## Importing required libraries

In [1]:

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

## Stroke Dataset: Loading

- Stroke prediction dataset (gathered from kaggle. Author: Fedesoriano. Name: Stroke-prediction-dataset)
- The purpose of the dataset is to forecast the possibility of an individual having a stroke, utilising input parameters such as gender, age, presence of different ailments, and smoking status. Each row of data provides pertinent information about the patient.
- The dataset includes 5110 rows and 12 columns, with each row representing a different patient and each column representing a different attribute or feature. The columns in the dataset are:

| Variable | Description |
|---:|---:|
| iD | Unique identifier for each patient |
| gender | Gender of the patient (Male/Female/Other) |
| age | Age of the patient in years |
| hypertension | Whether the patient has hypertension or not (0 - No, 1 - Yes) |
| heart_disease | Whether the patient has heart disease or not (0 - No, 1 - Yes) |
| ever_married | Whether the patient has ever been married or not (Yes/No) |
| work_type | Type of occupation of the patient (Private, Self-employed, Govt_job, children, Never_worked) |
| Residence_type | Area type of residence of the patient (Urban/Rural) |
| avg_glucose_level | Average glucose level in the patient's blood |
| bmi | Body mass index of the patient |
| smoking_status | Habitual infromation, patient's smoking status (formerly smoked, never smoked, smokes, unknown) |
| stroke | Whether the patient has had a stroke or not (0 - No, 1 - Yes) |

In [2]:

```
stroke_data = pd.read_csv("healthcare-dataset-stroke-data.csv")
```

In [3]:

```
stroke_data.head(10)
```

Out[3]:

|  | id | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi | smoking_status | strok |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 9046 | Male | 67.0 | 0 | 1 | Yes | Private | Urban | 228.69 | 36.6 | formerly smoked | |
| **1** | 51676 | Female | 61.0 | 0 | 0 | Yes | Self-employed | Rural | 202.21 | NaN | never smoked | |
| **2** | 31112 | Male | 80.0 | 0 | 1 | Yes | Private | Rural | 105.92 | 32.5 | never smoked | |
| **3** | 60182 | Female | 49.0 | 0 | 0 | Yes | Private | Urban | 171.23 | 34.4 | smokes | |
| **4** | 1665 | Female | 79.0 | 1 | 0 | Yes | Self-employed | Rural | 174.12 | 24.0 | never smoked | |
| **5** | 56669 | Male | 81.0 | 0 | 0 | Yes | Private | Urban | 186.21 | 29.0 | formerly smoked | |
| **6** | 53882 | Male | 74.0 | 1 | 1 | Yes | Private | Rural | 70.09 | 27.4 | never smoked | |
| **7** | 10434 | Female | 69.0 | 0 | 0 | No | Private | Urban | 94.39 | 22.8 | never smoked | |
| **8** | 27419 | Female | 59.0 | 0 | 0 | Yes | Private | Rural | 76.15 | NaN | Unknown | |
| **9** | 60491 | Female | 78.0 | 0 | 0 | Yes | Private | Urban | 58.57 | 24.2 | Unknown | |

***Checking the summary of statistics for each column of the DataFrame***

In [4]:

```
stroke_data.describe()
```

Out[4]:

| | id | age | hypertension | heart_disease | avg_glucose_level | bmi | stroke |
|---|---|---|---|---|---|---|---|
| **count** | 5110.000000 | 5110.000000 | 5110.000000 | 5110.000000 | 5110.000000 | 4909.000000 | 5110.000000 |
| **mean** | 36517.829354 | 43.226614 | 0.097456 | 0.054012 | 106.147677 | 28.893237 | 0.048728 |
| **std** | 21161.721625 | 22.612647 | 0.296607 | 0.226063 | 45.283560 | 7.854067 | 0.215320 |
| **min** | 67.000000 | 0.080000 | 0.000000 | 0.000000 | 55.120000 | 10.300000 | 0.000000 |
| **25%** | 17741.250000 | 25.000000 | 0.000000 | 0.000000 | 77.245000 | 23.500000 | 0.000000 |
| **50%** | 36932.000000 | 45.000000 | 0.000000 | 0.000000 | 91.885000 | 28.100000 | 0.000000 |
| **75%** | 54682.000000 | 61.000000 | 0.000000 | 0.000000 | 114.090000 | 33.100000 | 0.000000 |
| **max** | 72940.000000 | 82.000000 | 1.000000 | 1.000000 | 271.740000 | 97.600000 | 1.000000 |

In [5]:

```
stroke_data.info() # this is to obtain basic information about a DataFrame, and is often used as a first step in expl
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 5110 entries, 0 to 5109
Data columns (total 12 columns):
 #   Column             Non-Null Count  Dtype  
---  ------             --------------  -----  
 0   id                 5110 non-null   int64  
 1   gender             5110 non-null   object 
 2   age                5110 non-null   float64
 3   hypertension       5110 non-null   int64  
 4   heart_disease      5110 non-null   int64  
 5   ever_married       5110 non-null   object 
 6   work_type          5110 non-null   object 
 7   Residence_type     5110 non-null   object 
 8   avg_glucose_level  5110 non-null   float64
 9   bmi                4909 non-null   float64
 10  smoking_status     5110 non-null   object 
 11  stroke             5110 non-null   int64  
dtypes: float64(3), int64(4), object(5)
memory usage: 479.2+ KB
```

In [6]:

```
# Calculating the mean of the 'bmi' column
mean_value = stroke_data ['bmi'].mean()
stroke_data ['bmi'].fillna(value = mean_value, inplace = True)
```

In [7]:

```
stroke_data.head(10)
# it can be seen that all the missing values have been replaced by the mean
```

Out[7]:

| | id | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi | smoking_status |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 9046 | Male | 67.0 | 0 | 1 | Yes | Private | Urban | 228.69 | 36.600000 | formerly smoked |
| **1** | 51676 | Female | 61.0 | 0 | 0 | Yes | Self-employed | Rural | 202.21 | 28.893237 | never smoked |
| **2** | 31112 | Male | 80.0 | 0 | 1 | Yes | Private | Rural | 105.92 | 32.500000 | never smoked |
| **3** | 60182 | Female | 49.0 | 0 | 0 | Yes | Private | Urban | 171.23 | 34.400000 | smokes |
| **4** | 1665 | Female | 79.0 | 1 | 0 | Yes | Self-employed | Rural | 174.12 | 24.000000 | never smoked |
| **5** | 56669 | Male | 81.0 | 0 | 0 | Yes | Private | Urban | 186.21 | 29.000000 | formerly smoked |
| **6** | 53882 | Male | 74.0 | 1 | 1 | Yes | Private | Rural | 70.09 | 27.400000 | never smoked |
| **7** | 10434 | Female | 69.0 | 0 | 0 | No | Private | Urban | 94.39 | 22.800000 | never smoked |
| **8** | 27419 | Female | 59.0 | 0 | 0 | Yes | Private | Rural | 76.15 | 28.893237 | Unknown |
| **9** | 60491 | Female | 78.0 | 0 | 0 | Yes | Private | Urban | 58.57 | 24.200000 | Unknown |

## Exploratory Data Analysis (EDA)

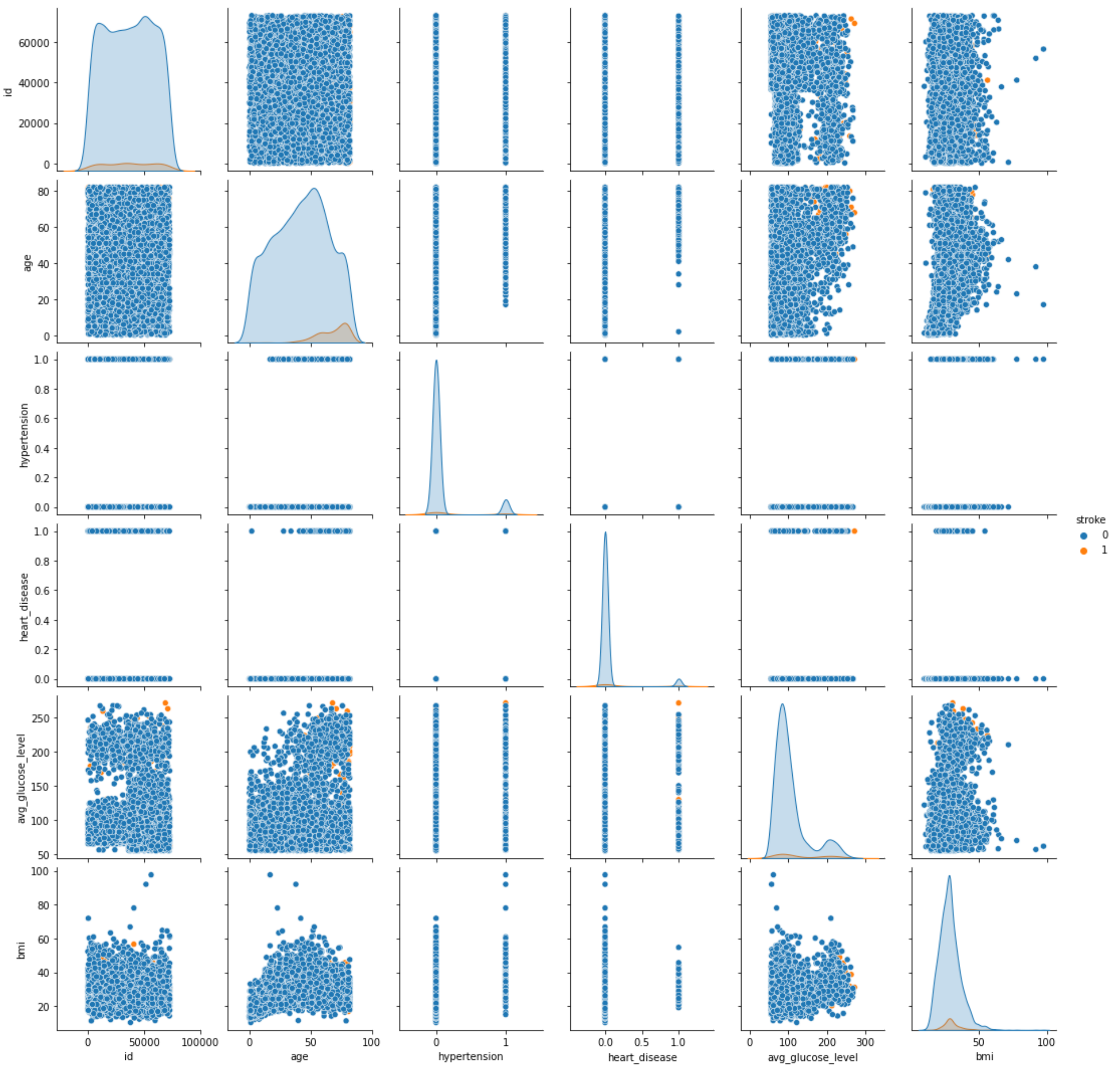
***Calculating the mean inside the 'bmi' attribute and replacing all the null and missing values with the mean***

In [8]:

```
sns.pairplot(stroke_data, hue="stroke")
```

Out[8]:

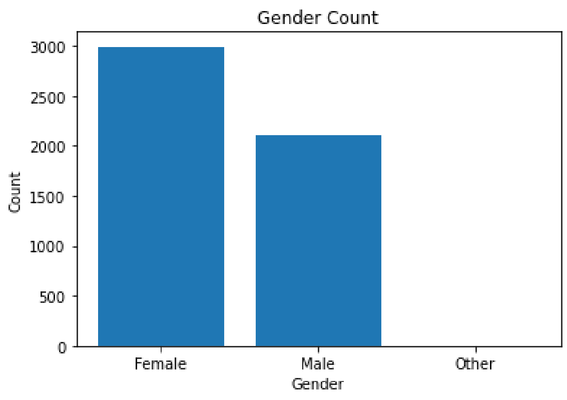
```
<seaborn.axisgrid.PairGrid at 0x7f7ba3b51040>
```



**Distribution by Gender**

In [9]:

```
# Count the occurences of each gender
gender_count = stroke_data['gender'].value_counts()

# Plotting a Bar chart
plt.bar(gender_count.index, gender_count.values)

# Adding the labels and the char title
plt.xlabel('Gender')
plt.ylabel('Count')
plt.title('Gender Count')

plt.show()
```



In [10]:

```
gender_count
```

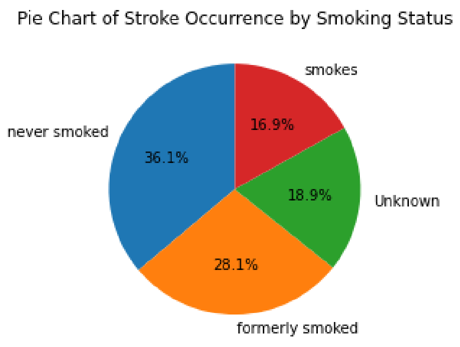
Out[10]:

```
Female    2994
Male      2115
Other        1
Name: gender, dtype: int64
```

***Distribution by Smoking Status***

In [11]:

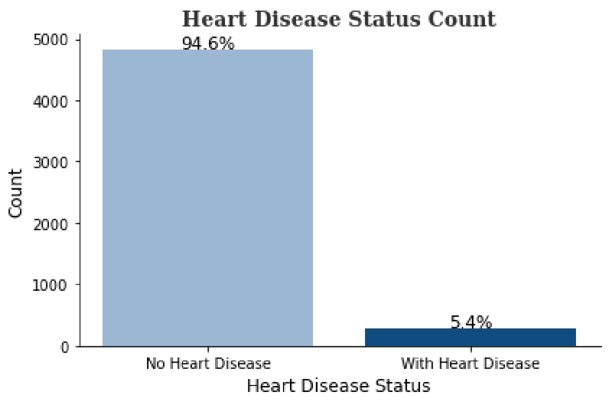
```
#Pie chart of stroke occurrence by smoking status
smoking_stroke = stroke_data[stroke_data["stroke"] == 1]["smoking_status"].value_counts()
plt.pie(smoking_stroke, labels=smoking_stroke.index, autopct='%1.1f%%', startangle=90)
plt.title("Pie Chart of Stroke Occurrence by Smoking Status")
plt.show()
```



***Distribution by Heart Disease***

In [12]:

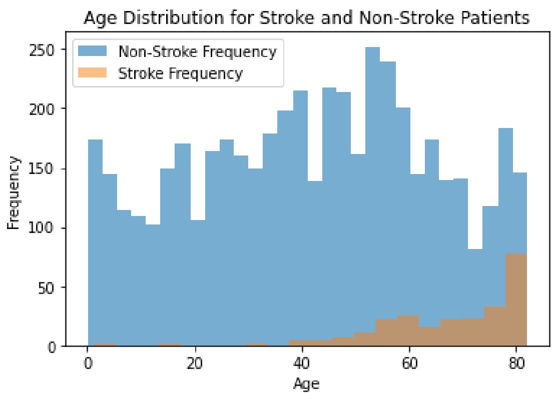
```
# Count the occurrences of each heart disease status
hd_count = stroke_data['heart_disease'].value_counts()

# Plotting a bar chart
plt.bar(['No Heart Disease', 'With Heart Disease'], hd_count.values, color=['#9bb7d4', '#0f4c81'])

# Adding the labels and the chart title
plt.xlabel('Heart Disease Status', fontsize=12)
plt.ylabel('Count', fontsize=12)
plt.title('Heart Disease Status Count', fontsize=14, fontweight='bold', fontfamily='serif', color="#323232")

# Adding the percentage values above the bars
for i, count in enumerate(hd_count.values):
    plt.text(i, count+10, str(round((count/len(stroke_data))*100, 1)) + '%', ha='center', fontsize=12)

# Removing the top and right spines
plt.gca().spines['top'].set_visible(False)
plt.gca().spines['right'].set_visible(False)

# Adjusting the layout
plt.tight_layout()

plt.show()
```



**Distribution of Frequency by Age**

In [13]:

```
#this is to check stroke frequency by age

stroke_positive = stroke_data[stroke_data['stroke'] == 1]
stroke_negative = stroke_data[stroke_data['stroke'] == 0]

# Plot the age distributions for stroke and non-stroke patients
plt.hist(stroke_negative['age'], bins=30, alpha=0.6, label='Non-Stroke Frequency')
plt.hist(stroke_positive['age'], bins=20, alpha=0.5, label='Stroke Frequency')
plt.title('Age Distribution for Stroke and Non-Stroke Patients')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.legend(loc='upper left')
plt.show()
```



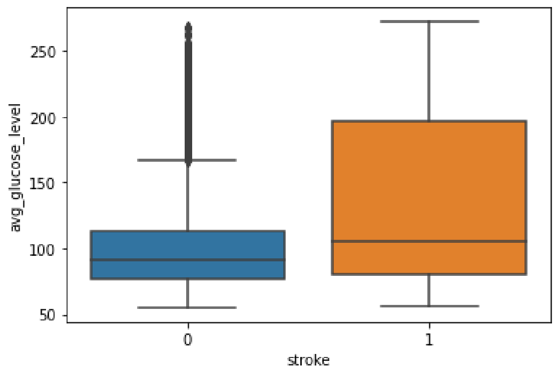
**Distribution by Stroke and Glucose Levels**

In [14]:

```
#Box plot of glucose levels by stroke occurrence
sns.boxplot(x="stroke", y="avg_glucose_level", data=stroke_data)
```

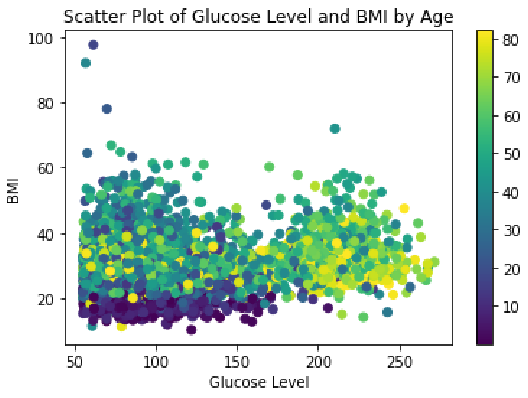
Out[14]:

```
<AxesSubplot:xlabel='stroke', ylabel='avg_glucose_level'>
```



In [15]:

```
#Scatter plot of glucose level and BMI by age:
plt.scatter(stroke_data["avg_glucose_level"], stroke_data["bmi"], c=stroke_data["age"], cmap="viridis")
plt.xlabel("Glucose Level")
plt.ylabel("BMI")
plt.title("Scatter Plot of Glucose Level and BMI by Age")
plt.colorbar()
plt.show()
```



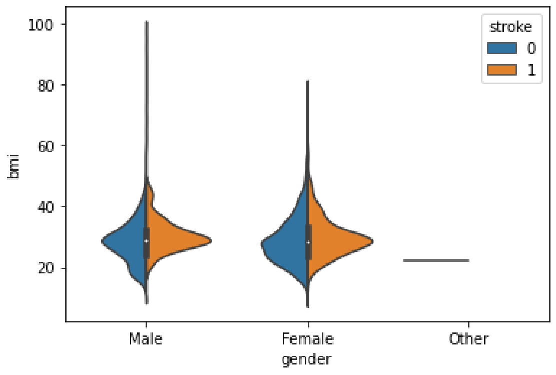
**Distribution Gender and BMI scores**

In [16]:

```
#Violin plot of BMI by stroke occurrence and gender
sns.violinplot(x="gender", y="bmi", hue="stroke", data=stroke_data, split=True)
```

Out[16]:

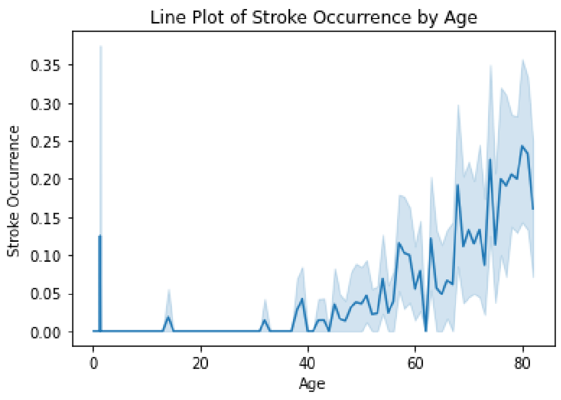
```
<AxesSubplot:xlabel='gender', ylabel='bmi'>
```



**Distribution frequency of Stroke occurances by Age**

In [17]:

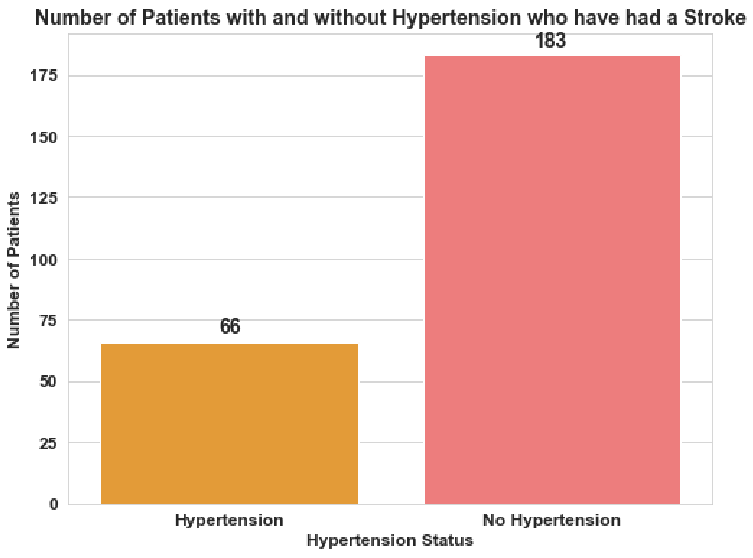
```
#Line plot of stroke occurrence by age
sns.lineplot(x="age", y="stroke", data=stroke_data)
plt.xlabel("Age")
plt.ylabel("Stroke Occurrence")
plt.title("Line Plot of Stroke Occurrence by Age")
plt.show()
```



**Distribution of Stroke patients filtered by Hypertension**

In [18]:

```
# Count the number of patients with and without hypertension who have had a stroke
hypertension_stroke = stroke_data.loc[(stroke_data['hypertension'] == 1) & (stroke_data['stroke'] == 1)].shape[0]
no_hypertension_stroke = stroke_data.loc[(stroke_data['hypertension'] == 0) & (stroke_data['stroke'] == 1)].shape[0]

# Create a bar chart to visualize the results
sns.set_style('whitegrid')
plt.figure(figsize=(8,6))
ax = sns.barplot(x=['Hypertension', 'No Hypertension'], y=[hypertension_stroke, no_hypertension_stroke], palette=['#F
plt.title('Number of Patients with and without Hypertension who have had a Stroke', fontsize=14, fontweight='bold')
plt.xlabel('Hypertension Status', fontsize=12, fontweight='bold')
plt.ylabel('Number of Patients', fontsize=12, fontweight='bold')
plt.xticks(fontsize=12, fontweight='bold')
plt.yticks(fontsize=12, fontweight='bold')
for p in ax.patches:
    ax.annotate(format(p.get_height(), '.0f'), (p.get_x() + p.get_width() / 2., p.get_height()), ha = 'center', va =
plt.show()
```



## Dataset Pre-Processing

***Dropping unwanted variables***

In [19]:

```
# Removing the 'id' column as it is redundant in this case
stroke_data = stroke_data.drop('id', axis=1)
```

In [20]:

```
#This is to take of the decimal value in age
stroke_data['age'] = stroke_data['age'].astype(int)
```

In [21]:

```
stroke_data.head()
```

Out[21]:

| | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi | smoking_status | stroke |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Male | 67 | 0 | 1 | Yes | Private | Urban | 228.69 | 36.600000 | formerly smoked | 1 |
| **1** | Female | 61 | 0 | 0 | Yes | Self-employed | Rural | 202.21 | 28.893237 | never smoked | 1 |
| **2** | Male | 80 | 0 | 1 | Yes | Private | Rural | 105.92 | 32.500000 | never smoked | 1 |
| **3** | Female | 49 | 0 | 0 | Yes | Private | Urban | 171.23 | 34.400000 | smokes | 1 |
| **4** | Female | 79 | 1 | 0 | Yes | Self-employed | Rural | 174.12 | 24.000000 | never smoked | 1 |

**Replacing the non-numerical categorical values with the numerical integers**

In [22]:

```
# Creating a dictionary to map non-numerical values with the numerical integers
gender_mapping = {'Male': 0, 'Female':1, 'Other':2} # this is to replace the gender values from 'Male', 'Female' to '
# replace non-numerical values with numerical values using the mapping dictionary
stroke_data['gender'] = stroke_data['gender'].replace(gender_mapping)
stroke_data.head()
```

Out[22]:

| | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi | smoking_status | stroke |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 0 | 67 | 0 | 1 | Yes | Private | Urban | 228.69 | 36.600000 | formerly smoked | 1 |
| **1** | 1 | 61 | 0 | 0 | Yes | Self-employed | Rural | 202.21 | 28.893237 | never smoked | 1 |
| **2** | 0 | 80 | 0 | 1 | Yes | Private | Rural | 105.92 | 32.500000 | never smoked | 1 |
| **3** | 1 | 49 | 0 | 0 | Yes | Private | Urban | 171.23 | 34.400000 | smokes | 1 |
| **4** | 1 | 79 | 1 | 0 | Yes | Self-employed | Rural | 174.12 | 24.000000 | never smoked | 1 |

In [23]:

```
# Replcing the 'ever_married' values from non numerical to numeriacal integers
marr_mapping = {'Yes':0, 'No':1}
stroke_data['ever_married'] = stroke_data['ever_married'].replace(marr_mapping)
```

In [24]:

```
stroke_data.head()
```

Out[24]:

| | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi | smoking_status | stroke |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 0 | 67 | 0 | 1 | 0 | Private | Urban | 228.69 | 36.600000 | formerly smoked | 1 |
| **1** | 1 | 61 | 0 | 0 | 0 | Self-employed | Rural | 202.21 | 28.893237 | never smoked | 1 |
| **2** | 0 | 80 | 0 | 1 | 0 | Private | Rural | 105.92 | 32.500000 | never smoked | 1 |
| **3** | 1 | 49 | 0 | 0 | 0 | Private | Urban | 171.23 | 34.400000 | smokes | 1 |
| **4** | 1 | 79 | 1 | 0 | 0 | Self-employed | Rural | 174.12 | 24.000000 | never smoked | 1 |

In [25]:

```
# Replcing the 'work_type' values from non numerical to numeriacal integers
stroke_data['work_type'].unique()
```

Out[25]:

```
array(['Private', 'Self-employed', 'Govt_job', 'children', 'Never_worked'],
      dtype=object)
```

In [26]:

```
work_mapping = {'Private':0, 'Self-employed':1, 'Govt_job':2, 'children':3, 'Never_worked':4}
stroke_data['work_type'] = stroke_data['work_type'].replace(work_mapping)
stroke_data.head()
```

Out[26]:

| | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi | smoking_status | stroke |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 0 | 67 | 0 | 1 | 0 | 0 | Urban | 228.69 | 36.600000 | formerly smoked | 1 |
| **1** | 1 | 61 | 0 | 0 | 0 | 1 | Rural | 202.21 | 28.893237 | never smoked | 1 |
| **2** | 0 | 80 | 0 | 1 | 0 | 0 | Rural | 105.92 | 32.500000 | never smoked | 1 |
| **3** | 1 | 49 | 0 | 0 | 0 | 0 | Urban | 171.23 | 34.400000 | smokes | 1 |
| **4** | 1 | 79 | 1 | 0 | 0 | 1 | Rural | 174.12 | 24.000000 | never smoked | 1 |

In [27]:

```
# Replcing the 'Residence_type' values from non numerical to numeriacal integers
stroke_data['Residence_type'].unique()
```

Out[27]:

```
array(['Urban', 'Rural'], dtype=object)
```

In [28]:

```
res_mapping = {'Urban':0, 'Rural':1}
stroke_data['Residence_type'] = stroke_data['Residence_type'].replace(res_mapping)
stroke_data.head()
```

Out[28]:

| | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi | smoking_status | stroke |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 0 | 67 | 0 | 1 | 0 | 0 | 0 | 228.69 | 36.600000 | formerly smoked | 1 |
| **1** | 1 | 61 | 0 | 0 | 0 | 1 | 1 | 202.21 | 28.893237 | never smoked | 1 |
| **2** | 0 | 80 | 0 | 1 | 0 | 0 | 1 | 105.92 | 32.500000 | never smoked | 1 |
| **3** | 1 | 49 | 0 | 0 | 0 | 0 | 0 | 171.23 | 34.400000 | smokes | 1 |
| **4** | 1 | 79 | 1 | 0 | 0 | 1 | 1 | 174.12 | 24.000000 | never smoked | 1 |

In [29]:

```
# Replcing the 'smoking_status' values from non numerical to numeriacal integers
stroke_data['smoking_status'].unique()
```

Out[29]:

```
array(['formerly smoked', 'never smoked', 'smokes', 'Unknown'],
      dtype=object)
```

In [30]:

```
res_mapping = {'formerly smoked':0, 'never smoked':1, 'smokes':2, 'Unknown':3}
stroke_data['smoking_status'] = stroke_data['smoking_status'].replace(res_mapping)
```

In [31]:

```
# Now all the non-numerical categorical values are replaced with Integers
stroke_data.head(10)
```

Out[31]:

| | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi | smoking_status | stroke |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 0 | 67 | 0 | 1 | 0 | 0 | 0 | 228.69 | 36.600000 | 0 | 1 |
| **1** | 1 | 61 | 0 | 0 | 0 | 1 | 1 | 202.21 | 28.893237 | 1 | 1 |
| **2** | 0 | 80 | 0 | 1 | 0 | 0 | 1 | 105.92 | 32.500000 | 1 | 1 |
| **3** | 1 | 49 | 0 | 0 | 0 | 0 | 0 | 171.23 | 34.400000 | 2 | 1 |
| **4** | 1 | 79 | 1 | 0 | 0 | 1 | 1 | 174.12 | 24.000000 | 1 | 1 |
| **5** | 0 | 81 | 0 | 0 | 0 | 0 | 0 | 186.21 | 29.000000 | 0 | 1 |
| **6** | 0 | 74 | 1 | 1 | 0 | 0 | 1 | 70.09 | 27.400000 | 1 | 1 |
| **7** | 1 | 69 | 0 | 0 | 1 | 0 | 0 | 94.39 | 22.800000 | 1 | 1 |
| **8** | 1 | 59 | 0 | 0 | 0 | 0 | 1 | 76.15 | 28.893237 | 3 | 1 |
| **9** | 1 | 78 | 0 | 0 | 0 | 0 | 0 | 58.57 | 24.200000 | 3 | 1 |

In [32]:

```
# this is to check the correlation
stroke_data.corr()
```

Out[32]:

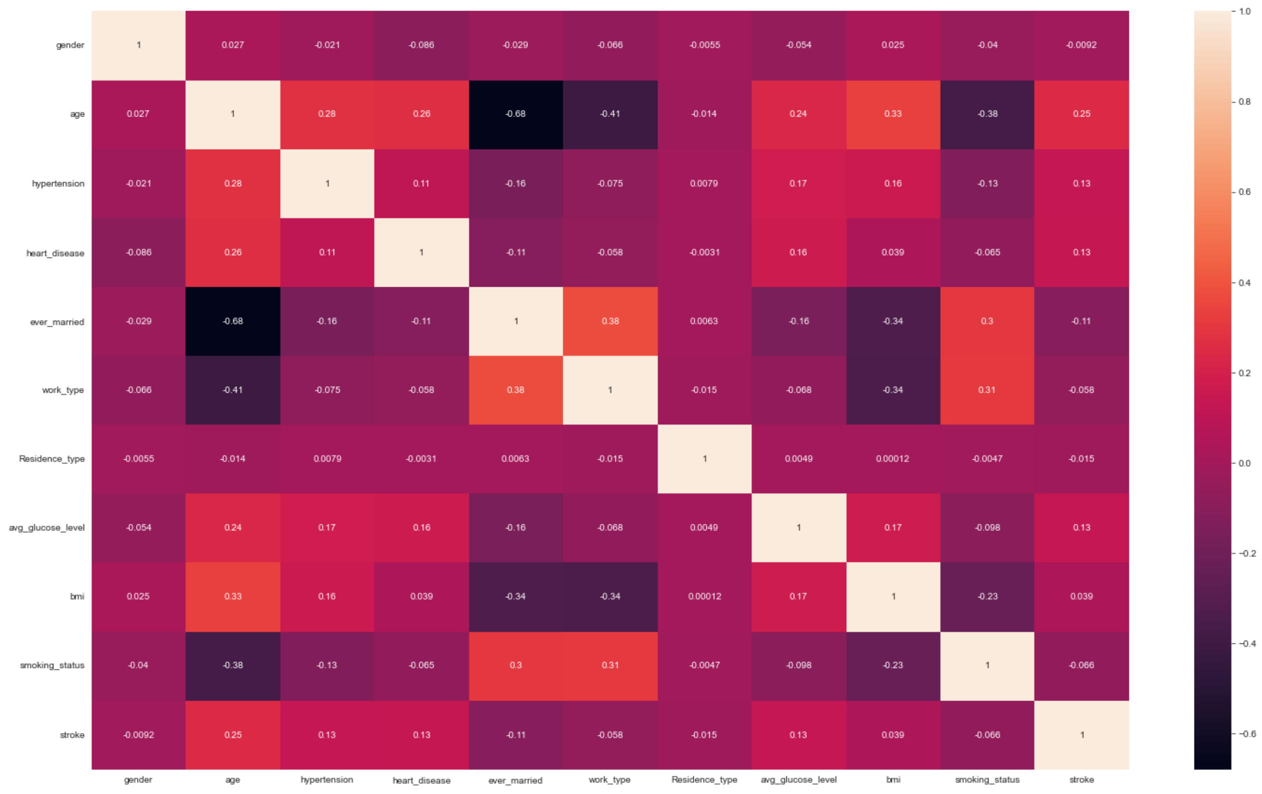
| | gender | age | hypertension | heart_disease | ever_married | work_type | Residence_type | avg_glucose_level | bmi |
|---|---|---|---|---|---|---|---|---|---|
| **gender** | 1.000000 | 0.027404 | -0.021390 | -0.085749 | -0.029366 | -0.066212 | -0.005529 | -0.054213 | 0.025110 |
| **age** | 0.027404 | 1.000000 | 0.276303 | 0.263668 | -0.679181 | -0.413852 | -0.014169 | 0.238060 | 0.326271 |
| **hypertension** | -0.021390 | 0.276303 | 1.000000 | 0.108306 | -0.164243 | -0.075097 | 0.007913 | 0.174474 | 0.160189 |
| **heart_disease** | -0.085749 | 0.263668 | 0.108306 | 1.000000 | -0.114644 | -0.058263 | -0.003092 | 0.161857 | 0.038899 |
| **ever_married** | -0.029366 | -0.679181 | -0.164243 | -0.114644 | 1.000000 | 0.375944 | 0.006261 | -0.155068 | -0.335705 |
| **work_type** | -0.066212 | -0.413852 | -0.075097 | -0.058263 | 0.375944 | 1.000000 | -0.014573 | -0.068135 | -0.341973 |
| **Residence_type** | -0.005529 | -0.014169 | 0.007913 | -0.003092 | 0.006261 | -0.014573 | 1.000000 | 0.004946 | 0.000120 |
| **avg_glucose_level** | -0.054213 | 0.238060 | 0.174474 | 0.161857 | -0.155068 | -0.068135 | 0.004946 | 1.000000 | 0.168751 |
| **bmi** | 0.025110 | 0.326271 | 0.160189 | 0.038899 | -0.335705 | -0.341973 | 0.000120 | 0.168751 | 1.000000 |
| **smoking_status** | -0.039693 | -0.376142 | -0.129012 | -0.064671 | 0.303694 | 0.307774 | -0.004656 | -0.097732 | -0.230553 |
| **stroke** | -0.009200 | 0.245128 | 0.127904 | 0.134914 | -0.108340 | -0.058224 | -0.015458 | 0.131945 | 0.038947 |

In [33]:

```
plt.figure(figsize=(25,15))
sns.heatmap(stroke_data.corr(),annot=True)
```

Out[33]:

```
<AxesSubplot:>
```



## Splitting the dataset into dependant and independant variables

In [34]:

```
X = stroke_data.drop(['stroke'], axis=1)
y = stroke_data['stroke']
```

### Class Distribution

In [35]:

```
# Checking the class distribution of the target variable
class_dist = pd.Series(y).value_counts(normalize=True)
print("Class distribution:\n{}".format(class_dist))
```

```
Class distribution:
0    0.951272
1    0.048728
Name: stroke, dtype: float64
```

### Creating a baseline prediction

In [36]:

```
# Creating a baseline prediction that always predicts the majority class (0) for the test set
baseline_pred = np.zeros(len(y))

# Calculating the accuracy of the baseline prediction for the test set
baseline_acc = sum(baseline_pred == y) / len(y)

print("Baseline accuracy: {:.2f}%".format(baseline_acc * 100))
```

```
Baseline accuracy: 95.13%
```

## Machine Learning Models

### 1: Logistic Regression

In [37]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import MinMaxScaler
from sklearn.metrics import confusion_matrix
from sklearn.model_selection import cross_val_score
```

In [38]:

```
# Spliting the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, stratify=y, random_state=0)
```

In [39]:

```
# Checking the class distribution of the target variable
class_dist = pd.Series(y_train).value_counts(normalize=True)
print("Class distribution:\n{}".format(class_dist))
```

```
Class distribution:
0    0.9512
1    0.0488
Name: stroke, dtype: float64
```

In [40]:

```
# Checking the class distribution of the target variable
class_dist = pd.Series(y_test).value_counts(normalize=True)
print("Class distribution:\n{}".format(class_dist))
```

```
Class distribution:
0    0.951487
1    0.048513
Name: stroke, dtype: float64
```

In [41]:

```
# Standardising the data
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

# Normalising the data
normalizer = MinMaxScaler()
X_train_norm = normalizer.fit_transform(X_train_scaled)
X_test_norm = normalizer.transform(X_test_scaled)
```

***Dummy classifer to perform baseline accuracy score***

In [42]:

```
from sklearn.dummy import DummyClassifier
dummy_clf = DummyClassifier(strategy="most_frequent")
dummy_clf.fit(X_train_scaled, y_train)
DummyClassifier(strategy='most_frequent')
#dummy_clf.predict(X_test_scaled)
dummy_clf.score(X_test_scaled, y_test)
```

Out[42]:

```
0.9514866979655712
```

## Training the Logistic Regression Classifier on the given training dataset

In [43]:

```
# Creating a logistic regression model object
logreg = LogisticRegression(penalty = "l2", C = 10, solver = "newton-cg")

# Fitting the model on the training data
logreg.fit(X_train_scaled, y_train)
```

Out[43]:

```
LogisticRegression(C=10, solver='newton-cg')
```

## Testing the Logistic Regression Classifier on testing dataset

In [44]:

```
# Predicting the labels of the test data
y_pred = logreg.predict(X_test_scaled)

# Printing the accuracy score of the model
print("Accuracy of the model on the test set is : {:.2f}".format(logreg.score(X_test_scaled, y_test)))
```

```
Accuracy of the model on the test set is : 0.95
```

In [45]:

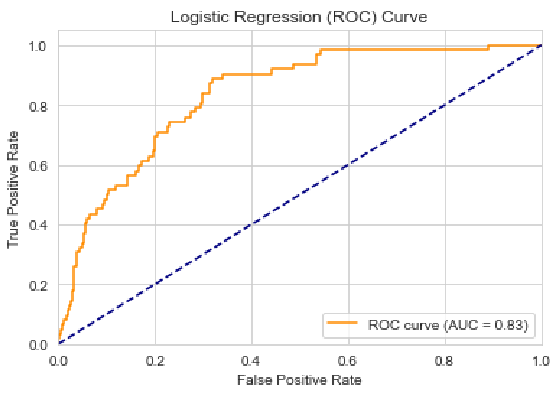
```
#Performing the k-fold cross-validation on the LR model
# here we define k=5
scores = cross_val_score(logreg, X, y, cv=5)

# Printing the accuracy for each fold and the mean accuracy across all folds
for i, score in enumerate(scores):
    print("Fold {} accuracy: {:.2f}%".format(i+1, score * 100))
print("Mean accuracy: {:.2f}%".format(scores.mean() * 100))
print("Standard deviation: {:.2f}%".format(scores.std() * 100))
```

```
Fold 1 accuracy: 95.11%
Fold 2 accuracy: 95.11%
Fold 3 accuracy: 95.11%
Fold 4 accuracy: 95.01%
Fold 5 accuracy: 95.21%
Mean accuracy: 95.11%
Standard deviation: 0.06%
```

### The ROC (Receiver Operating Characteristic) curve graphical representation

In [46]:

```
from sklearn.metrics import roc_curve, roc_auc_score

# Predicting the probability scores of the test data
y_prob = logreg.predict_proba(X_test_norm)

# Computing the false positive rate, true positive rate, and threshold values
fpr, tpr, thresholds = roc_curve(y_test, y_prob[:,1])

# Computing the AUC score
auc_score = roc_auc_score(y_test, y_prob[:,1])

# Creating a ROC curve plot
plt.plot(fpr, tpr, color='darkorange', label=f'ROC curve (AUC = {auc_score:.2f})')
plt.plot([0, 1], [0, 1], color='navy', linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Logistic Regression (ROC) Curve')
plt.legend(loc="lower right")
plt.show()
```



**2. Support Vector Machine (SVM)**

In [47]:

```
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import MinMaxScaler
```

### Training the SVM Classifier on the given training dataset

In [48]:

```
# Training the SVM classifier on the standardised data
svm = SVC(kernel='linear', C=1.0, random_state=0)
svm.fit(X_train_scaled, y_train)
```

Out[48]:

```
SVC(kernel='linear', random_state=0)
```

### Testing the SVM Classifier on testing dataset

In [49]:

```
# Evaluating the classifier on the testing data
score = svm.score(X_test_scaled, y_test)
print("Accuracy of SVM Classifier on Testing Dataset:", score)
```

```
Accuracy of SVM Classifier on Testing Dataset: 0.9514866979655712
```

In [50]:

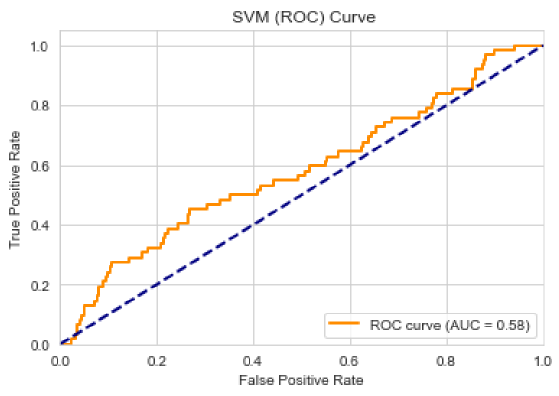
```
# Performing k-fold cross-validation on the SVM model
scores = cross_val_score(svm, X, y, cv=5)

# Printing the accuracy for each fold and the mean accuracy across all folds
for i, score in enumerate(scores):
    print("Fold {} accuracy: {:.2f}%".format(i+1, score * 100))
print("Mean accuracy: {:.2f}%".format(scores.mean() * 100))
print("Standard deviation: {:.2f}%".format(scores.std() * 100))
```

```
Fold 1 accuracy: 95.11%
Fold 2 accuracy: 95.11%
Fold 3 accuracy: 95.11%
Fold 4 accuracy: 95.11%
Fold 5 accuracy: 95.21%
Mean accuracy: 95.13%
Standard deviation: 0.04%
```

## Plotting the SVM ROC representation

In [51]:

```
from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt

# Computing the false positive rate (fpr) and true positive rate (tpr)
fpr, tpr, thresholds = roc_curve(y_test, svm.decision_function(X_test_scaled))

# Computing the area under the ROC curve (AUC)
roc_auc = auc(fpr, tpr)

# Plotting the ROC curve
plt.figure()
plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (AUC = %0.2f)' % roc_auc)
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title(' SVM (ROC) Curve')
plt.legend(loc="lower right")
plt.show()
```


SVM (ROC) Curve
True Positive Rate
False Positive Rate
ROC curve (AUC = 0.58)