Logistic Regression Modeling

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Part 1: Research Question

Question

For this analysis, my research question is, "Does High Blood Pressure correlate to any other specific conditions?".

Analysis Goals

Using a logistic regression model to answer our research question will give our organization/hospital the ability to predict patient cardiovascular requirements. This will allow us to make informed resource management decisions, to efficiently and effectively treat patients, and give the patients the ability to plan and estimate financially.

Part 2: Method Justification

Assumptions

1. Binary Dependent Variable: The Dependent Variable has to be a discrete binary option. It cannot be a continuous variable or a categorical variable with multiple options.
2. Relationship: The independent and dependent variables have to have a relationship - without a relationship, there is no point in including the variable.
3. No or little multicollinearity: Perfect Relationships between exploratory variables should be avoided. Multicollinearity leads to Type II errors (False Negatives) - we accept the Null Hypothesis when it should be rejected.
4. Independence: Each variable is independent of all other variables

Tool Benefits

Python is the chosen programming language. This is because it has:

1. Strong module/library support: For our analysis, we will need a method of calculating the variance inflation factor (VIF). By using Python, we can easily access the VIF method provided by the statsmodel library, this would not have been possible as simply in another language.
2. Integration with Jupyter Notebook: Python is the default language supported by Jupyter Notebook, giving us access to the features of Jupyter Notebook, particularly checkpoints, which are saved file states, giving us access to analysis states without rerunning intense calculations on every view. This will be handy when we are running OLS Regression, we will only want to run a model once, save its state, and then move to the next point - not rerun the model every time we want to move on.

Technique Explanation

For our research questions, we need to model the relationships between a discrete boolean variable, High Blood Pressure, against continuous and categorical indepedent variables - which Multiple Logistic Regression is used for. High Blood is provided as a discrete categorical option, "Yes" or "No", not a continuous variable, making it work as our dependent variable for analysis.

Part III: Data Preparation

Data Cleaning

The main goal of this data cleaning is to remove all unnecessary information from the dataset. Since we are only comparing High Blood Pressure to specific conditions, location data, and survey data will not be needed. Additionally, we will run duplicate checks, and missing value checks, then delete all records that are duplicates or missing values.

Steps:

1. Remove Duplicates
2. Handle Missing Values
3. Remove Usused Features

In [1]:
```
# Standard Imports
import math
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

# Statsmodels imports for Logistic Regression Model and Evaluation Methods
import statsmodels.api as sm
from statsmodels.stats.outliers_influence import variance_inflation_factor

# Sklearn imports for Logistic Regression Model and Evaluation Methods
from sklearn import metrics
from sklearn.metrics import ConfusionMatrixDisplay, confusion_matrix
from sklearn.model_selection import train_test_split

# Import Data
df = pd.read_csv('./medical_clean.csv')
```

In [2]:
```
# Get Shape of new dataframe of only duplicate values
df[df.duplicated()].shape
```

Out[2]:
```
(0, 50)
```

In [3]:
```
# Aggregate NaN Values, filter aggregates > 0, returns # records with NaN values
nullity = df.isna().sum()
nullity[~(nullity == 0)].shape
```

Out[3]:
```
(0,)
```

In [4]:
```
# Remove Unused Features
df.drop(
    columns=['CaseOrder', 'Customer_id', 'Interaction', 'UID', 'City', 'State', 'County', 'Zip', 'Lat', 'Lng', 'Area',
             'Population', 'TimeZone', 'Job', 'Item1', 'Item2', 'Item3', 'Item4', 'Item5', 'Item6', 'Item7', 'Item8'],
    inplace=True)
```

Summary Statistics

Summary Statistics are split into 3 sections: The Dependent Variable, The Continuous Independent Variables, and The Categorical/Qualitative Independent Variables. This is done since they each have their descriptive methods.

In [5]:
```
# Get Summary Stats of Dependent Variable
df['HighBlood'].value_counts()
```

Out[5]:
```
No     5910
Yes    4090
Name: HighBlood, dtype: int64
```

In [6]:
```
# Get Summary Stats of Continuous Independent Variables

features_continuous = ["Children", "Age", "Income", "VitD_levels", "Doc_visits", "Full_meals_eaten", "vitD_supp", "Initial_days",
    "Additional_charges", 'TotalCharge']

df[features_continuous].describe()
```

Out[6]:

	Children	Age	Income	VitD_levels	Doc_visits	Full_meals_eaten	vitD_supp	Initial_days	Additional_charges	TotalCharge
count	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000	10000.000000
mean	2.097200	53.511700	40490.495160	17.964262	5.012200	1.001400	0.398900	34.455299	12934.528587	5312.172769
std	2.163659	20.638538	28521.153293	2.017231	1.045734	1.008117	0.628505	26.309341	6542.601544	2180.393838
min	0.000000	18.000000	154.080000	9.806483	1.000000	0.000000	0.000000	1.001981	3125.703000	1938.312067
25%	0.000000	36.000000	19598.775000	16.626439	4.000000	0.000000	0.000000	7.896215	7986.487755	3179.374015
50%	1.000000	53.000000	33768.420000	17.951122	5.000000	1.000000	0.000000	35.836244	11573.977735	5213.952000
75%	3.000000	71.000000	54296.402500	19.347963	6.000000	2.000000	1.000000	61.161020	15626.490000	7459.699750
max	10.000000	89.000000	207249.100000	26.394449	9.000000	7.000000	5.000000	71.981490	30566.070000	9180.728000

In [7]:
```
# Get Summary Stats of Qualitative Independent Variables
features_categorical = ['Marital', 'Gender', 'ReAdmis', 'Soft_drink', 'Initial_admin', 'Overweight',
                        'Stroke', 'Complication_risk', 'Arthritis', 'Diabetes', 'Hyperlipidemia',
                        'BackPain', 'Anxiety', 'Allergic_rhinitis', 'Reflux_esophagitis',
                        'Asthma', 'Services']

for column in features_categorical:
    print(f"{df[column].name} Unique Values:")
    print(f"{df[column].value_counts()}\n")
```

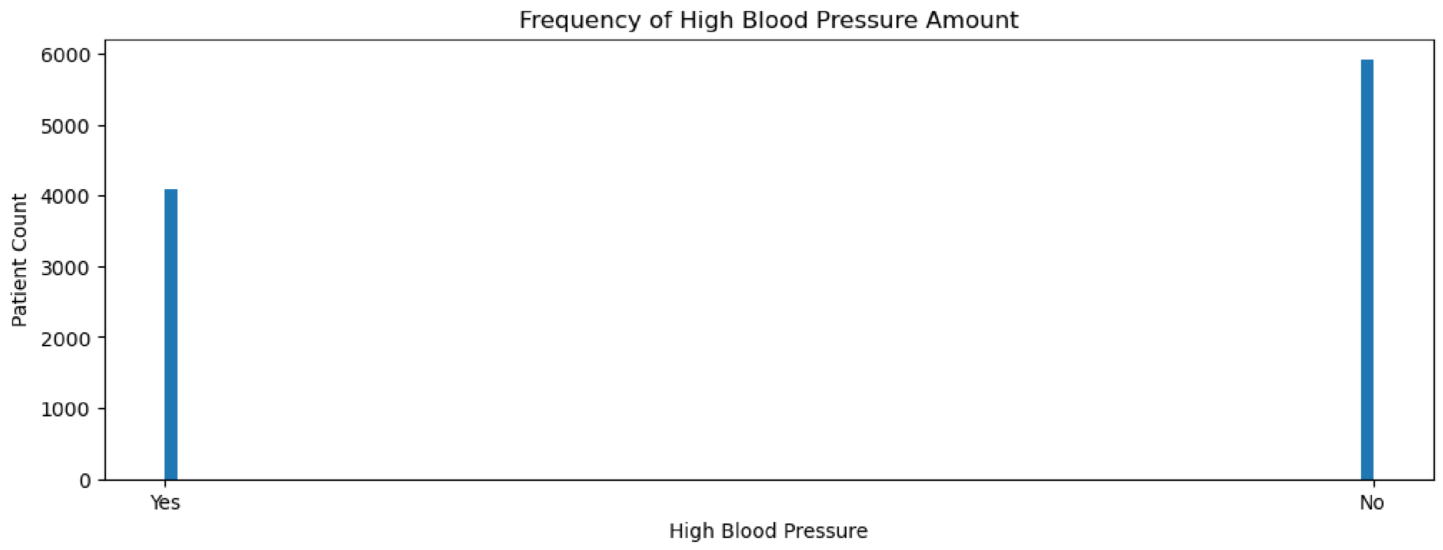
```
Marital Unique Values:
Widowed          2045
Married          2023
Separated        1987
Never Married    1984
Divorced         1961
Name: Marital, dtype: int64

Gender Unique Values:
Female       5018
Male         4768
Nonbinary     214
Name: Gender, dtype: int64

ReAdmis Unique Values:
No     6331
Yes    3669
Name: ReAdmis, dtype: int64

Soft_drink Unique Values:
No     7425
Yes    2575
Name: Soft_drink, dtype: int64

Initial_admin Unique Values:
Emergency Admission      5060
Elective Admission       2504
Observation Admission    2436
Name: Initial_admin, dtype: int64

Overweight Unique Values:
Yes    7094
No     2906
Name: Overweight, dtype: int64

Stroke Unique Values:
No     8007
Yes    1993
Name: Stroke, dtype: int64

Complication_risk Unique Values:
Medium    4517
High      3358
Low       2125
Name: Complication_risk, dtype: int64

Arthritis Unique Values:
No     6426
Yes    3574
Name: Arthritis, dtype: int64

Diabetes Unique Values:
No     7262
Yes    2738
Name: Diabetes, dtype: int64

Hyperlipidemia Unique Values:
No     6628
Yes    3372
Name: Hyperlipidemia, dtype: int64

BackPain Unique Values:
No     5886
Yes    4114
Name: BackPain, dtype: int64

Anxiety Unique Values:
No     6785
Yes    3215
Name: Anxiety, dtype: int64

Allergic_rhinitis Unique Values:
No     6059
Yes    3941
Name: Allergic_rhinitis, dtype: int64

Reflux_esophagitis Unique Values:
No     5865
Yes    4135
Name: Reflux_esophagitis, dtype: int64

Asthma Unique Values:
No     7107
Yes    2893
Name: Asthma, dtype: int64
```

```
Services Unique Values:
Blood Work      5265
Intravenous     3130
CT Scan         1225
MRI              380
Name: Services, dtype: int64
```

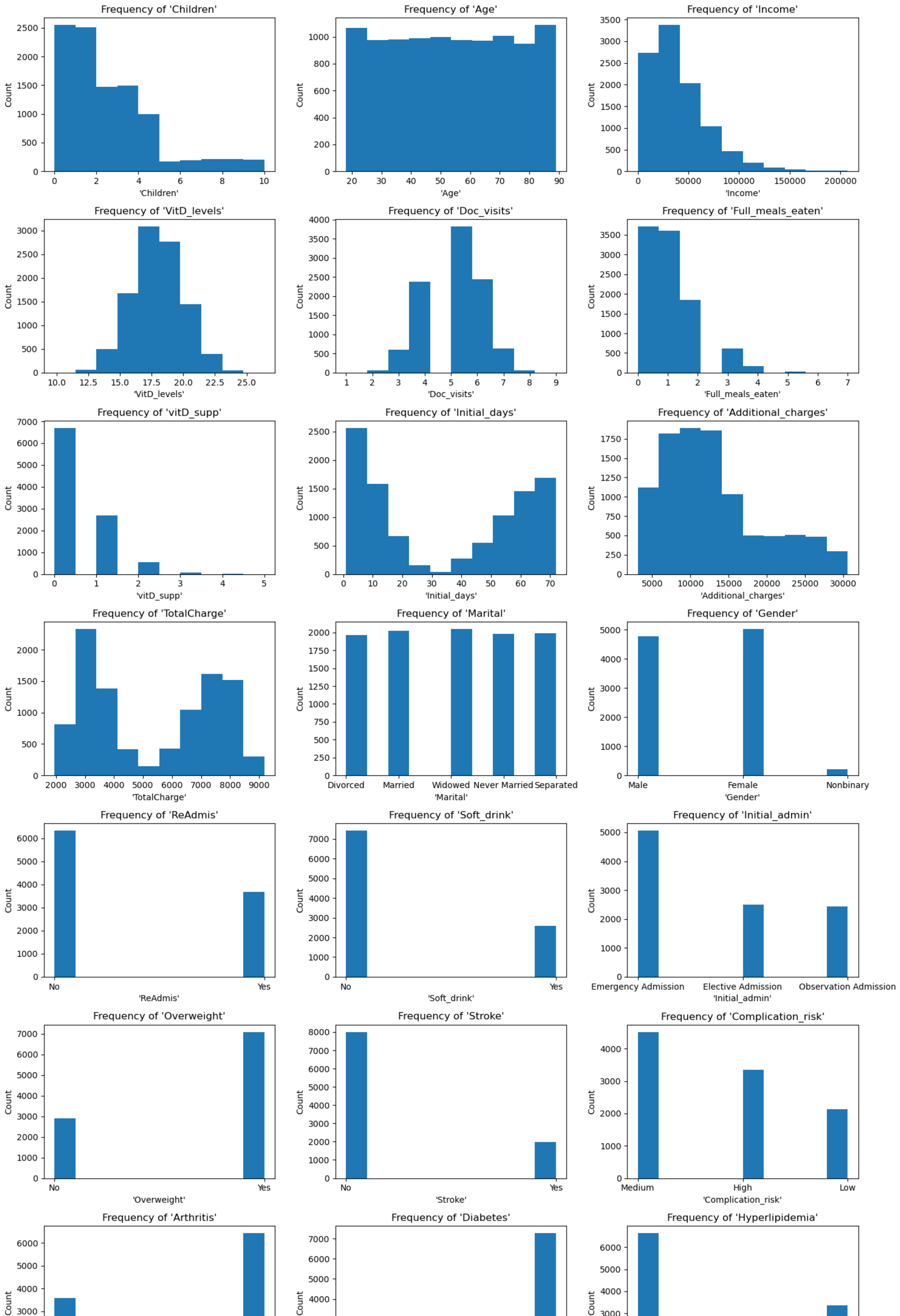
Distribution Visualizations

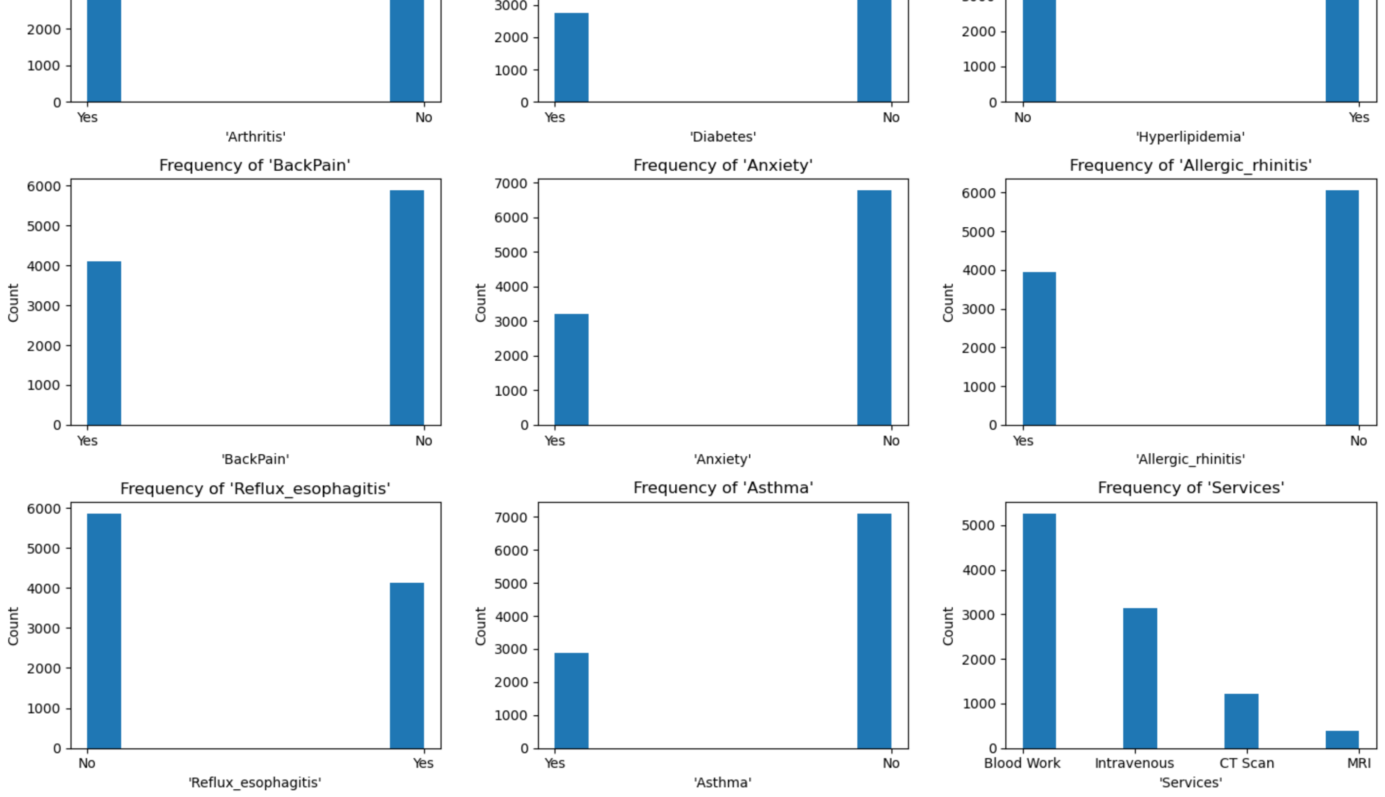
Univariate Distributions

In [8]:
```
# Dependent Variable (HighBlood) Visualization
plt.figure(figsize=(12,4))
plt.hist(data=df, x = "HighBlood", bins=100)
plt.xlabel("High Blood Pressure")
plt.ylabel("Patient Count");
plt.title("Frequency of High Blood Pressure Amount")
plt.show()
```



In [9]:
```
# Univariate Histograms for Independent Variables

num_cols = 3

var_independent = features_continuous + features_categorical

_, axs = plt.subplots(math.ceil(len(var_independent) / num_cols), num_cols, figsize=(15, 30), tight_layout=True)

for i, var in enumerate(var_independent):
    axs[i // num_cols, i % num_cols].hist(data=df, x = var, bins=10)
    name = f'{var=}'.split('=')[1]
    axs[i // num_cols, i % num_cols].set_xlabel(name)
    axs[i // num_cols, i % num_cols].set_ylabel("Count");
    axs[i // num_cols, i % num_cols].set_title(f"Frequency of {name}")

plt.show()
```


Frequency of 'Children'
Count
'Children'
Frequency of 'Age'
Count
'Age'
Frequency of 'Income'
Count
'Income'
Frequency of 'VitD_levels'
Count
'VitD_levels'
Frequency of 'Doc_visits'
Count
'Doc_visits'
Frequency of 'Full_meals_eaten'
Count
'Full_meals_eaten'
Frequency of 'vitD_supp'
Count
'vitD_supp'
Frequency of 'Initial_days'
Count
'Initial_days'
Frequency of 'Additional_charges'
Count
'Additional_charges'
Frequency of 'TotalCharge'
Count
'TotalCharge'
Frequency of 'Marital'
Count
Divorced
Married
Widowed
Never Married
Separated
'Marital'
Frequency of 'Gender'
Count
Male
Female
Nonbinary
'Gender'
Frequency of 'ReAdmis'
Count
No
Yes
'ReAdmis'
Frequency of 'Soft_drink'
Count
No
Yes
'Soft_drink'
Frequency of 'Initial_admin'
Count
Emergency Admission
Elective Admission
Observation Admission
'Initial_admin'
Frequency of 'Overweight'
Count
No
Yes
'Overweight'
Frequency of 'Stroke'
Count
No
Yes
'Stroke'
Frequency of 'Complication_risk'
Count
Medium
High
Low
'Complication_risk'
Frequency of 'Arthritis'
Count
Frequency of 'Diabetes'
Count
Frequency of 'Hyperlipidemia'
Count



Univariate Observations:

1. Additional Charges have a steep falloff at 15,000.
2. Age is fairly level. I would have thought there would be more elderly getting hospitalized than 20-year-olds.
3. It appears all types of martial status are equal in frequency. This is completely different from the US average, where notably Married is almost 50%, and separated is only 2% (US Census Bureau)

Bivariate Distributions are below Data Transformation. Dummy Variables / Conversions to Booleans make visualizations easier.

Data Transformation

The first step to transform our data for our analysis will be to convert features to the correct types:

1. Convert Object Data Types to Categorical for Marital, Gender, Initial_admin, Complication_risk, and Services.
2. Convert Boolean Data Types to Integers for ReAdmis, Soft_drink, Stroke, Overweight, Arthritis, Diabetes, Hyperlipidemia, BackPain, Anxiety, Allergic_rhinitis, Reflux_esophagitis, & Asthma.

The next step will be to convert categorical features into separate boolean features and remove unnecessary duplicates. This is completed using dummies and is important since the analysis will require binary values instead of strings. The removal of duplicate features will also avoid multicollinearity, and perfect relationships between variables.

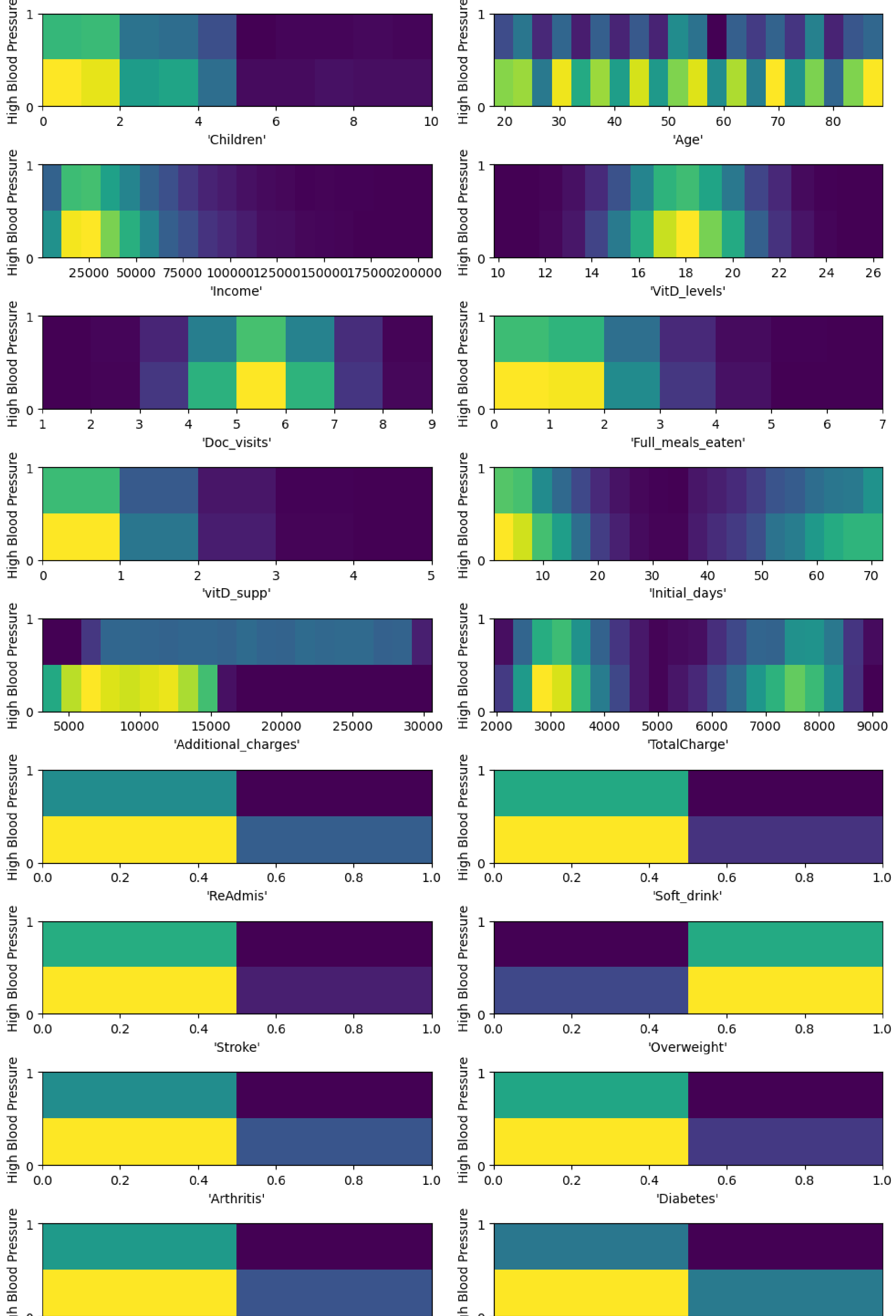
In [10]:
```python
# Convert Categorical
var_cat = ['Marital', 'Gender', 'Initial_admin', 'Complication_risk', 'Services']

for var in var_cat:
    df[var] = df[var].astype("category")

# Convert Boolean
var_bool = ['ReAdmis', 'Soft_drink', 'Stroke', 'Overweight', 'Arthritis', 'Diabetes', 'Hyperlipidemia',
            'BackPain', 'Anxiety', 'Allergic_rhinitis', 'Reflux_esophagitis', 'Asthma']

for var in var_bool:
    df[var] = df[var].replace({
        "Yes": 1,
        "No": 0
    })

df['HighBlood'] = df['HighBlood'].replace({
    "Yes": 1,
    "No": 0
})

var_numeric = ['Children', 'Age', 'Income', 'VitD_levels', 'Doc_visits', 'Full_meals_eaten',
               'vitD_supp', 'Initial_days','Additional_charges', 'TotalCharge']
```

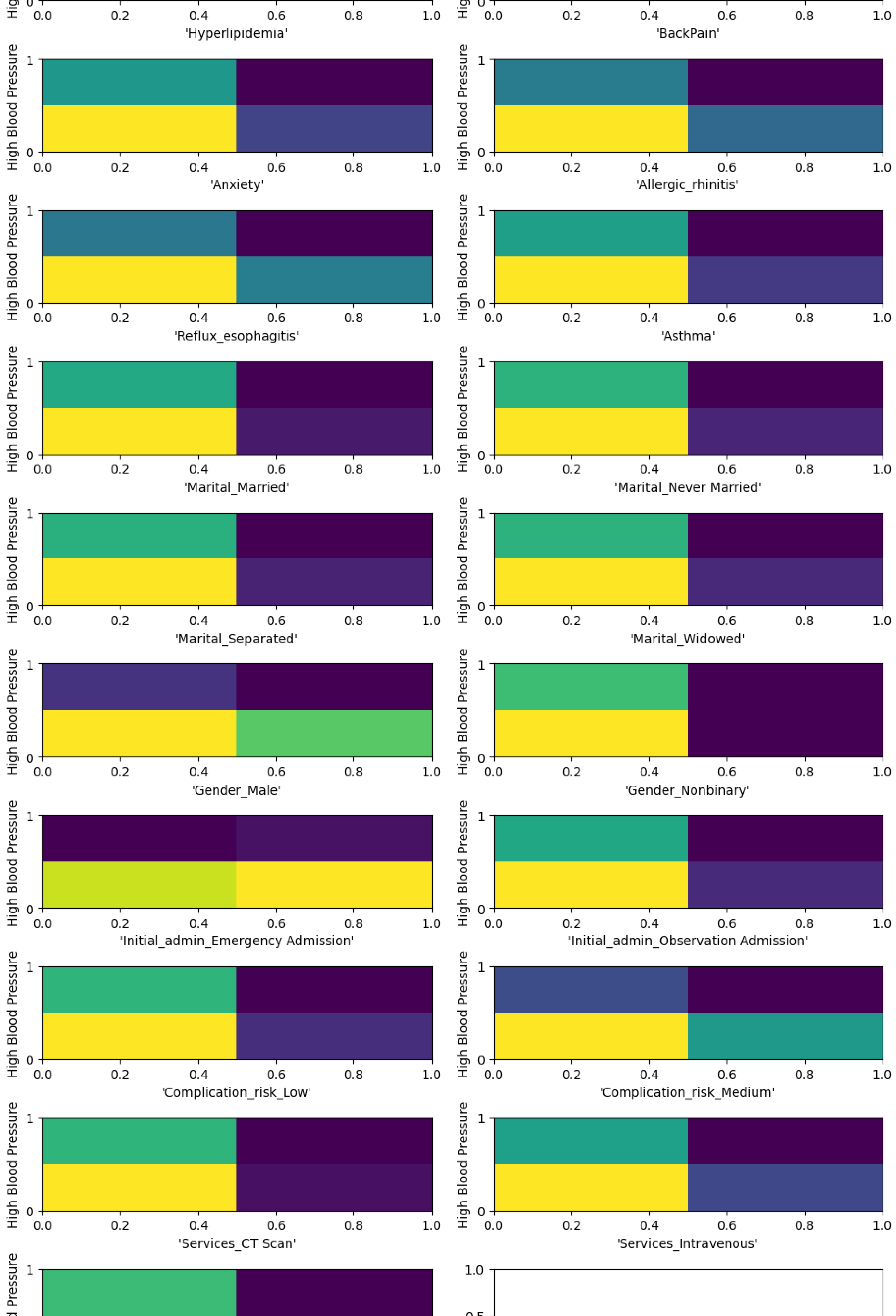
In [11]:
```python
# Convert String Categorical into Separate Boolean Features

var_cat_dumm = []

for var in var_cat:
    dummies = pd.get_dummies(df[var], prefix=var, drop_first=True).astype(np.int64)
    df.drop(var, axis=1, inplace=True)
    df = pd.concat([df, dummies], axis="columns")
    var_cat_dumm.extend(dummies.columns)
```

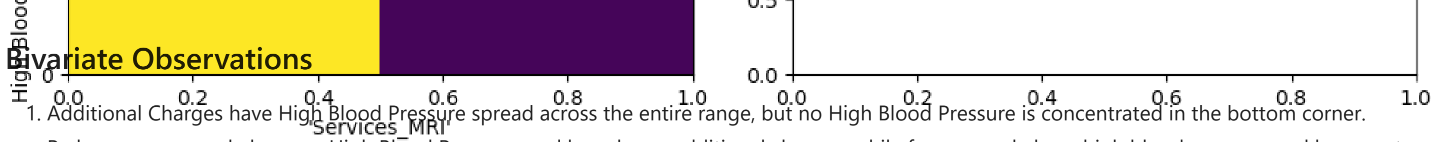
In [12]:
```python
# Combine Names of all independent variables into 1 list
var_independent = var_numeric + var_bool + var_cat_dumm
```

Bivariate Visualizations

In [13]:
```python
# Bivariate Histograms for Independent Variables

num_cols = 2

fig, axs = plt.subplots(math.ceil(len(var_independent) / num_cols), num_cols, figsize=(10, 30), tight_layout=True)

for i, var in enumerate(var_independent):
    # Min 2, Max 20 x bins
    x_bins = math.ceil(max(min(df[var].max() - df[var].min(), 20), 2))
    axs[i // num_cols, i % num_cols].hist2d(data=df, x=var, y='HighBlood', bins=[x_bins, 2])
    name = f'{var=}'.split('=')[1]
    axs[i // num_cols, i % num_cols].set_xlabel(name)
    axs[i // num_cols, i % num_cols].set_ylabel("High Blood Pressure");
    axs[i // num_cols, i % num_cols].set_yticks(range(0, 2))

plt.show()
```


High Blood Pressure
'Children'
'Age'
'Income'
'VitD_levels'
'Doc_visits'
'Full_meals_eaten'
'vitD_supp'
'Initial_days'
'Additional_charges'
'TotalCharge'
'ReAdmis'
'Soft_drink'
'Stroke'
'Overweight'
'Arthritis'
'Diabetes'


'Hyperlipidemia'
'BackPain'
High Blood Pressure
'Anxiety'
'Allergic_rhinitis'
'Reflux_esophagitis'
'Asthma'
'Marital_Married'
'Marital_Never Married'
'Marital_Separated'
'Marital_Widowed'
'Gender_Male'
'Gender_Nonbinary'
'Initial_admin_Emergency Admission'
'Initial_admin_Observation Admission'
'Complication_risk_Low'
'Complication_risk_Medium'
'Services_CT Scan'
'Services_Intravenous'
0.0
0.2
0.4
0.6
0.8
1.0
0
1



Bivariate Observations

1. Additional Charges have High Blood Pressure spread across the entire range, but no High Blood Pressure is concentrated in the bottom corner. Perhaps more people have no High Blood Pressure, and have lower additional charges, while fewer people have high blood pressure and have costs that are usually higher.
2. This is also the case with Total Charges.

CSV Export

In [14]:
```
# Export Data
df.to_csv('clean.csv', index=False)
```

Model Comparison and Analysis

Initial Logistic Regression Model

In [15]:
```
y = df['HighBlood']
X = df[var_independent].assign(const=1)

model = sm.Logit(y, X)
results = model.fit()

print(results.summary())
```

```
Warning: Maximum number of iterations has been exceeded.
         Current function value: 0.000000
         Iterations: 35
                           Logit Regression Results
==============================================================================
Dep. Variable:              HighBlood   No. Observations:                10000
Model:                          Logit   Df Residuals:                     9964
Method:                           MLE   Df Model:                           35
Date:                Fri, 15 Dec 2023   Pseudo R-squ.:                   1.000
Time:                        22:20:09   Log-Likelihood:            -8.2527e-05
converged:                      False   LL-Null:                       -6764.9
Covariance Type:            nonrobust   LLR p-value:                     0.000
=========================================================================================================
                                          coef    std err          z      P>|z|      [0.025      0.975]
---------------------------------------------------------------------------------------------------------
Children                               -0.2085     56.519     -0.004      0.997    -110.984     110.566
Age                                    -1.1234    140.454     -0.008      0.994    -276.408     274.161
Income                                6.73e-07      0.004      0.000      1.000      -0.008       0.008
VitD_levels                            -0.0241     59.944     -0.000      1.000    -117.513     117.465
Doc_visits                              0.0096    105.347   9.12e-05      1.000    -206.466     206.486
Full_meals_eaten                        0.0463    115.270      0.000      1.000    -225.879     225.972
vitD_supp                              -0.0055    175.036  -3.15e-05      1.000    -343.070     343.059
Initial_days                           -9.9830   1867.603     -0.005      0.996   -3670.418    3650.452
Additional_charges                      0.0072      0.872      0.008      0.993      -1.702       1.716
TotalCharge                             0.1218     22.793      0.005      0.996     -44.551      44.795
ReAdmis                                 0.0003    448.644   6.91e-07      1.000    -879.325     879.326
Soft_drink                             -0.0379    264.223     -0.000      1.000    -517.906     517.830
Stroke                                 -2.7151    437.923     -0.006      0.995    -861.028     855.598
Overweight                              0.0510    263.282      0.000      1.000    -515.972     516.074
Arthritis                              -8.6371   1676.695     -0.005      0.996   -3294.898    3277.624
Diabetes                               -9.8108   1660.084     -0.006      0.995   -3263.515    3243.894
Hyperlipidemia                        -11.4260   2161.000     -0.005      0.996   -4246.908    4224.056
BackPain                              -10.2834   1968.901     -0.005      0.996   -3869.258    3848.691
Anxiety                               -10.4019   2004.660     -0.005      0.996   -3939.463    3918.659
Allergic_rhinitis                      -7.2056   1439.921     -0.005      0.996   -2829.399    2814.988
Reflux_esophagitis                     -7.2178   1373.615     -0.005      0.996   -2699.454    2685.018
Asthma                                 -0.2908    283.657     -0.001      0.999    -556.249     555.668
Marital_Married                        -0.1099    371.357     -0.000      1.000    -727.956     727.737
Marital_Never Married                  -0.0373    365.568     -0.000      1.000    -716.538     716.463
Marital_Separated                       0.0143    367.221   3.89e-05      1.000    -719.726     719.754
Marital_Widowed                        -0.0680    357.272     -0.000      1.000    -700.308     700.172
Gender_Male                            -0.6039    240.499     -0.003      0.998    -471.972     470.765
Gender_Nonbinary                        0.0282    849.756   3.32e-05      1.000   -1665.464    1665.520
Initial_admin_Emergency Admission     -66.2415   1.12e+04     -0.006      0.995    -2.2e+04    2.19e+04
Initial_admin_Observation Admission     0.0710    322.517      0.000      1.000    -632.052     632.194
Complication_risk_Low                  54.0566   8982.067      0.006      0.995   -1.76e+04    1.77e+04
Complication_risk_Medium               53.0995   9114.780      0.006      0.995   -1.78e+04    1.79e+04
Services_CT Scan                       -0.1165    393.628     -0.000      1.000    -771.612     771.379
Services_Intravenous                   -0.1239    263.886     -0.000      1.000    -517.331     517.083
Services_MRI                           -0.1504    763.162     -0.000      1.000   -1495.921    1495.620
const                                -301.3410   5.11e+04     -0.006      0.995   -1.01e+05    9.99e+04
=========================================================================================================

Complete Separation: The results show that there iscomplete separation.
In this case the Maximum Likelihood Estimator does not exist and the parameters
are not identified.
```

```
C:\Users\Aaron\anaconda3\lib\site-packages\statsmodels\base\model.py:604: ConvergenceWarning: Maximum Likelihood optimization failed t
o converge. Check mle_retvals
  warnings.warn("Maximum Likelihood optimization failed to "
```

Reduction Justification

The original model had many features that were correlated and ones that provided little explanation for the variance of high blood pressure. To clean up this model the first step was to remove highly correlated features. This is done by getting the variance inflation factor (VIF) of each feature. Features with VIF values greater than 10 are removed from the model. In our case, these were TotalCharge, VitD_levels, Age, and Doc_visits. Next, any features with values greater than our 0.05 alpha value are removed since these are not significant in our model. This included Initial_admin_Observation Admission, Initial_admin_Emergency Admission, BackPain, Stroke, Marital_Widowed, Gender_Nonbinary, Diabetes, Reflux_esophagitis, Initial_days, Services_Intravenous, Hyperlipidemia, Services_MRI, Gender_Male, Children, Income, Complication_risk_Low, Marital_Separated, Soft_drink, ReAdmis, Arthritis, Asthma, Anxiety, Allergic_rhinitis, Marital_Married, Marital_Never Married, vitD_supp, Services_CT Scan, and Full_meals_eaten.

The only features left are not heavily correlated with each other, and ones that provide significance to the model. These will be the only ones important for answering our Research Question.

In [16]:
```
# vif_removal() is a recursive function that will remove features with VIF > 10.
# The VIF check has to be ran after each feature removal, which necessitates the recursive function
def vif_removal():
    # Create Dataframe for VIF Info
    vif_df = pd.DataFrame()
    vif_df["feature"] = df[var_independent].columns
    vif_df["VIF"] = [variance_inflation_factor(df[var_independent].values, i) for i in range(len(df[var_independent].columns))]
    # Highest VIF Variable Data
    highest = vif_df.sort_values('VIF').round(2).tail(1)
    highest_vif = int(highest.VIF)
    highest_column = str(list(highest.feature)[0])

    if highest_vif > 10:
        print(highest_column, " has a VIF Value of: ", highest_vif, " and will be removed from the dataset.")

        # Drop from Dataframe and from variable list, then run function again
        df.drop(highest_column, axis='columns', inplace=True)
        var_independent.remove(highest_column)
        vif_removal()
    else:
        print("All Features with VIF values > 10 Have been removed.")
        return False

# While VIF > 10, remove
remove = True

while remove:
    remove = vif_removal()
```

```
TotalCharge  has a VIF Value of:  826  and will be removed from the dataset.
VitD_levels  has a VIF Value of:  33  and will be removed from the dataset.
Age  has a VIF Value of:  15  and will be removed from the dataset.
Doc_visits  has a VIF Value of:  13  and will be removed from the dataset.
All Features with VIF values > 10 Have been removed.
```

In [17]:

```
y = df['HighBlood']
X = df[var_independent].assign(const=1)

model = sm.Logit(y, X)
results = model.fit()

print(results.summary())
```

```
Optimization terminated successfully.
         Current function value: 0.411870
         Iterations 7
                           Logit Regression Results
==============================================================================
Dep. Variable:              HighBlood   No. Observations:                10000
Model:                          Logit   Df Residuals:                     9968
Method:                           MLE   Df Model:                           31
Date:                Fri, 15 Dec 2023   Pseudo R-squ.:                  0.3912
Time:                        22:20:13   Log-Likelihood:                -4118.7
converged:                       True   LL-Null:                       -6764.9
Covariance Type:            nonrobust   LLR p-value:                     0.000
=====================================================================================================
                                        coef    std err          z      P>|z|      [0.025      0.975]
-----------------------------------------------------------------------------------------------------
Children                             -0.0093      0.013     -0.736      0.462      -0.034       0.015
Income                             6.612e-07   9.66e-07      0.684      0.494   -1.23e-06    2.55e-06
Full_meals_eaten                      0.0022      0.027      0.082      0.934      -0.051       0.056
vitD_supp                             0.0052      0.043      0.119      0.905      -0.080       0.090
Initial_days                         -0.0020      0.002     -0.993      0.321      -0.006       0.002
Additional_charges                    0.0003   7.27e-06     47.710      0.000       0.000       0.000
ReAdmis                               0.0450      0.109      0.413      0.680      -0.169       0.259
Soft_drink                           -0.0299      0.063     -0.472      0.637      -0.154       0.094
Stroke                               -0.1374      0.069     -1.992      0.046      -0.272      -0.002
Overweight                            0.1455      0.061      2.392      0.017       0.026       0.265
Arthritis                             0.0180      0.057      0.313      0.754      -0.094       0.130
Diabetes                             -0.0677      0.062     -1.098      0.272      -0.189       0.053
Hyperlipidemia                       -0.0524      0.058     -0.898      0.369      -0.167       0.062
BackPain                             -0.0785      0.056     -1.399      0.162      -0.188       0.031
Anxiety                               0.0156      0.059      0.265      0.791      -0.100       0.131
Allergic_rhinitis                     0.0144      0.056      0.255      0.798      -0.096       0.125
Reflux_esophagitis                    0.0589      0.056      1.053      0.292      -0.051       0.169
Asthma                               -0.0173      0.061     -0.284      0.777      -0.137       0.102
Marital_Married                       0.0144      0.087      0.165      0.869      -0.156       0.185
Marital_Never Married                -0.0123      0.088     -0.140      0.889      -0.184       0.160
Marital_Separated                    -0.0439      0.087     -0.503      0.615      -0.215       0.127
Marital_Widowed                      -0.1027      0.087     -1.178      0.239      -0.274       0.068
Gender_Male                           0.0429      0.056      0.769      0.442      -0.066       0.152
Gender_Nonbinary                      0.2184      0.191      1.146      0.252      -0.155       0.592
Initial_admin_Emergency Admission    -0.1004      0.068     -1.475      0.140      -0.234       0.033
Initial_admin_Observation Admission   0.1209      0.079      1.538      0.124      -0.033       0.275
Complication_risk_Low                 0.0476      0.077      0.620      0.536      -0.103       0.198
Complication_risk_Medium              0.1482      0.063      2.367      0.018       0.025       0.271
Services_CT Scan                     -0.0092      0.086     -0.106      0.915      -0.179       0.160
Services_Intravenous                 -0.0589      0.062     -0.944      0.345      -0.181       0.063
Services_MRI                         -0.1147      0.149     -0.769      0.442      -0.407       0.177
const                                -4.8468      0.166    -29.220      0.000      -5.172      -4.522
=====================================================================================================
```

In [18]:
```python
# Significant Variables < 0.05 (alpha value)
# Insignificant Variables are dropped from the DataFrame and removed from the list of independent variables

# p_removal() is a recursive function that will remove features with pvals > 0.05.
# The Pval check has to be ran after each feature removal, which necessitates the recursive function
def p_removal():
    # New Model after VIF Evaluation
    y = df['HighBlood']
    X = df[var_independent].assign(const=1)

    model = sm.OLS(y, X)
    results = model.fit()

    pvals = results.pvalues.sort_values()
    highest = pvals.tail(1)
    highest_name = list(highest.index)[0]
    highest_value = highest.values[0]

    if highest_value > 0.05:
        print(highest_name, " has a P Value of: ", highest_value.round(2), " and will be removed from the dataset.")

        # Drop from Dataframe and from variable list, then run function again
        df.drop(highest_name, axis='columns', inplace=True)
        var_independent.remove(highest_name)
        p_removal()
    else:
        print("All Features with P values > 0.05 Have been removed.")
        return False

# While pval > 0.05, remove
remove = True

while remove:
    remove = p_removal()
```

```
vitD_supp  has a P Value of:  0.96  and will be removed from the dataset.
Marital_Married  has a P Value of:  0.94  and will be removed from the dataset.
Anxiety  has a P Value of:  0.9  and will be removed from the dataset.
Services_CT Scan  has a P Value of:  0.87  and will be removed from the dataset.
Allergic_rhinitis  has a P Value of:  0.84  and will be removed from the dataset.
Full_meals_eaten  has a P Value of:  0.71  and will be removed from the dataset.
Arthritis  has a P Value of:  0.68  and will be removed from the dataset.
ReAdmis  has a P Value of:  0.66  and will be removed from the dataset.
Asthma  has a P Value of:  0.64  and will be removed from the dataset.
Gender_Male  has a P Value of:  0.64  and will be removed from the dataset.
Soft_drink  has a P Value of:  0.63  and will be removed from the dataset.
Marital_Never Married  has a P Value of:  0.54  and will be removed from the dataset.
Marital_Separated  has a P Value of:  0.59  and will be removed from the dataset.
Income  has a P Value of:  0.54  and will be removed from the dataset.
Services_MRI  has a P Value of:  0.45  and will be removed from the dataset.
Complication_risk_Low  has a P Value of:  0.43  and will be removed from the dataset.
Children  has a P Value of:  0.43  and will be removed from the dataset.
BackPain  has a P Value of:  0.36  and will be removed from the dataset.
Diabetes  has a P Value of:  0.33  and will be removed from the dataset.
Hyperlipidemia  has a P Value of:  0.3  and will be removed from the dataset.
Services_Intravenous  has a P Value of:  0.3  and will be removed from the dataset.
Gender_Nonbinary  has a P Value of:  0.29  and will be removed from the dataset.
Initial_days  has a P Value of:  0.23  and will be removed from the dataset.
Reflux_esophagitis  has a P Value of:  0.23  and will be removed from the dataset.
Marital_Widowed  has a P Value of:  0.14  and will be removed from the dataset.
Initial_admin_Emergency Admission  has a P Value of:  0.11  and will be removed from the dataset.
All Features with P values > 0.05 Have been removed.
```

Final Model

Prior to creating the Final Model, a training and test dataset will be be created to allow easy evaluation later.

In [19]:
```python
y = df['HighBlood']
X = df[var_independent].assign(const=1)

# Test and training split
X_train, X_test, y_train, y_test = train_test_split( X, y, test_size=0.2, random_state=100)
```

In [20]:
```python
model = sm.Logit(y_train, X_train)
results = model.fit()

print(results.summary())
```

```
Optimization terminated successfully.
         Current function value: 0.414381
         Iterations 7
                           Logit Regression Results
==============================================================================
Dep. Variable:              HighBlood   No. Observations:                 8000
Model:                          Logit   Df Residuals:                     7994
Method:                           MLE   Df Model:                            5
Date:                Fri, 15 Dec 2023   Pseudo R-squ.:                  0.3882
Time:                        22:20:13   Log-Likelihood:                -3315.1
converged:                       True   LL-Null:                       -5418.5
Covariance Type:            nonrobust   LLR p-value:                     0.000
==========================================================================================================
                                         coef    std err          z      P>|z|      [0.025      0.975]
----------------------------------------------------------------------------------------------------------
Additional_charges                     0.0003   8.06e-06     42.808      0.000       0.000       0.000
Stroke                                -0.1532      0.077     -1.987      0.047      -0.304      -0.002
Overweight                             0.1382      0.068      2.046      0.041       0.006       0.271
Initial_admin_Observation Admission    0.1776      0.071      2.511      0.012       0.039       0.316
Complication_risk_Medium               0.1455      0.062      2.360      0.018       0.025       0.266
const                                 -4.9522      0.122    -40.613      0.000      -5.191      -4.713
==========================================================================================================
```

Model Comparison

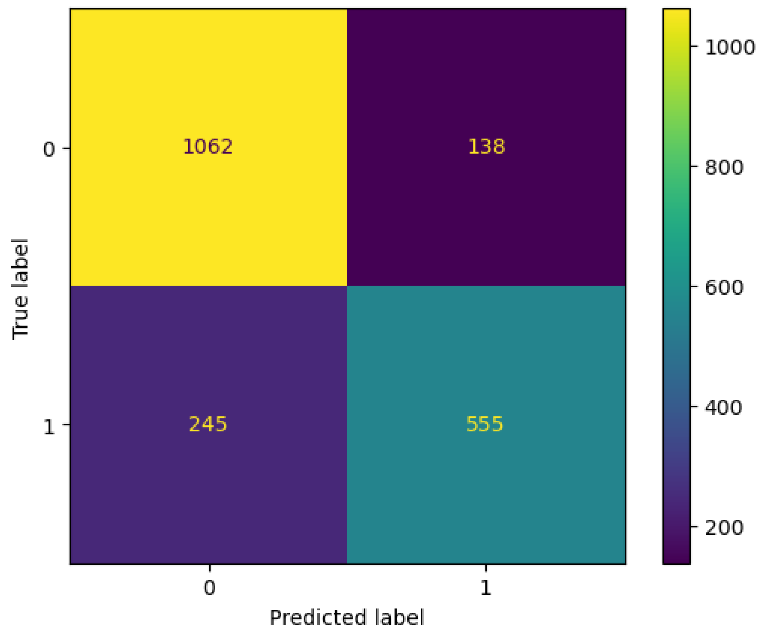
The comparison metric I have chosen for this evaluation is the Psuedo R-squared metric. A standard R-squared value cannot be applied to a logistic regression model, since we are modeling likelihoods, not direct values. Pseudo R-squared attempts to mimic the R-squared metric. However, since the error variance is different for each predicted value, it cannot be used analogously to an R-squared metric. We should have no problem using the metric to compare models on the same data, the metric just falls apart when comparing models on different data. (IBM)

When we compare Psuedo R-squared values, we still see the original model has a value of 1.00 and our final model has a value of 0.3882. After some research, this is because of the warning we are getting on the original model, "Complete Separation: The results show that there is complete separation.". Complete Separation meanings the dependent variable for our function separates (between 0 and 1) at an exact value for one of our independent variables. After some research, it turns out the TotalCharge variable is the culprit. The removal of these variables removes this separation. This means the first model's R-squared value of 1.0 is not an accurate metric. (OARC)

To simplify, the Psuedo R-squared metric does not have to be 1.0 for a perfect model, and the original model's Psuedo R-squared value does not hold water by itself. To accurately assess the accuracy of the final model we will need to run a training and test split against the model and evaluate the accuracy of predictions.

Evaluation

In [21]:
```python
# Predictions from Model using Training data to Fit,
# Values are returned as continuous between 0-1, and rounded to match binary High Blood Pressure Value
y_pred = round(results.predict(X_test))

cm = confusion_matrix(y_test, y_pred)
disp = ConfusionMatrixDisplay(confusion_matrix=cm)
disp.plot()

plt.show()

# All Confusion Matrix Metrics
print(f'Accuracy: {round(metrics.accuracy_score(y_test, y_pred),2)}')
print(f'Precision: {round(metrics.precision_score(y_test, y_pred),2)}')
print(f'Sensitivity (Recall): {round(metrics.recall_score(y_test, y_pred),2)}')
print(f'Specificity: {round(metrics.recall_score(y_test, y_pred, pos_label=0),2)}')
print(f'F-score: {round(metrics.f1_score(y_test, y_pred),2)}')
```



```
Accuracy: 0.81
Precision: 0.8
Sensitivity (Recall): 0.69
Specificity: 0.88
F-score: 0.74
```

Executable Code

I am not sure if the above code snippets suffice. If not an additional python file "d208_task2_e3.py" has been included. To run the file, numpy, pandas, matplotlib, seaborn, and statsmodels libraries have to be installed. That file executes all the above code snippets.

Part V: Data Summary and Implications

Results

Equation

ln (p / (1 - p)) = - 4.9522 + 0.0003 (Additional_charges) - 0.1532 (Stroke) + 0.1382 (Overweight) + 0.1776 (Initial_admin_Observation Admission) + 0.1455 (Complication_risk_Medium)

Practical Interpretation

A Patients chance of having High Blood Pressure can be interpreted as the following:

- All things constant, for each extra dollar in additional charges, the patient will be 0.03% more likely to have High Blood Pressure.
- All things constant, if the patient has a Stroke, the patient will be 15.32% more likely to have High Blood Pressure.
- All things constant, if the patient is overweight, the patient will be 13.82% more likely to have High Blood Pressure.
- All things constant, if the patient's initial admission is an Observation Admission, the patient will be 17.76% more likely to have High Blood Pressure.
- All things constant, if the patient has a medium complication risk, the patient will be 14.55% more likely to have High Blood Pressure.

Significance

This model has some practical and statistical significance; however, I have concerns with its practicality. We had 4 features that were statistically significant to our model, but our model was not accurate and effective at taking into account all variance in the model. The model could only predict with a ~81% accuracy, which while good, in my opinion, is not high enough to make financial or health-related suggestions. Additionally, practically speaking I'm not sure how useful the additional charges feature is to the model, since this value is calculated during/after a visit. It can not be used to predict or estimate high blood pressure in patients. By the time you have their additional charges, you will already have their blood pressure.

Limitations

- While logistic regression could not be used, I do believe a continuous variable for Blood Pressure would interesting to compare to this boolean option. It may provide more insight into patient health.

- There is a similar problem with overweight. In my experience weights are usually broken down into underweight, normal, overweight, obese, and morbidly obese. I think this categorical feature or a continuous BMI value would provide more insight, especially since being underweight can have negative health consequences as well.

Recommendations

At this time I cannot recommend any course of action when it comes to answering our question. I do not believe this model is good enough to be used to make any decisions, and I do not believe we can make any conclusions on features related to high blood pressure. It does appear that more research should be done in comparing overweight and high blood pressure, there may be a connection there.

Presentation

https://youtu.be/LWugYhTZ4xc

Web Sources

Model Building:

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Model Evaluation:

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