diabeties-prediction-eda-svm

November 30, 2023

```
[5]: import pandas as pd
     from sklearn.model_selection import train_test_split
     from sklearn.preprocessing import OneHotEncoder
     import numpy as np
     import seaborn as sns
     import matplotlib.pyplot as plt
```

```
[6]: df=pd.read_csv('D:/CodeCaulse/diabetes_prediction_dataset.csv')
```

```
[7]: df
```

```
[7]:        gender   age  hypertension  heart_disease smoking_history    bmi  \
     0      Female  80.0             0              1           never  25.19
     1      Female  54.0             0              0         No Info  27.32
     2        Male  28.0             0              0           never  27.32
     3      Female  36.0             0              0         current  23.45
     4        Male  76.0             1              1         current  20.14
     …         …     …             …              …               …      …
     99995  Female  80.0             0              0         No Info  27.32
     99996  Female   2.0             0              0         No Info  17.37
     99997    Male  66.0             0              0          former  27.83
     99998  Female  24.0             0              0           never  35.42
     99999  Female  57.0             0              0         current  22.43

            HbA1c_level  blood_glucose_level  diabetes
     0              6.6                  140         0
     1              6.6                   80         0
     2              5.7                  158         0
     3              5.0                  155         0
     4              4.8                  155         0
     …              …                    …         …
     99995          6.2                   90         0
     99996          6.5                  100         0
     99997          5.7                  155         0
     99998          4.0                  100         0
     99999          6.6                   90         0
```

```
[100000 rows x 9 columns]
```

[8]:

```
df.info()
```

```
<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
```

[9]:

```
print(df.duplicated())
print(df.duplicated().sum())
```

```
0        False
1        False
2        False
3        False
4        False
         …
99995     True
99996    False
99997    False
99998    False
99999    False
Length: 100000, dtype: bool
3854
```

[10]:

```
df.drop_duplicates(inplace=True)
```

[11]:

```
df.duplicated().sum()
```

[11]:

```
0
```

[12]:

```
df.isna().sum()
```

```
[12]: 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
```

```
[13]: df.describe(include='object')
```

```
[13]:         gender smoking_history
      count    96146           96146
      unique       3               6
      top     Female           never
      freq     56161           34398
```

```
[14]: df.describe()
```

```
[14]:                 age  hypertension  heart_disease           bmi   HbA1c_level  \
      count  96146.000000  96146.000000   96146.000000  96146.000000  96146.000000
      mean      41.794326      0.077601       0.040803     27.321461      5.532609
      std       22.462948      0.267544       0.197833      6.767716      1.073232
      min        0.080000      0.000000       0.000000     10.010000      3.500000
      25%       24.000000      0.000000       0.000000     23.400000      4.800000
      50%       43.000000      0.000000       0.000000     27.320000      5.800000
      75%       59.000000      0.000000       0.000000     29.860000      6.200000
      max       80.000000      1.000000       1.000000     95.690000      9.000000

             blood_glucose_level      diabetes
      count         96146.000000  96146.000000
      mean            138.218231      0.088220
      std              40.909771      0.283616
      min              80.000000      0.000000
      25%             100.000000      0.000000
      50%             140.000000      0.000000
      75%             159.000000      0.000000
      max             300.000000      1.000000
```

```
[15]: numeric_col=[]
      non_numeric_col=[]
      for column in df.columns:
          if pd.api.types.is_numeric_dtype(df[column]):
              if(df[column].nunique()<5):
                  non_numeric_col.append(column)
```

```python
        else:
            numeric_col.append(column)
    else:
        non_numeric_col.append(column)
```

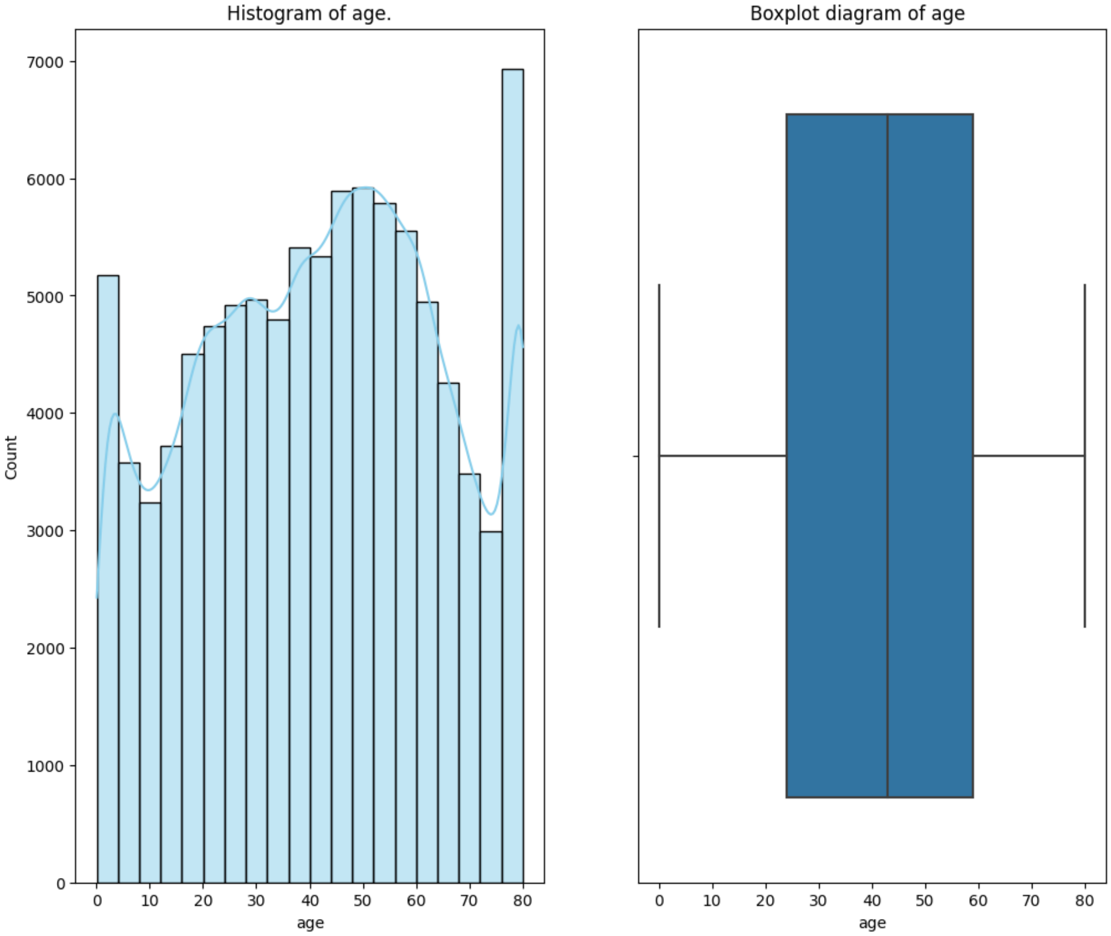
[16]:
```python
print(numeric_col)
print(non_numeric_col)
```

```
['age', 'bmi', 'HbA1c_level', 'blood_glucose_level']
['gender', 'hypertension', 'heart_disease', 'smoking_history', 'diabetes']
```

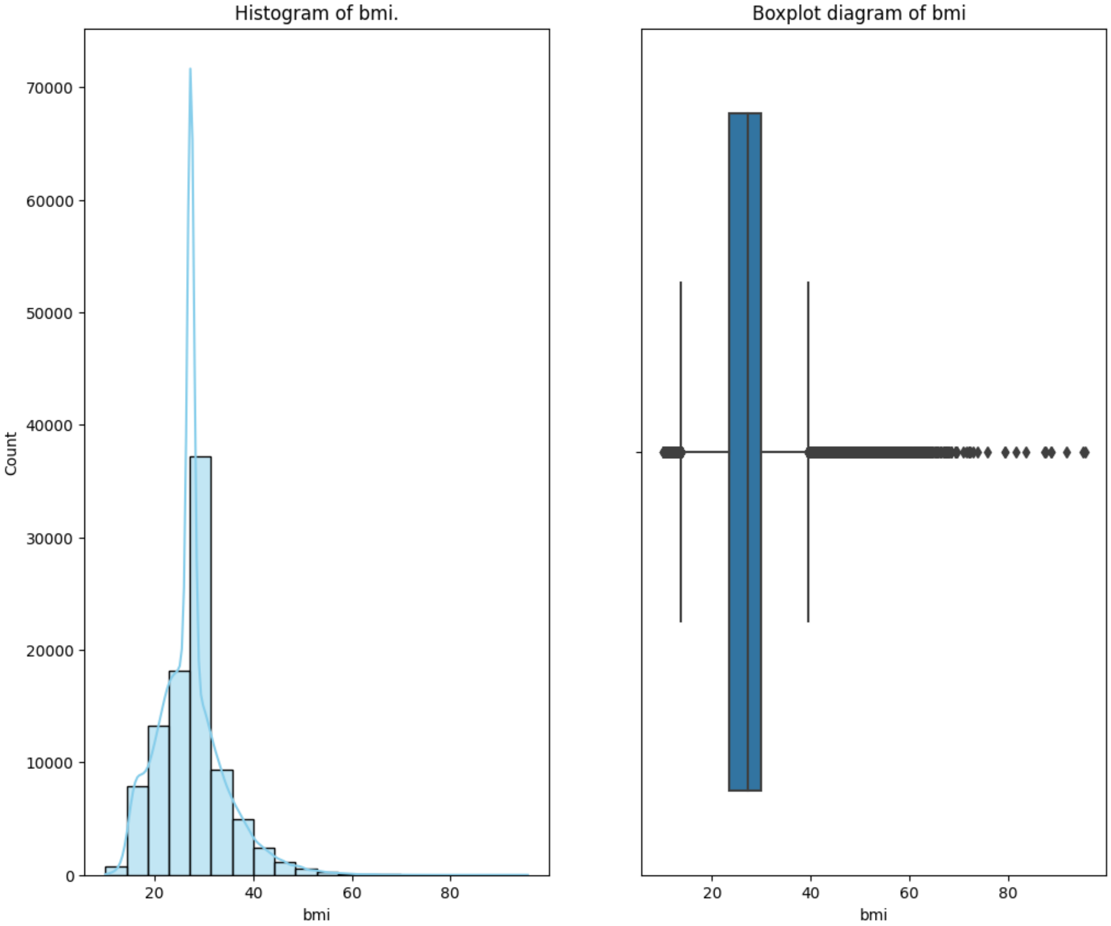
[17]:
```python
def univariate_analysis_numeric(col):
    fig, ax = plt.subplots(1, 2, figsize=(12,10))
    sns.histplot(x=df[col], kde=True, bins=20, color='skyblue',ax=ax[0])
    ax[0].set_title(f'Histogram of {col}.')

    sns.boxplot(x=df[col],ax=ax[1])
    ax[1].set_title(f'Boxplot diagram of {col}     ')
```

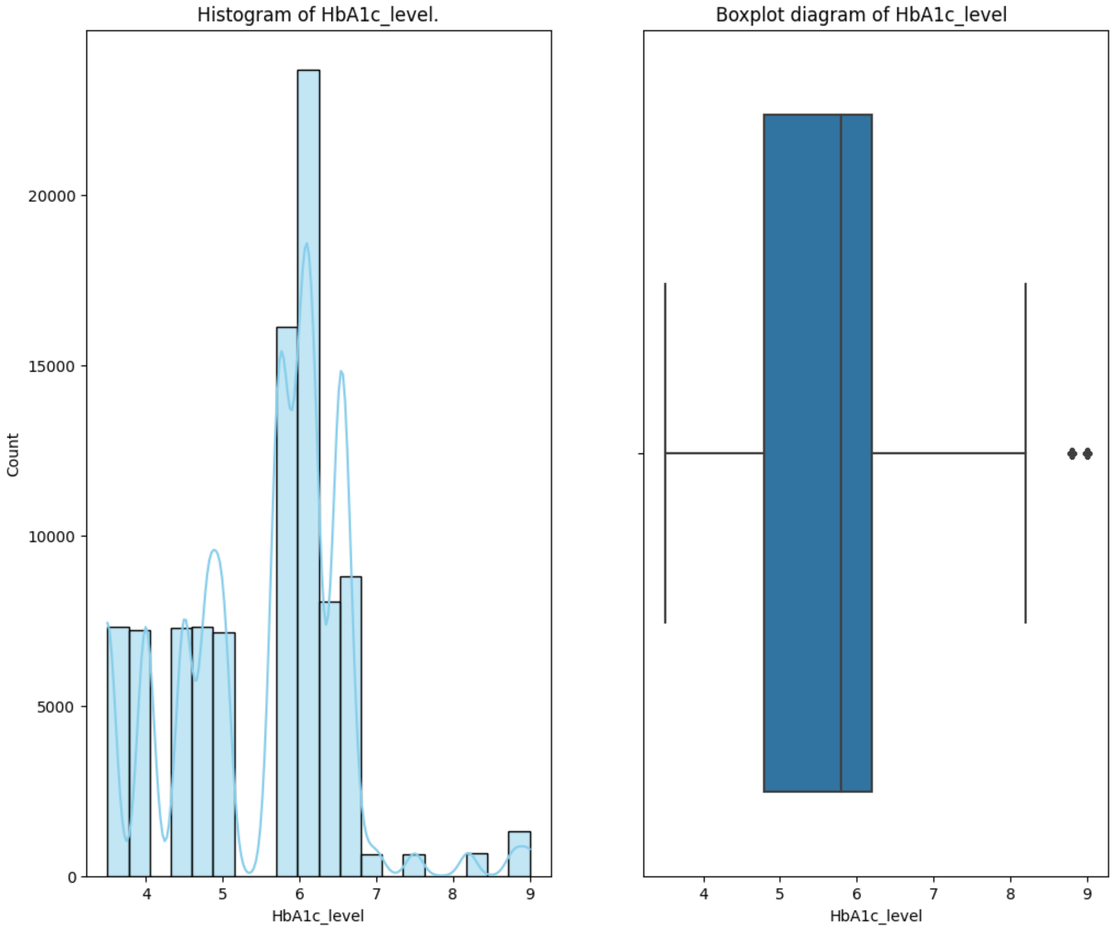
[18]:
```python
for col in numeric_col:
    print(f' Univariate analysis for {col} column:')
    univariate_analysis_numeric(col)
```

```
 Univariate analysis for age column:
 Univariate analysis for bmi column:
 Univariate analysis for HbA1c_level column:
 Univariate analysis for blood_glucose_level column:
```


Histogram of age.

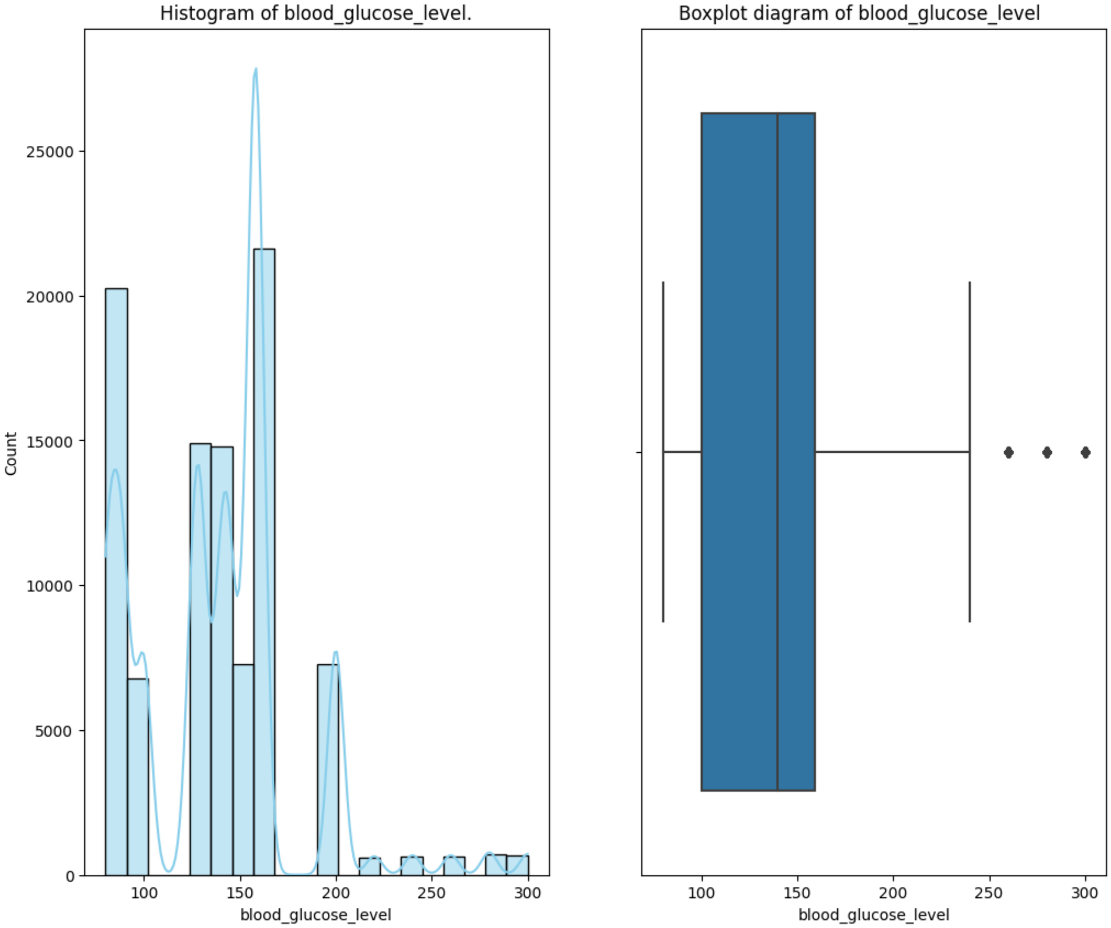
Boxplot diagram of age


Histogram of bmi.
Count
70000
60000
50000
40000
30000
20000
10000
0
20
40
60
80
bmi
Boxplot diagram of bmi
20
40
60
80
bmi



Histogram of HbA1c_level.

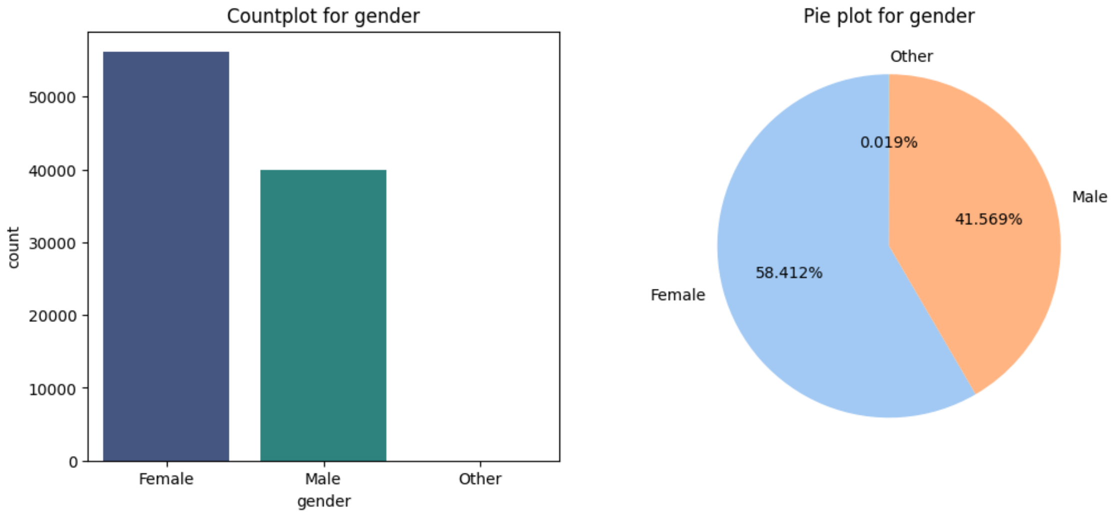
Boxplot diagram of HbA1c_level



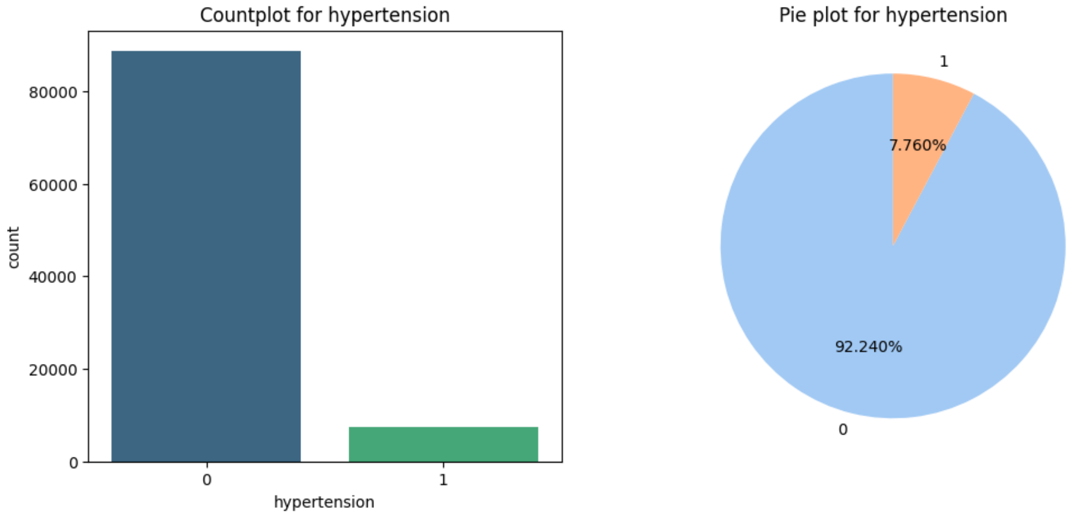
```
[19]: def univariate_analysis_cat(col):
          fig, ax = plt.subplots(1, 2, figsize=(12, 5))

          # Countplot
          sns.countplot(x=df[col],data=df ,palette='viridis', ax=ax[0])
          ax[0].set_title(f'Countplot for {col}')

          # Pie plot
          data_counts = df[col].value_counts()
          ax[1].pie(data_counts, labels=data_counts.index, autopct='%1.3f%%',␣
       ↪startangle=90, colors=sns.color_palette('pastel'))
          ax[1].set_title(f'Pie plot for {col}')

          plt.show()
```

```
[20]: for col in non_numeric_col:
          print(f' Univariate analysis for {col} column:')
          univariate_analysis_cat(col)
```

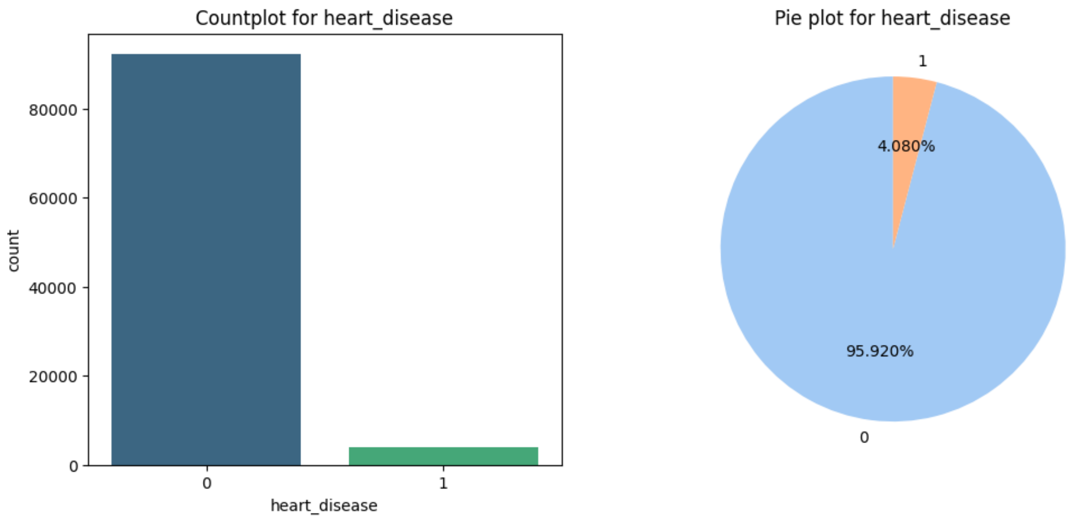
```
Univariate analysis for gender column:
```



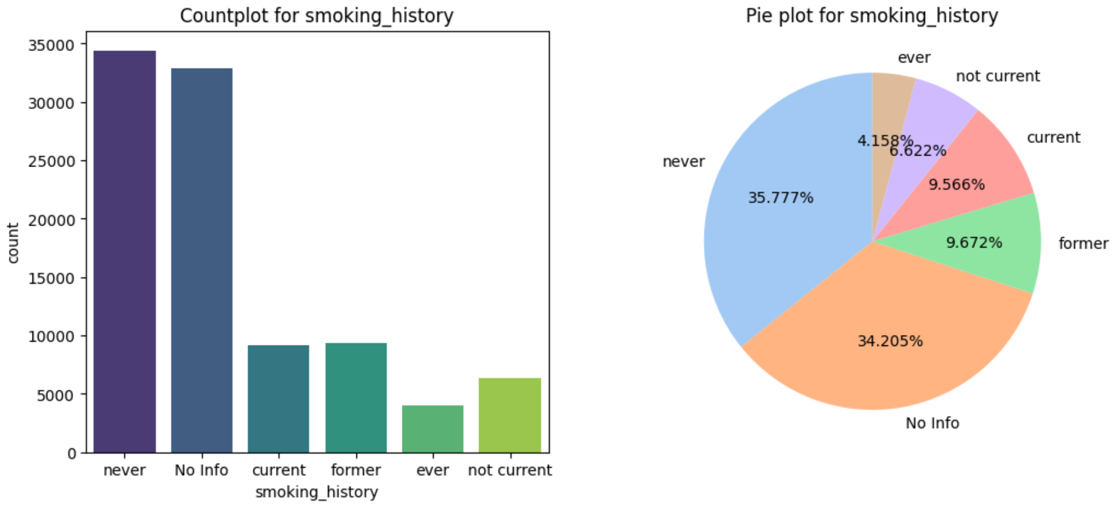
```
Univariate analysis for hypertension column:
```



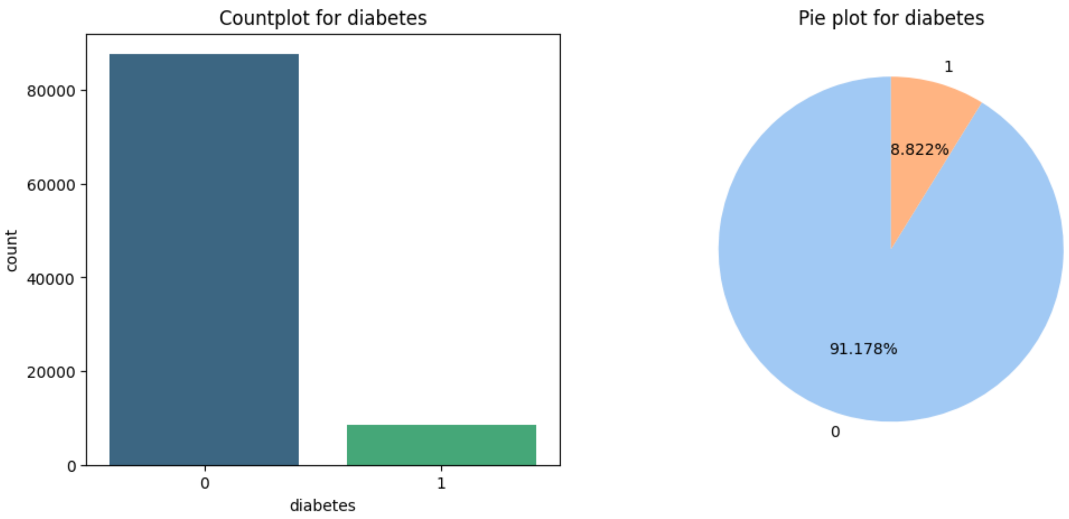
```
Univariate analysis for heart_disease column:
```



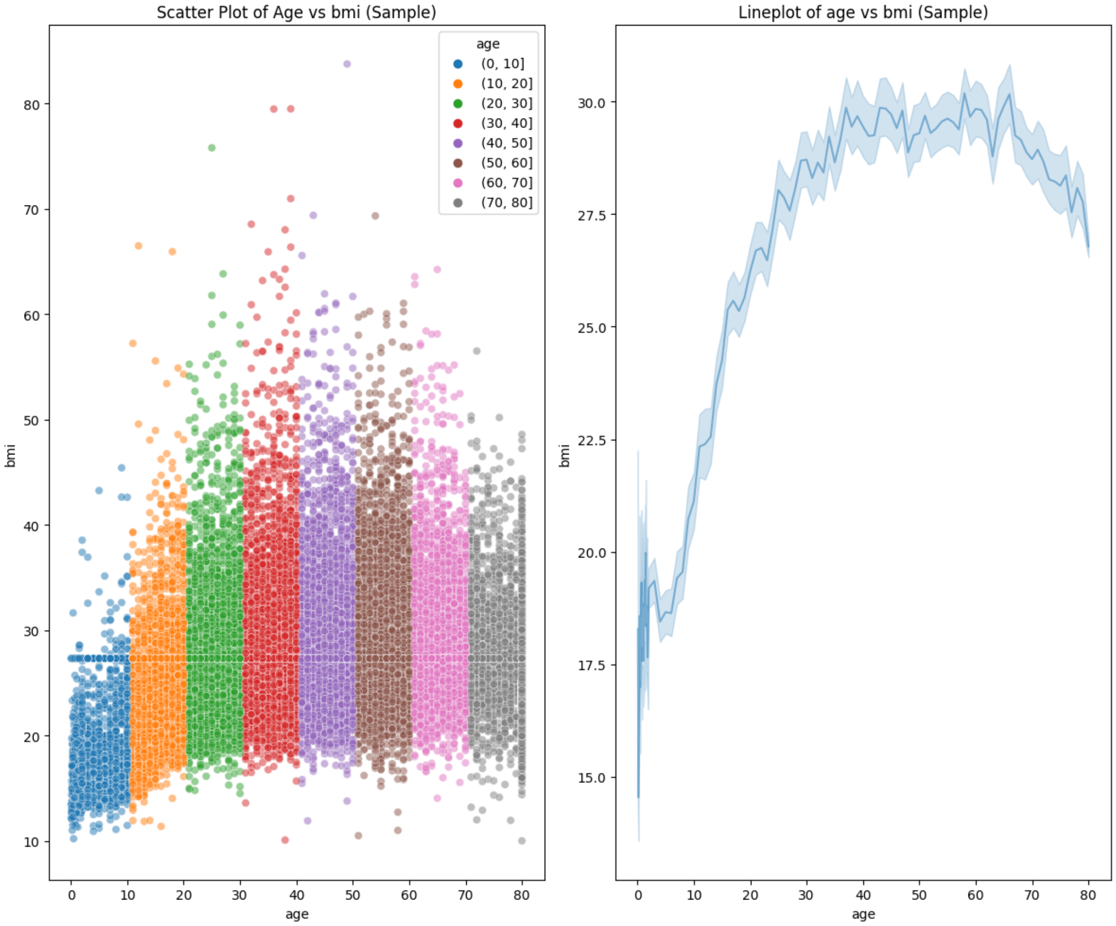
```
Univariate analysis for smoking_history column:
```

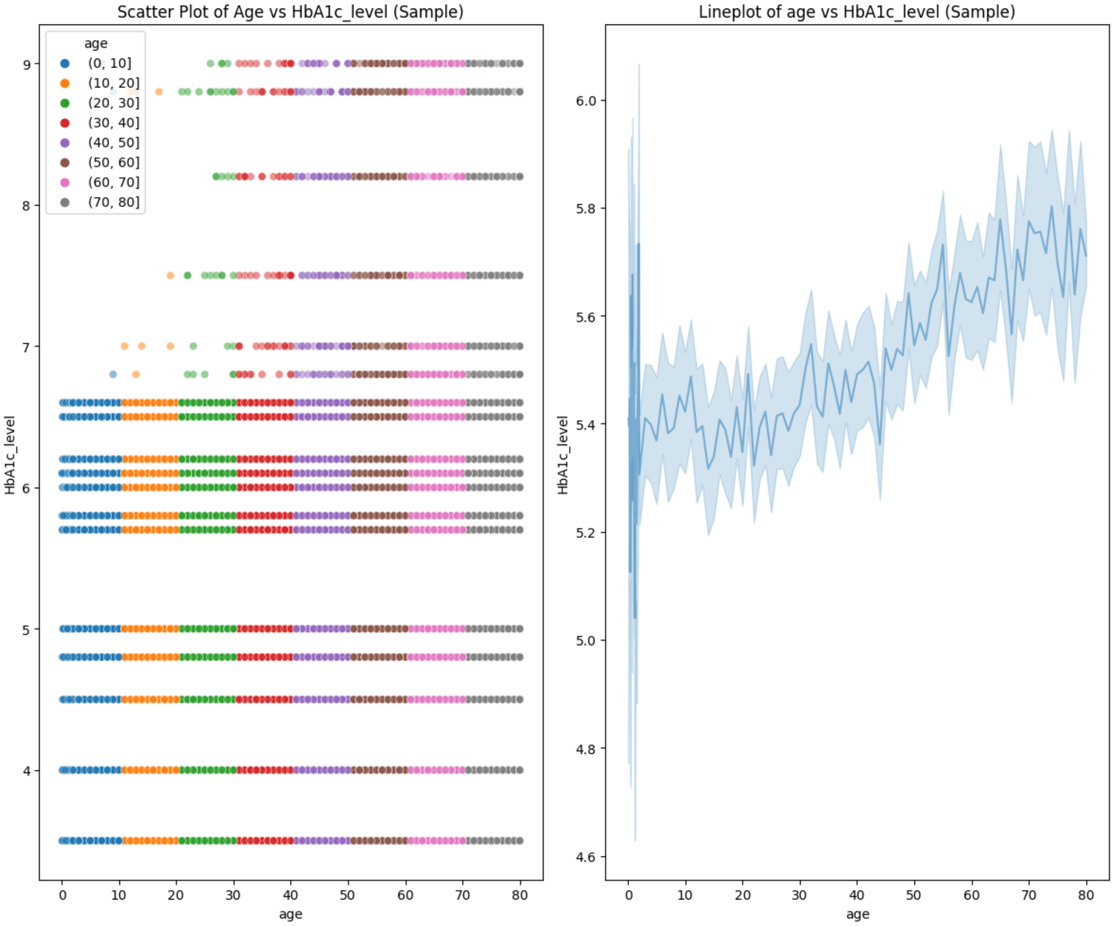


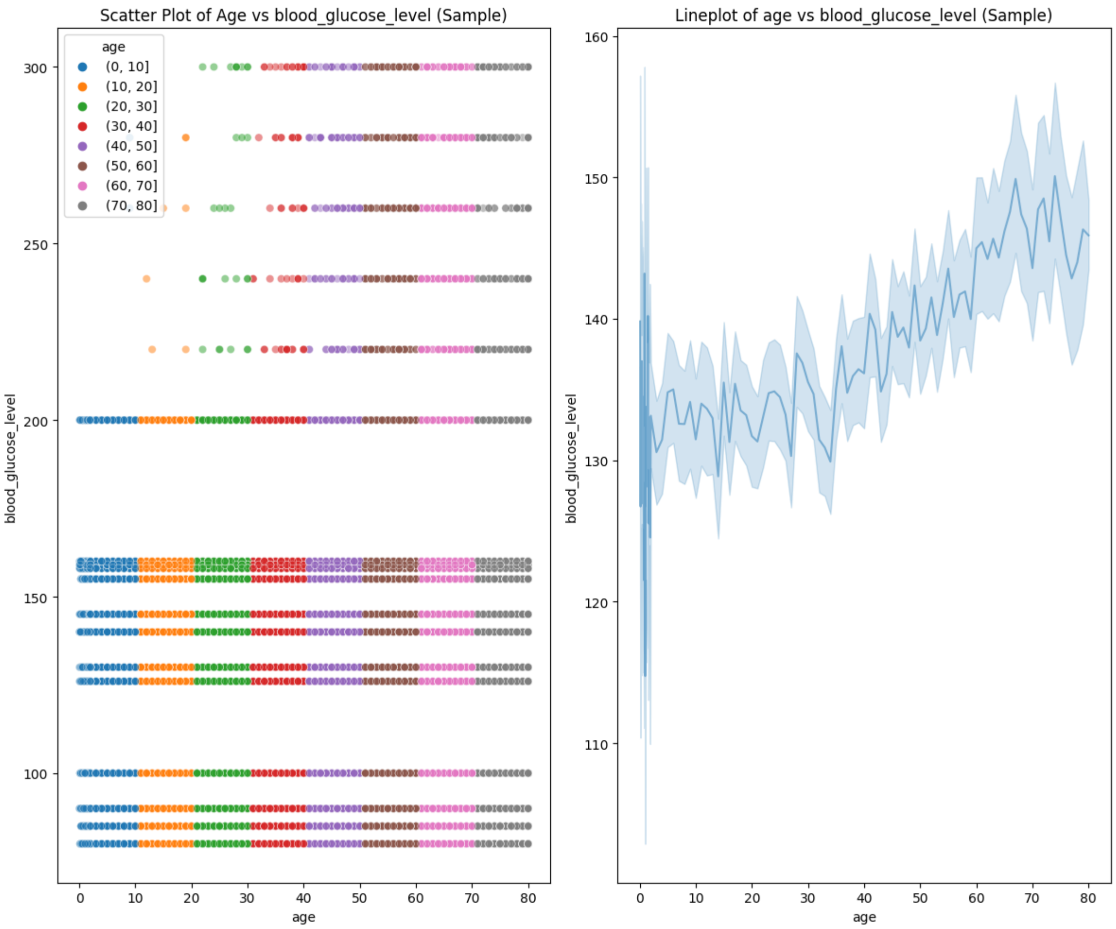
```
Univariate analysis for diabetes column:
```



[21]:
```
sample_size = 30000
sample_df = df.sample(n=sample_size, random_state=42)
age_group = pd.cut(df['age'], bins=[0, 10, 20, 30, 40, 50, 60, 70, 80])

for col in numeric_col[1:]:
    fig, ax = plt.subplots(1, 2, figsize=(12, 10))
    sns.scatterplot(x='age', y=df[col], data=sample_df,hue=age_group, alpha=0.
 ↪5,ax=ax[0])
    ax[0].set_title(f'Scatter Plot of Age vs {col} (Sample)')

    sns.lineplot(x='age',y=df[col],data=sample_df,alpha=0.5,ax=ax[1])
    ax[1].set_title(f'Lineplot of age vs {col} (Sample)')
    plt.tight_layout()
    plt.show()
```


Scatter Plot of Age vs bmi (Sample)
age
● (0, 10]
● (10, 20]
● (20, 30]
● (30, 40]
● (40, 50]
● (50, 60]
● (60, 70]
● (70, 80]
bmi
80
70
60
50
40
30
20
10
0
10
20
30
40
50
60
70
80
age
Lineplot of age vs bmi (Sample)
bmi
30.0
27.5
25.0
22.5
20.0
17.5
15.0
0
10
20
30
40
50
60
70
80
age

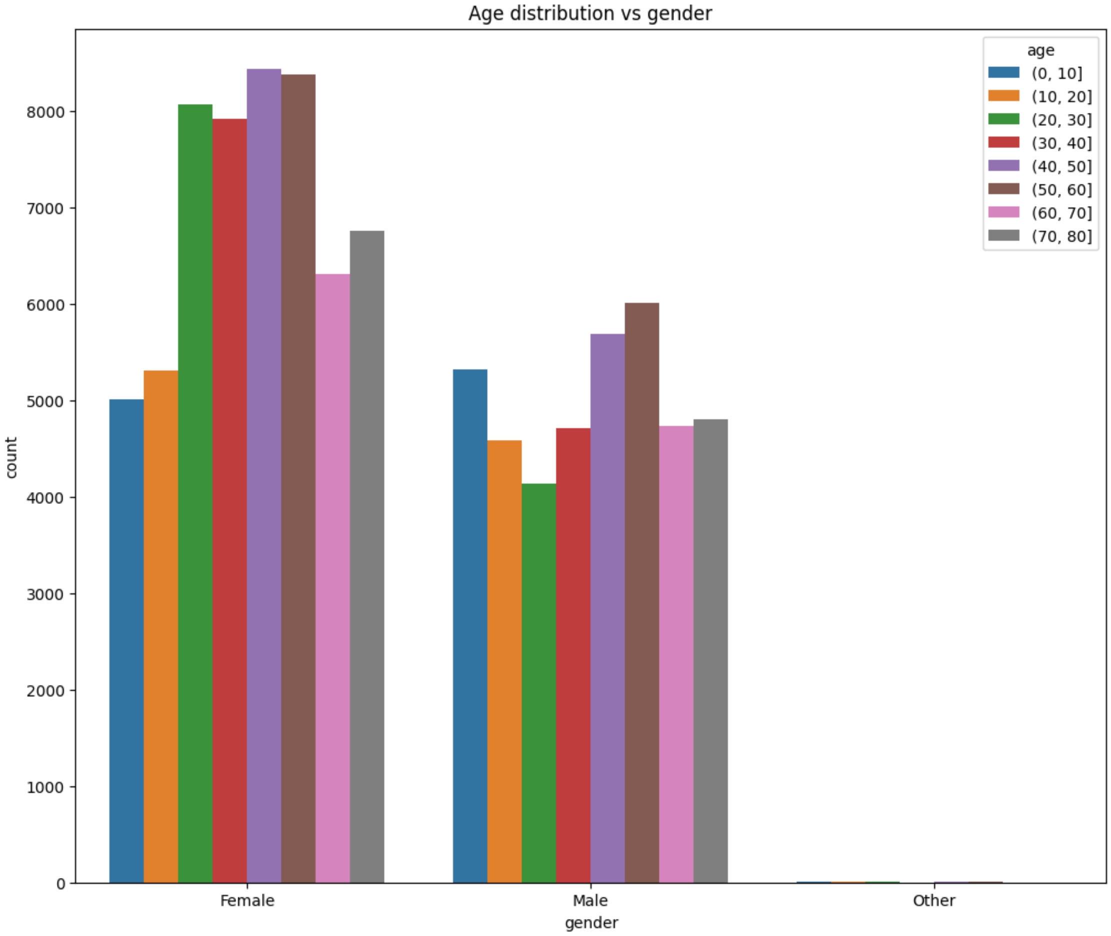

Scatter Plot of Age vs HbA1c_level (Sample)
age
(0, 10]
(10, 20]
(20, 30]
(30, 40]
(40, 50]
(50, 60]
(60, 70]
(70, 80]
HbA1c_level
9
8
7
6
5
4
0
10
20
30
40
50
60
70
80
age
Lineplot of age vs HbA1c_level (Sample)
HbA1c_level
6.0
5.8
5.6
5.4
5.2
5.0
4.8
4.6
0
10
20
30
40
50
60
70
80
age

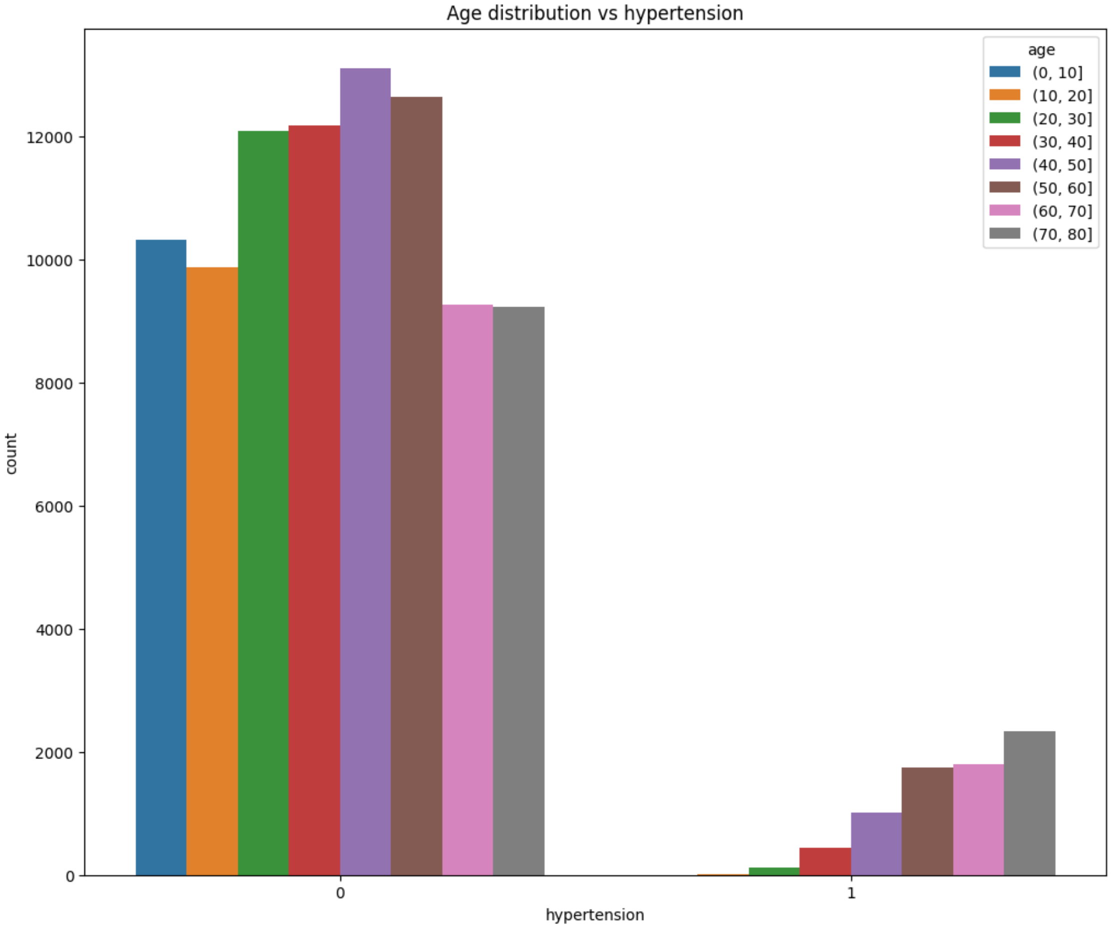


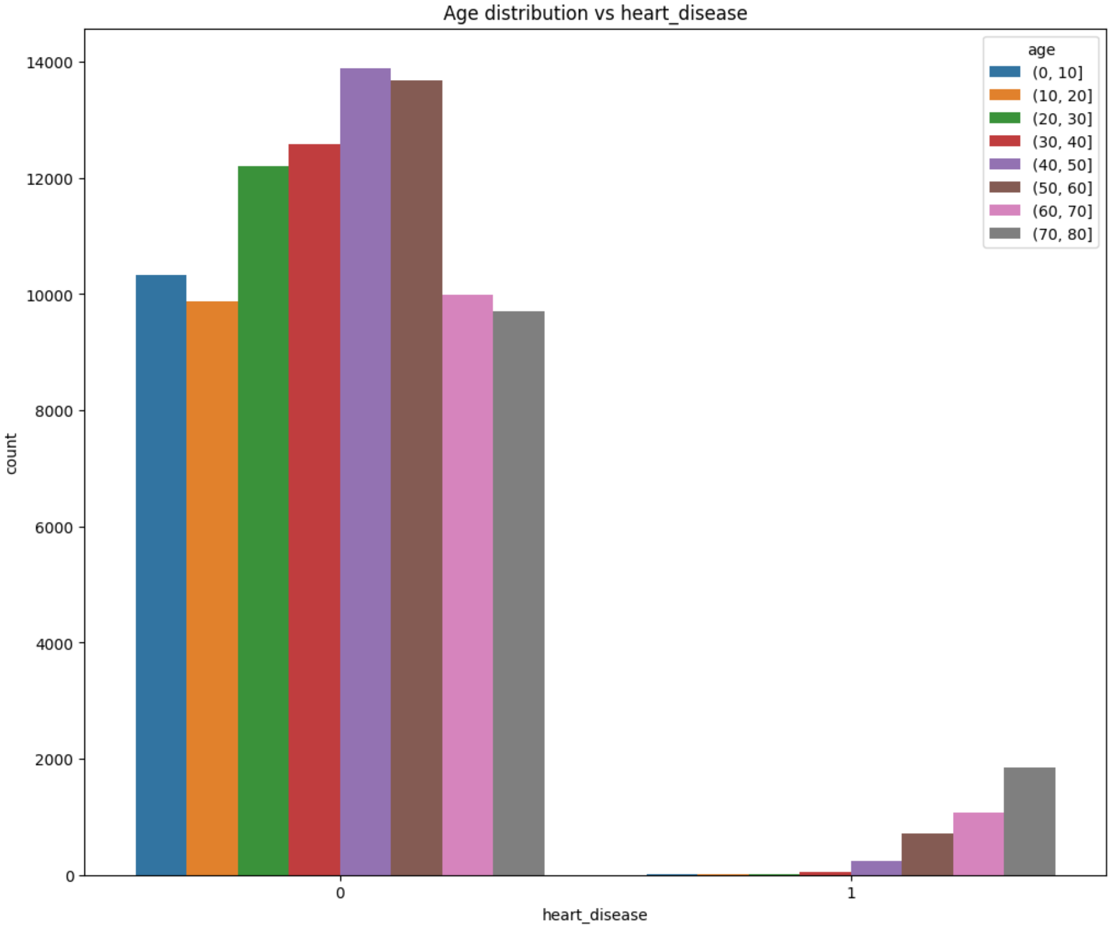
[22]:
```
print(sample_df['age'].mean())
print(df['age'].mean())
```

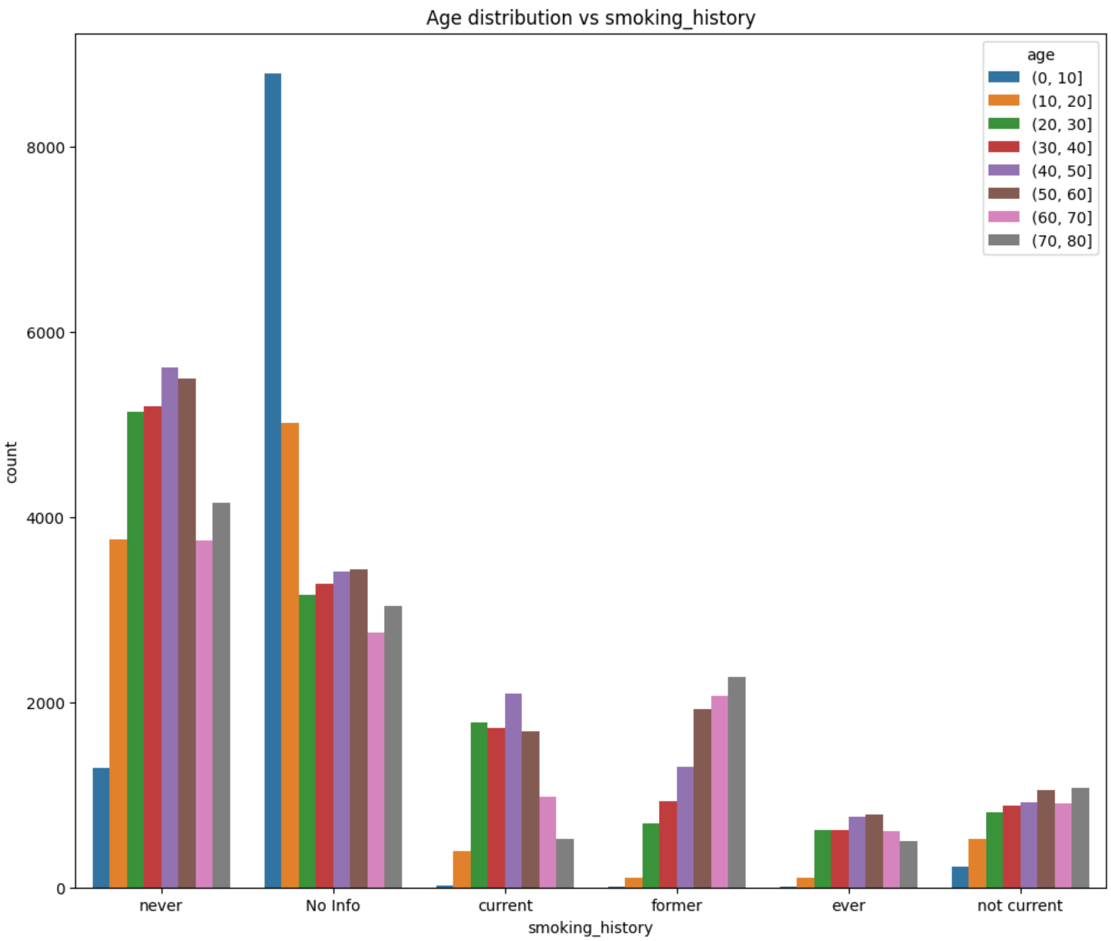
```
41.85690399999999
41.79432571297817
```

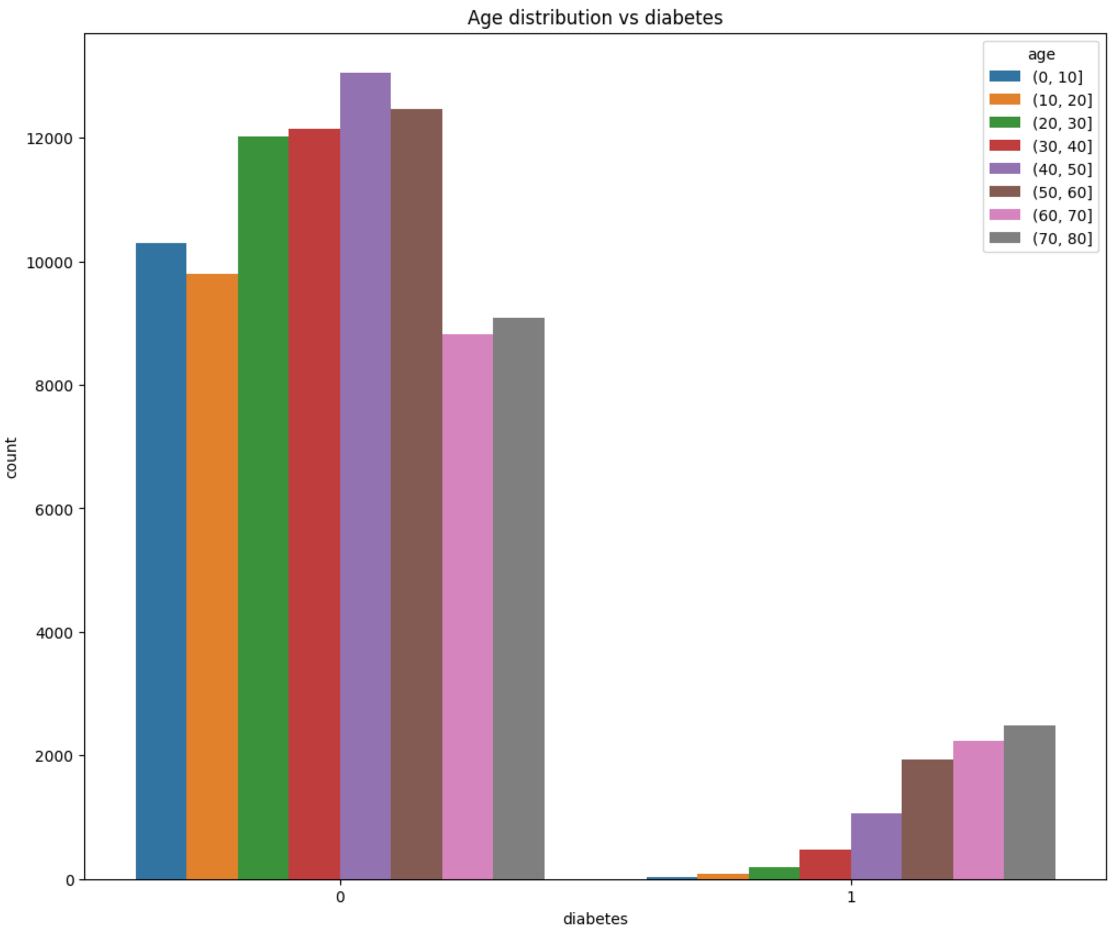
[23]:
```
age_group = pd.cut(df['age'], bins=[0, 10, 20, 30, 40, 50, 60, 70, 80])
for i in non_numeric_col:
    plt.figure(figsize=(12,10))
    sns.countplot(x=df[i],data=df,hue=age_group)
    plt.title(f'Age distribution vs {i}')
    plt.show()
```


Age distribution vs gender
age
(0, 10]
(10, 20]
(20, 30]
(30, 40]
(40, 50]
(50, 60]
(60, 70]
(70, 80]
count
0
1000
2000
3000
4000
5000
6000
7000
8000
Female
Male
Other
gender


Age distribution vs hypertension
age
(0, 10]
(10, 20]
(20, 30]
(30, 40]
(40, 50]
(50, 60]
(60, 70]
(70, 80]
count
0
2000
4000
6000
8000
10000
12000
0
1
hypertension


Age distribution vs heart_disease
count
14000
12000
10000
8000
6000
4000
2000
0
0
1
heart_disease
age
(0, 10]
(10, 20]
(20, 30]
(30, 40]
(40, 50]
(50, 60]
(60, 70]
(70, 80]


Age distribution vs smoking_history
age
(0, 10]
(10, 20]
(20, 30]
(30, 40]
(40, 50]
(50, 60]
(60, 70]
(70, 80]
count
0
2000
4000
6000
8000
never
No Info
current
former
ever
not current
smoking_history



[24]:
```
from sklearn.preprocessing import LabelEncoder
le=LabelEncoder()
for col in non_numeric_col:
    sample_df[col]=le.fit_transform(sample_df[col])
sample_df
```

[24]:
```
       gender   age  hypertension  heart_disease  smoking_history    bmi  
2547        0   5.0             0              0                0  15.14  \
34774       1  19.0             0              0                4  22.74
71084       0  52.0             0              0                4  24.27
50584       1  55.0             0              0                0  27.32
80788       0  22.0             0              0                4  28.78
…       …     …            …             …             …     …
54431       0  26.0             0              0                3  28.27
55182       0  57.0             0              0                4  22.12
92776       1  74.0             0              1                2  29.83
76035       0  11.0             0              0                0  27.32
81939       0  80.0             0              0                1  20.03
```

```
       HbA1c_level  blood_glucose_level  diabetes
2547           4.5                   90         0
34774          6.6                   85         0
71084          7.5                  220         1
50584          5.7                   85         0
80788          4.5                  200         0
…            …                    …       …
54431          6.2                  100         0
55182          5.0                  100         0
92776          4.8                  160         0
76035          6.2                   90         0
81939          6.6                   90         0

[30000 rows x 9 columns]
```

[25]:
```
x = sample_df.drop('diabetes', axis=1)
y = sample_df['diabetes']
```

[26]:
```
from sklearn.svm import SVC
from sklearn.metrics import classification_report, accuracy_score,␣
 ↪confusion_matrix
X_train, X_test, y_train, y_test = train_test_split(x, y, test_size = 0.3)
model_svm = SVC(kernel = 'linear', random_state = 0)
model_svm.fit(X_train, y_train)
```

[26]:
```
SVC(kernel='linear', random_state=0)
```

[27]:
```
y_pred = model_svm.predict(X_test)
```

[28]:
```
accuracy_svm = accuracy_score(y_test, y_pred)
print(accuracy_svm)
```

```
0.9582222222222222
```

[29]:
```
classification_rep_svm = classification_report(y_test, y_pred)
print(classification_rep_svm)
```

```
              precision    recall  f1-score   support

           0       0.96      1.00      0.98      8192
           1       0.93      0.58      0.71       808

    accuracy                           0.96      9000
   macro avg       0.95      0.79      0.85      9000
weighted avg       0.96      0.96      0.95      9000
```