```
!pip install pandas matplotlib seaborn markdown2 weasyprint
```

```
Requirement already satisfied: pandas in /usr/local/lib/python3.11/dist-packages (2.2.2)
Requirement already satisfied: matplotlib in /usr/local/lib/python3.11/dist-packages (3.10.0)
Requirement already satisfied: seaborn in /usr/local/lib/python3.11/dist-packages (0.13.2)
Collecting markdown2
  Downloading markdown2-2.5.3-py3-none-any.whl.metadata (2.1 kB)
Collecting weasyprint
  Downloading weasyprint-64.1-py3-none-any.whl.metadata (3.7 kB)
Requirement already satisfied: numpy>=1.23.2 in /usr/local/lib/python3.11/dist-packages (from pandas) (1.26.4)
Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/python3.11/dist-packages (from pandas) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.11/dist-packages (from pandas) (2025.1)
Requirement already satisfied: tzdata>=2022.7 in /usr/local/lib/python3.11/dist-packages (from pandas) (2025.1)
Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.11/dist-packages (from matplotlib) (1.3.1)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.11/dist-packages (from matplotlib) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.11/dist-packages (from matplotlib) (4.56.0)
Requirement already satisfied: kiwisolver>=1.3.1 in /usr/local/lib/python3.11/dist-packages (from matplotlib) (1.4.8)
Requirement already satisfied: packaging>=20.0 in /usr/local/lib/python3.11/dist-packages (from matplotlib) (24.2)
Requirement already satisfied: pillow>=8 in /usr/local/lib/python3.11/dist-packages (from matplotlib) (11.1.0)
Requirement already satisfied: pyparsing>=2.3.1 in /usr/local/lib/python3.11/dist-packages (from matplotlib) (3.2.1)
Collecting pydyf>=0.11.0 (from weasyprint)
  Downloading pydyf-0.11.0-py3-none-any.whl.metadata (2.5 kB)
Requirement already satisfied: cffi>=0.6 in /usr/local/lib/python3.11/dist-packages (from weasyprint) (1.17.1)
Collecting tinyhtml5>=2.0.0b1 (from weasyprint)
  Downloading tinyhtml5-2.0.0-py3-none-any.whl.metadata (2.9 kB)
Requirement already satisfied: tinycss2>=1.4.0 in /usr/local/lib/python3.11/dist-packages (from weasyprint) (1.4.0)
Collecting cssselect2>=0.1 (from weasyprint)
  Downloading cssselect2-0.7.0-py3-none-any.whl.metadata (2.9 kB)
Collecting Pyphen>=0.9.1 (from weasyprint)
  Downloading pyphen-0.17.2-py3-none-any.whl.metadata (3.2 kB)
Requirement already satisfied: pycparser in /usr/local/lib/python3.11/dist-packages (from cffi>=0.6->weasyprint) (2.22)
Requirement already satisfied: webencodings in /usr/local/lib/python3.11/dist-packages (from cssselect2>=0.1->weasyprint) (0.5.1)
Collecting brotli>=1.0.1 (from fonttools[woff]>=4.0.0->weasyprint)
  Downloading Brotli-1.1.0-cp311-cp311-manylinux_2_17_x86_64.manylinux2014_x86_64.whl.metadata (5.5 kB)
Collecting zopfli>=0.1.4 (from fonttools[woff]>=4.0.0->weasyprint)
  Downloading zopfli-0.2.3.post1-cp311-cp311-manylinux_2_17_x86_64.manylinux2014_x86_64.whl.metadata (2.9 kB)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.11/dist-packages (from python-dateutil>=2.8.2->pandas) (1.17.0)
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Downloading weasyprint-64.1-py3-none-any.whl (302 kB)
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Downloading cssselect2-0.7.0-py3-none-any.whl (15 kB)
Downloading pydyf-0.11.0-py3-none-any.whl (8.1 kB)
Downloading pyphen-0.17.2-py3-none-any.whl (2.1 MB)
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Downloading tinyhtml5-2.0.0-py3-none-any.whl (39 kB)
Downloading Brotli-1.1.0-cp311-cp311-manylinux_2_17_x86_64.manylinux2014_x86_64.whl (2.9 MB)
   ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 2.9/2.9 MB 22.5 MB/s eta 0:00:00
Downloading zopfli-0.2.3.post1-cp311-cp311-manylinux_2_17_x86_64.manylinux2014_x86_64.whl (850 kB)
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Installing collected packages: brotli, zopfli, tinyhtml5, Pyphen, pydyf, markdown2, cssselect2, weasyprint
Successfully installed Pyphen-0.17.2 brotli-1.1.0 cssselect2-0.7.0 markdown2-2.5.3 pydyf-0.11.0 tinyhtml5-2.0.0 weasyprint-64.1 zopfli-0
```

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import markdown2
import weasyprint
```

```
from google.colab import files
uploaded = files.upload()
```

```
Choose Files No file chosen    Upload widget is only available when the cell has been executed in the current browser session. Please rerun this cell to enable.
```

```
#import pandas as pd
```

```
df = pd.read_csv("diabetes_prediction_dataset.csv")
```

```
df.info()
df.head()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 100000 entries, 0 to 99999
Data columns (total 9 columns):
 #   Column               Non-Null Count   Dtype  
---  ------               --------------   -----  
 0   gender               100000 non-null  object 
 1   age                  100000 non-null  float64
 2   hypertension         100000 non-null  int64  
 3   heart_disease        100000 non-null  int64  
 4   smoking_history      100000 non-null  object 
 5   bmi                  100000 non-null  float64
 6   HbA1c_level          100000 non-null  float64
 7   blood_glucose_level  100000 non-null  int64  
 8   diabetes             100000 non-null  int64  
dtypes: float64(3), int64(4), object(2)
memory usage: 6.9+ MB
```

	gender	age	hypertension	heart_disease	smoking_history	bmi	HbA1c_level	blood_glucose_level	diabetes
0	Female	80.0	0	1	never	25.19	6.6	140	0
1	Female	54.0	0	0	No Info	27.32	6.6	80	0
2	Male	28.0	0	0	never	27.32	5.7	158	0
3	Female	36.0	0	0	current	23.45	5.0	155	0
4	Male	76.0	1	1	current	20.14	4.8	155	0

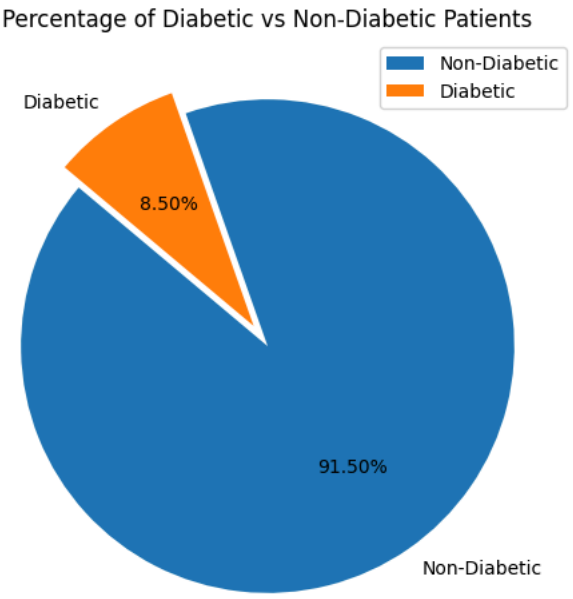
```
print(df.isnull().sum())
```

```
gender                 0
age                    0
hypertension           0
heart_disease          0
smoking_history        0
bmi                    0
HbA1c_level            0
blood_glucose_level    0
diabetes               0
dtype: int64
```

```
display(df.describe())
```

	age	hypertension	heart_disease	bmi	HbA1c_level	blood_glucose_level	diabetes
count	100000.000000	100000.00000	100000.000000	100000.000000	100000.000000	100000.000000	100000.000000
mean	41.885856	0.07485	0.039420	27.320767	5.527507	138.058060	0.085000
std	22.516840	0.26315	0.194593	6.636783	1.070672	40.708136	0.278883
min	0.080000	0.00000	0.000000	10.010000	3.500000	80.000000	0.000000
25%	24.000000	0.00000	0.000000	23.630000	4.800000	100.000000	0.000000
50%	43.000000	0.00000	0.000000	27.320000	5.800000	140.000000	0.000000
75%	60.000000	0.00000	0.000000	29.580000	6.200000	159.000000	0.000000
max	80.000000	1.00000	1.000000	95.690000	9.000000	300.000000	1.000000

```
# Count occurrences of diabetic vs non-diabetic cases
diabetes_counts = df['diabetes'].value_counts().to_dict()  # Convert to dictionary to avoid KeyError

# Ensure both labels exist in the correct order
sizes = [diabetes_counts.get(0, 0), diabetes_counts.get(1, 0)]  # Handles cases where values might be missing
labels = ['Non-Diabetic', 'Diabetic']
colors = ['#1f77b4', '#ff7f0e']  # Custom colors for clarity
explode = (0, 0.1)  # Slightly separate "Diabetic" slice for emphasis

# Create the pie chart
plt.figure(figsize=(6, 6))
plt.pie(sizes, labels=labels, colors=colors, autopct='%1.2f%%', startangle=140, explode=explode)
plt.title("Percentage of Diabetic vs Non-Diabetic Patients")
plt.legend(labels, loc="upper right")
plt.show()
```



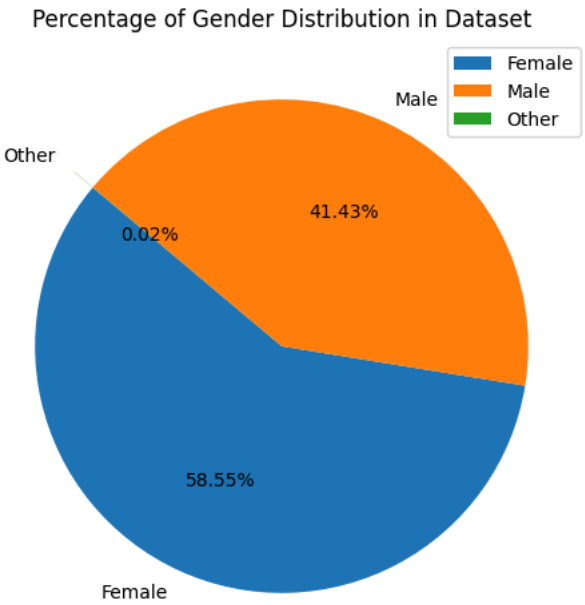

```
categorical_columns = ['gender', 'smoking_history']  # Adjust as needed
for col in categorical_columns:
    print(f"Unique values in {col}: {df[col].unique()}")
```

```
Unique values in gender: ['Female' 'Male' 'Other']
Unique values in smoking_history: ['never' 'No Info' 'current' 'former' 'ever' 'not current']
```

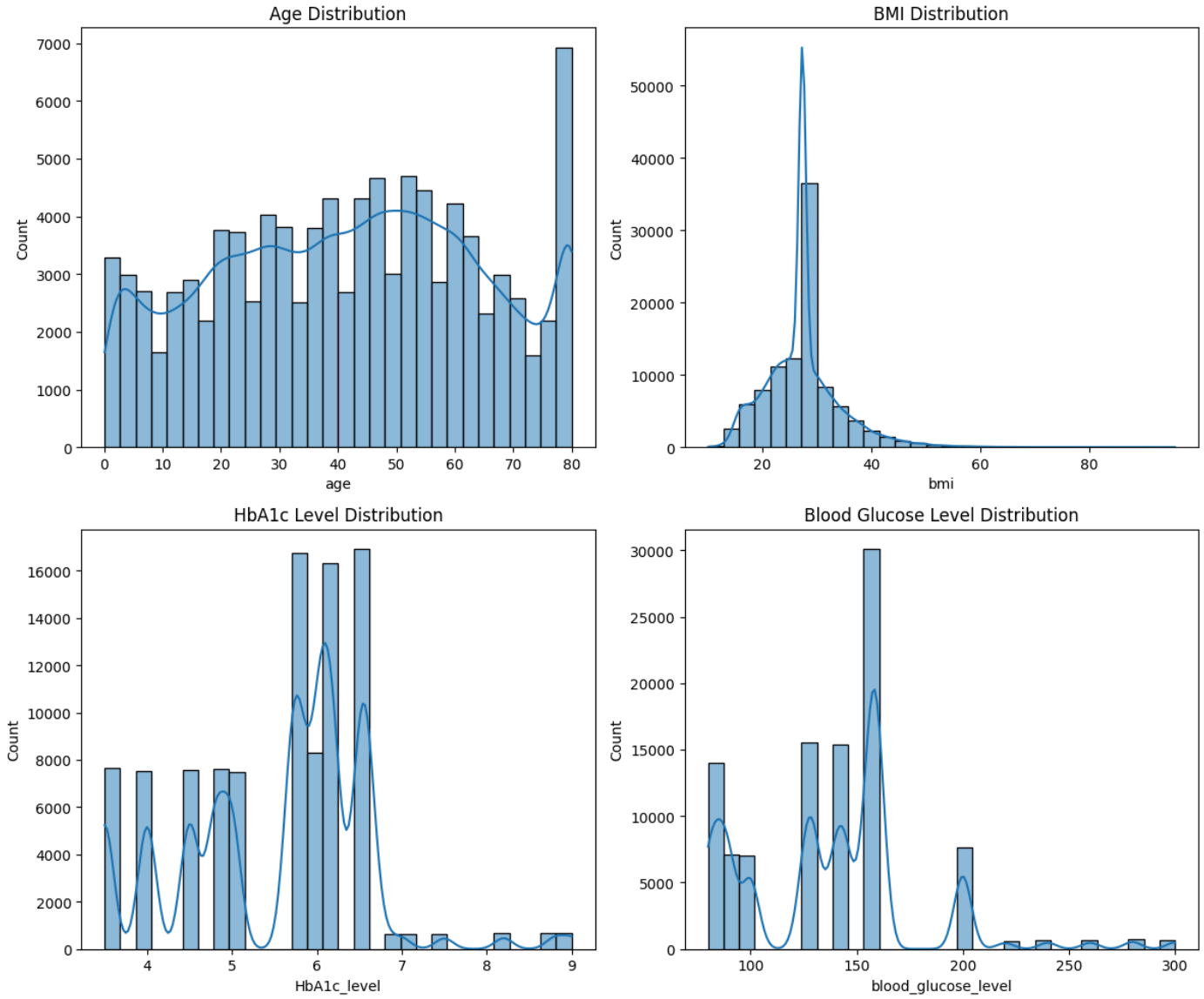
```
# Count occurrences of each gender category
gender_counts = df['gender'].value_counts()
print(gender_counts)
```

```
gender
Female    58552
Male      41430
Other        18
Name: count, dtype: int64
```

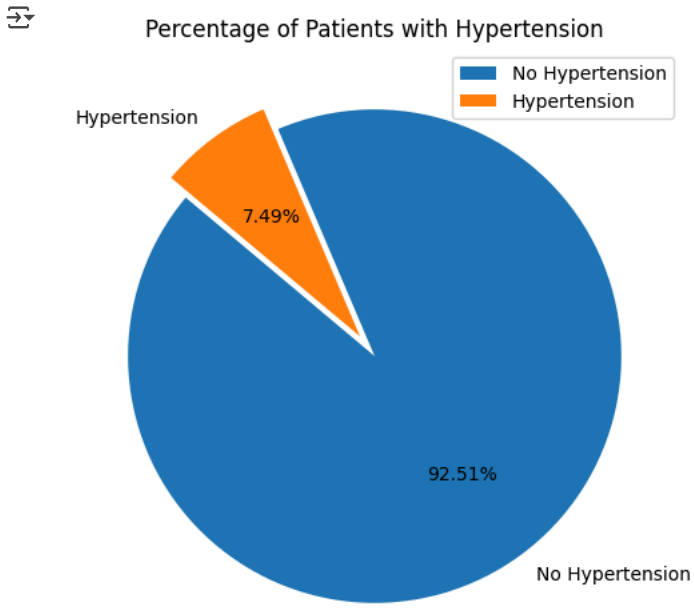
```
# Count occurrences of each gender category
gender_counts = df['gender'].value_counts()

# Data for the pie chart
labels = gender_counts.index.tolist()  # Extract unique gender labels
sizes = gender_counts.values  # Extract corresponding counts
colors = ['#1f77b4', '#ff7f0e', '#2ca02c']  # Assign colors
explode = (0, 0, 0.1) if 'Other' in labels else (0, 0)  # Slightly separate 'Other' if it exists

# Create the pie chart
plt.figure(figsize=(6, 6))
plt.pie(sizes, labels=labels, colors=colors, autopct='%1.2f%%', startangle=140, explode=explode)
plt.title("Percentage of Gender Distribution in Dataset")
plt.legend(labels, loc="upper right")
plt.show()
```



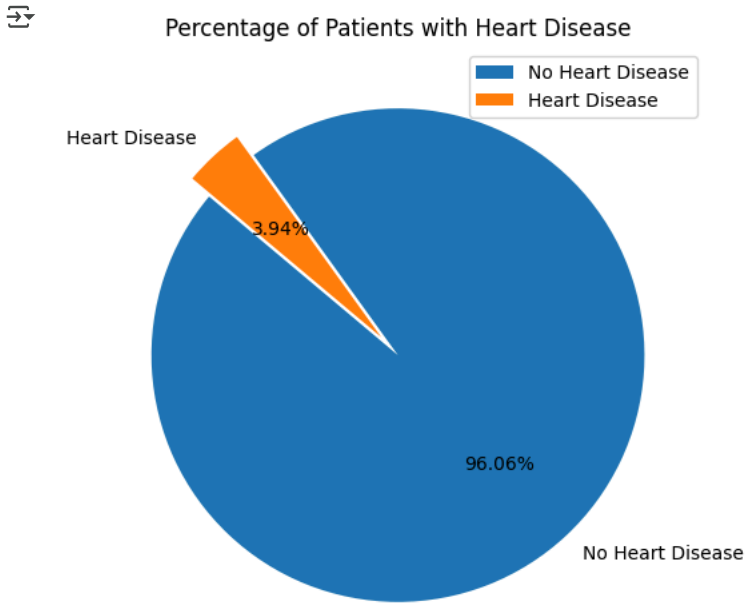

```
# Plot distributions
fig, axes = plt.subplots(2, 2, figsize=(12, 10))
sns.histplot(df['age'], bins=30, kde=True, ax=axes[0, 0])
axes[0, 0].set_title('Age Distribution')

sns.histplot(df['bmi'], bins=30, kde=True, ax=axes[0, 1])
axes[0, 1].set_title('BMI Distribution')

sns.histplot(df['HbA1c_level'], bins=30, kde=True, ax=axes[1, 0])
axes[1, 0].set_title('HbA1c Level Distribution')

sns.histplot(df['blood_glucose_level'], bins=30, kde=True, ax=axes[1, 1])
axes[1, 1].set_title('Blood Glucose Level Distribution')

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




```
# Count occurrences of each hypertension category
hypertension_counts = df['hypertension'].value_counts()

# Data for the pie chart
labels = ['No Hypertension', 'Hypertension']
sizes = [hypertension_counts[0], hypertension_counts[1]]  # Extract counts
colors = ['#1f77b4', '#ff7f0e']  # Custom colors for clarity
explode = (0, 0.1)  # Slightly separate "Hypertension" slice for emphasis

# Create the pie chart
plt.figure(figsize=(6, 6))
plt.pie(sizes, labels=labels, colors=colors, autopct='%1.2f%%', startangle=140, explode=explode)
plt.title("Percentage of Patients with Hypertension")
plt.legend(labels, loc="upper right")
plt.show()
```




```
# Count occurrences of each heart disease category
heart_disease_counts = df['heart_disease'].value_counts()

# Data for the pie chart
labels = ['No Heart Disease', 'Heart Disease']
sizes = [heart_disease_counts[0], heart_disease_counts[1]]  # Extract counts
colors = ['#1f77b4', '#ff7f0e']  # Custom colors for clarity
explode = (0, 0.1)  # Slightly separate "Heart Disease" slice for emphasis

# Create the pie chart
plt.figure(figsize=(6, 6))
plt.pie(sizes, labels=labels, colors=colors, autopct='%1.2f%%', startangle=140, explode=explode)
plt.title("Percentage of Patients with Heart Disease")
plt.legend(labels, loc="upper right")
plt.show()
```




```
# Count occurrences of each smoking history category
smoking_counts = df['smoking_history'].value_counts().reset_index()
```

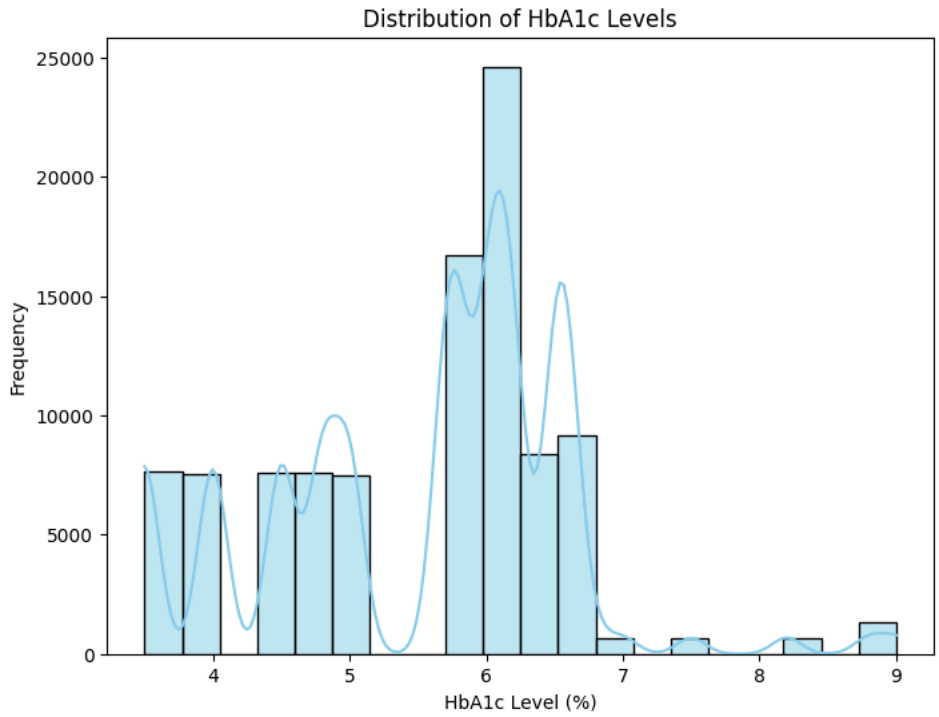
```
smoking_counts.columns = ['Smoking History', 'Count']

# Calculate frequency (percentage)
smoking_counts['Frequency (%)'] = (smoking_counts['Count'] / df.shape[0]) * 100

# Display the table
print(smoking_counts)
```

```
  Smoking History  Count  Frequency (%)
0         No Info  35816         35.816
1           never  35095         35.095
2          former   9352          9.352
3         current   9286          9.286
4     not current   6447          6.447
5            ever   4004          4.004
```

```
# Get the range of HbA1c levels
hbA1c_min = df['HbA1c_level'].min()
hbA1c_max = df['HbA1c_level'].max()

# Define HbA1c categories
hbA1c_bins = [0, 5.7, 6.4, float('inf')]
hbA1c_labels = ['≤ 5.7% (Non-Diabetic)', '5.7% - 6.4% (Prediabetic)', '≥ 6.5% (Diabetic)']

# Categorize patients based on HbA1c levels
df['HbA1c_Category'] = pd.cut(df['HbA1c_level'], bins=hbA1c_bins, labels=hbA1c_labels, include_lowest=True)

# Count occurrences in each category
hbA1c_counts = df['HbA1c_Category'].value_counts().reset_index()
hbA1c_counts.columns = ['HbA1c Category', 'Count']

# Calculate percentage
hbA1c_counts['Percentage (%)'] = (hbA1c_counts['Count'] / df.shape[0]) * 100

# Display the results
print(f"HbA1c levels range from {hbA1c_min}% to {hbA1c_max}%.\n")
print(hbA1c_counts)
```

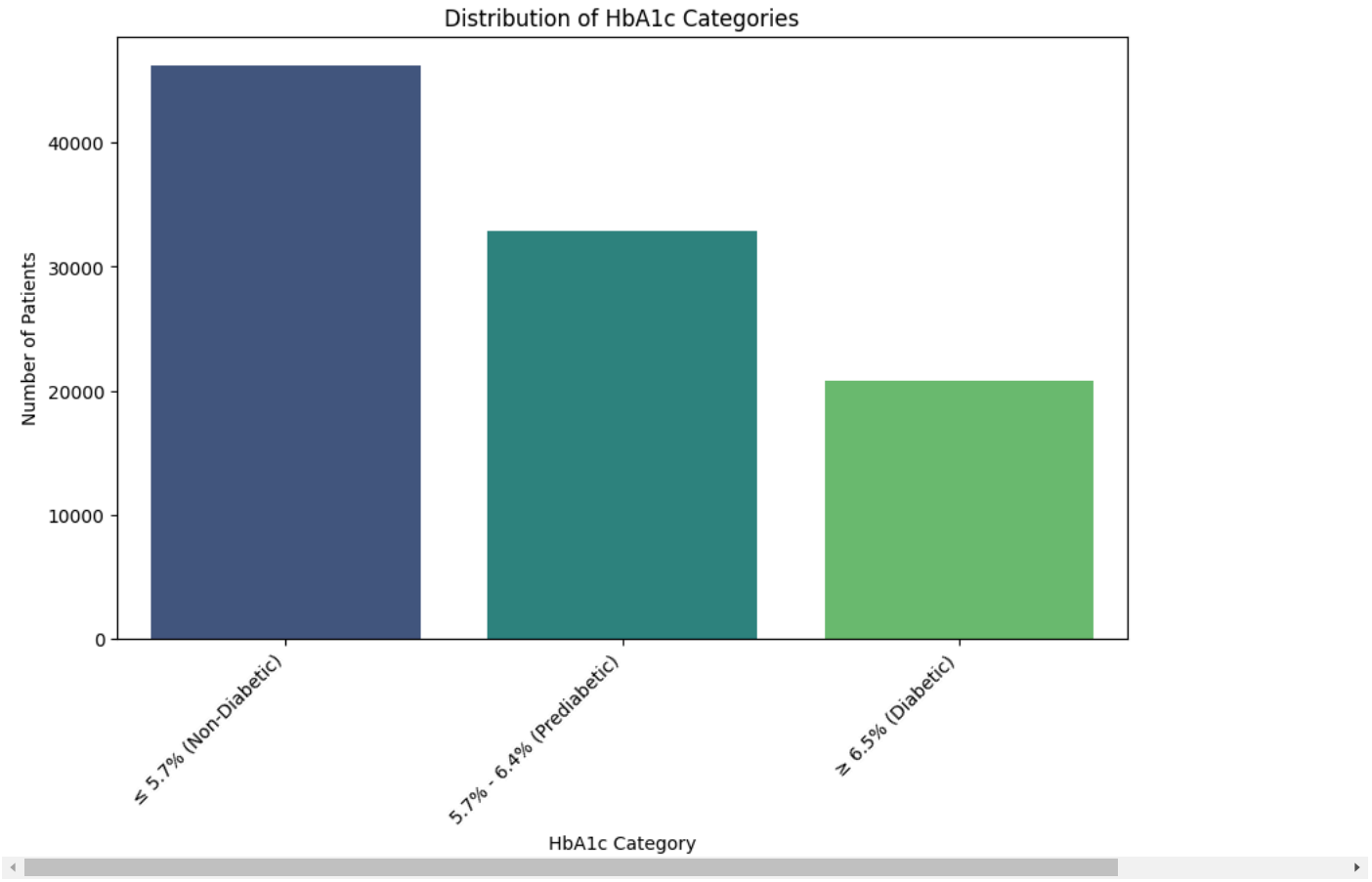
```
HbA1c levels range from 3.5% to 9.0%.

                HbA1c Category  Count  Percentage (%)
0      ≤ 5.7% (Non-Diabetic)  46270          46.270
1  5.7% - 6.4% (Prediabetic)  32933          32.933
2          ≥ 6.5% (Diabetic)  20797          20.797
```

```
# prompt: histogram for HbA1C

import matplotlib.pyplot as plt
# Plotting the histogram for HbA1c levels with a density curve
plt.figure(figsize=(8, 6))
sns.histplot(df['HbA1c_level'], bins=20, kde=True, color='skyblue')  # Increased bins for better granularity
plt.title('Distribution of HbA1c Levels')
plt.xlabel('HbA1c Level (%)')
plt.ylabel('Frequency')
plt.show()
```

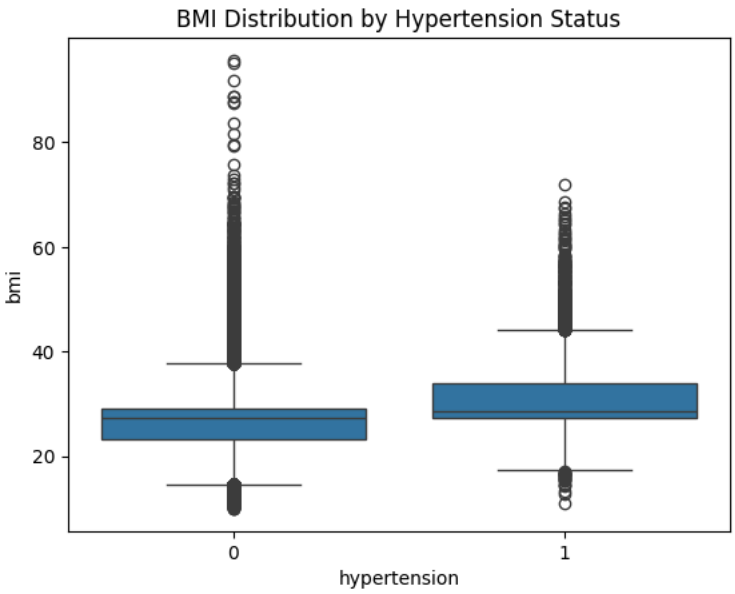



```
# prompt: historgram for this About ≤ 5.7% being non-diabetic, 5.7% - 6.4% being prediabetic, and ≥ 6.5% being diabetic.

import matplotlib.pyplot as plt
# Plotting the histogram for HbA1c categories
plt.figure(figsize=(10, 6))
sns.countplot(x='HbA1c_Category', data=df, palette='viridis')
plt.title('Distribution of HbA1c Categories')
plt.xlabel('HbA1c Category')
plt.ylabel('Number of Patients')
plt.xticks(rotation=45, ha='right')  # Rotate x-axis labels for better readability
plt.show()
```

```
<ipython-input-32-6feb8259eba6>:6: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend

  sns.countplot(x='HbA1c_Category', data=df, palette='viridis')
```

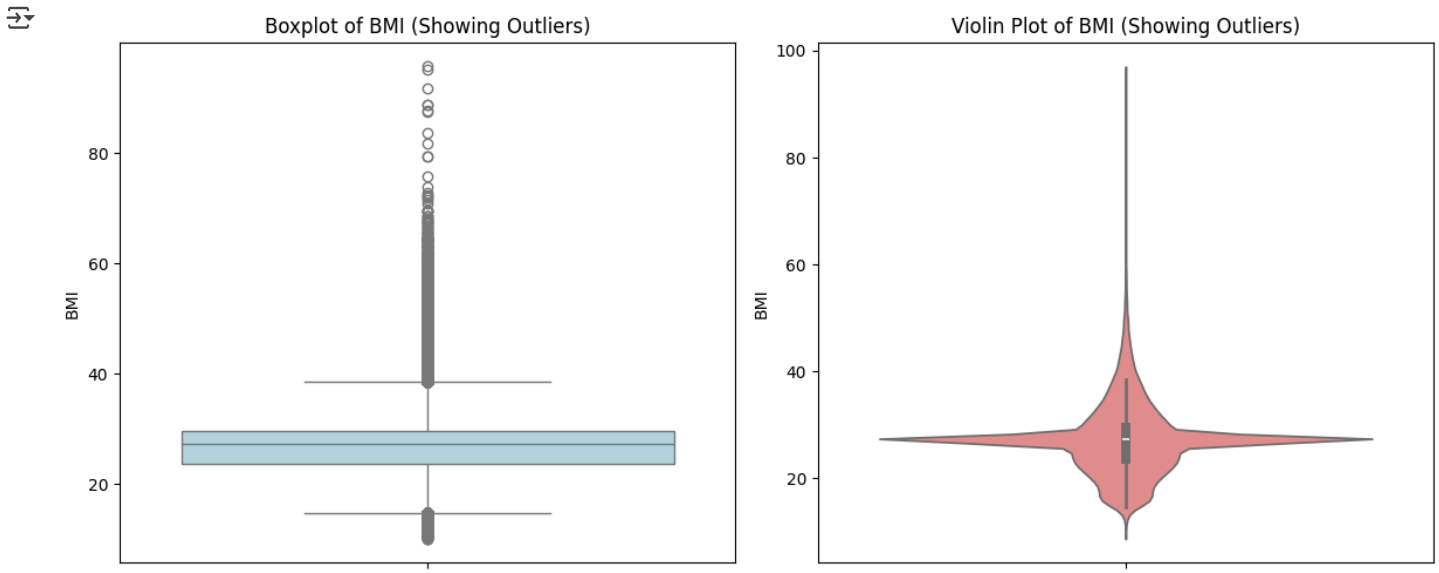



```
import seaborn as sns
import matplotlib.pyplot as plt

sns.boxplot(x=df['hypertension'], y=df['bmi'])
plt.title("BMI Distribution by Hypertension Status")
plt.show()
```




```
# Set figure size
plt.figure(figsize=(12, 5))
```

```
# Create a boxplot for BMI to show outliers
plt.subplot(1, 2, 1)  # 1 row, 2 columns, position 1
sns.boxplot(y=df['bmi'], color='lightblue')
plt.title("Boxplot of BMI (Showing Outliers)")
plt.ylabel("BMI")

# Create a violin plot for BMI to show distribution and outliers
plt.subplot(1, 2, 2)  # 1 row, 2 columns, position 2
sns.violinplot(y=df['bmi'], color='lightcoral')
plt.title("Violin Plot of BMI (Showing Outliers)")
plt.ylabel("BMI")

# Show the plots
plt.tight_layout()
plt.show()
```

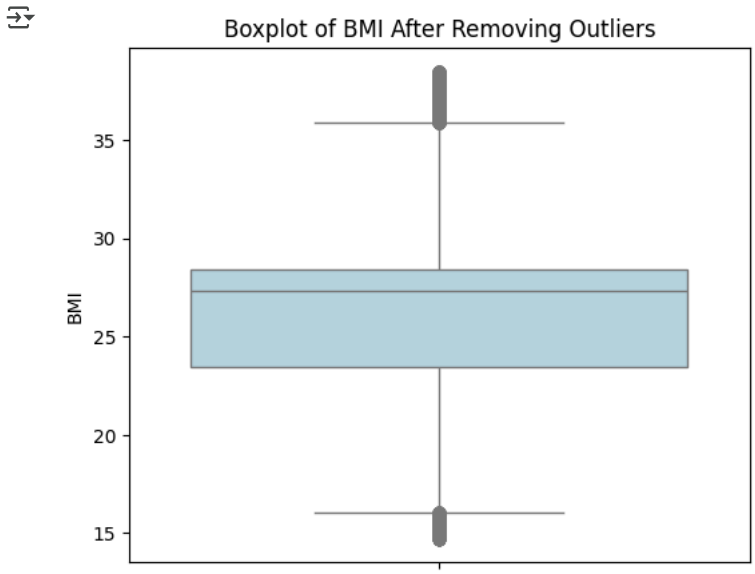



```
# Calculate IQR (Interquartile Range) for BMI
Q1 = df['bmi'].quantile(0.25)  # 25th percentile
Q3 = df['bmi'].quantile(0.75)  # 75th percentile
IQR = Q3 - Q1  # Interquartile Range

# Define lower and upper bounds for outliers
lower_bound = Q1 - 1.5 * IQR
upper_bound = Q3 + 1.5 * IQR

# Remove outliers
df_cleaned = df[(df['bmi'] >= lower_bound) & (df['bmi'] <= upper_bound)]

# Print before and after removing outliers
print(f"Original dataset size: {df.shape[0]} rows")
print(f"Dataset size after removing outliers: {df_cleaned.shape[0]} rows")

# Save the cleaned dataset (optional)
df_cleaned.to_csv("cleaned_diabetes_dataset.csv", index=False)
```

```
Original dataset size: 100000 rows
Dataset size after removing outliers: 92914 rows
```

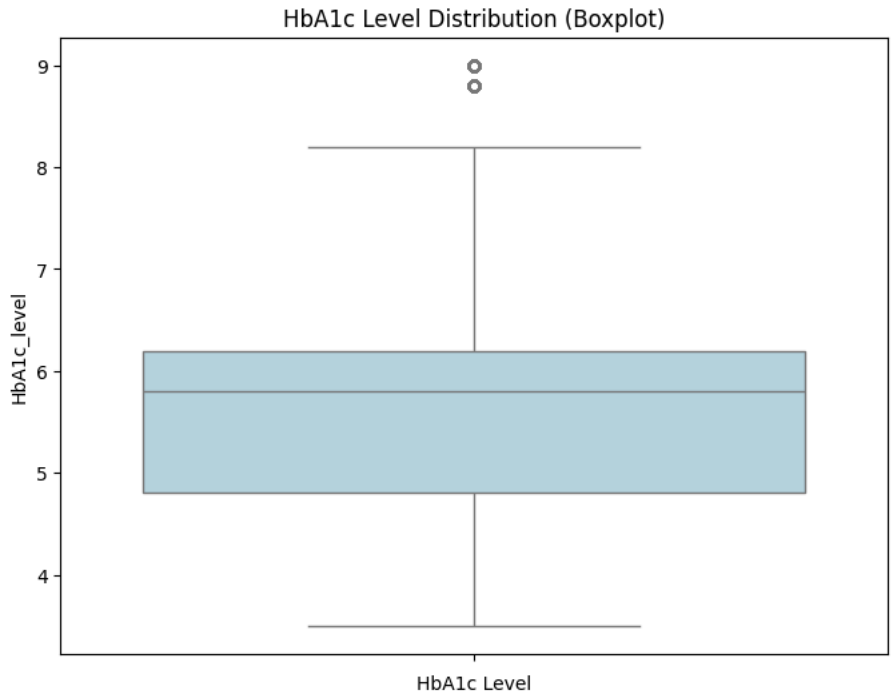
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

# Load dataset
file_path = "diabetes_prediction_dataset.csv"  # Update the path if needed
df = pd.read_csv(file_path)
```

```
# Calculate IQR (Interquartile Range) for BMI
Q1 = df['bmi'].quantile(0.25)  # 25th percentile
Q3 = df['bmi'].quantile(0.75)  # 75th percentile
IQR = Q3 - Q1  # Interquartile Range

# Define lower and upper bounds for outliers
lower_bound = Q1 - 1.5 * IQR
upper_bound = Q3 + 1.5 * IQR

# Remove outliers
df_cleaned = df[(df['bmi'] >= lower_bound) & (df['bmi'] <= upper_bound)]

# Plot the boxplot for BMI after removing outliers
plt.figure(figsize=(6, 5))
sns.boxplot(y=df_cleaned['bmi'], color='lightblue')
plt.title("Boxplot of BMI After Removing Outliers")
plt.ylabel("BMI")

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



Start coding or generate with AI.

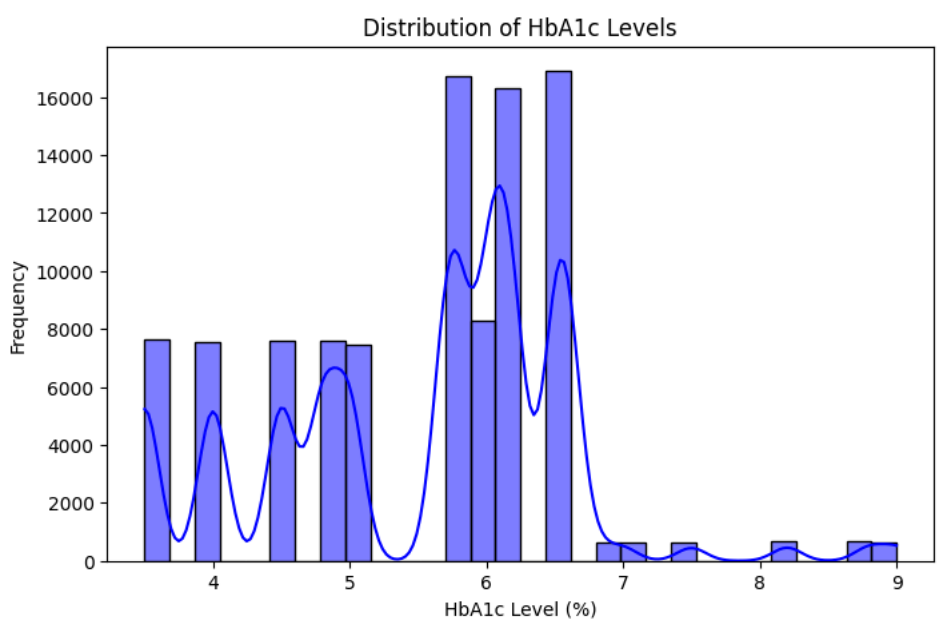
```
# Plot a boxplot for HbA1c level distribution
plt.figure(figsize=(8, 6))
sns.boxplot(y=df['HbA1c_level'], color="lightblue")
plt.title("HbA1c Level Distribution (Boxplot)")
plt.xlabel("HbA1c Level")
plt.show()
```



Start coding or generate with AI.

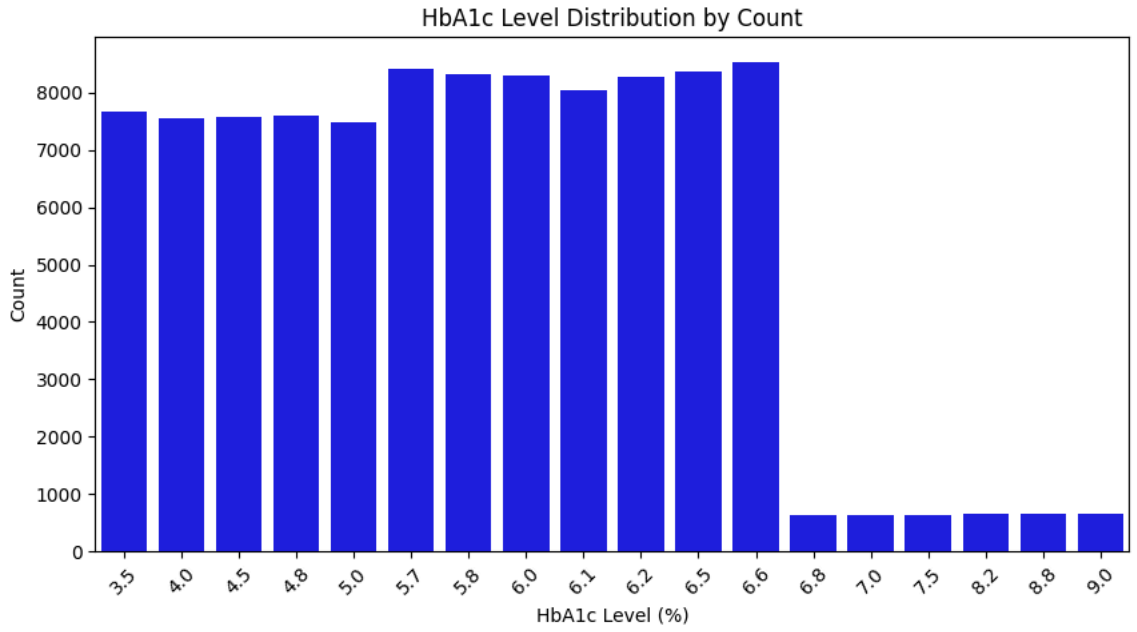
Start coding or generate with AI.

```
# Plot the distribution of HbA1c levels
plt.figure(figsize=(8, 5))
sns.histplot(df['HbA1c_level'], bins=30, kde=True, color='blue')
plt.title("Distribution of HbA1c Levels")
plt.xlabel("HbA1c Level (%)")
plt.ylabel("Frequency")
plt.show()
```




```
# Plot the distribution of HbA1c levels by count
plt.figure(figsize=(10, 5))
sns.barplot(x=hbA1c_distribution['HbA1c Level'], y=hbA1c_distribution['Count'], color='blue')
plt.title("HbA1c Level Distribution by Count")
plt.xlabel("HbA1c Level (%)")
```

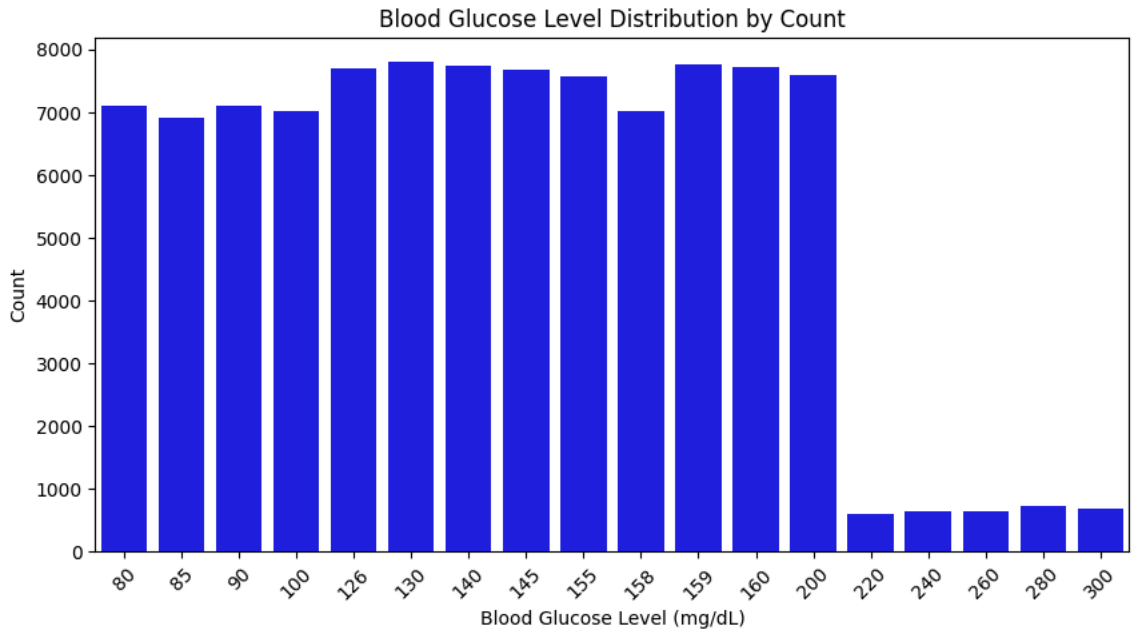
```
plt.ylabel("Count")
plt.xticks(rotation=45)
plt.show()
```



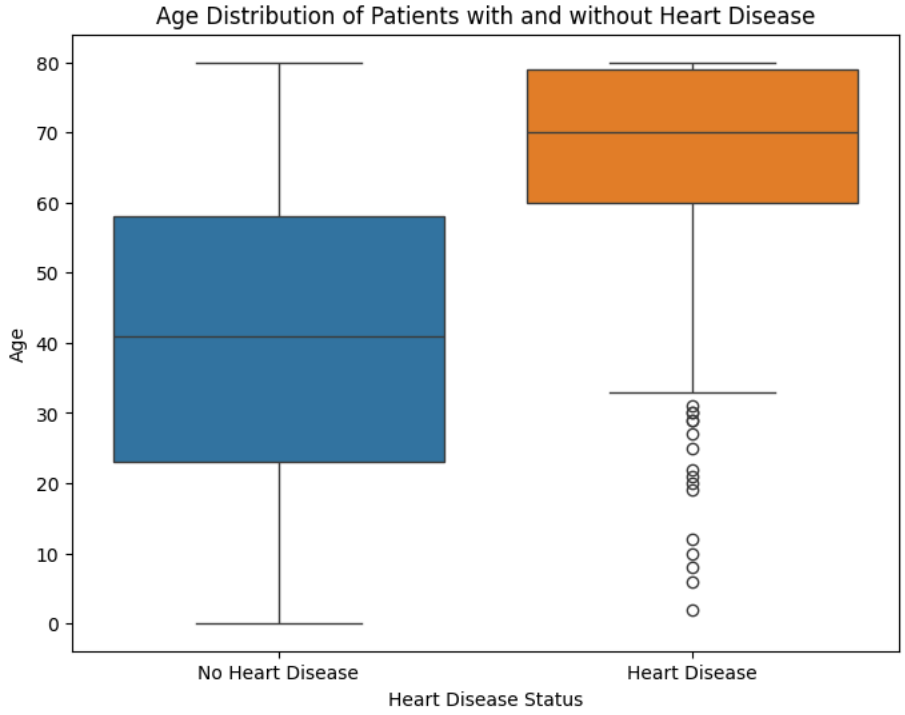

```
# Count occurrences of each Blood Glucose Level
blood_glucose_distribution = df['blood_glucose_level'].value_counts().reset_index()
blood_glucose_distribution.columns = ['Blood Glucose Level', 'Count']

# Display the distribution table
print(blood_glucose_distribution)
```

```
    Blood Glucose Level  Count
0                   130   7794
1                   159   7759
2                   140   7732
3                   160   7712
4                   126   7702
5                   145   7679
6                   200   7600
7                   155   7575
8                    90   7112
9                    80   7106
10                  158   7026
11                  100   7025
12                   85   6901
13                  280    729
14                  300    674
15                  240    636
16                  260    635
17                  220    603
```

```
# Plot the distribution of Blood Glucose Levels by count
plt.figure(figsize=(10, 5))
sns.barplot(x=blood_glucose_distribution['Blood Glucose Level'],
            y=blood_glucose_distribution['Count'],
            color='blue')
plt.title("Blood Glucose Level Distribution by Count")
plt.xlabel("Blood Glucose Level (mg/dL)")
plt.ylabel("Count")
plt.xticks(rotation=45)
plt.show()
```

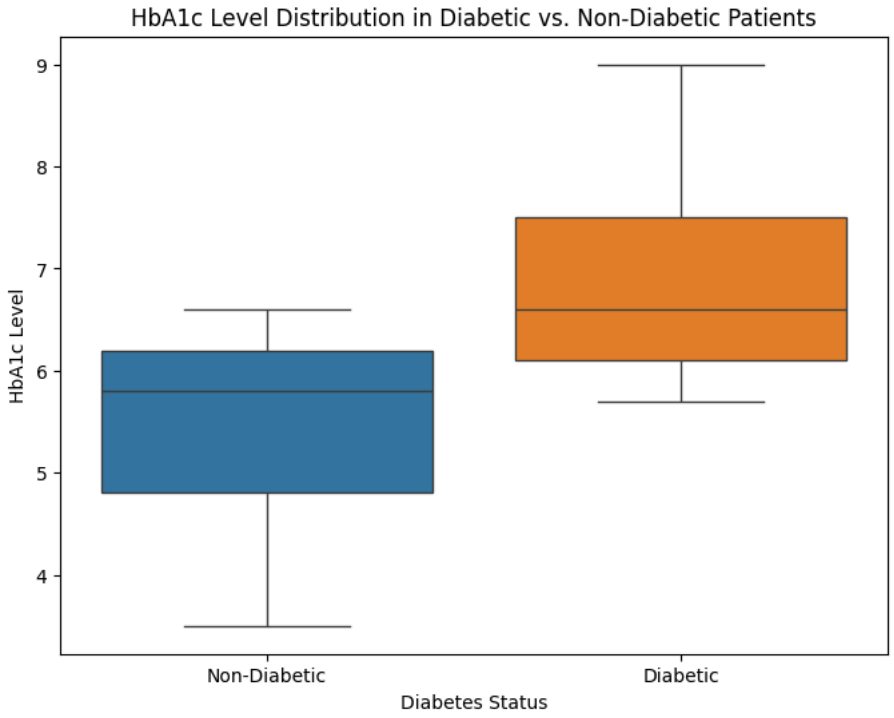



```
# Comparing the age distribution of patients with and without heart disease.
# Create a boxplot to compare age distribution between patients with and without heart disease
plt.figure(figsize=(8, 6))
sns.boxplot(x="heart_disease", y="age", data=df, hue="heart_disease", palette={0: "#1f77b4", 1: "#ff7f0e"}, legend=False)
plt.xticks([0, 1], ['No Heart Disease', 'Heart Disease'])
plt.title("Age Distribution of Patients with and without Heart Disease")
plt.xlabel("Heart Disease Status")
plt.ylabel("Age")
plt.show()
```

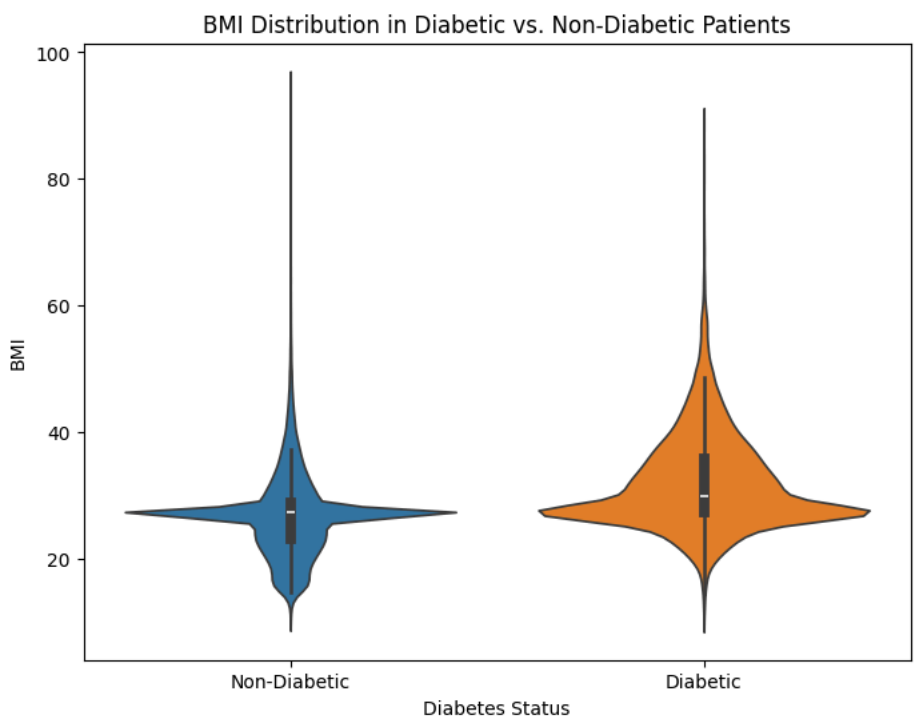



```
plt.figure(figsize=(8, 6))
sns.boxplot(x="diabetes", y="HbA1c_level", data=df, hue="diabetes", palette={0: "#1f77b4", 1: "#ff7f0e"}, legend=False)
plt.xticks([0, 1], ['Non-Diabetic', 'Diabetic'])
plt.title("HbA1c Level Distribution in Diabetic vs. Non-Diabetic Patients")
plt.xlabel("Diabetes Status")
plt.ylabel("HbA1c Level")
```

```
plt.show()
```




```
plt.figure(figsize=(8, 6))
sns.violinplot(x="diabetes", y="bmi", data=df, hue="diabetes", palette={0: "#1f77b4", 1: "#ff7f0e"}, legend=False)
plt.xticks([0, 1], ['Non-Diabetic', 'Diabetic'])
plt.title("BMI Distribution in Diabetic vs. Non-Diabetic Patients")
plt.xlabel("Diabetes Status")
plt.ylabel("BMI")
plt.show()
```

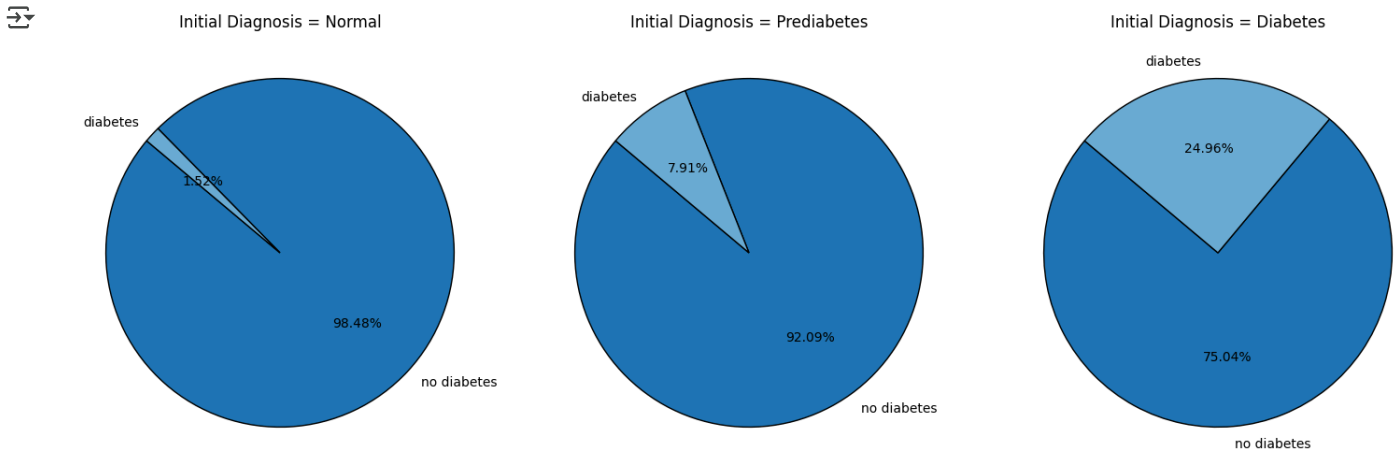



```
import pandas as pd

# Load the dataset
file_path = "diabetes_prediction_dataset.csv"  # Update if needed
```

```
df_new = pd.read_csv(file_path)

# Define HbA1c categories for initial diagnosis
hbA1c_bins = [0, 5.7, 6.4, float('inf')]
hbA1c_labels = ['Normal', 'Prediabetes', 'Diabetes']
df_new['HbA1c_Category'] = pd.cut(df_new['HbA1c_level'], bins=hbA1c_bins, labels=hbA1c_labels, include_lowest=True)

# Calculate the percentage of actual diabetes cases within each HbA1c category
hbA1c_diabetes_distribution = df_new.groupby('HbA1c_Category', observed=False)['diabetes'].mean() * 100

# Convert to DataFrame for better visualization
hbA1c_diabetes_summary = hbA1c_diabetes_distribution.reset_index()
hbA1c_diabetes_summary.columns = ['HbA1c Level', 'Percentage with Diabetes']

# Display the summary
print(hbA1c_diabetes_summary)
```

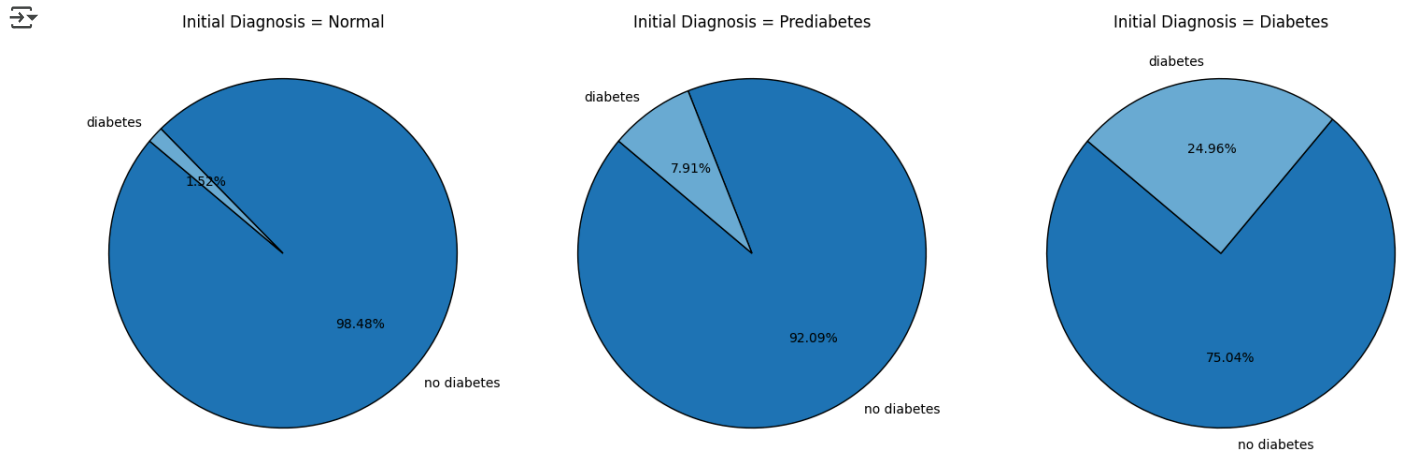
```
    HbA1c Level  Percentage with Diabetes
0        Normal                  1.521504
1   Prediabetes                  7.909999
2      Diabetes                 24.960331
```

```
# Define diabetes status labels
labels = ['no diabetes', 'diabetes']
colors = ['#1f77b4', '#6baed6']  # Different shades of blue

# Create subplots for each HbA1c category
fig, axes = plt.subplots(1, 3, figsize=(15, 5))

# Loop through each category and plot a pie chart
for i, category in enumerate(hbA1c_diabetes_summary['HbA1c Level']):
    diabetes_percentage = hbA1c_diabetes_summary.loc[hbA1c_diabetes_summary['HbA1c Level'] == category, 'Percentage with Diabetes'].values[0
    no_diabetes_percentage = 100 - diabetes_percentage

    axes[i].pie([no_diabetes_percentage, diabetes_percentage],
                labels=labels,
                autopct='%1.2f%%',
                colors=colors,
                startangle=140,
                wedgeprops={'edgecolor': 'black'})

    axes[i].set_title(f"Initial Diagnosis = {category}")

# Adjust layout and show the plots
plt.tight_layout()
plt.show()
```

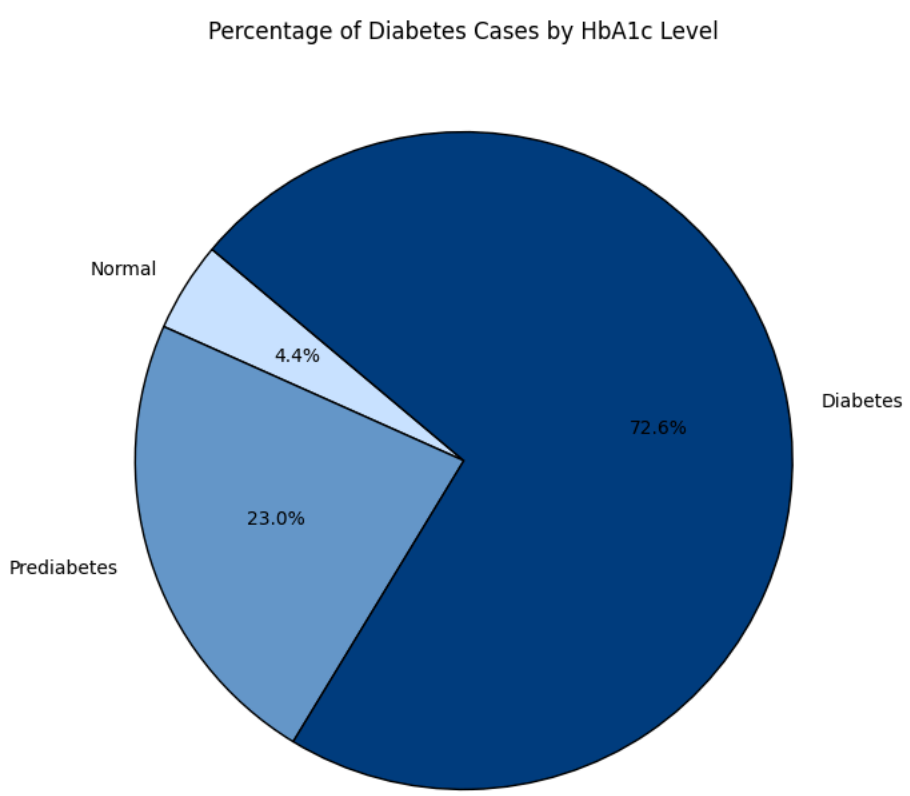


Double-click (or enter) to edit

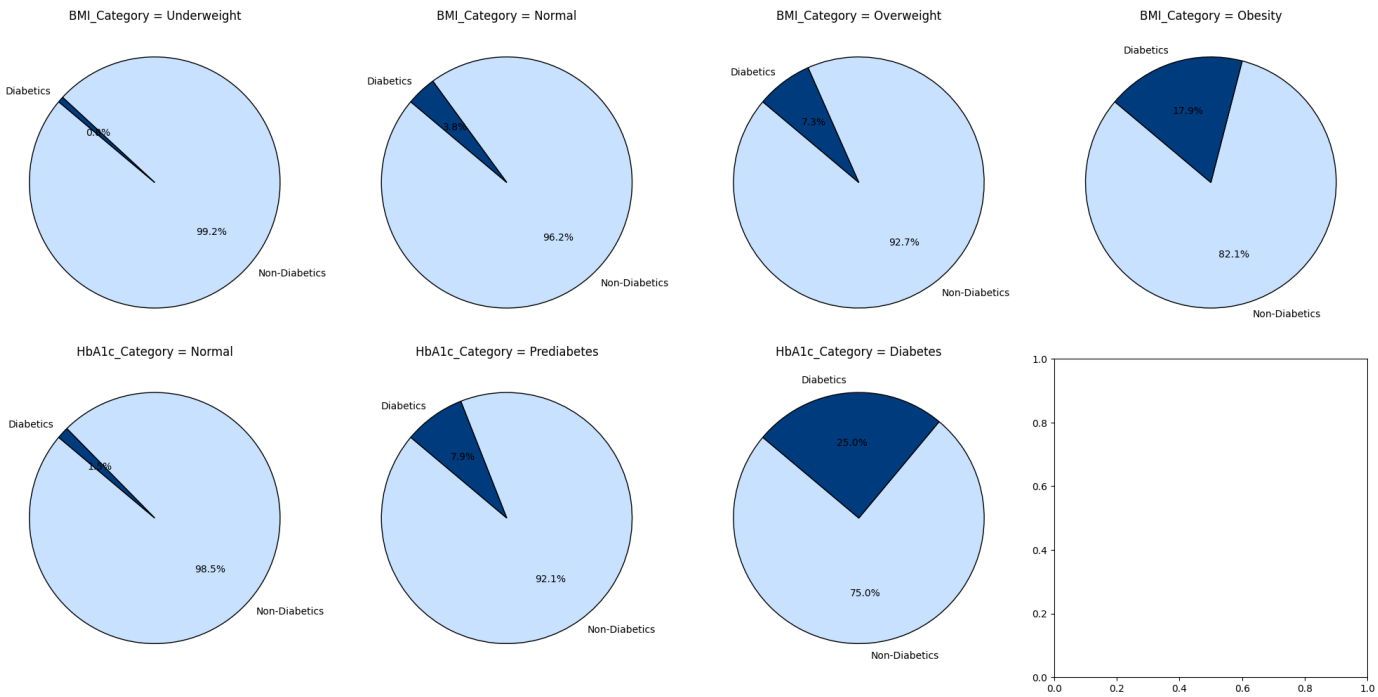
```
# prompt: add the title # Define diabetes status labels
# labels = ['no diabetes', 'diabetes']
# colors = ['#1f77b4', '#6baed6']  # Different shades of blue
# # Create subplots for each HbA1c category
# fig, axes = plt.subplots(1, 3, figsize=(15, 5))
# # Loop through each category and plot a pie chart
# for i, category in enumerate(hbA1c_diabetes_summary['HbA1c Level']):
#     diabetes_percentage = hbA1c_diabetes_summary.loc[hbA1c_diabetes_summary['HbA1c Level'] == category, 'Percentage with Diabetes'].values
#     no_diabetes_percentage = 100 - diabetes_percentage
#     axes[i].pie([no_diabetes_percentage, diabetes_percentage],
#                 labels=labels,
#                 autopct='%1.2f%%',
#                 colors=colors,
#                 startangle=140,
#                 wedgeprops={'edgecolor': 'black'})
#     axes[i].set_title(f"Initial Diagnosis = {category}")
# # Adjust layout and show the plots
# plt.tight_layout()
# plt.show()

import matplotlib.pyplot as plt
# Define diabetes status labels
labels = ['no diabetes', 'diabetes']
colors = ['#1f77b4', '#6baed6']  # Different shades of blue

# Create subplots for each HbA1c category
fig, axes = plt.subplots(1, 3, figsize=(15, 5))

# Loop through each category and plot a pie chart
for i, category in enumerate(hbA1c_diabetes_summary['HbA1c Level']):
    diabetes_percentage = hbA1c_diabetes_summary.loc[hbA1c_diabetes_summary['HbA1c Level'] == category, 'Percentage with Diabetes'].values[0
    no_diabetes_percentage = 100 - diabetes_percentage
    axes[i].pie([no_diabetes_percentage, diabetes_percentage],
                labels=labels,
                autopct='%1.2f%%',
                colors=colors,
                startangle=140,
                wedgeprops={'edgecolor': 'black'})
    axes[i].set_title(f"Initial Diagnosis = {category}")

# Adjust layout and show the plots
plt.tight_layout()
plt.show()
```




```
import matplotlib.pyplot as plt

# Define different shades of blue for the pie chart
colors = ['#cce5ff', '#6699cc', '#004080']  # Light to dark blue shades

# Create a pie chart for the distribution of diabetes cases within each HbA1c category
plt.figure(figsize=(8, 8))
plt.pie(hbA1c_diabetes_summary['Percentage with Diabetes'],
        labels=hbA1c_diabetes_summary['HbA1c Level'],
        autopct='%1.1f%%',
        colors=colors,
        startangle=140,
        wedgeprops={'edgecolor': 'black'})

# Set title
plt.title("Percentage of Diabetes Cases by HbA1c Level")

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

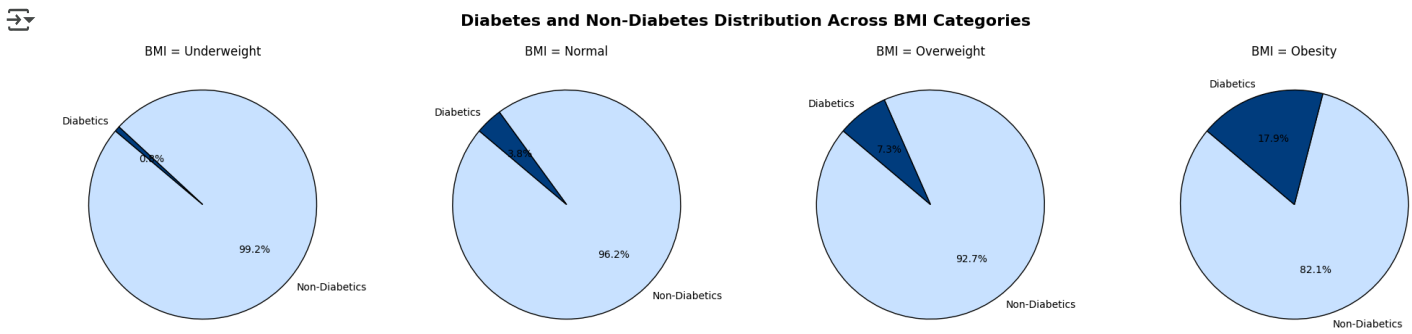



```
import matplotlib.pyplot as plt

# Define diabetes status labels and shades of blue
labels = ['Non-Diabetics', 'Diabetics']
colors = ['#cce5ff', '#004080']  # Light to dark blue shades

# Define ordinal categories
ordinal_categories = ['BMI_Category', 'HbA1c_Category']

# Create subplots for each ordinal category
fig, axes = plt.subplots(len(ordinal_categories), len(df_new['BMI_Category'].unique()), figsize=(20, 10))

# Loop through each ordinal category and plot a pie chart
for row, category in enumerate(ordinal_categories):
    category_distribution = df_new.groupby(category, observed=False)['diabetes'].value_counts(normalize=True).unstack() * 100

    for col, cat in enumerate(category_distribution.index):
        diabetes_percentage = category_distribution.loc[cat, 1] if 1 in category_distribution.columns else 0
        non_diabetes_percentage = category_distribution.loc[cat, 0] if 0 in category_distribution.columns else 100

        axes[row, col].pie([non_diabetes_percentage, diabetes_percentage],
                           labels=labels,
                           autopct='%1.1f%%',
                           colors=colors,
                           startangle=140,
                           wedgeprops={'edgecolor': 'black'})

        axes[row, col].set_title(f"{category} = {cat}")

# Adjust layout and show the plots
plt.tight_layout()
plt.show()
```

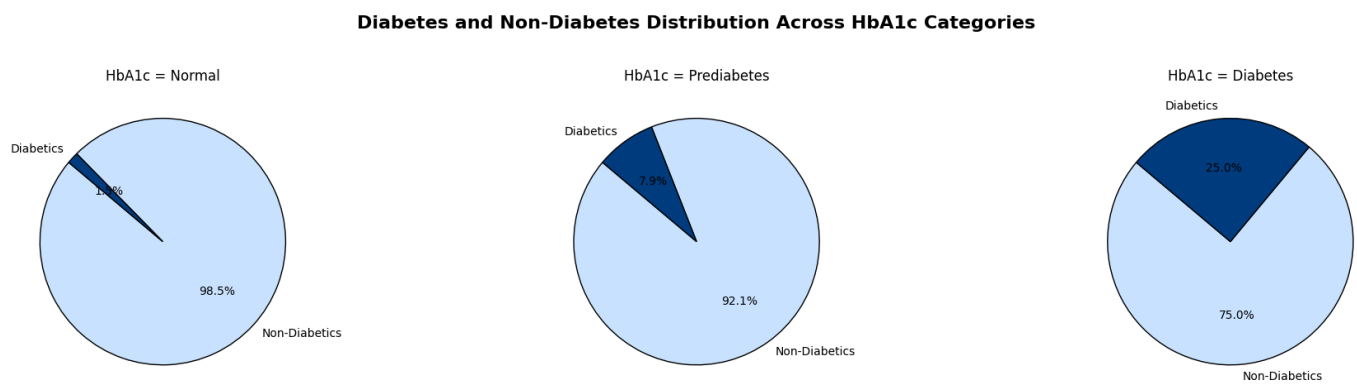



```
import matplotlib.pyplot as plt

# Define diabetes status labels and shades of blue
labels = ['Non-Diabetics', 'Diabetics']
colors = ['#cce5ff', '#004080']  # Light to dark blue shades

# Create subplots for BMI categories
fig, axes = plt.subplots(1, len(df_new['BMI_Category'].unique()), figsize=(20, 5))

# Group data by BMI category and diabetes status
bmi_distribution = df_new.groupby('BMI_Category', observed=False)['diabetes'].value_counts(normalize=True).unstack() * 100

# Loop through each BMI category and plot a pie chart
for col, category in enumerate(bmi_distribution.index):
    diabetes_percentage = bmi_distribution.loc[category, 1] if 1 in bmi_distribution.columns else 0
    non_diabetes_percentage = bmi_distribution.loc[category, 0] if 0 in bmi_distribution.columns else 100

    axes[col].pie([non_diabetes_percentage, diabetes_percentage],
                  labels=labels,
                  autopct='%1.1f%%',
                  colors=colors,
                  startangle=140,
                  wedgeprops={'edgecolor': 'black'})
```

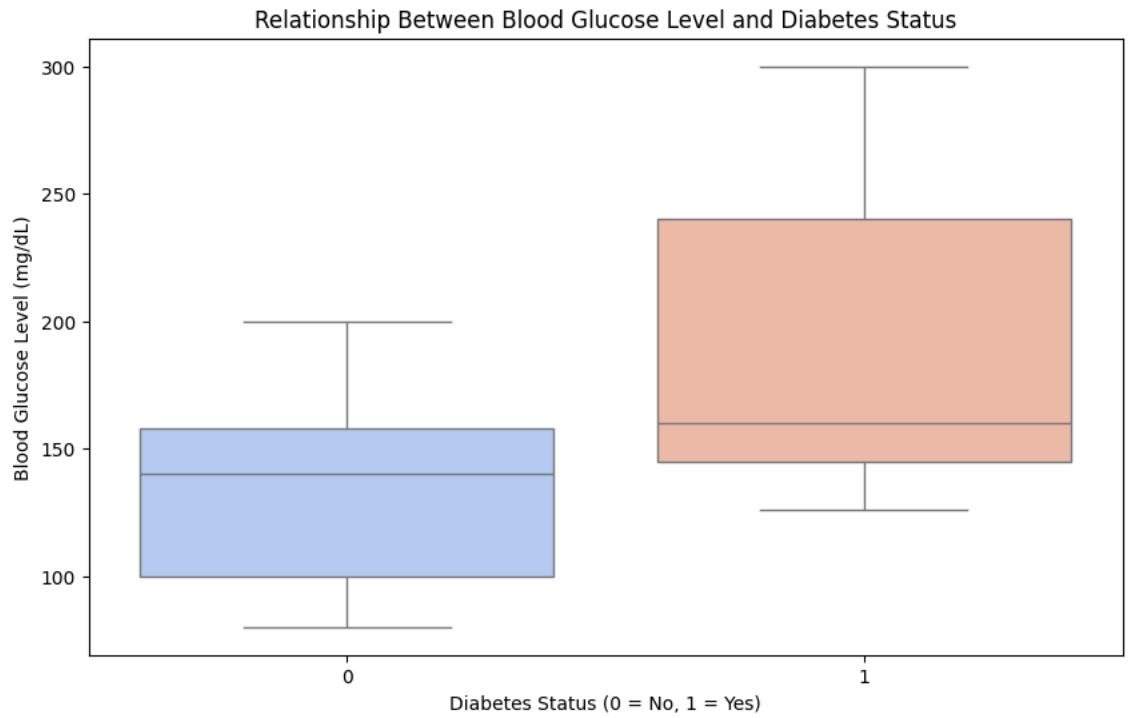
```
    axes[col].set_title(f"BMI = {category}")

# Add overall title
plt.suptitle("Diabetes and Non-Diabetes Distribution Across BMI Categories", fontsize=16, fontweight='bold')

# Adjust layout and show the plots
plt.tight_layout(rect=[0, 0.03, 1, 0.95])
plt.show()
```




```
import matplotlib.pyplot as plt

# Define diabetes status labels and shades of blue
labels = ['Non-Diabetics', 'Diabetics']
colors = ['#cce5ff', '#004080']  # Light to dark blue shades

# Create subplots for HbA1c categories
fig, axes = plt.subplots(1, len(df_new['HbA1c_Category'].unique()), figsize=(20, 5))

# Group data by HbA1c category and diabetes status
hba1c_distribution = df_new.groupby('HbA1c_Category', observed=False)['diabetes'].value_counts(normalize=True).unstack() * 100

# Loop through each HbA1c category and plot a pie chart
for col, category in enumerate(hba1c_distribution.index):
    diabetes_percentage = hba1c_distribution.loc[category, 1] if 1 in hba1c_distribution.columns else 0
    non_diabetes_percentage = hba1c_distribution.loc[category, 0] if 0 in hba1c_distribution.columns else 100

    axes[col].pie([non_diabetes_percentage, diabetes_percentage],
                  labels=labels,
                  autopct='%1.1f%%',
                  colors=colors,
                  startangle=140,
                  wedgeprops={'edgecolor': 'black'})

    axes[col].set_title(f"HbA1c = {category}")

# Add overall title
plt.suptitle("Diabetes and Non-Diabetes Distribution Across HbA1c Categories", fontsize=16, fontweight='bold')

# Adjust layout and show the plots
plt.tight_layout(rect=[0, 0.03, 1, 0.95])
plt.show()
```

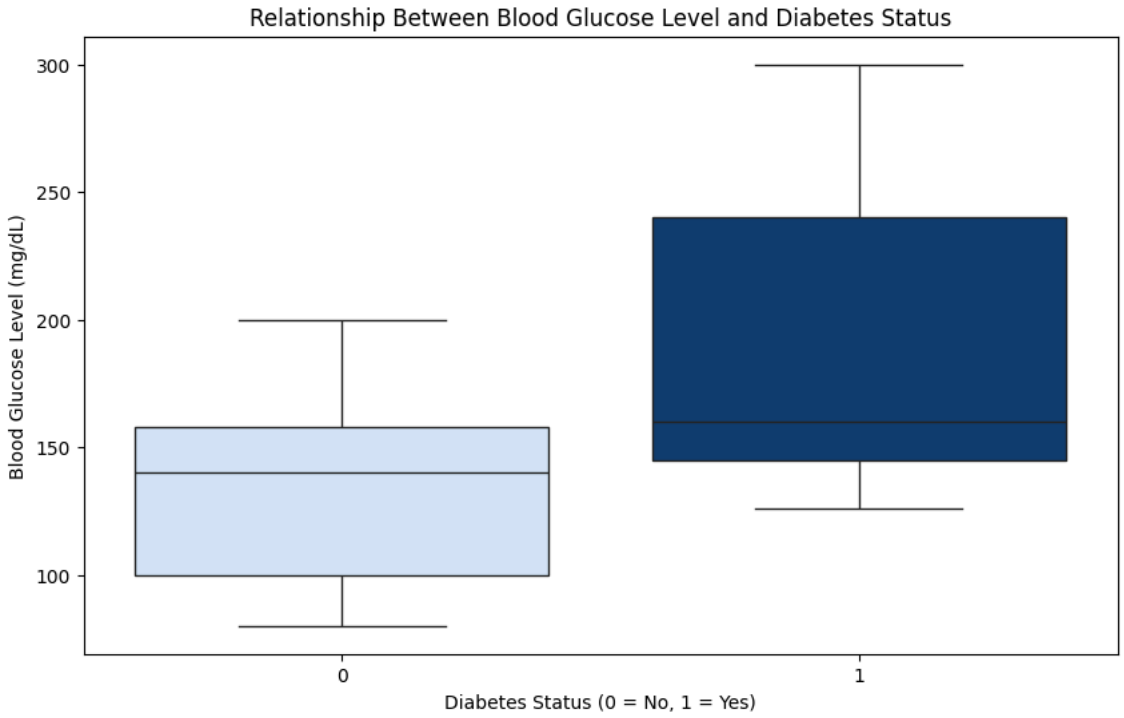



```
import matplotlib.pyplot as plt
import seaborn as sns

# Plot the distribution of Blood Glucose Levels vs. Diabetes Status
plt.figure(figsize=(10, 6))
sns.boxplot(x=df_new['diabetes'], y=df_new['blood_glucose_level'], hue=df_new['diabetes'], palette="coolwarm", legend=False)

# Set plot labels and title
plt.title("Relationship Between Blood Glucose Level and Diabetes Status")
plt.xlabel("Diabetes Status (0 = No, 1 = Yes)")
plt.ylabel("Blood Glucose Level (mg/dL)")

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




```
import matplotlib.pyplot as plt
import seaborn as sns
```

```
# Plot the distribution of Blood Glucose Levels vs. Diabetes Status using shades of blue
plt.figure(figsize=(10, 6))
sns.boxplot(x=df_new['diabetes'], y=df_new['blood_glucose_level'], hue=df_new['diabetes'],
            palette=['#cce5ff', '#004080'], legend=False)  # Light to dark blue shades

# Set plot labels and title
plt.title("Relationship Between Blood Glucose Level and Diabetes Status")
plt.xlabel("Diabetes Status (0 = No, 1 = Yes)")
plt.ylabel("Blood Glucose Level (mg/dL)")

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



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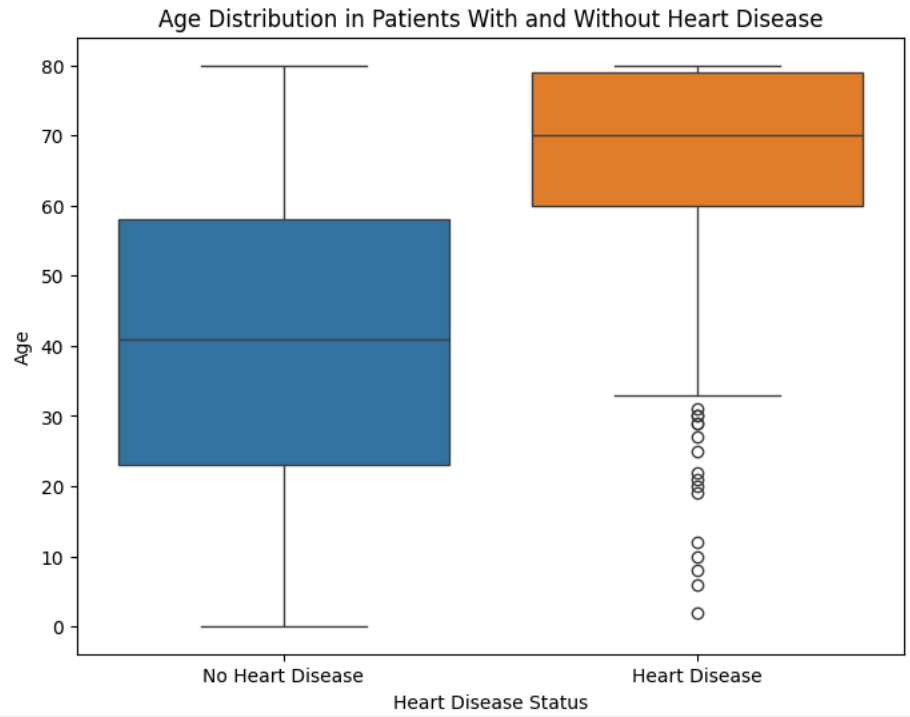
```
plt.figure(figsize=(8, 6))
sns.boxplot(x=df['heart_disease'], y=df['age'], palette=["#1f77b4", "#ff7f0e"])
plt.xticks([0, 1], ['No Heart Disease', 'Heart Disease'])
plt.title("Age Distribution in Patients With and Without Heart Disease")
plt.xlabel("Heart Disease Status")
plt.ylabel("Age")
plt.show()
```

```
<ipython-input-39-32f56af5aab9>:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend

  sns.boxplot(x=df['heart_disease'], y=df['age'], palette=["#1f77b4", "#ff7f0e"])
```




```
# Define HbA1c level categories based on diabetes classification
hba1c_bins = [0, 5.7, 6.4, float('inf')]
hba1c_labels = ['Normal', 'Prediabetes', 'Diabetes']
df['HbA1c_Category'] = pd.cut(df['HbA1c_level'], bins=hba1c_bins, labels=hba1c_labels)

# Calculate percentage of diabetics in each HbA1c category
hba1c_diabetes_counts = df.groupby('HbA1c_Category', observed=True)['diabetes'].mean() * 100

# Create a structured table
hba1c_table = pd.DataFrame({
    'HbA1c Level Category': hba1c_labels,
    'Prediction': [f"{hba1c_diabetes_counts.get(category, 0):.2f}% have diabetes" for category in hba1c_labels]
})

# Display the table
print(hba1c_table)
```

```
  HbA1c Level Category            Prediction
0               Normal   1.52% have diabetes
1          Prediabetes   7.91% have diabetes
2             Diabetes  24.96% have diabetes
```

```
# Define HbA1c level categories
hba1c_bins = [0, 5.7, 6.4, float('inf')]
hba1c_labels = ['< 5.7', '5.7 - 6.4', '>= 6.5']
df['HbA1c_Category'] = pd.cut(df['HbA1c_level'], bins=hba1c_bins, labels=hba1c_labels, include_lowest=True)

# Calculate percentage of diabetics in each HbA1c category
hba1c_diabetes_counts = df.groupby('HbA1c_Category', observed=True)['diabetes'].mean() * 100

# Create a structured table
hba1c_table = pd.DataFrame({
    'HbA1c Level': hba1c_labels,
    'Prediction': [f"{hba1c_diabetes_counts.get(category, 0):.2f}% have diabetes" for category in hba1c_labels]
})

# Display the table
print(hba1c_table)
```

```
  HbA1c Level            Prediction
0       < 5.7   1.52% have diabetes
1   5.7 - 6.4   7.91% have diabetes
2      >= 6.5  24.96% have diabetes
```

```
# Define BMI categories
bmi_bins = [0, 18.5, 24.9, 29.9, float('inf')]
bmi_labels = ['Underweight', 'Normal', 'Overweight', 'Obesity']
df['BMI_Category'] = pd.cut(df['bmi'], bins=bmi_bins, labels=bmi_labels, include_lowest=True)

# Calculate percentage of diabetics in each BMI category
bmi_diabetes_counts = df.groupby('BMI_Category', observed=True)['diabetes'].mean() * 100

# Create a structured table
bmi_table = pd.DataFrame({
    'BMI Category': bmi_labels,
    'Prediction': [f"{bmi_diabetes_counts.get(category, 0):.2f}% have diabetes" for category in bmi_labels]
})

# Display the table
print(bmi_table)
```

```
  BMI Category            Prediction
0  Underweight   0.75% have diabetes
1       Normal   3.84% have diabetes
2   Overweight   7.25% have diabetes
3      Obesity  17.91% have diabetes
```

```
# Define Blood Glucose Level categories
glucose_bins = [0, 99, 125, float('inf')]
glucose_labels = ['≤ 99', '100 – 125', '≥ 126']
df['Glucose_Category'] = pd.cut(df['blood_glucose_level'], bins=glucose_bins, labels=glucose_labels, include_lowest=True)

# Calculate percentage of diabetics in each Blood Glucose Level category
glucose_diabetes_counts = df.groupby('Glucose_Category', observed=True)['diabetes'].mean() * 100

# Create a structured table
glucose_table = pd.DataFrame({
    'Blood Glucose Level': glucose_labels,
    'Prediction': [f"{glucose_diabetes_counts.get(category, 0):.2f}% have diabetes" for category in glucose_labels]
})

# Display the table
print(glucose_table)
```

```
  Blood Glucose Level            Prediction
0               ≤ 99   0.00% have diabetes
1          100 – 125   0.00% have diabetes
2              ≥ 126  11.83% have diabetes
```

Double-click (or enter) to edit

```
# Define Blood Glucose Level categories
glucose_bins = [0, 99, 125, float('inf')]
glucose_labels = ['≤ 99', '100 – 125', '≥ 126']
df['Glucose_Category'] = pd.cut(df['blood_glucose_level'], bins=glucose_bins, labels=glucose_labels, include_lowest=True)

# Plot a bar chart for blood glucose categories (Fixing FutureWarning)
plt.figure(figsize=(8, 6))
sns.countplot(x="Glucose_Category", data=df, hue="Glucose_Category", palette="coolwarm", legend=False)
```