Diabetes Patients Predictive Analysis

Project Overview:

This project focuses on predictive analysis for diabetes diagnosis using a dataset originally sourced from the National Institute of Diabetes and Digestive and Kidney Diseases. The dataset contains various medical and demographic variables for a group of Pima Indian heritage females who are at least 21 years old.

The primary objective of this project is to develop a predictive model that can diagnostically predict whether a patient has diabetes based on the provided diagnostic measurements and demographic information.

Dataset Description:

Features	Description
Pregnancies	The number of pregnancies a patient has had.
Glucose	Plasma glucose concentration, an indicator of blood sugar levels.
BloodPressure	Diastolic blood pressure.
SkinThickness	Skinfold thickness, which may be related to body composition.
Insulin	2-Hour serum insulin level.
BMI	A measure of body weight and height, indicating body fat.
DiabetesPedigreeFunction	A measure of the diabetes heredity risk based on family history.
Age	The age of the patient in years.
Outcome	The target variable indicating whether the patient has diabetes (1 for positive, 0 for negative).

Importing Important Libraries For This Project

In [1]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
import math
#Spliting Data into Train and Test:
from sklearn.model_selection import train_test_split
#For Feature Scaling:
from sklearn.preprocessing import StandardScaler
#Support Vector Machine:
from sklearn.svm import SVC
#Logistic Regression:
from sklearn.linear_model import LogisticRegression
#Evaluation:
from sklearn.model_selection import cross_val_score
from sklearn.metrics import accuracy_score
#For ignoring  warnings:
import warnings
warnings.filterwarnings('ignore')
```

In [2]:
```
#Import Dataset
data = pd.read_csv("D:/Meri Skill/Project 2 - Diabetes Data-20231029T054108Z-001/Project 2 - Diabetes Data/Project 2 MeriSKILL/diabetes.csv")
```

In [3]:
```
#Copy the dataset
df = data.copy()
```

Data Exploration

In [4]:
```
df.head()
```

Out[4]:

	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 [5]:
```
df.tail()
```

Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

Number of Rows and Columns in Dataset

In [6]:
```
df.shape
print("Total Number of Rows in Dataset  :",data.shape[0])
print("Total Number of Columns in Dataset:",data.shape[1])
```

```
Total Number of Rows in Dataset  : 768
Total Number of Columns in Dataset: 9
```

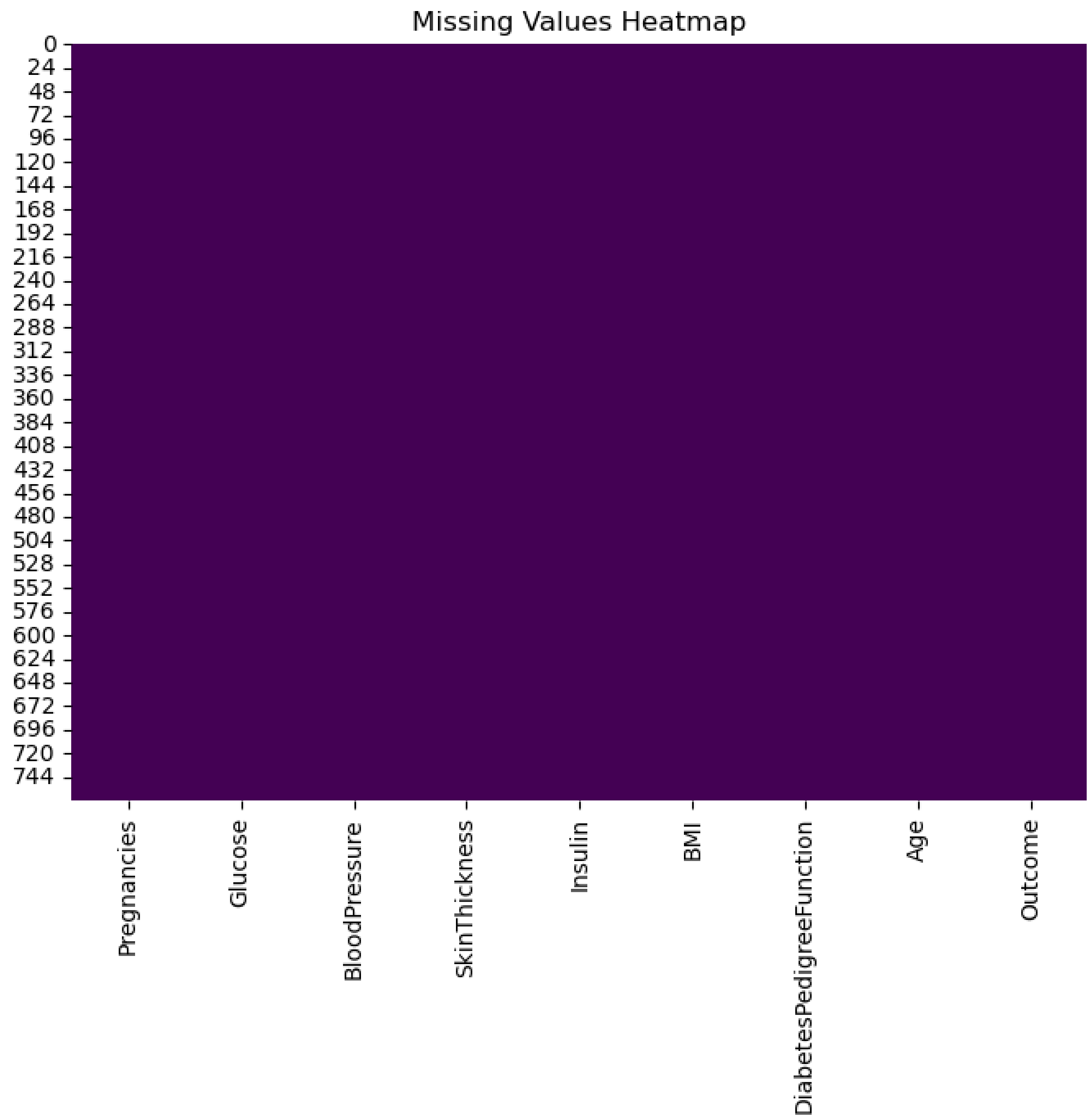
In [7]:
```
df.info()
```

```
<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
```

Heatmap to Check Missing Values in Dataset

In [8]:

```
plt.figure(figsize=(8, 6))
sns.heatmap(df.isnull(), cmap='viridis', cbar=False)
plt.title('Missing Values Heatmap')
plt.show()
```



We have verified that the dataset is free of any missing or null values.

Overall Statistics About The Dataset

In [9]:
```
df.describe()
```

Out[9]:

	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

Data Summary Report

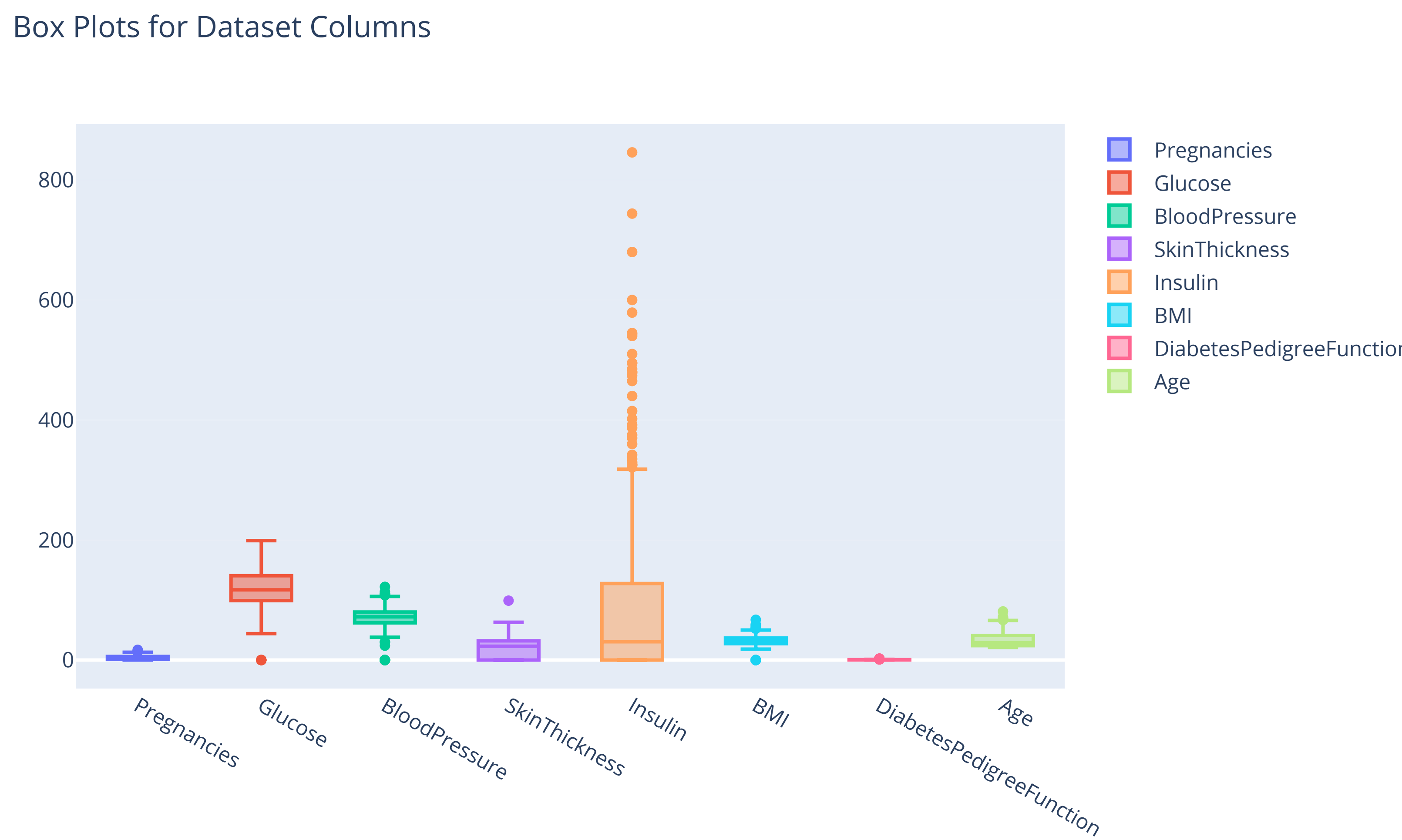
Features	Description
Pregnancies	Most data falls within the range of 1 to 6 pregnancies.
Glucose	Glucose levels are typically distributed between 99 to 140.
BloodPressure	Most values fall within the 62 to 80 range.
SkinThickness	A significant portion of the data has values between 0 and 32.
Insulin	A substantial portion of the data has low insulin values.
BMI	Most values fall in the range of 27.3 to 36.6.
DiabetesPedigreeFunction	The majority of values are below 0.626.
Age	Most of the data represents individuals between the ages of 24 and 41.
Outcome	The dataset appears to be imbalanced, with a lower number of positive outcomes (diabetes) compared to negative outcomes (no diabetes).

Checking Outliers

In [10]:

```
import plotly.graph_objs as go

# Create a list to store the box plot traces
box_traces = []

# Iterate through each column and create a box plot
for column in df.columns:
    if column != 'Outcome':  # Exclude 'Outcome' if it's the target variable
        trace = go.Box(y=df[column], name=column)
        box_traces.append(trace)

# Create a layout
layout = go.Layout(title='Box Plots for Dataset Columns')

# Create a figure and add the traces and layout
fig = go.Figure(data=box_traces, layout=layout)
```

```
# Show the figure
fig.show()
```



Outliers have been identified in our dataset.

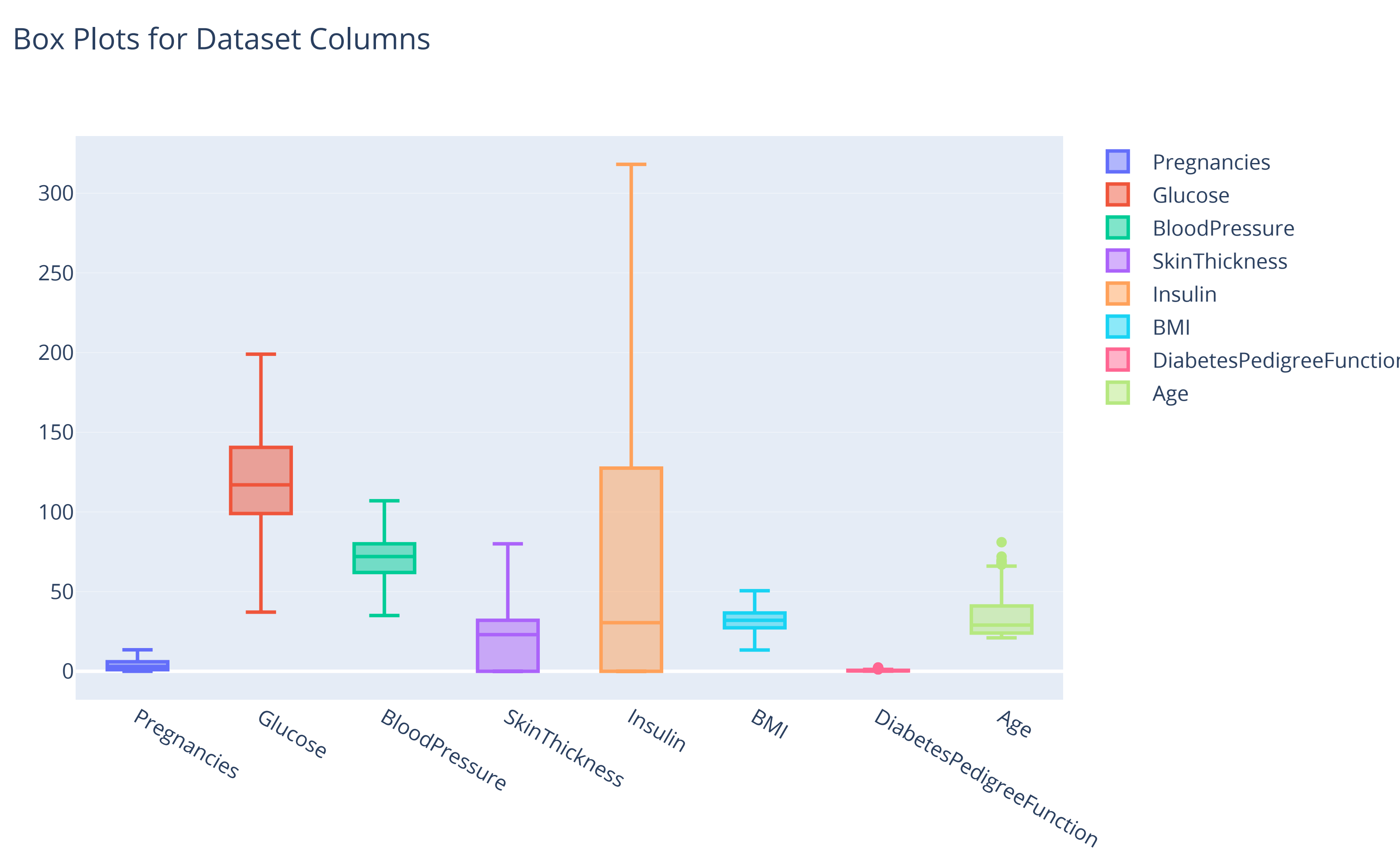
Managing Outliers in Dataset

In [11]:
```
#Create a function to handle Outliers
def remove_outliers(data, column_name):
    Q1 = data[column_name].quantile(0.25)
    Q3 = data[column_name].quantile(0.75)
    IQR = Q3 - Q1
    upper_limit = Q3 + 1.5 * IQR
    lower_limit = Q1 - 1.5 * IQR
    data[column_name] = data[column_name].clip(lower=lower_limit, upper=upper_limit)
    return data
```

In [12]:
```
#Handle outliers using "remove_outliers" function

df = remove_outliers(df, 'Pregnancies')
df = remove_outliers(df, 'Glucose')
df = remove_outliers(df, 'BloodPressure')
```

```python
df = remove_outliers(df, 'SkinThickness')
df = remove_outliers(df, 'Insulin')
df = remove_outliers(df, 'BMI')
```

In [13]:
```python
import plotly.graph_objs as go

# Create a list to store the box plot traces
box_traces = []

for column in df.columns:
    if column != 'Outcome':  # Exclude 'Outcome' if it's the target variable
        trace = go.Box(y=df[column], name=column)
        box_traces.append(trace)

# Create a layout
layout = go.Layout(title='Box Plots for Dataset Columns')

# Create a figure and add the traces and layout
fig = go.Figure(data=box_traces, layout=layout)

# Show the figure
fig.show()
```



After handling outliers , the datatype of some columns has changed to float. We also need to convert them back to int32.

In [14]:
```
df['Pregnancies']=round(df['Pregnancies'].astype('int32'))
df['Glucose']=round(df['Glucose'].astype('int32'))
df['Insulin']=round(df['Insulin'].astype('int32'))
```

In [15]:
```
df.info()
```

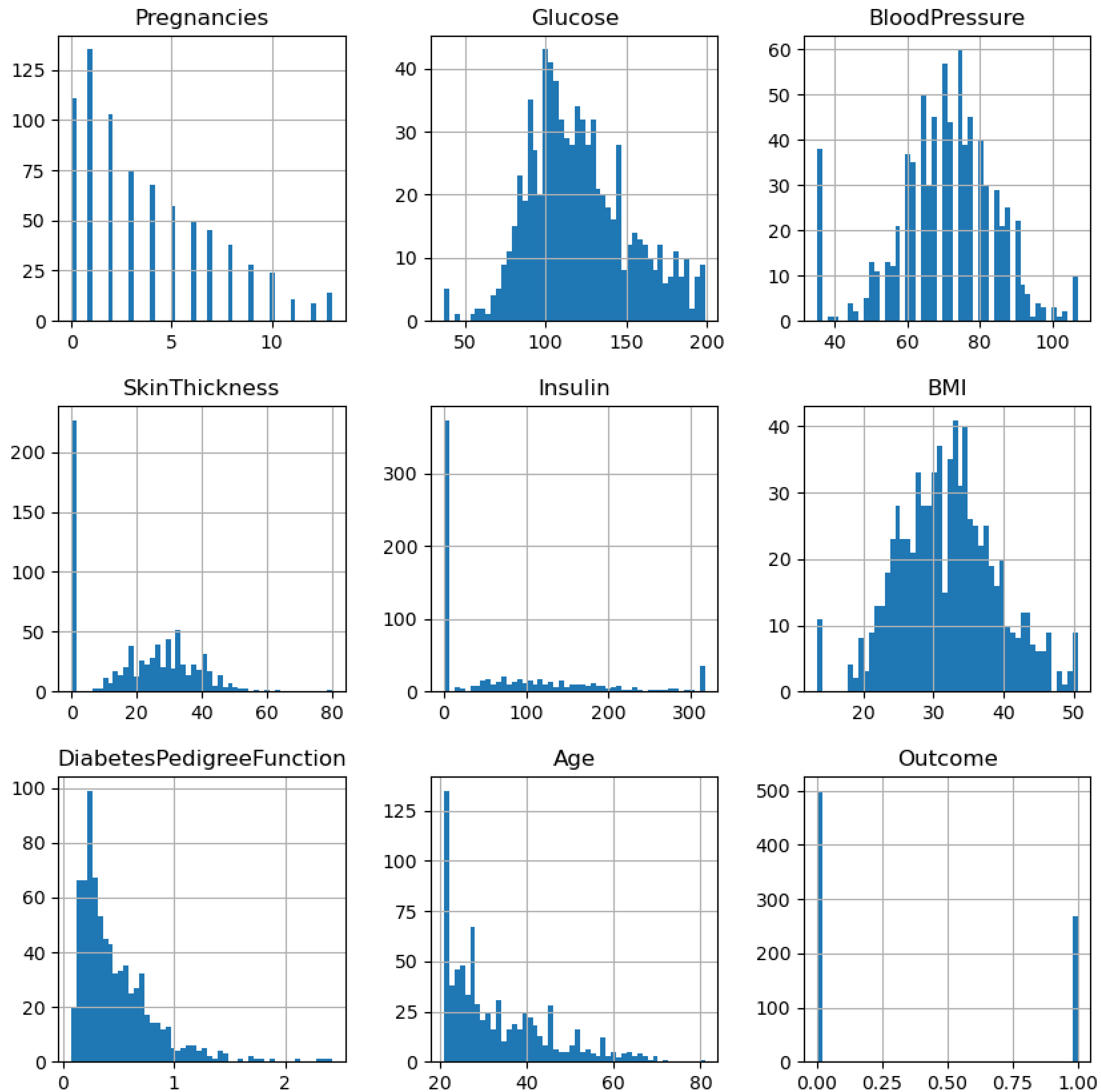
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int32  
 1   Glucose                   768 non-null    int32  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int32  
 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), int32(3), int64(4)
memory usage: 45.1 KB
```

Visualizing the Dataset for Better Understanding:

In [385…
```
df.columns
```

Out[385]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [16]:
```
import pandas as pd
import matplotlib.pyplot as plt

# Plot the histogram
fig, ax = plt.subplots(figsize=(10, 10))
df.hist(bins=50, ax=ax)

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



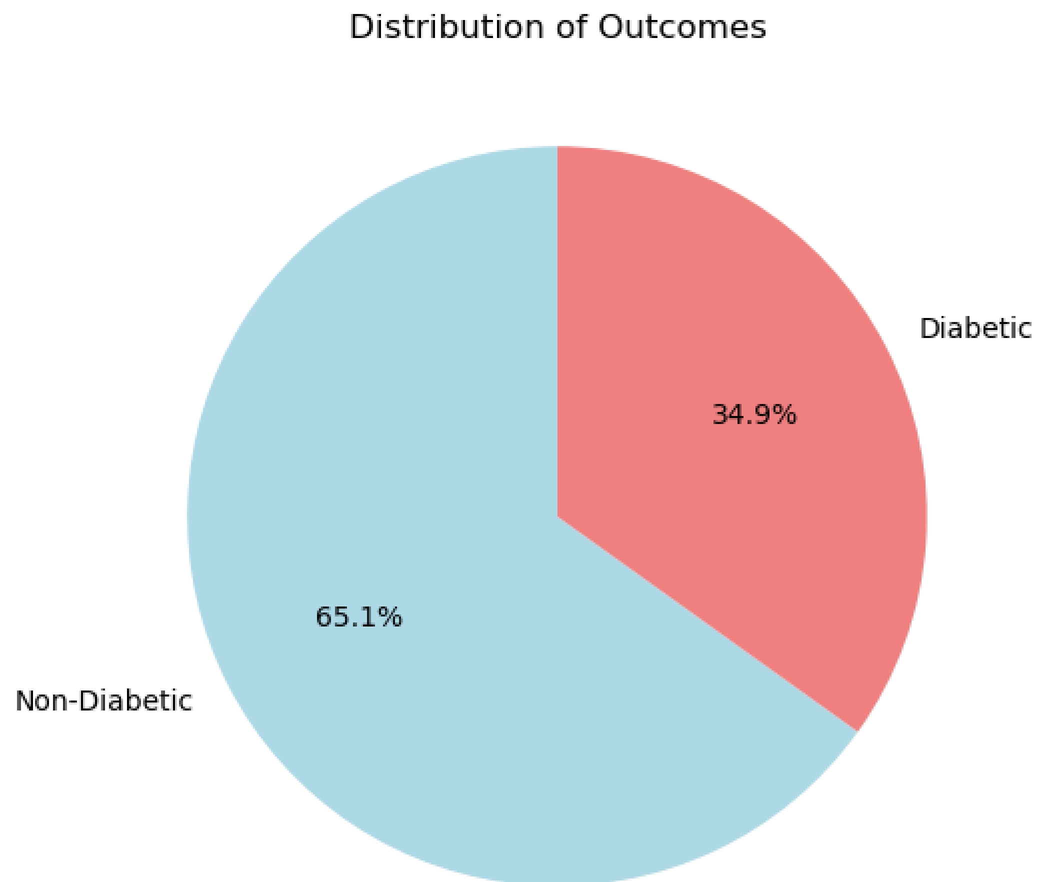
Observations:

Distributions are mostly skewed to the right

Small peaks at higher values for glucose, blood pressure, skin thickness, insulin, BMI, and diabetes pedigree function

Bimodal distribution for outcome variable (diabetes vs. no diabetes)

In [97]:
```
# Count the occurrences of each outcome value
outcome_counts = df['Outcome'].value_counts()

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

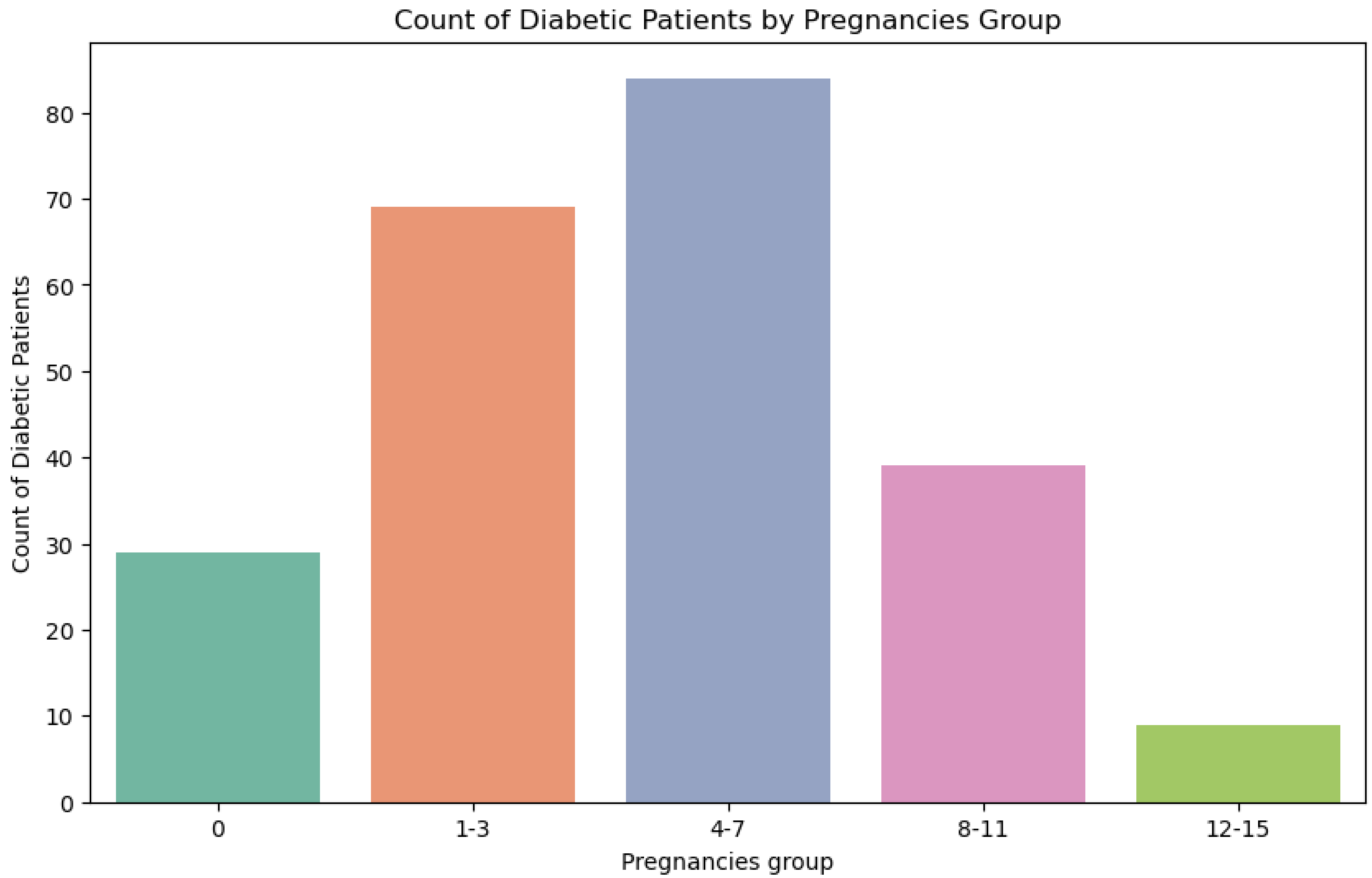


Converting Numerical Features into Categorical Features for Data Clarity:

Create bins for the 'Pregnancies' column

In [79]:
```
pregnancies_bins = [0, 1, 4, 8, 12, 16]
pregnancies_labels = ['0', '1-3', '4-7', '8-11', '12-15']
df['PregnanciesGroup'] = pd.cut(df['Pregnancies'], bins=pregnancies_bins, labels=pregnancies_labels)

# Filter the dataset to include only records with 'Outcome' equal to 1 (Diabetic patients)
diabetic_df = df[df['Outcome'] == 1]

# Create a bar chart for Diabetic patients with 'PregnanciesGroup' as the x-axis
plt.figure(figsize=(10, 6))
sns.countplot(data=diabetic_df, x='PregnanciesGroup', order=pregnancies_labels, palette="Set2")
plt.xlabel('Pregnancies group')
```

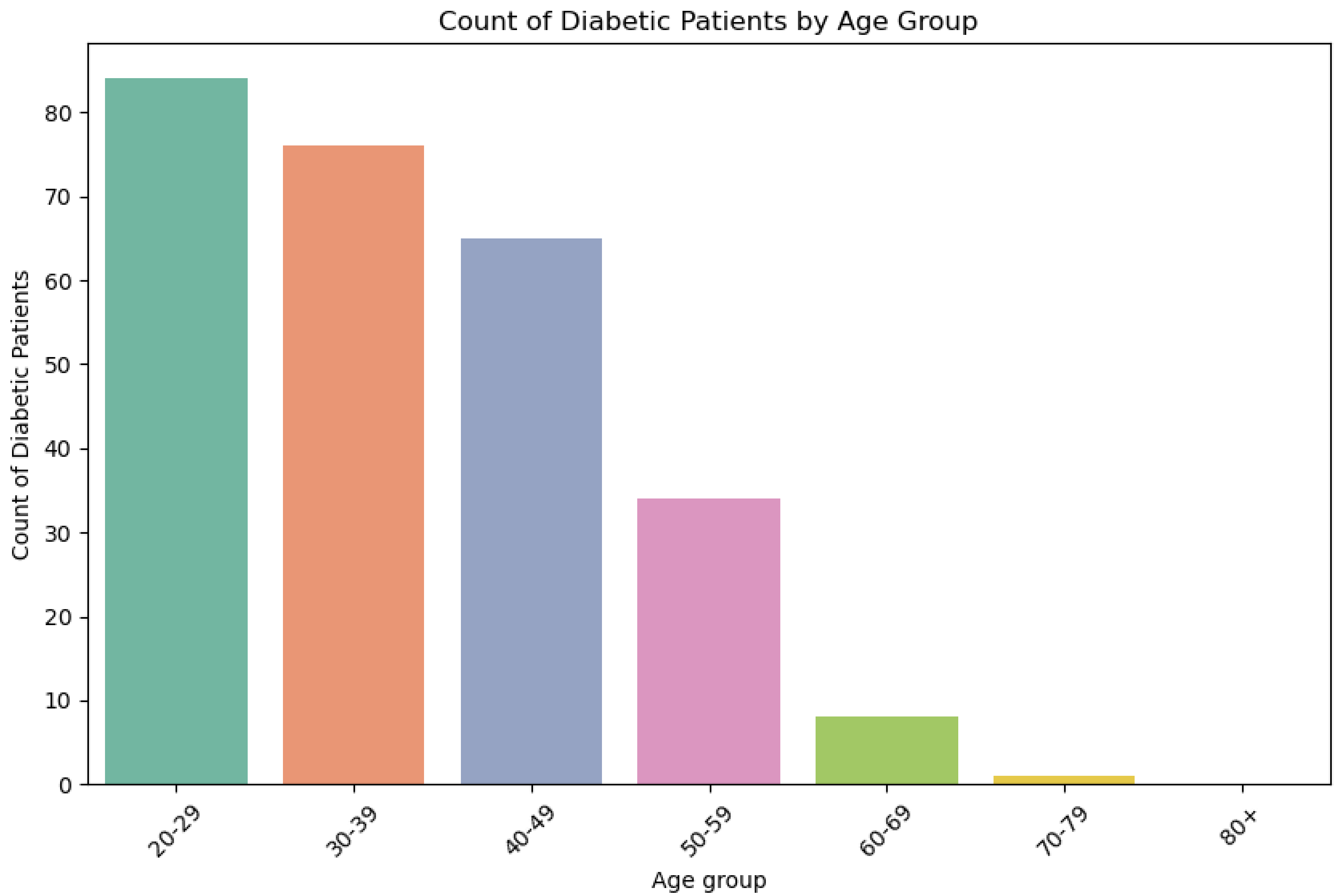
```
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Diabetic Patients by Pregnancies Group')
plt.show()
```



Create age groups based on the 'Age' column

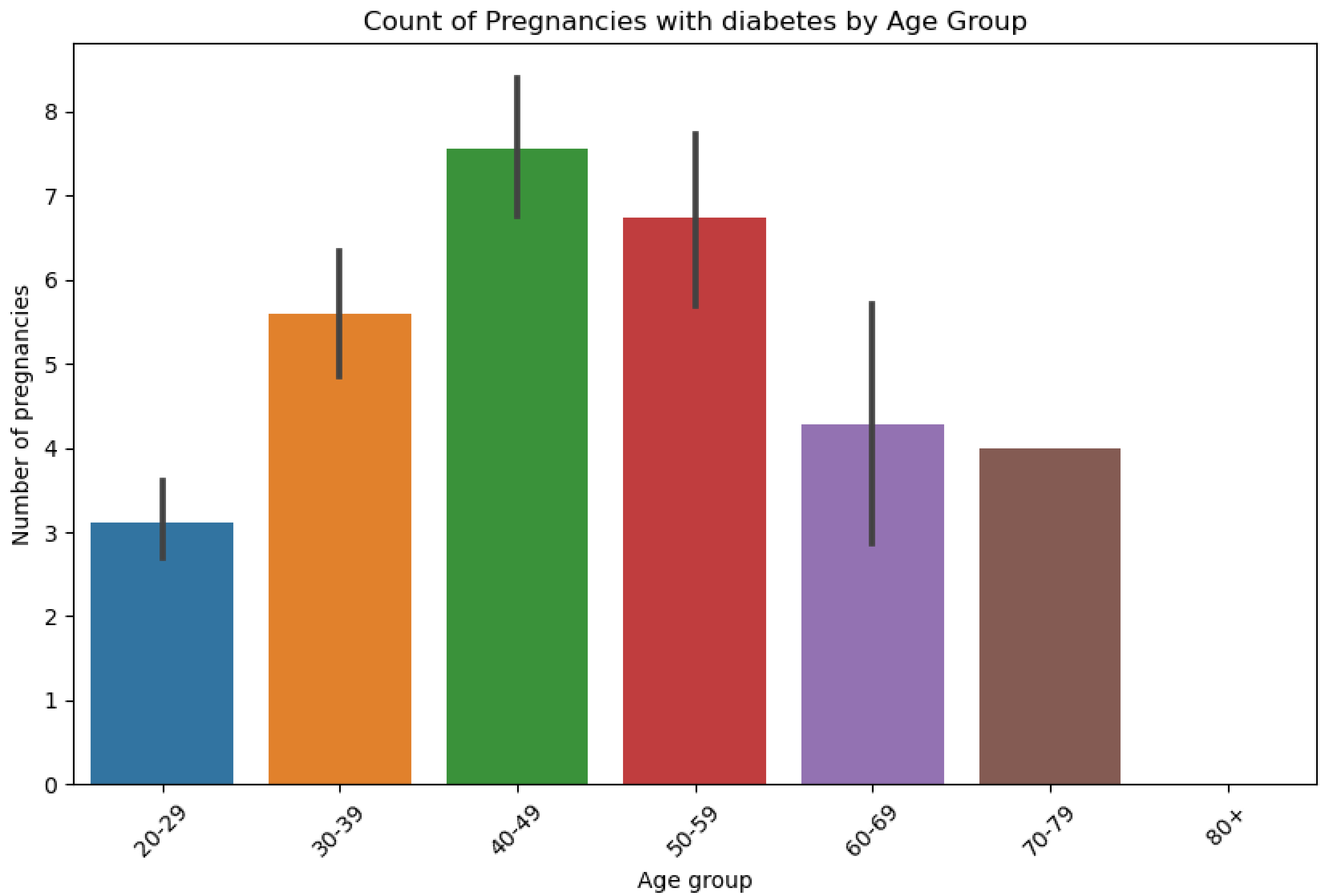
In [70]:
```
bins = [20, 30, 40, 50, 60, 70, 80, 200]
labels = ['20-29', '30-39', '40-49', '50-59', '60-69', '70-79', '80+']
df['AgeGroup'] = pd.cut(df['Age'], bins=bins, labels=labels, right=False)
```

In [80]:
```
# Filter the dataset to include only records with 'Outcome' equal to 1 (Diabetic patients)
diabetic_df = df[df['Outcome'] == 1]

# Create a bar chart for Diabetic patients with age groups
plt.figure(figsize=(10, 6))
sns.countplot(data=diabetic_df, x='AgeGroup', order=labels, palette="Set2")
plt.xlabel('Age group')
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Diabetic Patients by Age Group')
plt.xticks(rotation=45)
plt.show()
```



In [77]:

```
new_df = df[(df['Outcome'] == 1) & (df['Pregnancies'] > 0)]
# Create a bar chart with 'Outcome' as hue
plt.figure(figsize=(10, 6))
ax = sns.barplot(data=new_df, x='AgeGroup', y='Pregnancies')
plt.xlabel('Age group')
plt.ylabel('Number of pregnancies')
plt.title('Count of Pregnancies with diabetes by Age Group')
plt.xticks(rotation=45)


plt.show()
```



Define the bins and labels for 'BloodPressure'

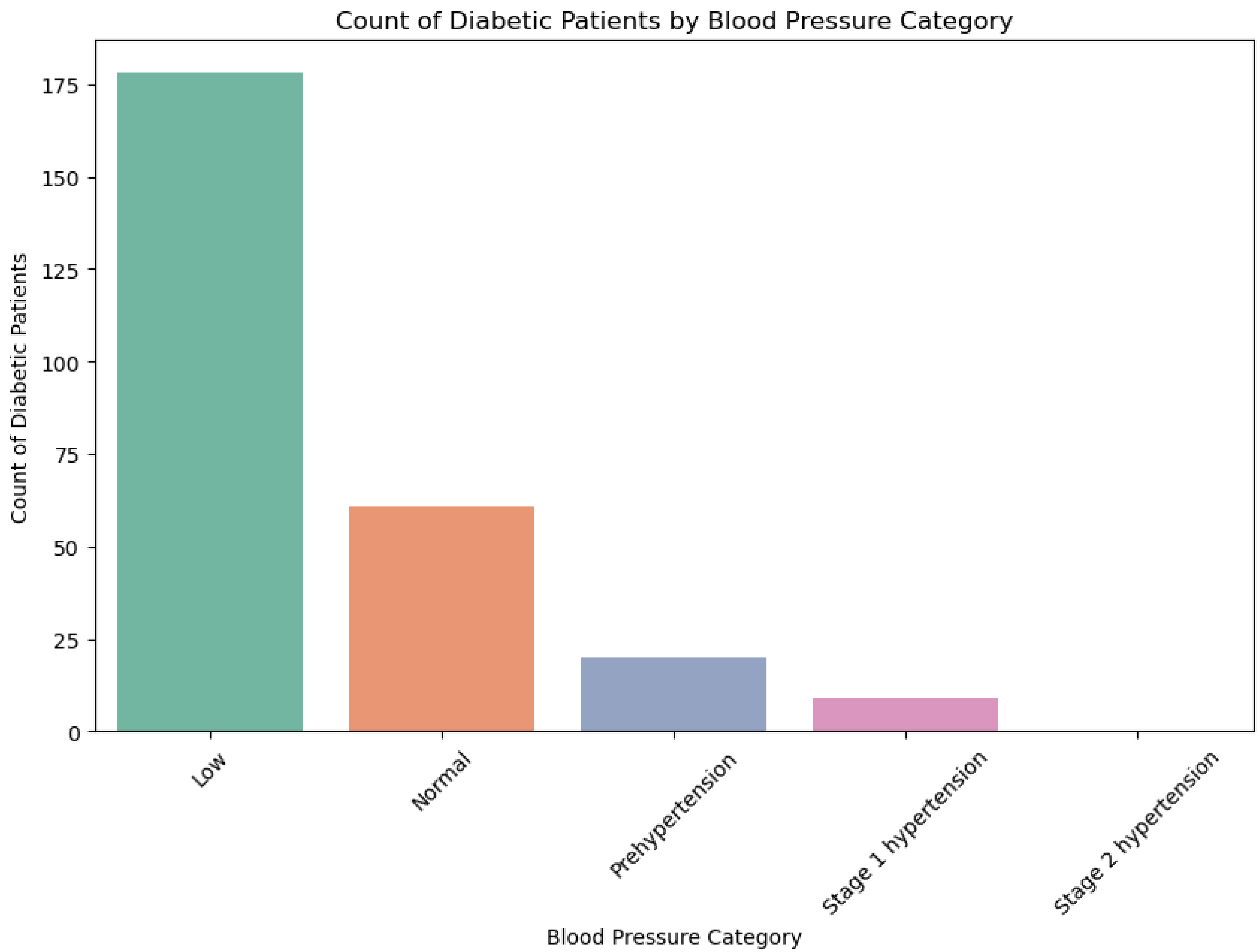
In [81]:

```
# Define the bins and labels for 'BloodPressure'
blood_pressure_bins = [0, 80, 89, 99, 119, 1000]  # Adjust the boundaries as needed
blood_pressure_labels = ['Low', 'Normal', 'Prehypertension', 'Stage 1 hypertension', 'Stage 2 hypertension']

# Create a new column 'BloodPressureCategory' based on the bins and labels
df['BloodPressureCategory'] = pd.cut(df['BloodPressure'], bins=blood_pressure_bins, labels=blood_pressure_labels,right=False)

df.head()
```

Out[81]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome	AgeGroup	PregnanciesGroup	BloodPressureCategory
0	6	148	72	35	0	33.6	0.627	50	1	50-59	4-7	Low
1	1	85	66	29	0	26.6	0.351	31	0	30-39	0	Low
2	8	183	64	0	0	23.3	0.672	32	1	30-39	4-7	Low
3	1	89	66	23	94	28.1	0.167	21	0	20-29	0	Low
4	0	137	40	35	168	43.1	2.288	33	1	30-39	NaN	Low

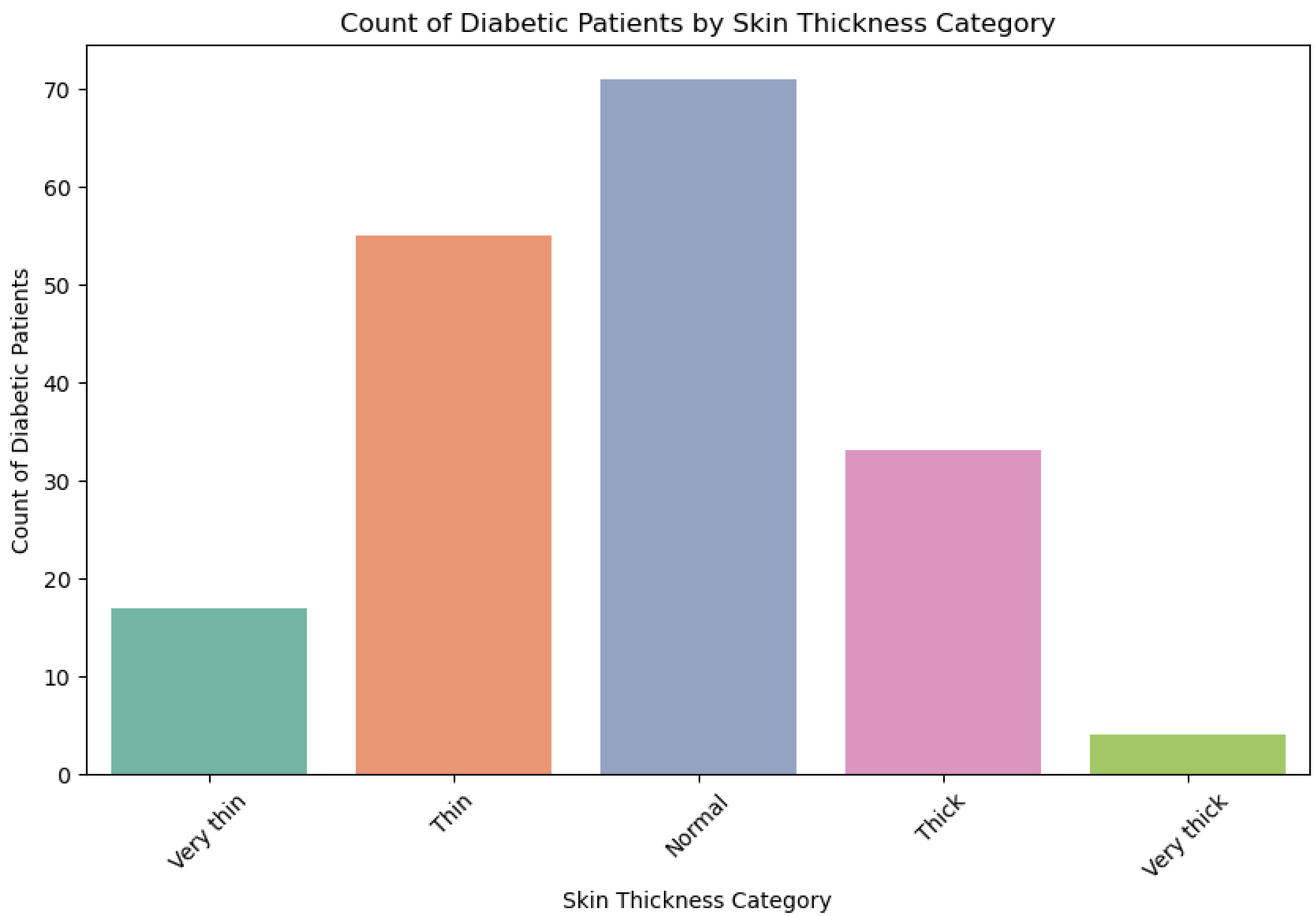
In [82]:
```
# Filter the dataset to include only records with 'Outcome' equal to 1 (Diabetic patients)
diabetic_df = df[df['Outcome'] == 1]

# Create a bar chart for Diabetic patients with 'BloodPressureCategory' as the x-axis
plt.figure(figsize=(10, 6))
sns.countplot(data=diabetic_df, x='BloodPressureCategory', order=blood_pressure_labels, palette="Set2")
plt.xlabel('Blood Pressure Category')
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Diabetic Patients by Blood Pressure Category')
plt.xticks(rotation=45)
plt.show()
```



Define the bins and labels for 'SkinThickness'

In [84]:
```
skin_thickness_bins = [0, 20, 30, 40, 50, 100]
skin_thickness_labels = ['Very thin', 'Thin', 'Normal', 'Thick', 'Very thick']
```

```python
# Create a new column 'SkinThicknessCategory' based on the bins and labels
df['SkinThicknessCategory'] = pd.cut(df['SkinThickness'], bins=skin_thickness_bins, labels=skin_thickness_labels)

# Filter the dataset to include only records with 'Outcome' equal to 1 (Diabetic patients)
diabetic_df = df[df['Outcome'] == 1]

# Create a bar chart for Diabetic patients with 'SkinThicknessCategory' as the x-axis
plt.figure(figsize=(10, 6))
sns.countplot(data=diabetic_df, x='SkinThicknessCategory', order=skin_thickness_labels, palette="Set2")
plt.xlabel('Skin Thickness Category')
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Diabetic Patients by Skin Thickness Category')
plt.xticks(rotation=45)
plt.show()
```

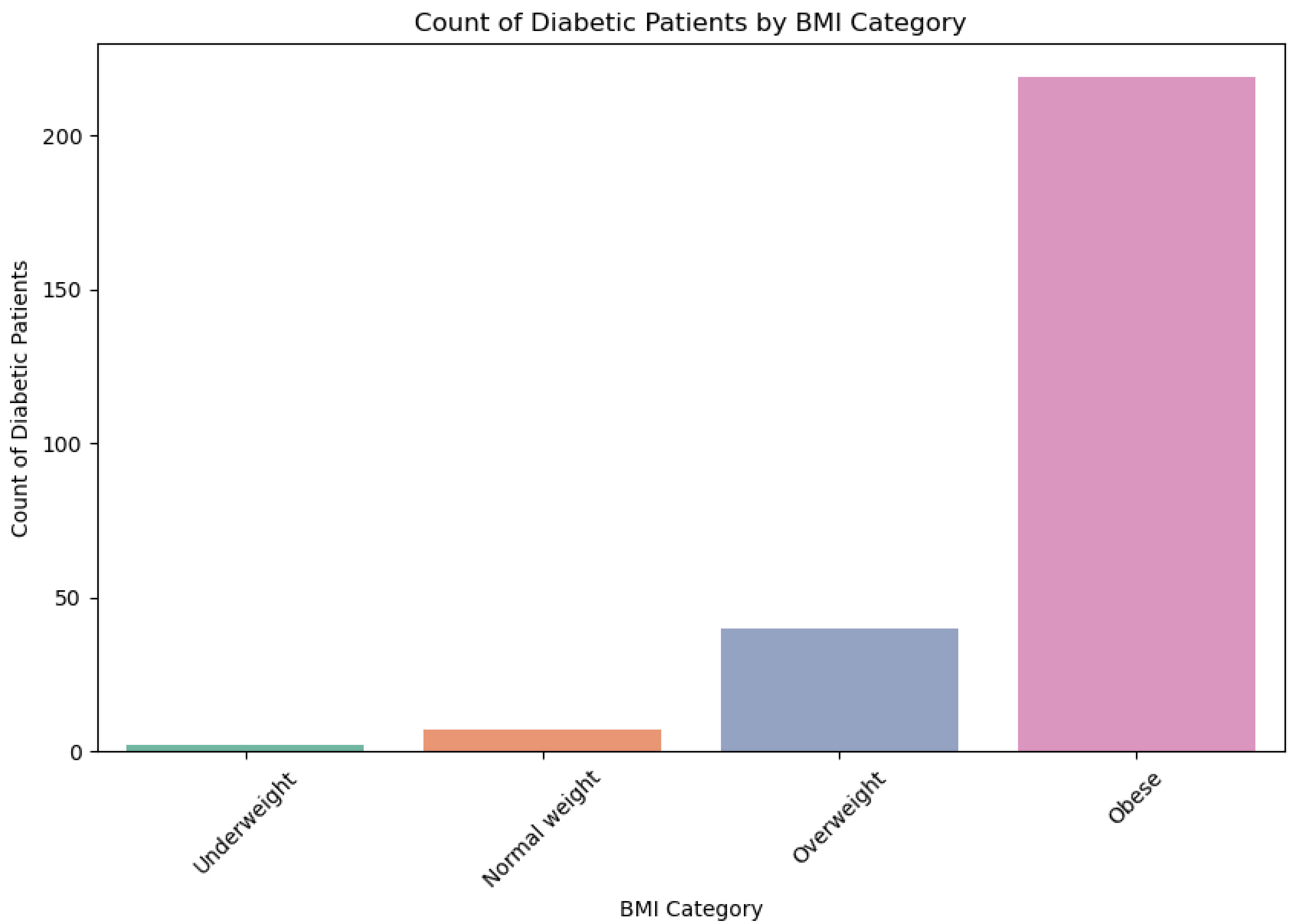


Define the custom bins and labels for 'BMI'

In [85]:

```python
# Define the custom bins and labels for 'BMI'
bmi_bins = [0, 18.5, 24.9, 29.9, 1000]
bmi_labels = ['Underweight', 'Normal weight', 'Overweight', 'Obese']

# Create a new column 'BMICategory' based on the custom bins and labels
```

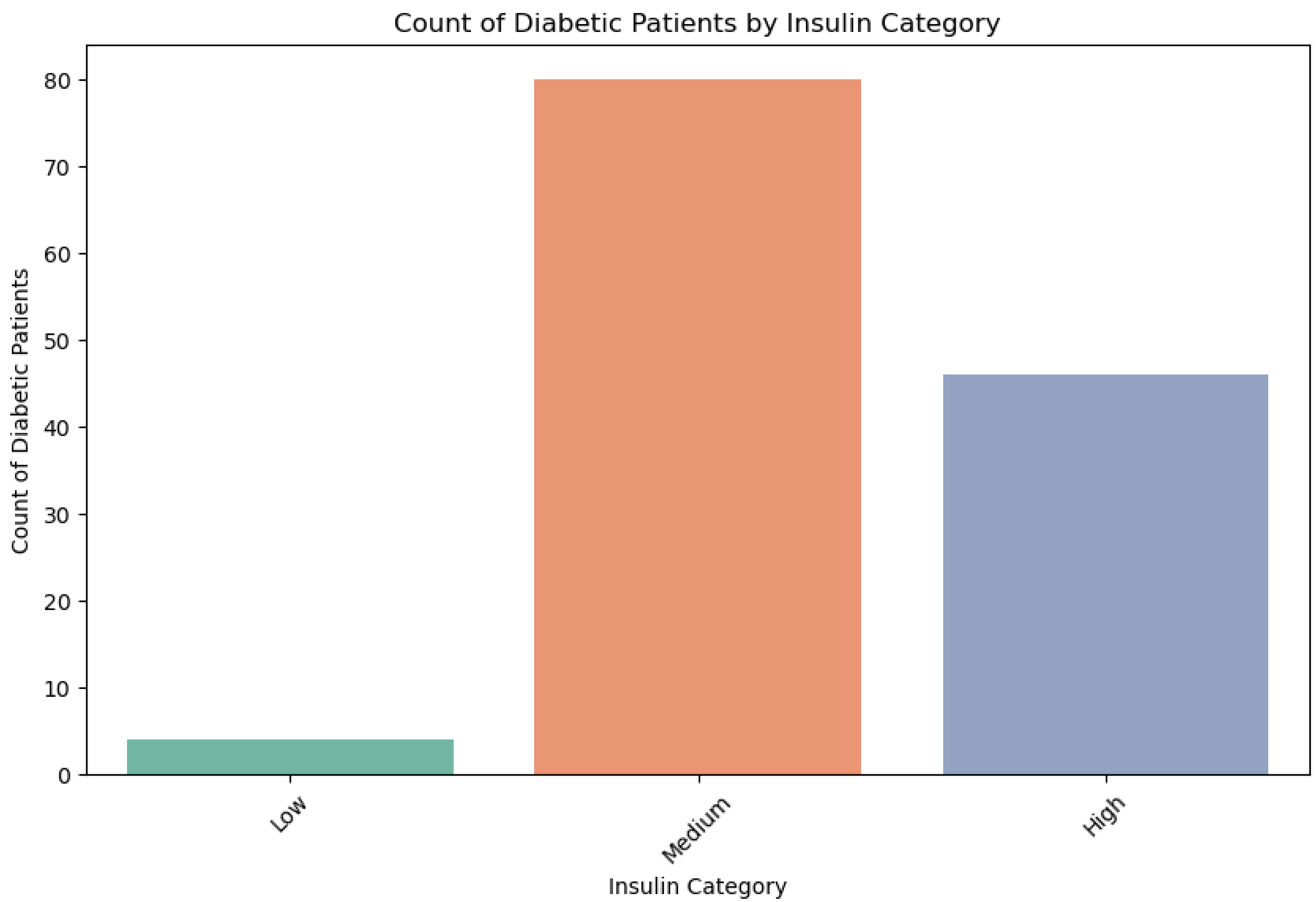
```
df['BMICategory'] = pd.cut(df['BMI'], bins=bmi_bins, labels=bmi_labels)

# Filter the dataset to include only records with 'Outcome' equal to 1 (Diabetic patients)
diabetic_df = df[df['Outcome'] == 1]

# Create a bar chart for Diabetic patients with 'BMICategory' as the x-axis
plt.figure(figsize=(10, 6))
sns.countplot(data=diabetic_df, x='BMICategory', order=bmi_labels, palette="Set2")
plt.xlabel('BMI Category')
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Diabetic Patients by BMI Category')
plt.xticks(rotation=45)
plt.show()
```



Define the custom bins and labels for 'Insulin'

In [86]:
```
insulin_bins = [0, 50, 200, 10000]
insulin_labels = ['Low', 'Medium', 'High']

# Create a new column 'InsulinCategory' based on the custom bins and labels
```

```python
df['InsulinCategory'] = pd.cut(df['Insulin'], bins=insulin_bins, labels=insulin_labels)

# Filter the dataset to include only records with 'Outcome' equal to 1 (Diabetic patients)
diabetic_df = df[df['Outcome'] == 1]

# Create a bar chart for Diabetic patients with 'InsulinCategory' as the x-axis
plt.figure(figsize=(10, 6))
sns.countplot(data=diabetic_df, x='InsulinCategory', order=insulin_labels, palette="Set2")
plt.xlabel('Insulin Category')
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Diabetic Patients by Insulin Category')
plt.xticks(rotation=45)
plt.show()
```

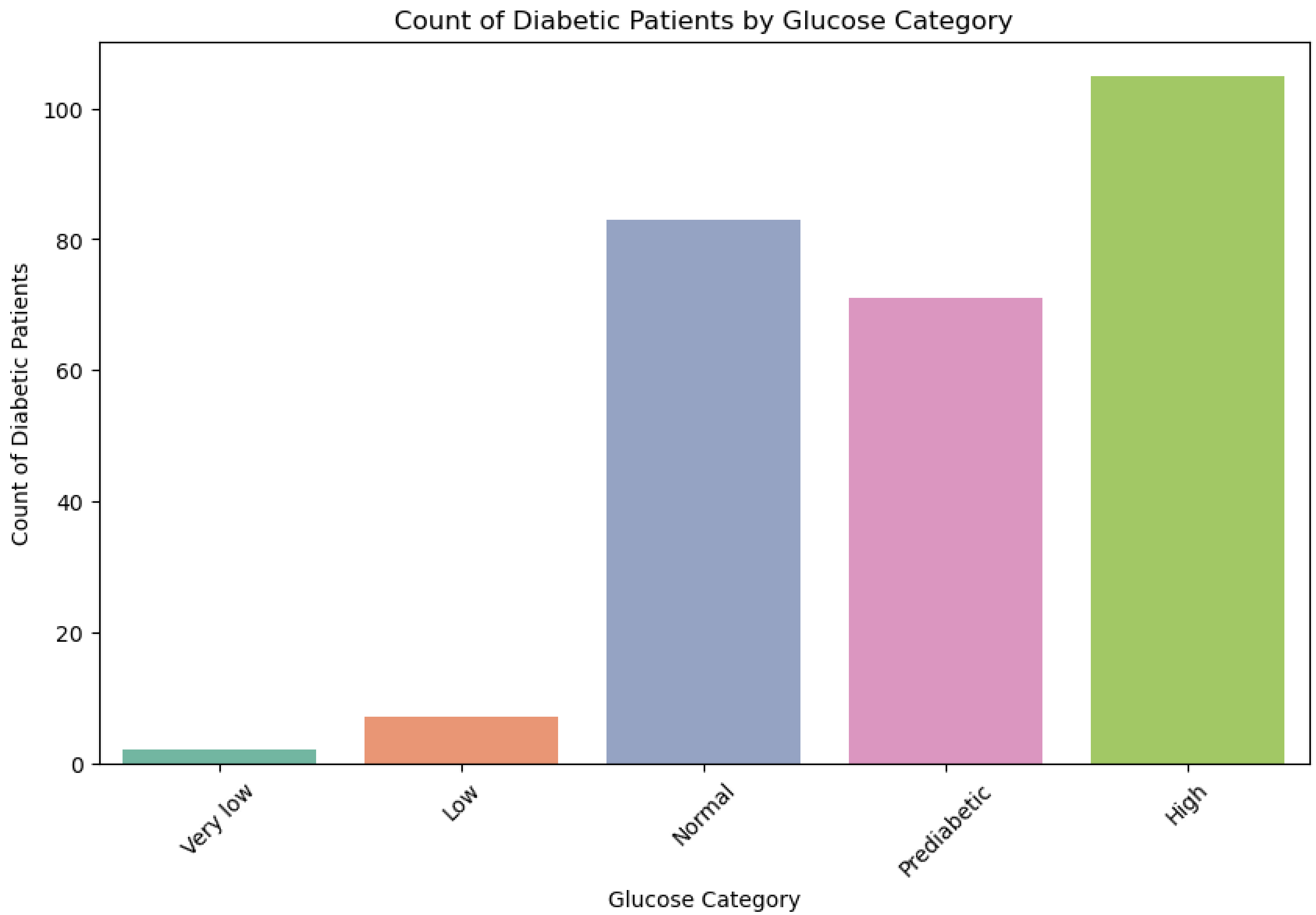


Define the custom bins and labels for 'Glucose'

In [88]:

```python
glucose_bins = [0, 75, 90, 125, 150, 1000]  # Adjust the boundaries as needed
glucose_labels = ['Very low', 'Low', 'Normal', 'Prediabetic', 'High']

# Create a new column 'GlucoseCategory' based on the custom bins and labels
df['GlucoseCategory'] = pd.cut(df['Glucose'], bins=glucose_bins, labels=glucose_labels)
```

```python
# Filter the dataset to include only records with 'Outcome' equal to 1 (Diabetic patients)
diabetic_df = df[df['Outcome'] == 1]

# Create a bar chart for Diabetic patients with 'GlucoseCategory' as the x-axis
plt.figure(figsize=(10, 6))
sns.countplot(data=diabetic_df, x='GlucoseCategory', order=glucose_labels, palette="Set2")
plt.xlabel('Glucose Category')
plt.ylabel('Count of Diabetic Patients')
plt.title('Count of Diabetic Patients by Glucose Category')
plt.xticks(rotation=45)
plt.show()
```



Data Wrangling:

Seprate Independent Variable(X) and Dependent Variable(y)

In [90]:

```python
df.columns
```

Out[90]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome', 'AgeGroup',
       'PregnanciesGroup', 'BloodPressureCategory', 'SkinThicknessCategory',
       'BMICategory', 'InsulinCategory', 'GlucoseCategory'],
      dtype='object')
```

In [18]:
```
#Independent Variables
X = df[['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age']]
#Target variable
y = df['Outcome']
```

In [95]:
```
X.head()
```

Out[95]:

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

In [96]:
```
y.head()
```

Out[96]:
```
0    1
1    0
2    1
3    0
4    1
Name: Outcome, dtype: int64
```

Split the data into training and testing sets

In [20]:
```
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.2,random_state=2)
```

Feature Scaling

In [21]:
```
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

In [22]:
```
X_train
```

Out[22]:
```
array([[-0.86394553,  0.06032628,  0.23252153, ..., -0.59426762,
        -1.10316947, -0.27704152],
       [-0.86394553, -0.86888624,  0.79598761, ...,  0.43404704,
        -0.71238555,  0.84376203],
       [-1.16313479, -0.90092805, -0.04921151, ...,  1.64802962,
        -0.37742791, -1.05298243],
       ...,
       [ 0.03362225,  0.09236809, -0.04921151, ..., -0.43716399,
         1.96433735,  1.01619334],
       [-0.26556701, -0.19600821,  0.23252153, ..., -0.80849984,
        -1.08260189, -0.79433546],
       [ 0.03362225, -0.38825908, -0.33094455, ..., -0.00869955,
        -0.01308802, -0.36325717]])
```

Train a Modal

SVM:

In [24]:
```python
sv_model = SVC(C= 0.1,kernel='linear',random_state=15)
sv_model.fit(X_train,y_train)

#Prediction on Traing Data
sv_pred_train = sv_model.predict(X_train)
#Prediction on Test Data
sv_pred_test = sv_model.predict(X_test)


#Evaluation
SVM_Train_Accuracy = accuracy_score(y_train,sv_pred_train)*100
SVM_Test_Accuracy = accuracy_score(y_test,sv_pred_test)*100
SVM_CV = cross_val_score(sv_model,X_test,y_test,cv=5,scoring="accuracy").mean()*100


print(f"Train Accuracy: {SVM_Train_Accuracy:.2f}%")
print(f"Test Accuracy: {SVM_Test_Accuracy:.2f}%")
print(f"cross Validataion Score: {SVM_CV:.2f}%")
```

```
Train Accuracy: 76.55%
Test Accuracy: 76.62%
cross Validataion Score: 74.69%
```

LogisticRegression

In [27]:
```python
logistic = LogisticRegression(C=100,penalty='l1',solver='liblinear',random_state=16)
logistic.fit(X_train,y_train)


#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 = accuracy_score(y_train,log_pred_train)*100
log_Test_Accuracy = accuracy_score(y_test,log_pred_test)*100
Log_CV = cross_val_score(logistic,X_test,y_test,cv=5,scoring="accuracy").mean()*100
```

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

```
Train Accuracy: 77.20%
Test Accuracy: 77.27%
cross Validataion Score: 75.94%
```

Conclusion

After evaluating the performance metrics of the models, specifically Support Vector Machine and Logistic Regression, and keeping in mind the objective of maximizing the accuracy in predicting Diabetic Patients, the **Logistic Regression** model stands out as the most suitable choice.

As a result, we recommend using Logistic Regression for predicting Diabetic Patients based on the available data and the assessed evaluation metrics.

Developing a Prediction System

In [98]:

```
input_data = (2,174,88,37,120,44.5,0.646,24)

# 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)

# standardize the input data
std_data = scaler.transform(input_data_reshaped)

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

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

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

Graphical User Interface

In [78]:

```
import tkinter as tk
from tkinter import Label, Entry, Button

# Function to make predictions
def predict():
    input_data = [
        pregnancies_entry.get(),
        glucose_entry.get(),
        blood_pressure_entry.get(),
        skin_thickness_entry.get(),
```

```python
        insulin_entry.get(),
        bmi_entry.get(),
        pedigree_function_entry.get(),
        age_entry.get()
    ]

    # Convert input_data to a NumPy array and standardize it
    input_data_as_numpy_array = np.asarray(input_data, dtype=float).reshape(1, -1)
    std_input_data = scaler.transform(input_data_as_numpy_array)

    # Make the prediction using sv_model
    prediction = logistic.predict(std_input_data)

    # Interpret the prediction
    result = 'diabetic' if prediction[0] == 1 else 'not diabetic'
    result_label.config(text=f'Prediction: {result}')

# Create the main window
root = tk.Tk()
root.title("Diabetes Prediction")

# Create labels and entry fields for input features
Label(root, text="Pregnancies").grid(row=0, column=0)
pregnancies_entry = Entry(root)
pregnancies_entry.grid(row=0, column=1)

Label(root, text="Glucose").grid(row=1, column=0)
glucose_entry = Entry(root)
glucose_entry.grid(row=1, column=1)

Label(root, text="Blood Pressure").grid(row=2, column=0)
blood_pressure_entry = Entry(root)
blood_pressure_entry.grid(row=2, column=1)

Label(root, text="Skin Thickness").grid(row=3, column=0)
skin_thickness_entry = Entry(root)
skin_thickness_entry.grid(row=3, column=1)

Label(root, text="Insulin").grid(row=4, column=0)
insulin_entry = Entry(root)
insulin_entry.grid(row=4, column=1)

Label(root, text="BMI").grid(row=5, column=0)
bmi_entry = Entry(root)
bmi_entry.grid(row=5, column=1)

Label(root, text="Diabetes Pedigree Function").grid(row=6, column=0)
pedigree_function_entry = Entry(root)
pedigree_function_entry.grid(row=6, column=1)

Label(root, text="Age").grid(row=7, column=0)
age_entry = Entry(root)
age_entry.grid(row=7, column=1)


# Create a button to make predictions
predict_button = Button(root, text="Predict", command=predict)
predict_button.grid(row=8, columnspan=2)

# Create a label to display predictions
```

```
result_label = Label(root, text="Prediction: ")
result_label.grid(row=9, columnspan=2)

# Start the main loop
root.mainloop()
```