STROKE PREDICTION USING MACHINE LEARNING

Dataset URL :

Dataset has been downloaded from Kaggle. URL:- https://www.kaggle.com/datasets/fedesoriano/stroke-prediction-dataset

Dataset description:

Based on input parameters such as gender, age, various diseases, and smoking status,this dataset is used to predict whether a patient is likely to have a stroke. Each row of data contains relevant information about the patient. The stroke data is organised into 12 columns in the dataset.

Attribute Information

1) id: unique identifier 2) gender: "Male", "Female" or "Other" 3) age: age of the patient 4) hypertension: 0 if the patient doesn't have hypertension, 1 if the patient has hypertension 5) heart_disease: 0 if the patient doesn't have any heart diseases, 1 if the patient has a heart disease 6) ever_married: "No" or "Yes" 7) work_type: "children", "Govt_jov", "Never_worked", "Private" or "Self-employed" 8) Residence_type: "Rural" or "Urban" 9) avg_glucose_level: average glucose level in blood 10) bmi: body mass index 11) smoking_status: "formerly smoked", "never smoked", "smokes" or "Unknown" *12) stroke: 1 if the patient had a stroke or 0 if not*Note: "Unknown" in smoking_status means that the information is unavailable for this patient

1. Data Collection and Initial Analysis

In [1]:
```
# To import pandas to read the raw data csv file to a dataframe
import pandas as pd

# To import numpy to perform different mathematical operations on arrays
import numpy as np

# Importing matplotlib and seaborn for data visualization
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
sns.set_style("ticks")

# To manage warnings
import warnings
warnings.filterwarnings("ignore")
```

In [2]:
```
# To Load the data: stroke_data
stroke_data = pd.read_csv("healthcare-dataset-stroke-data.csv")
```

In [3]:
```
# To print first and last 5 rows of the dataset
stroke_data
```

Out[3]:

	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	str
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	
...	...	...	...	...	...	...	...	...	...	...	...	
5105	18234	Female	80.0	1	0	Yes	Private	Urban	83.75	NaN	never smoked	
5106	44873	Female	81.0	0	0	Yes	Self-employed	Urban	125.20	40.0	never smoked	
5107	19723	Female	35.0	0	0	Yes	Self-employed	Rural	82.99	30.6	never smoked	
5108	37544	Male	51.0	0	0	Yes	Private	Rural	166.29	25.6	formerly smoked	
5109	44679	Female	44.0	0	0	Yes	Govt_job	Urban	85.28	26.2	Unknown	

5110 rows × 12 columns

In [4]:
```
# min, max count avg and percentile details of each column
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]:
```
# To understand the data types of the column data
stroke_data.info()
```

```
<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
```

2. Data Pre - Processing and Cleaning

In [6]:
```
stroke_data.isnull()
```

Out[6]:

	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	st
0	False	False	False	False	False	False	False	False	False	False	False	
1	False	False	False	False	False	False	False	False	False	True	False	
2	False	False	False	False	False	False	False	False	False	False	False	
3	False	False	False	False	False	False	False	False	False	False	False	
4	False	False	False	False	False	False	False	False	False	False	False	
...	...	...	...	...	...	...	...	...	...	...	...	
5105	False	False	False	False	False	False	False	False	False	True	False	
5106	False	False	False	False	False	False	False	False	False	False	False	
5107	False	False	False	False	False	False	False	False	False	False	False	
5108	False	False	False	False	False	False	False	False	False	False	False	
5109	False	False	False	False	False	False	False	False	False	False	False	

5110 rows × 12 columns

In [7]:
```
# To find the number of missing values in the data set
stroke_data.isnull().sum()
```

Out[7]:
```
id                   0
gender               0
age                  0
hypertension         0
heart_disease        0
ever_married         0
work_type            0
Residence_type       0
avg_glucose_level    0
```

```
bmi                 201
smoking_status        0
stroke                0
dtype: int64
```

In [8]:
```
# To get the count of values of column 'gender'
stroke_data.gender.value_counts()
```

Out[8]:
```
Female    2994
Male      2115
Other        1
Name: gender, dtype: int64
```

In [9]:
```
# To remove the unnecessary rows
stroke_data.drop(stroke_data[stroke_data['gender']=='Other'].index,inplace=True)
stroke_data.shape
```

Out[9]:
```
(5109, 12)
```

In [10]:
```
# To replace string values to numerical value
stroke_data.gender.replace({'Male':1,'Female':0},inplace = True)
stroke_data.ever_married.replace({'Yes':1,'No':0},inplace = True)
stroke_data.Residence_type.replace({'Urban':1,'Rural':0},inplace = True)
stroke_data
```

Out[10]:

	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	str
0	9046	1	67.0	0	1	1	Private	1	228.69	36.6	formerly smoked	
1	51676	0	61.0	0	0	1	Self-employed	0	202.21	NaN	never smoked	
2	31112	1	80.0	0	1	1	Private	0	105.92	32.5	never smoked	
3	60182	0	49.0	0	0	1	Private	1	171.23	34.4	smokes	
4	1665	0	79.0	1	0	1	Self-employed	0	174.12	24.0	never smoked	
...	...	...	...	...	...	...	...	...	...	...	...	
5105	18234	0	80.0	1	0	1	Private	1	83.75	NaN	never smoked	
5106	44873	0	81.0	0	0	1	Self-employed	1	125.20	40.0	never smoked	
5107	19723	0	35.0	0	0	1	Self-employed	0	82.99	30.6	never smoked	
5108	37544	1	51.0	0	0	1	Private	0	166.29	25.6	formerly smoked	
5109	44679	0	44.0	0	0	1	Govt_job	1	85.28	26.2	Unknown	

5109 rows × 12 columns

In [11]:
```
stroke_data.smoking_status.value_counts()
```

Out[11]:
```
never smoked       1892
Unknown            1544
formerly smoked     884
smokes              789
Name: smoking_status, dtype: int64
```

In [12]:
```
#To convert categorical data into dummy variables
stroke_data = pd.get_dummies(stroke_data, columns = ['work_type','smoking_status'])
stroke_data
```

Out[12]:

	id	gender	age	hypertension	heart_disease	ever_married	Residence_type	avg_glucose_level	bmi	stroke	work_type_Govt_job	wo
0	9046	1	67.0	0	1	1	1	228.69	36.6	1	0	
1	51676	0	61.0	0	0	1	0	202.21	NaN	1	0	
2	31112	1	80.0	0	1	1	0	105.92	32.5	1	0	
3	60182	0	49.0	0	0	1	1	171.23	34.4	1	0	
4	1665	0	79.0	1	0	1	0	174.12	24.0	1	0	
...	...	...	...	...	...	...	...	...	...	...	...	

5105	18234	0	80.0	1	0	1	1	83.75	NaN	0	0
5106	44873	0	81.0	0	0	1	1	125.20	40.0	0	0
5107	19723	0	35.0	0	0	1	0	82.99	30.6	0	0
5108	37544	1	51.0	0	0	1	0	166.29	25.6	0	0
5109	44679	0	44.0	0	0	1	1	85.28	26.2	0	1

5109 rows × 19 columns

In [13]:
```
# To show the columns
stroke_data.columns
```

Out[13]:
```
Index(['id', 'gender', 'age', 'hypertension', 'heart_disease', 'ever_married',
       'Residence_type', 'avg_glucose_level', 'bmi', 'stroke',
       'work_type_Govt_job', 'work_type_Never_worked', 'work_type_Private',
       'work_type_Self-employed', 'work_type_children',
       'smoking_status_Unknown', 'smoking_status_formerly smoked',
       'smoking_status_never smoked', 'smoking_status_smokes'],
      dtype='object')
```

In [14]:
```
cols = ['id', 'gender', 'age', 'hypertension', 'heart_disease', 'ever_married',
       'Residence_type', 'avg_glucose_level', 'bmi', 'stroke',
       'work_type_Govt_job', 'work_type_Never_worked', 'work_type_Private',
       'work_type_Self-employed', 'work_type_children',
       'smoking_status_Unknown', 'smoking_status_formerly smoked',
       'smoking_status_never smoked', 'smoking_status_smokes']
```

In [15]:
```
#SimpleImputer transformer for completing missing values.
from sklearn.impute import SimpleImputer
imp = SimpleImputer(missing_values = np.NaN,strategy='mean')
imp = imp.fit(stroke_data)
stroke_data = imp.transform(stroke_data)
```

In [16]:
```
stroke_data
```

Out[16]:
```
array([[9.0460e+03, 1.0000e+00, 6.7000e+01, ..., 1.0000e+00, 0.0000e+00,
        0.0000e+00],
       [5.1676e+04, 0.0000e+00, 6.1000e+01, ..., 0.0000e+00, 1.0000e+00,
        0.0000e+00],
       [3.1112e+04, 1.0000e+00, 8.0000e+01, ..., 0.0000e+00, 1.0000e+00,
        0.0000e+00],
       ...,
       [1.9723e+04, 0.0000e+00, 3.5000e+01, ..., 0.0000e+00, 1.0000e+00,
        0.0000e+00],
       [3.7544e+04, 1.0000e+00, 5.1000e+01, ..., 1.0000e+00, 0.0000e+00,
        0.0000e+00],
       [4.4679e+04, 0.0000e+00, 4.4000e+01, ..., 0.0000e+00, 0.0000e+00,
        0.0000e+00]])
```

In [17]:
```
# To assign columns names to the current data
stroke_data = pd.DataFrame(stroke_data,columns = cols)
stroke_data
```

Out[17]:

	id	gender	age	hypertension	heart_disease	ever_married	Residence_type	avg_glucose_level	bmi	stroke	work_type_Govt_jo
0	9046.0	1.0	67.0	0.0	1.0	1.0	1.0	228.69	36.60000	1.0	0
1	51676.0	0.0	61.0	0.0	0.0	1.0	0.0	202.21	28.89456	1.0	0
2	31112.0	1.0	80.0	0.0	1.0	1.0	0.0	105.92	32.50000	1.0	0
3	60182.0	0.0	49.0	0.0	0.0	1.0	1.0	171.23	34.40000	1.0	0
4	1665.0	0.0	79.0	1.0	0.0	1.0	0.0	174.12	24.00000	1.0	0
...	...	...	...	...	...	...	...	...	...	...	
5104	18234.0	0.0	80.0	1.0	0.0	1.0	1.0	83.75	28.89456	0.0	0
5105	44873.0	0.0	81.0	0.0	0.0	1.0	1.0	125.20	40.00000	0.0	0
5106	19723.0	0.0	35.0	0.0	0.0	1.0	0.0	82.99	30.60000	0.0	0
5107	37544.0	1.0	51.0	0.0	0.0	1.0	0.0	166.29	25.60000	0.0	0
5108	44679.0	0.0	44.0	0.0	0.0	1.0	1.0	85.28	26.20000	0.0	1

5109 rows × 19 columns

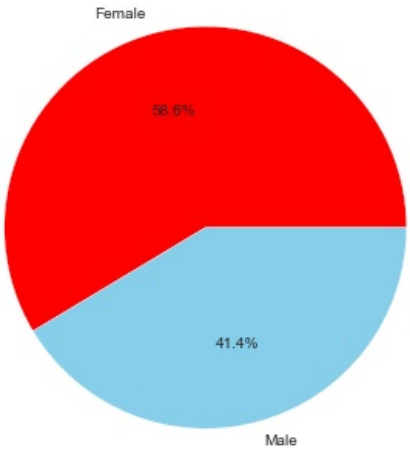
In [18]:
```
stroke_data.isnull().sum()
```

Out[18]:
```
id                                0
gender                            0
age                               0
hypertension                      0
heart_disease                     0
ever_married                      0
Residence_type                    0
avg_glucose_level                 0
bmi                               0
stroke                            0
work_type_Govt_job                0
work_type_Never_worked            0
work_type_Private                 0
work_type_Self-employed           0
work_type_children                0
smoking_status_Unknown            0
smoking_status_formerly smoked    0
smoking_status_never smoked       0
smoking_status_smokes             0
dtype: int64
```

3. Data Visualization

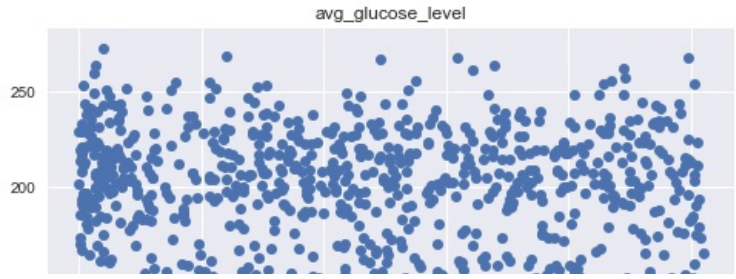
3.1 Univariate Distribution

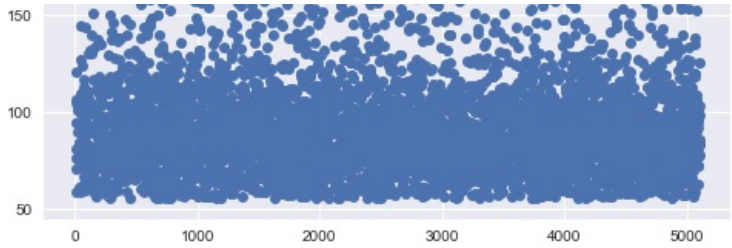
In [19]:
```
# To plot pie chart for the column 'gender'
plt.style.use('seaborn')

fig, ax = plt.subplots(figsize=(8, 6))
plt.pie(x=stroke_data.gender.value_counts(),
colors=['red', 'skyblue'],
labels=['Female', 'Male'], autopct='%1.1f%%')
plt.show()
```



Findings: The distribution of gender in the above pie chart shows 41.4 percentage of males and 58.6 percentage of female's stroke-related statuses are given in the dataset.

In [20]:
```
# To plot scatter graph for avgerage glucose level
plt.plot('avg_glucose_level', data=stroke_data, linestyle='none', marker='o')
plt.title('avg_glucose_level')
plt.show()
```

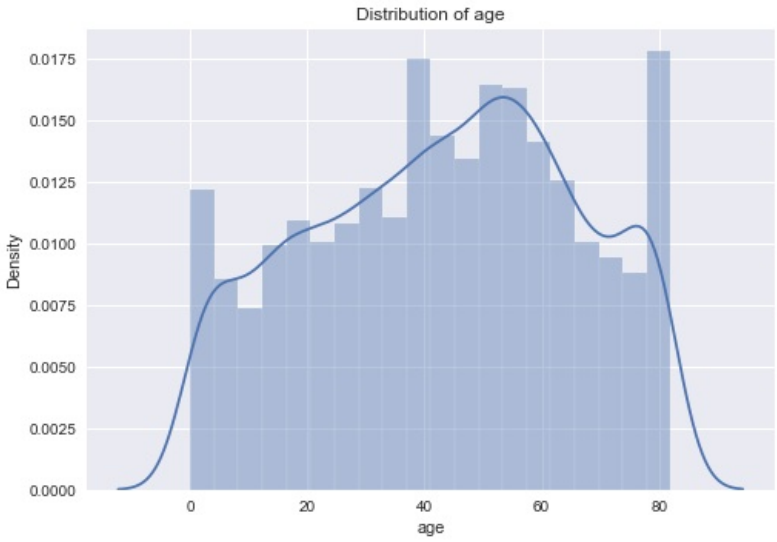




Findings: Scatter plot gives us an idea about the average glucose level of people in the dataset. Here in this plot most of the values are scattered over a range of 60 to 120 which shows most people have an average and below-average glucose level

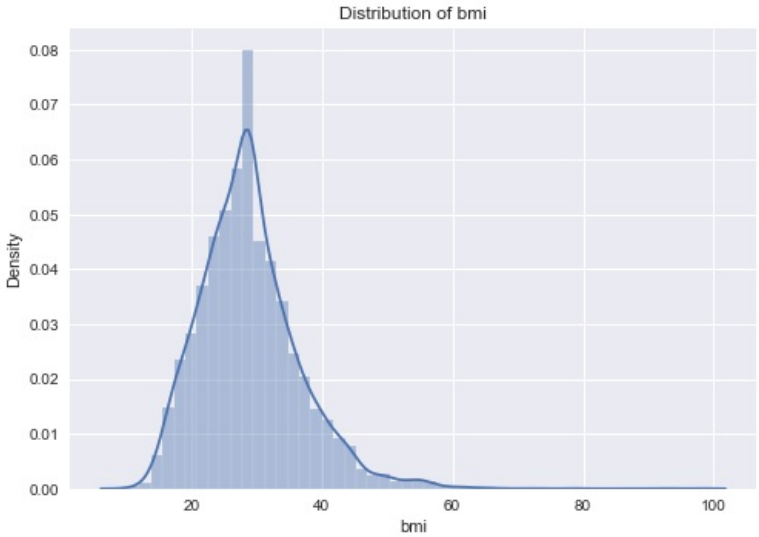
In [21]:
```
# To plot graph for age distribution
sns.distplot(stroke_data['age'])
plt.title('Distribution of age')
```

Out[21]: Text(0.5, 1.0, 'Distribution of age')



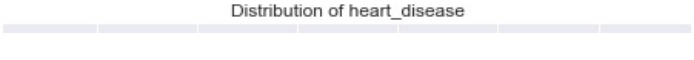
In [22]:
```
# To plot graph for bmi distribution
sns.distplot(stroke_data['bmi'])
plt.title('Distribution of bmi')
```

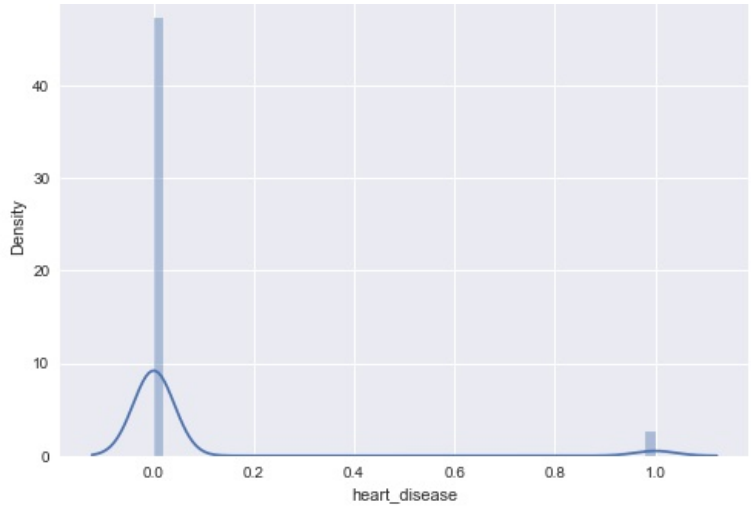
Out[22]: Text(0.5, 1.0, 'Distribution of bmi')



In [23]:
```
# To plot graph for column heart_disease
sns.distplot(stroke_data['heart_disease'])
plt.title('Distribution of heart_disease')
```

Out[23]: Text(0.5, 1.0, 'Distribution of heart_disease')

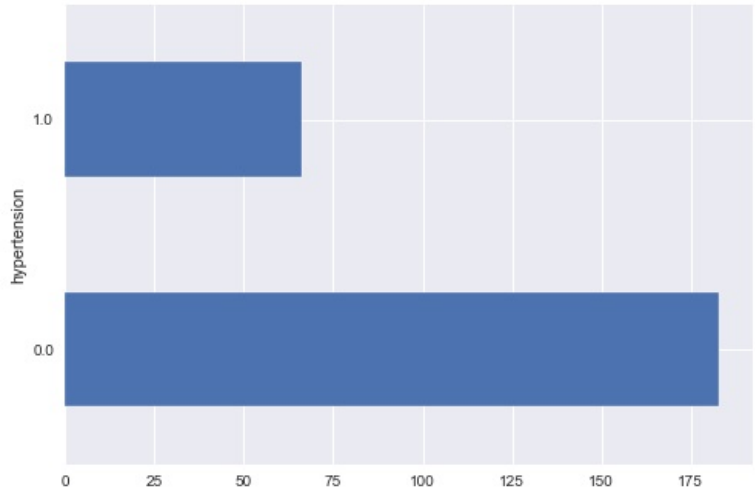




3.2 Multvariate Distribution

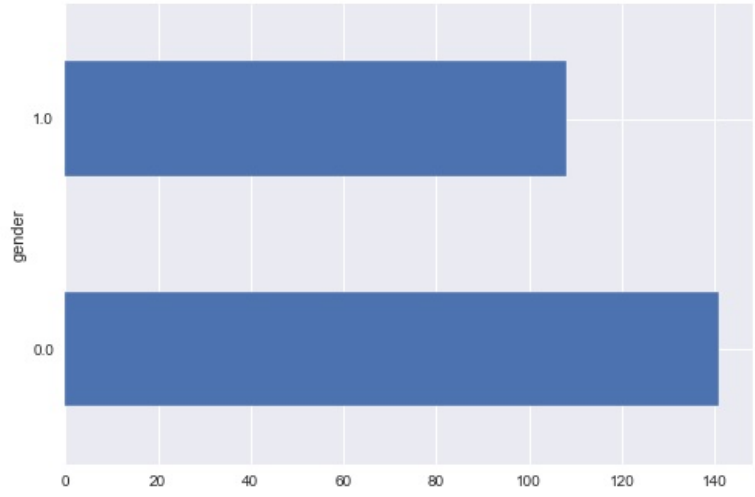
In [24]:
```
#comparing the relation with hypertension and stroke
stroke_data.groupby('hypertension')['stroke'].sum().plot(kind = 'barh')
```

Out[24]: <AxesSubplot:ylabel='hypertension'>



In [25]:
```
#comparing the relation with gender and stroke
stroke_data.groupby('gender')['stroke'].sum().plot(kind = 'barh')
```

Out[25]: <AxesSubplot:ylabel='gender'>

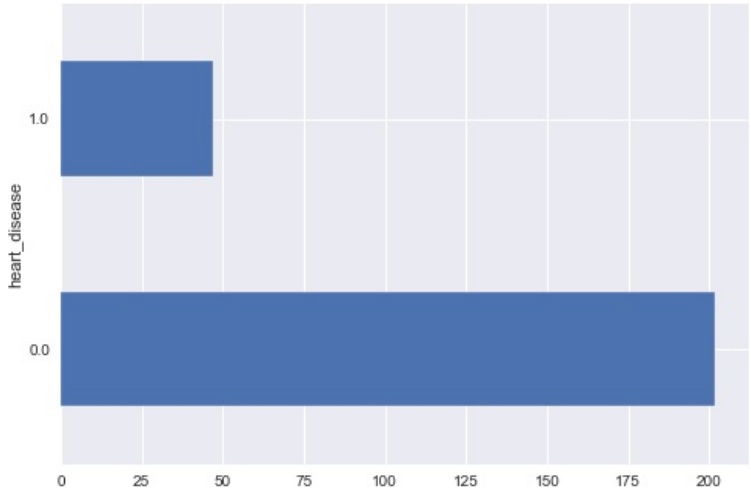


In [26]:
```
stroke_data.heart_disease.value_counts()
```

Out[26]:
```
0.0    4833
1.0     276
Name: heart_disease, dtype: int64
```

In [27]:
```
#comparing the relation with heart_disease and stroke
stroke_data.groupby('heart_disease')['stroke'].sum().plot(kind = 'barh')
```

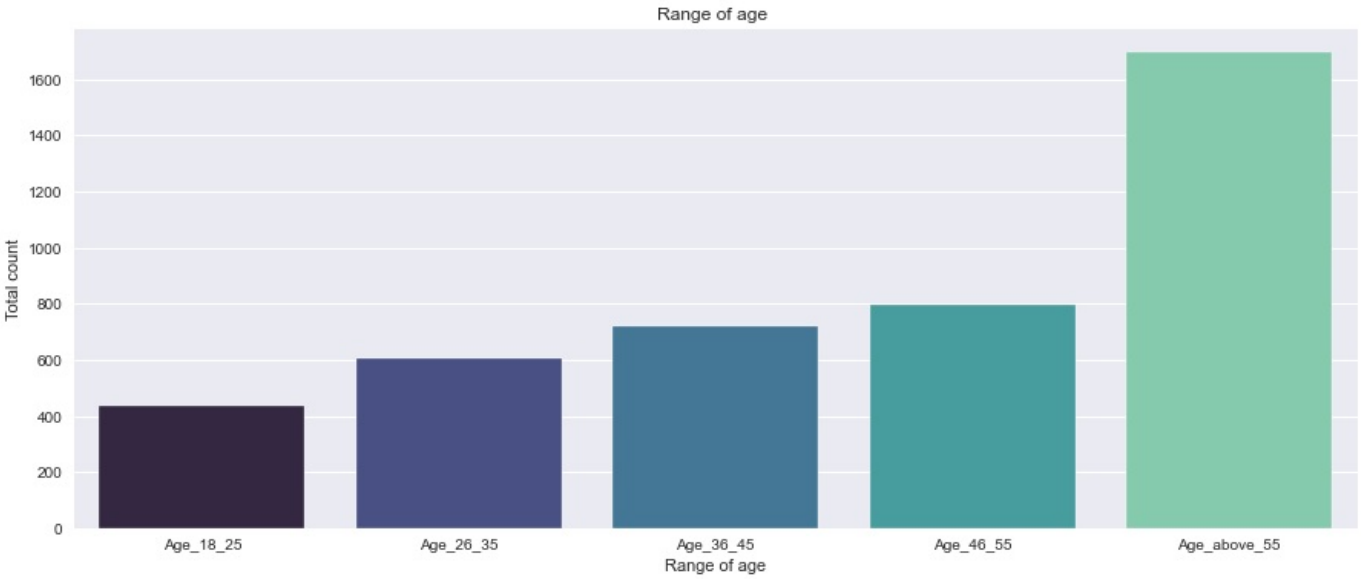
Out[27]:
```
<AxesSubplot:ylabel='heart_disease'>
```



In [28]:
```
Age_18_25 = stroke_data.age[(stroke_data.age >= 18)& (stroke_data.age<=25)]
Age_26_35 = stroke_data.age[(stroke_data.age >= 26)& (stroke_data.age<=35)]
Age_36_45 = stroke_data.age[(stroke_data.age >= 36)& (stroke_data.age<=45)]
Age_46_55 = stroke_data.age[(stroke_data.age >= 46)& (stroke_data.age<=55)]
Age_above_55 = stroke_data.age[stroke_data.age >= 56]
```

In [29]:
```
agex = ['Age_18_25','Age_26_35','Age_36_45','Age_46_55','Age_above_55']
agey = [len(Age_18_25.values),len(Age_26_35.values),len(Age_36_45.values),len(Age_46_55.values),len(Age_above_55.
```

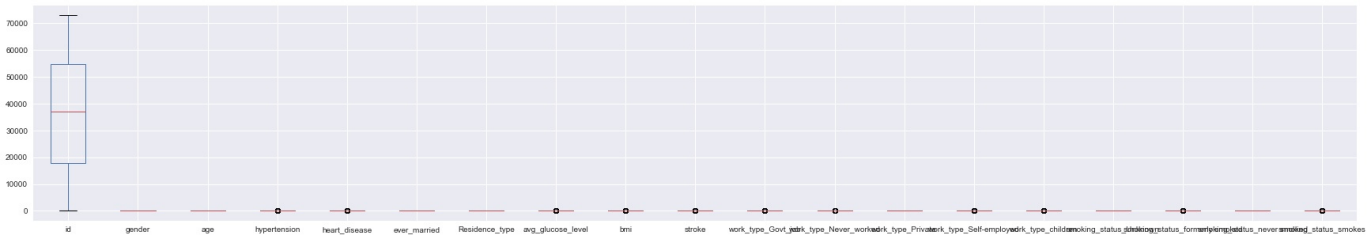
In [30]:
```
#To plot the range of age
plt.figure(figsize=(15,6))
sns.barplot(x = agex,y = agey , palette='mako')
plt.title("Range of age ")
plt.xlabel(" Range of age ")
plt.ylabel('Total count')
plt.show()
```



Findings: From the above bar graph we can understand that a very high number of the people in this dataset belong to the age group of above 55 years old who are likely to have more chance to get a stroke rather than people below the age group of 55.

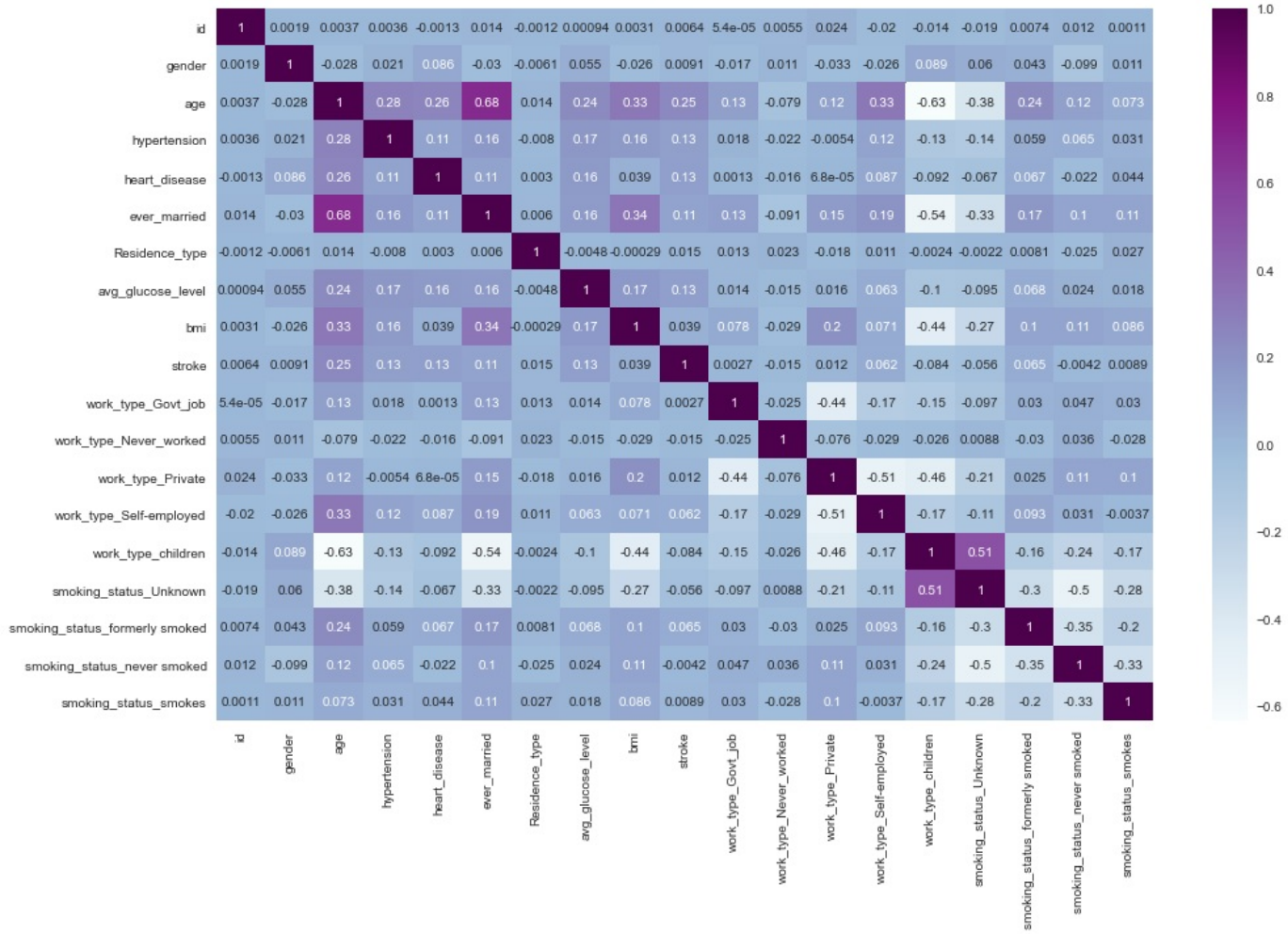
In [31]:
```
#To plot boxplot for entire columns for checking outliers
plt.figure(figsize=(30,5))
stroke_data.boxplot()
```

Out[31]:
```
<AxesSubplot:>
```



Findings: The above Box plot is plotted to check the outliers. There were no outliers were found for the columns of the dataset. If there were outliers, by removing them we could increase the accuracy of the machine learning algorithms.

In [32]:
```
#To visualize relationships between variables
plt.figure(figsize = (16,10))
sns.heatmap(stroke_data.corr(),annot = True,cmap='BuPu')
plt.show()
```



Findings: The above correlation matrix (Fig 11) depicts the relationship between distinct columns. Since we're focusing on the stroke variable, we can see that “gender”, “age”, “hypertension”, “heart disease”, “marital status”, “residence type”, “average glucose level”, “BMI”, “work type govt job”, “work type private”, “work type self-employed”, “smoking status formerly smoked” and “smoking status smokes” all have a positive correlation with Stroke. Because the Correlation matrix displays numbers, it is simple to discern the negative and positive correlation between distinct columns.

4. Applying Algorithms

In [33]:
```
y = stroke_data['stroke']
X = stroke_data.drop('stroke',axis = 1)
```

In [34]:
```
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import make_pipeline
from sklearn.model_selection import train_test_split
from sklearn.metrics import confusion_matrix,classification_report,plot_confusion_matrix

# Splitting the data
```

```
X_train,X_test,y_train,y_test = train_test_split(X,y)
```

In [35]:
```
print(X_train.shape)
print(X_test.shape)
print(y_train.shape)
print(y_test.shape)
```

```
(3831, 18)
(1278, 18)
(3831,)
(1278,)
```

4.1 Logistic Regression

In [36]:
```
from sklearn.linear_model import LogisticRegression
score = {}
model_1 = make_pipeline(StandardScaler(),LogisticRegression())
model_1.fit(X_train,y_train)
score['logistic_Regression'] = model_1.score(X_test,y_test)
predictions = model_1.predict(X_test)
print(classification_report(y_test, predictions))
```

```
              precision    recall  f1-score   support

         0.0       0.95      1.00      0.97      1210
         1.0       1.00      0.01      0.03        68

    accuracy                           0.95      1278
   macro avg       0.97      0.51      0.50      1278
weighted avg       0.95      0.95      0.92      1278
```

In [37]:
```
scaler = StandardScaler()
scaled_X_test = scaler.fit_transform(X_test)
scaled_X_train = scaler.fit_transform(X_train)
y_pred = model_1.predict(scaled_X_test)
confusion_matrix(y_test,y_pred)
```

Out[37]:
```
array([[1210,    0],
       [  68,    0]], dtype=int64)
```

4.2 KNeighbor Classifier

In [38]:
```
from sklearn.neighbors import KNeighborsClassifier
model_2 = make_pipeline(StandardScaler(),KNeighborsClassifier())
model_2.fit(X_train,y_train)
score['KNN'] = model_2.score(X_test,y_test)
predictions = model_2.predict(X_test)
print(classification_report(y_test, predictions))
```

```
              precision    recall  f1-score   support

         0.0       0.95      1.00      0.97      1210
         1.0       0.00      0.00      0.00        68

    accuracy                           0.94      1278
   macro avg       0.47      0.50      0.49      1278
weighted avg       0.90      0.94      0.92      1278
```

In [39]:
```
scaler = StandardScaler()
scaled_X_test = scaler.fit_transform(X_test)
scaled_X_train = scaler.fit_transform(X_train)
y_pred = model_2.predict(scaled_X_test)
confusion_matrix(y_test,y_pred)
```

Out[39]:
```
array([[1210,    0],
       [  68,    0]], dtype=int64)
```

4.3 Random Forest Classifier

In [40]:
```
from sklearn.ensemble import RandomForestClassifier
model_3 = make_pipeline(StandardScaler(),RandomForestClassifier())
model_3.fit(X_train,y_train)
score['RandomForest'] = model_3.score(X_test,y_test)
predictions = model_3.predict(X_test)
```

In [41]:
```
scaler = StandardScaler()
scaled_X_test = scaler.fit_transform(X_test)
scaled_X_train = scaler.fit_transform(X_train)
```

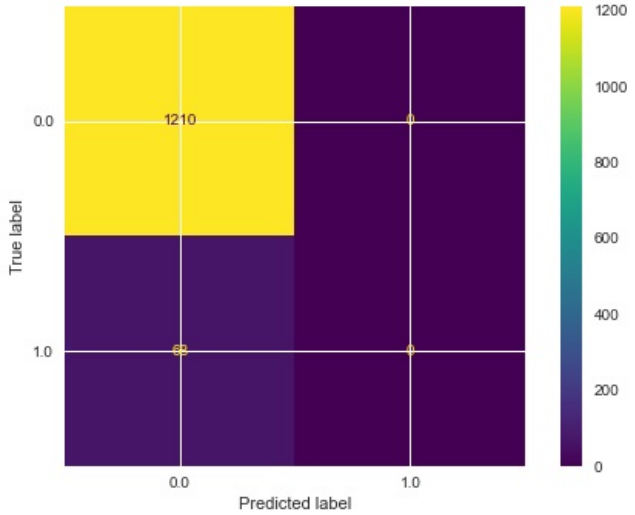
In [42]:
```
model_3 = RandomForestClassifier()
model_3.fit(X_train,y_train)
```

Out[42]:
```
RandomForestClassifier()
```

In [43]:
```
y_pred = model_3.predict(scaled_X_test)
confusion_matrix(y_test,y_pred)
```

Out[43]:
```
array([[1210,    0],
       [  68,    0]], dtype=int64)
```

In [44]:
```
plot_confusion_matrix(model_3,scaled_X_test,y_test);
```



In [45]:
```
print(classification_report(y_test, predictions))
```

```
              precision    recall  f1-score   support

         0.0       0.95      1.00      0.97      1210
         1.0       0.00      0.00      0.00        68

    accuracy                           0.95      1278
   macro avg       0.47      0.50      0.49      1278
weighted avg       0.90      0.95      0.92      1278
```

4.4 XG Boost Classifier

In [46]:
```
from xgboost import XGBClassifier
model_4 = make_pipeline(StandardScaler(),XGBClassifier())
model_4.fit(X_train,y_train)
score['XGB'] = model_4.score(X_test,y_test)
predictions = model_4.predict(X_test)
print(classification_report(y_test, predictions))
```

```
              precision    recall  f1-score   support

         0.0       0.95      0.99      0.97      1210
         1.0       0.31      0.06      0.10        68

    accuracy                           0.94      1278
   macro avg       0.63      0.53      0.53      1278
weighted avg       0.92      0.94      0.92      1278
```

In [47]:
```
scaler = StandardScaler()
scaled_X_test = scaler.fit_transform(X_test)
scaled_X_train = scaler.fit_transform(X_train)
y_pred = model_4.predict(scaled_X_test)
confusion_matrix(y_test,y_pred)
```

Out[47]:
```
array([[1210,    0],
       [  68,    0]], dtype=int64)
```

5. Score Comparison

In [48]:
```
score
```

Out[48]:
```
{'logistic_Regression': 0.9475743348982786,
 'KNN': 0.9444444444444444,
 'RandomForest': 0.94679186228482,
 'XGB': 0.9428794992175273}
```

In [49]:
```
A = score['logistic_Regression']*100
B = score['KNN']*100
C = score['RandomForest']*100
D = score['XGB']*100
```

In [50]:
```
algorithms = ['logistic_Regression','KNN','RandomForest','XGB']
score = [A, B, C, D]
plt.figure(figsize=(11,6))
sns.barplot(algorithms,score)
plt.show()
```