Diabetes_Pred

March 7, 2024

Diabetes Prediction using Machine Learning:

Diabetes is a group of metabolic disorders in which there are high blood sugar levels over a prolonged period. Symptoms of high blood sugar include frequent urination, increased thirst, and increased hunger. If left untreated, diabetes can cause many complications. Acute complications can include diabetic ketoacidosis, hyperosmolar hyperglycemic state, or death. Serious long-term complications include cardiovascular disease, stroke, chronic kidney disease, foot ulcers, and damage to the eyes.

This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective of the dataset is to diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Several constraints were placed on the selection of these instances from a larger database. All patients here are females at least 21 years old of Pima Indian heritage.

Objective We will try to build a machine learning model to accurately predict whether or not the patients in the dataset have diabetes or not?

Details about the dataset: The datasets consist of several medical predictor variables and one target variable, Outcome. Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and so on.

Pregnancies: Number of times pregnant Glucose: Plasma glucose concentration 2 hours in an oral glucose tolerance test Blood Pressure: Diastolic blood pressure (mm Hg) Skin Thickness: Triceps skin fold thickness (mm) Insulin: 2-Hour serum insulin (mu U/ml) BMI: Body mass index (weight in kg/(height in m)^2) Diabetes Pedigree Function: Diabetes pedigree function Age: Age (years) Outcome: Class variable (0 or 1) Number of Observation Units: 768

Variable Number: 9

1. Exploratory Data Analysis

[1]:
```
#Installation of required libraries
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, roc_auc_score,␣
 ↪roc_curve,auc,classification_report
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.preprocessing import StandardScaler
```

[2]:
```
#Reading the dataset
df=pd.read_csv('diabetes.csv')
df.head()
```

[2]:
```
   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
```

[3]:
```
#Feature information
df.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
```

[4]:
```
df.columns
```

[4]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

[5]:
```
# The size of the data set was examined. It consists of 768 observation units␣
↪and 9 variables.
df.shape
```

[5]:
```
(768, 9)
```

[6]:
```
# Descriptive statistics of the data
df.describe()
```

[6]:
```
       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
```

[7]:
```
for i in df:
    print(df.groupby("Outcome").agg({i:"mean"}),'\n')
```

```
         Pregnancies
Outcome
0           3.298000
1           4.865672

            Glucose
Outcome
0        109.980000
1        141.257463

         BloodPressure
Outcome
0            68.184000
1            70.824627
```

```
         SkinThickness
Outcome
0            19.664000
1            22.164179

            Insulin
Outcome
0         68.792000
1        100.335821

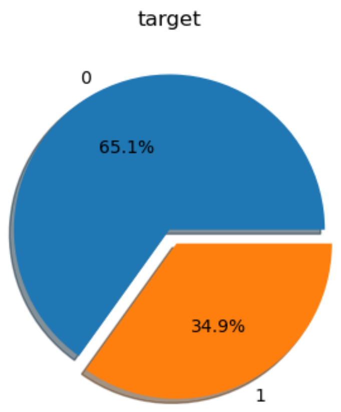
               BMI
Outcome
0        30.304200
1        35.142537

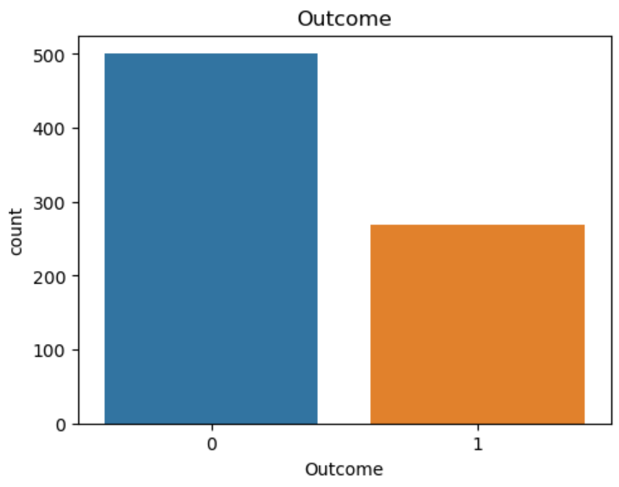
         DiabetesPedigreeFunction
Outcome
0                        0.429734
1                        0.550500

               Age
Outcome
0        31.190000
1        37.067164

         Outcome
Outcome
0            0.0
1            1.0
```

[8]:
```
# The distribution of the outcome variable in the data was examined and␣
 ↪visualized.
f,ax=plt.subplots(1,2,figsize=(12,4))
df['Outcome'].value_counts().plot.pie(explode=[0,0.1],autopct='%1.
 ↪1f%%',ax=ax[0],shadow=True)
ax[0].set_title('target')
ax[0].set_ylabel('')
sns.countplot(data=df, x='Outcome')
ax[1].set_title('Outcome')
plt.show()
```

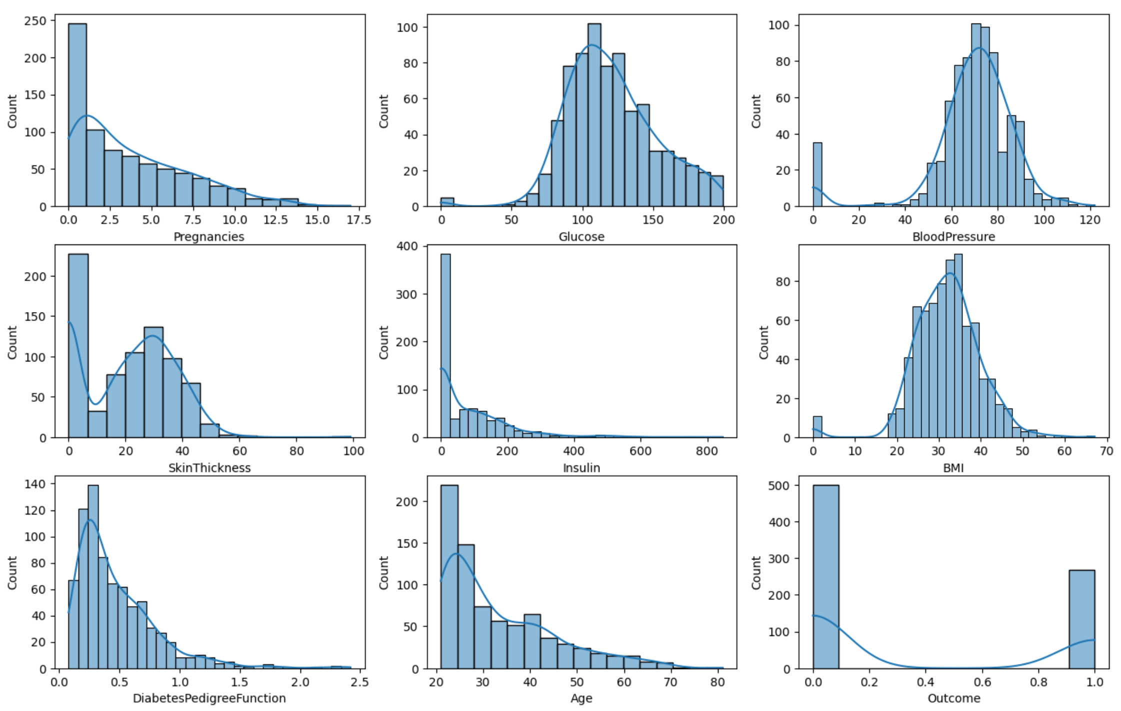




[9]:
```
#Histograms of each feature was accessed
k=1
plt.figure(figsize=(16,10))
for i in df.columns:
    plt.subplot(3,3,k)
    sns.histplot(df[i],kde=True)
    plt.xlabel(i)
    k=k+1
plt.suptitle('Histograms of each feature')
```

[9]:
```
Text(0.5, 0.98, 'Histograms of each feature')
```

Histograms of each feature



```
[10]: # Access to the correlation of the data set was provided. What kind of␣
      ↪relationship is examined between the variables.
      # If the correlation value is> 0, there is a positive correlation. While the␣
      ↪value of one variable increases, the value of the other variable also␣
      ↪increases.
      # Correlation = 0 means no correlation.
      # If the correlation is <0, there is a negative correlation. While one variable␣
      ↪increases, the other variable decreases.
      # When the correlations are examined, there are 2 variables which has␣
      ↪considerable correlation to the Outcome dependent variable.
      # The variable is Glucose. As these increases, Outcome variable also increases.
      df.corr()
```

```
[10]:                           Pregnancies   Glucose  BloodPressure  SkinThickness  \
      Pregnancies                  1.000000  0.129459       0.141282      -0.081672
      Glucose                      0.129459  1.000000       0.152590       0.057328
      BloodPressure                0.141282  0.152590       1.000000       0.207371
      SkinThickness               -0.081672  0.057328       0.207371       1.000000
      Insulin                     -0.073535  0.331357       0.088933       0.436783
      BMI                          0.017683  0.221071       0.281805       0.392573
      DiabetesPedigreeFunction    -0.033523  0.137337       0.041265       0.183928
      Age                          0.544341  0.263514       0.239528      -0.113970
```

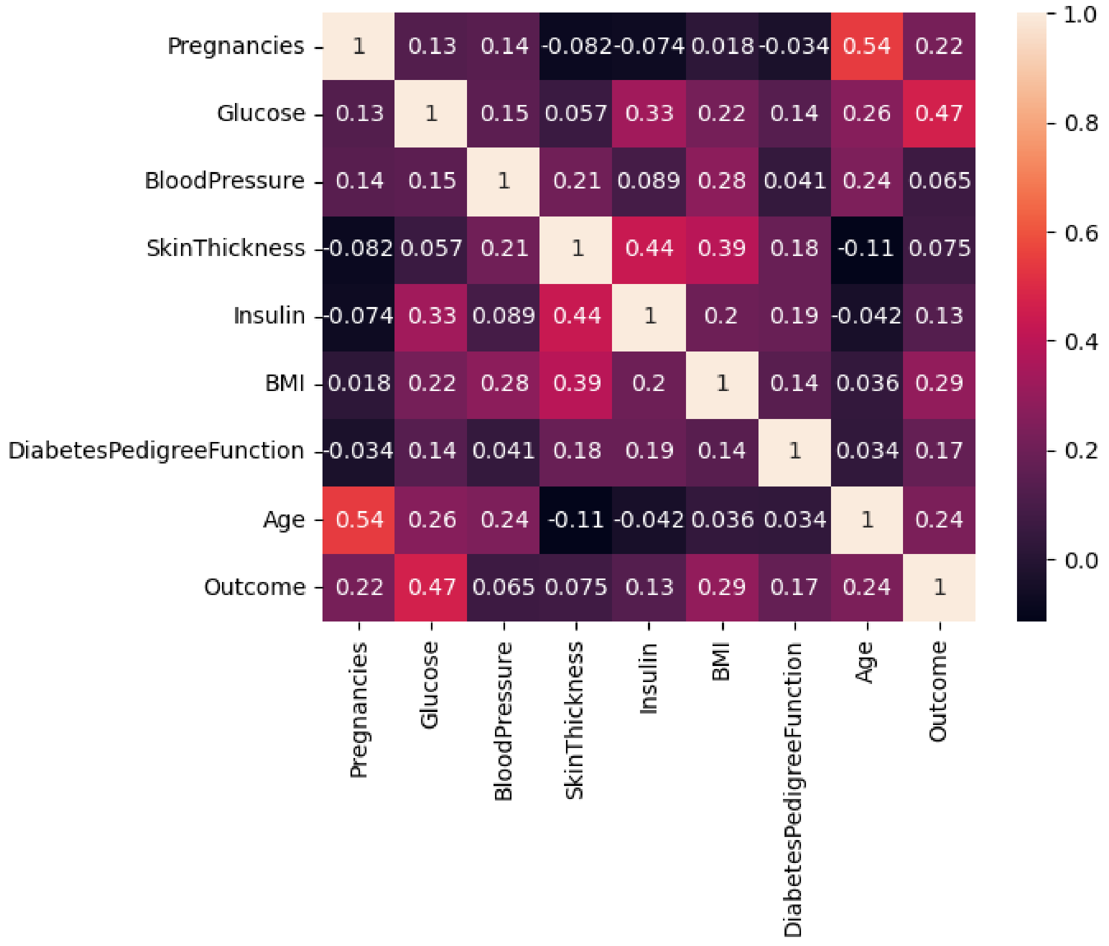
```
Outcome                       0.221898  0.466581       0.065068       0.074752

                           Insulin       BMI  DiabetesPedigreeFunction  \
Pregnancies              -0.073535  0.017683                 -0.033523
Glucose                   0.331357  0.221071                  0.137337
BloodPressure             0.088933  0.281805                  0.041265
SkinThickness             0.436783  0.392573                  0.183928
Insulin                   1.000000  0.197859                  0.185071
BMI                       0.197859  1.000000                  0.140647
DiabetesPedigreeFunction  0.185071  0.140647                  1.000000
Age                      -0.042163  0.036242                  0.033561
Outcome                   0.130548  0.292695                  0.173844

                               Age   Outcome
Pregnancies               0.544341  0.221898
Glucose                   0.263514  0.466581
BloodPressure             0.239528  0.065068
SkinThickness            -0.113970  0.074752
Insulin                  -0.042163  0.130548
BMI                       0.036242  0.292695
DiabetesPedigreeFunction  0.033561  0.173844
Age                       1.000000  0.238356
Outcome                   0.238356  1.000000
```

[11]:
```
sns.heatmap(df.corr(),annot=True)
# correlation of Glucose w.r.t. outcome is highest in this case which is 0.47␣
 ↪as visible in Heatmap
```

[11]:
```
<AxesSubplot: >
```



2) Data Preprocessing

2.1. Checking any Null or duplicated values in the dataset

[12]:
```
df.isnull().sum()
```

[12]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[13]:
```
df.duplicated().sum()
```

[13]: 0

2.2 Outlier Observation Analysis

[14]:
```
for feature in df:

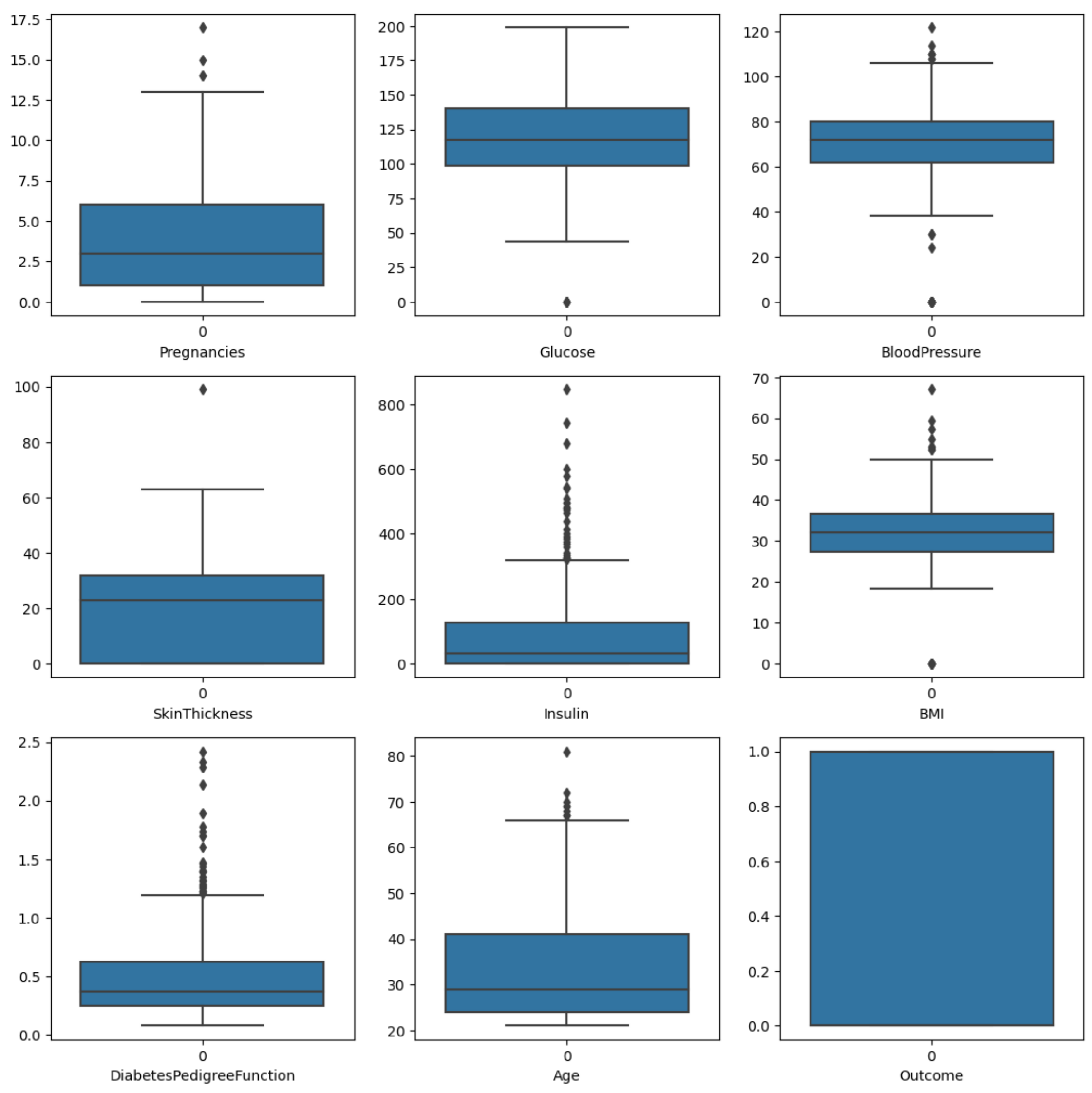
    Q1 = df[feature].quantile(0.25)
    Q3 = df[feature].quantile(0.75)
    IQR = Q3-Q1
    lower = Q1- 1.5*IQR
    upper = Q3 + 1.5*IQR

    if df[(df[feature] > upper)].any(axis=None):
        print(feature,"yes")
    else:
        print(feature, "no")
```

```
Pregnancies yes
Glucose no
BloodPressure yes
SkinThickness yes
Insulin yes
BMI yes
DiabetesPedigreeFunction yes
Age yes
Outcome no
```

[15]:
```
#check outliers in the dataset using box plot
k=1
plt.figure(figsize=(13,13))
for j in df.columns:
    plt.subplot(3,3,k)
    sns.boxplot(df[j])
    plt.xlabel(j)
    k=k+1
    plt.suptitle('Outlier detection using Boxplots')
```

Outlier detection using Boxplots

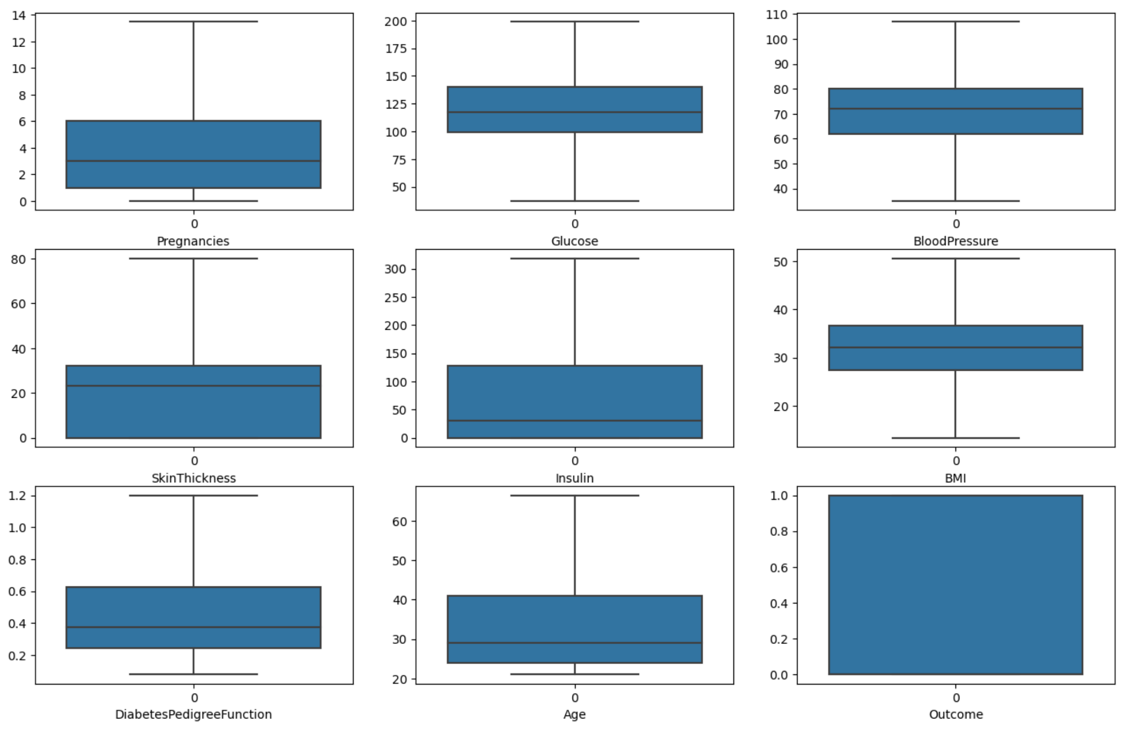


2.3. Outlier removal through imputations

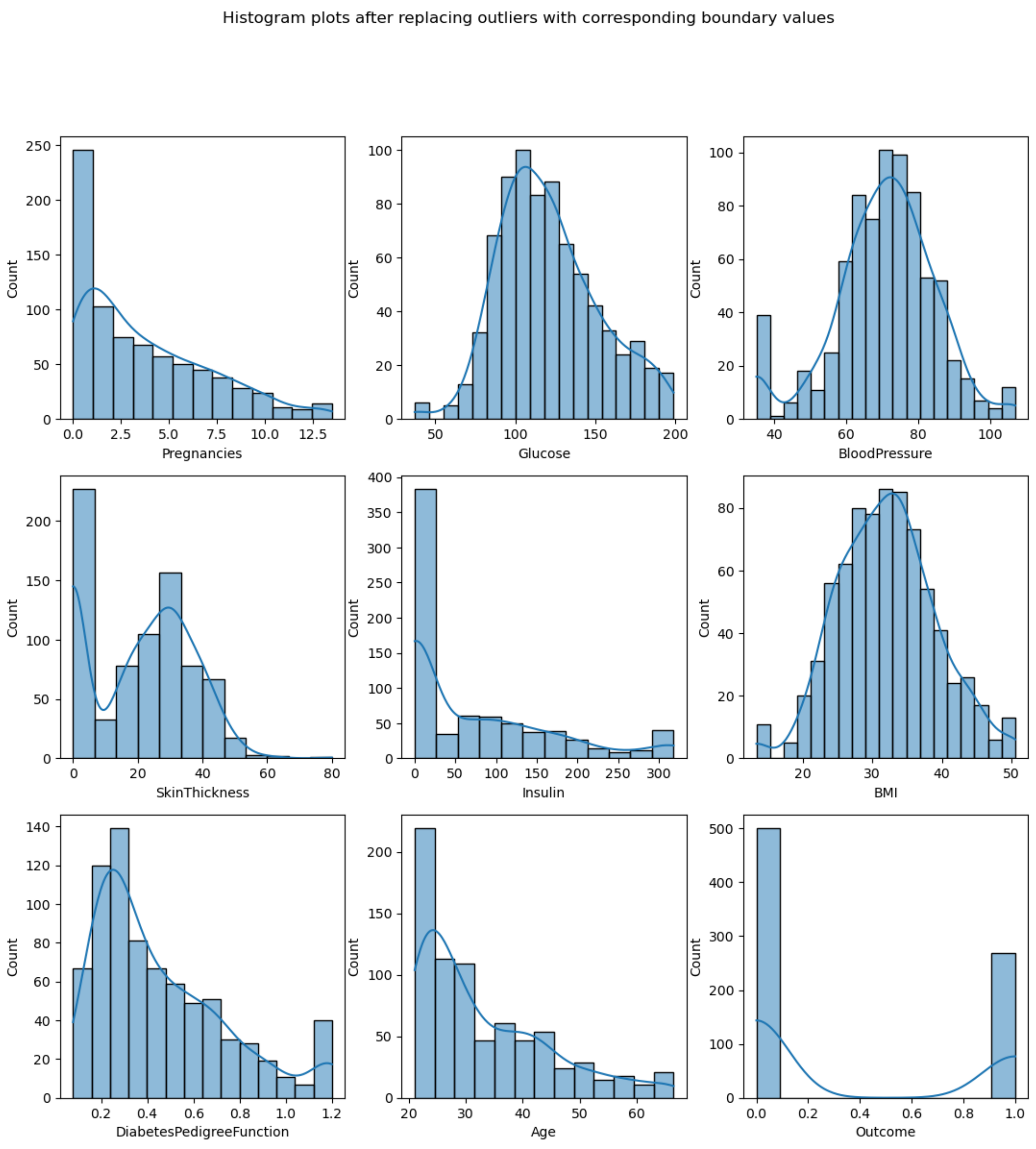
[16]:
```
#Detect outliers using IQR method and replace them with corresponding boundary␣
↪values to remove outliers.
for i in df.columns:
    Q1 = df[i].quantile(0.25)
    Q3 = df[i].quantile(0.75)
    IQR = Q3-Q1
    lower = Q1 - 1.5*IQR
    upper = Q3 + 1.5*IQR
    df.loc[df[i] > upper,i] = upper
    df.loc[df[i] < lower,i] = lower
```

```
[17]: #box plot after imputations:
k=1
plt.figure(figsize=(16,10))
for j in df.columns:
    plt.subplot(3,3,k)
    sns.boxplot(df[j])
    plt.xlabel(j)
    k=k+1
    plt.suptitle('Boxplots after replacing outliers with corresponding boundary␣
 ↪values')
```

Boxplots after replacing outliers with corresponding boundary values



```
[18]: #Histogram plots after imputations
k=1
plt.figure(figsize=(13,13))
for i in df.columns:
    plt.subplot(3,3,k)
    sns.histplot(df[i],kde=True)
    plt.xlabel(i)
    k=k+1
    plt.suptitle('Histogram plots after replacing outliers with corresponding␣
↪boundary values')
```



```
[19]: X=df.drop(['Outcome'], axis=1)
      y=df['Outcome']
      X.head()
```

[19]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0          6.0    148.0             72             35      0.0  33.6
1          1.0     85.0             66             29      0.0  26.6
2          8.0    183.0             64              0      0.0  23.3
3          1.0     89.0             66             23     94.0  28.1
4          0.0    137.0             40             35    168.0  43.1

   DiabetesPedigreeFunction   Age
0                     0.627  50.0
1                     0.351  31.0
2                     0.672  32.0
3                     0.167  21.0
4                     1.200  33.0
```

[20]:
```
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.
↪30,random_state=42)
```

[21]:
```
# Scale the features using StandardScaler
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

3. Base Models

[22]:
```
# Initialize models
models = {
    'Logistic Regression': LogisticRegression(),
    'Random Forest': RandomForestClassifier(),
    'Support Vector Machine': SVC(probability=True)
}

# Train and evaluate models
for name, model in models.items():
    model.fit(X_train_scaled, y_train)
    y_pred = model.predict(X_test_scaled)

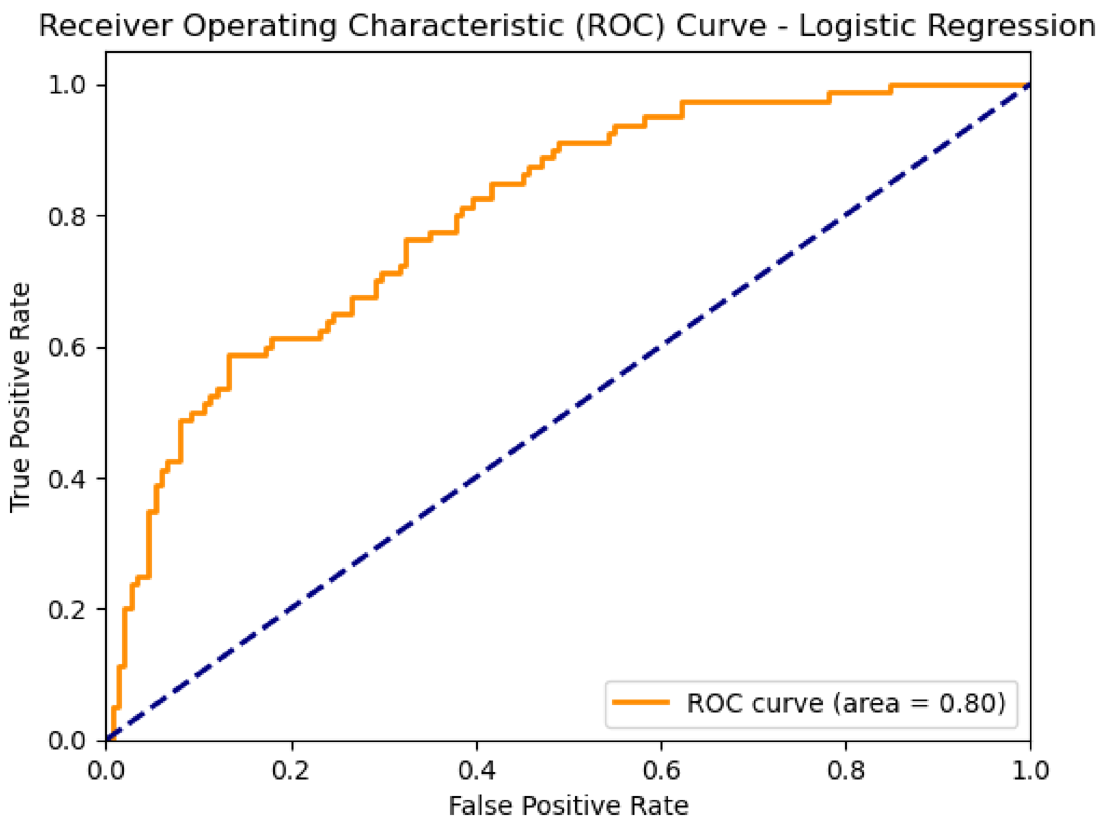
    print(f"\nResults for {name}:")
    print("Confusion Matrix:")
    print(confusion_matrix(y_test, y_pred))
    print("\nClassification Report:")
    print(classification_report(y_test, y_pred))
    if name != 'Support Vector Machine':  # SVC does not provide probabilities␣
↪for roc_curve
        y_prob = model.predict_proba(X_test_scaled)[:, 1]
        fpr, tpr, thresholds = roc_curve(y_test, y_prob)
        roc_auc = roc_auc_score(y_test, y_prob)
        plt.figure()
        plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area =␣
↪%0.2f)' % roc_auc)
        plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
        plt.xlim([0.0, 1.0])
        plt.ylim([0.0, 1.05])
        plt.xlabel('False Positive Rate')
        plt.ylabel('True Positive Rate')
        plt.title(f'Receiver Operating Characteristic (ROC) Curve - {name}')
        plt.legend(loc="lower right")
        plt.show()
```

```
Results for Logistic Regression:
Confusion Matrix:
[[123  28]
 [ 31  49]]

Classification Report:
              precision    recall  f1-score   support

         0.0       0.80      0.81      0.81       151
         1.0       0.64      0.61      0.62        80

    accuracy                           0.74       231
   macro avg       0.72      0.71      0.72       231
weighted avg       0.74      0.74      0.74       231
```

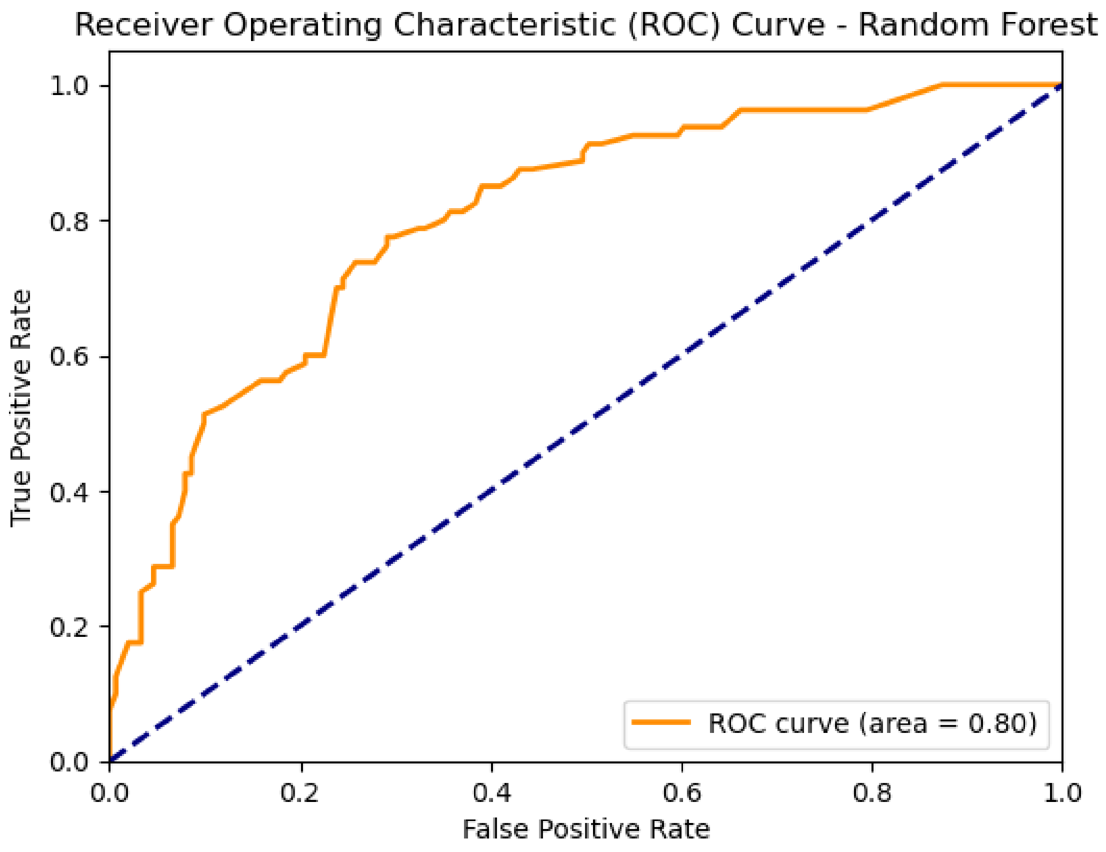


```
Results for Random Forest:
Confusion Matrix:
[[120  31]
 [ 32  48]]

Classification Report:
              precision    recall  f1-score   support

         0.0       0.79      0.79      0.79       151
         1.0       0.61      0.60      0.60        80

    accuracy                           0.73       231
   macro avg       0.70      0.70      0.70       231
weighted avg       0.73      0.73      0.73       231
```



```
Results for Support Vector Machine:
Confusion Matrix:
[[122  29]
 [ 31  49]]

Classification Report:
              precision    recall  f1-score   support

         0.0       0.80      0.81      0.80       151
         1.0       0.63      0.61      0.62        80

    accuracy                           0.74       231
   macro avg       0.71      0.71      0.71       231
weighted avg       0.74      0.74      0.74       231
```

4. Reporting

The aim of this study was to create classification models for the diabetes data set and to predict whether a person is sick by establishing models. The work done is as follows:

1) Diabetes Data Set read.

2) With Exploratory Data Analysis: The data set's structural data were checked. The types of variables in the dataset were examined. Size information of the dataset was accessed. The values in the data set was checked to see if there were any missing or duplicated values. Descriptive statistics of the data set were examined.

3) Data Preprocessing section: The outliers were determined by IQR method and it caps the outliers by replacing values above the upper bound with the upper bound value, and values below the lower bound with the lower bound value.

4) During Model Building: Logistic Regression, SVM, Random Forests were employed for this dataset. I used the confusion matrix values, Classification report to ananlyse the best performing model.

5) Result: Based on the provided results, we can compare the models in terms of accuracy, precision, recall, and F1-score. The Random Forest model seems to perform better in terms of accuracy compared to Logistic Regression and SVM. It also demonstrates better accuracy precision, recall, and F1-score for both classes. Therefore, the Random Forest model appears to be the best among the three models based on the provided evaluation metrics.

```
[ ]:
```

```
[ ]:
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[ ]:
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[ ]:
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[ ]:
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