EDA, FE and Logistic Regression (Classification) Models (Diabetes Dataset)

1. EDA and FE Data Profiling Stastical analysis Graphical Analysis Data Cleaning Data Scaling Outlier Trimming
2. Logistic Regression (Classification) Models Logistic Regression Performance metrics for above models

Importing Dataset

In [172…

```
import pandas as pd
import numpy as np

### Visualisation libraries
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline

### To ignore warnings
import warnings
warnings.filterwarnings('ignore')

### Machine Learning libraries
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, accuracy_score, precision_score, recall_score, fbeta_score

### To be able to see maximum columns on screen
pd.set_option('display.max_columns', 500)
```

In [25]:

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

In [26]:

```
### exporting file to csv for future use
dataset.to_csv("diabetes.csv")
```

1.1 Stastical Analysis

In [27]:

```
dataset.head()
```

Out[27]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

In [28]:

```
dataset.columns
```

Out[28]:

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

In [29]:

```
dataset.describe()
```

Out[29]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	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	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000

50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

In [30]:

```
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int64  
 1   Glucose                   768 non-null    int64  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int64  
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64  
 8   Outcome                   768 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

In [31]:

```
dataset.shape
```

Out[31]:

```
(768, 9)
```

1.2 Checking Missing values

dataset.isnull().sum()

In [33]:

```
for feature in dataset.columns:
    print("{} has {} no of unique categories".format(feature, dataset[feature].nunique()))
```

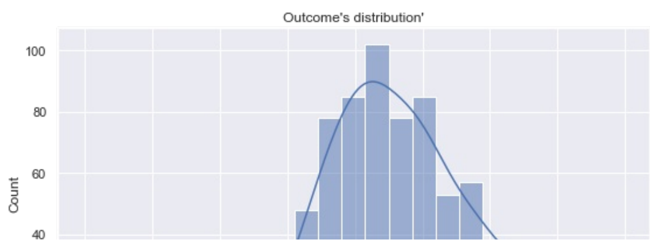
```
Pregnancies has 17 no of unique categories
Glucose has 136 no of unique categories
BloodPressure has 47 no of unique categories
SkinThickness has 51 no of unique categories
Insulin has 186 no of unique categories
BMI has 248 no of unique categories
DiabetesPedigreeFunction has 517 no of unique categories
Age has 52 no of unique categories
Outcome has 2 no of unique categories
```

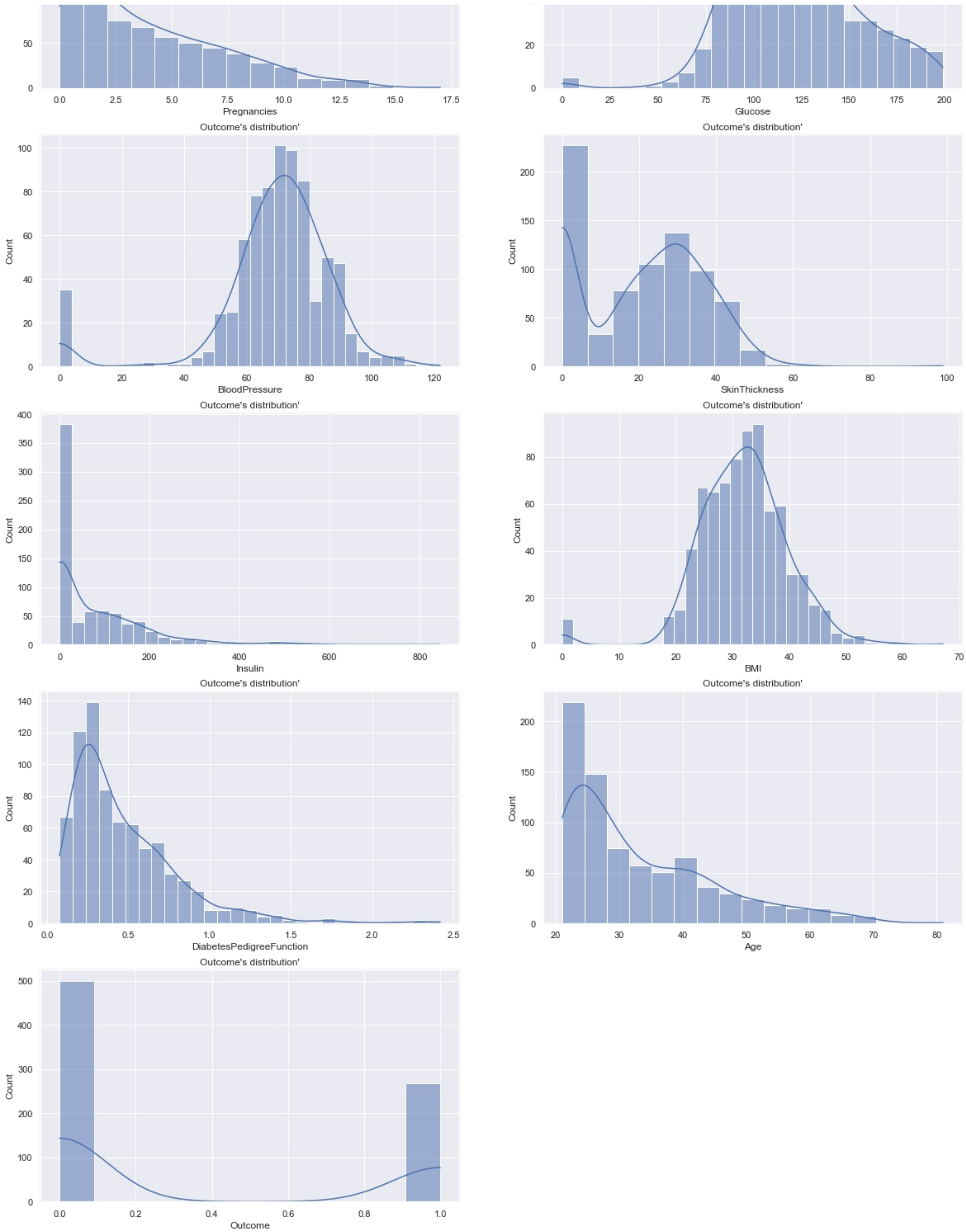
2.0 Graphical Analysis

2.1 Checking Distribution of features

In [34]:

```
plt.figure(figsize=(20,30))
for i in enumerate(dataset.columns):
    plt.subplot(5, 2, i[0]+1)
    sns.set(rc={'figure.figsize':(7,5)})
    sns.histplot(data=dataset, x=i[1], kde=True)
    plt.title("{}'s distribution'".format(feature))
```





Observations

1. Pregnancies has right skewed distribution, this indicates this feature has outliers towards right side of distribution.
2. Glucose has outliers towards left side of distribution.
3. BloodPressure has outliers towards left side of distribution.
4. Insulin has right skewed distribution, this indicates this feature has outliers towards right side of distribution.
5. BMI has outliers towards left side of distribution.
6. DiabetesPedigreeFunction has outliers towards left side of distribution.
7. Age has outliers towards left side of distribution.

8. Features like Glucose, BloodPressure, SkinThickness, Insulin, BMI have lot of zero values so replace these values with its mean.

2.2 Replacing zero values with mean and rechecking Distribution of features

Note: In place of mean we can also use median, mode or any random value.

In [86]:

```
### creating copy of dataset for further analysis so that we can also perform data cleaning on copied dataset.

data=dataset.copy()
data.head()
```

Out[86]:

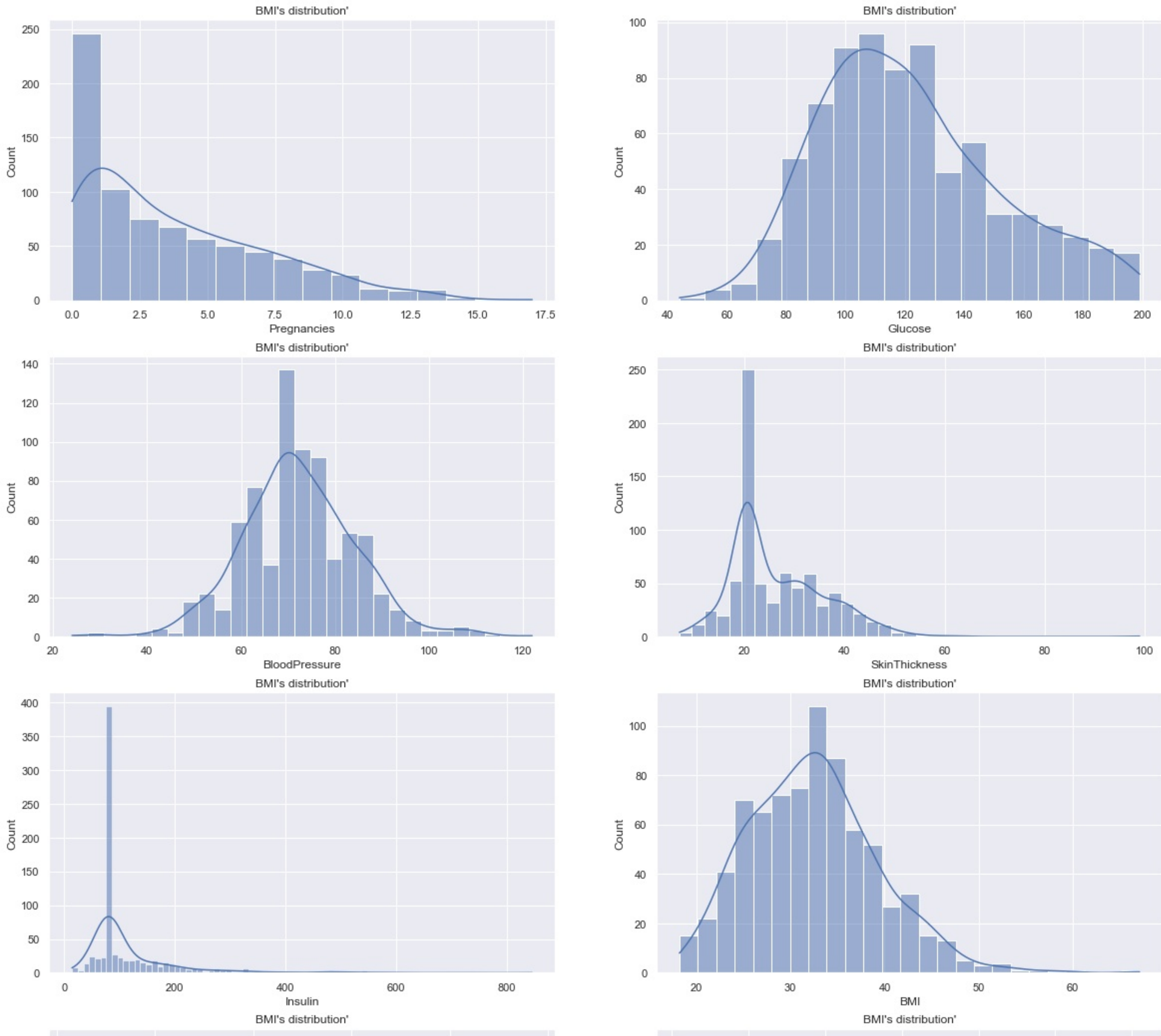
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

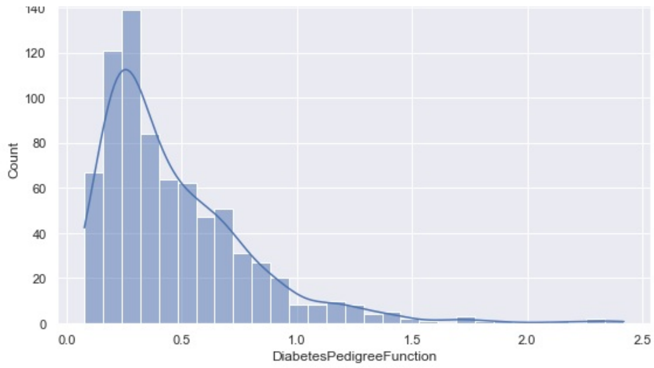
In [87]:

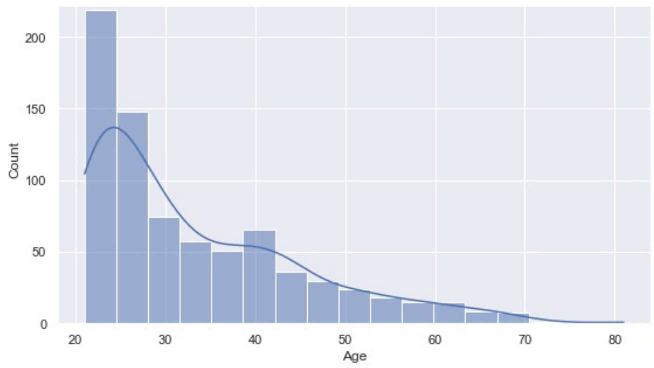
```
### Replacing zero values in feature with mean values of that feature

for feature in ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']:
    data[feature]=data[feature].replace(0,data[feature].mean())
```

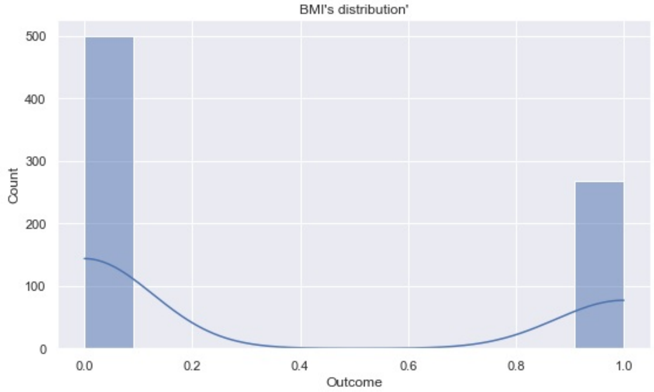
In [88]:

```
plt.figure(figsize=(20,30))
for i in enumerate(data.columns):
    plt.subplot(5, 2, i[0]+1)
    sns.set(rc={'figure.figsize':(7,5)})
    sns.histplot(data=data, x=i[1], kde=True)
    plt.title("{}'s distribution'".format(feature))
```









Observations

1. After replacing zero values with means of these features Glucose, BloodPressure, SkinThickness, Insulin, BMI the distribution skewness managed a little bit.

2.3 Checking Outliers in independent features

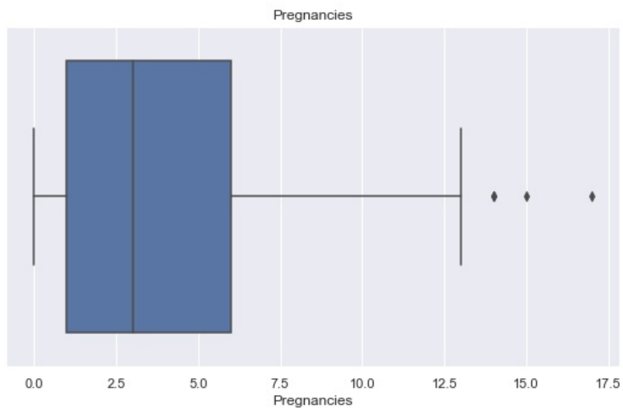
In [89]:

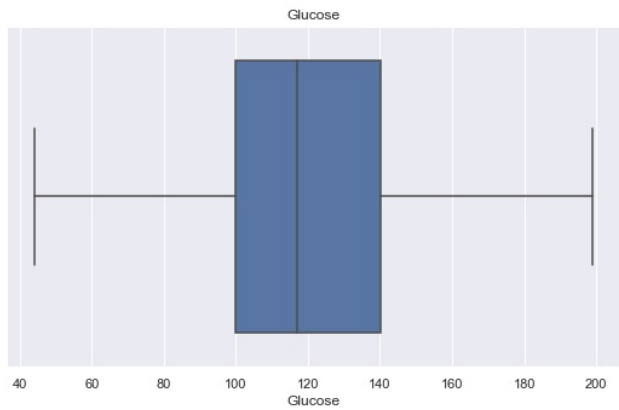
```
### Getting independent features
independent_features=[feature for feature in data.columns if feature not in ['Outcome']]
print(independent_features)
```

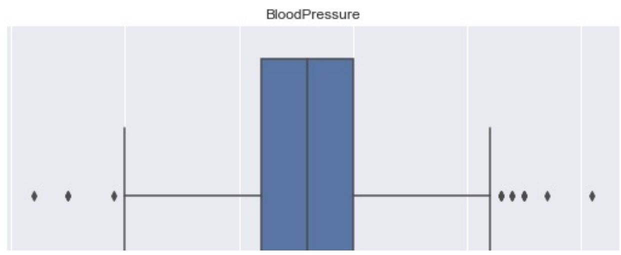
```
['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age']
```

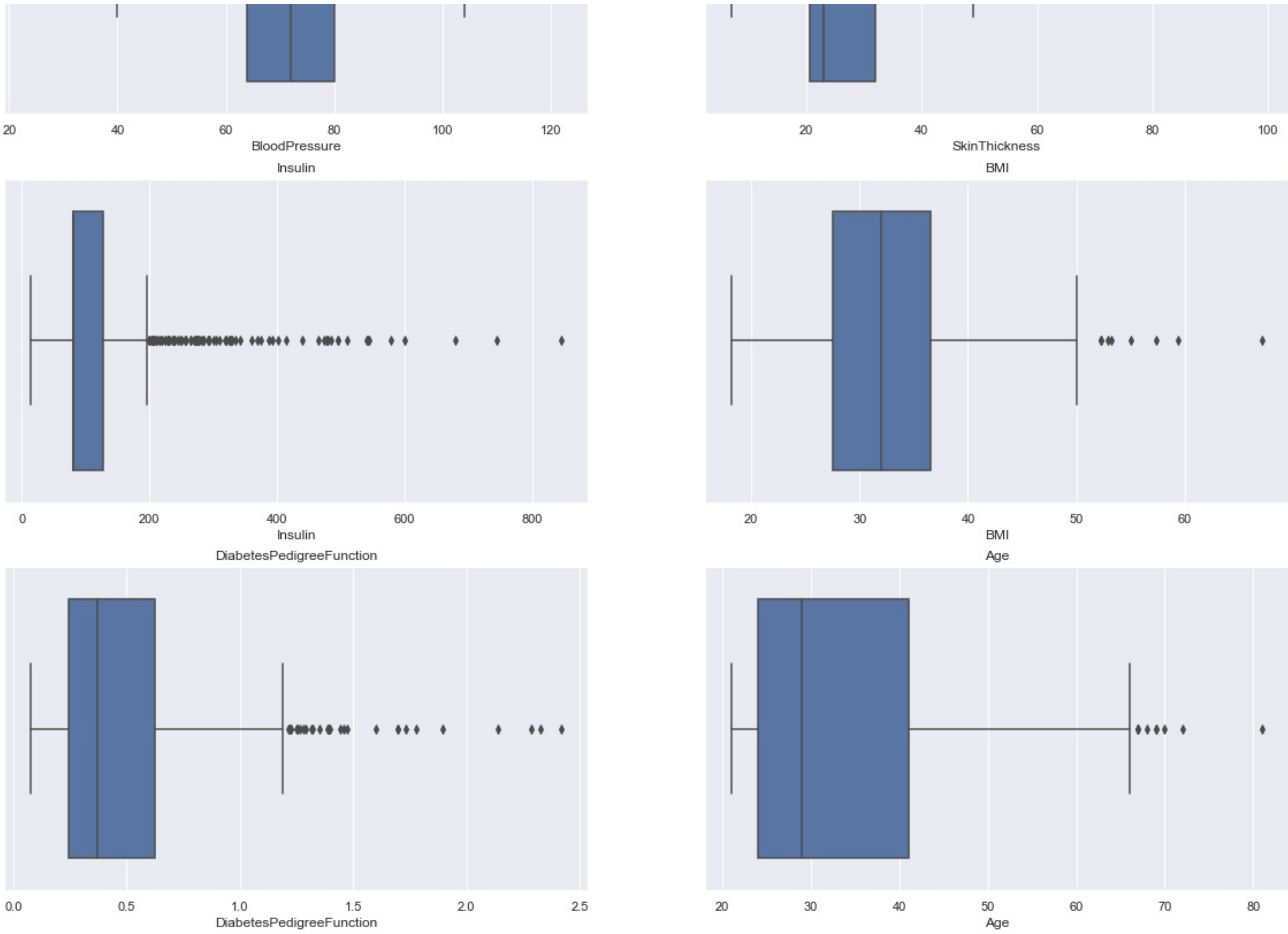
In [90]:

```
plt.figure(figsize=(20,30))
for i in enumerate(independent_features):
    plt.subplot(5, 2, i[0]+1)
    sns.set(rc={'figure.figsize':(7,5)})
    sns.boxplot(data=data, x=i[1])
    plt.title("{}".format(i[1]))
```









Observations

Note: Some outliers are already handled when we replaced the zreo values with mean.

1. Glucose has zero outliers.
2. Pregnancies has some outliers on upper boundary side.
3. BloodPressure has outliers on both sides of boundary.
4. SkinThickness, BMI and Age have outliers on upper boundary side.
5. Insulin and DiabetesPedigreeFunction has large no of outliers on upper boundary side.

2.4 Trimming outliers

In [91]:

```
def outlier_trimmer_upper(data_set, feature, trimming_value):
    """This function takes dataset, feature to be trimmed and the value after which we have to trim the data
    and returns the dataset after trimming outliers in input feature.
    """
    threshold=data_set[feature].quantile(trimming_value/100)
    data_set=data_set[data_set[feature]<threshold]
    return data_set

def outlier_trimmer_lower(data_set, feature, trimming_value):
    """This function takes dataset, feature to be trimmed and the value after which we have to trim the data
    and returns the dataset after trimming outliers in input feature.
    """
    threshold=data_set[feature].quantile(trimming_value/100)
    data_set=data_set[data_set[feature]>threshold]
    return data_set
```

In [92]:

```
### shape of data before trimming
data.shape
```

Out[92]:

```
(768, 9)
```

In [93]:

```
### removing 1 percent outliers in BloodPressure, SkinThickness, BMI and Age as these feature has less no of outl
```

```python
for feature in ['BloodPressure', 'SkinThickness', 'BMI', 'Age']:
    data=outlier_trimmer_upper(data, feature, 99)
```

In [94]:

```python
### shape of data after trimming
data.shape
```

Out[94]: (733, 9)

In [95]:

```python
### removing 2 percent outliers in Insulin and DiabetesPedigreeFunction as they have large no of outliers

for feature in ['Insulin', 'DiabetesPedigreeFunction']:
    data=outlier_trimmer_upper(data, feature, 98)
```

In [96]:

```python
data.shape
```

Out[96]: (703, 9)

In [98]:

```python
### removing 0.5 percent outliers in BMI, Glucose, BloodPressure on lower side

for feature in ['Glucose', 'BloodPressure', 'BMI' ]:
    data=outlier_trimmer_lower(data, feature, 0.5)
```

In [99]:

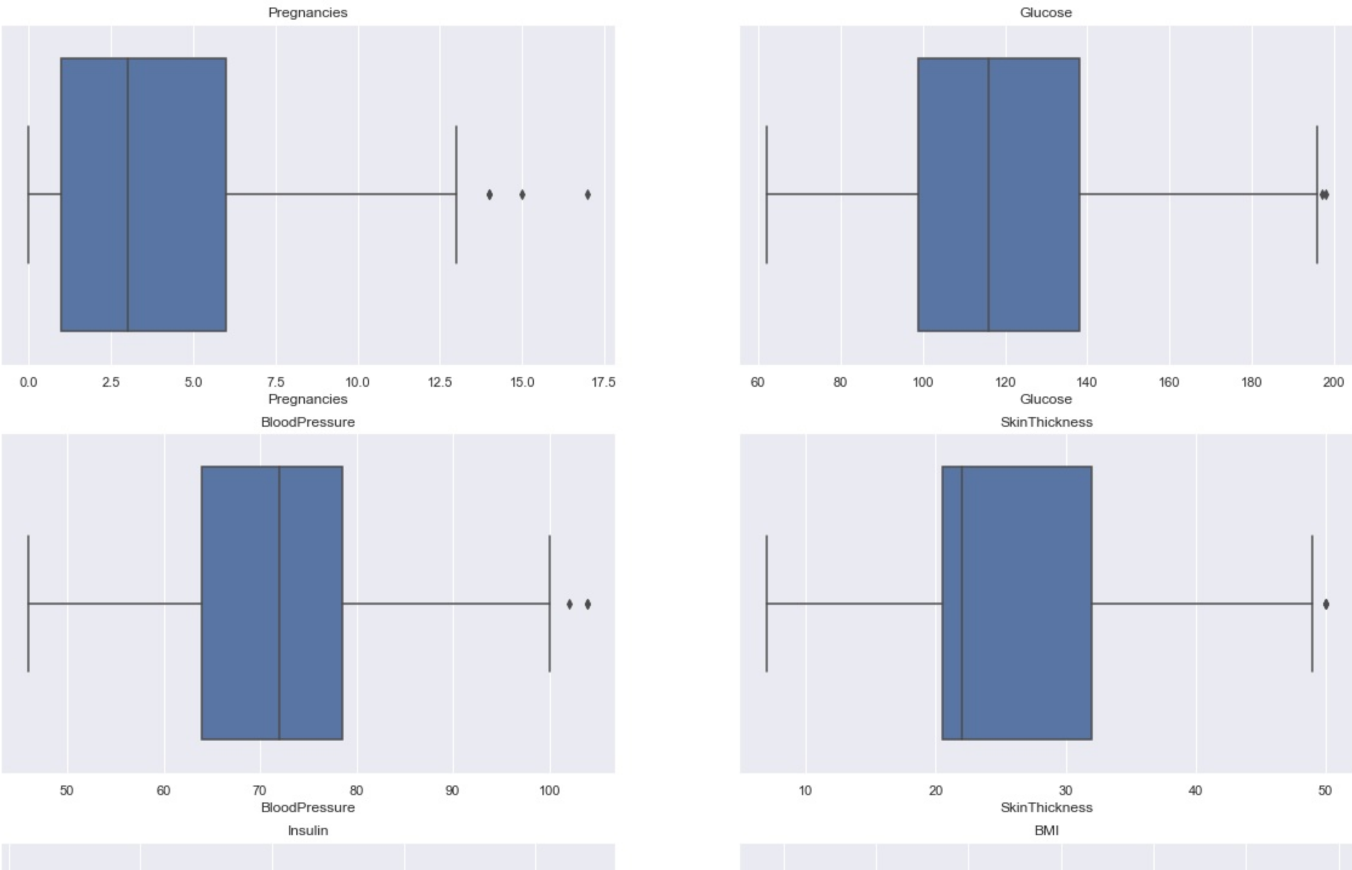
```python
data.shape
```

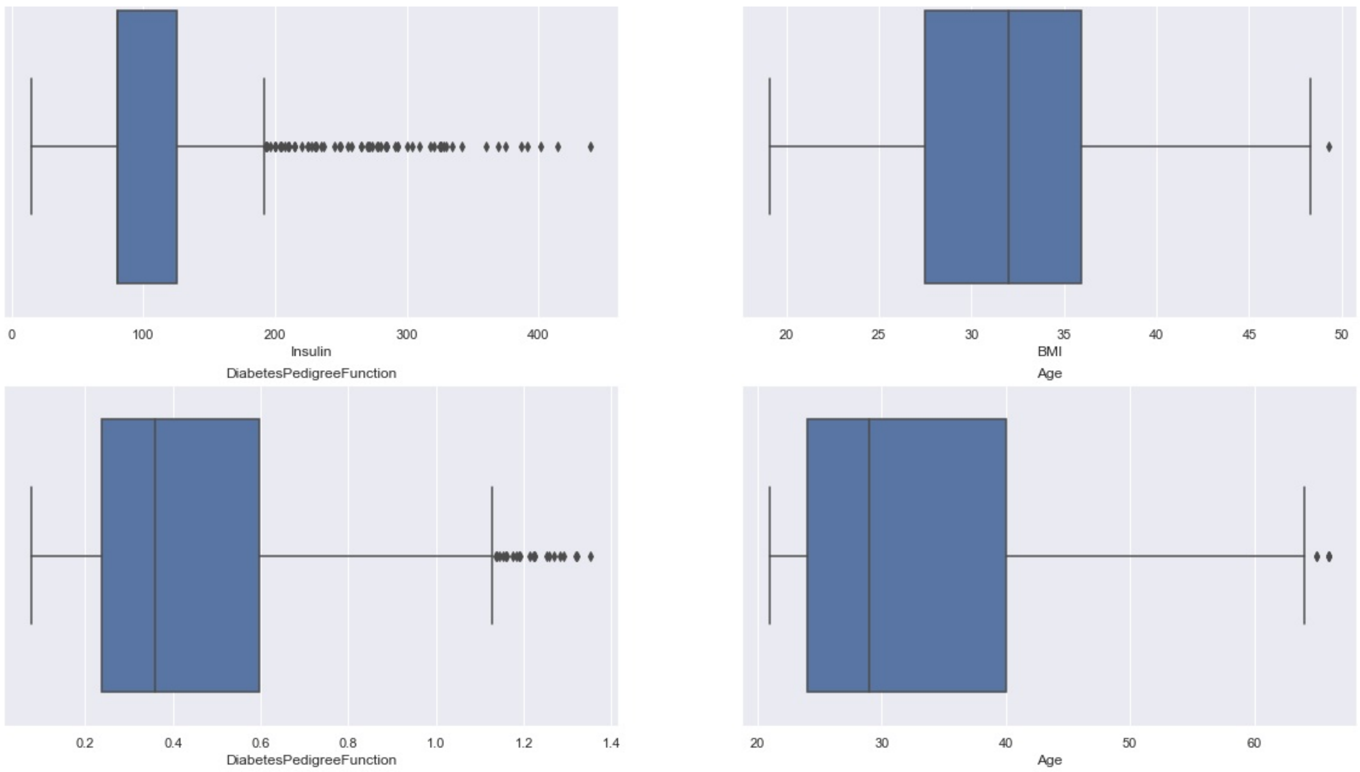
Out[99]: (688, 9)

2.5 Re-checking outliers after trimming outliers in independent features

In [100…

```python
plt.figure(figsize=(20,30))
for i in enumerate(independent_features):
    plt.subplot(5, 2, i[0]+1)
    sns.set(rc={'figure.figsize':(7,5)})
    sns.boxplot(data=data, x=i[1])
    plt.title("{}".format(i[1]))
```





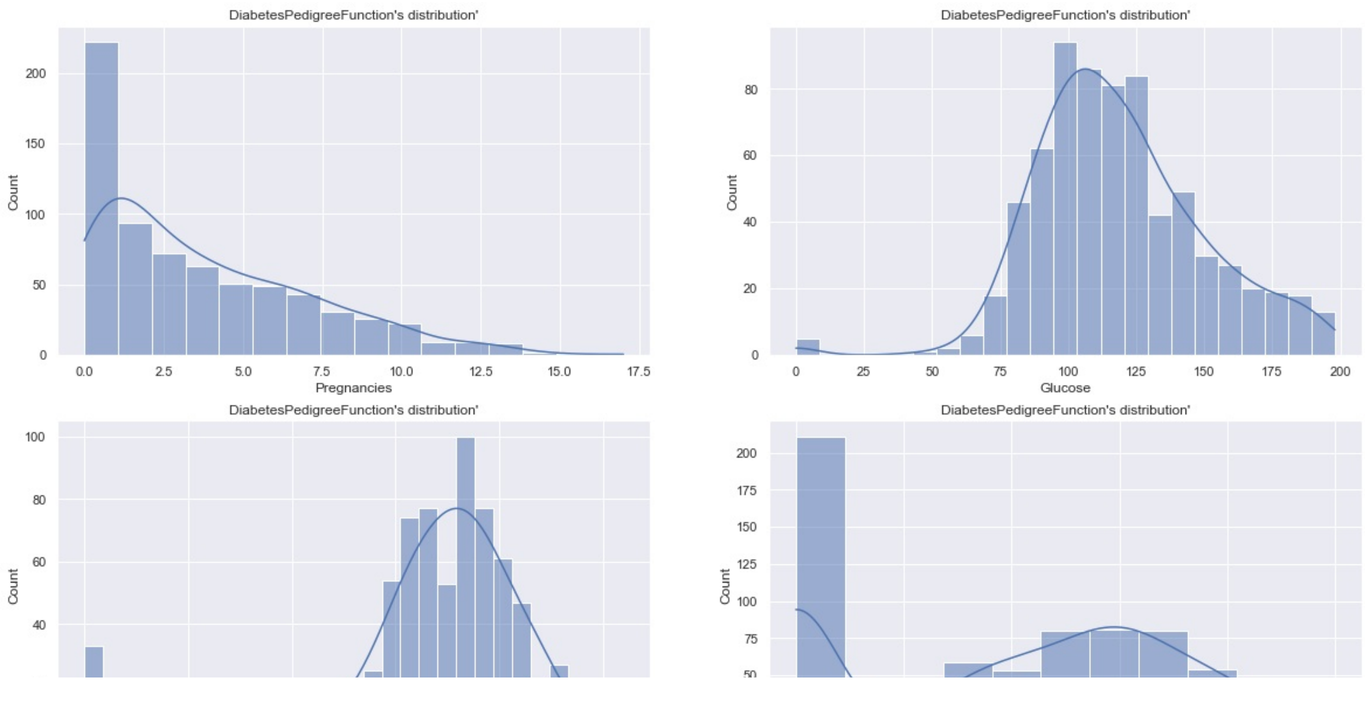
Observations

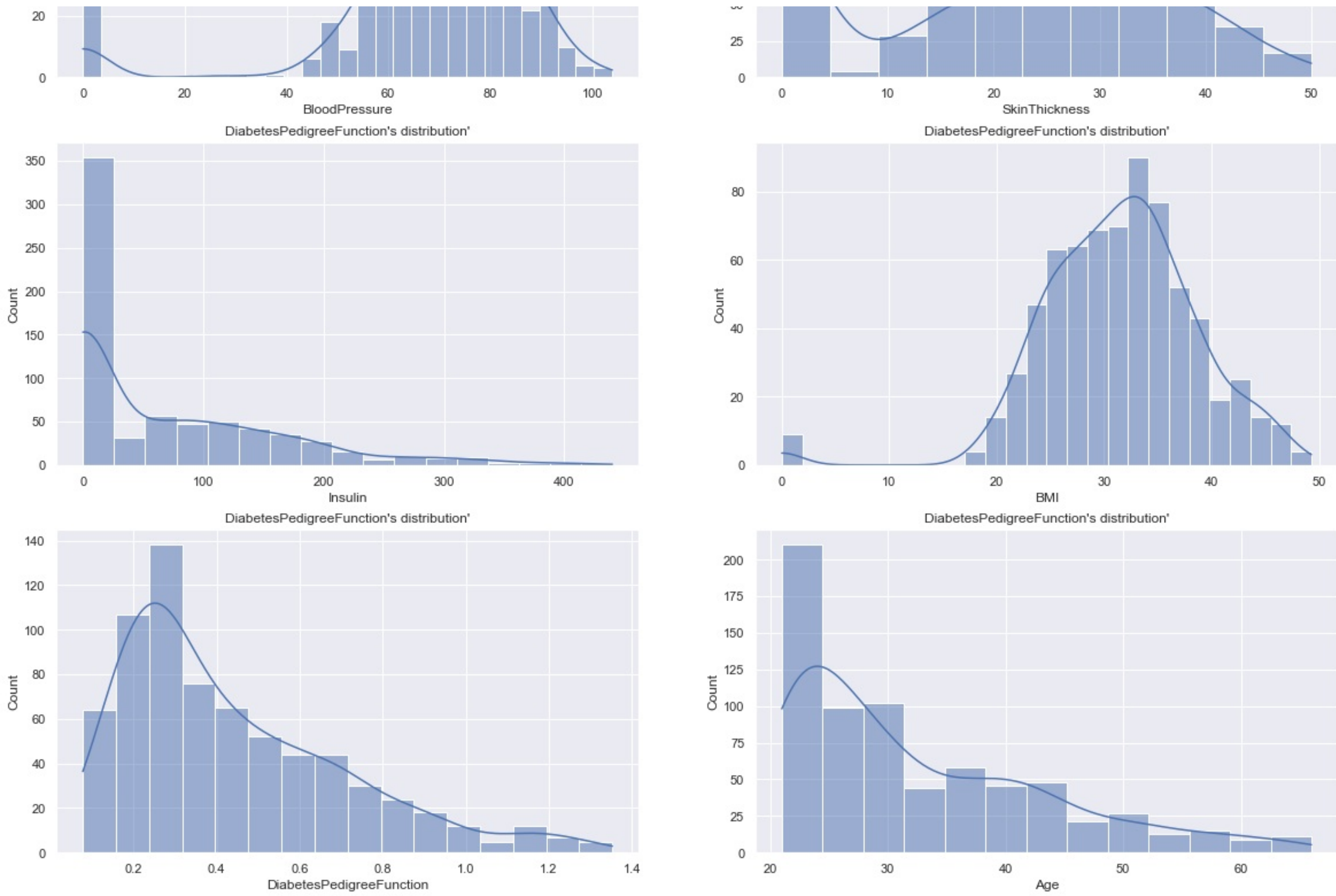
After Trimming Outliers

1. BloodPressure has very few outliers on left sides of boundary now.
2. SkinThickness has no outliers now.
3. BMI and Age have very few outliers on upper boundary side now.
4. No of outliers is reduced for Insulin and DiabetesPedigreeFunction.
5. Now no feature has outliers on lower side.

2.6 Rechecking distribution of independent feature after trimming outlies

In [69]:
```
plt.figure(figsize=(20,30))
for i in enumerate(independent_features):
    plt.subplot(5, 2, i[0]+1)
    sns.set(rc={'figure.figsize':(7,5)})
    sns.histplot(data=data, x=i[1], kde=True)
    plt.title("{}'s distribution'".format(feature))
```





2.7 Checking imbalance of data before and after trimming outliers

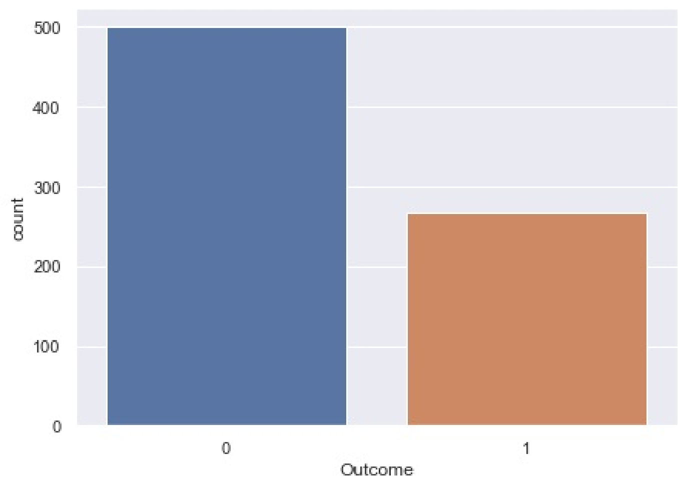
2.7.1 Before trimming outliers

In [101…

```
sns.countplot(data=dataset, x='Outcome')
```

Out[101…

```
<AxesSubplot:xlabel='Outcome', ylabel='count'>
```



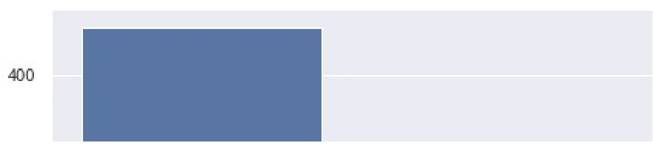
2.7.2 After trimming outliers

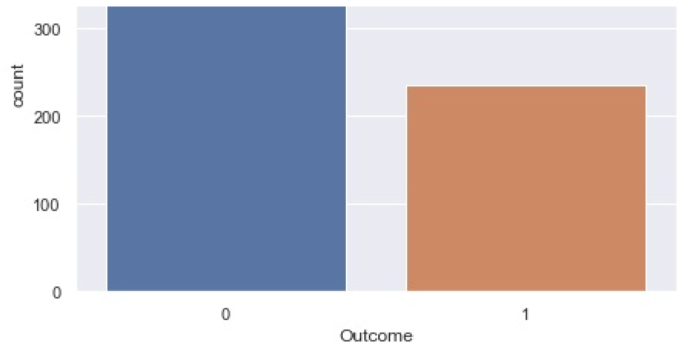
In [102…

```
sns.countplot(data=data, x='Outcome')
```

Out[102…

```
<AxesSubplot:xlabel='Outcome', ylabel='count'>
```





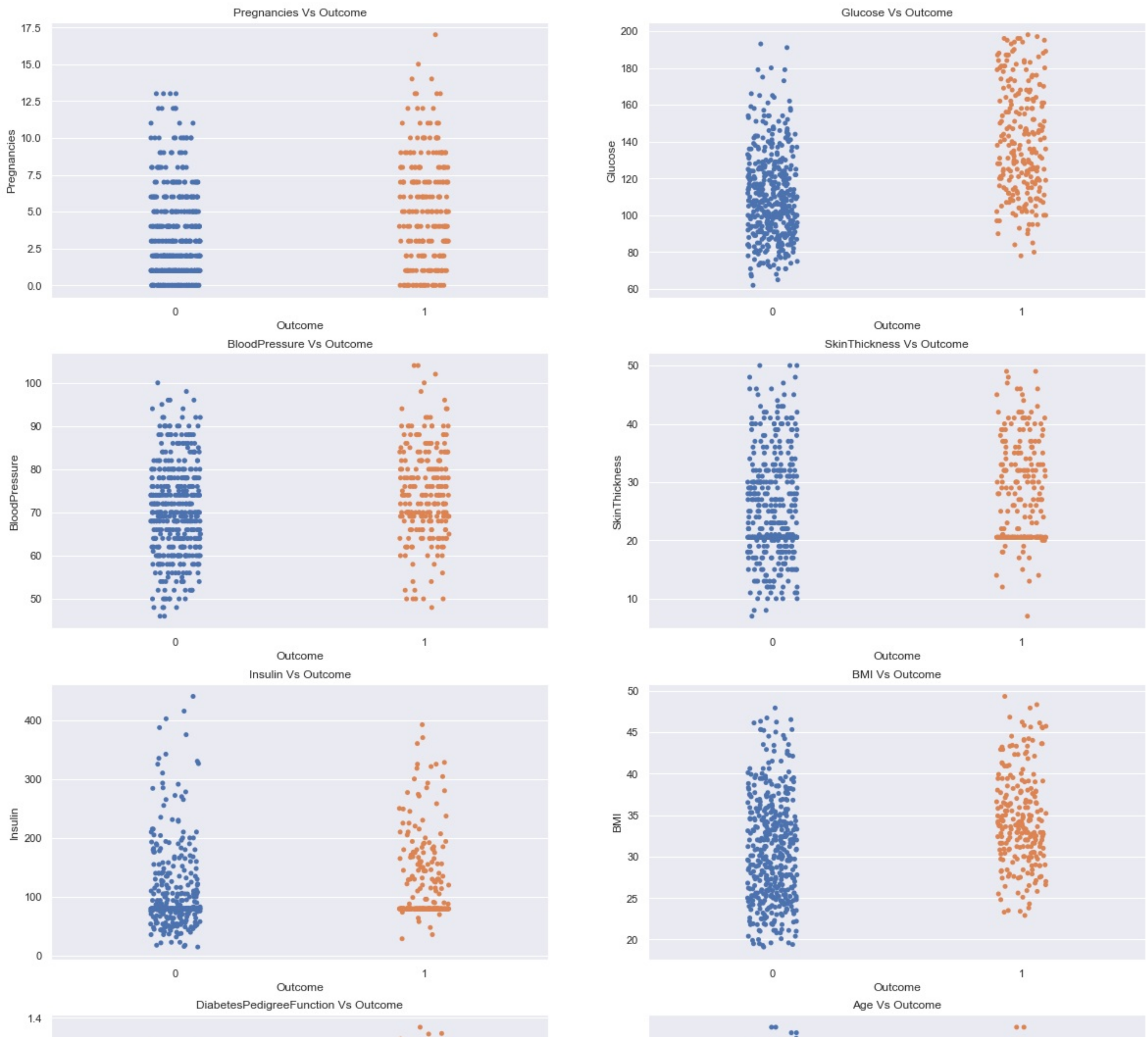
Observations

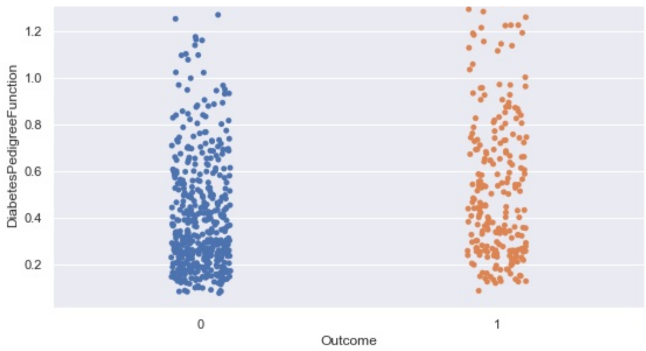
1. We have imbalance in our dataset, lets not handle this imbalance and check accuracy, precision and recall
2. Then handle this imbalance and check accuracy, precision and recall

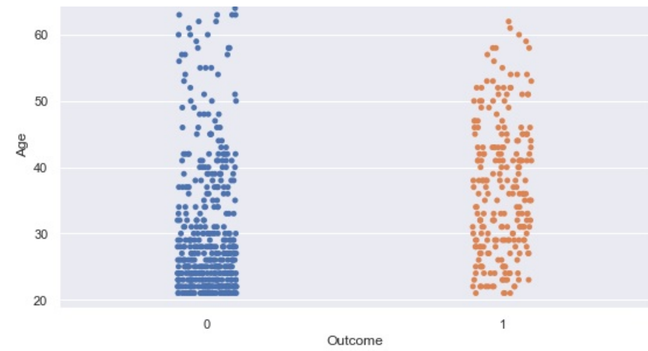
2.8 Relationship between independent features and dependent feature

In [118…

```
plt.figure(figsize=(20,30))
for i in enumerate(independent_features):
    plt.subplot(5, 2, i[0]+1)
    sns.set(rc={'figure.figsize':(7,5)})
    sns.stripplot(data=data, y=i[1], x='Outcome')
    plt.title("{} Vs Outcome".format(i[1]))
```



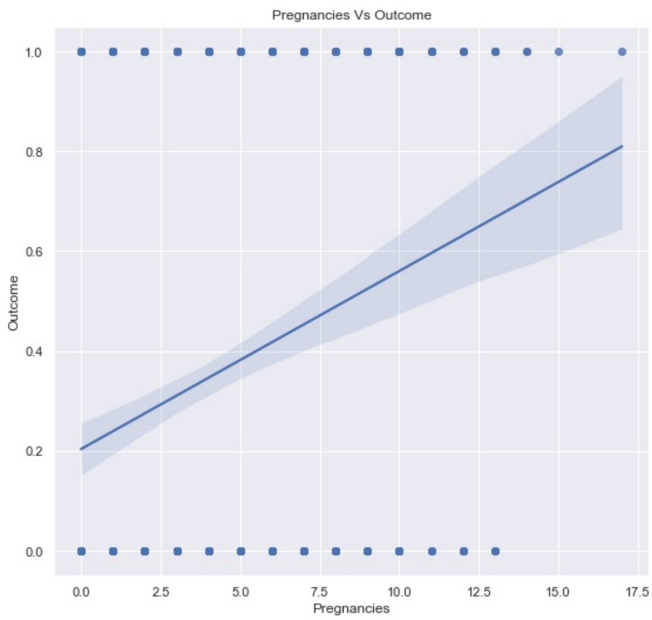


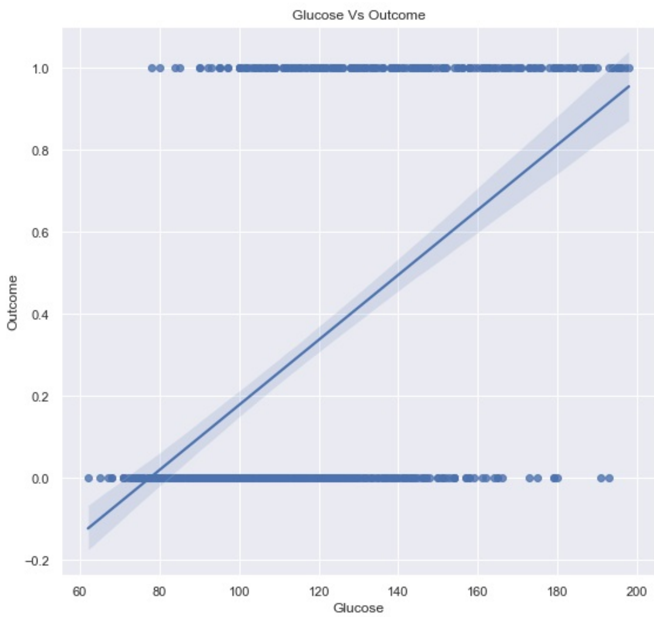


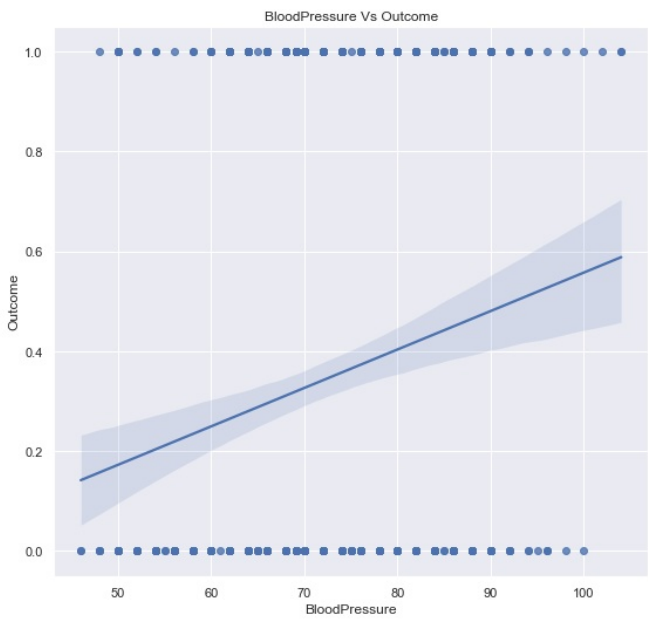
2.9 Checking the variation of slope between independent features and dependent feature

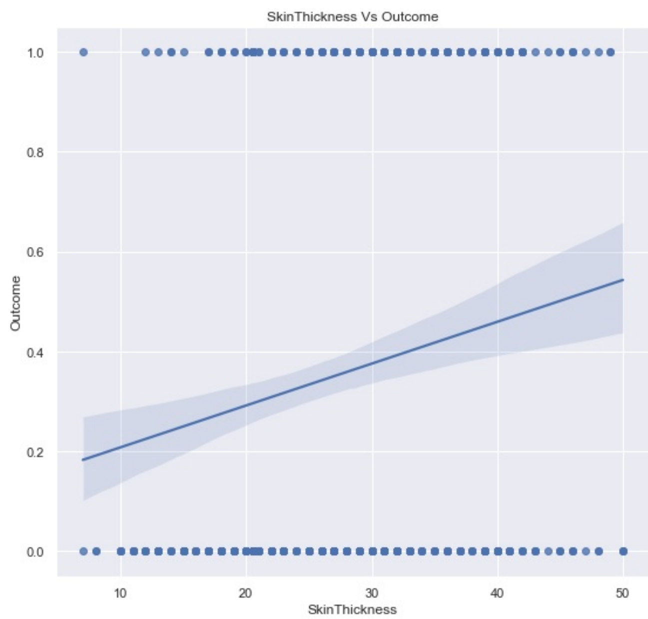
In [142…

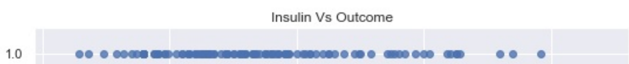
```
plt.figure(figsize=(20,50))
for i in enumerate(independent_features):
    plt.subplot(5, 2, i[0]+1)
    sns.set(rc={'figure.figsize':(8,10)})
    sns.regplot(x=data[i[1]], y=data['Outcome'])
    plt.xlabel(i[1])
    plt.ylabel("Outcome")
    plt.title("{} Vs Outcome".format(i[1]))
```

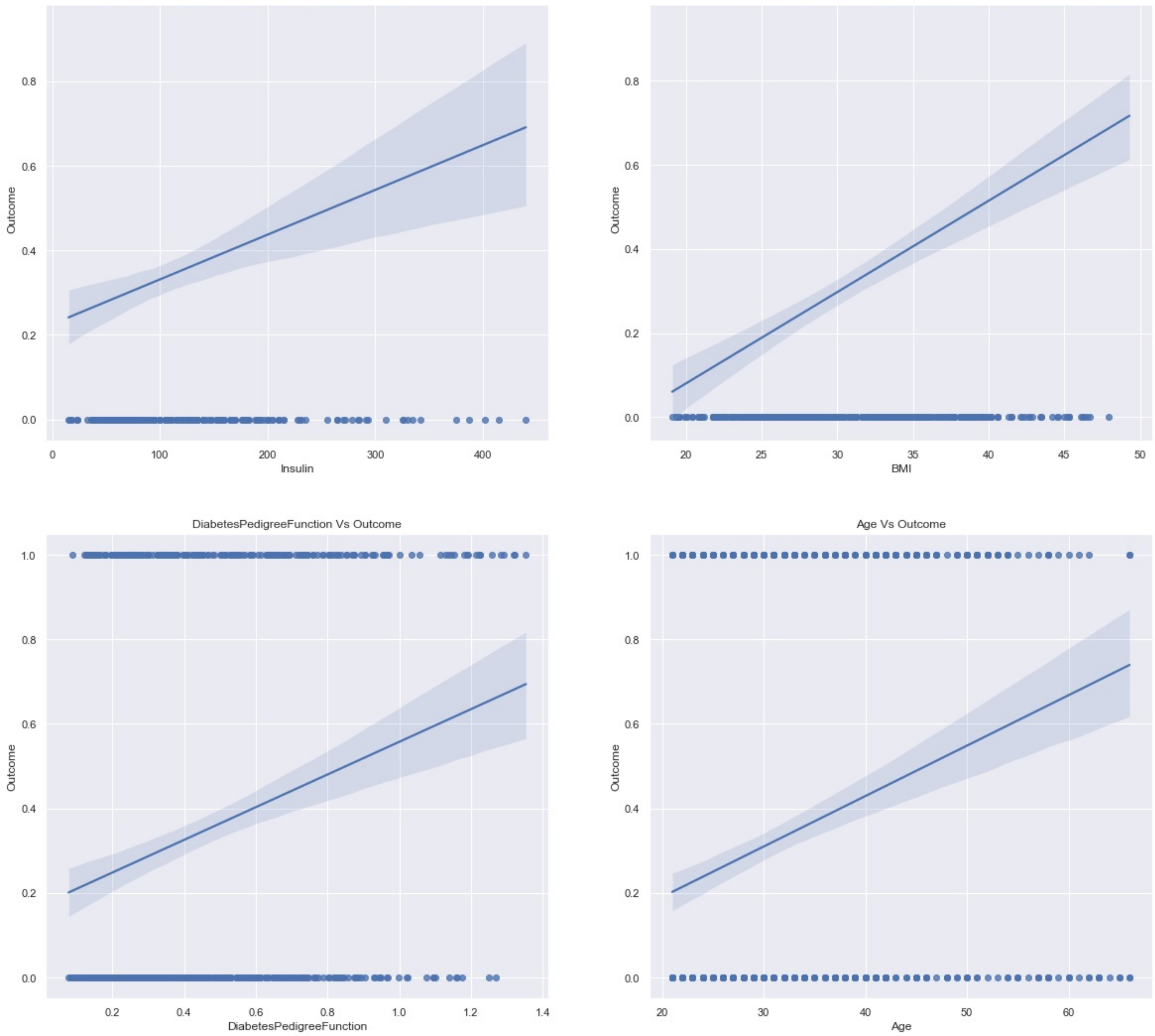












2.10 Checking correlation between independent features and dependent feature

In [122…

```
corr=round(data[[feature for feature in data.columns]].corr(),2)
corr
```

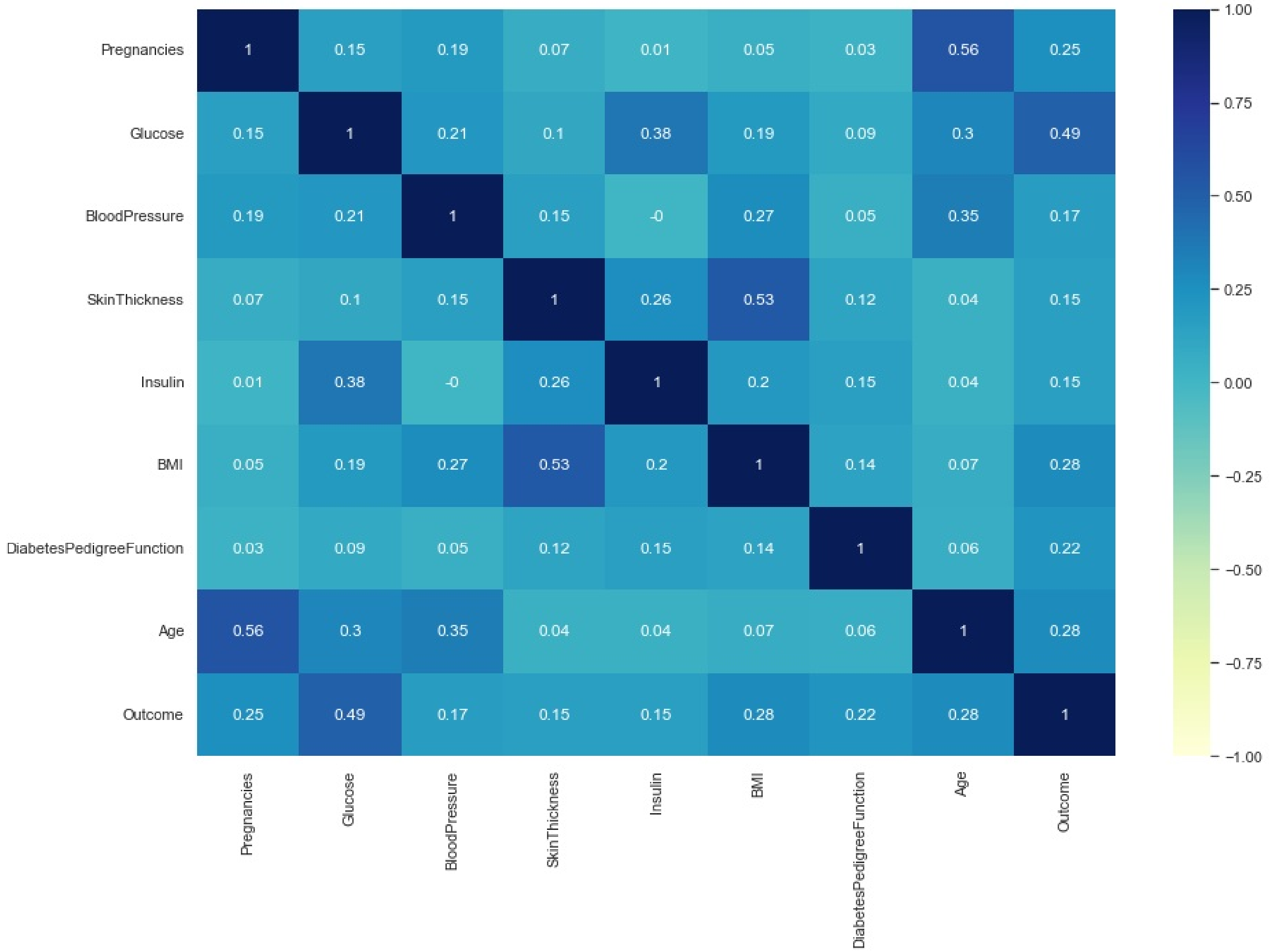
Out[122…

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1.00	0.15	0.19	0.07	0.01	0.05	0.03	0.56	0.25
Glucose	0.15	1.00	0.21	0.10	0.38	0.19	0.09	0.30	0.49
BloodPressure	0.19	0.21	1.00	0.15	-0.00	0.27	0.05	0.35	0.17
SkinThickness	0.07	0.10	0.15	1.00	0.26	0.53	0.12	0.04	0.15
Insulin	0.01	0.38	-0.00	0.26	1.00	0.20	0.15	0.04	0.15
BMI	0.05	0.19	0.27	0.53	0.20	1.00	0.14	0.07	0.28
DiabetesPedigreeFunction	0.03	0.09	0.05	0.12	0.15	0.14	1.00	0.06	0.22
Age	0.56	0.30	0.35	0.04	0.04	0.07	0.06	1.00	0.28
Outcome	0.25	0.49	0.17	0.15	0.15	0.28	0.22	0.28	1.00

In [124…

```
### Plotting heatmap for visualising the correlation between features
sns.set(rc={'figure.figsize':(15,10)})
sns.heatmap(data=corr, annot=True,cmap="YlGnBu", vmin=-1, vmax=1)
```

Out[124… <AxesSubplot:>



3.0 Model Building

3.1 Getting independent features in dataset(X) and dependent feature in series(y)

In [126…

```
data.head()
```

Out[126…

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.000000	79.799479	33.6	0.627	50	1
1	1	85.0	66.0	29.000000	79.799479	26.6	0.351	31	0
2	8	183.0	64.0	20.536458	79.799479	23.3	0.672	32	1
3	1	89.0	66.0	23.000000	94.000000	28.1	0.167	21	0
5	5	116.0	74.0	20.536458	79.799479	25.6	0.201	30	0

In [129…

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

X.head()
```

Out[129…

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
0	6	148.0	72.0	35.000000	79.799479	33.6	0.627	50
1	1	85.0	66.0	29.000000	79.799479	26.6	0.351	31
2	8	183.0	64.0	20.536458	79.799479	23.3	0.672	32
3	1	89.0	66.0	23.000000	94.000000	28.1	0.167	21
5	5	116.0	74.0	20.536458	79.799479	25.6	0.201	30

In [130…

```
y.head()
```

Out[130…
```
0    1
1    0
2    1
3    0
5    0
Name: Outcome, dtype: int64
```

3.2 Splitting data into Training and Test data

In [226…
```
### random state train test split will be same with all people using random_state=16

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.15, random_state=16)
```

In [227…
```
X_train.head()
```

Out[227…

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
746	1	147.0	94.0	41.000000	79.799479	49.3	0.358	27
264	4	123.0	62.0	20.536458	79.799479	32.0	0.226	35
340	1	130.0	70.0	13.000000	105.000000	25.9	0.472	22
322	0	124.0	70.0	20.000000	79.799479	27.4	0.254	36
565	2	95.0	54.0	14.000000	88.000000	26.1	0.748	22

In [228…
```
y_train.head()
```

Out[228…
```
746    1
264    1
340    0
322    1
565    0
Name: Outcome, dtype: int64
```

In [229…
```
X_test.head()
```

Out[229…

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
705	6	80.0	80.0	36.000000	79.799479	39.8	0.177	28
728	2	175.0	88.0	20.536458	79.799479	22.9	0.326	22
242	3	139.0	54.0	20.536458	79.799479	25.6	0.402	22
687	1	107.0	50.0	19.000000	79.799479	28.3	0.181	29
638	7	97.0	76.0	32.000000	91.000000	40.9	0.871	32

In [230…
```
y_test.head()
```

Out[230…
```
705    0
728    0
242    1
687    0
638    1
Name: Outcome, dtype: int64
```

In [231…
```
### both will have same shape
X_train.shape, y_train.shape
```

Out[231…
```
((584, 8), (584,))
```

In [232…
```
### both will have same shape
X_test.shape, y_test.shape
```

Out[232…
```
((104, 8), (104,))
```

3.3 Standardisation/ feature scaling the dataset

In [233…

```
### Crating a standard scaler object
scaler=StandardScaler()
scaler
```

Out[233…

```
StandardScaler()
```

In [234…

```
### using fit_transform to Standardize the train data
X_train=scaler.fit_transform(X_train)
X_train
```

Out[234…

```
array([[-0.86019009,  0.94854966,  2.01983918, ...,  2.89360233,
        -0.31591105, -0.51401632],
       [ 0.04169683,  0.1172319 , -0.91556073, ...,  0.016956  ,
        -0.79724224,  0.20241693],
       [-0.86019009,  0.35969958, -0.18171075, ..., -0.99735282,
         0.09978406, -0.9617871 ],
       ...,
       [ 0.3423258 , -0.47161818,  0.91906421, ...,  1.26405701,
        -0.57845534,  0.47107939],
       [ 1.84547065, -0.64480938,  1.2859892 , ...,  2.27836583,
         2.52102579,  0.47107939],
       [ 1.54484168,  1.74522918,  0.18521424, ...,  2.01231762,
        -0.15182088,  0.91885017]])
```

In [235…

```
### here using transform only to avoid data leakage
### (training mean and training std will be used for standardisation when we use transform)
X_test=scaler.transform(X_test)
X_test
```

Out[235…

```
array([[ 6.42954768e-01, -1.37221242e+00,  7.35601720e-01,
         1.18101174e+00, -4.38881751e-01,  1.31394105e+00,
        -9.75918211e-01, -4.24462162e-01],
       [-5.59561115e-01,  1.91842038e+00,  1.46945170e+00,
        -6.29808456e-01, -4.38881751e-01, -1.49619322e+00,
        -4.32597403e-01, -9.61787095e-01],
       [-2.58932144e-01,  6.71443739e-01, -1.64941070e+00,
        -6.29808456e-01, -4.38881751e-01, -1.04723686e+00,
        -1.55467326e-01, -9.61787095e-01],
       [-8.60190086e-01, -4.36979943e-01, -2.01633569e+00,
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        -9.61332418e-01, -3.34908006e-01],
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         7.12601531e-01, -2.66275971e-01,  1.49684920e+00,
         1.55471696e+00, -6.62455397e-02],
       [-1.16081906e+00, -6.44809383e-01, -7.32098232e-01,
        -1.04393675e+00, -4.38881751e-01, -1.81212547e+00,
        -7.02434583e-01, -1.05134125e+00],
       [ 1.24421271e+00,  1.08710262e+00,  5.52139226e-01,
         7.12601531e-01,  1.56757517e+00,  1.82940947e+00,
         2.60227790e-01,  2.91971082e-01],
       [ 2.74735756e+00, -4.71618183e-01, -1.81710750e-01,
        -6.29808456e-01, -4.38881751e-01,  3.82772301e-01,
        -7.06081031e-01,  1.72483757e+00],
       [ 4.16968264e-02, -1.02583002e+00,  1.46945170e+00,
         2.46913981e+00, -8.36464981e-01,  9.64752771e-01,
        -3.01325261e-01, -3.34908006e-01],
       [-8.60190086e-01, -1.23365946e+00, -7.32098232e-01,
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         9.61376125e-02, -4.24462162e-01],
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        -6.29808456e-01, -4.38881751e-01, -1.39642514e+00,
        -9.39453727e-01, -8.72232940e-01],
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        -5.93041131e-01,  1.12862771e-01],
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         7.45205424e-01, -8.72232940e-01],
       [-5.59561115e-01, -2.63788742e-01,  1.28598920e+00,
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        -7.24313273e-01, -4.24462162e-01],
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        -8.25383581e-02, -6.93124629e-01],
       [ 3.42325797e-01,  1.67595270e+00, -7.32098232e-01,
```

```
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```

```
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```

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  4.78396426e-01, -1.89223402e-01,  4.49284354e-01,
  3.07631619e-01, -6.62455397e-02]])
```

4.0 Model

1.0 Logistic Regression

In [236…
```
### Creating a Logistic regression object
logistic_reg=LogisticRegression()
logistic_reg
```
Out[236…
```
LogisticRegression()
```

In [237…
```
### Passing independant and dependant training data to the model
logistic_reg.fit(X_train,y_train)
```
Out[237…
```
LogisticRegression()
```

1.1 Using Above Model to get prediction for test data

In [238…
```
logistic_reg_pred=logistic_reg.predict(X_test)
logistic_reg_pred
```
Out[238…
```
array([0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0,
       1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 1, 1, 1, 1, 0, 0,
       0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0, 0, 0, 1, 0, 0, 1, 0,
       1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0], dtype=int64)
```

1.2.0 Performance Metrics

1.2.1 Confusion Matrix

In [239…
```
confusion_mat=confusion_matrix(y_test, logistic_reg_pred)
confusion_mat
```
Out[239…
```
array([[56,  8],
       [16, 24]], dtype=int64)
```

In [240…
```
truly_positive=confusion_mat[0][0]
falsely_positive=confusion_mat[0][1]
falsely_negative=confusion_mat[1][0]
truly_negative=confusion_mat[1][1]
```

1.2.2 Accuracy Score

In [241…
```
### accuracy using accuracy_score
accuracy=round(accuracy_score(y_test, logistic_reg_pred),4)
accuracy
```
Out[241…
```
0.7692
```

In [242…
```
### manual calcualtion for accuracy
accuracy_manual=round(((truly_positive+truly_negative)/(truly_positive+falsely_positive+falsely_negative+truly_ne
print("Accuracy of our model is {}".format(accuracy_manual))
```
```
Accuracy of our model is 0.7692
```

1.2.3 Precision Score

In [243…

```
precision_manual_diabetic=round(truly_positive/(truly_positive+falsely_positive),4)
print("Precision of our model is {}".format(precision_manual_diabetic))
```

```
Precision of our model is 0.875
```

1.2.4 Recall Score

In [244…

```
recall_manual_diabetic=round(truly_positive/(truly_positive+falsely_negative),4)
print("Recall of our model is {}".format(recall_manual_diabetic))
```

```
Recall of our model is 0.7778
```

1.2.5 F-1 Score

1. Giving equal importance to falsely positive and falsely negative

In [245…

```
f1_score=2*(precision_manual_diabetic*recall_manual_diabetic)/(precision_manual_diabetic+recall_manual_diabetic)
print("F-1 Score of our model is {} ".format(round(f1_score,4)))
```

```
F-1 Score of our model is 0.8235
```