

```
In [1]: #Import the Libraries needed
from pandas import Series, DataFrame
from pylab import rcParams
from scipy.stats import spearmann
from sklearn import datasets
from sklearn import metrics
from sklearn import preprocessing
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import scale
from statsmodels.formula.api import ols
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import scipy
import seaborn as sns
import sklearn as sl
import sklearn.metrics as sm
import statsmodels.api as sm
import statsmodels.formula.api as smf
```

```
In [2]: pip install statsmodels
```

```
Requirement already satisfied: statsmodels in c:\users\brittany\anaconda3\lib\site-packages (0.13.2)
Requirement already satisfied: numpy>=1.17 in c:\users\brittany\anaconda3\lib\site-packages (from statsmodels) (1.21.5)
Requirement already satisfied: scipy>=1.3 in c:\users\brittany\anaconda3\lib\site-packages (from statsmodels) (1.7.3)
Requirement already satisfied: pandas>=0.25 in c:\users\brittany\anaconda3\lib\site-packages (from statsmodels) (1.4.3)
Requirement already satisfied: patsy>=0.5.2 in c:\users\brittany\anaconda3\lib\site-packages (from statsmodels) (0.5.2)
Requirement already satisfied: packaging>=21.3 in c:\users\brittany\anaconda3\lib\site-packages (from statsmodels) (21.3)
Requirement already satisfied: pyparsing!=3.0.5,>=2.0.2 in c:\users\brittany\anaconda3\lib\site-packages (from packaging>=21.3->statsmodels) (3.0.4)
Requirement already satisfied: python-dateutil>=2.8.1 in c:\users\brittany\anaconda3\lib\site-packages (from pandas>=0.25->statsmodels) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in c:\users\brittany\anaconda3\lib\site-packages (from pandas>=0.25->statsmodels) (2022.1)
Requirement already satisfied: six in c:\users\brittany\anaconda3\lib\site-packages (from patsy>=0.5.2->statsmodels) (1.16.0)
Note: you may need to restart the kernel to use updated packages.
```

```
In [3]: #Load the dataset
df = pd.read_csv("medical clean 1.1.23.csv")
```

```
In [4]: #Check total rows/columns
rows = df.shape[0]
cols = df.shape[1]
# display the number of rows and columns
print("Number of Rows: " + str(rows))
print("Number of Columns: " + str(cols))
```

```
Number of Rows: 10000
Number of Columns: 50
```

```
In [5]: #check for nan and null values  
df.isna().any()
```

```
Out[5]: CaseOrder      False  
Customer_id     False  
Interaction     False  
UID             False  
City            False  
State           False  
County          False  
Zip             False  
Lat             False  
Lng              False  
Population      False  
Area             False  
TimeZone         False  
Job              False  
Children         False  
Age              False  
Income           False  
Marital          False  
Gender           False  
ReAdmis          False  
VitD_levels     False  
Doc_visits      False  
Full_meals_eaten False  
vitD_supp        False  
Soft_drink        False  
Initial_admin    False  
HighBlood        False  
Stroke           False  
Complication_risk False  
Overweight        False  
Arthritis         False  
Diabetes          False  
Hyperlipidemia   False  
BackPain          False  
Anxiety           False  
Allergic_rhinitis False  
Reflux_esophagitis False  
Asthma            False  
Services          False  
Initial_days      False  
TotalCharge       False  
Additional_charges False  
Item1             False  
Item2             False  
Item3             False  
Item4             False  
Item5             False  
Item6             False  
Item7             False  
Item8             False  
dtype: bool
```

```
In [6]: df.isnull().any()
```

```
Out[6]: CaseOrder      False
Customer_id     False
Interaction     False
UID             False
City            False
State           False
County          False
Zip             False
Lat             False
Lng             False
Population      False
Area            False
TimeZone         False
Job             False
Children        False
Age              False
Income           False
Marital          False
Gender           False
ReAdmis          False
VitD_levels     False
Doc_visits      False
Full_meals_eaten False
vitD_supp       False
Soft_drink       False
Initial_admin    False
HighBlood        False
Stroke           False
Complication_risk False
Overweight        False
Arthritis         False
Diabetes          False
Hyperlipidemia   False
BackPain          False
Anxiety           False
Allergic_rhinitis False
Reflux_esophagitis False
Asthma            False
Services          False
Initial_days     False
TotalCharge      False
Additional_charges False
Item1            False
Item2            False
Item3            False
Item4            False
Item5            False
Item6            False
Item7            False
Item8            False
dtype: bool
```

```
In [7]: # count of unique values in each column  
print(df.nunique())
```

```
CaseOrder      10000  
Customer_id    10000  
Interaction    10000  
UID           10000  
City            6072  
State            52  
County          1607  
Zip             8612  
Lat              8588  
Lng              8725  
Population     5951  
Area              3  
TimeZone         26  
Job              639  
Children         11  
Age              72  
Income           9993  
Marital            5  
Gender             3  
ReAdmis           2  
VitD_levels     9976  
Doc_visits        9  
Full_meals_eaten   8  
vitD_supp         6  
Soft_drink         2  
Initial_admin      3  
HighBlood          2  
Stroke             2  
Complication_risk  3  
Overweight          2  
Arthritis           2  
Diabetes            2  
Hyperlipidemia      2  
BackPain            2  
Anxiety             2  
Allergic_rhinitis    2  
Reflux_esophagitis   2  
Asthma              2  
Services            4  
Initial_days       9997  
TotalCharge        9997  
Additional_charges  9418  
Item1              8  
Item2              7  
Item3              8  
Item4              7  
Item5              7  
Item6              7  
Item7              7  
Item8              7  
dtype: int64
```

```
In [10]: #drop all columns and rows not being used  
to_drop = ['CaseOrder', 'Customer_id', 'Interaction', 'UID', 'City', 'State', 'County', 'Zip', 'Lat', 'Lng', 'Population', 'Area',  
df.drop(to_drop, inplace=True, axis=1)
```

```
In [15]: #Change object to category for ReAdmis
df["ReAdmis"] = df["ReAdmis"].astype('category')
#Change object to category for Anxiety
df["Anxiety"] = df["Anxiety"].astype('category')
#Change object to category for Overweight
df["Overweight"] = df["Overweight"].astype('category')
#Change object to category for Arthritis
df["Arthritis"] = df["Arthritis"].astype('category')
#Change object to category for HighBlood
df["HighBlood"] = df["HighBlood"].astype('category')
#Change object to category for Stroke
df["Stroke"] = df["Stroke"].astype('category')
#Change object to category for Gender
df["Gender"] = df["Gender"].astype('category')
#Change object to category for Diabetes
df["Diabetes"] = df["Diabetes"].astype('category')
#Change object to category for Asthma
df["Asthma"] = df["Asthma"].astype('category')
#Change object to category for back pain
df["BackPain"] = df["BackPain"].astype('category')
#Change object to category for Hyperlipidemia
df["Hyperlipidemia"] = df["Hyperlipidemia"].astype('category')
```

```
In [16]: #check data types
df.dtypes
```

```
Out[16]: Gender      category
ReAdmis    category
Doc_visits   int64
HighBlood    category
Stroke       category
Overweight    category
Arthritis    category
Diabetes     category
Hyperlipidemia category
BackPain     category
Anxiety      category
Asthma       category
dtype: object
```

```
In [18]: #Run get_dummies on categorical
pd.get_dummies(df, columns = ['Gender', 'ReAdmis', 'Anxiety', 'Overweight', 'HighBlood', 'Arthritis', 'Stroke', 'Diabetes', 'Asthma'])
```

```
Out[18]:
```

	Doc_visits	Gender_Female	Gender_Male	Gender_Nonbinary	ReAdmis_No	ReAdmis_Yes	Anxiety_No	Anxiety_Yes	Overweight_No	Overweight_Yes	...
0	6	0	1	0	1	0	0	1	1	1	0 ...
1	4	1	0	0	1	0	1	0	0	0	1 ...
2	4	1	0	0	1	0	1	0	0	0	1 ...
3	4	0	1	0	1	0	1	0	1	0	0 ...
4	5	1	0	0	1	0	1	0	0	1	0 ...
...
9995	4	0	1	0	1	0	0	1	1	0	0 ...
9996	5	0	1	0	0	1	1	0	0	1	0 ...
9997	4	1	0	0	0	1	0	1	0	1	0 ...
9998	5	0	1	0	0	1	1	0	0	0	1 ...
9999	5	1	0	0	0	1	1	0	0	1	0 ...

10000 rows × 24 columns

```
In [19]: #create new df with the get_dummies responses
dfupdated = pd.get_dummies(df, columns = ['ReAdmis', 'Anxiety', 'Overweight', 'Arthritis', 'HighBlood', 'Gender', 'Stroke', 'Diabe
```

```
In [20]: #Drop columns to avoid dummy variable trap
to_drop = ['Gender_Male', 'Gender_Nonbinary', 'ReAdmis_No', 'Anxiety_No', 'Overweight_No', 'Stroke_No', 'Diabetes_No', 'Asthma_No']
dfupdated.drop(to_drop, inplace=True, axis=1)
```

```
In [21]: #Run a describe
dfupdated.describe()
```

Out[21]:

	Doc_visits	ReAdmis_Yes	Anxiety_Yes	Overweight_Yes	Arthritis_Yes	HighBlood_Yes	Gender_Female	Stroke_Yes	Diabetes_Yes	Asthma_Yes	Hy
count	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000
mean	5.012200	0.366900	0.321500	0.709400	0.357400	0.409000	0.501800	0.199300	0.27380	0.28930	
std	1.045734	0.481983	0.467076	0.454062	0.479258	0.491674	0.50022	0.399494	0.44593	0.45346	
min	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	4.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
50%	5.000000	0.000000	0.000000	1.000000	0.000000	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000
75%	6.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000
max	9.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000

```
In [23]: # Import statistics Library
import statistics
```

```
In [26]: #view the mean
print(dfupdated.mean())
```

```
Doc_visits      5.0122
ReAdmis_Yes    0.3669
Anxiety_Yes    0.3215
Overweight_Yes  0.7094
Arthritis_Yes   0.3574
HighBlood_Yes   0.4090
Gender_Female   0.5018
Stroke_Yes     0.1993
Diabetes_Yes    0.2738
Asthma_Yes      0.2893
Hyperlipidemia_Yes 0.3372
BackPain_Yes    0.4114
dtype: float64
```

```
In [30]: print(dfupdated['ReAdmis_Yes'].mode())
0    0
Name: ReAdmis_Yes, dtype: uint8
```

```
In [32]: print(dfupdated['Anxiety_Yes'].mode())
0    0
Name: Anxiety_Yes, dtype: uint8
```

```
In [33]: print(dfupdated['Overweight_Yes'].mode())
0    1
Name: Overweight_Yes, dtype: uint8
```

```
In [34]: print(dfupdated['Arthritis_Yes'].mode())
0    0
Name: Arthritis_Yes, dtype: uint8
```

```
In [35]: print(dfupdated['HighBlood_Yes'].mode())
0    0
Name: HighBlood_Yes, dtype: uint8
```

```
In [36]: print(dfupdated['Asthma_Yes'].mode())
0    0
Name: Asthma_Yes, dtype: uint8
```

```
In [37]: print(dfupdated['Gender_Female'].mode())
0    1
Name: Gender_Female, dtype: uint8
```

```
In [38]: print(dfupdated['Stroke_Yes'].mode())
0    0
Name: Stroke_Yes, dtype: uint8
```

```
In [39]: print(dfupdated['Diabetes_Yes'].mode())
```

```
0    0  
Name: Diabetes_Yes, dtype: uint8
```

```
In [40]: print(dfupdated['Hyperlipidemia_Yes'].mode())
```

```
0    0  
Name: Hyperlipidemia_Yes, dtype: uint8
```

```
In [41]: print(dfupdated['BackPain_Yes'].mode())
```

```
0    0  
Name: BackPain_Yes, dtype: uint8
```

```
In [42]: print(dfupdated['Doc_visits'].mode())
```

```
0    5  
Name: Doc_visits, dtype: int64
```

```
In [43]: #Check independence of each variable with Spearman Coefficient
```

```
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]  
Doc_visits = dfupdated["Doc_visits"]  
#Find the Spearmen Cofficient.  
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Doc_visits)  
spearmanr_coff
```

```
Out[43]: -0.0006162697767207155
```

```
In [44]: #Check independence of each variable with Spearman Coefficient
```

```
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]  
Gender_Female = dfupdated["Gender_Female"]  
#Find the Spearmen Cofficient.  
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Gender_Female)  
spearmanr_coff
```

```
Out[44]: -0.011662563587899893
```

```
In [45]: #Check independence of each variable with Spearman Coefficient
```

```
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]  
Anxiety_Yes = dfupdated["Anxiety_Yes"]  
#Find the Spearmen Cofficient.  
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Anxiety_Yes)  
spearmanr_coff
```

```
Out[45]: 0.0024062642580066325
```

```
In [46]: #Check independence of each variable with Spearman Coefficient
```

```
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]  
Overweight_Yes = dfupdated["Overweight_Yes"]  
#Find the Spearmen Cofficient.  
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Overweight_Yes)  
spearmanr_coff
```

```
Out[46]: -0.008586002506313991
```

```
In [47]: #Check independence of each variable with Spearman Coefficient
```

```
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]  
Stroke_Yes = dfupdated["Stroke_Yes"]  
#Find the Spearmen Cofficient.  
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Stroke_Yes)  
spearmanr_coff
```

```
Out[47]: 0.0009184539170458379
```

```
In [48]: #Check independence of each variable with Spearman Coefficient
```

```
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]  
Diabetes_Yes = dfupdated["Diabetes_Yes"]  
#Find the Spearmen Cofficient.  
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Diabetes_Yes)  
spearmanr_coff
```

```
Out[48]: -0.00305812979631911
```

```
In [49]: #Check independence of each variable with Spearman Coefficient
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]
Asthma_Yes = dfupdated["Asthma_Yes"]
#Find the Spearmen Coefficient.
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Asthma_Yes)
spearmanr_coff
```

Out[49]: -0.017132793168549827

```
In [50]: #Check independence of each variable with Spearman Coefficient
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]
Hyperlipidemia_Yes = dfupdated["Hyperlipidemia_Yes"]
#Find the Spearmen Coefficient.
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Hyperlipidemia_Yes)
spearmanr_coff
```

Out[50]: 0.004306908097121766

```
In [51]: #Check independence of each variable with Spearman Coefficient
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]
BackPain_Yes = dfupdated["BackPain_Yes"]
#Find the Spearmen Coefficient.
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,BackPain_Yes)
spearmanr_coff
```

Out[51]: 0.013312789543203096

```
In [52]: #Check independence of each variable with Spearman Coefficient
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]
HighBlood_Yes = dfupdated["HighBlood_Yes"]
#Find the Spearmen Coefficient.
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,HighBlood_Yes)
spearmanr_coff
```

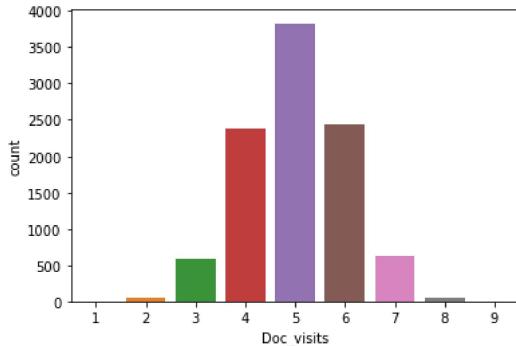
Out[52]: 0.0022700537328705066

```
In [53]: #Check independence of each variable with Spearman Coefficient
ReAdmis_Yes= dfupdated["ReAdmis_Yes"]
Arthritis_Yes = dfupdated["Arthritis_Yes"]
#Find the Spearmen Coefficient.
spearmanr_coff, p_value = spearmanr(ReAdmis_Yes,Arthritis_Yes)
spearmanr_coff
```

Out[53]: 0.007663036548941127

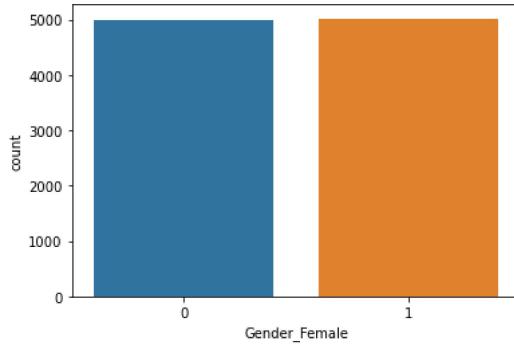
```
In [54]: # Check the Prevalence of Each Classification Category with visual plot
sns.countplot(x='Doc_visits', data=dfupdated)
```

Out[54]: <AxesSubplot:xlabel='Doc_visits', ylabel='count'>



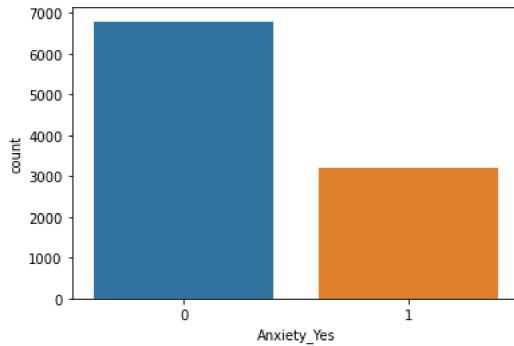
```
In [55]: # Check the Prevalence of Each Classification Category with visual plot  
sns.countplot(x='Gender_Female', data=dfupdated)
```

```
Out[55]: <AxesSubplot:xlabel='Gender_Female', ylabel='count'>
```



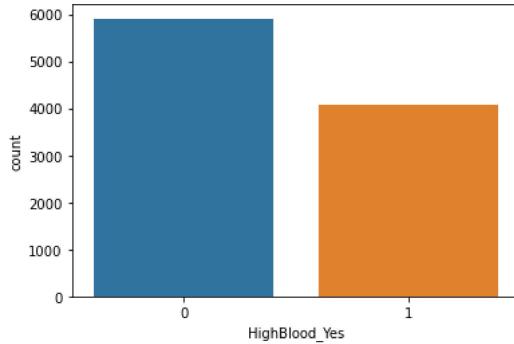
```
In [56]: # Check the Prevalence of Each Classification Category with visual plot  
sns.countplot(x='Anxiety_Yes', data=dfupdated)
```

```
Out[56]: <AxesSubplot:xlabel='Anxiety_Yes', ylabel='count'>
```



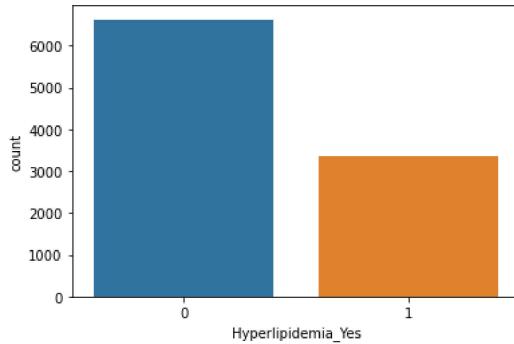
```
In [57]: # Check the Prevalence of Each Classification Category with visual plot  
sns.countplot(x='HighBlood_Yes', data=dfupdated)
```

```
Out[57]: <AxesSubplot:xlabel='HighBlood_Yes', ylabel='count'>
```



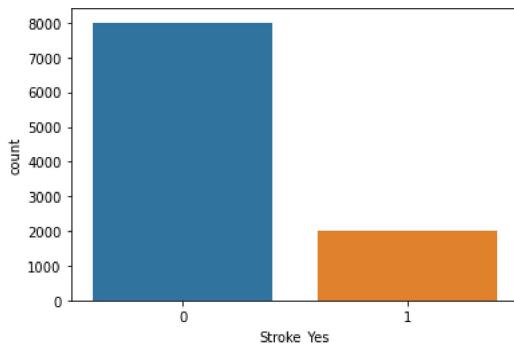
```
In [58]: # Check the Prevalence of Each Classification Category with visual plot  
sns.countplot(x='Hyperlipidemia_Yes', data=dfupdated)
```

```
Out[58]: <AxesSubplot:xlabel='Hyperlipidemia_Yes', ylabel='count'>
```



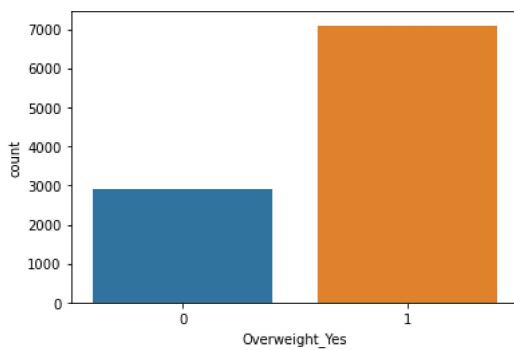
```
In [59]: # Check the Prevalence of Each Classification Category with visual plot  
sns.countplot(x='Stroke_Yes', data=dfupdated)
```

```
Out[59]: <AxesSubplot:xlabel='Stroke_Yes', ylabel='count'>
```



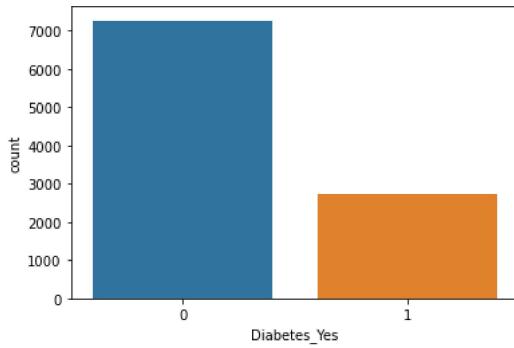
```
In [60]: # Check the Prevalence of Each Classification Category with visual plot  
sns.countplot(x='Overweight_Yes', data=dfupdated)
```

```
Out[60]: <AxesSubplot:xlabel='Overweight_Yes', ylabel='count'>
```



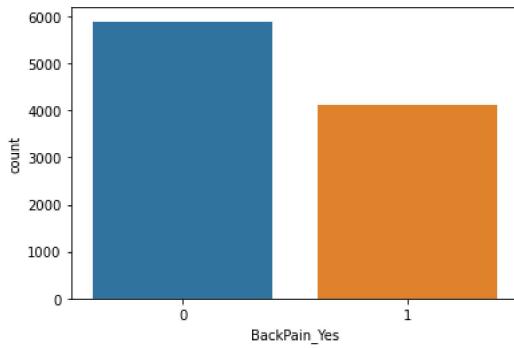
```
In [61]: # Check the Prevalence of Each Classification Category with visual plot  
sns.countplot(x='Diabetes_Yes', data=dfupdated)
```

```
Out[61]: <AxesSubplot:xlabel='Diabetes_Yes', ylabel='count'>
```



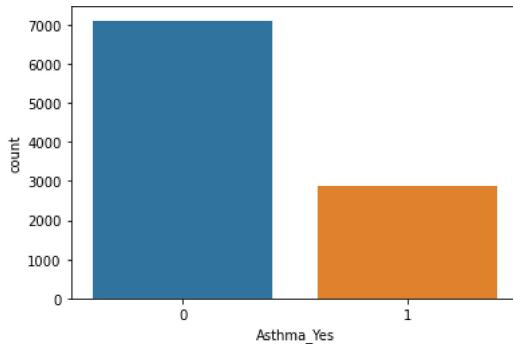
```
In [62]: # Check the Prevalence of Each Classification Category with visual plot  
sns.countplot(x='BackPain_Yes', data=dfupdated)
```

```
Out[62]: <AxesSubplot:xlabel='BackPain_Yes', ylabel='count'>
```



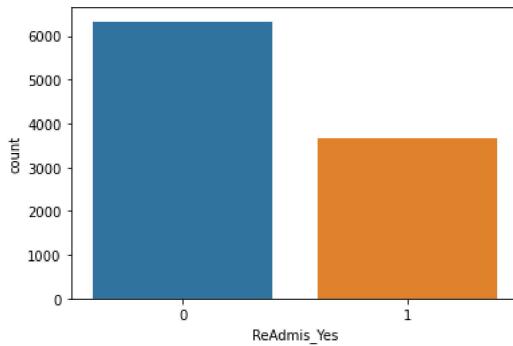
```
In [63]: # Check the Prevalence of Each Classification Category with visual plot
sns.countplot(x='Asthma_Yes', data=dfupdated)
```

```
Out[63]: <AxesSubplot:xlabel='Asthma_Yes', ylabel='count'>
```



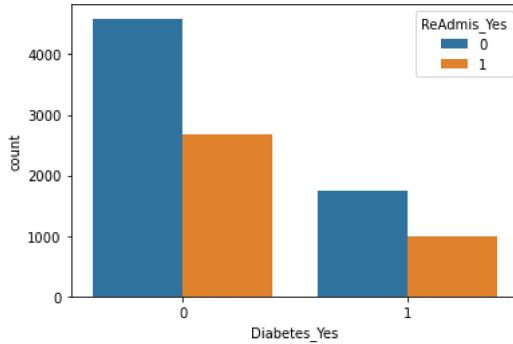
```
In [64]: # Predictor Variable Plot
sns.countplot(x='ReAdmis_Yes', data=dfupdated)
```

```
Out[64]: <AxesSubplot:xlabel='ReAdmis_Yes', ylabel='count'>
```



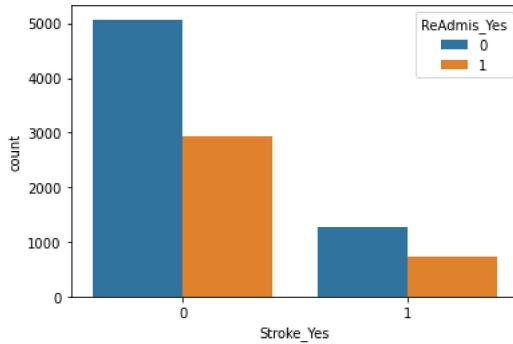
```
In [65]: #Compare readmissions to patients who have diabetes
sns.countplot(x='Diabetes_Yes', hue='ReAdmis_Yes', data=dfupdated)
```

```
Out[65]: <AxesSubplot:xlabel='Diabetes_Yes', ylabel='count'>
```



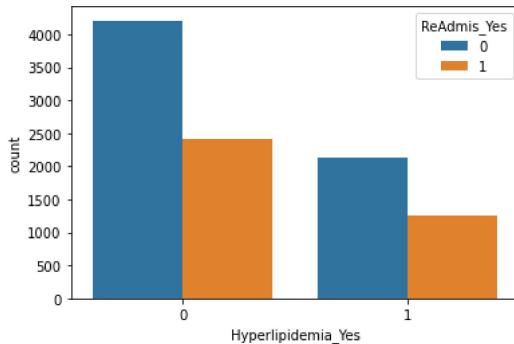
```
In [66]: #Compare readmissions to patients who have had a stroke
sns.countplot(x='Stroke_Yes', hue='ReAdmis_Yes', data=dfupdated)
```

```
Out[66]: <AxesSubplot:xlabel='Stroke_Yes', ylabel='count'>
```



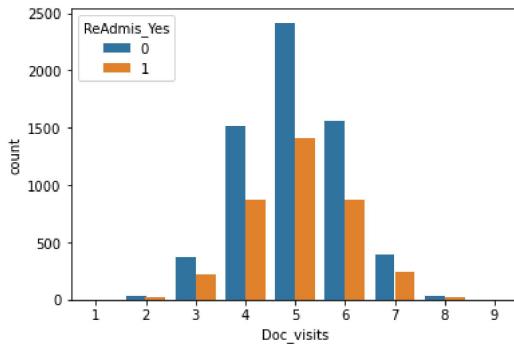
```
In [67]: #Compare readmissions to patients who have hyperlipidemia
sns.countplot(x='Hyperlipidemia_Yes', hue='ReAdmis_Yes', data=dfupdated)
```

```
Out[67]: <AxesSubplot:xlabel='Hyperlipidemia_Yes', ylabel='count'>
```



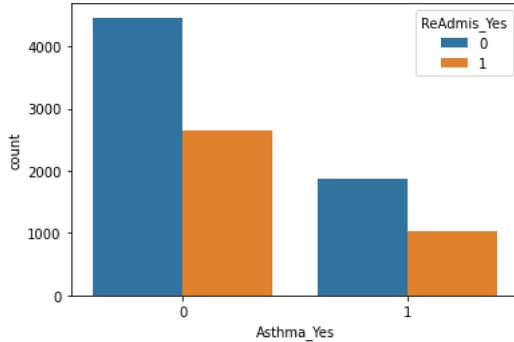
```
In [68]: #Compare readmissions to doctor visits
sns.countplot(x='Doc_visits', hue='ReAdmis_Yes', data=dfupdated)
```

```
Out[68]: <AxesSubplot:xlabel='Doc_visits', ylabel='count'>
```



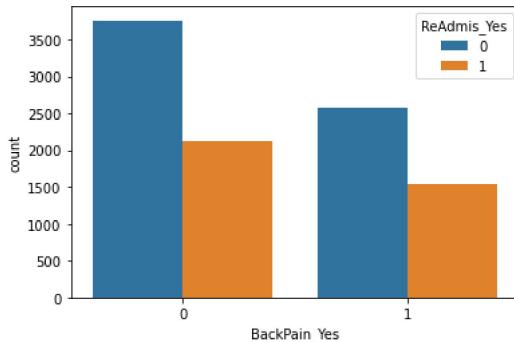
```
In [69]: #Compare readmissions patients with asthma
sns.countplot(x='Asthma_Yes', hue='ReAdmis_Yes', data=dfupdated)
```

```
Out[69]: <AxesSubplot:xlabel='Asthma_Yes', ylabel='count'>
```



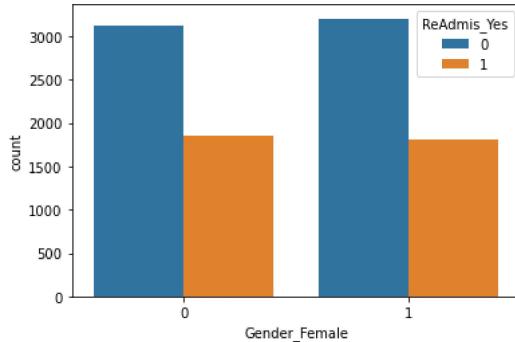
```
In [70]: #Compare readmissions patients with back pain
sns.countplot(x='BackPain_Yes', hue='ReAdmis_Yes', data=dfupdated)
```

```
Out[70]: <AxesSubplot:xlabel='BackPain_Yes', ylabel='count'>
```



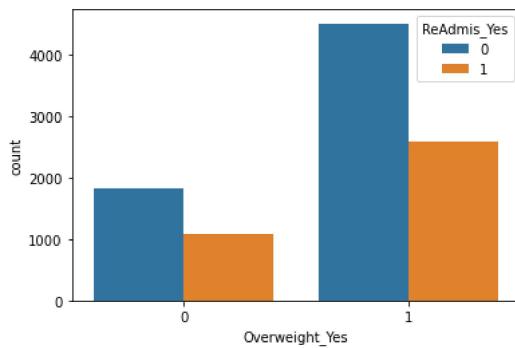
```
In [71]: #Compare readmissions for female patients  
sns.countplot(x='Gender_Female', hue='ReAdmis_Yes', data=dfupdated)
```

```
Out[71]: <AxesSubplot:xlabel='Gender_Female', ylabel='count'>
```



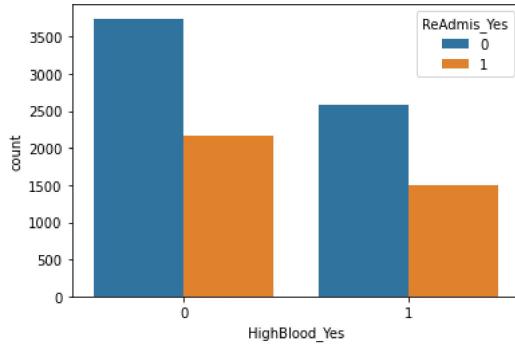
```
In [72]: #Compare readmissions for overweight patients  
sns.countplot(x='Overweight_Yes', hue='ReAdmis_Yes', data=dfupdated)
```

```
Out[72]: <AxesSubplot:xlabel='Overweight_Yes', ylabel='count'>
```

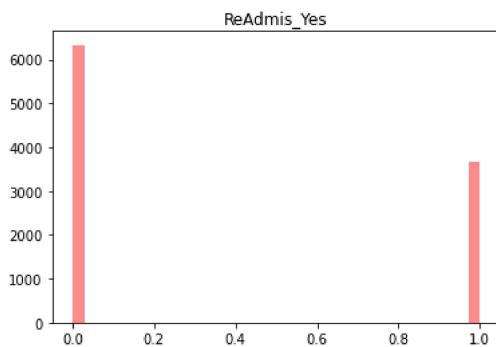


```
In [73]: #Compare readmissions for patients with high blood pressure  
sns.countplot(x='HighBlood_Yes', hue='ReAdmis_Yes', data=dfupdated)
```

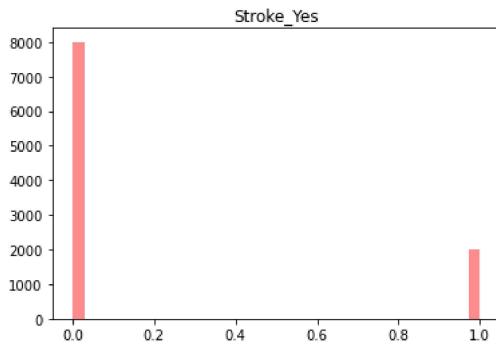
```
Out[73]: <AxesSubplot:xlabel='HighBlood_Yes', ylabel='count'>
```



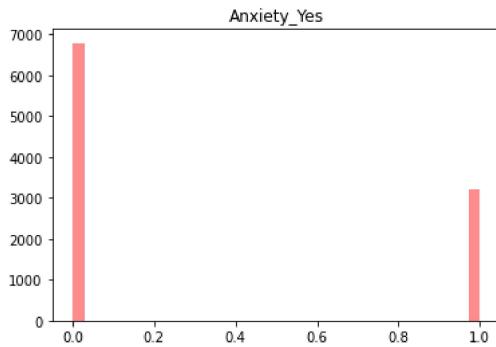
```
In [74]: # plotting histogram  
plt.hist(dfupdated['ReAdmis_Yes'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("ReAdmis_Yes")  
plt.show()
```



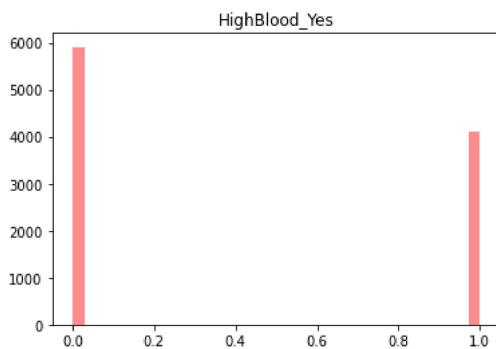
```
In [75]: # plotting histogram  
plt.hist(dfupdated['Stroke_Yes'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("Stroke_Yes")  
plt.show()
```



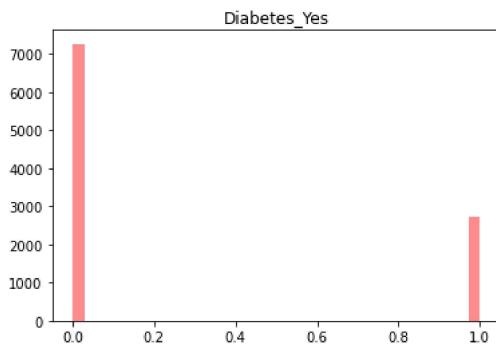
```
In [77]: # plotting histogram  
plt.hist(dfupdated['Anxiety_Yes'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("Anxiety_Yes")  
plt.show()
```



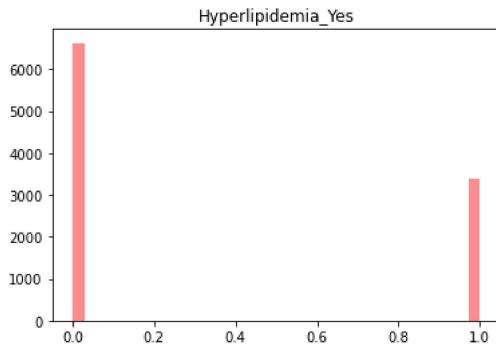
```
In [80]: # plotting histogram  
plt.hist(dfupdated['HighBlood_Yes'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("HighBlood_Yes")  
plt.show()
```



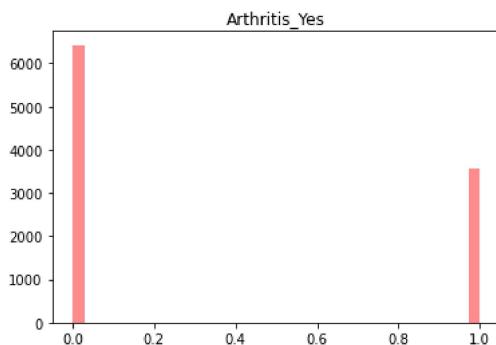
```
In [81]: # plotting histogram  
plt.hist(dfupdated['Diabetes_Yes'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("Diabetes_Yes")  
plt.show()
```



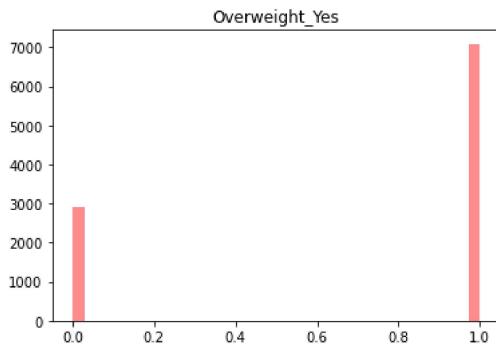
```
In [83]: # plotting histogram  
plt.hist(dfupdated['Hyperlipidemia_Yes'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("Hyperlipidemia_Yes")  
plt.show()
```



```
In [84]: # plotting histogram  
plt.hist(dfupdated['Arthritis_Yes'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("Arthritis_Yes")  
plt.show()
```

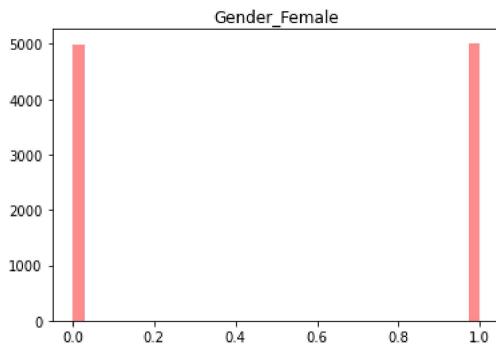


```
In [85]: # plotting histogram  
plt.hist(dfupdated['Overweight_Yes'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("Overweight_Yes")  
plt.show()
```

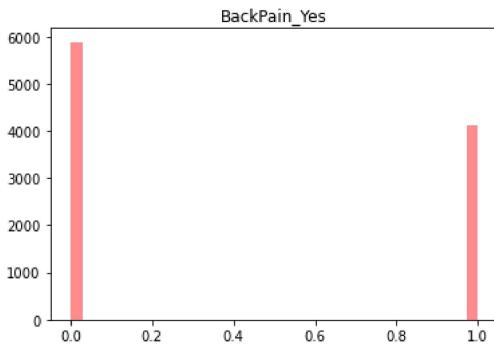


```
In [86]: # plotting histogram  
plt.hist(dfupdated['Gender_Female'],bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("Gender_Female")
```

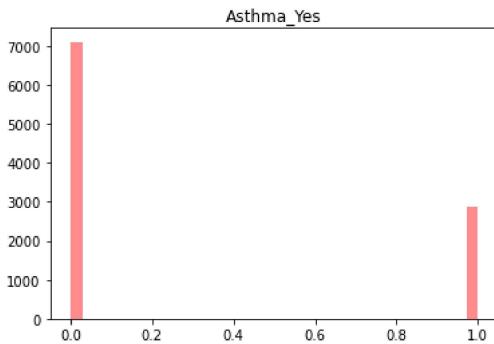
Out[86]: Text(0.5, 1.0, 'Gender_Female')



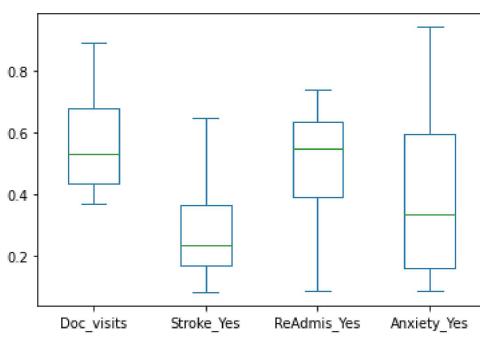
```
In [87]: # plotting histogram  
plt.hist(dfupdated['BackPain_Yes'], bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("BackPain_Yes")  
plt.show()
```



```
In [88]: # plotting histogram  
plt.hist(dfupdated['Asthma_Yes'], bins = 35,  
         alpha = 0.45, color = 'red')  
plt.title("Asthma_Yes")  
plt.show()
```

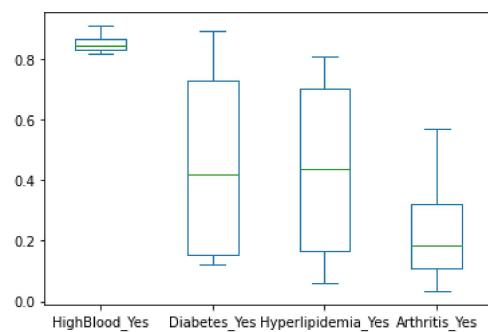


```
In [89]: #boxplots  
df = pd.DataFrame(data = np.random.random(size=(4,4)), columns = ['Doc_visits', 'Stroke_Yes', 'ReAdmis_Yes', 'Anxiety_Yes'])  
df.plot(kind='box')  
plt.show()
```



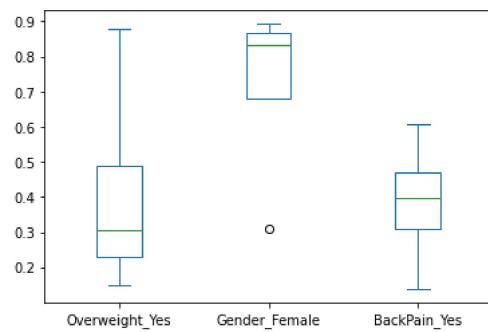
```
In [90]: df = pd.DataFrame(data = np.random.random(size=(4,4)), columns = ['HighBlood_Yes', 'Diabetes_Yes', 'Hyperlipidemia_Yes', 'Arthritis_Yes'])

df.plot(kind='box')
plt.show()
```



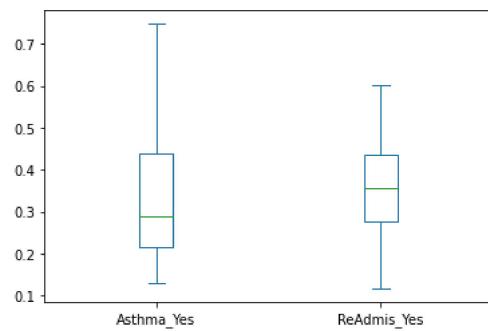
```
In [91]: df = pd.DataFrame(data = np.random.random(size=(4,3)), columns = ['Overweight_Yes', 'Gender_Female', 'BackPain_Yes'])

df.plot(kind='box')
plt.show()
```

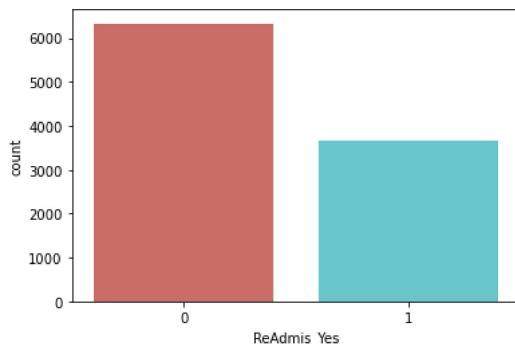


```
In [92]: df = pd.DataFrame(data = np.random.random(size=(4,2)), columns = ['Asthma_Yes', 'ReAdmis_Yes'])

df.plot(kind='box')
plt.show()
```



```
In [93]: #how does the Y data stack up?
dfupdated['ReAdmis_Yes'].value_counts()
sns.countplot(x='ReAdmis_Yes', data=dfupdated, palette='hls')
plt.show()
plt.savefig('count_plot')
```



<Figure size 432x288 with 0 Axes>

```
In [94]: #review percentage of patients who readmitted/versus not readmitted
count_no_sub = len(dfupdated[dfupdated['ReAdmis_Yes']==0])
count_sub = len(dfupdated[dfupdated['ReAdmis_Yes']==1])
pct_of_no_sub = count_no_sub/(count_no_sub+count_sub)
print("patients who did not readmit", pct_of_no_sub*100)
pct_of_sub = count_sub/(count_no_sub+count_sub)
print("patients who readmitted", pct_of_sub*100)
```

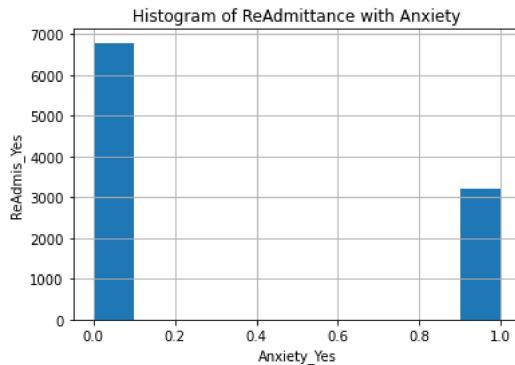
patients who did not readmit 63.31
 patients who readmitted 36.69

```
In [95]: #Check the means
dfupdated.groupby('ReAdmis_Yes').mean()
```

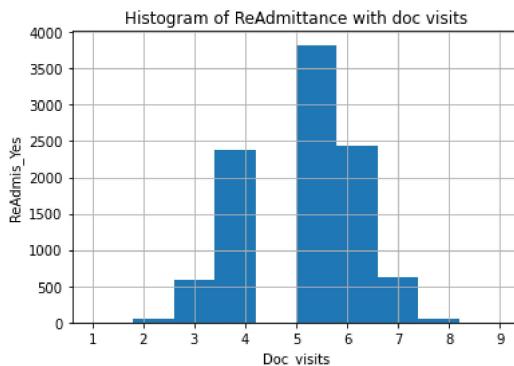
Out[95]:

	Doc_visits	Anxiety_Yes	Overweight_Yes	Arthritis_Yes	HighBlood_Yes	Gender_Female	Stroke_Yes	Diabetes_Yes	Asthma_Yes	Hyperlipidemia_
ReAdmis_Yes										
0	5.012004	0.320644	0.712368	0.354604	0.408150	0.506239	0.199021	0.274838	0.295214	0.3351
1	5.012537	0.322976	0.704279	0.362224	0.410466	0.494140	0.199782	0.272009	0.279095	0.3391

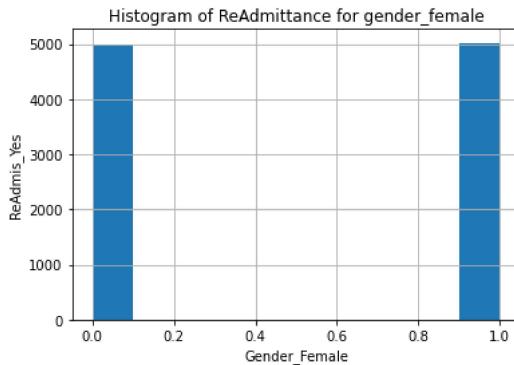
```
In [96]: #review histogram visual aides
dfupdated.Anxiety_Yes.hist()
plt.title('Histogram of ReAdmittance with Anxiety')
plt.xlabel('Anxiety_Yes')
plt.ylabel('ReAdmis_Yes')
plt.savefig('hist_anxiety')
```



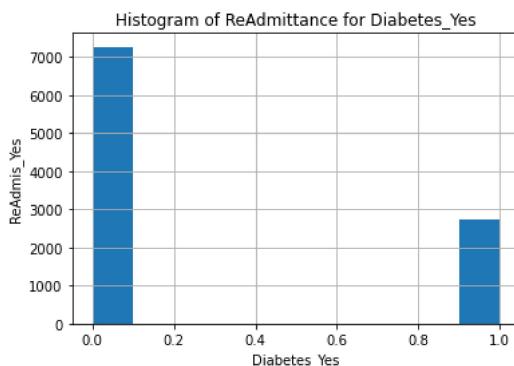
```
In [97]: dfupdated.Doc_visits.hist()  
plt.title('Histogram of ReAdmittance with doc visits')  
plt.xlabel('Doc_visits')  
plt.ylabel('ReAdmis_Yes')  
plt.savefig('hist_docvisits')
```



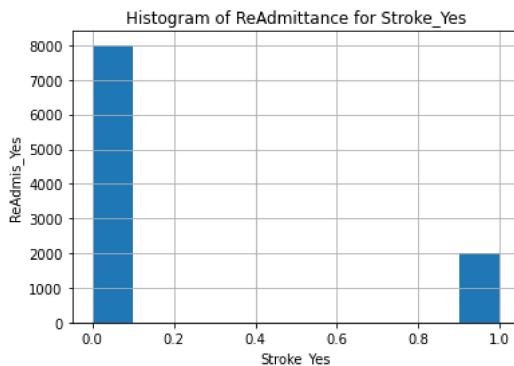
```
In [98]: dfupdated.Gender_Female.hist()  
plt.title('Histogram of ReAdmittance for gender_female')  
plt.xlabel('Gender_Female')  
plt.ylabel('ReAdmis_Yes')  
plt.savefig('hist_GenderFemale')
```



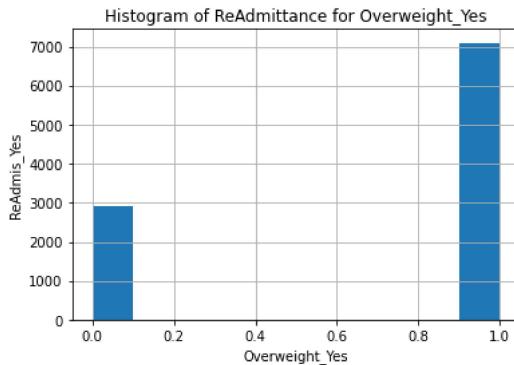
```
In [99]: dfupdated.Diabetes_Yes.hist()  
plt.title('Histogram of ReAdmittance for Diabetes_Yes')  
plt.xlabel('Diabetes_Yes')  
plt.ylabel('ReAdmis_Yes')  
plt.savefig('hist_DiabetesYes')
```



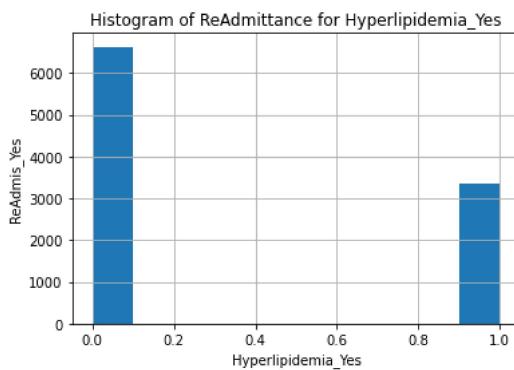
```
In [100]: dfupdated.Stroke_Yes.hist()  
plt.title('Histogram of ReAdmittance for Stroke_Yes')  
plt.xlabel('Stroke_Yes')  
plt.ylabel('ReAdmis_Yes')  
plt.savefig('hist_StrokeYes')
```



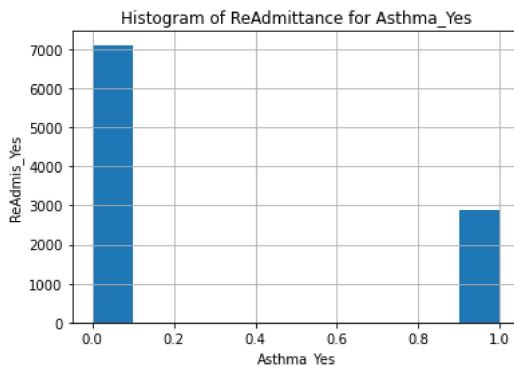
```
In [101]: dfupdated.Overweight_Yes.hist()  
plt.title('Histogram of ReAdmittance for Overweight_Yes')  
plt.xlabel('Overweight_Yes')  
plt.ylabel('ReAdmis_Yes')  
plt.savefig('hist_OverweightYes')
```



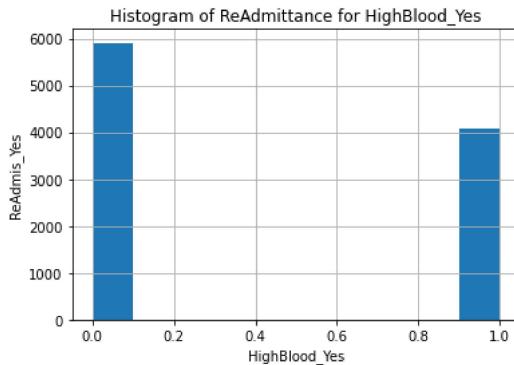
```
In [102]: dfupdated.Hyperlipidemia_Yes.hist()  
plt.title('Histogram of ReAdmittance for Hyperlipidemia_Yes')  
plt.xlabel('Hyperlipidemia_Yes')  
plt.ylabel('ReAdmis_Yes')  
plt.savefig('hist_HyperlipidemiaYes')
```



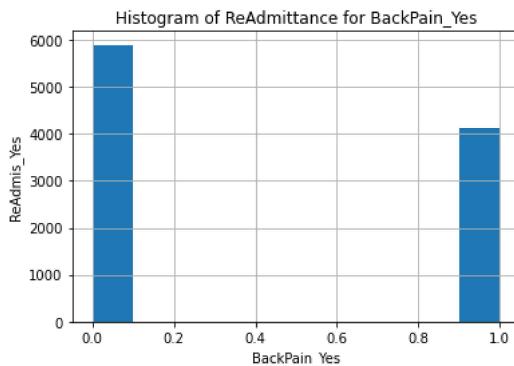
```
In [103]: dfupdated.Asthma_Yes.hist()
plt.title('Histogram of ReAdmittance for Asthma_Yes')
plt.xlabel('Asthma_Yes')
plt.ylabel('ReAdmis_Yes')
plt.savefig('hist_AsthmaYes')
```



```
In [104]: dfupdated.HighBlood_Yes.hist()
plt.title('Histogram of ReAdmittance for HighBlood_Yes')
plt.xlabel('HighBlood_Yes')
plt.ylabel('ReAdmis_Yes')
plt.savefig('hist_HighBloodYes')
```



```
In [105]: dfupdated.BackPain_Yes.hist()
plt.title('Histogram of ReAdmittance for BackPain_Yes')
plt.xlabel('BackPain_Yes')
plt.ylabel('ReAdmis_Yes')
plt.savefig('hist_BackPainYes')
```



```
In [106]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Overweight_Yes + Stroke_Yes + HighBlood_Yes + Anxiety_Yes + Diabetes_Yes + Hyperlipidemia_Yes")
Optimization terminated successfully.
    Current function value: 0.656892
    Iterations 4
```

```
In [107]: #print the model
# Summary of results
print(log_reg.summary())
```

Logit Regression Results

Dep. Variable:	ReAdmis_Yes	No. Observations:	10000			
Model:	Logit	Df Residuals:	9988			
Method:	MLE	Df Model:	11			
Date:	Wed, 18 Jan 2023	Pseudo R-squ.:	0.0005985			
Time:	20:20:54	Log-Likelihood:	-6568.9			
converged:	True	LL-Null:	-6572.9			
Covariance Type:	nonrobust	LLR p-value:	0.7251			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-0.5197	0.116	-4.480	0.000	-0.747	-0.292
Overweight_Yes	-0.0389	0.046	-0.853	0.394	-0.128	0.051
Stroke_Yes	0.0061	0.052	0.118	0.906	-0.096	0.108
HighBlood_Yes	0.0101	0.042	0.240	0.811	-0.073	0.093
Anxiety_Yes	0.0107	0.044	0.241	0.810	-0.076	0.098
Diabetes_Yes	-0.0127	0.047	-0.273	0.785	-0.104	0.079
Hyperlipidemia_Yes	0.0179	0.044	0.407	0.684	-0.068	0.104
Arthritis_Yes	0.0335	0.043	0.774	0.439	-0.051	0.118
Gender_Female	-0.0486	0.042	-1.171	0.242	-0.130	0.033
BackPain_Yes	0.0583	0.042	1.384	0.167	-0.024	0.141
Asthma_Yes	-0.0790	0.046	-1.717	0.086	-0.169	0.011
Doc_visits	0.0003	0.020	0.013	0.990	-0.039	0.039

```
In [108]: #define the predictor variables and the response variable
X = dfupdated[['Overweight_Yes', 'Stroke_Yes', 'HighBlood_Yes', 'Anxiety_Yes', 'Diabetes_Yes', 'Hyperlipidemia_Yes', 'Arthritis_Yes']]
y = dfupdated['ReAdmis_Yes']
```

```
In [109]: #split the dataset into training (70%) and testing (30%) sets
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.3,random_state=0)
```

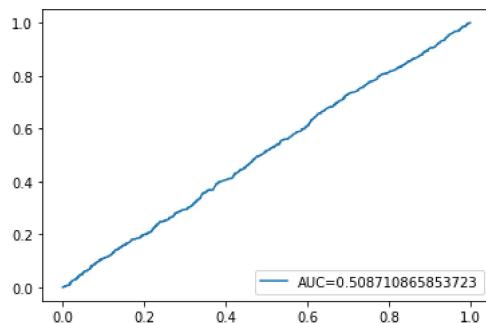
```
In [110]: #instantiate the model
log_regression = LogisticRegression()
```

```
In [111]: #fit the model using the training data
log_regression.fit(X_train,y_train)
```

```
Out[111]: LogisticRegression()
LogisticRegression()
```

```
In [112]: #define metrics
y_pred_proba = log_regression.predict_proba(X_test)[:,1]
fpr, tpr, _ = metrics.roc_curve(y_test, y_pred_proba)
auc = metrics.roc_auc_score(y_test, y_pred_proba)
```

```
In [113]: #create ROC curve
plt.plot(fpr,tpr,label="AUC="+str(auc))
plt.legend(loc=4)
plt.show()
```

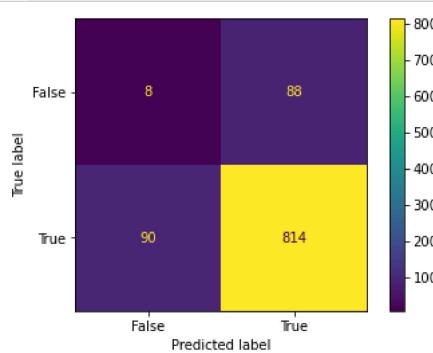


```
In [115]: #plot confusion matrix
actual = np.random.binomial(1,.9,size = 1000)
predicted = np.random.binomial(1,.9,size = 1000)

confusion_matrix = metrics.confusion_matrix(actual, predicted)

cm_display = metrics.ConfusionMatrixDisplay(confusion_matrix = confusion_matrix, display_labels = [False, True])

cm_display.plot()
plt.show()
```



```
In [116]: #drop highest p-value
to_drop = ['Doc_visits']
dfupdated.drop(to_drop, inplace=True, axis=1)
```

```
In [117]: #new dataframe for second model
```

```
dfupdated2 = dfupdated[['ReAdmis_Yes', 'Stroke_Yes', 'HighBlood_Yes', 'Anxiety_Yes', 'Hyperlipidemia_Yes', 'Arthritis_Yes', 'Overweight_Yes', 'Gender_Female', 'BackPain_Yes', 'Asthma_Yes']]
```

```
In [118]: #Prepare and fit the model
```

```
log_reg = smf.logit("ReAdmis_Yes ~ Overweight_Yes + Stroke_Yes + HighBlood_Yes + Anxiety_Yes + Diabetes_Yes + Hyperlipidemia_Yes + Arthritis_Yes + Gender_Female + BackPain_Yes + Asthma_Yes")
```

```
Optimization terminated successfully.
```

```
Current function value: 0.656892
Iterations 4
```

```
In [119]: #print the model
```

```
# Summary of results
print(log_reg.summary())
```

Logit Regression Results						
Dep. Variable:	ReAdmis_Yes	No. Observations:	10000			
Model:	Logit	Df Residuals:	9989			
Method:	MLE	Df Model:	10			
Date:	Wed, 18 Jan 2023	Pseudo R-squ.:	0.0005985			
Time:	20:22:41	Log-Likelihood:	-6568.9			
converged:	True	LL-Null:	-6572.9			
Covariance Type:	nonrobust	LLR p-value:	0.6418			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-0.5184	0.060	-8.646	0.000	-0.636	-0.401
Overweight_Yes	-0.0389	0.046	-0.853	0.394	-0.128	0.051
Stroke_Yes	0.0061	0.052	0.118	0.906	-0.096	0.108
HighBlood_Yes	0.0101	0.042	0.240	0.811	-0.073	0.093
Anxiety_Yes	0.0107	0.044	0.241	0.810	-0.076	0.098
Diabetes_Yes	-0.0127	0.047	-0.273	0.785	-0.104	0.079
Hyperlipidemia_Yes	0.0178	0.044	0.407	0.684	-0.068	0.104
Arthritis_Yes	0.0335	0.043	0.774	0.439	-0.051	0.118
Gender_Female	-0.0486	0.042	-1.171	0.242	-0.130	0.033
BackPain_Yes	0.0583	0.042	1.384	0.166	-0.024	0.141
Asthma_Yes	-0.0790	0.046	-1.718	0.086	-0.169	0.011

```
In [120]: #new dataframe for third model
```

```
dfupdated3 = dfupdated[['ReAdmis_Yes', 'HighBlood_Yes', 'Anxiety_Yes', 'Hyperlipidemia_Yes', 'Arthritis_Yes', 'Overweight_Yes', 'Gender_Female', 'BackPain_Yes', 'Asthma_Yes']]
```

```
In [121]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Overweight_Yes + HighBlood_Yes + Anxiety_Yes + Diabetes_Yes + Hyperlipidemia_Yes + Arthritis_Yes + Gender_Female + BackPain_Yes + Asthma_Yes")
Optimization terminated successfully.
    Current function value: 0.656892
    Iterations 4
```

```
In [122]: #print the model
# Summary of results
print(log_reg.summary())
```

Logit Regression Results						
Dep. Variable:	ReAdmis_Yes	No. Observations:	10000			
Model:	Logit	Df Residuals:	9990			
Method:	MLE	Df Model:	9			
Date:	Wed, 18 Jan 2023	Pseudo R-squ.:	0.0005974			
Time:	20:23:05	Log-Likelihood:	-6568.9			
converged:	True	LL-Null:	-6572.9			
Covariance Type:	nonrobust	LLR p-value:	0.5489			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-0.5172	0.059	-8.767	0.000	-0.633	-0.402
Overweight_Yes	-0.0389	0.046	-0.853	0.394	-0.128	0.051
HighBlood_Yes	0.0102	0.042	0.241	0.810	-0.073	0.093
Anxiety_Yes	0.0106	0.044	0.239	0.811	-0.076	0.098
Diabetes_Yes	-0.0127	0.047	-0.272	0.786	-0.104	0.079
Hyperlipidemia_Yes	0.0178	0.044	0.405	0.686	-0.068	0.104
Arthritis_Yes	0.0334	0.043	0.772	0.440	-0.051	0.118
Gender_Female	-0.0486	0.042	-1.170	0.242	-0.130	0.033
BackPain_Yes	0.0583	0.042	1.384	0.166	-0.024	0.141
Asthma_Yes	-0.0790	0.046	-1.717	0.086	-0.169	0.011

```
In [123]: #new dataframe for 4th model
Dfupdated4 = dfupdated[['ReAdmis_Yes', 'HighBlood_Yes', 'Hyperlipidemia_Yes', 'Arthritis_Yes', 'Overweight_Yes', 'Gender_Female', 'BackPain_Yes', 'Asthma_Yes']]
```

```
In [124]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Overweight_Yes + HighBlood_Yes + Diabetes_Yes + Hyperlipidemia_Yes + Arthritis_Yes + Gender_Female + BackPain_Yes + Asthma_Yes")
Optimization terminated successfully.
    Current function value: 0.656895
    Iterations 4
```

```
In [125]: #print the model
# Summary of results
print(log_reg.summary())
```

Logit Regression Results						
Dep. Variable:	ReAdmis_Yes	No. Observations:	10000			
Model:	Logit	Df Residuals:	9991			
Method:	MLE	Df Model:	8			
Date:	Wed, 18 Jan 2023	Pseudo R-squ.:	0.0005931			
Time:	20:23:28	Log-Likelihood:	-6569.0			
converged:	True	LL-Null:	-6572.9			
Covariance Type:	nonrobust	LLR p-value:	0.4536			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-0.5138	0.057	-8.971	0.000	-0.626	-0.402
Overweight_Yes	-0.0391	0.046	-0.856	0.392	-0.129	0.050
HighBlood_Yes	0.0102	0.042	0.243	0.808	-0.073	0.093
Diabetes_Yes	-0.0127	0.047	-0.273	0.785	-0.104	0.079
Hyperlipidemia_Yes	0.0176	0.044	0.402	0.688	-0.068	0.104
Arthritis_Yes	0.0335	0.043	0.775	0.438	-0.051	0.118
Gender_Female	-0.0485	0.042	-1.169	0.242	-0.130	0.033
BackPain_Yes	0.0584	0.042	1.386	0.166	-0.024	0.141
Asthma_Yes	-0.0789	0.046	-1.715	0.086	-0.169	0.011

```
In [126]: #new dataframe for 5th model
Dfupdated5 = dfupdated[['ReAdmis_Yes', 'Hyperlipidemia_Yes', 'Arthritis_Yes', 'Overweight_Yes', 'Gender_Female', 'BackPain_Yes', 'Asthma_Yes']]
```

```
In [127]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Overweight_Yes + Diabetes_Yes + Hyperlipidemia_Yes + Arthritis_Yes + Gender_Female + BackPain_Yes")
Optimization terminated successfully.
    Current function value: 0.656898
    Iterations 4
```

```
In [128]: #print the model
# Summary of results
print(log_reg.summary())
```

Logit Regression Results						
Dep. Variable:	ReAdmis_Yes	No. Observations:	10000			
Model:	Logit	Df Residuals:	9992			
Method:	MLE	Df Model:	7			
Date:	Wed, 18 Jan 2023	Pseudo R-squ.:	0.0005886			
Time:	20:23:50	Log-Likelihood:	-6569.0			
converged:	True	LL-Null:	-6572.9			
Covariance Type:	nonrobust	LLR p-value:	0.3563			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-0.5098	0.055	-9.301	0.000	-0.617	-0.402
Overweight_Yes	-0.0388	0.046	-0.850	0.396	-0.128	0.051
Diabetes_Yes	-0.0128	0.047	-0.274	0.784	-0.104	0.079
Hyperlipidemia_Yes	0.0175	0.044	0.399	0.690	-0.068	0.104
Arthritis_Yes	0.0336	0.043	0.776	0.437	-0.051	0.118
Gender_Female	-0.0486	0.042	-1.171	0.242	-0.130	0.033
BackPain_Yes	0.0585	0.042	1.387	0.165	-0.024	0.141
Asthma_Yes	-0.0788	0.046	-1.713	0.087	-0.169	0.011

```
In [129]: #new dataframe for 6th model
Dfupdated6 = dfupdated[['ReAdmis_Yes', 'Hyperlipidemia_Yes', 'Arthritis_Yes', 'Overweight_Yes', 'Gender_Female', 'BackPain_Yes']]
```

```
In [130]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Overweight_Yes + Hyperlipidemia_Yes + Arthritis_Yes + Gender_Female + BackPain_Yes + Asthma_Yes")
Optimization terminated successfully.
    Current function value: 0.656902
    Iterations 4
```

```
In [131]: #print the model
# Summary of results
print(log_reg.summary())
```

Logit Regression Results						
Dep. Variable:	ReAdmis_Yes	No. Observations:	10000			
Model:	Logit	Df Residuals:	9993			
Method:	MLE	Df Model:	6			
Date:	Wed, 18 Jan 2023	Pseudo R-squ.:	0.0005829			
Time:	20:24:13	Log-Likelihood:	-6569.0			
converged:	True	LL-Null:	-6572.9			
Covariance Type:	nonrobust	LLR p-value:	0.2639			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-0.5132	0.053	-9.622	0.000	-0.618	-0.409
Overweight_Yes	-0.0387	0.046	-0.848	0.397	-0.128	0.051
Hyperlipidemia_Yes	0.0174	0.044	0.396	0.692	-0.069	0.103
Arthritis_Yes	0.0335	0.043	0.774	0.439	-0.051	0.118
Gender_Female	-0.0487	0.042	-1.172	0.241	-0.130	0.033
BackPain_Yes	0.0586	0.042	1.391	0.164	-0.024	0.141
Asthma_Yes	-0.0790	0.046	-1.718	0.086	-0.169	0.011

```
In [132]: #new dataframe for 7th model
Dfupdated7 = dfupdated[['ReAdmis_Yes', 'Arthritis_Yes', 'Overweight_Yes', 'Gender_Female', 'BackPain_Yes', 'Asthma_Yes']]
```

```
In [133]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Overweight_Yes + Arthritis_Yes + Gender_Female + BackPain_Yes + Asthma_Yes", data=Dfupdated7)

Optimization terminated successfully.
    Current function value: 0.656910
    Iterations 4
```

```
In [134]: #print the model
# Summary of results
print(log_reg.summary())

Logit Regression Results
=====
Dep. Variable: ReAdmis_Yes No. Observations: 10000
Model: Logit Df Residuals: 9994
Method: MLE Df Model: 5
Date: Wed, 18 Jan 2023 Pseudo R-squ.: 0.0005710
Time: 20:24:34 Log-Likelihood: -6569.1
converged: True LL-Null: -6572.9
Covariance Type: nonrobust LLR p-value: 0.1857
=====
            coef  std err      z  P>|z|  [0.025  0.975]
-----
Intercept   -0.5070   0.051  -9.943  0.000  -0.607  -0.407
Overweight_Yes -0.0388   0.046  -0.850  0.395  -0.128  0.051
Arthritis_Yes  0.0334   0.043   0.771  0.441  -0.051  0.118
Gender_Female -0.0490   0.042  -1.179  0.238  -0.130  0.032
BackPain_Yes   0.0586   0.042   1.391  0.164  -0.024  0.141
Asthma_Yes    -0.0792   0.046  -1.722  0.085  -0.169  0.011
=====
```

```
In [135]: #new dataframe for 8th model
Dfupdated8 = dfupdated[['ReAdmis_Yes', 'Overweight_Yes', 'Gender_Female', 'BackPain_Yes', 'Asthma_Yes']]
```

```
In [136]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Overweight_Yes + Gender_Female + BackPain_Yes + Asthma_Yes", data=Dfupdated8).fit()

Optimization terminated successfully.
    Current function value: 0.656940
    Iterations 4
```

```
In [137]: #print the model
# Summary of results
print(log_reg.summary())

Logit Regression Results
=====
Dep. Variable: ReAdmis_Yes No. Observations: 10000
Model: Logit Df Residuals: 9995
Method: MLE Df Model: 4
Date: Wed, 18 Jan 2023 Pseudo R-squ.: 0.0005258
Time: 20:24:55 Log-Likelihood: -6569.4
converged: True LL-Null: -6572.9
Covariance Type: nonrobust LLR p-value: 0.1406
=====
            coef  std err      z  P>|z|  [0.025  0.975]
-----
Intercept   -0.4947   0.048  -10.221  0.000  -0.590  -0.400
Overweight_Yes -0.0386   0.046  -0.847  0.397  -0.128  0.051
Gender_Female -0.0493   0.042  -1.188  0.235  -0.131  0.032
BackPain_Yes   0.0580   0.042   1.376  0.169  -0.025  0.141
Asthma_Yes    -0.0794   0.046  -1.727  0.084  -0.170  0.011
=====
```

```
In [138]: #new dataframe for 9th model
Dfupdated9 = dfupdated[['ReAdmis_Yes', 'Gender_Female', 'BackPain_Yes', 'Asthma_Yes']]
```

```
In [139]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Gender_Female + BackPain_Yes + Asthma_Yes", data=Dfupdated9).fit()

Optimization terminated successfully.
    Current function value: 0.656975
    Iterations 4
```

```
In [140]: #print the model
# Summary of results
print(log_reg.summary())
```

Logit Regression Results						
Dep. Variable:		ReAdmis_Yes	No. Observations:	10000		
Model:		Logit	Df Residuals:	9996		
Method:		MLE	Df Model:	3		
Date:		Wed, 18 Jan 2023	Pseudo R-squ.:	0.0004713		
Time:		20:25:15	Log-Likelihood:	-6569.8		
converged:		True	LL-Null:	-6572.9		
Covariance Type:		nonrobust	LLR p-value:	0.1025		
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-0.5217	0.036	-14.331	0.000	-0.593	-0.450
Gender_Female	-0.0494	0.042	-1.189	0.234	-0.131	0.032
BackPain_Yes	0.0576	0.042	1.368	0.171	-0.025	0.140
Asthma_Yes	-0.0800	0.046	-1.739	0.082	-0.170	0.010

```
In [141]: #new dataframe for 10th model
Dfupdated10 = dfupdated[['ReAdmis_Yes', 'BackPain_Yes', 'Asthma_Yes']]
```

```
In [142]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ BackPain_Yes + Asthma_Yes", data=Dfupdated10).fit()
Optimization terminated successfully.
    Current function value: 0.657046
    Iterations 4
```

```
In [143]: #print the model
# Summary of results
print(log_reg.summary())
```

Logit Regression Results						
Dep. Variable:		ReAdmis_Yes	No. Observations:	10000		
Model:		Logit	Df Residuals:	9997		
Method:		MLE	Df Model:	2		
Date:		Wed, 18 Jan 2023	Pseudo R-squ.:	0.0003637		
Time:		20:25:38	Log-Likelihood:	-6570.5		
converged:		True	LL-Null:	-6572.9		
Covariance Type:		nonrobust	LLR p-value:	0.09155		
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-0.5463	0.030	-18.197	0.000	-0.605	-0.487
BackPain_Yes	0.0571	0.042	1.356	0.175	-0.025	0.140
Asthma_Yes	-0.0797	0.046	-1.732	0.083	-0.170	0.010

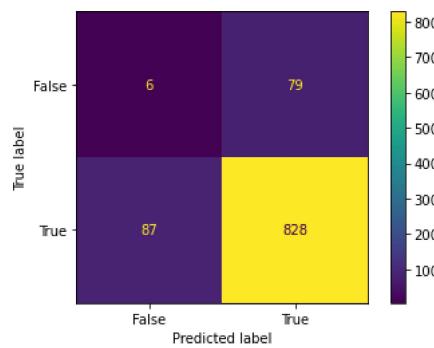
```
In [144]: #new dataframe for final model
DfupdatedFinal = dfupdated[['ReAdmis_Yes', 'Asthma_Yes']]
```

```
In [145]: #Prepare and fit the model
log_reg = smf.logit("ReAdmis_Yes ~ Asthma_Yes", data=DfupdatedFinal).fit()
Optimization terminated successfully.
    Current function value: 0.657138
    Iterations 4
```

```
In [146]: #print the model
# Summary of results
print(log_reg.summary())
```

```
Logit Regression Results
=====
Dep. Variable: ReAdmis_Yes No. Observations: 10000
Model: Logit Df Residuals: 9998
Method: MLE Df Model: 1
Date: Wed, 18 Jan 2023 Pseudo R-squ.: 0.0002240
Time: 20:26:00 Log-Likelihood: -6571.4
converged: True LL-Null: -6572.9
Covariance Type: nonrobust LLR p-value: 0.08618
=====
            coef    std err      z   P>|z|    [0.025    0.975]
-----
Intercept  -0.5229    0.025  -21.310    0.000   -0.571   -0.475
Asthma_Yes -0.0788    0.046   -1.713    0.087   -0.169    0.011
=====
```

```
In [147]: #Run confusion matrix on final model
actual = np.random.binomial(1,.9,size = 1000)
predicted = np.random.binomial(1,.9,size = 1000)
confusion_matrix = metrics.confusion_matrix(actual, predicted)
cm_display = metrics.ConfusionMatrixDisplay(confusion_matrix = confusion_matrix, display_labels = [False, True])
cm_display.plot()
plt.show()
```



```
In [ ]:
```