Diabetes_Prediction_Different_ML_Moodels

October 5, 2022

[1]:
```
import pandas as pd
import  numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

0.0.1 2.Loading the dataset

[2]:
```
# loading the diabetes dataset to a pandas DataFrame
diabetes_dataset = pd.read_csv('diabetes.csv')
```

0.0.2 3. Exploratory Data Analysis

[3]:
```
# printing the first 5 rows of the dataset
diabetes_dataset.head()
```

[3]:
```
   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
```

[4]:
```
# number of rows and Columns in this dataset
diabetes_dataset.shape
```

[4]:
```
(768, 9)
```

[5]:
```
#learning about the columns
diabetes_dataset.columns
```

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

```
[6]: #knowledge of data type helps for computation
     diabetes_dataset.dtypes
```

```
[6]: Pregnancies                   int64
     Glucose                       int64
     BloodPressure                 int64
     SkinThickness                 int64
     Insulin                       int64
     BMI                         float64
     DiabetesPedigreeFunction    float64
     Age                           int64
     Outcome                       int64
     dtype: object
```

```
[7]: #Print a concise summary of a DataFrame
     diabetes_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
```

```
[8]: # getting the statistical measures of the data
     diabetes_dataset.describe()
```

```
[8]:        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
```

CONCLUSION :- We observe that min value of some columns is 0 which cannot be possible medically.Hence in the data cleaning process we'll have to replace them with median/mean value depending on the distribution. Also in the max column we can see insulin levels as high as 846! We have to treat outliers.

0.0.3 Data cleaning

- Dropping duplicate values
- Checking NULL values
- Checking for 0 value and replacing it :- It isn't medically possible for some data record to have 0 value such as Blood Pressure or Glucose levels. Hence we replace them with the mean value of that particular column.

[9]:
```
#dropping duplicate values
diabetes_dataset = diabetes_dataset.drop_duplicates()
```

[10]:
```
#check for missing values
diabetes_dataset.isnull().sum()
```

[10]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[11]:
```
#checking for 0 values in 5 columns
print(diabetes_dataset[diabetes_dataset['BloodPressure']==0].shape[0])
print(diabetes_dataset[diabetes_dataset['Glucose']==0].shape[0])
print(diabetes_dataset[diabetes_dataset['SkinThickness']==0].shape[0])
print(diabetes_dataset[diabetes_dataset['Insulin']==0].shape[0])
print(diabetes_dataset[diabetes_dataset['BMI']==0].shape[0])
```

```
35
5
227
374
11
```

[12]:
```
#Age & DiabetesPedigreeFunction do not have have minimum 0 value so no need to␣
↪replace
```

Some of the columns have a skewed distribution, so the mean is more affected by outliers than the median. Glucose and Blood Pressure have normal distributions hence we replace 0 values in those columns by mean value. SkinThickness, Insulin,BMI have skewed distributions hence median is a better choice as it is less affected by outliers.

[13]:
```
#replacing 0 values with median of that column
diabetes_dataset['Glucose']=diabetes_dataset['Glucose'].
 ↪replace(0,diabetes_dataset['Glucose'].mean())
#normal distribution
diabetes_dataset['BloodPressure']=diabetes_dataset['BloodPressure'].
 ↪replace(0,diabetes_dataset['BloodPressure'].mean())
#normal distribution
diabetes_dataset['SkinThickness']=diabetes_dataset['SkinThickness'].
 ↪replace(0,diabetes_dataset['SkinThickness'].median())
#skewed distribution
diabetes_dataset['Insulin']=diabetes_dataset['Insulin'].
 ↪replace(0,diabetes_dataset['Insulin'].median())
#skewed distribution
diabetes_dataset['BMI']=diabetes_dataset['BMI'].
 ↪replace(0,diabetes_dataset['BMI'].median())
#skewed distribution
```

0.0.4 4.Data Visualization

Here we are going to plot :-

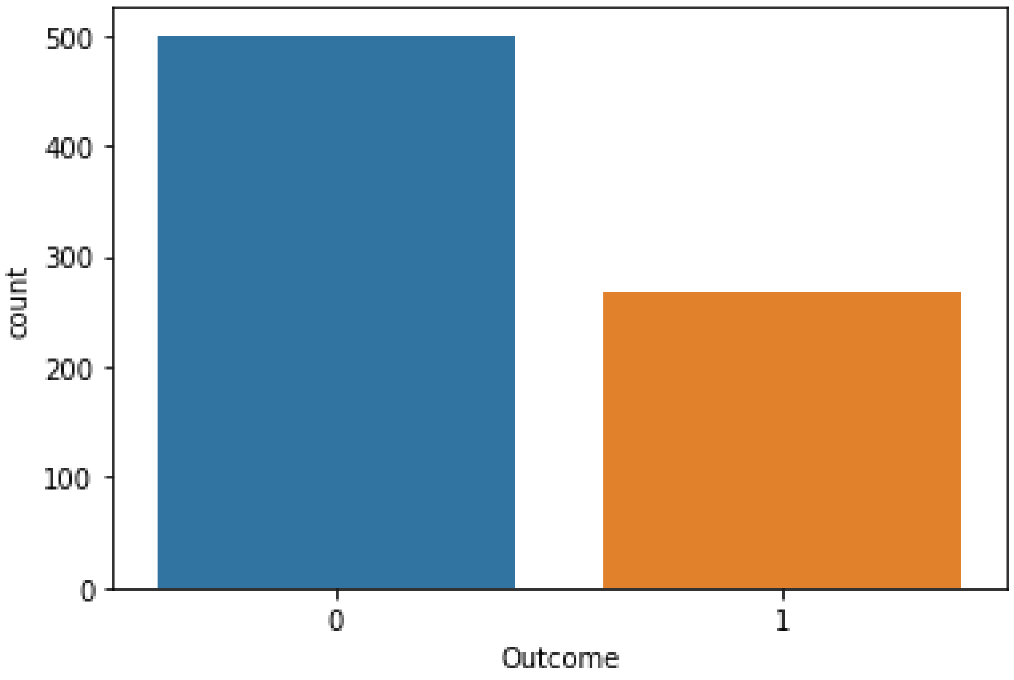
- Count Plot :- to see if the dataset is balanced or not
- Histograms :- to see if data is normally distributed or skewed
- Box Plot :- to analyse the distribution and see the outliers

[14]:
```
diabetes_dataset['Outcome'].value_counts()
```

[14]:
```
0    500
1    268
Name: Outcome, dtype: int64
```

[15]:
```
sns.countplot('Outcome',data=diabetes_dataset)
```

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

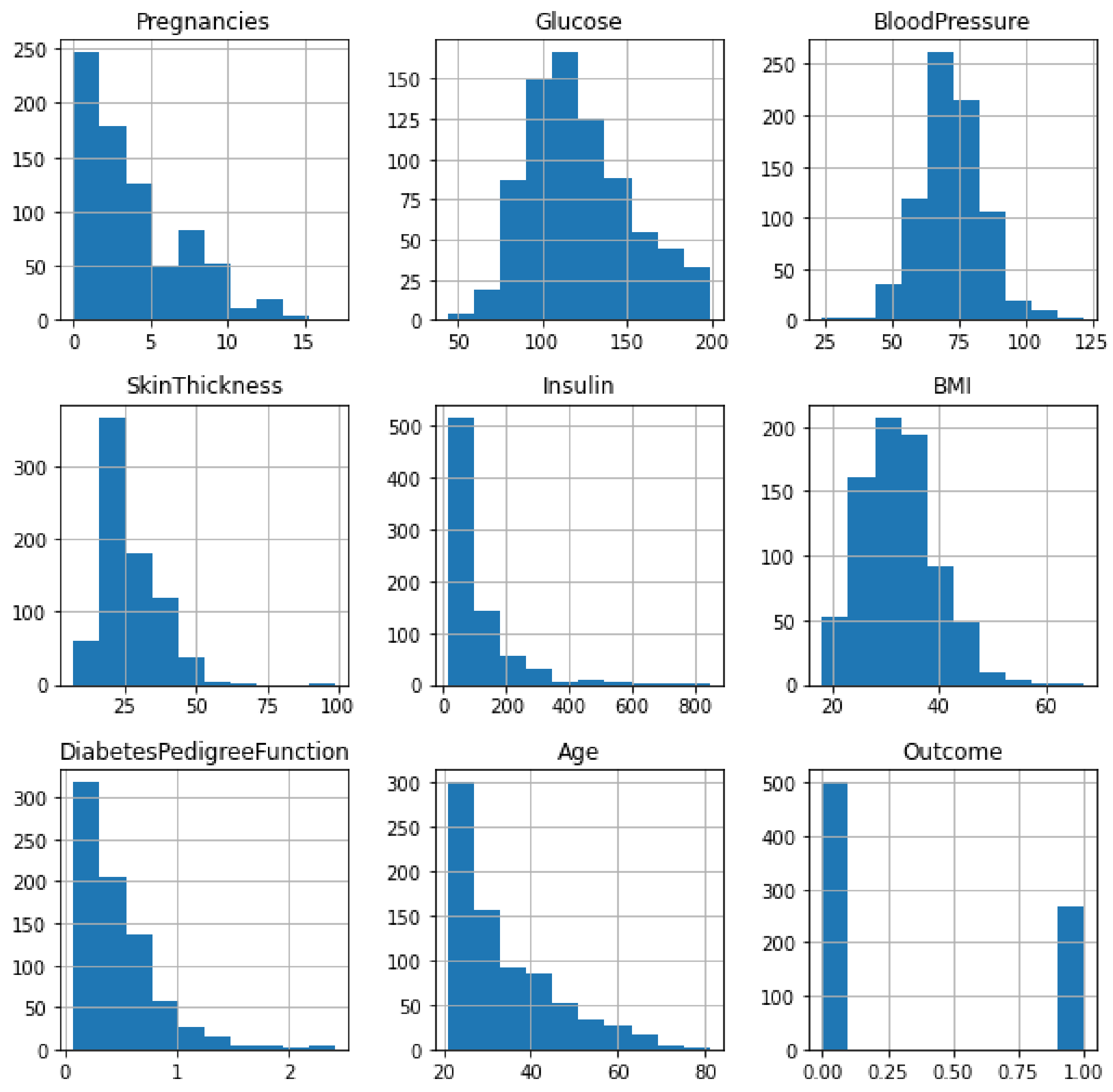


0 –> Non-Diabetic

1 –> Diabetic

Conclusion :- We observe that number of people who do not have diabetes is far more than people who do which indicates that our data is imbalanced.

```
[16]: #histogram for each  feature
diabetes_dataset.hist(bins=10,figsize=(10,10))
plt.show()
```

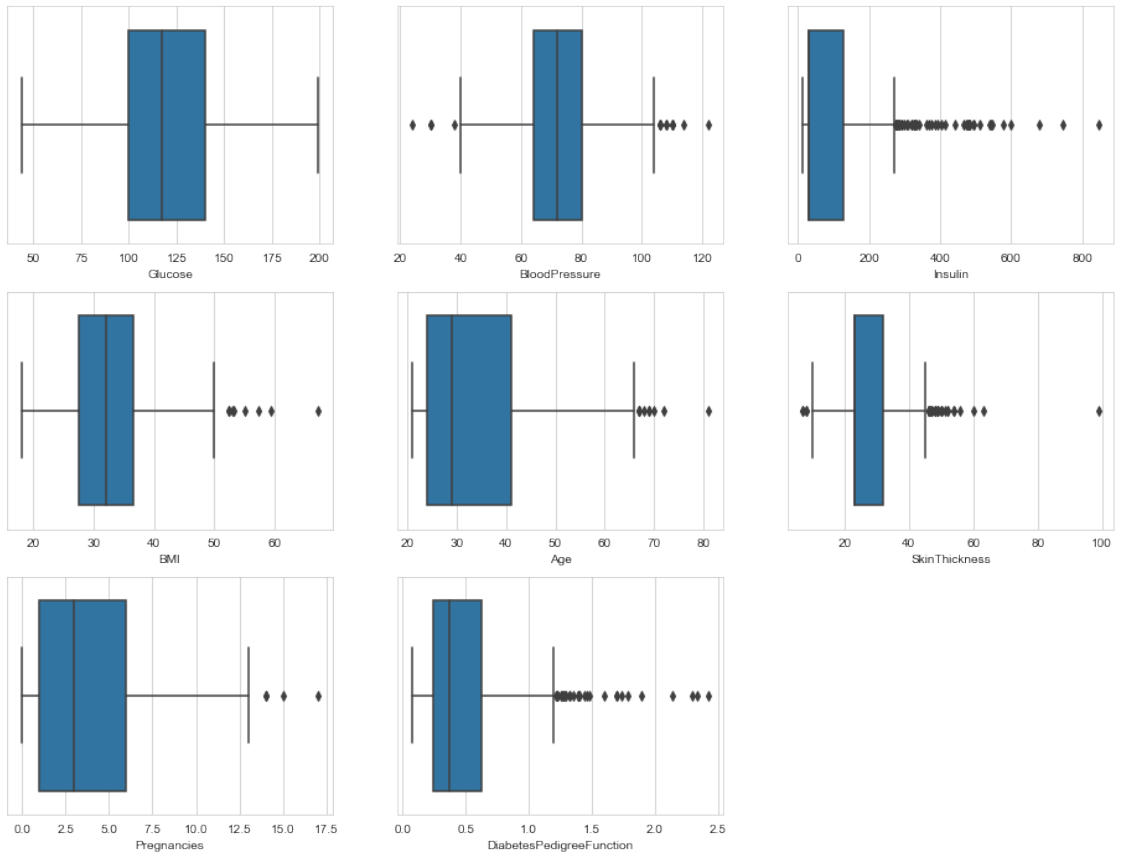


Conclusion :- We observe that only glucose and Blood Pressure are normally distributed rest others are skewed and have outliers

[17]:
```
plt.figure(figsize=(16,12))
sns.set_style(style='whitegrid')
plt.subplot(3,3,1)
sns.boxplot(x='Glucose',data=diabetes_dataset)
plt.subplot(3,3,2)
sns.boxplot(x='BloodPressure',data=diabetes_dataset)
plt.subplot(3,3,3)
sns.boxplot(x='Insulin',data=diabetes_dataset)
plt.subplot(3,3,4)
sns.boxplot(x='BMI',data=diabetes_dataset)
plt.subplot(3,3,5)
```

```
sns.boxplot(x='Age',data=diabetes_dataset)
plt.subplot(3,3,6)
sns.boxplot(x='SkinThickness',data=diabetes_dataset)
plt.subplot(3,3,7)
sns.boxplot(x='Pregnancies',data=diabetes_dataset)
plt.subplot(3,3,8)
sns.boxplot(x='DiabetesPedigreeFunction',data=diabetes_dataset)
```

```
[17]: <AxesSubplot:xlabel='DiabetesPedigreeFunction'>
```

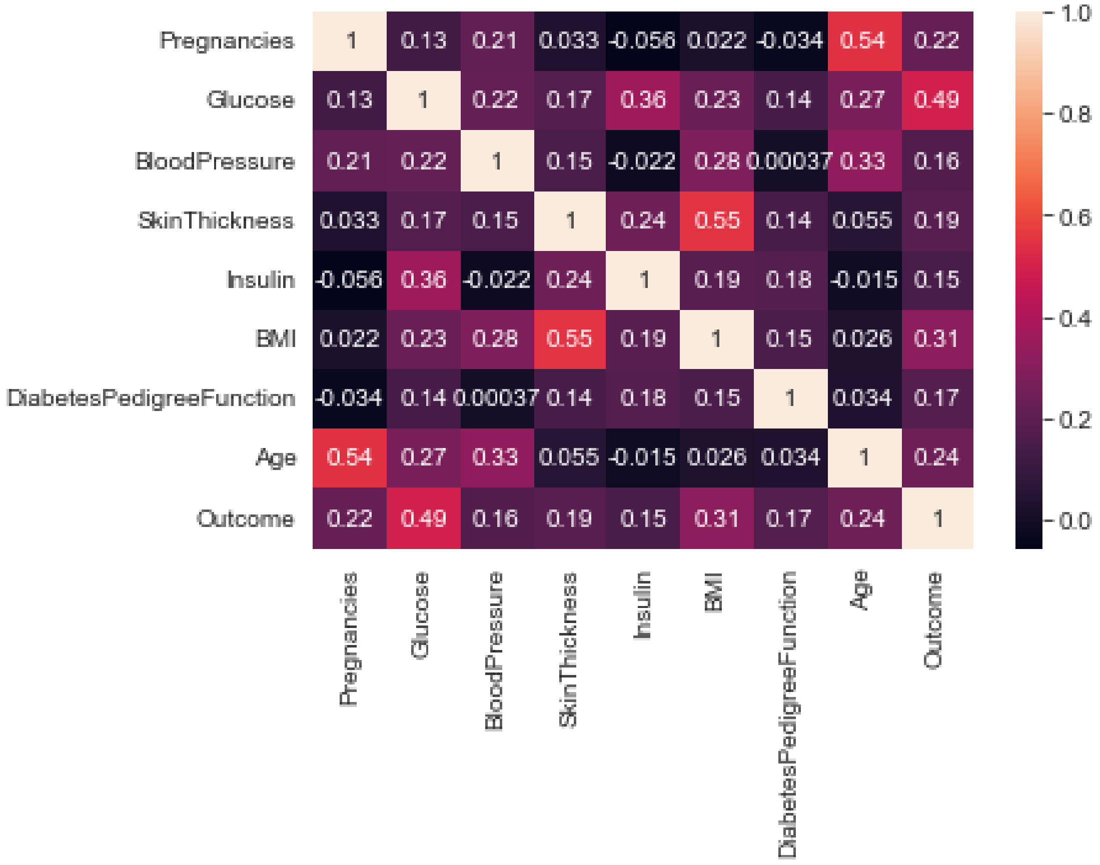


Outliers are unusual values in your dataset, and they can distort statistical analyses and violate their assumptions. Hence it is of most importance to deal with them. In this case removing outliers can cause data loss so we have to deal with it using various scaling and transformation techniques.

0.0.5 5.Feature Selection

[18]:
```
corrmat=diabetes_dataset.corr()
sns.heatmap(corrmat, annot=True)
```

[18]:
```
<AxesSubplot:>
```



CONCLUSION :- Observe the last row 'Outcome' and note its correlation scores with different features. We can observe that Glucose, BMI and Age are the most correlated with Outcome. BloodPressure, Insulin, DiabetesPedigreeFunction are the least correlated, hence they don't contribute much to the model so we can drop them.

[19]:
```
diabetes_selected=diabetes_dataset.
  ↪drop(['BloodPressure','Insulin','DiabetesPedigreeFunction'],axis='columns')
```

0.0.6 6.handing Outliers

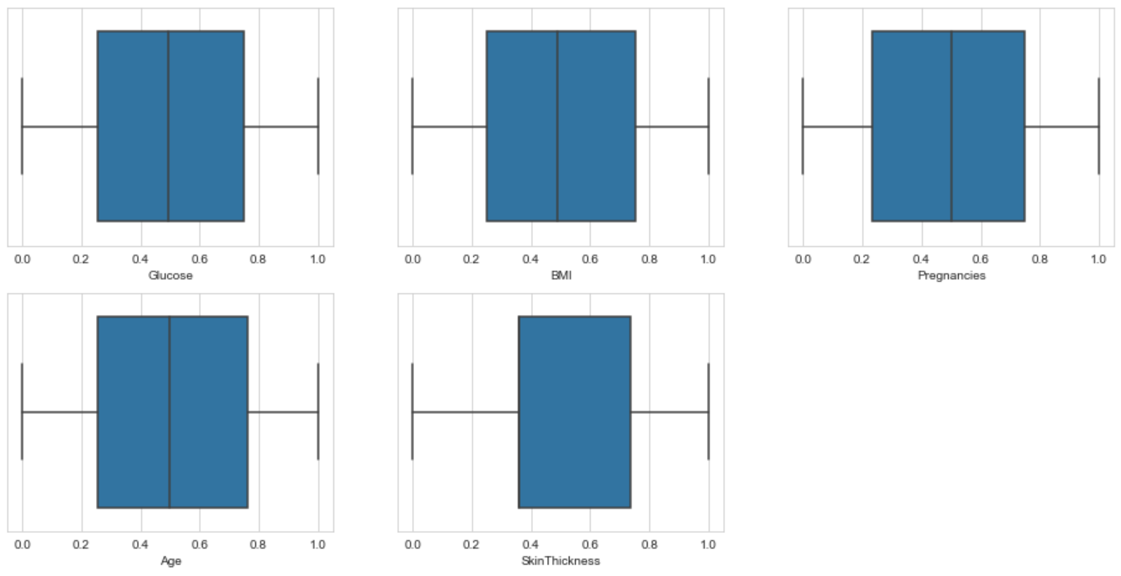
[20]:
```
from sklearn.preprocessing import QuantileTransformer
x=diabetes_selected
quantile  = QuantileTransformer()
```

```
X = quantile.fit_transform(x)
diabetes_new=quantile.transform(X)
diabetes_new=pd.DataFrame(X)
diabetes_new.columns =['Pregnancies',␣
 ↪'Glucose','SkinThickness','BMI','Age','Outcome']
diabetes_new.head(10)
```

[20]:
```
   Pregnancies   Glucose  SkinThickness       BMI       Age  Outcome
0     0.747718  0.810300       0.801825  0.591265  0.889831      1.0
1     0.232725  0.091265       0.644720  0.213168  0.558670      0.0
2     0.863755  0.956975       0.357888  0.077575  0.585398      1.0
3     0.232725  0.124511       0.357888  0.284224  0.000000      0.0
4     0.000000  0.721643       0.801825  0.926988  0.606258      1.0
5     0.677966  0.483703       0.357888  0.171447  0.529335      0.0
6     0.503259  0.039765       0.735332  0.433507  0.368970      1.0
7     0.940678  0.473272       0.357888  0.691656  0.496741      0.0
8     0.387223  0.996089       0.956323  0.408083  0.919166      1.0
9     0.863755  0.604302       0.357888  0.487614  0.926336      1.0
```

[21]:
```
plt.figure(figsize=(16,12))
sns.set_style(style='whitegrid')
plt.subplot(3,3,1)
sns.boxplot(x=diabetes_new['Glucose'],data=diabetes_new)
plt.subplot(3,3,2)
sns.boxplot(x=diabetes_new['BMI'],data=diabetes_new)
plt.subplot(3,3,3)
sns.boxplot(x=diabetes_new['Pregnancies'],data=diabetes_new)
plt.subplot(3,3,4)
sns.boxplot(x=diabetes_new['Age'],data=diabetes_new)
plt.subplot(3,3,5)
sns.boxplot(x=diabetes_new['SkinThickness'],data=diabetes_new)
```

[21]:
```
<AxesSubplot:xlabel='SkinThickness'>
```



0.0.7 7.Split the Data Frame into X and Y

```
[22]: target_name='Outcome'
      y= diabetes_new[target_name]#given predictions - training data
      X=diabetes_new.drop(target_name,axis=1)
```

```
[23]: X.head()
```

```
[23]:    Pregnancies   Glucose  SkinThickness       BMI       Age
      0     0.747718  0.810300       0.801825  0.591265  0.889831
      1     0.232725  0.091265       0.644720  0.213168  0.558670
      2     0.863755  0.956975       0.357888  0.077575  0.585398
      3     0.232725  0.124511       0.357888  0.284224  0.000000
      4     0.000000  0.721643       0.801825  0.926988  0.606258
```

```
[24]: y.head()
```

```
[24]: 0    1.0
      1    0.0
      2    1.0
      3    0.0
      4    1.0
      Name: Outcome, dtype: float64
```

0.0.8 8.Train Test Split

[25]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test= train_test_split(X,y,test_size=0.
 ↪2,random_state=0)
#splitting data in 80% train, 20%test
```

[26]:
```
X_train.shape,y_train.shape
```

[26]:
```
((614, 5), (614,))
```

[27]:
```
X_test.shape,y_test.shape
```

[27]:
```
((154, 5), (154,))
```

0.0.9 9.Classification Algorithms

- **9.1 K Nearest Neighbours** :- KNN algorithm, is a non-parametric algorithm that classifies data points based on their proximity and association to other available data.

[28]:
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import RepeatedStratifiedKFold
from sklearn.metrics import classification_report,confusion_matrix
from sklearn.metrics import f1_score, precision_score, recall_score
from sklearn.model_selection import GridSearchCV
```

[29]:
```
#List Hyperparameters to tune
knn= KNeighborsClassifier()
n_neighbors = list(range(15,25))
p=[1,2]
weights = ['uniform', 'distance']
metric = ['euclidean', 'manhattan', 'minkowski']

#convert to dictionary
hyperparameters = dict(n_neighbors=n_neighbors,␣
 ↪p=p,weights=weights,metric=metric)

#Making model
cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3, random_state=1)
grid_search = GridSearchCV(estimator=knn, param_grid=hyperparameters,␣
 ↪n_jobs=-1, cv=cv, scoring='f1',error_score=0)
```

[30]:
```
best_model = grid_search.fit(X_train,y_train)
```

[31]:
```
#Best Hyperparameters Value
print('Best leaf_size:', best_model.best_estimator_.get_params()['leaf_size'])
print('Best p:', best_model.best_estimator_.get_params()['p'])
print('Best n_neighbors:', best_model.best_estimator_.
 ↪get_params()['n_neighbors'])
```

```
Best leaf_size: 30
Best p: 1
Best n_neighbors: 19
```

[32]:
```
#Predict testing set
knn_pred = best_model.predict(X_test)
```

[33]:
```
print("\n Confusion Matrix:\n",confusion_matrix(y_test,knn_pred))
print("\n Classification Report is:\n",classification_report(y_test,knn_pred))
print("\n F1:\n",f1_score(y_test,knn_pred))
print("\n Precision score is:\n",precision_score(y_test,knn_pred))
print("\n Recall score is:\n",recall_score(y_test,knn_pred))
```

```

 Confusion Matrix:
 [[94 13]
 [17 30]]

 Classification Report is:
               precision    recall  f1-score   support

         0.0       0.85      0.88      0.86       107
         1.0       0.70      0.64      0.67        47

    accuracy                           0.81       154
   macro avg       0.77      0.76      0.76       154
weighted avg       0.80      0.81      0.80       154


 F1:
 0.6666666666666666

 Precision score is:
 0.6976744186046512

 Recall score is:
 0.6382978723404256
```

- **9.2 Naive Bayes** :- Naive Bayes is classification approach that adopts the principle of class conditional independence from the Bayes Theorem. This means that the presence of one feature does not impact the presence of another in the probability of a given outcome, and each predictor has an equal effect on that result

[34]:
```
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import GridSearchCV
```

```
param_grid_nb = {
    'var_smoothing': np.logspace(0,-2, num=100)
}
nbModel_grid = GridSearchCV(estimator=GaussianNB(), param_grid=param_grid_nb,␣
 ↪verbose=1, cv=10, n_jobs=-1)
```

[35]:
```
best_model= nbModel_grid.fit(X_train, y_train)
```

```
Fitting 10 folds for each of 100 candidates, totalling 1000 fits
```

[36]:
```
nb_pred=best_model.predict(X_test)
```

[37]:
```
print("\n Confusion Matrix:\n", confusion_matrix(y_test,nb_pred))
print("\n Classification Report is:\n",classification_report(y_test,nb_pred))
print("\n F1:\n",f1_score(y_test,nb_pred))
print("\n Precision score is:\n",precision_score(y_test,nb_pred))
print("\n Recall score is:\n",recall_score(y_test,nb_pred))
```

```

 Confusion Matrix:
 [[93 14]
 [22 25]]

 Classification Report is:
               precision    recall  f1-score   support

         0.0       0.81      0.87      0.84       107
         1.0       0.64      0.53      0.58        47

    accuracy                           0.77       154
   macro avg       0.72      0.70      0.71       154
weighted avg       0.76      0.77      0.76       154


 F1:
 0.5813953488372093

 Precision score is:
 0.6410256410256411

 Recall score is:
 0.5319148936170213
```

- **9.3 Support Vector Machine** :- It is typically leveraged for classification problems, constructing a hyperplane where the distance between two classes of data points is at its maximum. This hyperplane is known as the decision boundary, separating the classes of data points (e.g., has diabetes vs doesn't have diabetes) on either side of the plane.

[38]:
```
from sklearn.model_selection import RepeatedStratifiedKFold
from sklearn.model_selection import GridSearchCV
from sklearn.svm import SVC
from sklearn.metrics import classification_report,confusion_matrix
from sklearn.metrics import f1_score, precision_score, recall_score
```

[39]:
```
model = SVC()
kernel = ['poly', 'rbf', 'sigmoid']
C = [50, 10, 1.0, 0.1, 0.01]
gamma = ['scale']
```

[40]:
```
# define grid search
grid = dict(kernel=kernel,C=C,gamma=gamma)
cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3, random_state=1)
grid_search = GridSearchCV(estimator=model, param_grid=grid, n_jobs=-1, cv=cv,␣
  ↪scoring='f1',error_score=0)
```

[41]:
```
grid_result = grid_search.fit(X, y)
```

[42]:
```
svm_pred=grid_result.predict(X_test)
```

[43]:
```
print("\n Confusion Matrix:\n", confusion_matrix(y_test,svm_pred))
print("\n Classification Report is:\n",classification_report(y_test,svm_pred))
print("\n F1:\n",f1_score(y_test,knn_pred))
print("\n Precision score is:\n",precision_score(y_test,knn_pred))
print("\n Recall score is:\n",recall_score(y_test,knn_pred))
```

```
 Confusion Matrix:
 [[95 12]
 [15 32]]

 Classification Report is:
               precision    recall  f1-score   support

         0.0       0.86      0.89      0.88       107
         1.0       0.73      0.68      0.70        47

    accuracy                           0.82       154
   macro avg       0.80      0.78      0.79       154
weighted avg       0.82      0.82      0.82       154


 F1:
 0.6666666666666666

 Precision score is:
 0.6976744186046512
```

```
Recall score is:
0.6382978723404256
```

- **9.4 Logistic Regression** :- Logistical regression is selected when the dependent variable is categorical, meaning they have binary outputs, such as “true” and “false” or “yes” and “no.”
- Logistic regression does not really have any critical hyperparameters to tune. Sometimes, you can see useful differences in performance or convergence with different solvers (solver).Regularization (penalty) can sometimes be helpful.

[44]:
```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report,confusion_matrix
from sklearn.metrics import f1_score, precision_score,␣
↪recall_score,accuracy_score
```

[45]:
```
reg = LogisticRegression()
reg.fit(X_train,y_train)
```

[45]:
```
LogisticRegression()
```

[46]:
```
lr_pred=reg.predict(X_test)
```

[47]:
```
print("\n Confusion Matrix:\n", confusion_matrix(y_test,lr_pred))
print("\n Classification Report is:\n",classification_report(y_test,lr_pred))
print("\n F1:\n",f1_score(y_test,lr_pred))
print("\n Precision score is:\n",precision_score(y_test,lr_pred))
print("\n Recall score is:\n",recall_score(y_test,lr_pred))
```

```
 Confusion Matrix:
 [[95 12]
 [20 27]]

 Classification Report is:
               precision    recall  f1-score   support

         0.0       0.83      0.89      0.86       107
         1.0       0.69      0.57      0.63        47

    accuracy                           0.79       154
   macro avg       0.76      0.73      0.74       154
weighted avg       0.79      0.79      0.79       154


 F1:
 0.627906976744186

 Precision score is:
 0.6923076923076923
```

```
Recall score is:
0.574468085106383
```

0.0.10 Accuracy Score

K Nearest Neighbours :- 81%

Naive Bayes :- 77%

Support Vector Machine :- 82%

Logistic Regression :- 79%