1=model1.predict(x_test)
```

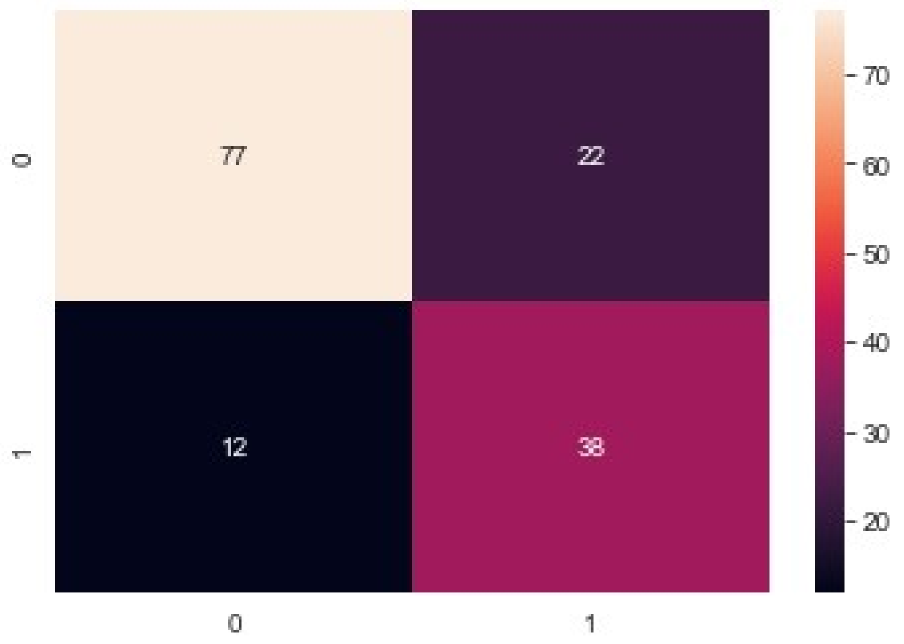
```
model1.score(x_test,y_test)
```

```
0.7718120805369127
```

```
from sklearn.metrics import confusion_matrix,classification_report
cm=confusion_matrix(y_test,y_pred1)
cm
```

```
array([[77, 22],
       [12, 38]], dtype=int64)
```

```
plt.figure(figsize=(6,4))
sns.heatmap(confusion_matrix(y_test,y_pred1),annot=True,fmt='0.0f');
```



```
print(classification_report(y_test, y_pred1))
```

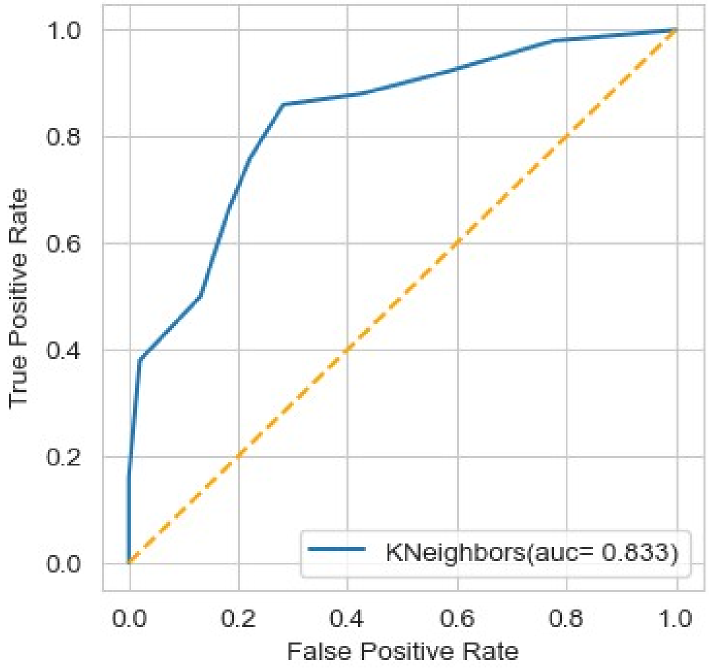
```
              precision    recall  f1-score   support

           0       0.87      0.78      0.82        99
           1       0.63      0.76      0.69        50

    accuracy                           0.77       149
   macro avg       0.75      0.77      0.76       149
weighted avg       0.79      0.77      0.78       149
```

```
sensitivity=cm[1,1]/(cm[1,1]+cm[1,0])
specificity=cm[0,0]/(cm[0,0]+cm[0,1])
print("Sensitivity:",  sensitivity)
print("Specificity:", np.round((specificity),2))
```

```
Sensitivity: 0.76
Specificity: 0.78
```

ROC Curve & AUC

```
from sklearn.metrics import roc_curve,auc
y_curve=model1.predict_proba(x_test)[:,1]
FPR,TPR,threshold=roc_curve(y_test,y_curve)
auc=auc(FPR,TPR)

plt.figure(figsize=(4,4),dpi=100)
plt.plot(FPR,TPR,label="KNeighbors(auc= %0.3f)"% auc)
plt.plot([0,1],[0,1],color='orange',linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.legend()
plt.show()
```



Model Building Using Random Forest Classifier

```
model3=RandomForestClassifier(n_estimators=70,max_depth=20,criterion='
entropy',min_samples_split=4,

max_leaf_nodes=25,min_samples_leaf=3,max_samples=0.2,max_features=3)

model3.fit(x_os,y_os)

RandomForestClassifier(criterion='entropy', max_depth=20,
max_features=3,
                       max_leaf_nodes=25, max_samples=0.2,
min_samples_leaf=3,
                       min_samples_split=4, n_estimators=70)
```

```
model3.score(x_test,y_test)
```

```
0.7651006711409396
```

```
model3.score(x_os,y_os)
```

```
0.8337595907928389
```

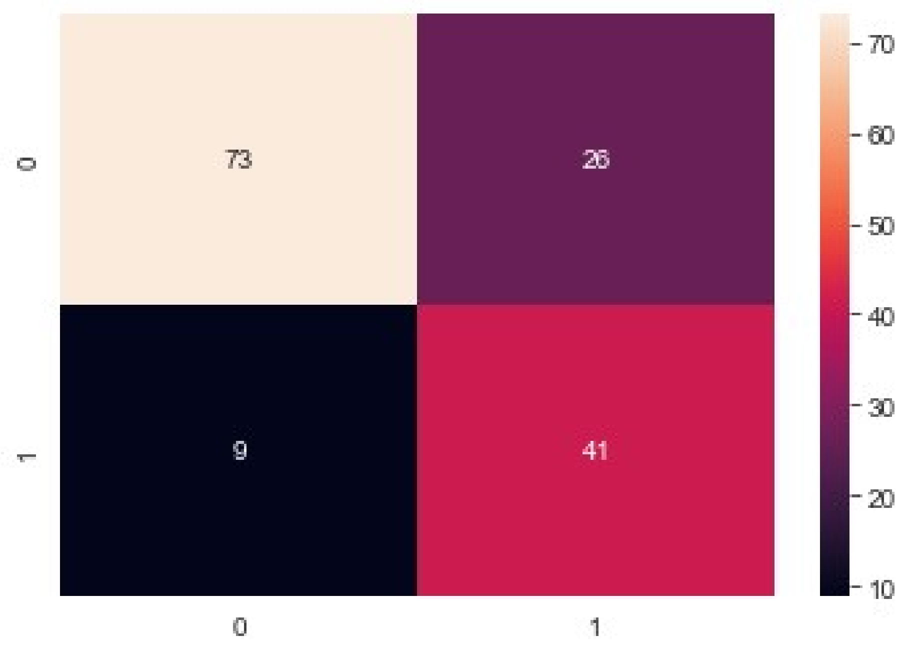
```
y_pred3=model3.predict(x_test)
```

Classification metrics

```
from sklearn.metrics import confusion_matrix, classification_report
confusion_matrix(y_test,y_pred3)
cm=confusion_matrix(y_test,y_pred3)
```

```
plt.figure(figsize=(6,4))
sns.heatmap(confusion_matrix(y_test, y_pred3), annot = True, fmt =
'0.0f')
```

```
<AxesSubplot:>
```



```
print(classification_report(y_test, y_pred3))
```

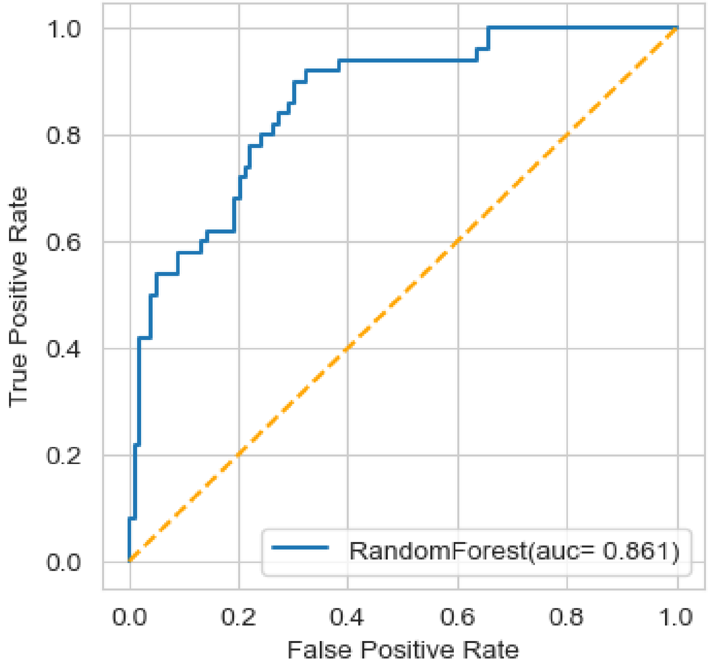
```
              precision    recall  f1-score   support

           0       0.89      0.74      0.81        99
           1       0.61      0.82      0.70        50

    accuracy                           0.77       149
   macro avg       0.75      0.78      0.75       149
weighted avg       0.80      0.77      0.77       149
```

```
sensitivity=cm[1,1]/(cm[1,1]+cm[1,0])
specificity=cm[0,0]/(cm[0,0]+cm[0,1])
print("Sensitivity:",  sensitivity)
print("Specificity:", np.round((specificity),2))
```

```
Sensitivity: 0.82
Specificity: 0.74
```

Roc curve & AUC

```
from sklearn.metrics import roc_curve,auc
y_curve=model3.predict_proba(x_test)[:,1]

FPR,TPR,threshold=roc_curve(y_test,y_curve)
auc_RF=auc(FPR,TPR)

plt.figure(figsize=(4,4),dpi=100)
plt.plot(FPR,TPR,label="RandomForest(auc= %0.3f)"% auc_RF)
plt.plot([0,1],[0,1],color='orange',linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.legend()
plt.show()
```



Model Building Using Logistic Regression

```
from sklearn.linear_model import LogisticRegression
model2=LogisticRegression(solver = 'newton-cg', C = 1000,
penalty='l2')

model2.fit(x_os,y_os)
```

```
LogisticRegression(C=1000, solver='newton-cg')
```

```
model2.score(x_os,y_os)
```

```
0.7506393861892583
```

```
model2.score(x_test,y_test)
```

```
0.7583892617449665
```

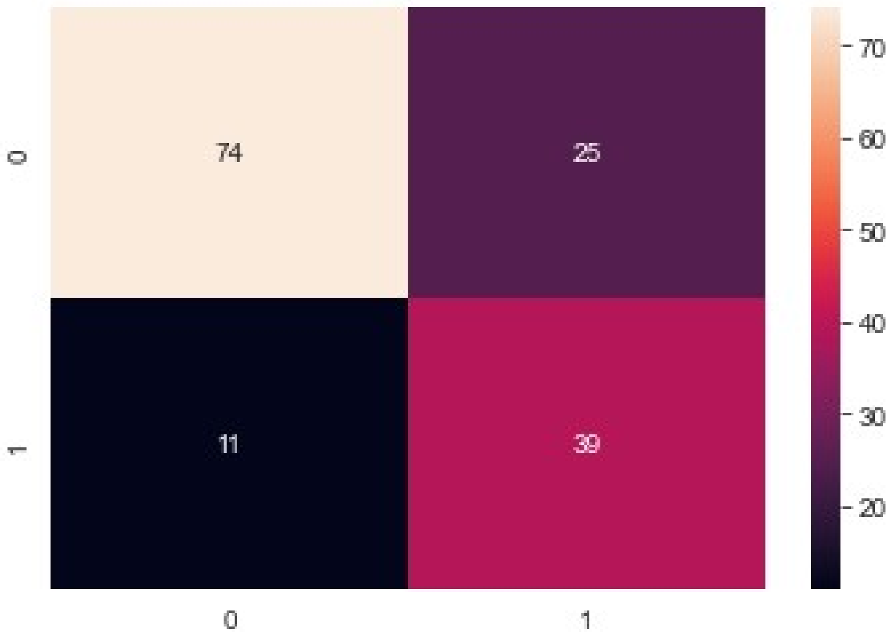
```
y_pred2=model2.predict(x_test)
```

Classification Metrics

```
from sklearn.metrics import confusion_matrix, classification_report
confusion_matrix(y_test,y_pred2)
cm=confusion_matrix(y_test,y_pred2)
```

```
plt.figure(figsize=(6,4))
sns.heatmap(confusion_matrix(y_test, y_pred2), annot = True, fmt = 
'0.0f')
```

```
<AxesSubplot:>
```



```
print(classification_report(y_test, y_pred2))
```

```
              precision    recall  f1-score   support

           0       0.87      0.75      0.80        99
           1       0.61      0.78      0.68        50

    accuracy                           0.76       149
   macro avg       0.74      0.76      0.74       149
```

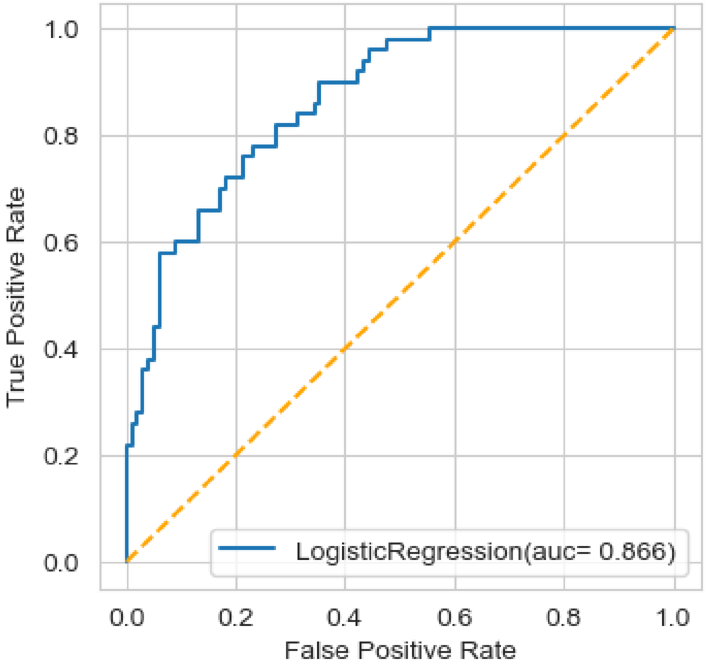
```
weighted avg       0.78      0.76      0.76       149
```

```
sensitivity=cm[1,1]/(cm[1,1]+cm[1,0])
specificity=cm[0,0]/(cm[0,0]+cm[0,1])
print("Sensitivity:", np.round((sensitivity),2))
print("Specificity:", np.round((specificity),2))
```

```
Sensitivity: 0.78
Specificity: 0.75
```

ROC Curve & AUC

```
from sklearn.metrics import roc_curve,auc
y_curve=model2.predict_proba(x_test)[:,1]

FPR,TPR,threshold=roc_curve(y_test,y_curve)
auc=auc(FPR,TPR)

plt.figure(figsize=(4,4),dpi=100)
plt.plot(FPR,TPR,label="LogisticRegression(auc= %0.3f)"% auc)
plt.plot([0,1],[0,1],color='orange',linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.legend()
plt.show()
```



Model Building Using SVM

```
from sklearn.svm import SVC
model4=SVC(C=10,gamma=0.0001,probability=True)
```

```
model4.fit(x_os,y_os)
```

```
SVC(C=10, gamma=0.0001, probability=True)
```

```
model4.score(x_os,y_os)
```

```
0.7800511508951407
```

```
model4.score(x_test,y_test)
```

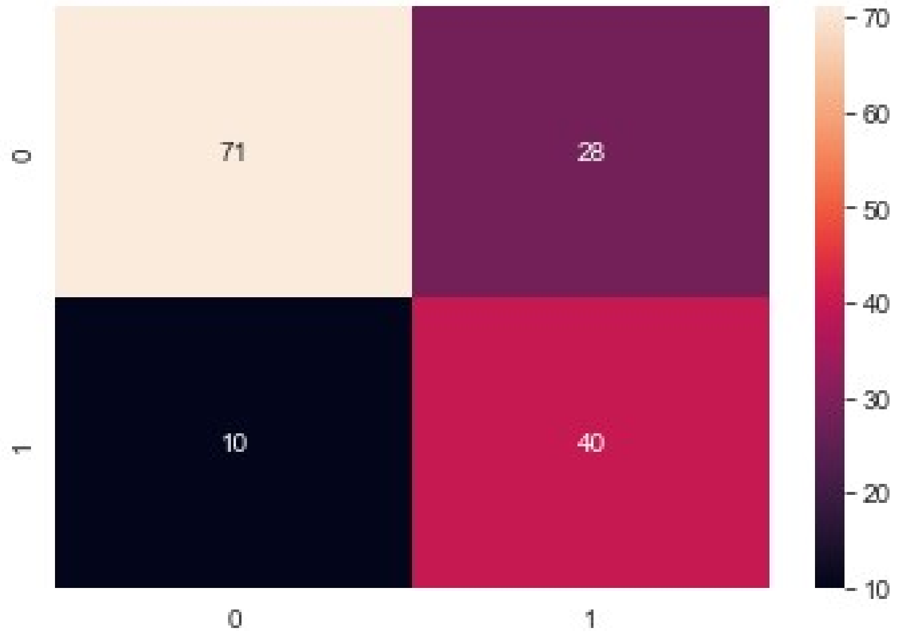
```
0.7449664429530202
```

```
y_pred4=model4.predict(x_test)
```

Classifiaction Metrics

```
from sklearn.metrics import confusion_matrix, classification_report
confusion_matrix(y_test,y_pred4)
cm=confusion_matrix(y_test,y_pred4)

plt.figure(figsize=(6,4))
sns.heatmap(confusion_matrix(y_test, y_pred4), annot = True, fmt =
'0.0f')
```

```
<AxesSubplot:>
```



```
print(classification_report(y_test, y_pred4))
```

```
              precision    recall  f1-score   support

           0       0.88      0.72      0.79        99
           1       0.59      0.80      0.68        50
```

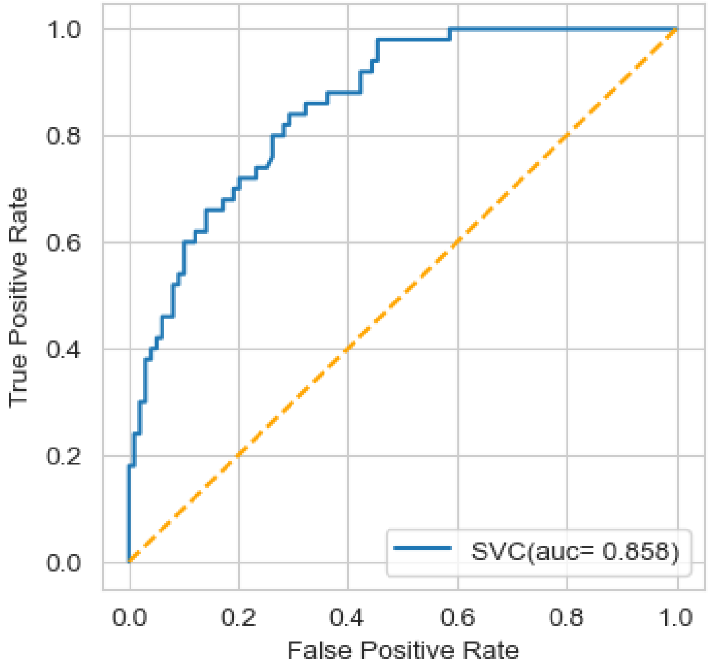
```
    accuracy                           0.74       149
   macro avg       0.73      0.76      0.73       149
weighted avg       0.78      0.74      0.75       149
```

```
sensitivity=cm[1,1]/(cm[1,1]+cm[1,0])
specificity=cm[0,0]/(cm[0,0]+cm[0,1])
print("Sensitivity:", np.round((sensitivity),2))
print("Specificity:", np.round((specificity),2))
```

```
Sensitivity: 0.8
Specificity: 0.72
```

Roc Curve & AUC

```
from sklearn.metrics import roc_curve,auc
y_curve=model4.predict_proba(x_test)[:,1]

FPR,TPR,threshold=roc_curve(y_test,y_curve)
auc=auc(FPR,TPR)

plt.figure(figsize=(4,4),dpi=100)
plt.plot(FPR,TPR,label="SVC(auc= %0.3f)"% auc)
plt.plot([0,1],[0,1],color='orange',linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.legend()
plt.show()
```

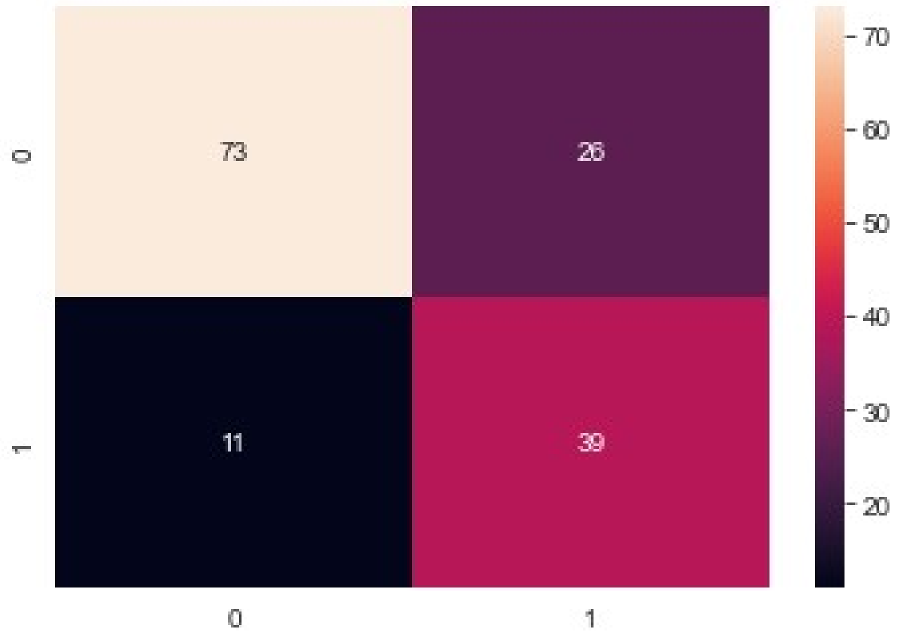


Model Building Using Naive Bayes

```
from sklearn.naive_bayes import GaussianNB
model5=GaussianNB(var_smoothing=1e-07)

model5.fit(x_os,y_os)

GaussianNB(var_smoothing=1e-07)

model5.score(x_os,y_os)

0.7468030690537084

model5.score(x_test,y_test)

0.7516778523489933

y_pred5=model5.predict(x_test)
```

Classification Metrics

```
from sklearn.metrics import confusion_matrix, classification_report
confusion_matrix(y_test,y_pred5)
cm=confusion_matrix(y_test,y_pred5)

plt.figure(figsize=(6,4))
sns.heatmap(confusion_matrix(y_test, y_pred5), annot = True, fmt =
'0.0f')

<AxesSubplot:>
```



```
print(classification_report(y_test, y_pred5))
```

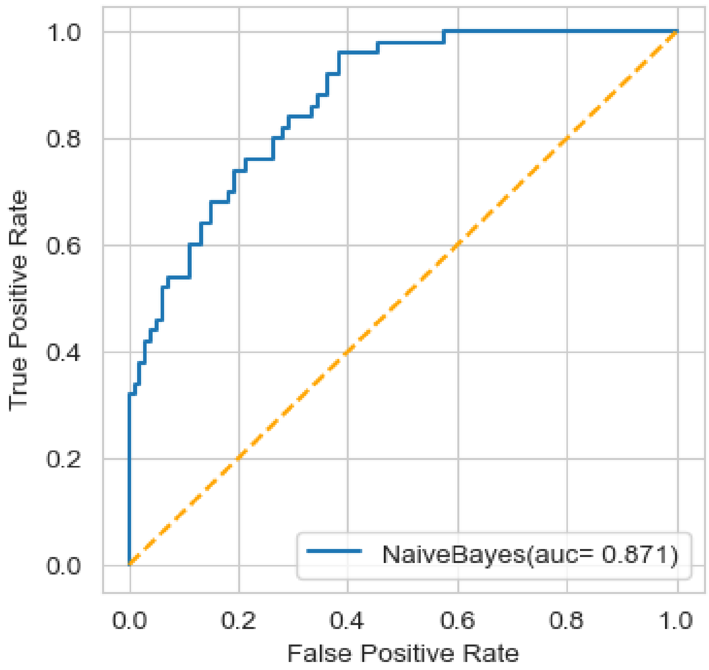
```
              precision    recall  f1-score   support

           0       0.87      0.74      0.80        99
           1       0.60      0.78      0.68        50

    accuracy                           0.75       149
   macro avg       0.73      0.76      0.74       149
weighted avg       0.78      0.75      0.76       149
```

```
sensitivity=cm[1,1]/(cm[1,1]+cm[1,0])
specificity=cm[0,0]/(cm[0,0]+cm[0,1])
print("Sensitivity:", np.round((sensitivity),2))
print("Specificity:", np.round((specificity),2))
```

```
Sensitivity: 0.78
Specificity: 0.74
```

ROC Curve & AUC

```
from sklearn.metrics import roc_curve,auc
y_curve=model5.predict_proba(x_test)[:,1]

FPR,TPR,threshold=roc_curve(y_test,y_curve)
auc=auc(FPR,TPR)

plt.figure(figsize=(4,4),dpi=100)
plt.plot(FPR,TPR,label="NaiveBayes(auc= %0.3f)"% auc)
plt.plot([0,1],[0,1],color='orange',linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.legend()
plt.show()
```



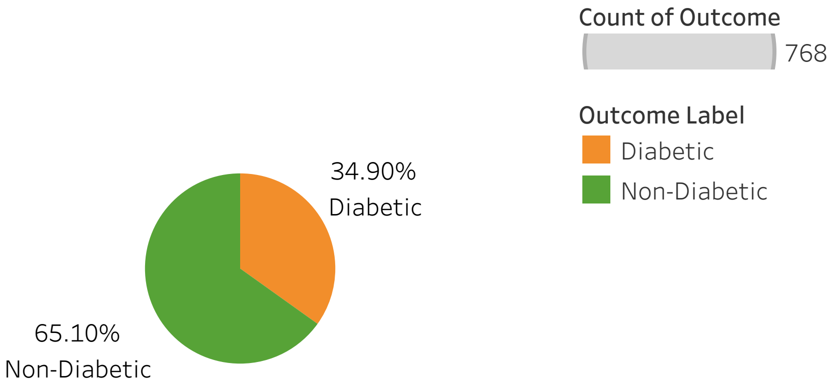
Comparing the results of all the models taking into account F1-score,precision,accuracy & AUC.

Considering AUC , Naive Baiyes Tops the list.

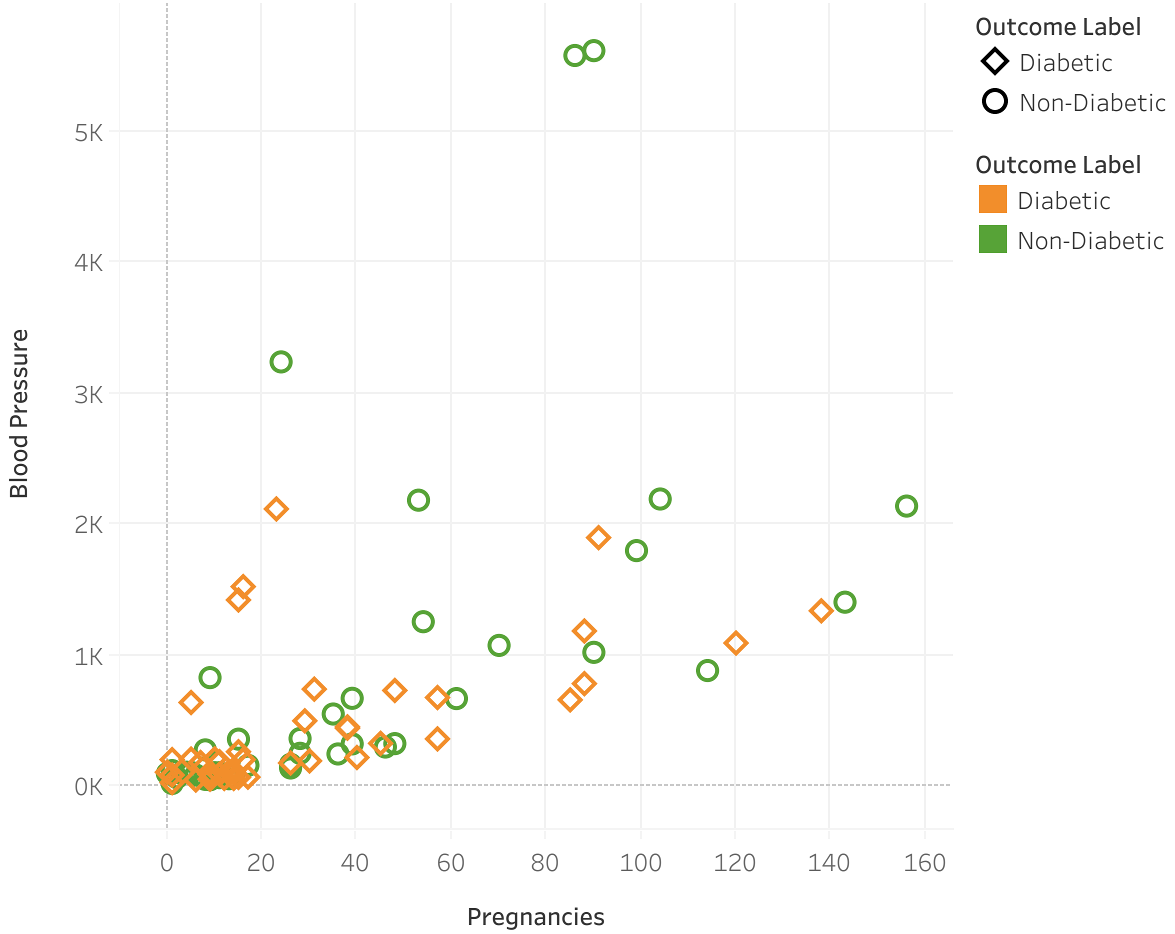
considering F1-score,precision,accuracy, Random Forest Classifier is at the top.

Here, I choose Random Forest Classifier as the best model.

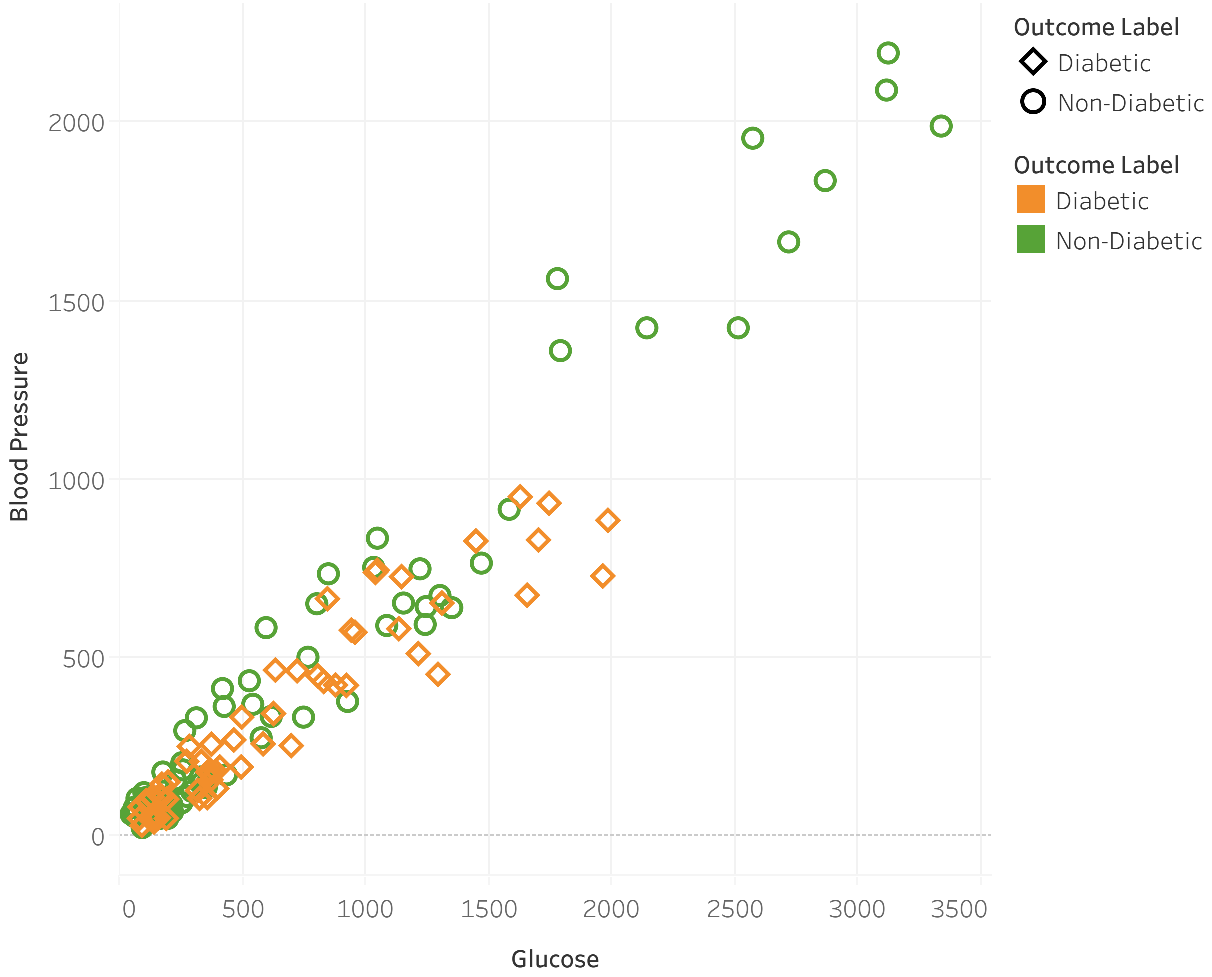
Pie Chart


Count of Outcome
768
Outcome Label
Diabetic
Non-Diabetic
34.90%
Diabetic
65.10%
Non-Diabetic

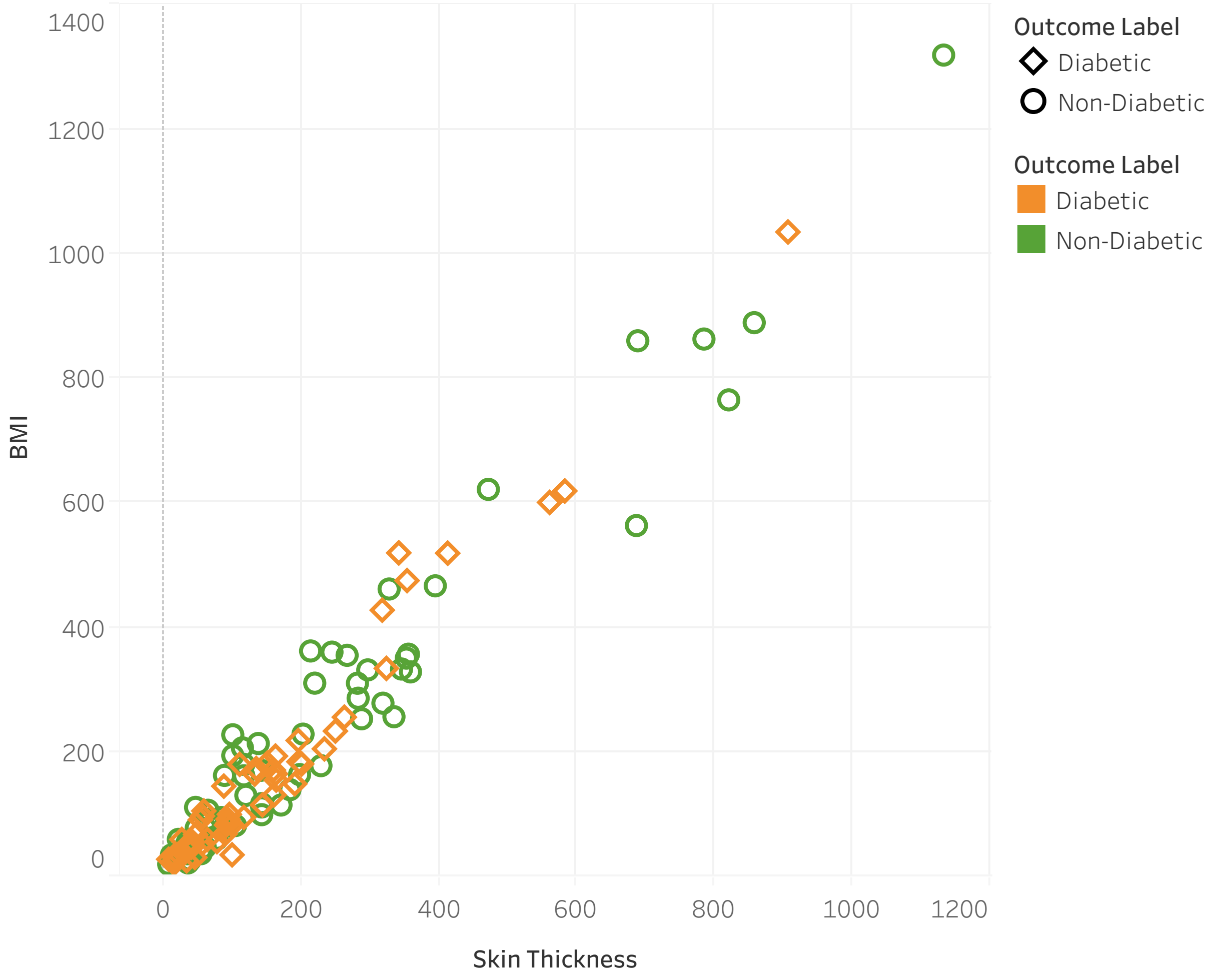
Pregnancy vs BP



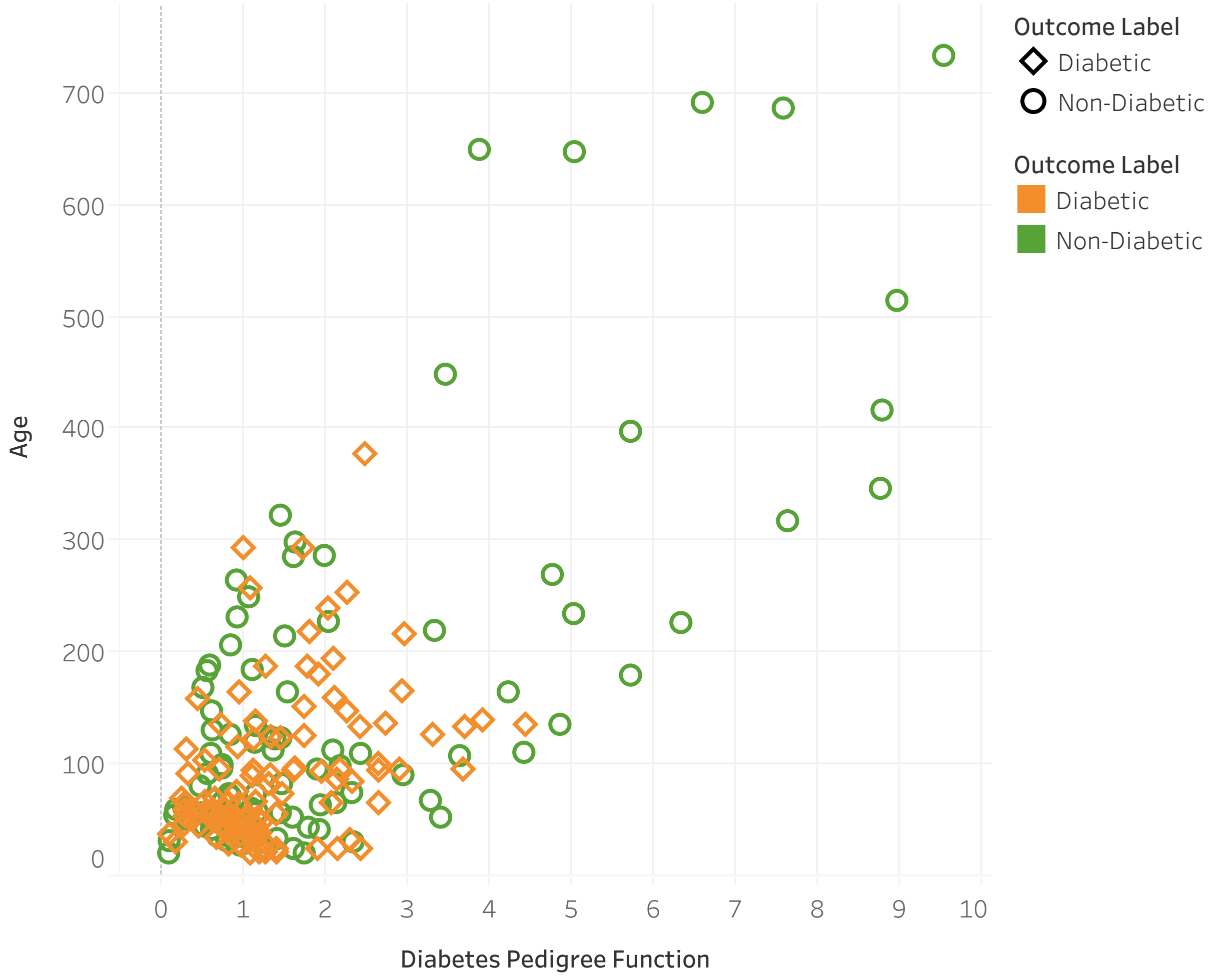
BP vs Glucose



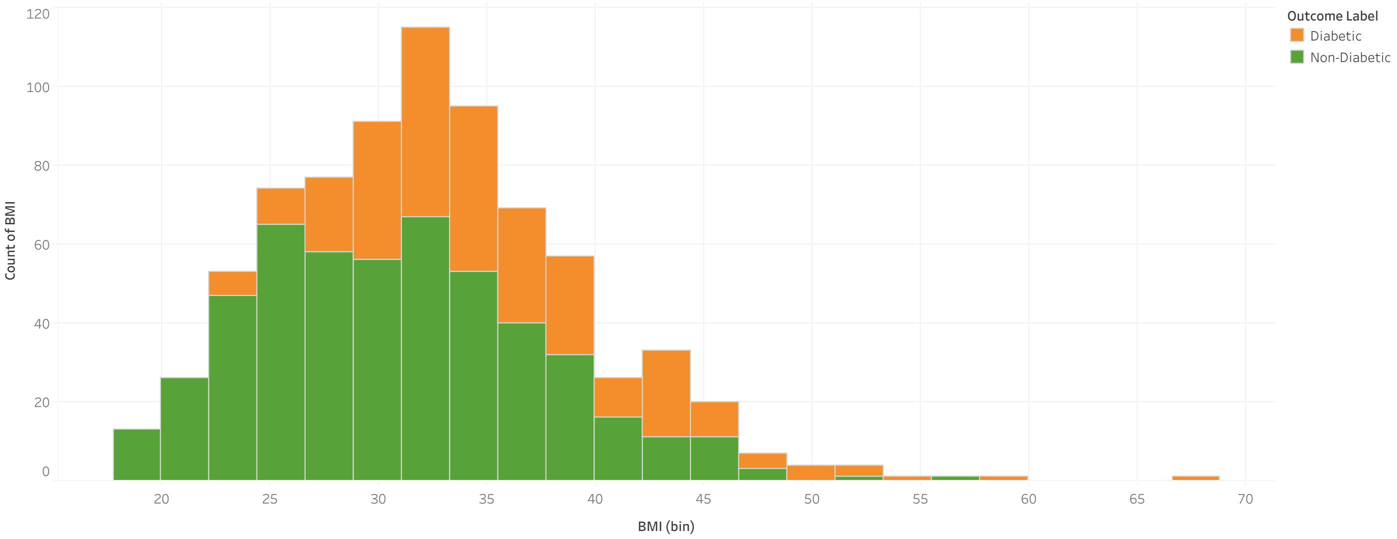
SkinThickness & BMI



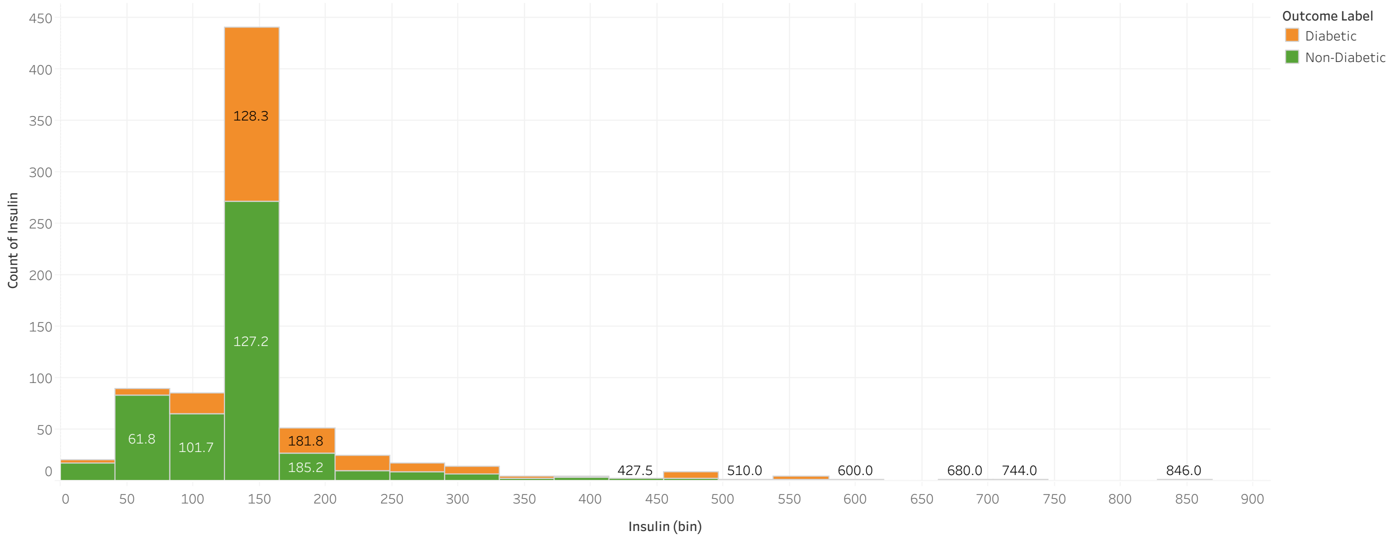
Age & DPF


Outcome Label
◇ Diabetic
○ Non-Diabetic
Outcome Label
🟧 Diabetic
🟩 Non-Diabetic
Age
700
600
500
400
300
200
100
0
0
1
2
3
4
5
6
7
8
9
10
Diabetes Pedigree Function

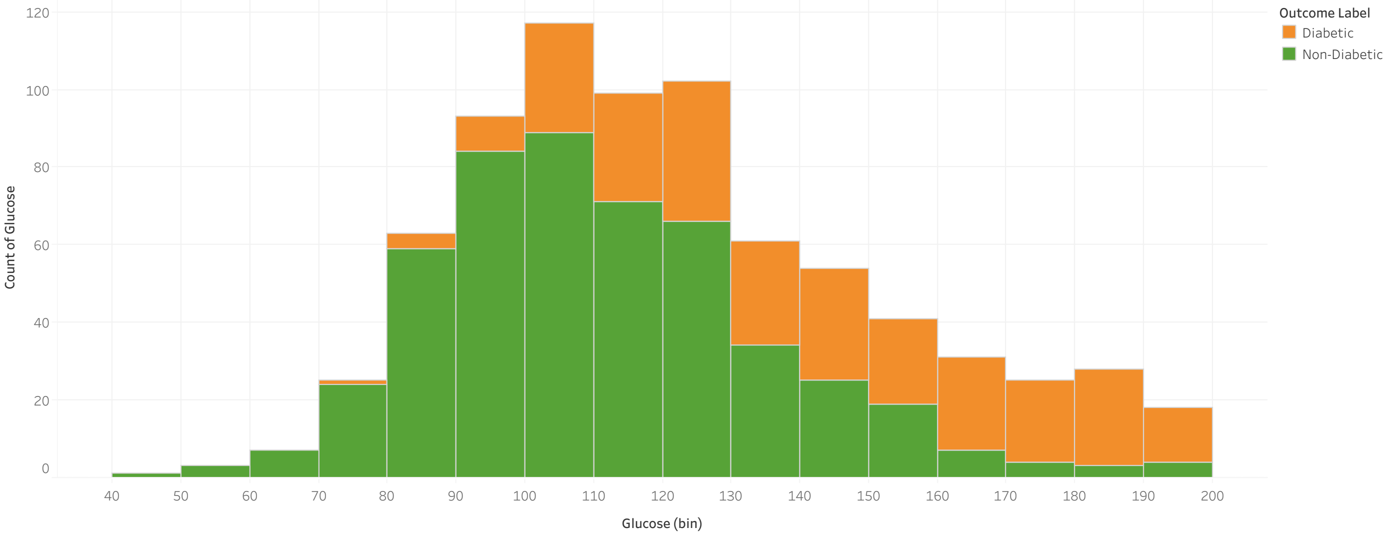
Histogram BMI



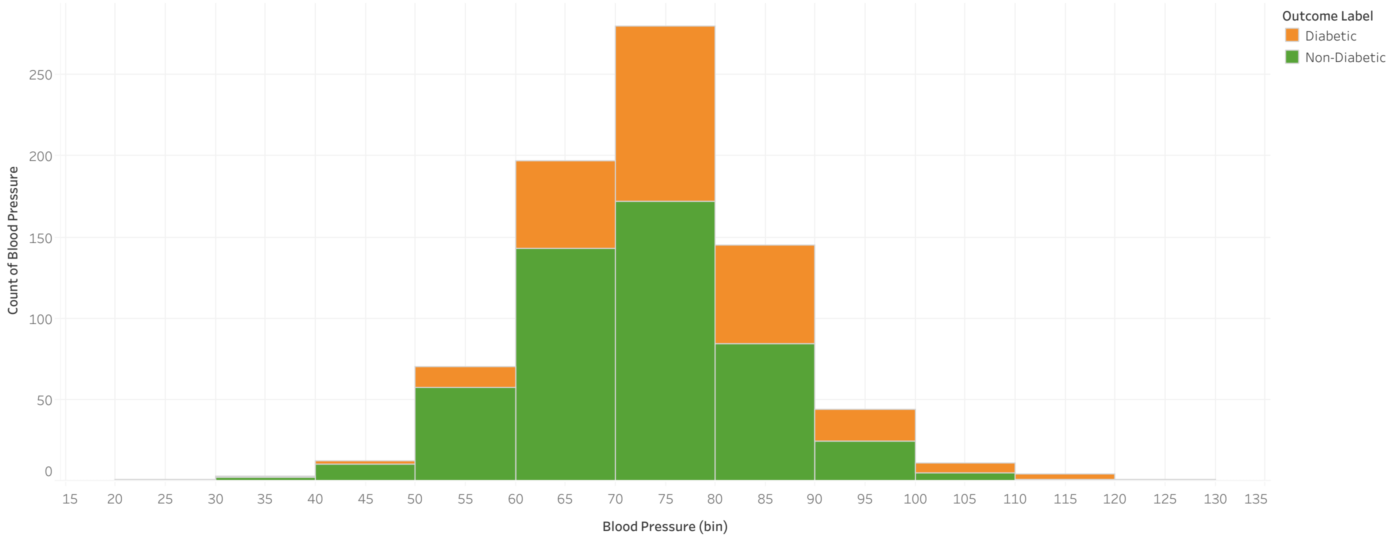
Histogram Insulin



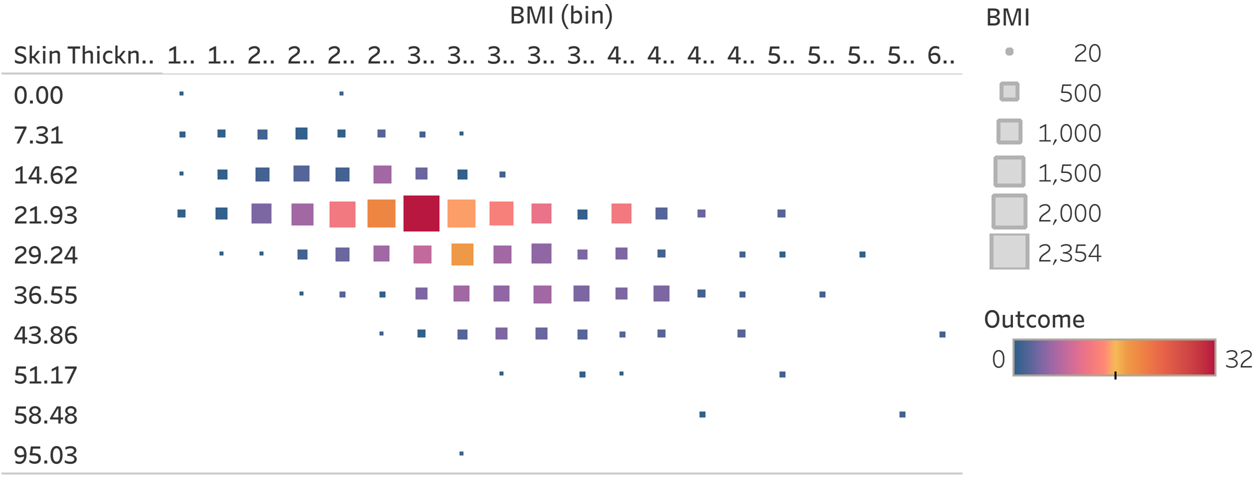
Histogram Glucose



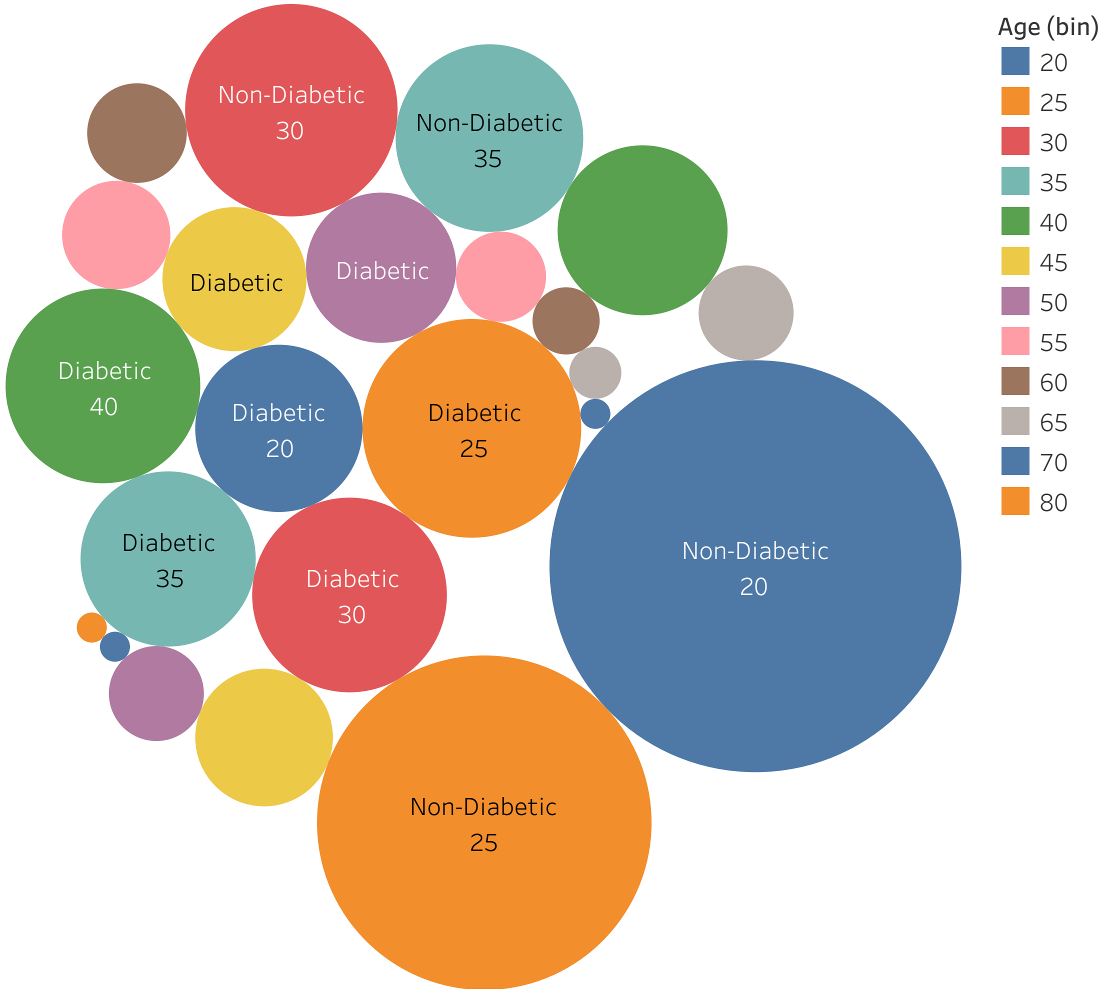
Histogram BP

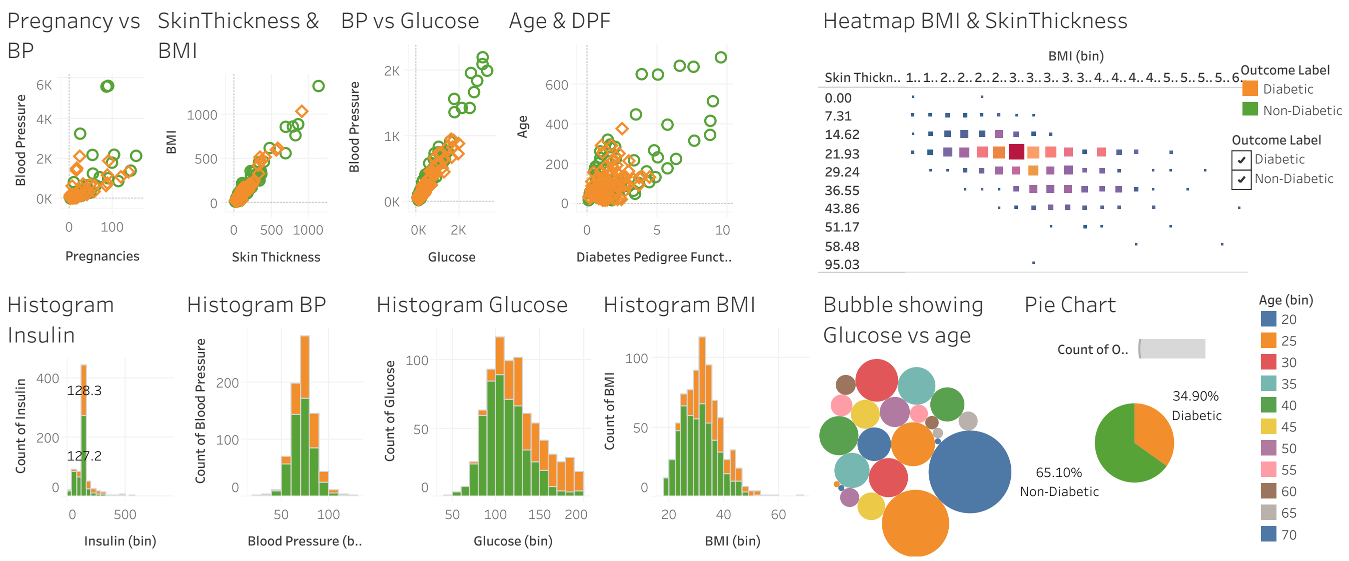


Heatmap BMI & SkinThickness



Bubble showing Glucose vs age




Pregnancy vs BP
6K
4K
2K
0K
Blood Pressure
0
100
Pregnancies
SkinThickness & BMI
1000
500
0
BMI
0
500
1000
Skin Thickness
BP vs Glucose
2K
1K
0K
Blood Pressure
0K
2K
Glucose
Age & DPF
600
400
200
0
Age
0
5
10
Diabetes Pedigree Funct..
Heatmap BMI & SkinThickness
BMI (bin)
Skin Thickn..
1..
1..
2..
2..
2..
2..
3..
3..
3..
3.
3..
4..
4..
4..
4..
5..
5..
5..
5..
6..
0.00
7.31
14.62
21.93
29.24
36.55
43.86
51.17
58.48
95.03
Outcome Label
🟧 Diabetic
🟩 Non-Diabetic
Outcome Label
☑ Diabetic
☑ Non-Diabetic
Histogram Insulin
400
200
0
Count of Insulin
128.3
127.2
0
500
Insulin (bin)
Histogram BP
200
100
0
Count of Blood Pressure
50
100
Blood Pressure (b..
Histogram Glucose
100
50
0
Count of Glucose
50
100
150
200
Glucose (bin)
Histogram BMI
100
50
0
Count of BMI
20
40
60
BMI (bin)
Bubble showing Glucose vs age
Pie Chart
Count of O..
34.90%
Diabetic
65.10%
Non-Diabetic
Age (bin)
20
25
30
35
40
45
50
55
60
65
70