Group12_Project_Implementation

April 18, 2024

1 Project Title: Diabetes Prediction - SVM Random Forest

1.1 Group Number: 12

1.1.1 Group Members:

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2 Diabetes Prediction System

2.1 Import Required Dependencies

[162]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from imblearn.over_sampling import SMOTE
```

2.2 Dataset

[163]:
```
# laod the diabetes dataset
diabetes_dataset = pd.read_csv('diabetes.csv')

# print first 5 data rows in the dataset
diabetes_dataset.head(5)
```

[163]:
```
   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
```

[164]:
```
# to check the number of columns and rows in the dataset
diabetes_dataset.shape
```

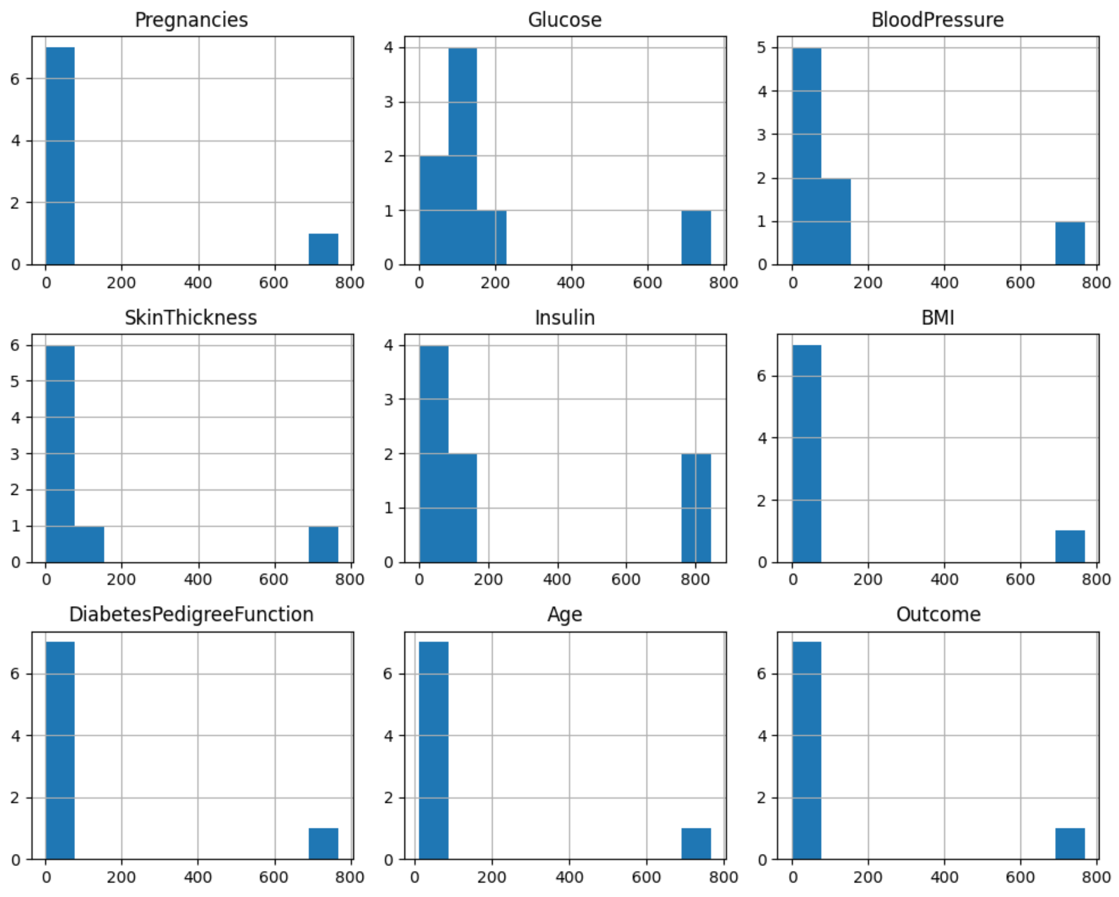
[164]:
```
(768, 9)
```

[165]:
```
# Getting the statistical measures of the data
diabetes_dataset.describe()
```

[165]:
```
       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
```

2.2.1 Dataset colums

[166]:
```
# data analysis and visualization to get a quick overview of the distribution␣
↪of data


diabetes_dataset.describe().hist(figsize=(10, 8))
plt.tight_layout()
plt.show()
```

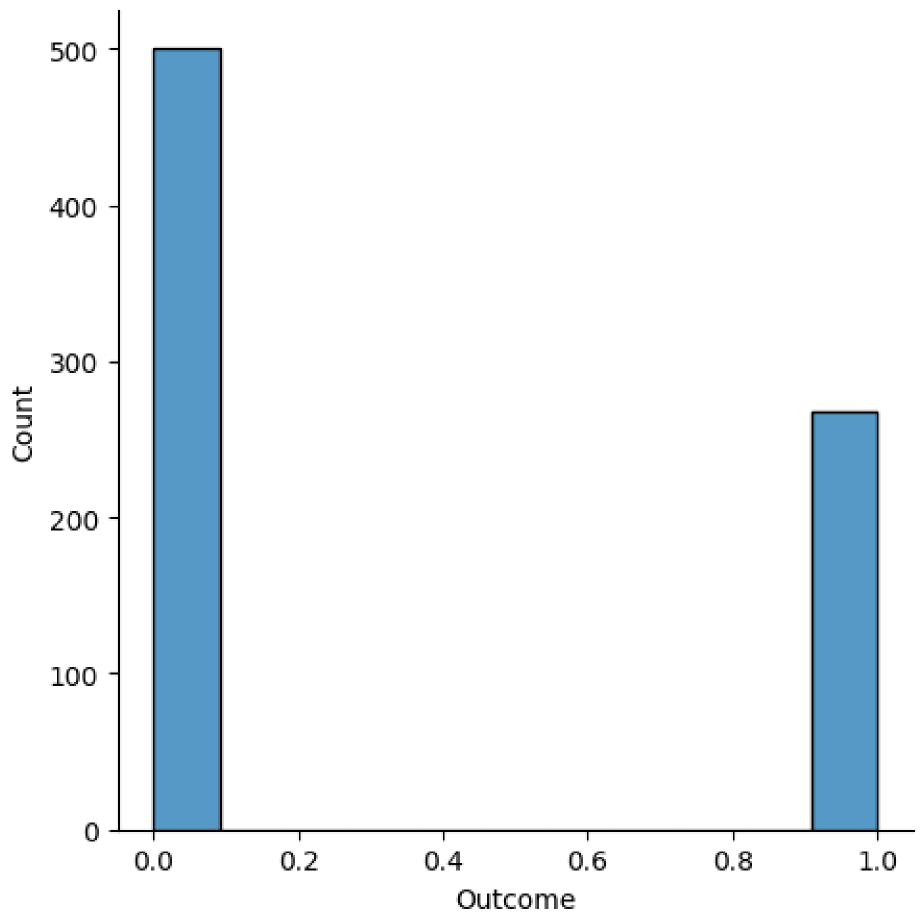


[167]:
```
# to get idea about lables in Target Variable
diabetes_dataset['Outcome'].value_counts()
```

[167]:
```
Outcome
0    500
1    268
Name: count, dtype: int64
```

[168]:
```
#Visualization to get idea about lables in Target Variable
import seaborn as sns
sns.displot(diabetes_dataset['Outcome'])
```

[168]:
```
<seaborn.axisgrid.FacetGrid at 0x78065cf8ecb0>
```



0 - Non diabetic 1 - diabetic

[169]:
```
# Mean values of the colums
diabetes_dataset.groupby('Outcome').mean()
```

[169]:
```
         Pregnancies     Glucose  BloodPressure  SkinThickness     Insulin  \
Outcome
0           3.298000  109.980000      68.184000      19.664000   68.792000
1           4.865672  141.257463      70.824627      22.164179  100.335821

               BMI  DiabetesPedigreeFunction        Age
Outcome
0        30.304200                  0.429734  31.190000
1        35.142537                  0.550500  37.067164
```

2.3 Data Preprocessing

2.3.1 Handling null / missing values

[170]:
```
#view dataframe summary
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
```

[171]:
```
#Checking the null values
diabetes_dataset.isnull().sum()
```

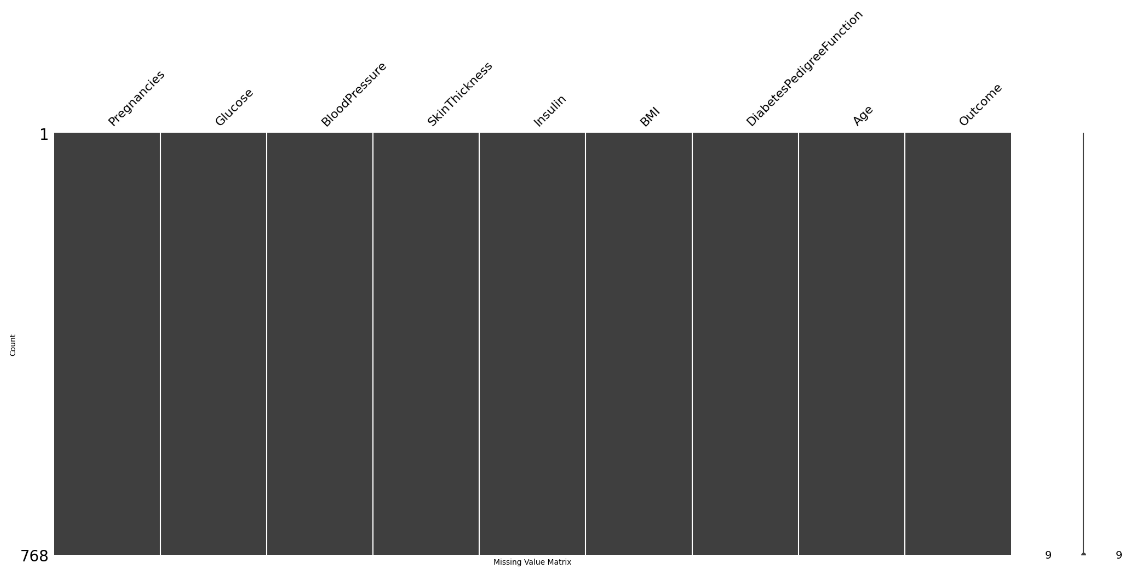
[171]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[172]:
```
#Visualizing Missing data
!pip install missingno
import missingno as msno
msno.matrix(diabetes_dataset)
plt.xlabel("Missing Value Matrix")
plt.ylabel("Count")
```

```
Requirement already satisfied: missingno in /usr/local/lib/python3.10/dist-
packages (0.5.2)
Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages
```

```
(from missingno) (1.25.2)
Requirement already satisfied: matplotlib in /usr/local/lib/python3.10/dist-
packages (from missingno) (3.7.1)
Requirement already satisfied: scipy in /usr/local/lib/python3.10/dist-packages
(from missingno) (1.11.4)
Requirement already satisfied: seaborn in /usr/local/lib/python3.10/dist-
packages (from missingno) (0.13.1)
Requirement already satisfied: contourpy>=1.0.1 in
/usr/local/lib/python3.10/dist-packages (from matplotlib->missingno) (1.2.1)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.10/dist-
packages (from matplotlib->missingno) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in
/usr/local/lib/python3.10/dist-packages (from matplotlib->missingno) (4.51.0)
Requirement already satisfied: kiwisolver>=1.0.1 in
/usr/local/lib/python3.10/dist-packages (from matplotlib->missingno) (1.4.5)
Requirement already satisfied: packaging>=20.0 in
/usr/local/lib/python3.10/dist-packages (from matplotlib->missingno) (24.0)
Requirement already satisfied: pillow>=6.2.0 in /usr/local/lib/python3.10/dist-
packages (from matplotlib->missingno) (9.4.0)
Requirement already satisfied: pyparsing>=2.3.1 in
/usr/local/lib/python3.10/dist-packages (from matplotlib->missingno) (3.1.2)
Requirement already satisfied: python-dateutil>=2.7 in
/usr/local/lib/python3.10/dist-packages (from matplotlib->missingno) (2.8.2)
Requirement already satisfied: pandas>=1.2 in /usr/local/lib/python3.10/dist-
packages (from seaborn->missingno) (2.0.3)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-
packages (from pandas>=1.2->seaborn->missingno) (2023.4)
Requirement already satisfied: tzdata>=2022.1 in /usr/local/lib/python3.10/dist-
packages (from pandas>=1.2->seaborn->missingno) (2024.1)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-
packages (from python-dateutil>=2.7->matplotlib->missingno) (1.16.0)
```

```
[172]: Text(0, 0.5, 'Count')
```



So, there is no any missing values in the dataset

2.3.2 Handling duplicated values

[173]:
```
# Check for duplicated values
duplicated_rows = diabetes_dataset.duplicated()

# Display rows with duplicated values
duplicated_data = diabetes_dataset[duplicated_rows]
print("Duplicated Rows:")
print(duplicated_data)
```

```
Duplicated Rows:
Empty DataFrame
Columns: [Pregnancies, Glucose, BloodPressure, SkinThickness, Insulin, BMI,
DiabetesPedigreeFunction, Age, Outcome]
Index: []
```

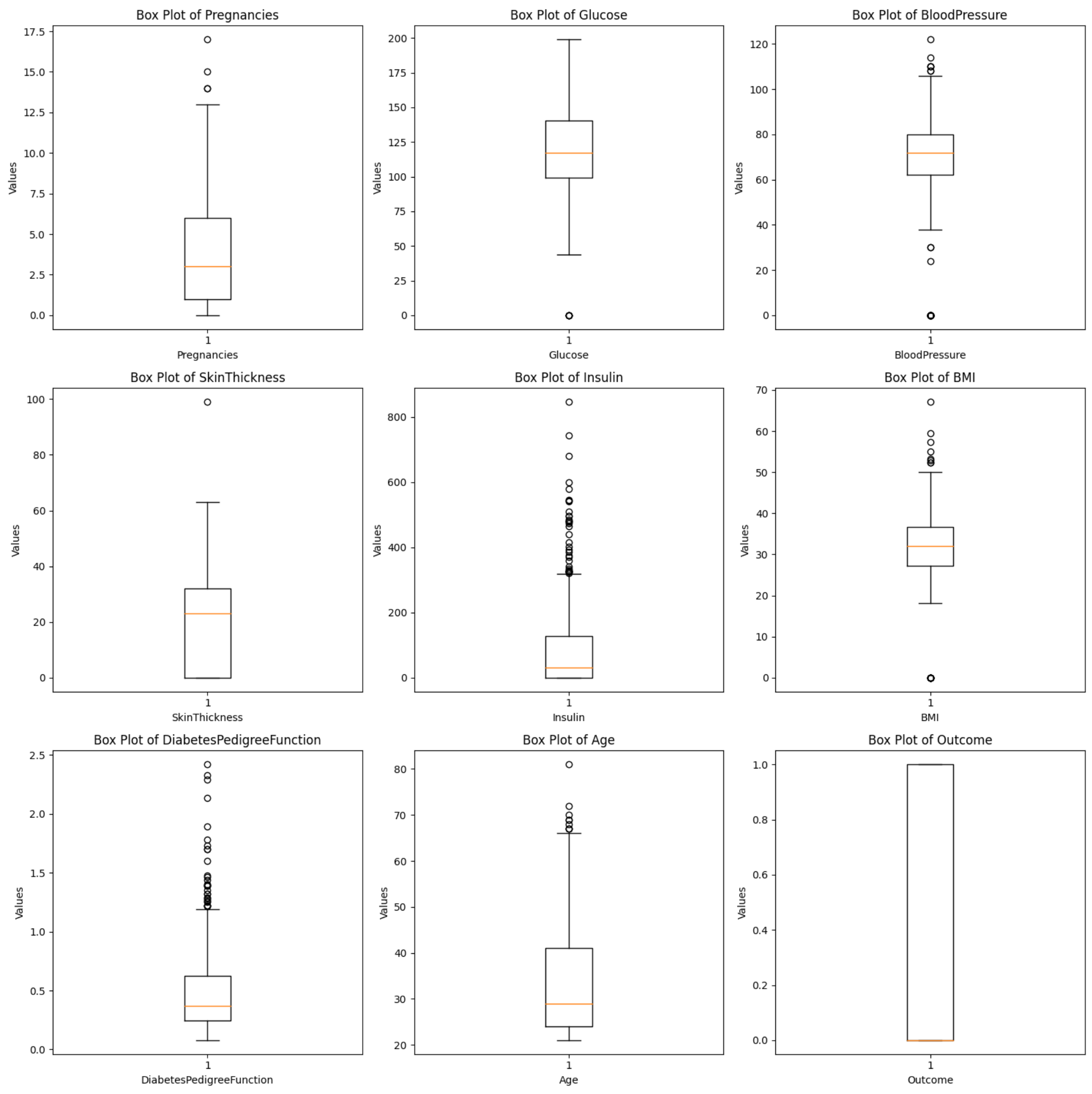
So, there is no any duplicated data

2.3.3 Handling Outliers

Detect outliers using Box-Plot

[174]:
```
# Get list of features
features = diabetes_dataset.columns.tolist()

# Calculate the number of rows and columns for subplots
num_rows = 3
num_cols = 3
```

```python
# Create subplots
fig, axes = plt.subplots(num_rows, num_cols, figsize=(15, 15))

# Flatten the axes array
axes = axes.flatten()

# Create separate box plots for each feature
for i, feature in enumerate(features):
    ax = axes[i]
    ax.boxplot(diabetes_dataset[feature])
    ax.set_title('Box Plot of {}'.format(feature))
    ax.set_xlabel('{}'.format(feature))
    ax.set_ylabel('Values')

# Hide any extra subplots if the number of features is less than 9
for j in range(len(features), num_rows * num_cols):
    fig.delaxes(axes[j])

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



Treat to the outliers In our analysis to predict diabetes, we have chosen not to treat outliers in the dataset. Since outliers may contain valuable information relevant to the prediction task, such as DiabetesPedigreeFunction or insulin levels that could be indicative of diabetes, we have opted to retain them in our analysis. By keeping outliers, we aim to capture the full range of variability in the data, which may contribute to the accuracy and robustness of our predictive models.

2.3.4 Train Test Split

[175]:
```python
# Separate the data and labels
x = diabetes_dataset.drop('Outcome',axis=1)
y = diabetes_dataset['Outcome']
```

```python
# print x and y
print(x)
print(y)
```

```
     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
..           …      …            …            …      …   …
763           10      101             76             48      180  32.9
764            2      122             70             27        0  36.8
765            5      121             72             23      112  26.2
766            1      126             60              0        0  30.1
767            1       93             70             31        0  30.4

     DiabetesPedigreeFunction  Age
0                       0.627   50
1                       0.351   31
2                       0.672   32
3                       0.167   21
4                       2.288   33
..                        …  …
763                     0.171   63
764                     0.340   27
765                     0.245   30
766                     0.349   47
767                     0.315   23

[768 rows x 8 columns]
0      1
1      0
2      1
3      0
4      1
      ..
763    0
764    0
765    0
766    1
767    0
Name: Outcome, Length: 768, dtype: int64
```

2.3.5 Treat for Imbalance dataset

[176]:
```
# check the count of the target variable
y.value_counts()
```

[176]:
```
Outcome
0    500
1    268
Name: count, dtype: int64
```

[177]:
```
# Apply SMOTE
smote = SMOTE()
x_balanced, y_balanced = smote.fit_resample(x, y)

# Check the balanced target variable
print(pd.Series(y_balanced).value_counts())

# Check the x_balanced
print(x_balanced)
```

```
Outcome
1    500
0    500
Name: count, dtype: int64
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin        BMI  \
0              6      148             72             35        0  33.600000
1              1       85             66             29        0  26.600000
2              8      183             64              0        0  23.300000
3              1       89             66             23       94  28.100000
4              0      137             40             35      168  43.100000
..           …        …            …             …        …        …
995            3      157             69             29      327  35.231892
996            6      146             89             25      479  31.110435
997            7      163             88              0        0  30.727504
998            3      173             82             24      160  31.365758
999            7      153             77             32        0  32.546891

     DiabetesPedigreeFunction  Age
0                    0.627000   50
1                    0.351000   31
2                    0.672000   32
3                    0.167000   21
4                    2.288000   33
..                        …  …
995                  0.332693   34
996                  0.145426   40
997                  0.439279   53
998                  1.007771   51
```

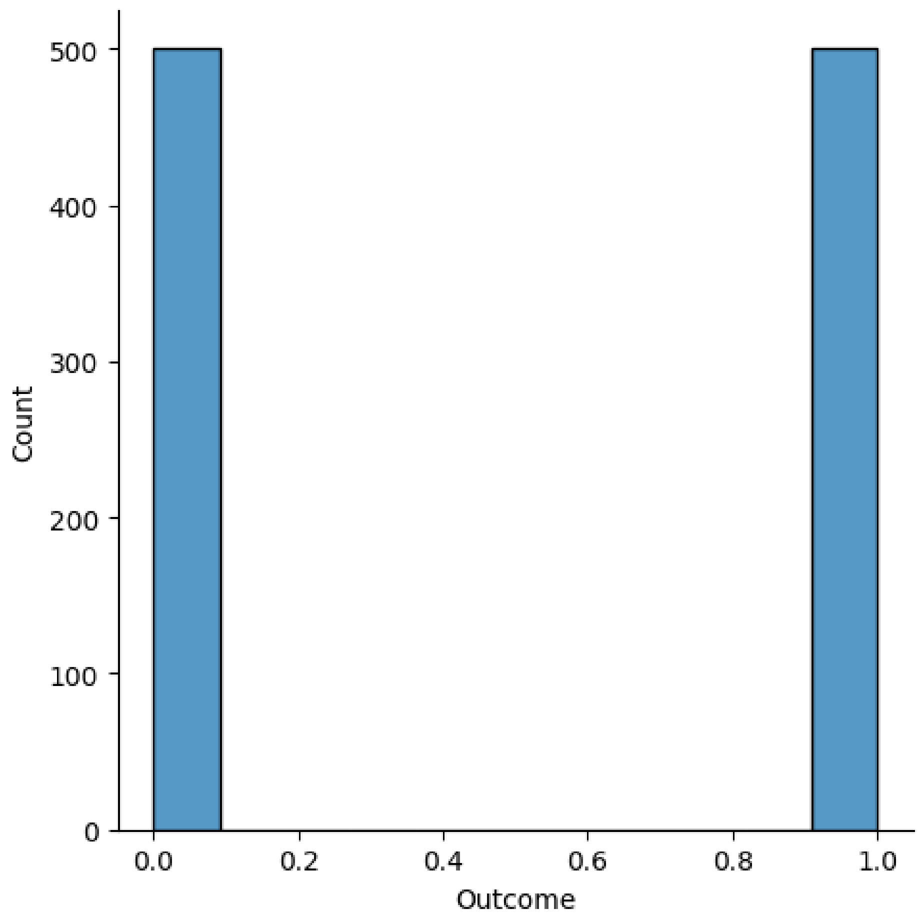
```
999                  0.465523   45

[1000 rows x 8 columns]
```

[178]:
```python
diabetes_indicators = pd.DataFrame(x_balanced, columns=x.columns)
diabetes_indicators['Outcome'] = y_balanced

# Check the class distribution after applying SMOTE
diabetes_counts = diabetes_indicators['Outcome'].value_counts()

# Print the counts
for value, count in diabetes_counts.items():
    print(f"Count {value}: {count}")
```

```
Count 1: 500
Count 0: 500
```

[179]:
```python
#Visualization to get idea about lables in Target Variable after Smote
import seaborn as sns
sns.displot(diabetes_indicators['Outcome'])
```

[179]:
```
<seaborn.axisgrid.FacetGrid at 0x78065ce8a560>
```

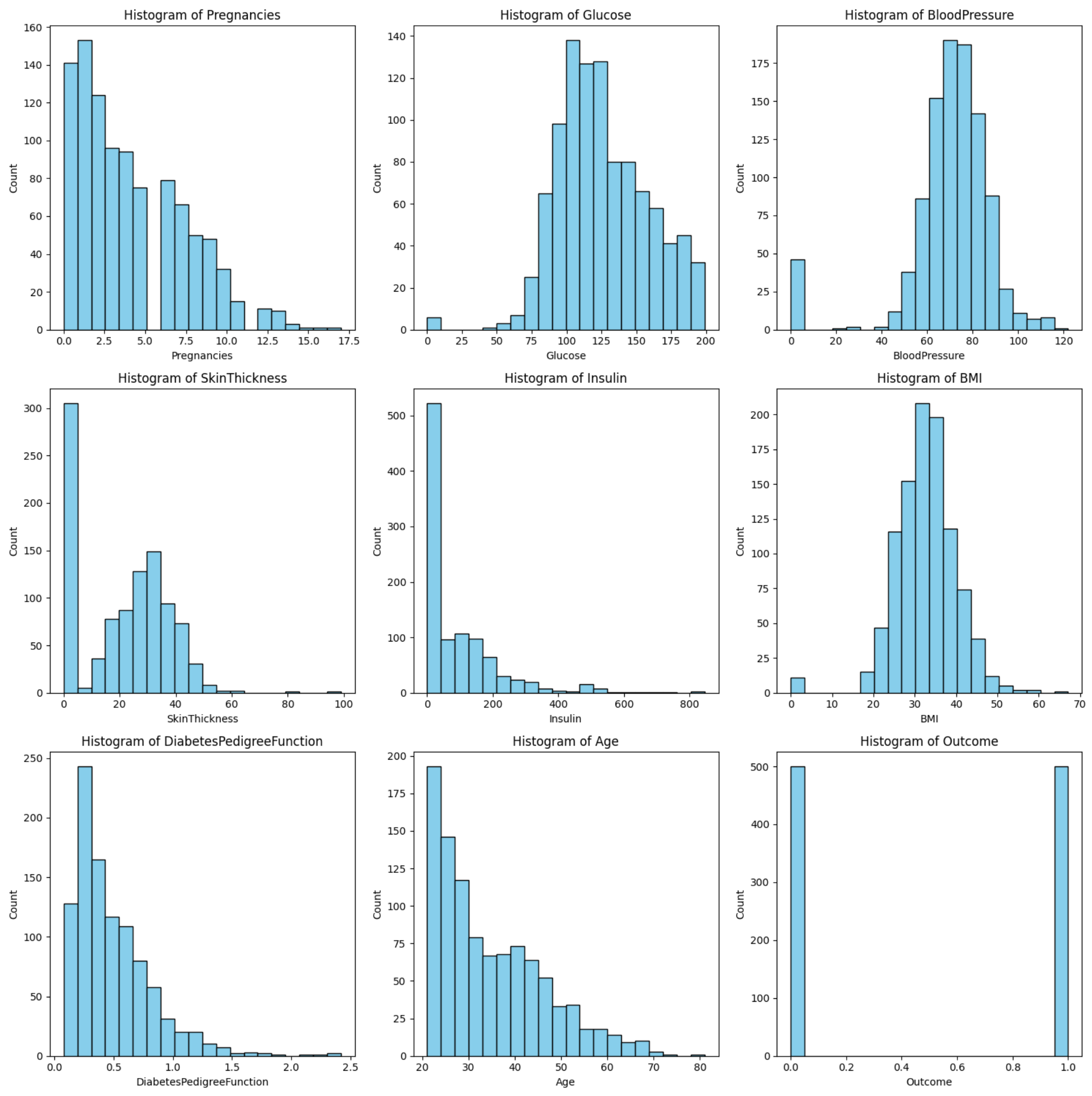


[180]:
```
diabetes_indicators.describe()
```

[180]:
```
       Pregnancies      Glucose  BloodPressure  SkinThickness      Insulin  \
count  1000.000000  1000.000000    1000.000000    1000.000000  1000.000000
mean      4.045000   126.018000      69.773000      20.738000    84.793000
std       3.369619    32.829917      19.420469      16.133308   123.387766
min       0.000000     0.000000       0.000000       0.000000     0.000000
25%       1.000000   102.750000      64.000000       0.000000     0.000000
50%       3.000000   122.000000      72.000000      24.000000     0.000000
75%       6.000000   148.000000      80.000000      33.000000   136.250000
max      17.000000   199.000000     122.000000      99.000000   846.000000

               BMI  DiabetesPedigreeFunction          Age     Outcome
count  1000.000000               1000.000000  1000.000000  1000.00000
mean     32.736158                  0.489805    34.292000     0.50000
std       7.478839                  0.323174    11.587709     0.50025
min       0.000000                  0.078000    21.000000     0.00000
25%      28.300000                  0.256000    25.000000     0.00000
```

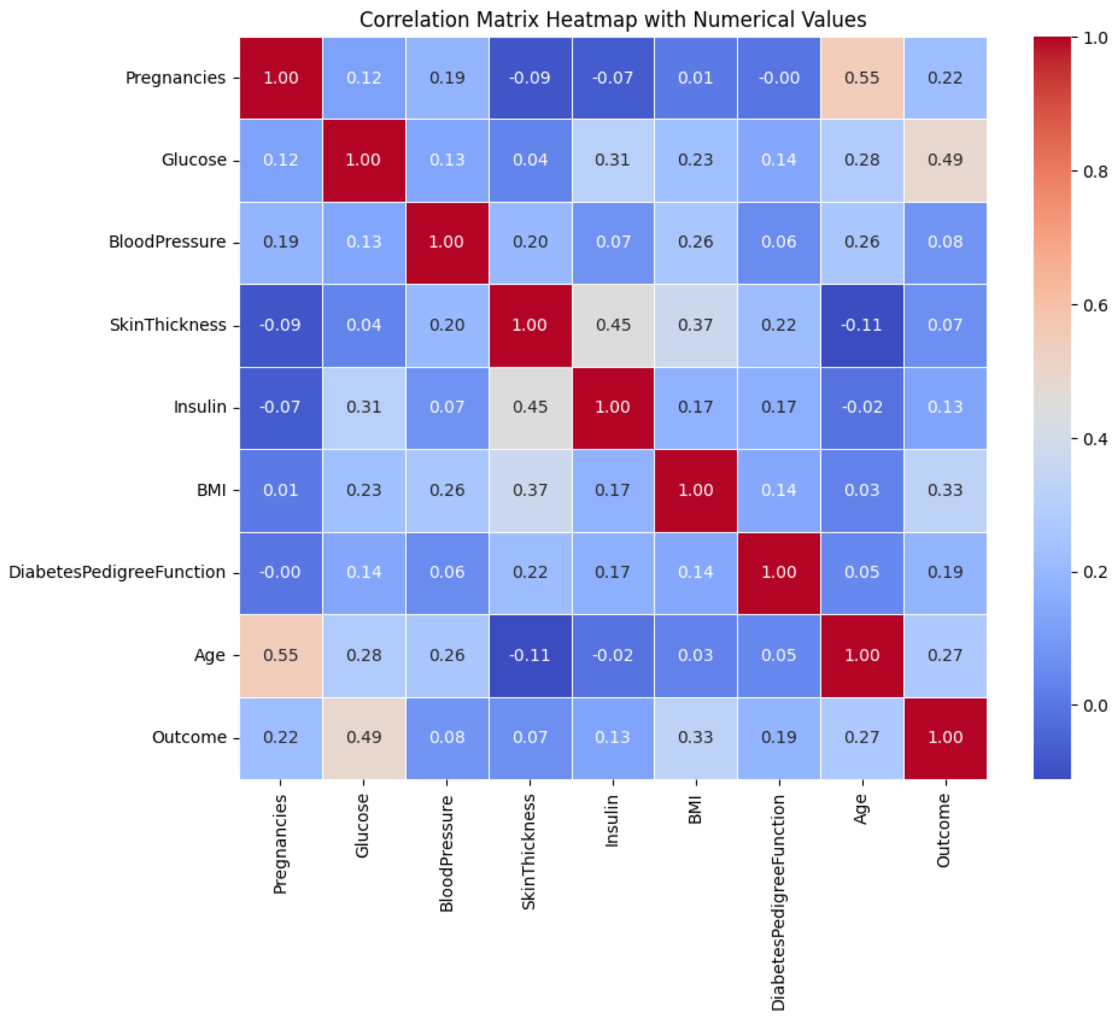
```
50%      32.800000                    0.398500   31.000000     0.50000
75%      37.056576                    0.647398   42.000000     1.00000
max      67.100000                    2.420000   81.000000     1.00000
```

[181]:
```
feature_names = diabetes_indicators.columns

# Create subplots for each feature
num_features = len(feature_names)
num_cols = 3  # Number of columns in the subplot grid
num_rows = (num_features + num_cols - 1) // num_cols  # Number of rows needed

plt.figure(figsize=(15, 5*num_rows))

for i, feature in enumerate(feature_names, 1):
    plt.subplot(num_rows, num_cols, i)
    plt.hist(diabetes_indicators[feature], bins=20, color='skyblue',␣
 ↪edgecolor='black')
    plt.xlabel(feature)
    plt.ylabel('Count')
    plt.title(f'Histogram of {feature}')

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



2.3.6 Correlation Matrix

```
[182]: # Plot the correlation matrix as a heatmap
correlation_matrix = diabetes_indicators.corr()

# Create a heatmap of the correlation matrix
plt.figure(figsize=(10, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt=".2f",␣
  ↪linewidths=.5)
plt.title('Correlation Matrix Heatmap with Numerical Values')
plt.show()
```



	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1.00	0.12	0.19	-0.09	-0.07	0.01	-0.00	0.55	0.22
Glucose	0.12	1.00	0.13	0.04	0.31	0.23	0.14	0.28	0.49
BloodPressure	0.19	0.13	1.00	0.20	0.07	0.26	0.06	0.26	0.08
SkinThickness	-0.09	0.04	0.20	1.00	0.45	0.37	0.22	-0.11	0.07
Insulin	-0.07	0.31	0.07	0.45	1.00	0.17	0.17	-0.02	0.13
BMI	0.01	0.23	0.26	0.37	0.17	1.00	0.14	0.03	0.33
DiabetesPedigreeFunction	-0.00	0.14	0.06	0.22	0.17	0.14	1.00	0.05	0.19
Age	0.55	0.28	0.26	-0.11	-0.02	0.03	0.05	1.00	0.27
Outcome	0.22	0.49	0.08	0.07	0.13	0.33	0.19	0.27	1.00

[183]:
```python
# separating the data and labels
x_balanced = diabetes_indicators.drop(columns = 'Outcome', axis=1)
y_balanced = diabetes_indicators['Outcome']
```

##Feature Scaling

2.3.7 Data Standadization

[184]:
```python
scaler = StandardScaler()
scaler.fit(x_balanced)
```

[184]:
```
StandardScaler()
```

[185]:
```python
standardized_data = scaler.transform(x_balanced)

# print the data
```

```
standardized_data
```

[185]:
```
array([[ 0.58047467,  0.66990724,  0.1147302 , …,  0.11556261,
         0.4247363 ,  1.3562525 ],
       [-0.90411528, -1.25003435, -0.19437676, …, -0.82087991,
        -0.42972118, -0.28423626],
       [ 1.17431065,  1.73654145, -0.29741242, …, -1.26234567,
         0.56405002, -0.19789475],
       …,
       [ 0.87739266,  1.12703618,  0.93901543, …, -0.26871267,
        -0.15642186,  1.61527704],
       [-0.3102793 ,  1.43178882,  0.62990847, …, -0.18332873,
         1.60355106,  1.44259401],
       [ 0.87739266,  0.82228355,  0.37231934, …, -0.0253197 ,
        -0.07517313,  0.92454493]])
```

[186]:
```
# again assign the standardized data into X variable
X = standardized_data

Y = y_balanced
```

2.3.8 Divide the data into two parts

[187]:
```
x_train, x_test, y_train, y_test = train_test_split(X,Y, test_size = 0.2,␣
↪stratify =Y , random_state = 2)
```

[188]:
```
# check the split

print(f'Original X : {X.shape}')
print(f'Original X : {Y.shape}')
print(f'Traing X   : {x_train.shape}')
print(f'Testing X  : {x_test.shape}')
print(f'Traing X   : {y_train.shape}')
print(f'Testing X  : {y_test.shape}')
```

```
Original X : (1000, 8)
Original X : (1000,)
Traing X   : (800, 8)
Testing X  : (200, 8)
Traing X   : (800,)
Testing X  : (200,)
```

2.4 Training the model

2.4.1 Using SVC (Support Vector Classifier)

[189]:
```
# import the svc library
from sklearn import svm

# Train the model
model_svc = svm.SVC(kernel = 'linear')
model_svc.fit(x_train,y_train)
```

[189]:
```
SVC(kernel='linear')
```

2.4.2 Using Random Forest

[190]:
```
# import the svc library
from sklearn.ensemble import RandomForestClassifier


max_depth_value=5


# Train the model
model_RF = RandomForestClassifier(n_estimators=500,max_depth=max_depth_value)
model_RF.fit(x_train,y_train)
```

[190]:
```
RandomForestClassifier(max_depth=5, n_estimators=500)
```

2.5 Model evaluation

2.5.1 Using accuracy score

[191]:
```
# for svc model

# for train data
pred_svc_train = model_svc.predict(x_train)
accuracyScore_svc_train = accuracy_score(pred_svc_train,y_train)
print('Accuracy score of the train data using SVC           : ',␣
 ↪accuracyScore_svc_train)


# for test data
pred_svc = model_svc.predict(x_test)
accuracyScore_svc = accuracy_score(pred_svc,y_test)
print('Accuracy score of the test data using SVC            : ',␣
 ↪accuracyScore_svc)
```

```
# for Fandom Forest model

# for train data
pred_RF_train = model_RF.predict(x_train)
accuracyScore_RF_train = accuracy_score(pred_RF_train,y_train)
print('Accuracy score of the train data using RF  : ', accuracyScore_RF_train)

# for test data
pred_RF = model_RF.predict(x_test)
accuracyScore_RF = accuracy_score(pred_RF,y_test)
print('Accuracy score of the test data using RF   : ', accuracyScore_RF)
```

```
Accuracy score of the train data using SVC           :  0.7625
Accuracy score of the test data using SVC            :  0.765
Accuracy score of the train data using RF  :  0.85625
Accuracy score of the test data using RF   :  0.805
```

2.5.2 confusion matrix, classification report, and accuracy score to assess its performance.

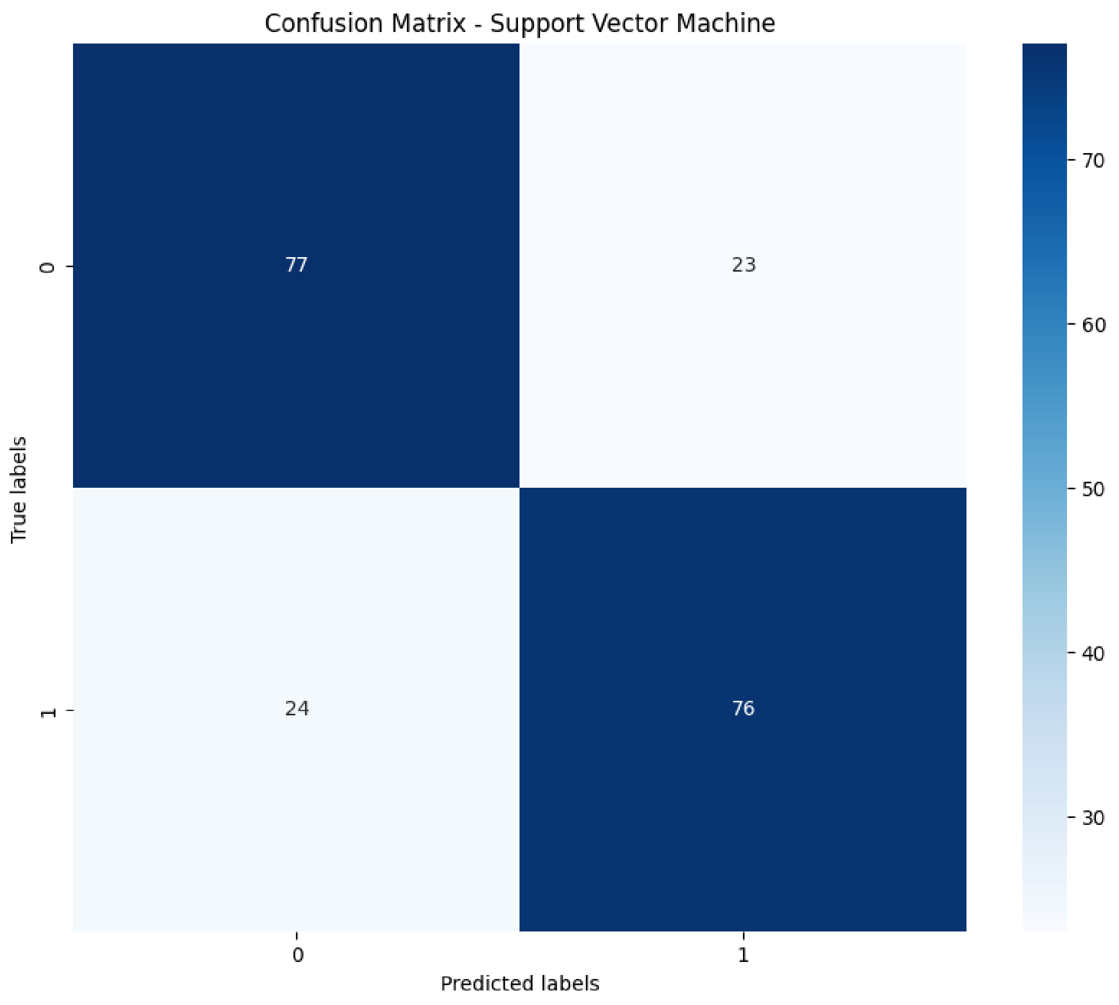
```
[192]: from sklearn.metrics import classification_report, confusion_matrix,␣
         ↪accuracy_score
print('Metrics for Support Vector Machine')
print('-----------------------------------------------------')
print("Confusion Matrix :")
print(confusion_matrix(y_test,pred_svc))
print('-----------------------------------------------------')
print("Classification Report :")
print(classification_report(y_test,pred_svc))
print('-----------------------------------------------------')
print("accuracy score :",accuracy_score(y_test, pred_svc))
```

```
Metrics for Support Vector Machine
----------------------------------------------------
Confusion Matrix :
[[77 23]
 [24 76]]
----------------------------------------------------
Classification Report :
              precision    recall  f1-score   support

           0       0.76      0.77      0.77       100
           1       0.77      0.76      0.76       100

    accuracy                           0.77       200
   macro avg       0.77      0.77      0.76       200
weighted avg       0.77      0.77      0.76       200
```

```
----------------------------------------------------
accuracy score : 0.765
```

[193]:

```
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.metrics import confusion_matrix

# Get confusion matrix
cm = confusion_matrix(y_test, pred_svc)

# Define the unique class labels
classes = [0, 1]  # Replace [0, 1] with your actual unique class labels

# Plot confusion matrix as heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(cm, annot=True, cmap='Blues', fmt='g',
            xticklabels=classes, yticklabels=classes)
plt.xlabel('Predicted labels')
plt.ylabel('True labels')
plt.title('Confusion Matrix - Support Vector Machine')
plt.show()
```

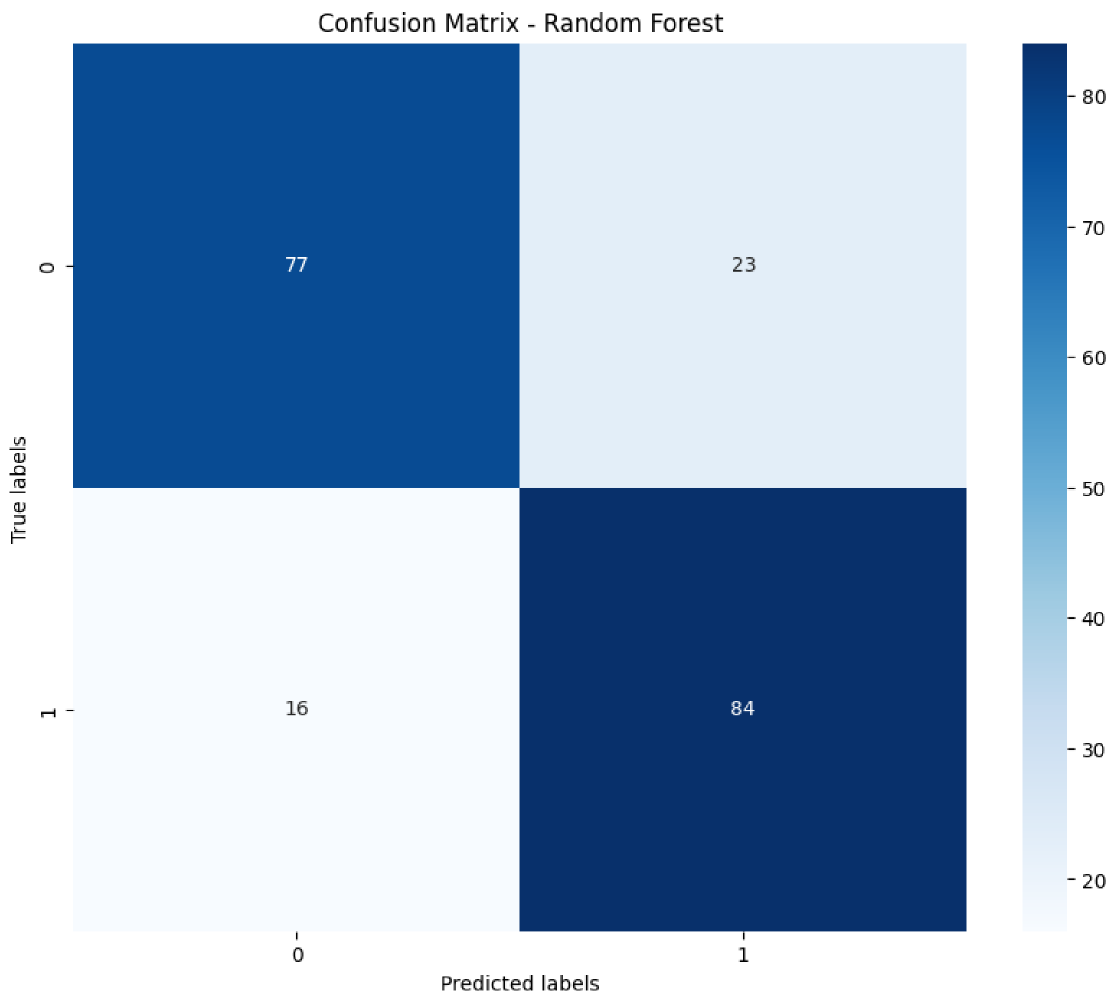


```
[194]: from sklearn.metrics import classification_report, confusion_matrix,␣
         ↪accuracy_score
       print('Metrics for Random Forest')
       print('-----------------------------------------------------')
       print("Confusion Matrix :")
       print(confusion_matrix(y_test,pred_RF))
       print('-----------------------------------------------------')
       print("Classification Report :")
       print(classification_report(y_test,pred_RF))
       print('-----------------------------------------------------')
       print("accuracy score :",accuracy_score(y_test, pred_RF))
```

```
Metrics for Random Forest
-----------------------------------------------------
Confusion Matrix :
[[77 23]
```

```
 [16 84]]
----------------------------------------------------
Classification Report :
              precision    recall  f1-score   support

           0       0.83      0.77      0.80       100
           1       0.79      0.84      0.81       100

    accuracy                           0.81       200
   macro avg       0.81      0.80      0.80       200
weighted avg       0.81      0.81      0.80       200

----------------------------------------------------
accuracy score : 0.805
```

[195]:
```python
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.metrics import confusion_matrix

# Get confusion matrix
cm = confusion_matrix(y_test, pred_RF)

# Define the unique class labels
classes = [0, 1]  # Replace [0, 1] with your actual unique class labels

# Plot confusion matrix as heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(cm, annot=True, cmap='Blues', fmt='g',
            xticklabels=classes, yticklabels=classes)
plt.xlabel('Predicted labels')
plt.ylabel('True labels')
plt.title('Confusion Matrix - Random Forest')
plt.show()
```



2.6 Making the predictive system

[196]:
```
input_data = (5,166,72,19,175,25.8,0.587,51)

# changing the input_data to numpy array
input_data_as_numpy_array = np.asarray(input_data)

# reshape the array as we are predicting for one instance
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)
```

2.6.1 Predict the diabetes using SVM

[197]:
```
# Prediction using SVM classifier
svm_prediction = model_svc.predict(input_data_reshaped)
print("SVM Classifier Prediction:", svm_prediction[0])
```

```
if (svm_prediction[0] == 0):
  print('SVM : The person is not diabetic')
else:
  print('SVM: The person is diabetic')
```

```
SVM Classifier Prediction: 1
SVM: The person is diabetic
```

2.6.2 Predict the diabetes using RF

[198]:
```
rf_prediction = model_RF.predict(input_data_reshaped)
print("Random Forest Classifier Prediction:", rf_prediction[0])

# Output prediction interpretation
if rf_prediction[0] == 0:
    print('Random Forest: The person is not diabetic')
else:
    print('Random Forest: The person is diabetic')
```

```
Random Forest Classifier Prediction: 1
Random Forest: The person is diabetic
```

2.6.3 Saving the trained SVM model & Random Forest model

[199]:
```
import pickle

# Save the svm trained model using pickle
filename = 'DiabetesPrediction_svm_model.sav'
pickle.dump(model_svc, open(filename,'wb'))

# Save the RF trained model using pickle
filename = 'DiabetesPrediction_rf_model.sav'
pickle.dump(model_RF, open(filename, 'wb'))
```

2.6.4 Loading the Save SVM model and Testing

[200]:
```
load_model_svm = pickle.load(open('DiabetesPrediction_svm_model.sav','rb'))
```

[201]:
```
# Prediction using SVM classifier
svm_prediction = load_model_svm.predict(input_data_reshaped)
print("SVM Classifier Prediction:", svm_prediction[0])

if (svm_prediction[0] == 0):
  print('SVM : The person is not diabetic')
else:
  print('SVM: The person is diabetic')
```

```
SVM Classifier Prediction: 1
SVM: The person is diabetic
```

2.6.5 Loading the Save RF model and Testing

```
[202]: load_model_RF = pickle.load(open('DiabetesPrediction_rf_model.sav','rb'))
```

```
[203]: # Prediction using SVM classifier
svm_prediction = load_model_RF.predict(input_data_reshaped)
print("SVM Classifier Prediction:", svm_prediction[0])

if (svm_prediction[0] == 0):
  print('SVM : The person is not diabetic')
else:
  print('SVM: The person is diabetic')
```

```
SVM Classifier Prediction: 1
SVM: The person is diabetic
```