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AP19110010030

CSE-A

Problem Statement:

Stroke is a leading cause of death across the world and a major cause of severe disability in adults. The sudden death of living brain cells due to loss of blood flow or lack of oxygen flow to brain is almost fatal.

So, here I am using the stroke prediction dataset here contains data like age, average glucose level in body, whether or not they had a heart disease or hypertension, etc of patients.The data is split into training and test data and the training data is used to create models that predict whether or not an entry from the test data will suffer a stroke.

Importing the required libraries and loading the dataset

In [1]:

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

In [2]:

```
df = pd.read_csv("stroke.csv")
df
```

Out[2]:

	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_ty
0	9046	Male	67.0	0	1	Yes	Private	Urb
1	51676	Female	61.0	0	0	Yes	Self-employed	Ru
2	31112	Male	80.0	0	1	Yes	Private	Ru
3	60182	Female	49.0	0	0	Yes	Private	Urb
4	1665	Female	79.0	1	0	Yes	Self-employed	Ru
...	...	...	...	...	...	...	...	
5105	18234	Female	80.0	1	0	Yes	Private	Urb
5106	44873	Female	81.0	0	0	Yes	Self-employed	Urb
5107	19723	Female	35.0	0	0	Yes	Self-employed	Ru
5108	37544	Male	51.0	0	0	Yes	Private	Ru
5109	44679	Female	44.0	0	0	Yes	Govt_job	Urb

5110 rows × 12 columns

In [3]:

```
print('Shape of dataframe:',df.shape)
```

```
Shape of dataframe: (5110, 12)
```

Data Cleaning and Preprocessing

- Data cleaning is the process of fixing or removing incorrect, corrupted, incorrectly formatted, duplicate, or incomplete data within a dataset and it is the process of preparing raw data for analysis by removing bad data, organizing the raw data, and filling in the null values
- Data preprocessing is the process of transforming raw data into an understandable format. It is also an important step in data mining as we cannot work with raw data. The quality of the data should be checked before applying data mining algorithms.

Checking for null values

In [4]:

```
df.isnull().sum()
```

Out[4]:

```
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 [5]:

```
#Only the bmi column has missing data so we need to fill it.
#1. Creating a function to classify bmi values into different groups.
#2. Based on the classification we will create box plots.
#3. Based on the averages obtained through box plots we will fill the average value

def bmi_values(bmi_values):
    if bmi_values<20:
        return 'undernourished'
    elif 20<=bmi_values<30:
        return 'normal_weight_1'
    elif 30<=bmi_values<40:
        return 'overweight'
    elif 40<=bmi_values<50:
        return 'Obese I'
    elif 50<=bmi_values<70:
        return 'Obese II'
    elif 70<=bmi_values<100:
        return 'Obese III'
    else:
        pass
df['bmi_classification']=df['bmi'].apply(bmi_values)
```

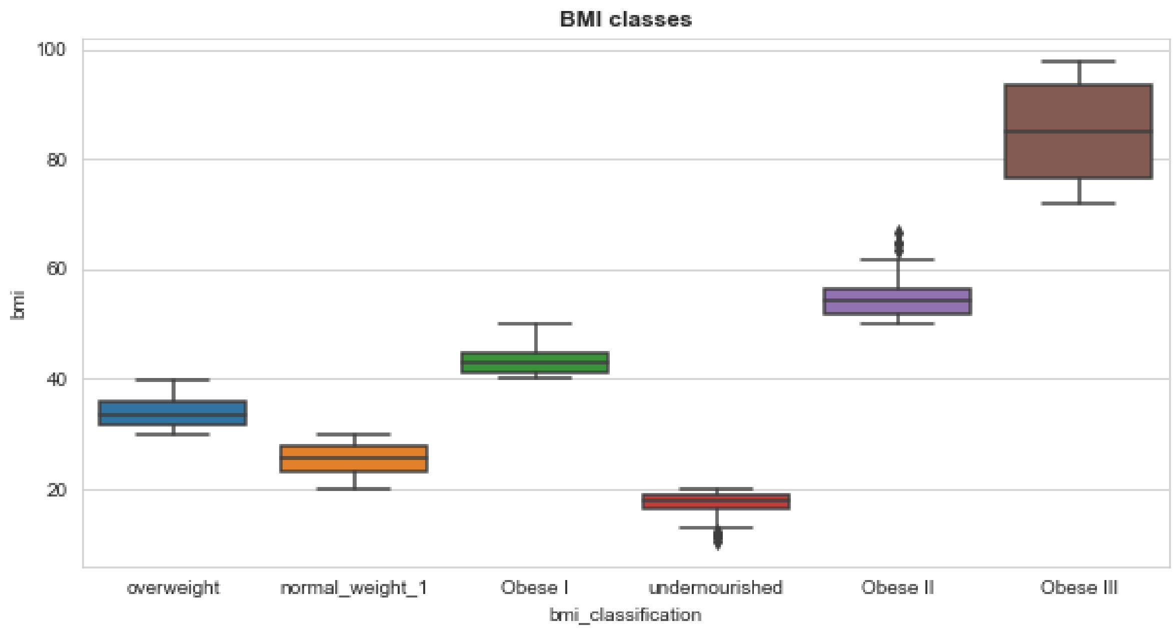
In [6]:

```
print(df.groupby('bmi_classification').stroke.value_counts())
plt.figure(figsize=(10,5))
sns.set_style('whitegrid')
sns.boxplot(x='bmi_classification',y='bmi',data=df)
plt.title('BMI classes',fontweight='bold',fontsize=12)
```

```
bmi_classification  stroke
Obese I             0          317
                    1           18
Obese II            0           74
                    1            1
Obese III           0            4
normal_weight_1     0         2361
                    1          108
overweight          0         1427
                    1           79
undernourished      0          517
                    1            3
Name: stroke, dtype: int64
```

Out[6]:

```
Text(0.5, 1.0, 'BMI classes')
```



In [7]:

```
#Filling in values based on the results obatined from the box plot.
def bmi_fill(bmi_value):
    if pd.isnull(bmi_value):
        if bmi_value<=20:
            return 17
        elif 20<bmi_value<=30:
            return 26
        elif 30<bmi_value<=40:
            return 33
        elif 40<bmi_value<=50:
            return 43
        elif 50<bmi_value<=70:
            return 55
        elif 70<bmi_value<=100:
            return 63
        else:
            return 105
    else:
        return bmi_value

df['bmi']=df['bmi'].apply(bmi_fill)
```

In [8]:

```
df['bmi'].isnull().sum()
```

Out[8]:

```
0
```

In [9]:

```
df.describe()
```

Out[9]:

	id	age	hypertension	heart_disease	avg_glucose_level	bmi
count	5110.000000	5110.000000	5110.000000	5110.000000	5110.000000	5110.000000
mean	36517.829354	43.226614	0.097456	0.054012	106.147677	31.886869
std	21161.721625	22.612647	0.296607	0.226063	45.283560	16.678613
min	67.000000	0.080000	0.000000	0.000000	55.120000	10.300000
25%	17741.250000	25.000000	0.000000	0.000000	77.245000	23.800000
50%	36932.000000	45.000000	0.000000	0.000000	91.885000	28.400000
75%	54682.000000	61.000000	0.000000	0.000000	114.090000	34.000000
max	72940.000000	82.000000	1.000000	1.000000	271.740000	105.000000

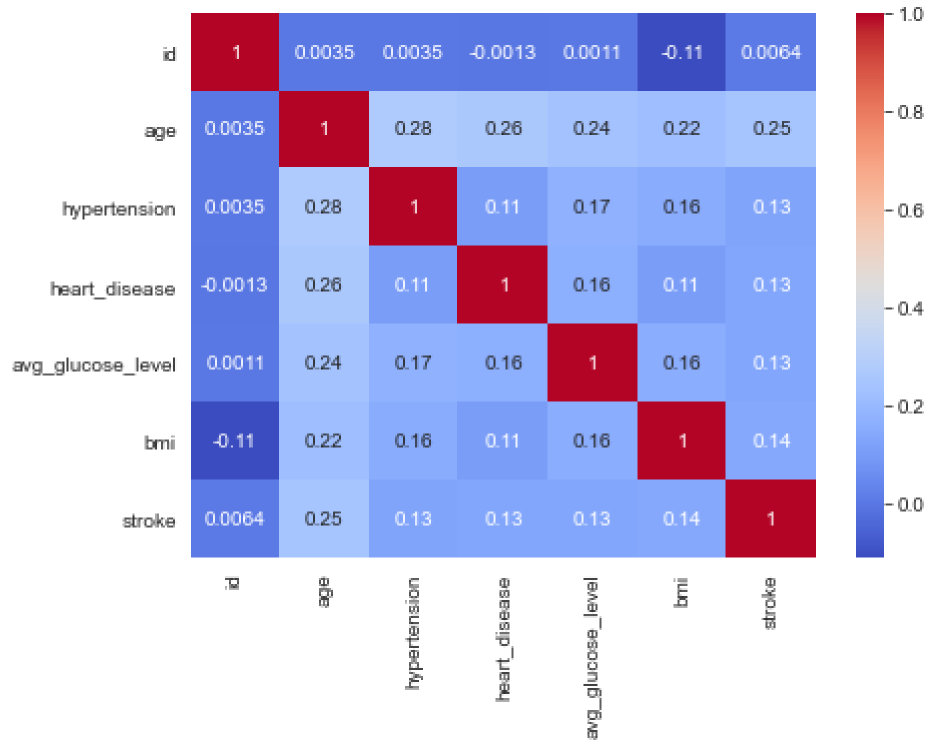
Plotting a heatmap to find correlations between the variables

In [10]:

```
plt.figure(figsize=(7,5))
sns.heatmap(df.corr(),cmap='coolwarm',annot=True)
```

Out[10]:

```
<AxesSubplot:>
```



	id	age	hypertension	heart_disease	avg_glucose_level	bmi	stroke
id	1	0.0035	0.0035	-0.0013	0.0011	-0.11	0.0064
age	0.0035	1	0.28	0.26	0.24	0.22	0.25
hypertension	0.0035	0.28	1	0.11	0.17	0.16	0.13
heart_disease	-0.0013	0.26	0.11	1	0.16	0.11	0.13
avg_glucose_level	0.0011	0.24	0.17	0.16	1	0.16	0.13
bmi	-0.11	0.22	0.16	0.11	0.16	1	0.14
stroke	0.0064	0.25	0.13	0.13	0.13	0.14	1

Statistical Analysis of the Data

Gender and chances of stroke

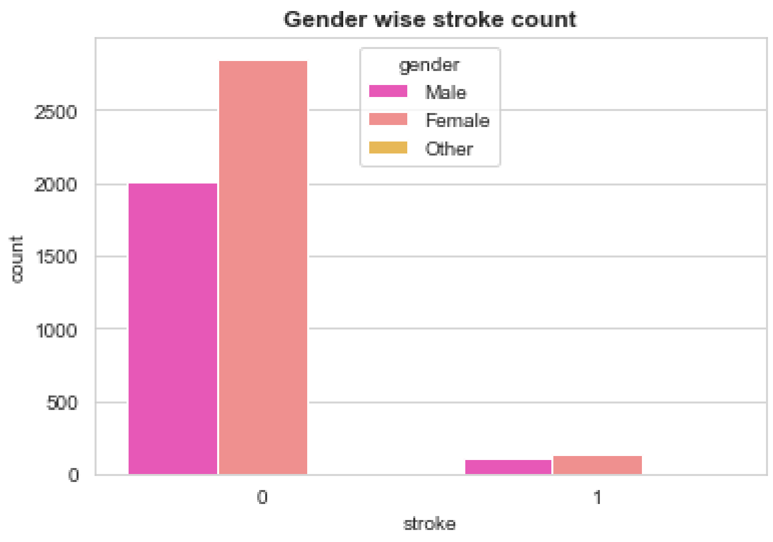
In [11]:

```
print(df.groupby('gender').stroke.value_counts().to_frame())
sns.set_style('whitegrid')
sns.countplot(x='stroke',data=df,hue='gender',palette='spring')
plt.title('Gender wise stroke count',fontweight='bold')
```

```
               stroke
gender stroke
Female 0         2853
       1          141
Male   0         2007
       1          108
Other  0            1
```

Out[11]:

```
Text(0.5, 1.0, 'Gender wise stroke count')
```



Relation between gender and hypertension

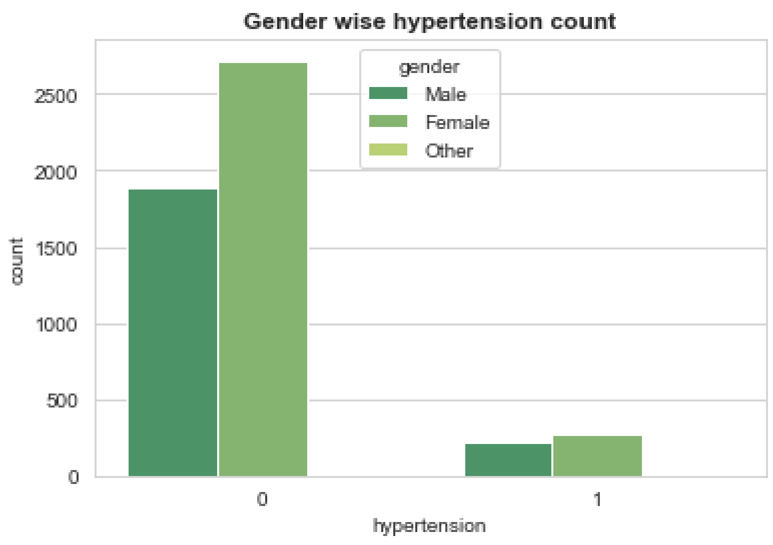
In [12]:

```
print(df.groupby('gender').hypertension.value_counts())
sns.countplot(x='hypertension',data=df,hue='gender',palette='summer')
plt.title('Gender wise hypertension count',fontweight='bold')
```

```
gender  hypertension
Female  0               2718
        1                276
Male    0               1893
        1                222
Other   0                  1
Name: hypertension, dtype: int64
```

Out[12]:

```
Text(0.5, 1.0, 'Gender wise hypertension count')
```



Relation between gender and heart disease

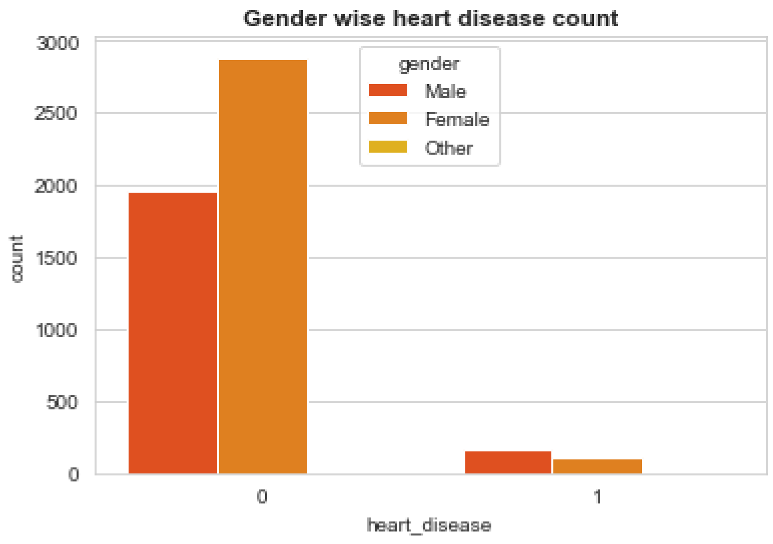
In [13]:

```
print(df.groupby('gender').heart_disease.value_counts())
sns.countplot(x='heart_disease',data=df,hue='gender',palette='autumn')
plt.title('Gender wise heart disease count',fontweight='bold')
```

```
gender  heart_disease
Female  0                2881
        1                 113
Male    0                1952
        1                 163
Other   0                   1
Name: heart_disease, dtype: int64
```

Out[13]:

```
Text(0.5, 1.0, 'Gender wise heart disease count')
```



Relation between gender and heart disease

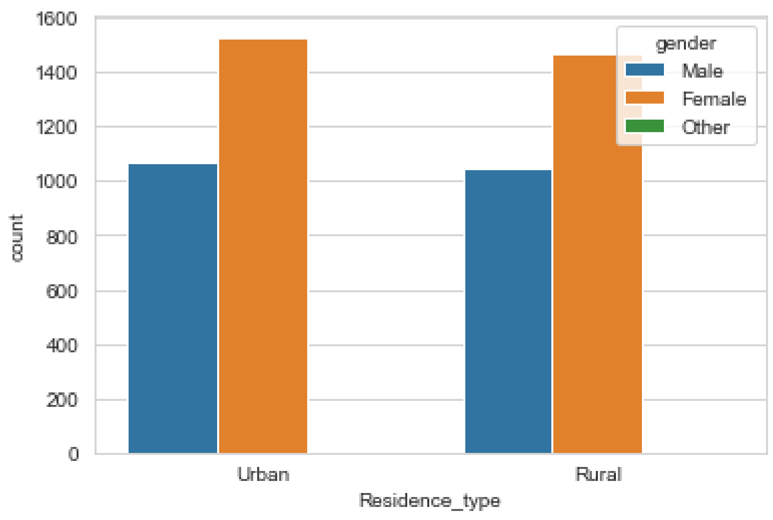
In [14]:

```
print(df.groupby('stroke').Residence_type.value_counts())
sns.countplot(x='Residence_type',data=df,hue='gender')
```

```
stroke  Residence_type
0       Urban             2461
        Rural             2400
1       Urban              135
        Rural              114
Name: Residence_type, dtype: int64
```

Out[14]:

```
<AxesSubplot:xlabel='Residence_type', ylabel='count'>
```



In [15]:

```
#Finding the relation between stroke, gender and their average glucose level
def glucose_level(amount):
    if amount<60:
        return 'Dangerously low'
    elif 60<=amount<90:
        return 'Low'
    elif 90<=amount<110:
        return 'Normal'
    elif 110<=amount<140:
        return 'Slightly high'
    elif 140<=amount<240:
        return 'High'
    elif 240<=amount<300:
        return 'Extremely high'
    else:
        return 'Dangerously high, requires medical attention'
df['Glucose_level_chart']=df['avg_glucose_level'].apply(glucose_level)
```

Relation between age and chances of stroke

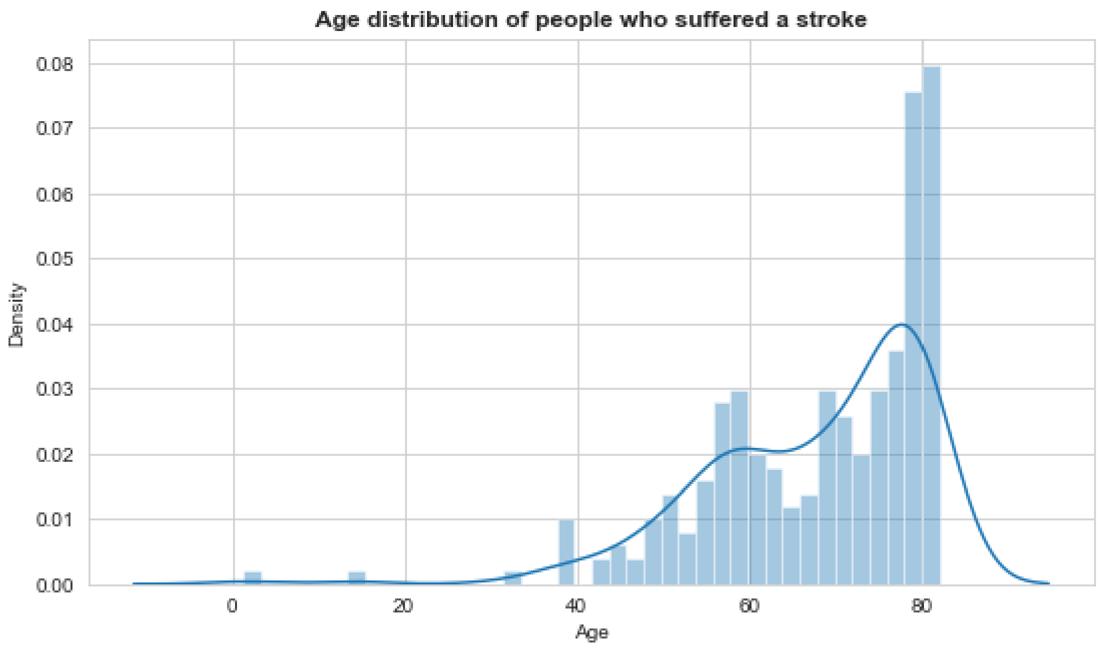
In [16]:

```
list_stroke=[]
for i in df['age'].index:
    if (df['stroke'][i]==1):
        list_stroke.append(df['age'][i])
print('Total number of people who suffered a stroke:', len(list_stroke))
sns.set_style('whitegrid')
plt.figure(figsize=(9,5))
plt.title('Age distribution of people who suffered a stroke',fontweight='bold',fontsize=12)
plt.xlabel('Age')
sns.distplot(list_stroke,bins=40)
```

```
Total number of people who suffered a stroke: 249
```

Out[16]:

```
<AxesSubplot:title={'center':'Age distribution of people who suffered a stro
ke'}, xlabel='Age', ylabel='Density'>
```



Work type and stroke analysis

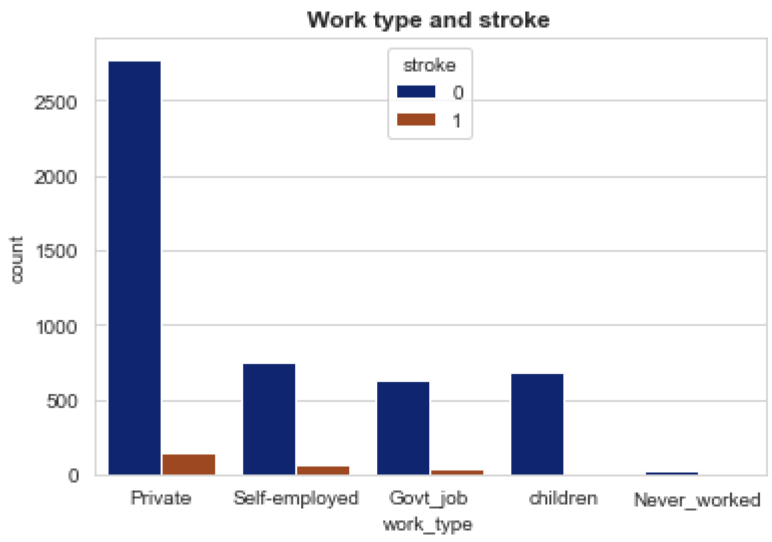
In [17]:

```
print(df.groupby('work_type').stroke.value_counts())
plt.figure(figsize=(6,4))
plt.title('Work type and stroke',fontweight='bold')
plt.xlabel('Work')
sns.countplot(x='work_type',data=df,hue='stroke',palette='dark')
```

```
work_type      stroke
Govt_job       0          624
               1           33
Never_worked   0           22
Private        0         2776
               1          149
Self-employed  0          754
               1           65
children       0          685
               1            2
Name: stroke, dtype: int64
```

Out[17]:

```
<AxesSubplot:title={'center':'Work type and stroke'}, xlabel='work_type', yl
abel='count'>
```



Relation between smoking status and stroke

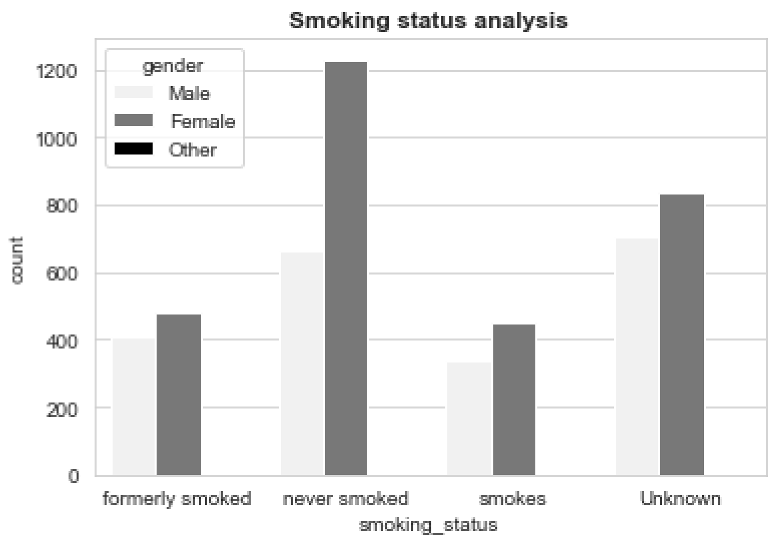
In [18]:

```
print(df.groupby('smoking_status').stroke.value_counts())
plt.title('Smoking status analysis',fontweight='bold')
plt.xlabel('Smoking status')
sns.countplot(x='smoking_status',data=df,hue='gender',color='black')
```

```
smoking_status   stroke
Unknown          0         1497
                 1           47
formerly smoked  0          815
                 1           70
never smoked     0         1802
                 1           90
smokes           0          747
                 1           42
Name: stroke, dtype: int64
```

Out[18]:

```
<AxesSubplot:title={'center':'Smoking status analysis'}, xlabel='smoking_sta
tus', ylabel='count'>
```



Getting dummies for categorical column

In [19]:

```
Gender =pd.get_dummies(df['gender'],drop_first=True)
#Getting dummies for categorical column -'gender' (that has strings)
df=pd.concat([df,Gender],axis=1)
```

Dropping the columns that are not required for training the model.

In [20]:

```
#Now there are no missing values in the bmi column.
df.drop(['id','bmi_classification','work_type','ever_married','Residence_type',
         'smoking_status','Glucose_level_chart','gender'],axis=1,inplace=True)
df.head()
```

Out[20]:

	age	hypertension	heart_disease	avg_glucose_level	bmi	stroke	Male	Other
0	67.0	0	1	228.69	36.6	1	1	0
1	61.0	0	0	202.21	105.0	1	0	0
2	80.0	0	1	105.92	32.5	1	1	0
3	49.0	0	0	171.23	34.4	1	0	0
4	79.0	1	0	174.12	24.0	1	0	0

Creating model and making predictions

Decision Tree

In [21]:

```
X = df.drop(columns=["stroke"])
y = df["stroke"]
```

In [22]:

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3,random_state=101)
from sklearn.tree import DecisionTreeClassifier
```

In [23]:

```
lm=DecisionTreeClassifier()
```

In [24]:

```
lm.fit(X_train,y_train)
```

Out[24]:

```
DecisionTreeClassifier()
```

In [25]:

```
lm_predictions=lm.predict(X_test)
```

In [26]:

```
lm.score(X_test,y_test)*100
```

Out[26]:

```
90.73711676451403
```

Conclusion

The decision tree is the best predictive model as it allows for a comprehensive analysis of the consequences of each possible decision, such as what the decision leads to, whether it ends in uncertainty or a definite conclusion and after creating and training my model I achieved an accuracy score of 90.1%