Diabetes Prediction

The objective of this project is to create a diabetes diagnostic prediction model based on particular health metrics. The National Institute of Diabetes and Digestive and Kidney Diseases provided the dataset utilized in this investigation, which is intended to identify patients with or without diabetes. It is significant to emphasize that the dataset was selected using strict criteria: all patients included had to be female, Pima Indian, and at least 21 years old.

Using these medical variables to create a machine learning model that can precisely determine whether a patient has diabetes is the main goal of this study. A model like this can have a big impact on clinical practice by helping medical practitioners identify and treat patients at an early stage.

```
import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn import metrics as m
##for visualization
import seaborn as sns
import matplotlib.pyplot as plt
from scipy.stats import zscore
 # For standardizing numerical features
from sklearn.preprocessing import StandardScaler
```

```
## read out the dataset
df = pd.read_csv('diabetes.csv')
```

Data Exploration

```
df.head(5)
```

	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

Here’s a brief explanation of each column:

Pregnancies : Number of times pregnant.

Glucose : Plasma glucose concentration after 2 hours in an oral glucose tolerance test.

BloodPressure : Diastolic blood pressure (mm Hg).

SkinThickness : Triceps skinfold thickness (mm).

Insulin : 2-Hour serum insulin (mu U/ml).

BMI : Body mass index (weight in kg/(height in m)^2).

DiabetesPedigreeFunction : Diabetes pedigree function (a function which scores likelihood of dia-betes based on family history).

Age : Age in years.

Outcome : Class variable (0 or 1) indicating whether the person has diabetes or not.

```
df.describe()
```

```
       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
```

- The minimum blood pressure,SkinThickness,BMI and Insulin is 0 that is not biologically possible, so we can say that like 0 might be a placeholder for missing values.

```
df.isnull().sum()
```

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

```
df.shape
```

```
(768, 9)
```

```
df.columns
```

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

```
df.dtypes
```

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

Data Processing

```
columns = ['Glucose', 'BloodPressure', 'SkinThickness',
'Insulin','BMI', 'Age'] df[columns] = df[columns].replace(0, np.nan)
df.isnull().sum()
```

```
Pregnancies                 0
Glucose                     5
```

```
BloodPressure              35
SkinThickness             227
Insulin                   374
BMI                        11
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

```
for column in columns :
    df[column].fillna(df[column].median(),inplace = True)
df.isnull().sum()
```

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

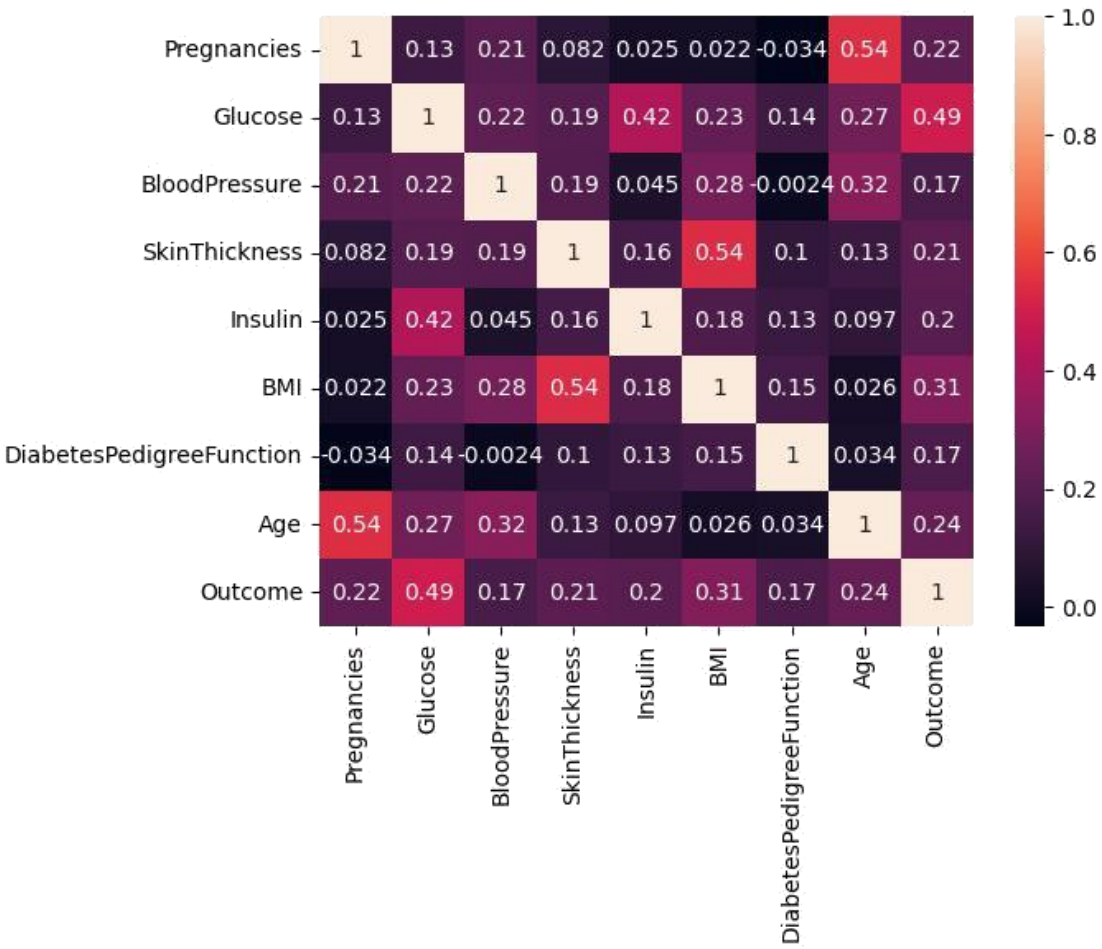
```
df.head()
```

```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin  BMI   \
0            6    148.0           72.0           35.0    125.0  33.6
1            1     85.0           66.0           29.0    125.0  26.6
2            8    183.0           64.0           29.0    125.0  23.3
3            1     89.0           66.0           23.0     94.0  28.1
4            0    137.0           40.0           35.0    168.0  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
```

Data Visualisation

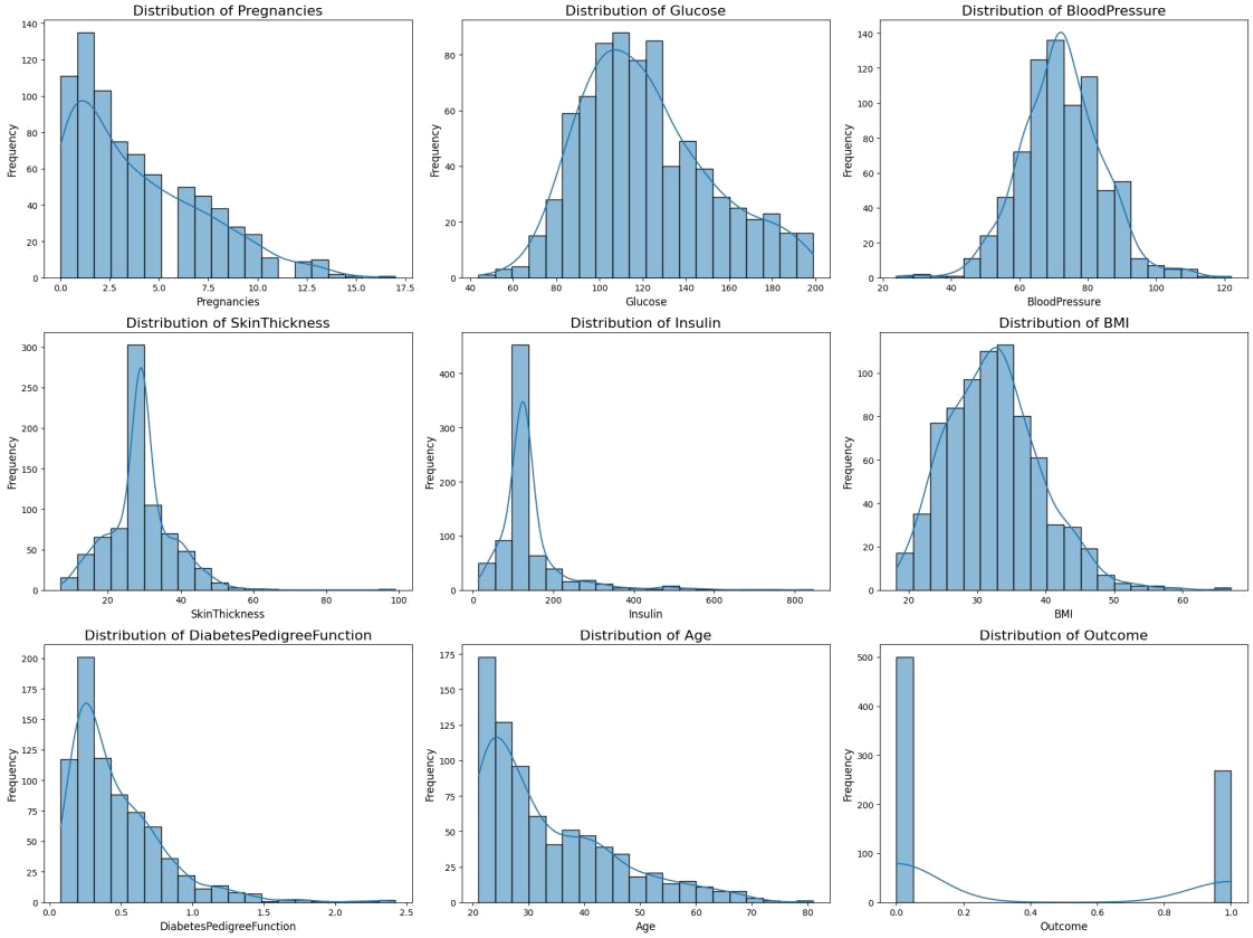
Visualizing Correlations with a Heatmap

```
sns.heatmap(df.corr(), annot=True)
plt.show()
```



Visualizing the Distribution of Features using Histograms

```
plt.figure(figsize=(20, 15))

for i, column in enumerate(df.columns, 1):
    plt.subplot(3, 3, i)
    sns.histplot(df[column], bins=20, kde=True)
    plt.title(f'Distribution of {column}', fontsize=16)
    plt.xlabel(column, fontsize=12)
    plt.ylabel('Frequency', fontsize=12)

# Adjust layout for better
spacing plt.tight_layout()

# Show the plot
plt.show()
```



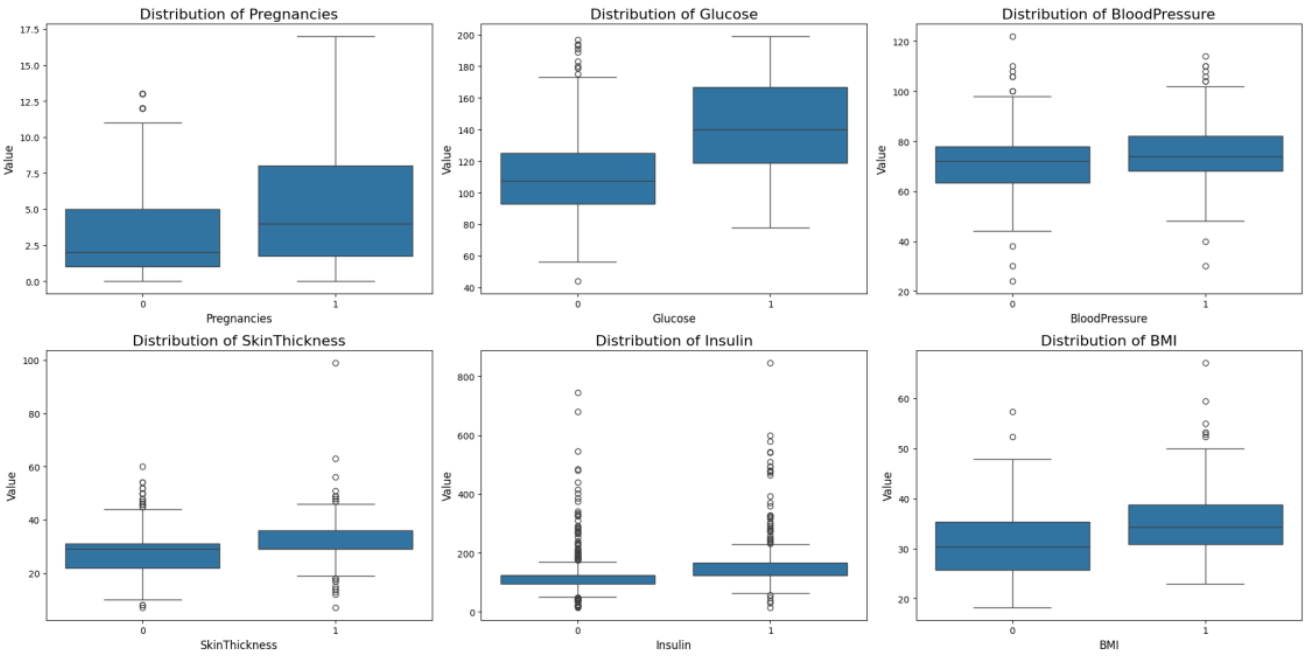
Insights, that we got from histogram,

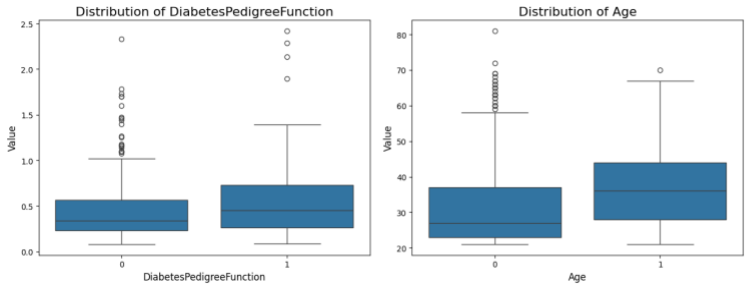
- **Pregnancies:** Most of the women in the dataset have had either no pregnancies or only 1 or 2 pregnancies. There are fewer women who have had more pregnancies.
- **Glucose:** The levels of glucose (sugar in the blood) follow a somewhat normal pattern, but there is a small group of people with lower glucose levels.
- **Blood Pressure:** Blood pressure values tend to center around 70. It's like the average or typical blood pressure in the dataset.
- **Skin Thickness:** Many people in the dataset have lower skin thickness values, and there's a peak around those values. It means that a significant number of individuals have relatively thinner skin.
- **Insulin:** Most people have lower insulin levels, but there are a few individuals with higher insulin values.
- **BMI (Body Mass Index):** BMI values are slightly skewed to the right, with a peak around 30. This suggests that many people have a BMI around 30, which is considered overweight.
- **Diabetes Pedigree Function:** The majority of individuals in the dataset have a low value for this function, indicating that, based on their family history, they have a lower likelihood of developing diabetes.

- **Age:** Most people in the dataset are in their 20s and 40s, with relatively fewer individuals in other age groups.
- **Outcome**: More people in the dataset do not have diabetes (labeled as 0) compared to those who do have diabetes (labeled as 1).

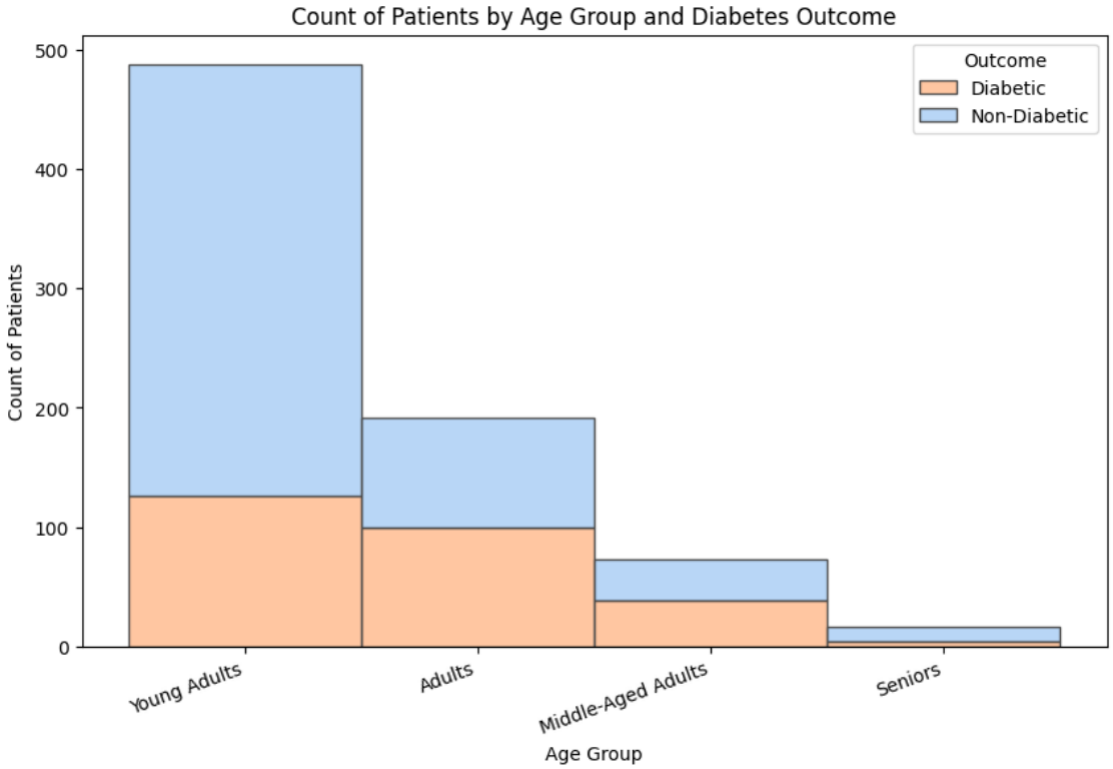
Visualizing the Distribution of Features using Box Plot

```
df_No_Outcome = df.iloc[:,:-1]

num_cols = len(df_No_Outcome.columns)
num_rows = (num_cols - 1) // 3 + 1 # Calculate the number of rows needed
fig, axes = plt.subplots(num_rows, 3, figsize=(20, 5 * num_rows))

axes = axes.flatten()
for i, column in enumerate(df_No_Outcome.columns):
    sns.boxplot(data=df,y=df[column],x = df['Outcome'] ,     ax=axes[i])

    axes[i].set_title(f'Distribution of {column}', fontsize=16)
    axes[i].set_xlabel(column, fontsize=12)
    axes[i].set_ylabel('Value', fontsize=12)

# Remove any empty subplots
for i in range(num_cols, num_rows * 3):
    fig.delaxes(axes[i])

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

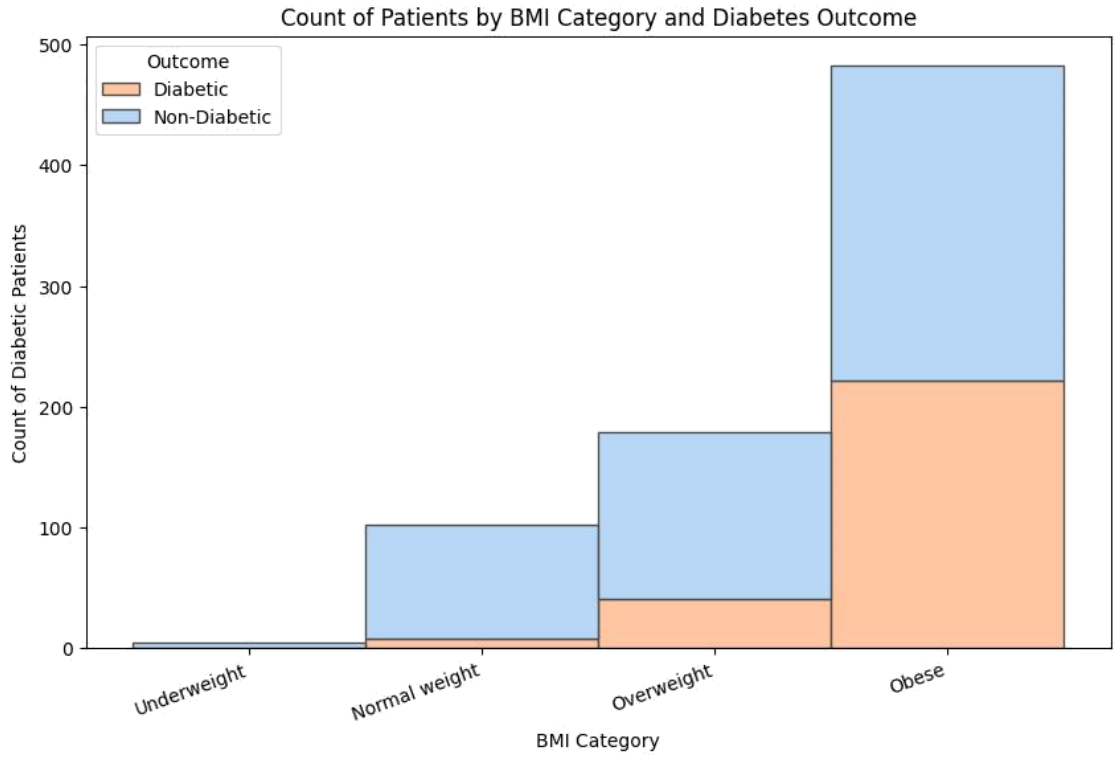





```
bins = [20, 35, 50, 65, 200]
labels = ['Young Adults', 'Adults', 'Middle-Aged Adults', 'Seniors']

df['AgeGroup'] = pd.cut(df['Age'], bins=bins, labels=labels, right=False)

plt.figure(figsize=(10, 6))
sns.histplot(data=df, x='AgeGroup', hue='Outcome',
 multiple='stack', palette='pastel', edgecolor=".3")
plt.xlabel('Age Group')
plt.ylabel('Count of Patients')
plt.title('Count of Patients by Age Group and Diabetes Outcome')
plt.xticks(rotation=20, ha='right')
plt.legend(title='Outcome', labels=[ 'Diabetic', 'Non-Diabetic'])
plt.show()
```



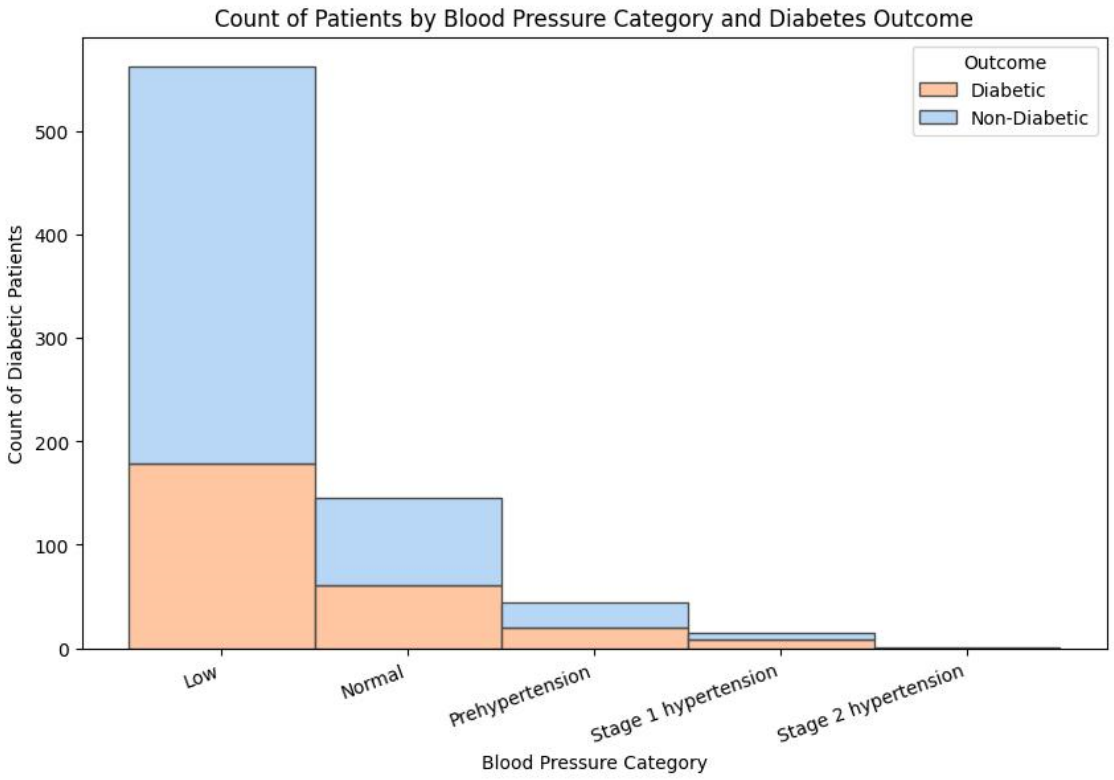
```
bmi_bins = [0, 18.5, 24.9, 29.9, 1000]
bmi_labels = ['Underweight', 'Normal weight', 'Overweight', 'Obese']

df['BMICategory'] = pd.cut(df['BMI'], bins=bmi_bins, labels=bmi_labels)

plt.figure(figsize=(10, 6))
sns.histplot(data=df, x='BMICategory', hue='Outcome',
 multiple='stack', palette='pastel', edgecolor=".3")
plt.xlabel('BMI Category')
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Patients by BMI Category and Diabetes Outcome')
plt.xticks(rotation=20, ha='right')
plt.legend(title='Outcome', labels=[ 'Diabetic', 'Non-Diabetic'])
plt.show()
```




```
blood_pressure_bins = [0, 80, 89, 99, 119, 1000]
blood_pressure_labels = ['Low', 'Normal', 'Prehypertension', 'Stage 1
 hypertension', 'Stage 2 hypertension']
df['BloodPressureCategory'] = pd.cut(df['BloodPressure'],
 bins=blood_pressure_bins, labels=blood_pressure_labels,right=False)
df.head()
```

```
   Pregnancies Glucose BloodPressure SkinThickness Insulin BMI   \
0            6   148.0          72.0          35.0   125.0  33.6
1            1    85.0          66.0          29.0   125.0  26.6
2            8   183.0          64.0          29.0   125.0  23.3
3            1    89.0          66.0          23.0    94.0  28.1
4            0   137.0          40.0          35.0   168.0  43.1

   DiabetesPedigreeFunction  Age  Outcome          AgeGroup BMICategory  \
0                     0.627   50        1  Middle-Aged Adults        Obese
1                     0.351   31        0      Young Adults   Overweight
2                     0.672   32        1      Young Adults Normal weight
3                     0.167   21        0      Young Adults   Overweight
4                     2.288   33        1      Young Adults        Obese

BloodPressureCategory
0                   Low
1                   Low
2                   Low
3                   Low
4                   Low
```

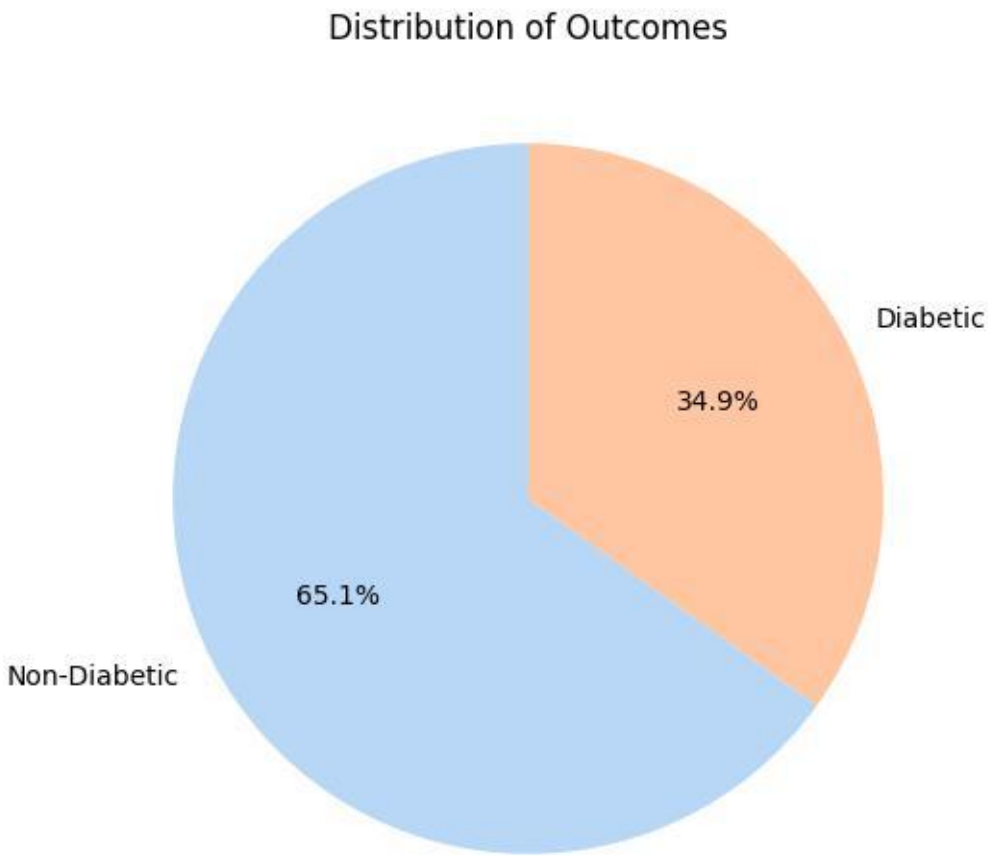
```
plt.figure(figsize=(10, 6))
sns.histplot(data=df, x='BloodPressureCategory', hue='Outcome',␣
 ↪multiple='stack', palette='pastel', edgecolor=".3")
plt.xlabel('Blood Pressure Category')
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Patients by Blood Pressure Category and Diabetes Outcome')
plt.xticks(rotation=20, ha='right')
plt.legend(title='Outcome', labels=[ 'Diabetic', 'Non-Diabetic'])
plt.show()
```




```
outcome_counts = df['Outcome'].value_counts()
outcome_counts
```

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

```
plt.figure(figsize=(6, 6))
plt.pie(outcome_counts, labels=['Non-Diabetic',
'Diabetic'], autopct='%1.1f%%', startangle=90,
colors=['#B8D6F6','#FFC6A1']) plt.title('Distribution
of Outcomes') plt.show()
```



Data Wrangling

```
#Independent Variables
X = df[['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness',
'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age']]
#Target Variable
y = df['Outcome']
```

```
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.2,random_state=2)
print(X_train.shape  )
```

```
(614, 8)
```

Feature Scaling

```
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
X_train
```

```
array([[-0.85811767,  0.04869548, 0.12833387, …, -0.66090407,
       -1.10316947, -0.27704152],
      [-0.85811767, -0.89788944, 0.7953984 , …, 0.40034496,
       -0.71238555,  0.84376203],
      [-1.15412006, -0.9305303 , -0.20519839, …, 1.65320841,
       -0.37742791, -1.05298243],
       …,
       [ 0.02988949,  0.08133634, -0.20519839, …, -
         0.4987688 ,  1.96433735,  1.01619334],
       [-0.2661129 , -0.21243139, 0.12833387, …, -
        0.88199762, -1.08260189, -0.79433546],
       [ 0.02988949, -0.40827655, -0.53873066, …, -
        0.0565817 , -0.01308802, -0.36325717]])
```

Model Training and Evaluation

```
logistic = LogisticRegression()
logistic.fit(X_train,y_train)
```

```
LogisticRegression()
```

```
#Prediction on Traing Data
log_pred_train = logistic.predict(X_train)
#Prediction on Test Data
log_pred_test = logistic.predict(X_test)
```

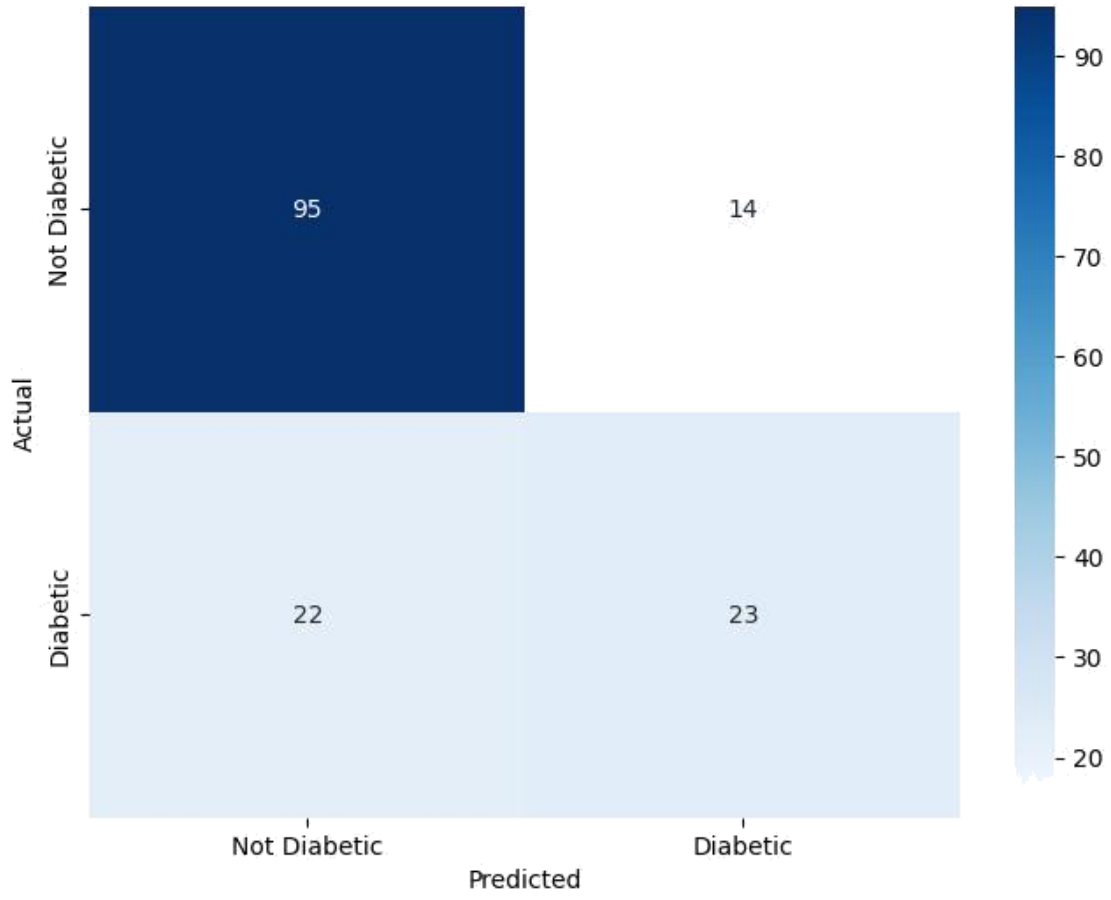
```
log_Train_Accuracy = m.accuracy_score(y_train,log_pred_train)*100
log_Test_Accuracy = m.accuracy_score(y_test,log_pred_test)*100

print(f"Train Accuracy: {log_Train_Accuracy:.2f}%")
print(f"Test Accuracy: {log_Test_Accuracy:.2f}%")
```

```
Train Accuracy: 77.52%
Test Accuracy: 76.62%
```

```
print('Classification_Report')
print(m.classification_report(y_test,log_pred_test))
print('Confusion_Matrix')
print(m.confusion_matrix(y_test,log_pred_test))
```

```
Classification_Report
              precision    recall  f1-score   support

           0       0.81      0.87      0.84       109
           1       0.62      0.51      0.56        45

    accuracy                           0.77       154
   macro avg       0.72      0.69      0.70       154
weighted avg       0.76      0.77      0.76       154

Confusion_Matrix
[[95 14]
 [22 23]]
```

```
plt.figure(figsize=(8, 6))
cm = m.confusion_matrix(y_test, log_pred_test)
sns.heatmap(cm, annot=True, fmt="d", cmap=plt.cm.Blues, xticklabels=["Not␣
 ↪Diabetic", "Diabetic"], yticklabels=["Not Diabetic", "Diabetic"])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.show()
```



Diabetes Prediction

```
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)

prediction = logistic.predict(input_data_reshaped)
print(prediction)

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

```
[1]
The person is diabetic
```

Web Application