Diabetes Dataset:

```
1- EDA
2- Graphical and Statistical Analysis
3- Outlier Trimming
4- Feature Engineering
5- Model Building : Logistic Regression
```

Link to dataset: "https://raw.githubusercontent.com/plotly/datasets/master/diabetes.csv (https://raw.githubusercontent.com/plotly/datasets/master/diabetes.csv)

Importing Required Libraries

In [55]:

```
import numpy as np
import pandas as pd

import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline

import warnings
warnings.filterwarnings('ignore')

from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, accuracy_score, precision_score, recall_score
from sklearn.metrics import classification_report
```

In [2]:

```
df = pd.read_csv("https://raw.githubusercontent.com/plotly/datasets/master/diabetes.csv")
```

In [3]:

```
df.head()
```

Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
0	6	148	72	35	0	33.6	0.62
1	1	85	66	29	0	26.6	0.35
2	8	183	64	0	0	23.3	0.67
3	1	89	66	23	94	28.1	0.16
4	0	137	40	35	168	43.1	2.28

In [4]:

```
df.shape
```

Out[4]:

```
(768, 9)
```

In [5]:

```
df.columns
```

Out[5]:

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

In [6]:

```
df.describe()
```

Out[6]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Diabet
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

Checking missing Values

In [7]:

```
df.isnull().sum()   # no null values
```

Out[7]:

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [8]:

```
df.duplicated().sum()   # No Duplicate values
```

Out[8]:

```
0
```

In [9]:

```
for feature in df.columns:
    print("{} has {} unique values".format(feature,df[feature].nunique()))
```

```
Pregnancies has 17 unique values
Glucose has 136 unique values
BloodPressure has 47 unique values
SkinThickness has 51 unique values
Insulin has 186 unique values
BMI has 248 unique values
DiabetesPedigreeFunction has 517 unique values
Age has 52 unique values
Outcome has 2 unique values
```

```
In [10]:
```

```
df.corr()
```

```
Out[10]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.0
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.2
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.2
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.3
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.1
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.0
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.1
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.0
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.2

```
In [11]:
```

```
df.skew()
```

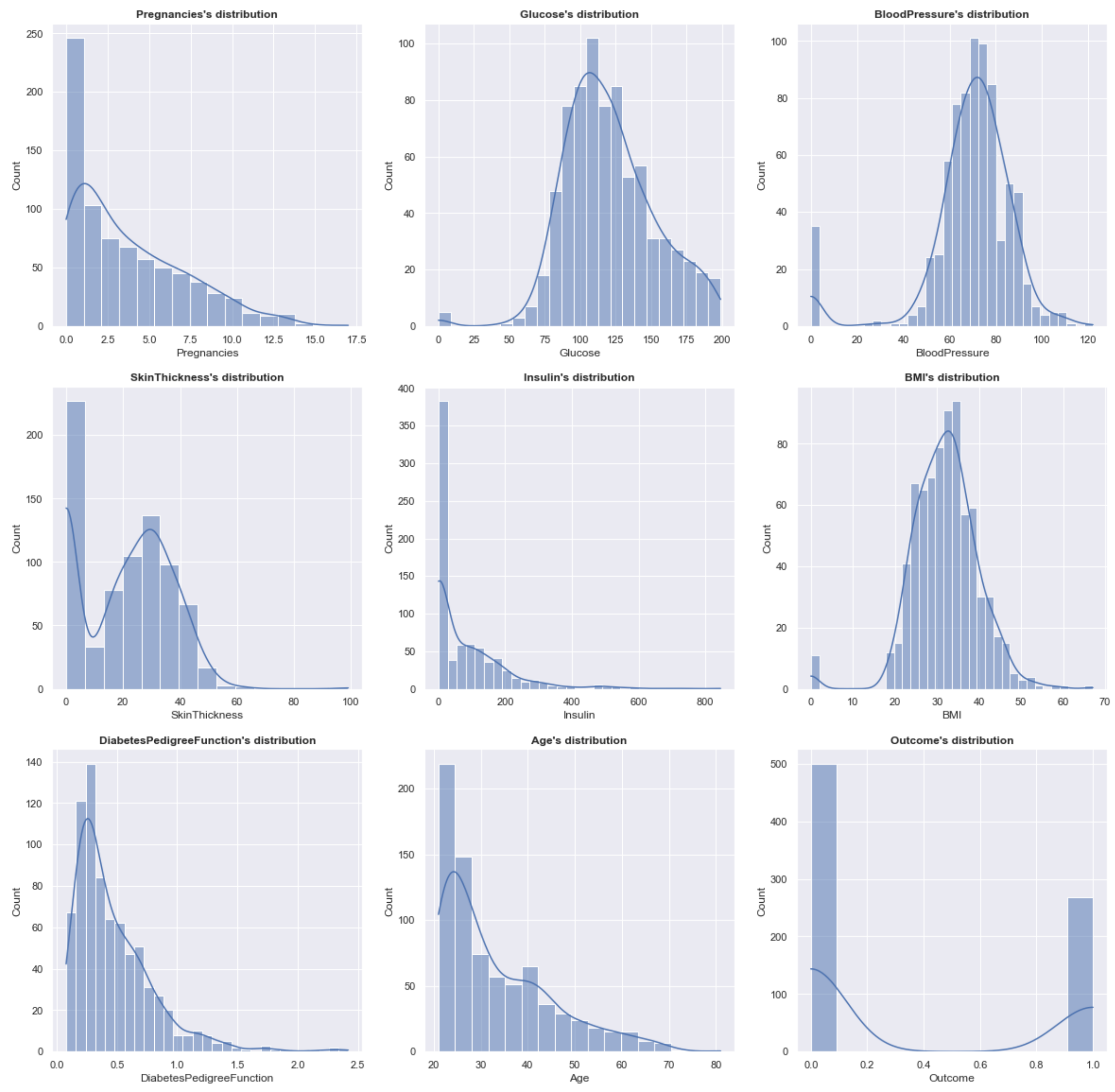
```
Out[11]:
```

```
Pregnancies                 0.901674
Glucose                     0.173754
BloodPressure              -1.843608
SkinThickness               0.109372
Insulin                     2.272251
BMI                        -0.428982
DiabetesPedigreeFunction    1.919911
Age                         1.129597
Outcome                     0.635017
dtype: float64
```

Graphical Analysis

In [12]:

```
plt.figure(figsize=(20,20))
for i in enumerate(df.columns):
    sns.set(style='darkgrid')
    plt.subplot(3,3,i[0]+1)
    sns.histplot(data=df,x=i[1],kde=True)
    plt.title("{}'s distribution".format(i[1]),fontweight="bold")
```



Observation:

```
1- No probable logical correlation i.e. no feature can be dropped in feature selec
tion
2- Features like Pregnancies, Insulin, DiabetesPedigreeFunction are Right-Skewed o
f distribution.
3- Features like BloodPressure, BMI,  are Left-Skewed of distribution.
```

There are lot of 0 values , we will try to replace it

In [13]:

```
df_copy= df.copy()
df_copy.head(3)
```

Out[13]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
0	6	148	72	35	0	33.6	0.62
1	1	85	66	29	0	26.6	0.35
2	8	183	64	0	0	23.3	0.67

In [14]:

```
for i in df_copy.columns:
    if 0 in df_copy[i].value_counts():
        print(i,'have',df_copy[i].value_counts()[0],'values as 0')
```

```
Pregnancies have 111 values as 0
Glucose have 5 values as 0
BloodPressure have 35 values as 0
SkinThickness have 227 values as 0
Insulin have 374 values as 0
BMI have 11 values as 0
Outcome have 500 values as 0
```

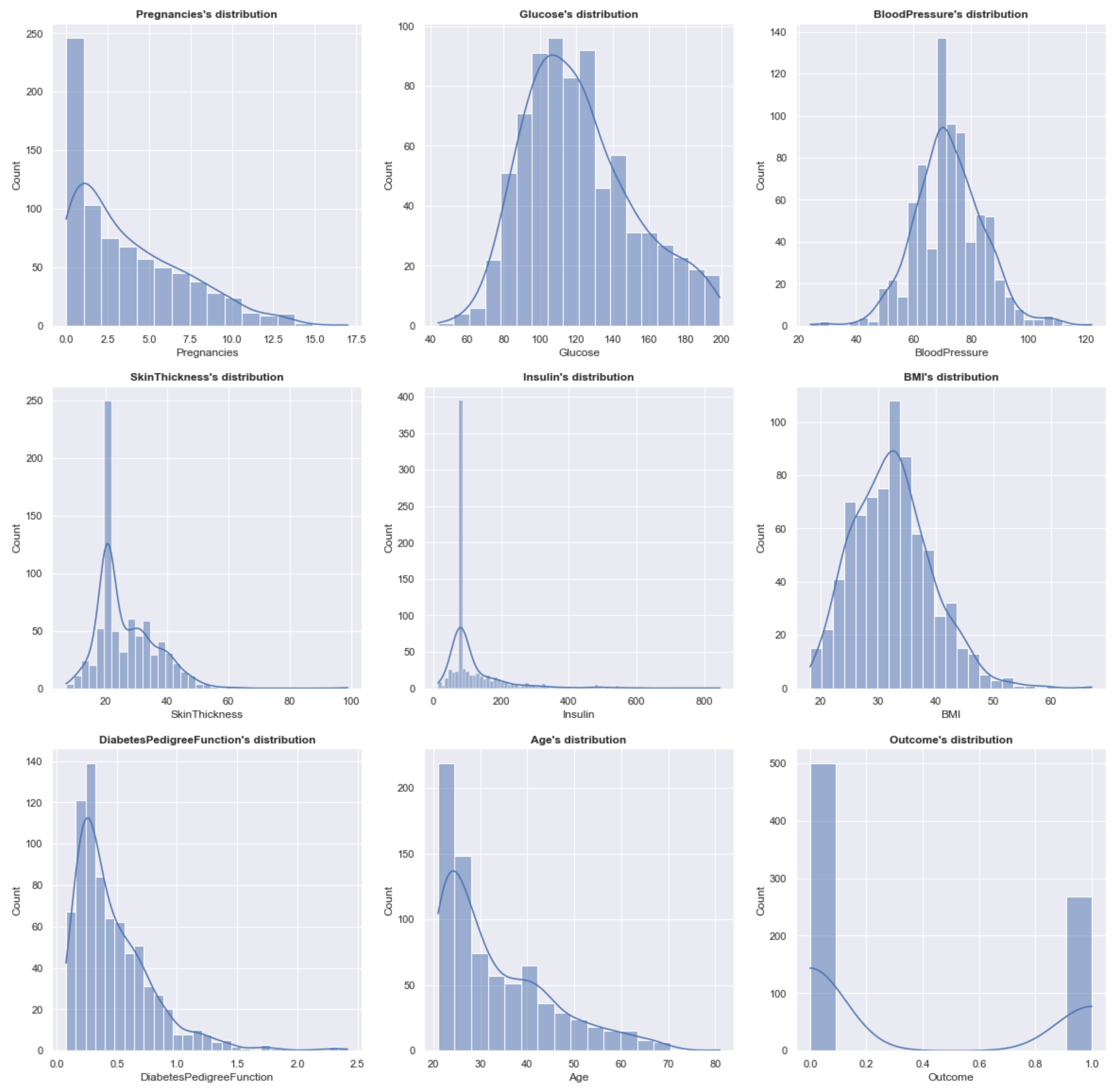
Replacing 0 value with 'Mean' as there is less impact with median

In [15]:

```
# We don't need to replace 0 value in pregnancies and outcome
for i in ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin','BMI']:
    df_copy[i] = df_copy[i].replace(0,df_copy[i].mean())
```

In [16]:

```
plt.figure(figsize=(20,20))
for i in enumerate(df_copy.columns):
    sns.set(style='darkgrid')
    plt.subplot(3,3,i[0]+1)
    sns.histplot(data=df_copy,x=i[1],kde=True)
    plt.title("{}'s distribution".format(i[1]),fontweight="bold")
```



Observation:

After replacing 0 values with mean , distribution improved

In [17]:

```
df_copy.columns
```

Out[17]:

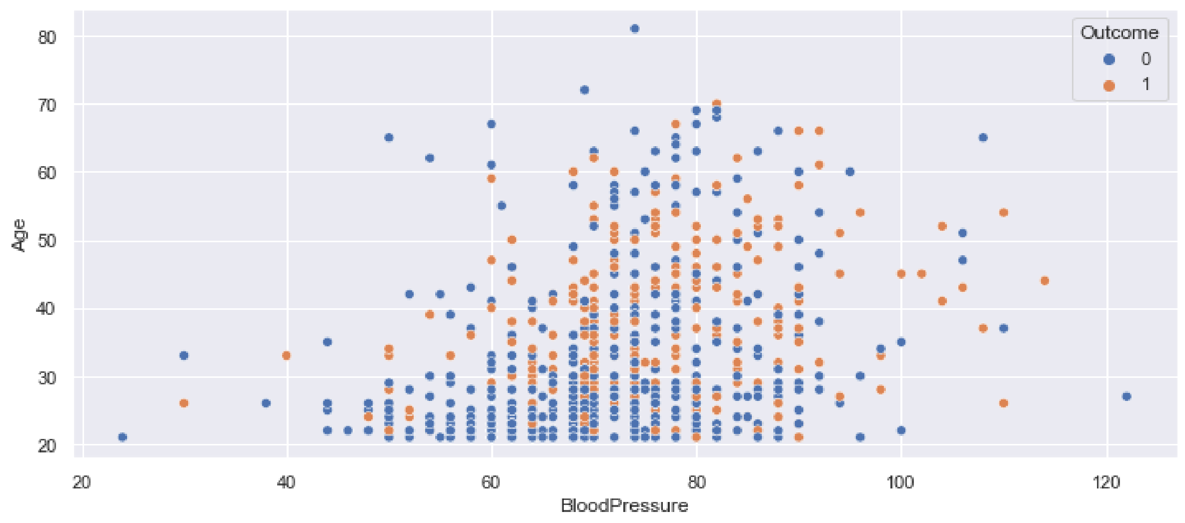
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insuli
n',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [18]:

```
plt.figure(figsize=(12,5))
sns.scatterplot(df_copy['BloodPressure'],df_copy['Age'],hue=df_copy['Outcome'])
```

Out[18]:

```
<AxesSubplot:xlabel='BloodPressure', ylabel='Age'>
```



Observation:

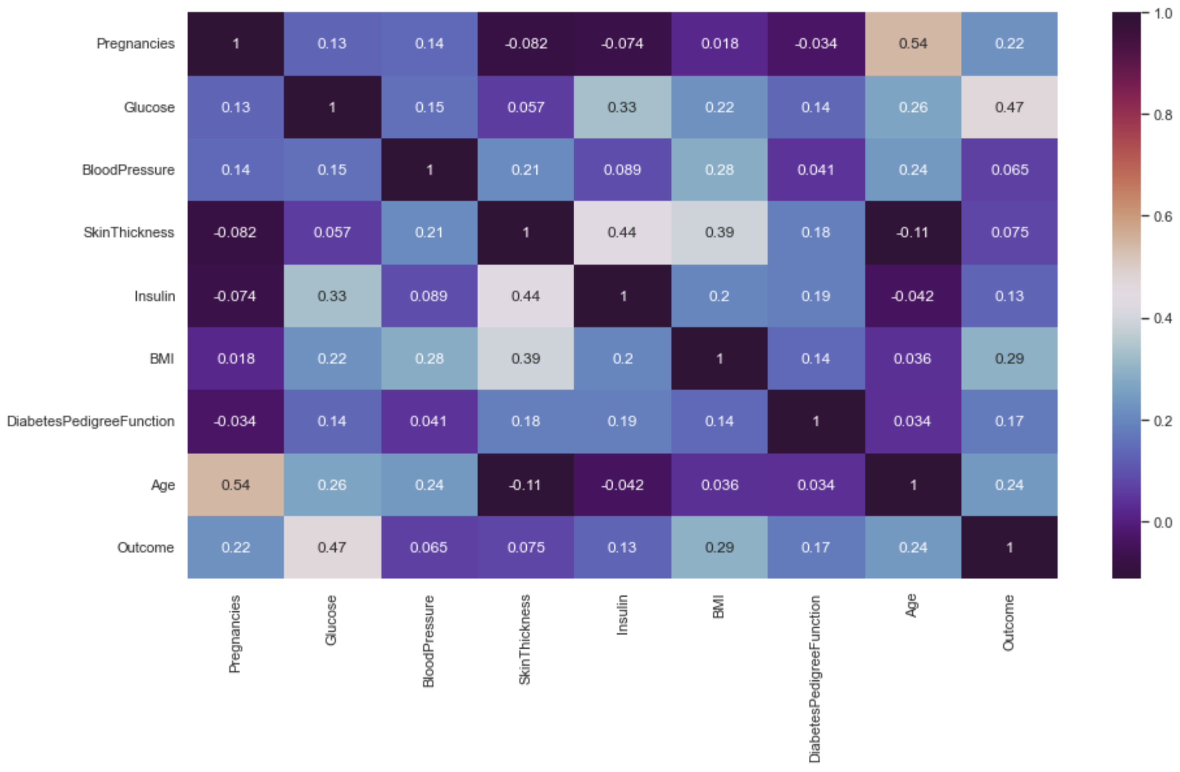
```
1- After plotting all scatter plot , There is linear relationship among any featur
es.
2- Mostly are normally distributed.
```

In [19]:

```
plt.figure(figsize=(15,8))
sns.heatmap(df.corr(),annot=True,cmap='twilight_shifted')
```

Out[19]:

```
<AxesSubplot:>
```

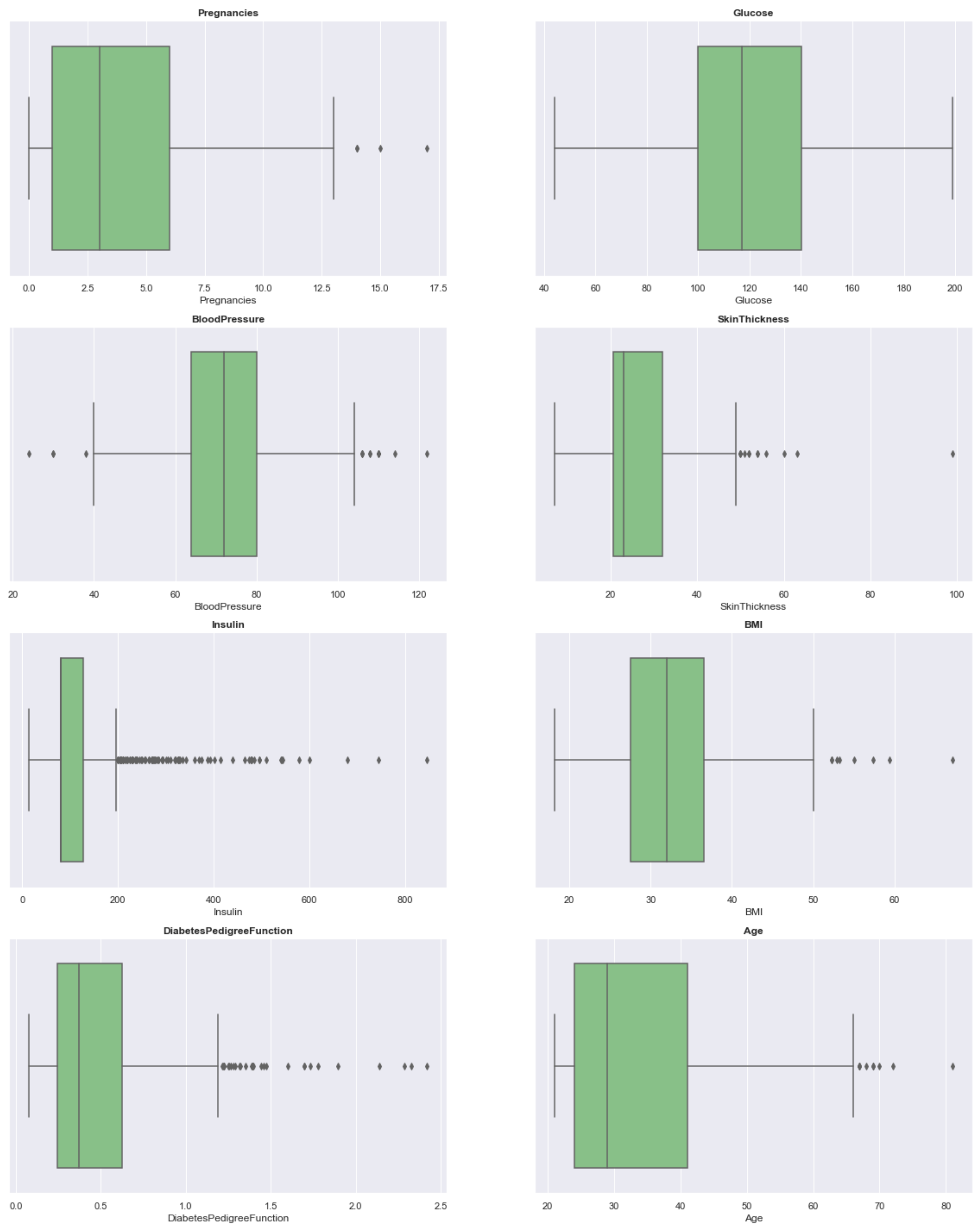


	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1	0.13	0.14	-0.082	-0.074	0.018	-0.034	0.54	0.22
Glucose	0.13	1	0.15	0.057	0.33	0.22	0.14	0.26	0.47
BloodPressure	0.14	0.15	1	0.21	0.089	0.28	0.041	0.24	0.065
SkinThickness	-0.082	0.057	0.21	1	0.44	0.39	0.18	-0.11	0.075
Insulin	-0.074	0.33	0.089	0.44	1	0.2	0.19	-0.042	0.13
BMI	0.018	0.22	0.28	0.39	0.2	1	0.14	0.036	0.29
DiabetesPedigreeFunction	-0.034	0.14	0.041	0.18	0.19	0.14	1	0.034	0.17
Age	0.54	0.26	0.24	-0.11	-0.042	0.036	0.034	1	0.24
Outcome	0.22	0.47	0.065	0.075	0.13	0.29	0.17	0.24	1

Checking Outliers

In [20]:

```
plt.figure(figsize=(20,25))
for i in enumerate([i for i in df_copy.columns if i!='Outcome']):
    sns.set(style='darkgrid')
    plt.subplot(4,2,i[0]+1)
    sns.boxplot(data=df_copy,x=i[1],palette='Accent')
    plt.title("{}".format(i[1]),fontweight="bold")
```



Observation:

```
1- Glucose has no outliers.
2- BloodPressure has outliers on both sides.
3- Rest all the features have outliers on upper quantile.
4- Insulin and DiabetesPedigreeFunction have many Outliers..
```

Treating Outliers

In [21]:

```
def outlier_threshold(df,variable):
    """Function to find threshold"""
    q1=df[variable].quantile(0.25)
    q3=df[variable].quantile(0.75)
    IQR = q3 - q1
    up_limit = q3+(1.5*IQR)
    lower_limit = q1-(1.5*IQR)
    return lower_limit,up_limit
```

In [22]:

```
for variable in enumerate([i for i in df_copy.columns if i!='Outcome']):
    low_limit,upper_limit=outlier_threshold(df_copy,variable[1])
    print(variable[1],':',low_limit,upper_limit)
```

```
Pregnancies : -6.5 13.5
Glucose : 39.0 201.0
BloodPressure : 40.0 104.0
SkinThickness : 3.341145833333332 49.1953125
Insulin : 8.623697916666671 198.42578125
BMI : 13.849999999999998 50.25
DiabetesPedigreeFunction : -0.32999999999999996 1.2
Age : -1.5 66.5
```

Replacing outliers values wiht threshold value i.e. CAPPING

In [23]:

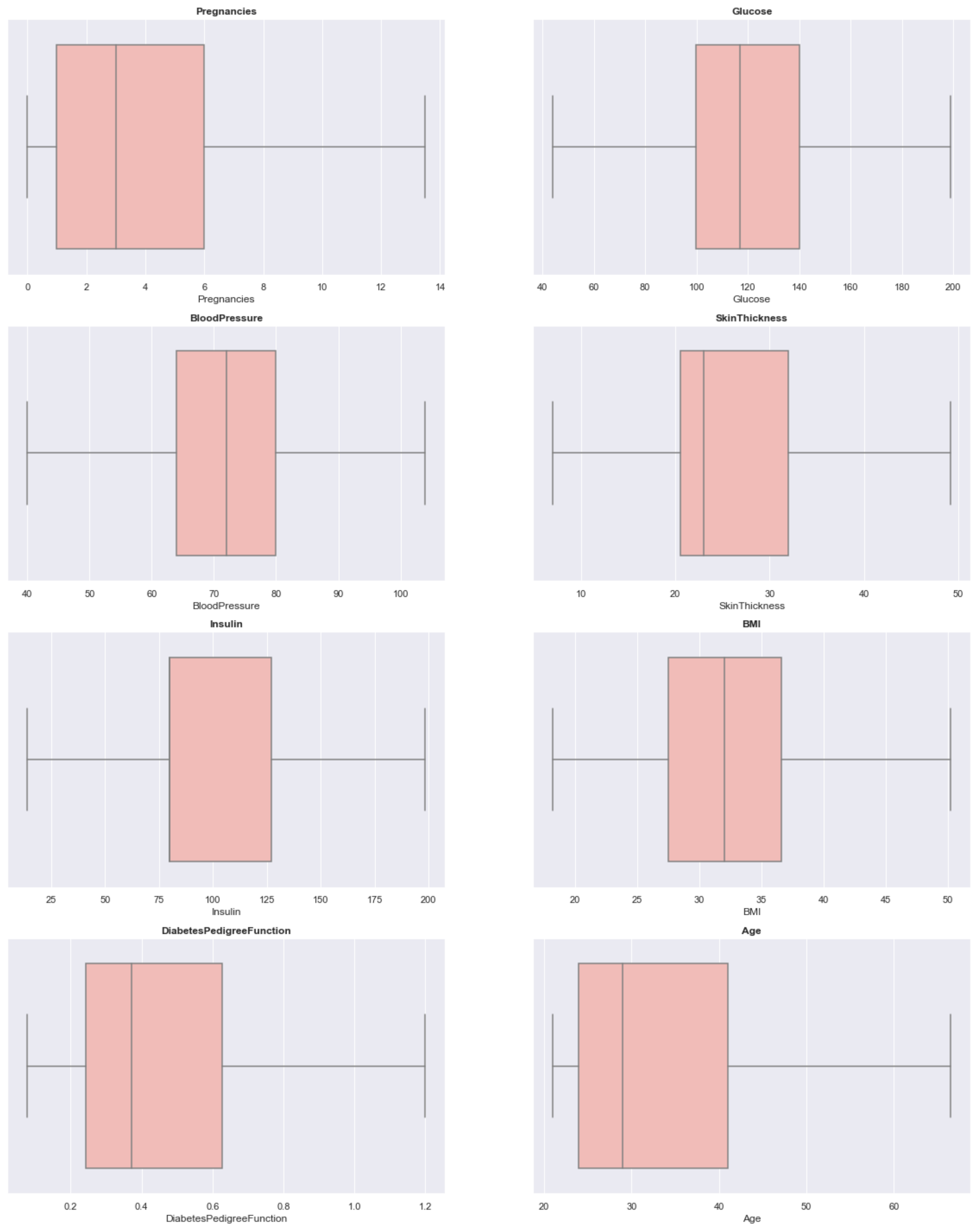
```
def replace_with_threshold(df,col):
    for variable in col:
        low_limit,upper_limit=outlier_threshold(df,variable)
        df.loc[df[variable]<low_limit,variable]=low_limit
        df.loc[df[variable]>upper_limit,variable]=upper_limit

replace_with_threshold(df_copy,df_copy.columns)
```

Rechecking the outliers again

In [24]:

```
plt.figure(figsize=(20,25))
for i in enumerate([i for i in df_copy.columns if i!='Outcome']):
    sns.set(style='darkgrid')
    plt.subplot(4,2,i[0]+1)
    sns.boxplot(data=df_copy,x=i[1],palette='Pastel1')
    plt.title("{}".format(i[1]),fontweight="bold")
```



In [25]:

```
df_copy.shape
```

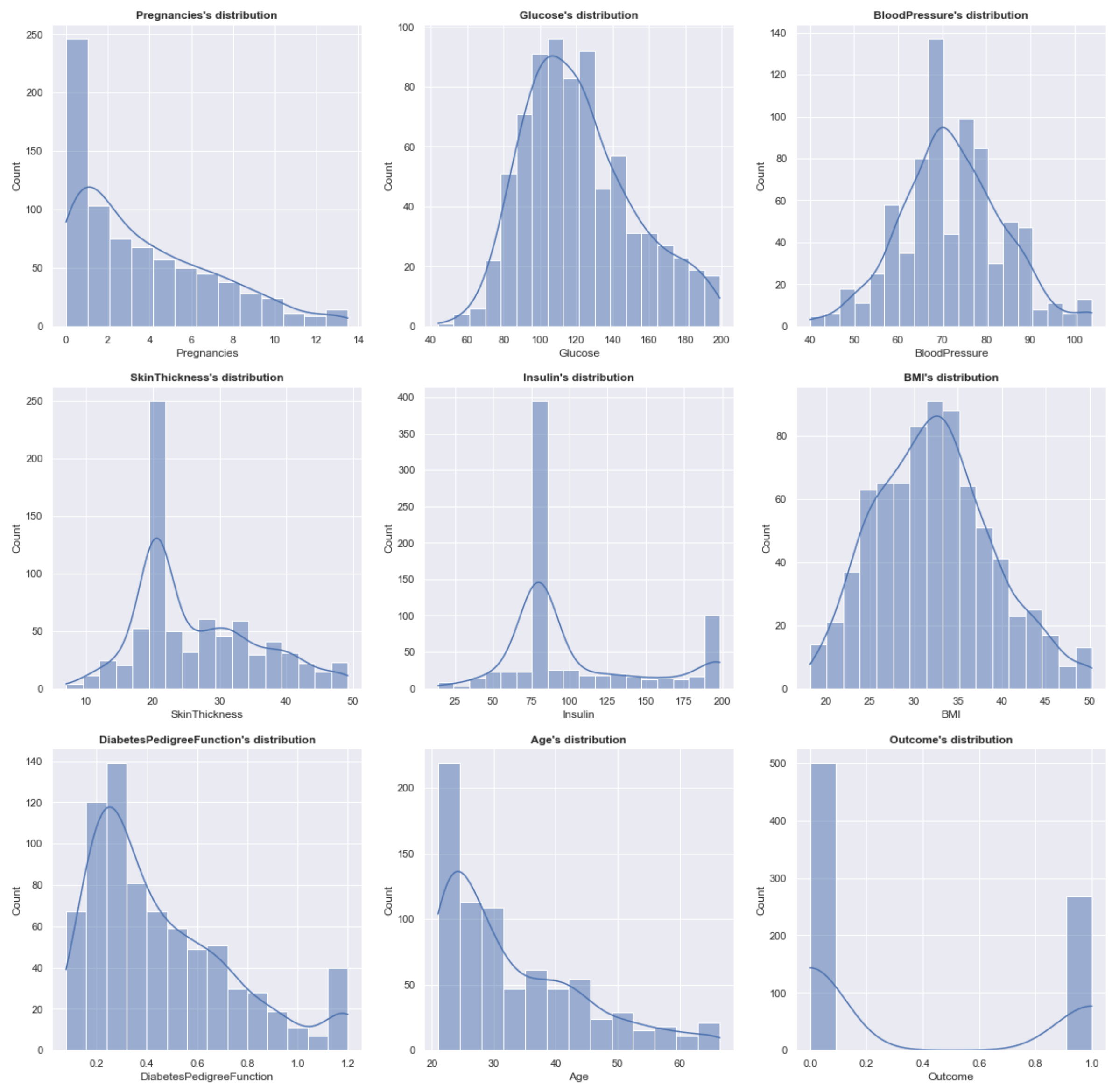
Out[25]:

```
(768, 9)
```

Rechecking Distribution

In [26]:

```
plt.figure(figsize=(20,20))
for i in enumerate(df_copy.columns):
    sns.set(style='darkgrid')
    plt.subplot(3,3,i[0]+1)
    sns.histplot(data=df_copy,x=i[1],kde=True)
    plt.title("{}'s distribution".format(i[1]),fontweight="bold")
```



Observation:

1- Outliers are handled but distribution is slightly changed towards right side.

Model Building

In [27]:

```
# Differenciating Independent and dependent variable
```

In [28]:

```
X = df_copy.iloc[:,:-1]
y = df_copy.iloc[:,-1]
```

In [29]:

```
X.head()
```

Out[29]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFun
0	6.0	148.0	72.0	35.000000	79.799479	33.6	
1	1.0	85.0	66.0	29.000000	79.799479	26.6	
2	8.0	183.0	64.0	20.536458	79.799479	23.3	
3	1.0	89.0	66.0	23.000000	94.000000	28.1	
4	0.0	137.0	40.0	35.000000	168.000000	43.1	

In [30]:

```
y.head()
```

Out[30]:

```
0    1.0
1    0.0
2    1.0
3    0.0
4    1.0
Name: Outcome, dtype: float64
```

Split dataframe in train and test data:

In [31]:

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

In [32]:

```
X_train.head()
```

Out[32]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedi
60	2.0	84.0	69.105469	20.536458	79.799479	31.992578	
618	9.0	112.0	82.000000	24.000000	79.799479	28.200000	
346	1.0	139.0	46.000000	19.000000	83.000000	28.700000	
294	0.0	161.0	50.000000	20.536458	79.799479	21.900000	
231	6.0	134.0	80.000000	37.000000	198.425781	46.200000	

In [33]:

```
X_test.head()
```

Out[33]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeF
668	6.0	98.0	58.0	33.000000	190.000000	34.0	
324	2.0	112.0	75.0	32.000000	79.799479	35.7	
624	2.0	108.0	64.0	20.536458	79.799479	30.8	
690	8.0	107.0	80.0	20.536458	79.799479	24.6	
473	7.0	136.0	90.0	20.536458	79.799479	29.9	

In [34]:

```
y_train.head()
```

Out[34]:

```
60     0.0
618    1.0
346    0.0
294    0.0
231    1.0
Name: Outcome, dtype: float64
```

Scaling the dataset

scaler = StandardScaler() scaler

In [35]:

```
from sklearn.preprocessing import MaxAbsScaler
scaler = MaxAbsScaler()
scaler
```

Out[35]:

```
MaxAbsScaler()
```

In [36]:

```
X_train_scaled = scaler.fit_transform(X_train)
```

In [37]:

```
X_test_scaled = scaler.transform(X_test)
```

In [38]:

```
X_train_scaled
```

Out[38]:

```
array([[0.14814815, 0.42211055, 0.66447566, ..., 0.63666822, 0.25333333,
        0.31578947],
       [0.66666667, 0.56281407, 0.78846154, ..., 0.56119403, 1.        ,
        0.7518797 ],
       [0.07407407, 0.69849246, 0.44230769, ..., 0.57114428, 0.545     ,
        0.33082707],
       ...,
       [0.74074074, 0.50753769, 0.82692308, ..., 0.90746269, 0.94666667,
        0.57142857],
       [0.        , 0.70854271, 0.66447566, ..., 0.84378109, 0.17083333,
        0.43609023],
       [0.        , 0.6281407 , 0.92307692, ..., 0.44776119, 0.21833333,
        0.31578947]])
```

Model Selection

Logistic Regression

In [39]:

```
log_reg = LogisticRegression()
log_reg
```

Out[39]:

```
LogisticRegression()
```

In [40]:

```
log_reg.fit(X_train_scaled,y_train)
```

Out[40]:

```
LogisticRegression()
```

In [41]:

```
# prediction
log_reg_pred = log_reg.predict(X_test_scaled)
log_reg_pred
```

Out[41]:

```
array([0., 0., 0., 0., 0., 0., 0., 0., 0., 1., 0., 1., 0., 0., 0., 0., 0.,
       0., 1., 0., 0., 0., 0., 0., 1., 1., 0., 0., 0., 0., 1., 1., 1., 1.,
       1., 1., 1., 0., 0., 0., 0., 0., 0., 0., 0., 1., 1., 0., 0., 1., 0.,
       1., 1., 0., 0., 0., 1., 0., 0., 1., 1., 0., 0., 0., 0., 1., 0., 1.,
       0., 1., 1., 0., 0., 0., 0., 1., 0., 0., 0., 0., 1., 0., 0., 0., 0.,
       1., 1., 0., 0., 0., 0., 0., 0., 0., 0., 1., 0., 0., 1., 0., 1., 0.,
       1., 0., 1., 0., 0., 1., 0., 1., 0., 0., 0., 1., 0., 0., 1., 0., 0.,
       0., 0., 0., 0., 0., 0., 1., 0., 1., 1., 1., 1., 1., 0., 0., 1., 0.,
       0., 1., 1., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 1., 0., 0., 0.,
       0.])
```

Performance Matrix

Accuracy Score

In [42]:

```
accuracy=round(accuracy_score(y_test, log_reg_pred),4)
accuracy
```

Out[42]:

```
0.7792
```

In [51]:

```
accuracy_manual = round((true_positive+true_negative)/(true_positive+false_positive+false_n
accuracy_manual
```

Out[51]:

```
0.7792
```

Confusion Matrix

In [43]:

```
confusion_mat=confusion_matrix(y_test, log_reg_pred)
confusion_mat
```

Out[43]:

```
array([[86, 13],
       [21, 34]], dtype=int64)
```

In [44]:

```
true_positive=confusion_mat[0][0]
false_positive=confusion_mat[0][1]
false_negative=confusion_mat[1][0]
true_negative=confusion_mat[1][1]
```

Precision Score

In [54]:

```
precision_score_manual = round(true_positive/(true_positive+false_positive),4)
precision_score_manual
```

Out[54]:

```
0.8687
```

Recall

In [59]:

```
recall_score_manual = round(true_positive/(true_positive+false_negative),4)
recall_score_manual
```

Out[59]:

```
0.8037
```

F-1 Score or F-Beta Score

In [61]:

```
f1_score = 2*((precision_score_manual*recall_score_manual)/(precision_score_manual+recall_s
f1_score
```

Out[61]:

```
0.8349368452523319
```

Classification Report

In [71]:

```
classification_rep = classification_report(y_test, log_reg_pred)
print(classification_rep)
```

```
              precision    recall  f1-score   support

         0.0       0.80      0.87      0.83        99
         1.0       0.72      0.62      0.67        55

    accuracy                           0.78       154
   macro avg       0.76      0.74      0.75       154
weighted avg       0.78      0.78      0.77       154
```

In [ ]:

```
```