Data Mining Project (Personal Key Indicators of Heart Disease)

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Introduction

The dataset come from the CDC (Centers For Disease Control Prevention) and is a major part of the Behavioral Risk Factor Surveillance System (BRFSS), which conducts annual telephone surveys to gather data on the health status of U.S. residents.

According to the CDC, heart disease is one of the leading causes of death for people of most races in the US (African Americans, American Indians and Alaska Natives, and white people). About half of all Americans (47%) have at least 1 of 3 key risk factors for heart disease:

-High blood pressure

-High cholesterol

-Smoking

Other key indicator include diabetic status, obesity (high BMI), not getting enough physical activity or drinking too much alcohol. Detecting and preventing the factors that have the greatest impact on heart disease is very important in healthcare. Computational developments, in turn, allow the application of machine learning methods to detect "patterns" from the data that can predict a patient's condition.

Dataset attributes

● **HeartDisease**: Respondents that have ever reported having coronary heart disease (CHD) or myocardial infarction (MI).

● **BMI**: Body Mass Index.

● **Smoking**: Have you smoked at least 100 cigarettes in your entire life?

● **AlcoholDrinking**: Heavy drinkers (adult men having more than 14 drinks per week and adult women having more than 7 drinks per week.

● **Stroke**: Ever told you had a stroke?

● **PhysicalHealth**: Now thinking about your physical health, which includes physical illness and injury, for how many days during the past 30.

● **MentalHealth**: Thinking about your mental health, for how many days during the past 30 days was your mental health not good?

● **DiffWalking**: Do you have serious difficulty walking or climbing stairs?

● **Sex**: Male or Female?

● **AgeCategory**: Fourteen-level age range.

● **Race(strain)**: Imputed race/ethnicity value.

● **Diabetic**: Ever told you have Diabetes?

● **PhysicalActivity**: Adults who reported doing physical activity or exercise during the past 30 days other than their regular job.

● **GenHealth**: Your general health is... (Poor,Fair,Good,Very good,Excellent).

● **SleepTime**: On average, how many hours of sleep do you get in a 24-hour period?

● **Asthma**: Ever told you had asthma?

● **KidneyDisease**: Not including kidney stones, bladder infection or incontinence, were you ever told you had kidney disease?

● **SkinCancer** : Ever told you had skin cancer?

In [1]:
```
#importing the required libraries
import pandas as pd
import numpy as np
import seaborn as snb
import matplotlib.pyplot as plt
%matplotlib inline
from sklearn.preprocessing import KBinsDiscretizer
import warnings
warnings.filterwarnings('ignore')
```

Data Wrangling Phase

A phase were the process of cleaning, organizing, and unifying raw, complex, unorganized data sets is done so that they are more accessible for future data analysis.

> **steps**:
>
> - Loading Dataset
> - Display Data Content
> - General Data Properties
> - Cleaning Phase

Loading Dataset

In [2]:
```
data=pd.read_csv("E:\heart_2020_cleaned.csv")
```

Diplay Data Content

In [3]:
```
data.head(15)
```

Out[3]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	PhysicalHealth	MentalHealth	DiffWalking	Sex	Age
0	No	16.60	Yes	No	No	3.0	30.0	No	Female	
1	No	20.34	No	No	Yes	0.0	0.0	No	Female	
2	No	26.58	Yes	No	No	20.0	30.0	No	Male	
3	No	24.21	No	No	No	0.0	0.0	No	Female	
4	No	23.71	No	No	No	28.0	0.0	Yes	Female	
5	Yes	28.87	Yes	No	No	6.0	0.0	Yes	Female	
6	No	21.63	No	No	No	15.0	0.0	No	Female	
7	No	31.64	Yes	No	No	5.0	0.0	Yes	Female	
8	No	26.45	No	No	No	0.0	0.0	No	Female	
9	No	40.69	No	No	No	0.0	0.0	Yes	Male	
10	Yes	34.30	Yes	No	No	30.0	0.0	Yes	Male	
11	No	28.71	Yes	No	No	0.0	0.0	No	Female	
12	No	28.37	Yes	No	No	0.0	0.0	Yes	Male	
13	No	28.15	No	No	No	7.0	0.0	Yes	Female	
14	No	29.29	Yes	No	No	0.0	30.0	Yes	Female	

General Properties :

In [4]:
```
#number of rows and columns
data.shape
```

Out[4]:
```
(319795, 18)
```

In [5]:
```
#data types and checking of missing values
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 319795 entries, 0 to 319794
Data columns (total 18 columns):
 #   Column            Non-Null Count   Dtype
---  ------            --------------   -----
 0   HeartDisease      319795 non-null  object
 1   BMI               319795 non-null  float64
 2   Smoking           319795 non-null  object
 3   AlcoholDrinking   319795 non-null  object
```

```
 4   Stroke            319795 non-null  object
 5   PhysicalHealth    319795 non-null  float64
 6   MentalHealth      319795 non-null  float64
 7   DiffWalking       319795 non-null  object
 8   Sex               319795 non-null  object
 9   AgeCategory       319795 non-null  object
 10  Race              319795 non-null  object
 11  Diabetic          319795 non-null  object
 12  PhysicalActivity  319795 non-null  object
 13  GenHealth         319795 non-null  object
 14  SleepTime         319795 non-null  float64
 15  Asthma            319795 non-null  object
 16  KidneyDisease     319795 non-null  object
 17  SkinCancer        319795 non-null  object
dtypes: float64(4), object(14)
memory usage: 43.9+ MB
```

No missing values

In [6]:
```
#some statistical Values
data.describe()
```

Out[6]:

	BMI	PhysicalHealth	MentalHealth	SleepTime
count	319795.000000	319795.00000	319795.000000	319795.000000
mean	28.325399	3.37171	3.898366	7.097075
std	6.356100	7.95085	7.955235	1.436007
min	12.020000	0.00000	0.000000	1.000000
25%	24.030000	0.00000	0.000000	6.000000
50%	27.340000	0.00000	0.000000	7.000000
75%	31.420000	2.00000	3.000000	8.000000
max	94.850000	30.00000	30.000000	24.000000

There is an error in "SleepTime" column as its maximum value is 24 hours and that's immpossible (will be handled in data cleaning phase)

Cleaning Phase

In [7]:
```
#checking wether data have duplicated rows or not.
data.duplicated().sum()
```

Out[7]:
```
18078
```

There are 18078 duplicated rows that we have to drop

In [8]:
```
data.drop_duplicates(inplace=True)
```

In [9]:
```
data.duplicated().sum()
```

Out[9]:
```
0
```

No more duplicated rows

In [10]:
```
#checking for errors in data entry
error = data.query("PhysicalHealth==0")
error
```

Out[10]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	PhysicalHealth	MentalHealth	DiffWalking	Sex
1	No	20.34	No	No	Yes	0.0	0.0	No	Female
3	No	24.21	No	No	No	0.0	0.0	No	Female
8	No	26.45	No	No	No	0.0	0.0	No	Female
9	No	40.69	No	No	No	0.0	0.0	Yes	Male
11	No	28.71	Yes	No	No	0.0	0.0	No	Female
...	...	...	...	...	...	...	...	...	...
319789	No	22.22	No	No	No	0.0	0.0	No	Female
319791	No	29.84	Yes	No	No	0.0	0.0	No	Male
319792	No	24.24	No	No	No	0.0	0.0	No	Female
319793	No	32.81	No	No	No	0.0	0.0	No	Female
319794	No	46.56	No	No	No	0.0	0.0	No	Female

208611 rows × 18 columns

There are 226589 rows containing 0 value of 'PhysicalHealth' attribute so, column must be dropped as it will ruin the analysis process

In [11]:
```
data.drop('PhysicalHealth',axis=1,inplace=True)
```

In [12]:
```
#checking for errors in data entry
error = data.query("MentalHealth==0")
error
```

Out[12]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	MentalHealth	DiffWalking	Sex	AgeCategory
1	No	20.34	No	No	Yes	0.0	No	Female	80 or older
3	No	24.21	No	No	No	0.0	No	Female	75-79
4	No	23.71	No	No	No	0.0	Yes	Female	40-44
5	Yes	28.87	Yes	No	No	0.0	Yes	Female	75-79
6	No	21.63	No	No	No	0.0	No	Female	70-74
...	...	...	...	...	...	...	...	...	...
319790	Yes	27.41	Yes	No	No	0.0	Yes	Male	60-64
319791	No	29.84	Yes	No	No	0.0	No	Male	35-39
319792	No	24.24	No	No	No	0.0	No	Female	45-49
319793	No	32.81	No	No	No	0.0	No	Female	25-29
319794	No	46.56	No	No	No	0.0	No	Female	80 or older

187898 rows × 17 columns

There are 205401 rows containing 0 value of 'MentalHealth' attribute So, column must be dropped as it will ruin the analysis process

In [13]:
```
data.drop('MentalHealth',axis=1,inplace=True)
```

In [14]:
```
#How many rows do contain 24 hrs "SleepTime" entry?
error = data.query("SleepTime==24")
error
```

Out[14]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race
12339	No	28.15	Yes	No	No	No	Female	55-59	American Indian/Alaskan Native
15736	Yes	24.41	No	No	No	Yes	Female	80 or older	White
17845	No	38.09	No	No	No	Yes	Female	55-59	White
28794	No	28.51	No	No	Yes	Yes	Male	18-24	Other
37508	No	48.82	No	No	No	No	Male	18-24	White
40015	No	36.36	Yes	No	No	Yes	Female	25-29	White
40288	No	21.46	No	No	No	Yes	Female	35-39	Hispanic
40858	No	31.09	No	No	No	Yes	Female	50-54	Black
43212	Yes	29.05	Yes	No	No	No	Female	60-64	Black
44608	No	32.50	No	No	No	No	Male	50-54	Black
52970	No	45.04	No	No	No	Yes	Male	65-69	White
63281	No	27.37	Yes	Yes	No	No	Male	30-34	Hispanic
90985	No	46.94	Yes	No	No	Yes	Female	55-59	White
101359	No	38.89	No	No	No	No	Male	25-29	Black
102691	No	25.04	No	No	Yes	No	Male	55-59	Black
119663	Yes	22.67	Yes	No	No	Yes	Female	50-54	Black
120188	No	32.61	No	No	No	No	Female	35-39	Black
134017	No	35.43	No	No	No	No	Female	55-59	Black
163829	Yes	54.91	Yes	Yes	No	Yes	Male	18-24	Black
191913	No	29.18	No	Yes	No	No	Male	50-54	Hispanic
220180	No	27.41	Yes	No	No	Yes	Male	45-49	Black
223641	No	25.09	Yes	No	No	Yes	Male	60-64	White
225626	Yes	35.25	Yes	No	No	Yes	Male	55-59	White
248202	No	24.75	No	No	No	No	Male	70-74	White
248700	No	43.05	No	No	No	No	Female	45-49	Black
264143	Yes	36.90	No	No	No	Yes	Female	65-69	Other
273779	No	30.92	No	No	No	No	Male	75-79	White
307770	No	37.41	No	No	No	No	Female	55-59	American Indian/Alaskan Native

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race
309745	No	19.64	No	No	No	No	Female	65-69	White
310560	No	29.84	No	No	No	No	Female	18-24	Other

In [15]:
```
#here we will create a list containig the indices of the wrong entry rows to be passed to
Error_index_list = error.index
Error_index_list
```

Out[15]:
```
Int64Index([ 12339,  15736,  17845,  28794,  37508,  40015,  40288,  40858,
             43212,  44608,  52970,  63281,  90985, 101359, 102691, 119663,
            120188, 134017, 163829, 191913, 220180, 223641, 225626, 248202,
            248700, 264143, 273779, 307770, 309745, 310560],
           dtype='int64')
```

In [16]:
```
#removing these rows
data.drop(index=Error_index_list,inplace=True)
```

In [17]:
```
#Checking
error = data.query("SleepTime==24")
error
```

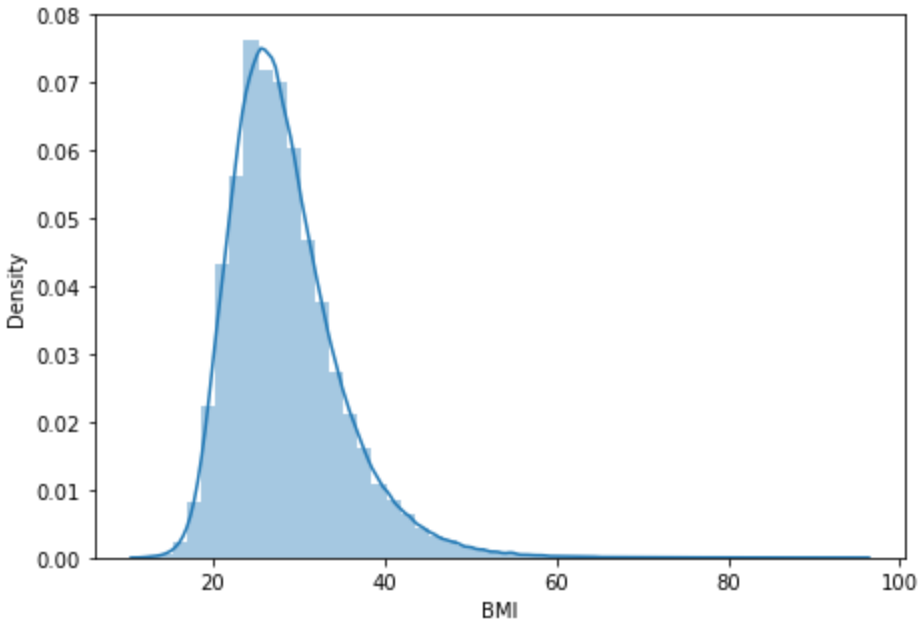
Out[17]:

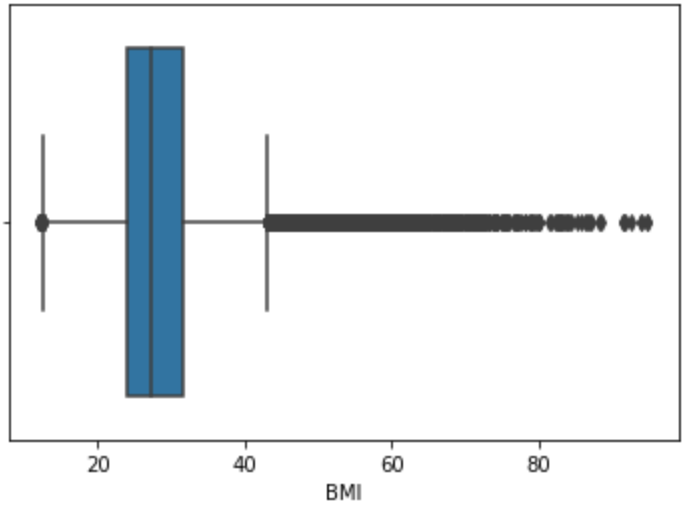
HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	PhysicalA

24 Hrs "SleepTime" rows are now dropped

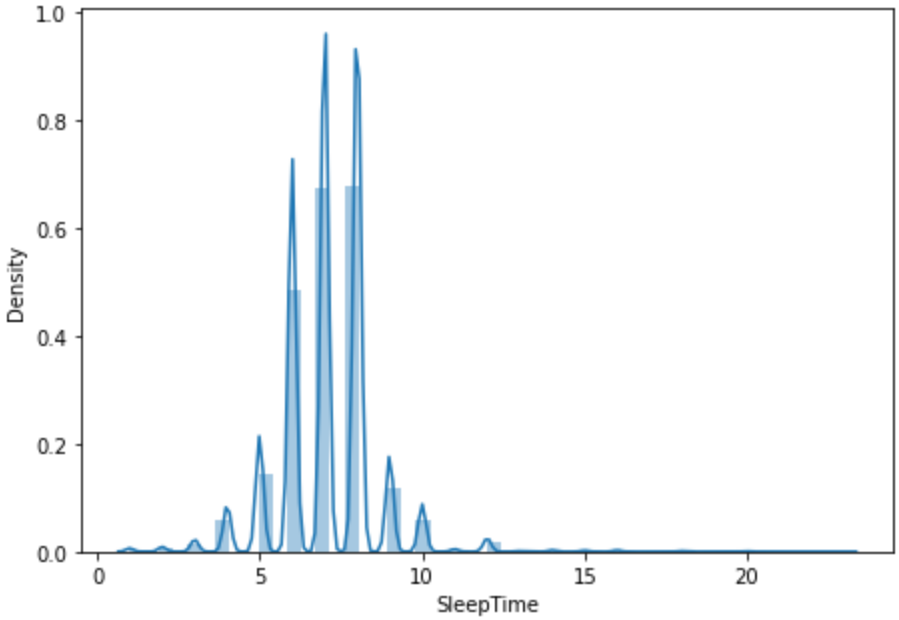
In [18]:
```
def detectOutliers(x):

    plt.figure(figsize=(16,5))
    plt.subplot(1,2,1)
    snb.distplot(data[x])
    plt.show()
    snb.boxplot(data[x])
```

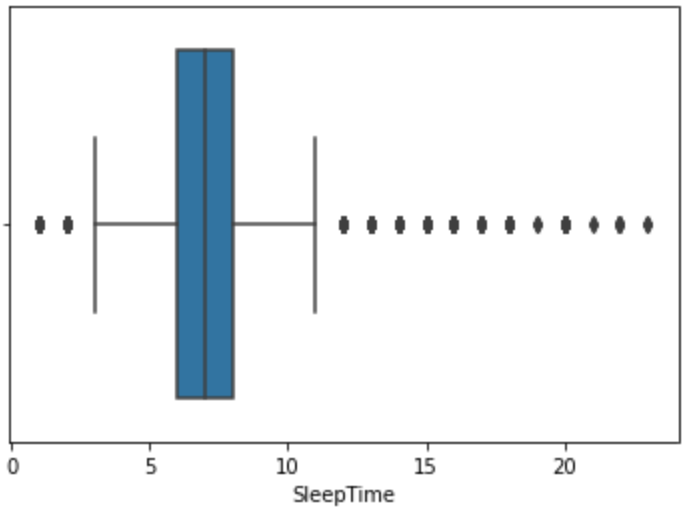
In [19]:
```
detectOutliers("BMI")
```





In [20]:
```
detectOutliers("SleepTime")
```





In [21]:
```
array=['BMI','SleepTime']
```

In [22]:
```
#function to remove outliers
def removeOutliers(data,g):
    for i in g:
```

```
        percentile25 = data[i].quantile(0.25)
        percentile75 = data[i].quantile(0.75)
        iqr=percentile75-percentile25
        upper_limit = percentile75 + 1.5 * iqr
        lower_limit = percentile25 - 1.5 * iqr
        data=data[(data[i]>lower_limit)&(data[i]<upper_limit)]
    return data
```

In [23]:
```
data=removeOutliers(data,array)
```

In [24]:
```
data
```

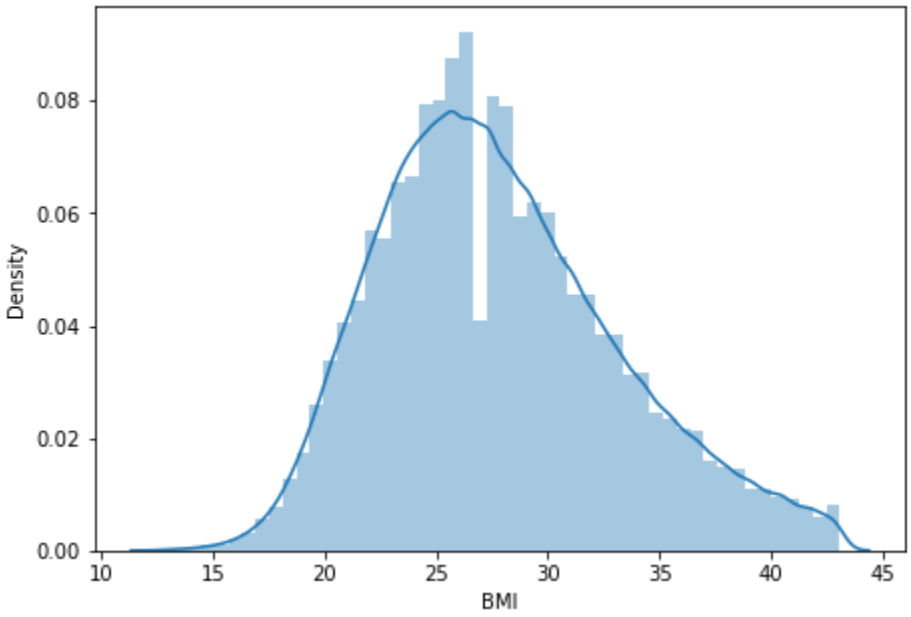
Out[24]:

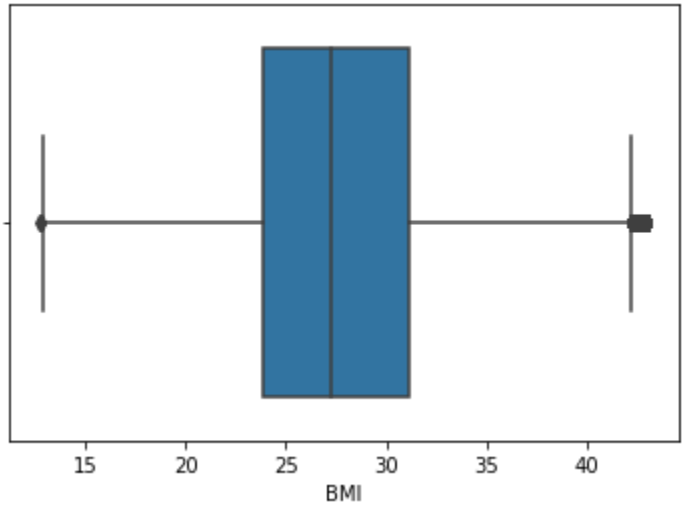
	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabe
0	No	16.60	Yes	No	No	No	Female	55-59	White	Y
1	No	20.34	No	No	Yes	No	Female	80 or older	White	
2	No	26.58	Yes	No	No	No	Male	65-69	White	Y
3	No	24.21	No	No	No	No	Female	75-79	White	
4	No	23.71	No	No	No	Yes	Female	40-44	White	
...	...	...	...	...	...	...	...	...	...	
319788	No	23.38	No	No	No	No	Female	60-64	Hispanic	
319789	No	22.22	No	No	No	No	Female	18-24	Hispanic	
319790	Yes	27.41	Yes	No	No	Yes	Male	60-64	Hispanic	Y
319791	No	29.84	Yes	No	No	No	Male	35-39	Hispanic	
319792	No	24.24	No	No	No	No	Female	45-49	Hispanic	

286216 rows × 16 columns

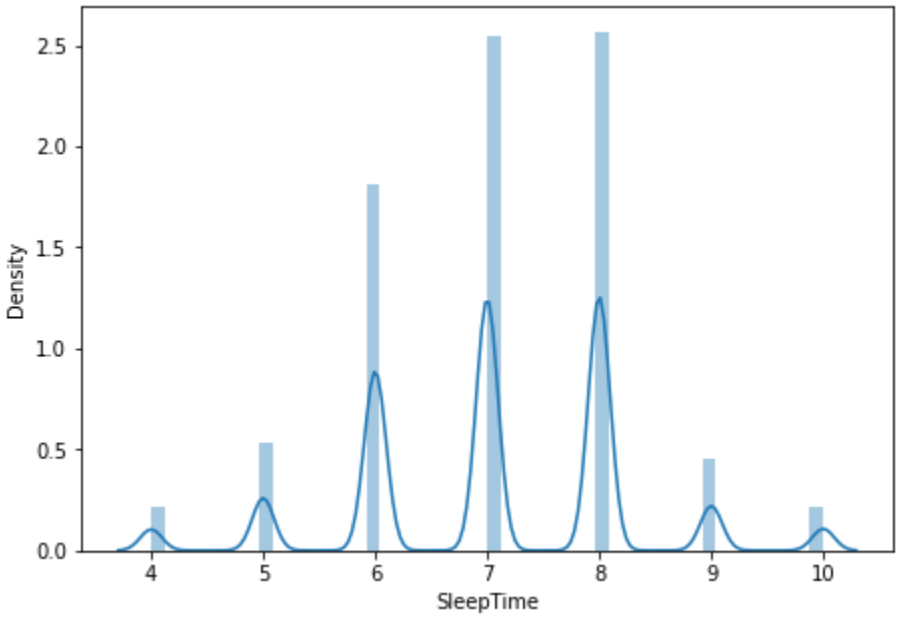
There are about 25000 rows have been removed as they are outliers

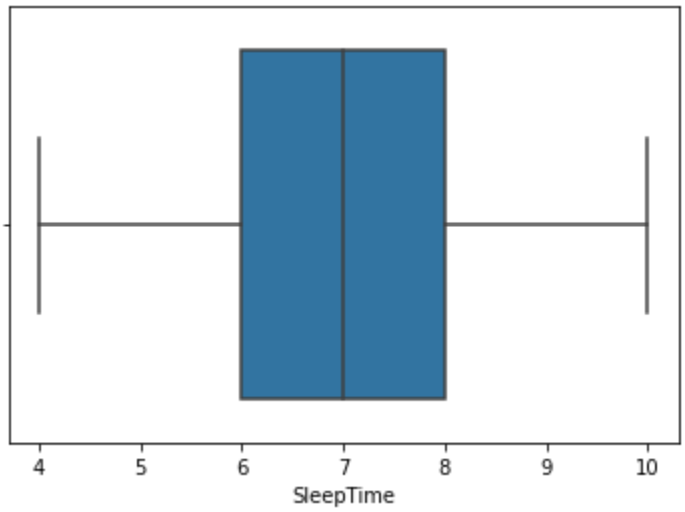
In [25]:
```
detectOutliers("BMI")
```





In [26]:
```
detectOutliers("SleepTime")
```





All data is in range as shown in both figures

In [27]:
```
arr=['HeartDisease','Smoking','AlcoholDrinking','Stroke','DiffWalking','Sex','Diabetic','R
#encoding binary attributes
def encode(data):
    for i in arr:
        pd.get_dummies(data[i])
```

```
        if i =='Sex':
            data[i]=df['Male']
        else:
            data[i]=df['Yes']
    return data

encode(data)
```

Out[27]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic
0	0	16.60	1	0	0	0	0	55-59	White	1
1	0	20.34	0	0	1	0	0	80 or older	White	0
2	0	26.58	1	0	0	0	1	65-69	White	1
3	0	24.21	0	0	0	0	0	75-79	White	0
4	0	23.71	0	0	0	1	0	40-44	White	0
...	...	...	...	...	...	...	...	...	...	...
319788	0	23.38	0	0	0	0	0	60-64	Hispanic	0
319789	0	22.22	0	0	0	0	0	18-24	Hispanic	0
319790	1	27.41	1	0	0	1	1	60-64	Hispanic	1
319791	0	29.84	1	0	0	0	1	35-39	Hispanic	0
319792	0	24.24	0	0	0	0	0	45-49	Hispanic	0

286216 rows × 16 columns

In [28]:

```
#Checking for values of  GenHealth attribute
data['GenHealth'].unique()
```

Out[28]:

```
array(['Very good', 'Fair', 'Good', 'Excellent', 'Poor'], dtype=object)
```

In [29]:

```
#encoding Ordinal Attribute
dataMapping={
    'Poor': 1,
    'Fair' : 2,
    'Good' : 3,
    'Very good': 4,
    'Excellent' :5
}
data['GenHealth']=data['GenHealth'].map(dataMapping)
```

In [30]:

```
data
```

Out[30]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic
0	0	16.60	1	0	0	0	0	55-59	White	1
1	0	20.34	0	0	1	0	0	80 or older	White	0
2	0	26.58	1	0	0	0	1	65-69	White	1
3	0	24.21	0	0	0	0	0	75-79	White	0
4	0	23.71	0	0	0	1	0	40-44	White	0
...	...	...	...	...	...	...	...	...	...	...
319788	0	23.38	0	0	0	0	0	60-64	Hispanic	0

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic
319789	0	22.22	0	0	0	0	0	18-24	Hispanic	0
319790	1	27.41	1	0	0	1	1	60-64	Hispanic	1
319791	0	29.84	1	0	0	0	1	35-39	Hispanic	0
319792	0	24.24	0	0	0	0	0	45-49	Hispanic	0

286216 rows × 16 columns

In [31]:
```
#showing race values
arr=data['Race'].unique()
arr
```

Out[31]:
```
array(['White', 'Black', 'Asian', 'American Indian/Alaskan Native',
       'Other', 'Hispanic'], dtype=object)
```

In [32]:
```
#encoding nominal attributes
data['Race']=data['Race'].replace(arr,[0,1,2,3,4,5])
data
```

Out[32]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	P
0	0	16.60	1	0	0	0	0	55-59	0	1	
1	0	20.34	0	0	1	0	0	80 or older	0	0	
2	0	26.58	1	0	0	0	1	65-69	0	1	
3	0	24.21	0	0	0	0	0	75-79	0	0	
4	0	23.71	0	0	0	1	0	40-44	0	0	
...	...	...	...	...	...	...	...	...	...	...	
319788	0	23.38	0	0	0	0	0	60-64	5	0	
319789	0	22.22	0	0	0	0	0	18-24	5	0	
319790	1	27.41	1	0	0	1	1	60-64	5	1	
319791	0	29.84	1	0	0	0	1	35-39	5	0	
319792	0	24.24	0	0	0	0	0	45-49	5	0	

286216 rows × 16 columns

In [33]:
```
arr=data['AgeCategory'].unique()
arr
```

Out[33]:
```
array(['55-59', '80 or older', '65-69', '75-79', '40-44', '70-74',
       '60-64', '50-54', '45-49', '18-24', '35-39', '30-34', '25-29'],
      dtype=object)
```

In [34]:
```
#Replacing age category values with logical numerical values to be used in calculations
data["AgeCategory"].replace({"55-59": 57, "80 or older": 95,'65-69':66,'75-79':77,'40-44'
```

In [35]:
```
data
```

Out[35]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	P
0	0	16.60	1	0	0	0	0	57	0	1	
1	0	20.34	0	0	1	0	0	95	0	0	
2	0	26.58	1	0	0	0	1	66	0	1	
3	0	24.21	0	0	0	0	0	77	0	0	
4	0	23.71	0	0	0	1	0	43	0	0	
...	...	...	...	...	...	...	...	...	...	...	
319788	0	23.38	0	0	0	0	0	63	5	0	
319789	0	22.22	0	0	0	0	0	20	5	0	
319790	1	27.41	1	0	0	1	1	63	5	1	
319791	0	29.84	1	0	0	0	1	38	5	0	
319792	0	24.24	0	0	0	0	0	48	5	0	

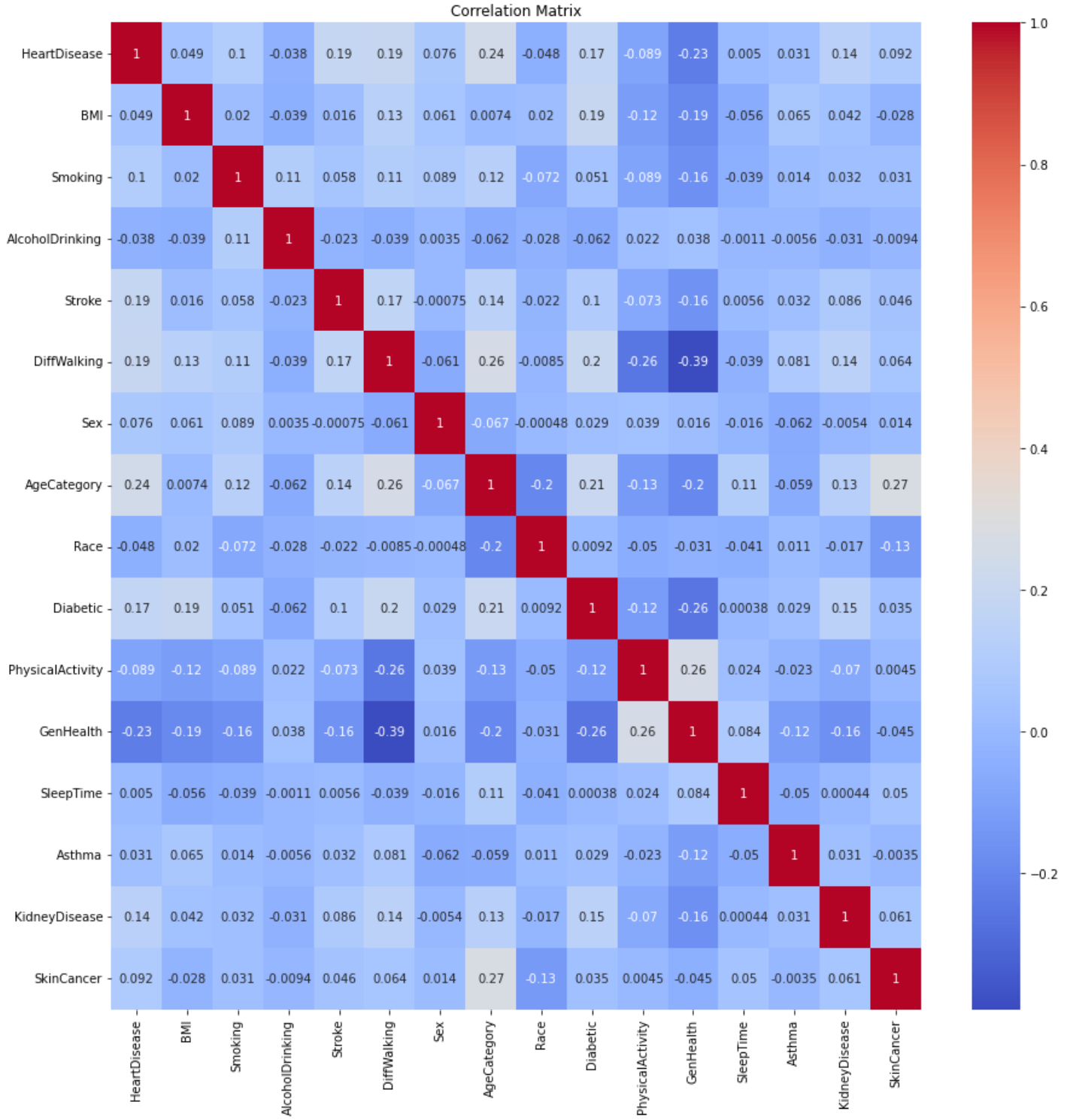
286216 rows × 16 columns

In [36]:

```
#correaltion Matrix
plt.figure(figsize=(15,15))
snb.heatmap(data.corr(), annot=True, cmap="coolwarm").set_title('Correlation Matrix')
```

Out[36]:

```
Text(0.5, 1.0, 'Correlation Matrix')
```



There's No Attributes With Correlation rate Greater than or equal 0.8 for +ve correlation

There's No Attributes With Correlation rate less than or equal -0.8 for -ve correlation

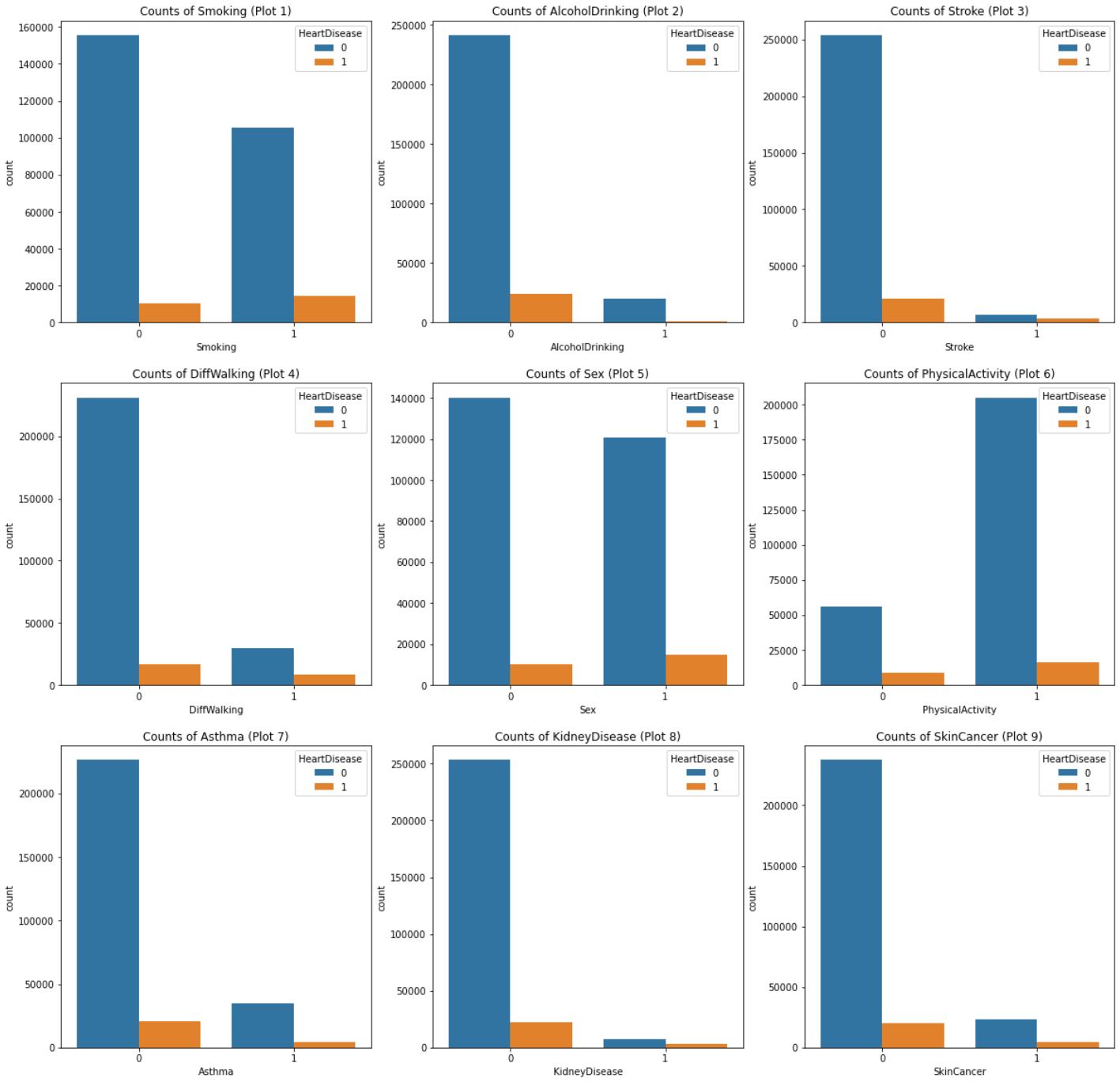
So no attributes need to be removed

Exploratory Data Analysis

In [37]:

```
#General look
#This list of lists contains all the columns which have binary categorical values
colRange = [['Smoking','AlcoholDrinking','Stroke'],['DiffWalking','Sex','PhysicalActivity'
#This function prints the countplots counting the number of people in each category
def printCount(cols):
    = plt.subplots(3, 3, figsize=(20, 20))
```

```
    row=0
    col=0
    p_count=1
    for row in range(3):
        for col in range(3):
            #reads column name from the list
            column = colRange[row][col]
            #plots the counts of the particular column
            snb.countplot(ax=axes[row,col],x=data[column],hue=data['HeartDisease'])
            #sets the title of the corresponding plot along with plot number
            axes[row,col].set_title("Counts of {} (Plot {})".format(column,p_count))
            p_count += 1
#Calling the function
printCount(colRange)
```



General Observations

Plot 1 : According to the plot people who smoke have a higher chance of Heart Diseases than people who don't

Plot 2 : According to the plot people who do not drink alcohol have a lower of Heart Disease

Plot 3 : According to the plot people having Heart Disease have a lower chance of having a Stroke

Plot 4 : According to the plot people who do not have any difficulty in walking have a lower chance of Heart Disease

Plot 5 : According to the plot Males have a higher chance of Heart Disease than Females

Plot 6 : According to the plot People who participate in Physical Activity cause Heart Diseases

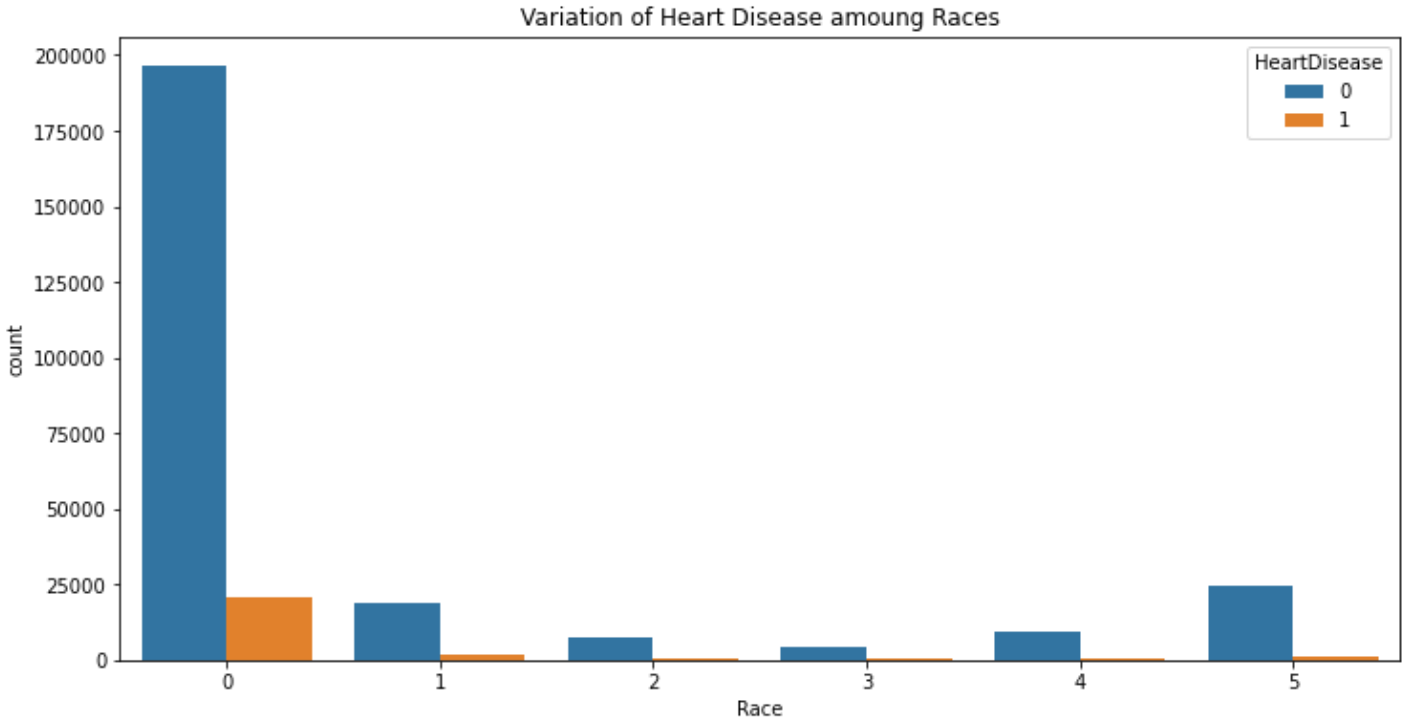
Plot 7 : According to the plot People who have asthma have a lower chance of Heart Disease

Plot 8 : People who have kidney diseases have low chance of having heart diseases.

plot 9 : People who have skin cancer have low chance of having heart diseases.

In [38]:
```
#Checking heart Disease among races
plt.figure(figsize=(12,6))
snb.countplot(data['Race'],hue=data['HeartDisease'])
plt.title('Variation of Heart Disease amoung Races')
```

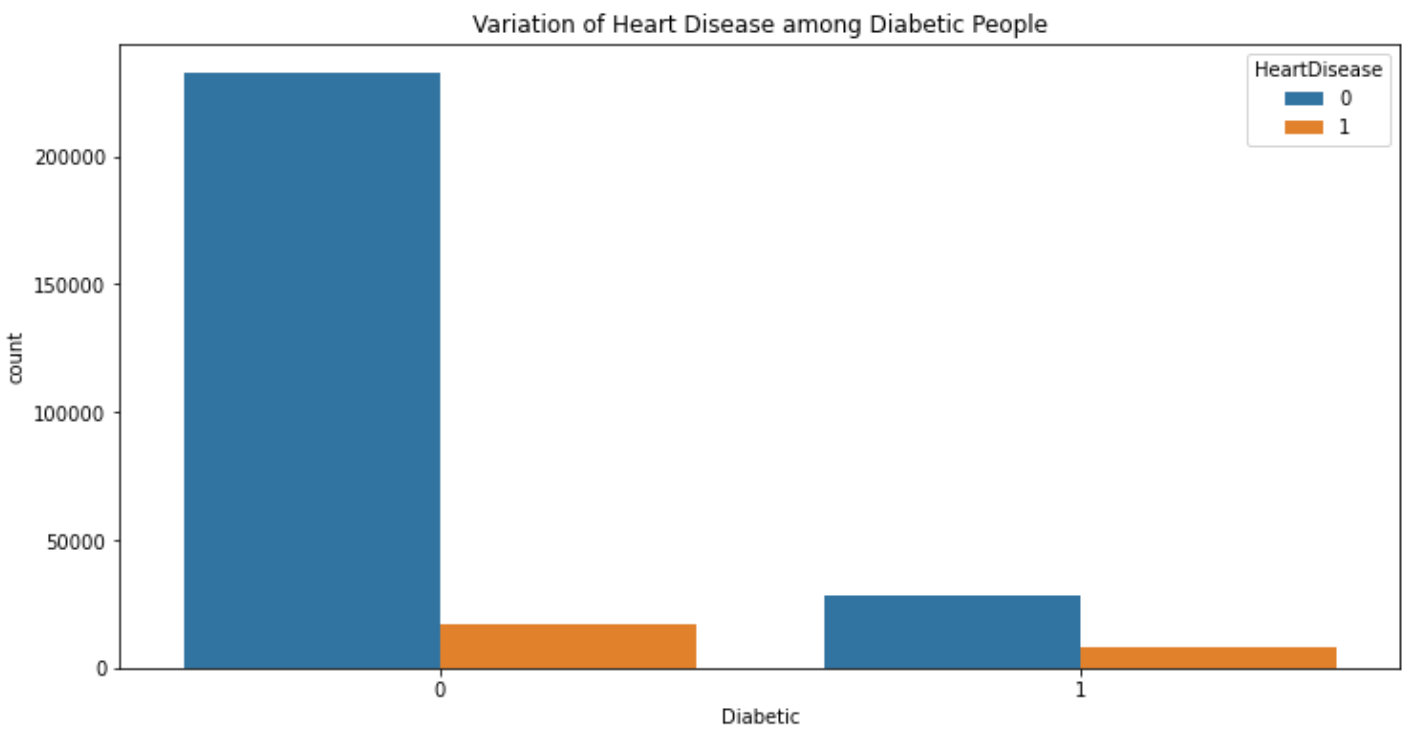
Out[38]:
```
Text(0.5, 1.0, 'Variation of Heart Disease amoung Races')
```



As 0 stands for white people...white people are more likely to have heart diseases

In [39]:
```
#checking heart diseases for diabetic people
plt.figure(figsize=(12,6))
snb.countplot(data['Diabetic'],hue=data['HeartDisease'])
plt.title('Variation of Heart Disease among Diabetic People')
```

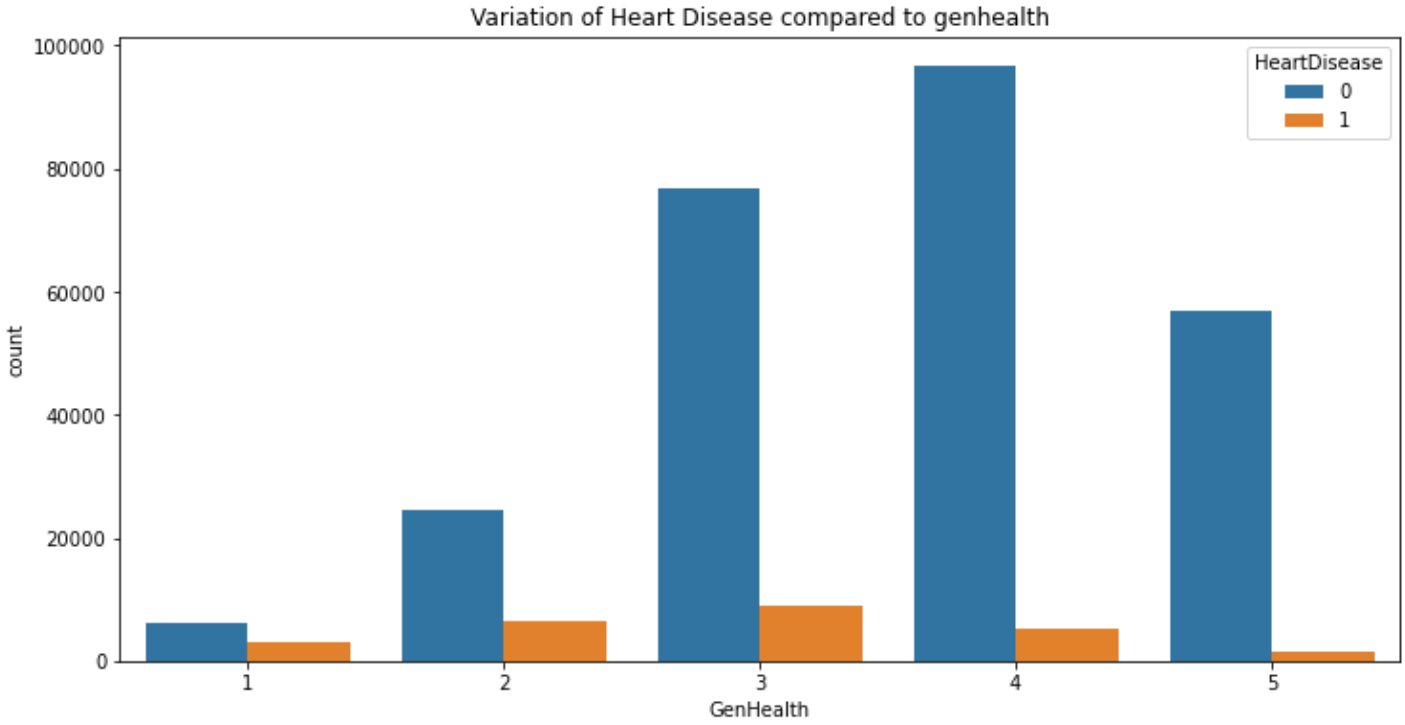
Out[39]:
```
Text(0.5, 1.0, 'Variation of Heart Disease among Diabetic People')
```



people who don't suffer from diabetes have higher risk of heart diseases

In [40]:
```
#checking heart diseases compared to general health
plt.figure(figsize=(12,6))
snb.countplot(data['GenHealth'],hue=data['HeartDisease'])
plt.title('Variation of Heart Disease compared to genhealth')
```

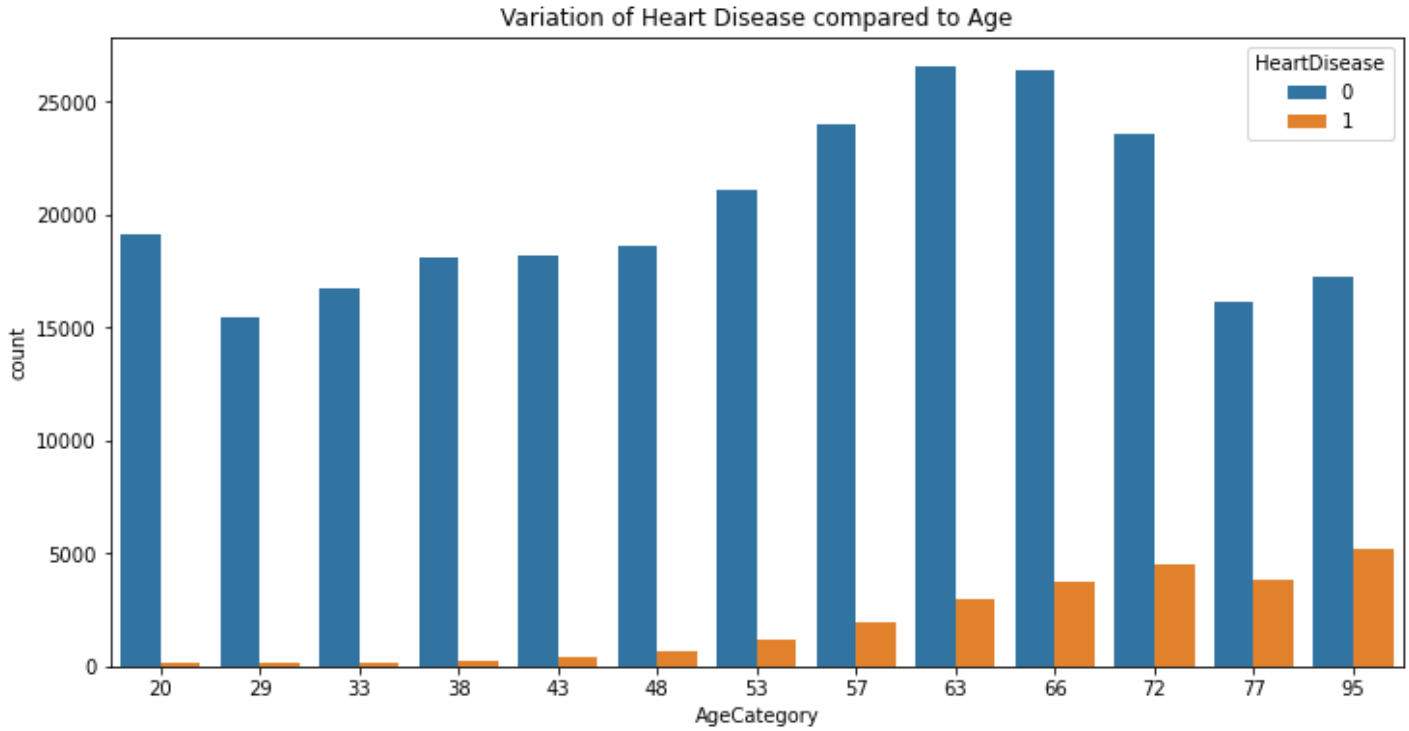
Out[40]:
```
Text(0.5, 1.0, 'Variation of Heart Disease compared to genhealth')
```



People ranked with above good health have the lowest chance of heart diseases

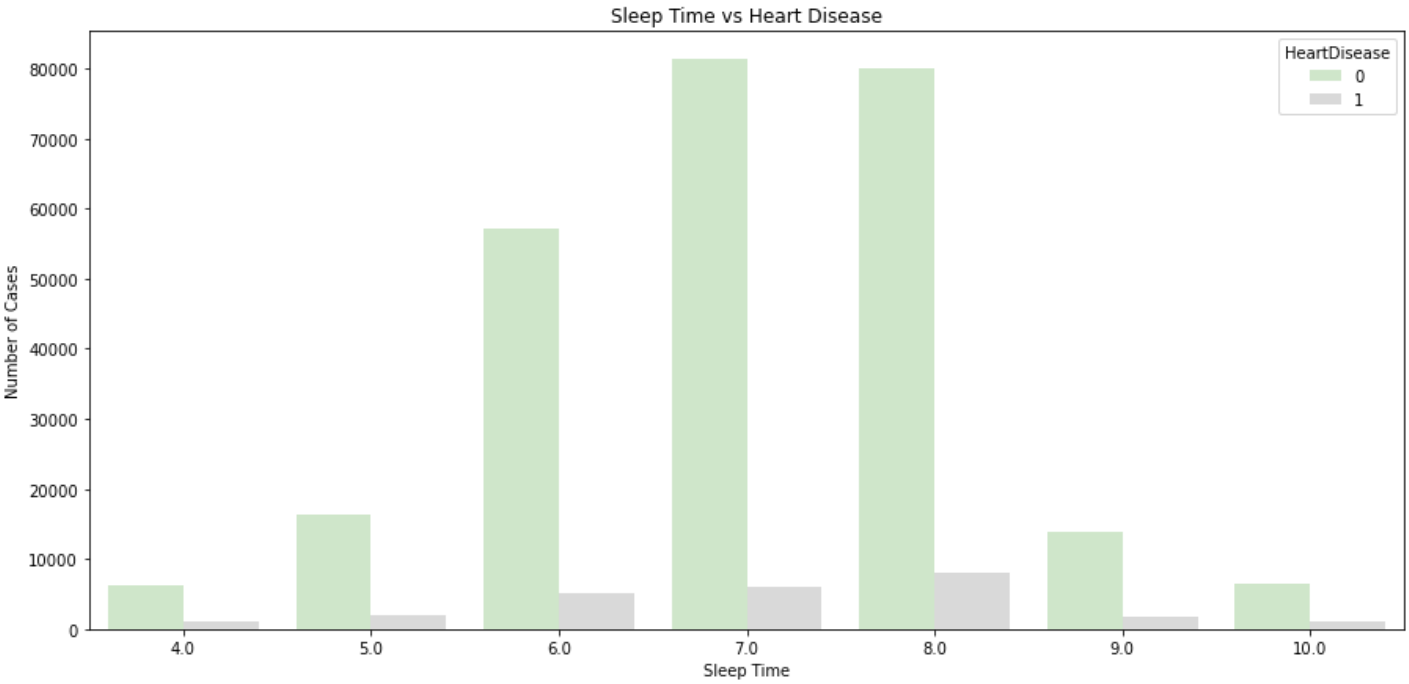
In [41]:
```
#checking heart diseases compared to Age
plt.figure(figsize=(12,6))
snb.countplot(data['AgeCategory'],hue=data['HeartDisease'])
plt.title('Variation of Heart Disease compared to Age')
```

Out[41]:
```
Text(0.5, 1.0, 'Variation of Heart Disease compared to Age')
```



-People above 80 are more likely to have heart diseases

In [42]:
```
#Heart disease compared to sleep time factor
snb.set_palette('Set3_r')
plt.figure(figsize=(15,7))
snb.countplot(data=data, x='SleepTime', hue='HeartDisease')
plt.title('Sleep Time vs Heart Disease')
plt.xlabel('Sleep Time')
plt.ylabel('Number of Cases')
plt.show()
```



Seems like 7 hours of sleeping is the better for your health

In [43]:
```
data.describe()
```

Out[43]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Se
count	286216.000000	286216.000000	286216.000000	286216.000000	286216.000000	286216.000000	286216.00000
mean	0.087822	27.813980	0.419903	0.072494	0.038359	0.134136	0.47441
std	0.283036	5.375851	0.493544	0.259305	0.192062	0.340799	0.49934
min	0.000000	12.650000	0.000000	0.000000	0.000000	0.000000	0.00000
25%	0.000000	23.830000	0.000000	0.000000	0.000000	0.000000	0.00000
50%	0.000000	27.260000	0.000000	0.000000	0.000000	0.000000	0.00000
75%	0.000000	31.180000	1.000000	0.000000	0.000000	0.000000	1.00000
max	1.000000	43.070000	1.000000	1.000000	1.000000	1.000000	1.00000

In [44]:

```
discretizer  = KBinsDiscretizer(n_bins=5, encode='ordinal', strategy='uniform')
data['discreteBMI'] = discretizer.fit_transform(data['BMI'].values.reshape(-1,1)).astype(
```

In [45]:

```
data['discreteBMI'].unique()
```

Out[45]:

```
array([0, 1, 2, 3, 4])
```

In [46]:

```
dataMapping={
    0:'Under Weight' ,
    1 : 'Normal',
    2: 'Over Weight',
    3: 'Obese',
    4 :'Extremely Obese'
}
data['discreteBMI']=data['discreteBMI'].map(dataMapping)
```

In [47]:

```
data
```

Out[47]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	P
0	0	16.60	1	0	0	0	0	57	0	1	
1	0	20.34	0	0	1	0	0	95	0	0	
2	0	26.58	1	0	0	0	1	66	0	1	
3	0	24.21	0	0	0	0	0	77	0	0	
4	0	23.71	0	0	0	1	0	43	0	0	
...	...	...	...	...	...	...	...	...	...	...	
319788	0	23.38	0	0	0	0	0	63	5	0	
319789	0	22.22	0	0	0	0	0	20	5	0	
319790	1	27.41	1	0	0	1	1	63	5	1	
319791	0	29.84	1	0	0	0	1	38	5	0	
319792	0	24.24	0	0	0	0	0	48	5	0	

286216 rows × 17 columns

In [48]:
```
discretizer  = KBinsDiscretizer(n_bins=7, encode='ordinal', strategy='uniform')
data['discreteST'] = discretizer.fit_transform(data['SleepTime'].values.reshape(-1,1)).ast
```

In [49]:
```
data['discreteST'].unique()
```

Out[49]:
```
array([1, 3, 4, 2, 0, 5, 6])
```

In [50]:
```
dataMapping={
    0:'Very Low' ,
    1 : 'Low',
    2: 'Good',
    3: 'Excellent',
    4 :'Very good',
    5 : 'Low',
    6 :'Very Low'
}
data['discreteST']=data['discreteST'].map(dataMapping)
```

In [51]:
```
data
```

Out[51]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	P
0	0	16.60	1	0	0	0	0	57	0	1	
1	0	20.34	0	0	1	0	0	95	0	0	
2	0	26.58	1	0	0	0	1	66	0	1	
3	0	24.21	0	0	0	0	0	77	0	0	
4	0	23.71	0	0	0	1	0	43	0	0	
...	...	...	...	...	...	...	...	...	...	...	
319788	0	23.38	0	0	0	0	0	63	5	0	
319789	0	22.22	0	0	0	0	0	20	5	0	
319790	1	27.41	1	0	0	1	1	63	5	1	
319791	0	29.84	1	0	0	0	1	38	5	0	
319792	0	24.24	0	0	0	0	0	48	5	0	

286216 rows × 18 columns

Training and Testing

> **Algorithms**:
>
> - K Nearest Neighbors Algorithm
> - Decision Tree Algorithm
> - Naive Bayes
> - Logistic Regression

In [52]:
```
#importing MinMax function to normalize data
from sklearn.preprocessing import MinMaxScaler
```

K Nearest Neighbors Algorithm

In [53]:
```
#dividing data into features (x) and target (y)
y=data.HeartDisease
x=data.iloc[:,1:16]
```

In [54]:
```
#normalizing data
scaler = MinMaxScaler()
names = x.columns
d = scaler.fit_transform(x)
scaled_df = pd.DataFrame(d, columns=names)
scaled_df
```

Out[54]:

	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	PhysicalActiv
0	0.129849	1.0	0.0	0.0	0.0	0.0	0.493333	0.0	1.0	
1	0.252794	0.0	0.0	1.0	0.0	0.0	1.000000	0.0	0.0	
2	0.457922	1.0	0.0	0.0	0.0	1.0	0.613333	0.0	1.0	
3	0.380013	0.0	0.0	0.0	0.0	0.0	0.760000	0.0	0.0	
4	0.363577	0.0	0.0	0.0	1.0	0.0	0.306667	0.0	0.0	
...	...	...	...	...	...	...	...	...	...	
286211	0.352728	0.0	0.0	0.0	0.0	0.0	0.573333	1.0	0.0	
286212	0.314596	0.0	0.0	0.0	0.0	0.0	0.000000	1.0	0.0	
286213	0.485207	1.0	0.0	0.0	1.0	1.0	0.573333	1.0	1.0	
286214	0.565089	1.0	0.0	0.0	0.0	1.0	0.240000	1.0	0.0	
286215	0.380999	0.0	0.0	0.0	0.0	0.0	0.373333	1.0	0.0	

286216 rows × 15 columns

In [55]:
```
#importing required libraries for the algorithm
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix
from sklearn.metrics import ConfusionMatrixDisplay
from sklearn.metrics import precision_score,recall_score
```

In [56]:
```
#splitting data into training and test data with ratio 8:2 (train:test)
X_train, X_test, y_train, y_test = train_test_split(
            x, y, test_size = 0.2, random_state=42)
```

In [57]:
```
X_train.to_csv(r"E:\Data Mining train&test data sets\x_train.csv")
```

In [58]:
```
X_test.to_csv(r"E:\Data Mining train&test data sets\x_test.csv")
```

In [59]:
```
y_test.to_csv(r"E:\Data Mining train&test data sets\y_test.csv")
```

In [60]:
```
y_train.to_csv(r"E:\Data Mining train&test data sets\y_train.csv")
```

In [61]:
```
y
```

Out[61]:
```
0         0
1         0
2         0
3         0
4         0
         ..
319788    0
319789    0
319790    1
319791    0
319792    0
Name: HeartDisease, Length: 286216, dtype: uint8
```

In [62]:
```
x
```

Out[62]:

	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	PhysicalActivity
0	16.60	1	0	0	0	0	57	0	1	1
1	20.34	0	0	1	0	0	95	0	0	1
2	26.58	1	0	0	0	1	66	0	1	1
3	24.21	0	0	0	0	0	77	0	0	0
4	23.71	0	0	0	1	0	43	0	0	1
...	...	...	...	...	...	...	...	...	...	...
319788	23.38	0	0	0	0	0	63	5	0	1
319789	22.22	0	0	0	0	0	20	5	0	1
319790	27.41	1	0	0	1	1	63	5	1	0
319791	29.84	1	0	0	0	1	38	5	0	1
319792	24.24	0	0	0	0	0	48	5	0	1

286216 rows × 15 columns

In [63]:
```
X_train
```

Out[63]:

	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	PhysicalActivity
152437	21.79	0	0	0	0	0	33	0	0	1
90603	33.15	1	0	0	0	1	66	0	1	1
215091	40.89	0	0	0	0	1	63	0	0	1
312023	22.81	0	0	0	0	0	72	0	0	1
242260	30.81	1	0	0	0	1	77	1	1	0
...	...	...	...	...	...	...	...	...	...	...
139647	19.26	1	0	0	1	0	33	0	0	1

	BMI	Smoking	AlcoholDrinking	Stroke	DiffWalking	Sex	AgeCategory	Race	Diabetic	PhysicalActivity
288673	34.33	0	0	0	0	0	43	0	0	1
143157	21.77	0	0	0	0	1	43	4	0	1
160067	35.61	0	0	0	0	0	63	0	0	0
131965	26.31	1	0	0	0	1	38	0	0	1

228972 rows × 15 columns

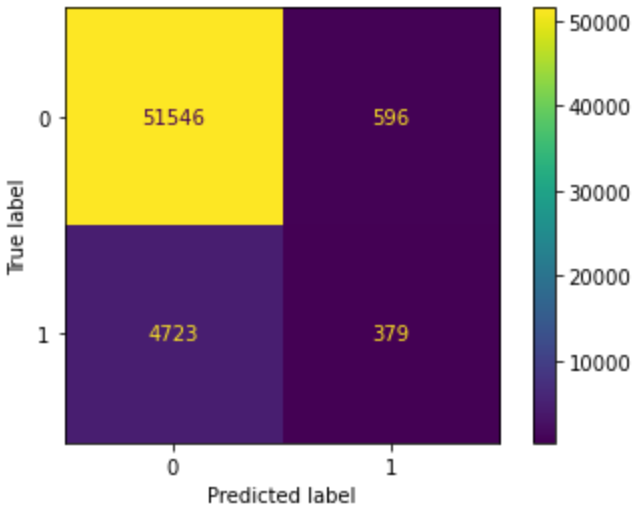
In [64]:

```
# declaring a object of K Neighbors Classifier class
knn = KNeighborsClassifier(n_neighbors=7)
knn.fit(X_train, y_train)
y_pred1 = knn.predict(X_test)
cm1 = confusion_matrix(y_test,y_pred1)
print("Accuracy: \n")
knnacc=accuracy_score(y_test,y_pred1)
print(accuracy_score(y_test,y_pred1)*100)
print()
print("Confusion Matrix\n ")
disp = ConfusionMatrixDisplay(confusion_matrix=cm1, display_labels= np.asarray([0,1]))
disp.plot()
```

```
Accuracy:

90.7081964922088

Confusion Matrix
```

Out[64]:

```
<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x1e1e89d99d0>
```



In [65]:

```
print(f'model: {str(knn)}')
print(f'Accuracy_score: {accuracy_score(y_test,y_pred1)}')
print(f'Precission_score: {precision_score(y_test,y_pred1)}')
print(f'Recall_score: {recall_score(y_test,y_pred1)}')
print( '\n')
```

```
model: KNeighborsClassifier(n_neighbors=7)
Accuracy_score: 0.9070819649220879
Precission_score: 0.38871794871794874
Recall_score: 0.07428459427675421
```

First: the code printed the confusion matrix which is compares the actual target values with those predicted by the KNN algorithm

-TN (True NoHeartDisease): 51546 (Values that actually havenot heart diseases)

-FP (False HeartDisease): 596 (represents the number of misclassified patients with the disease but actually they are healthy)

-TP (True HeartDisease): 379 (Number of patients which are truely predicted with heart disease)

-FN (False NoHeartDisease): 4723 (Number of patients misclassified as healthy but actually they are suffering from the disease)

-Accuarcy= (TP+TN)/(TP+TN+FP+FN)

-Precision score = (TP)/(TP+FP)..... Ratio of correctly classified patients with the disease (TP) to the total patients predicted to have the disease (TP+FP)

-Recall score = (TP)/(TP+FN).....Ratio of correctly classified diseased patients (TP) divided by total number of patients who have actually the disease

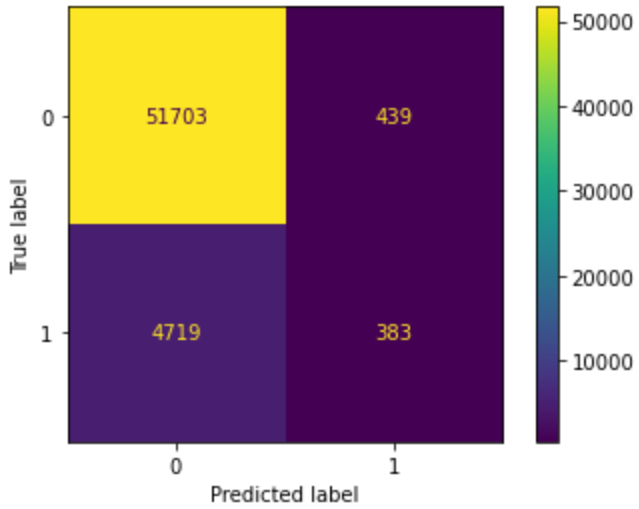
Decision Tree Algorithm

In [66]:
```
#importing required Libraries
from sklearn.tree import DecisionTreeClassifier
```

In [67]:
```
# declaring a object of Decision Tree Classifier class
# entropy is the criterion for calculating information gain
clf = DecisionTreeClassifier(criterion='entropy',max_depth=4,min_samples_leaf=5)
clf.fit(X_train, y_train)
y_pred2 = clf.predict(X_test)
cm2 = confusion_matrix(y_test,y_pred2)
print("Accuracy: \n")
dt=accuracy_score(y_test,y_pred2)
print(accuracy_score(y_test,y_pred2)*100)
print()
print("Confusion Matrix\n ")
disp = ConfusionMatrixDisplay(confusion_matrix=cm2, display_labels= np.asarray([0,1]))
disp.plot()
```

```
Accuracy:

90.98944867584376

Confusion Matrix
```

Out[67]:
```
<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x1e1e62e0610>
```



First: the code printed the confusion matrix which is compares the actual target values with those predicted by the KNN algorithm

-TN (True NoHeartDisease): 48289 (Values that actually havenot heart diseases)

-FP (False HeartDisease): 3853 (represents the number of misclassified patients with the disease but actually they are healthy)

-TP (True HeartDisease): 1216 (Number of patients which are truely predicted with heart disease)

-FN (False NoHeartDisease): 3886 (Number of patients misclassified as healthy but actually they are suffering from the disease)

Naive Bayes

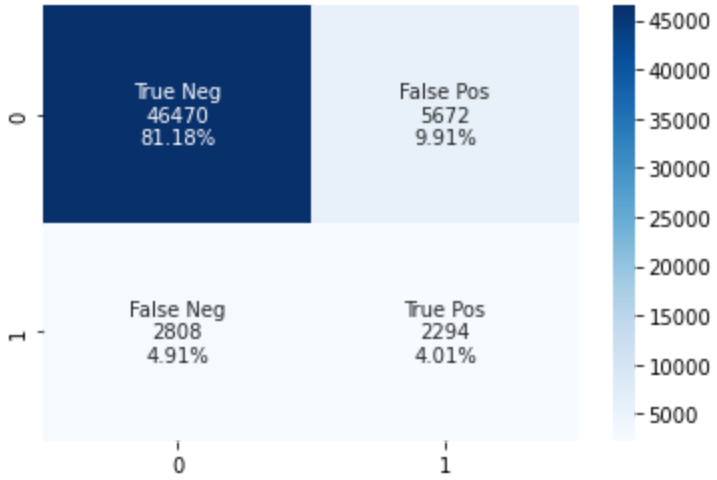
In [68]:
```
#Importing Naive bayes function
from sklearn.naive_bayes import GaussianNB
```

In [69]:
```
# declaring a object of GaussianNB class
clf3 = GaussianNB()
clf3.fit(X_train, y_train)
y_pred3 = clf3.predict(X_test)
cm3 = confusion_matrix(y_test,y_pred3)
naive=accuracy_score(y_test,y_pred3)
print(cm3)
print(accuracy_score(y_test,y_pred3)*100)
```

```
[[46470  5672]
 [ 2808  2294]]
85.18622038990986
```

In [70]:
```
group_names = ['True Neg','False Pos','False Neg','True Pos']
group_counts = ['{0:0.0f}'.format(value) for value in
                cm3.flatten()]
group_percentages = ['{0:.2%}'.format(value) for value in
                     cm3.flatten()/np.sum(cm3)]
labels = [f'{v1}\n{v2}\n{v3}' for v1, v2, v3 in
          zip(group_names,group_counts,group_percentages)]
labels = np.asarray(labels).reshape(2,2)
snb.heatmap(cm3, annot=labels, fmt='', cmap='Blues')
```

Out[70]: <AxesSubplot:>



First: the code printed the confusion matrix which is compares the actual target values with those predicted by the KNN algorithm

-TN (True NoHeartDisease): 46470 (Values that actually havenot heart diseases)

-FP (False HeartDisease): 5672 (represents the number of misclassified patients with the disease but actually they are healthy)

-TP (True HeartDisease): 2294 (Number of patients which are truely predicted with heart disease)

-FN (False NoHeartDisease): 2808 (Number of patients misclassified as healthy but actually they are suffering from the disease)

Logistic Regression

In [71]:
```
from sklearn.linear_model import LogisticRegression
```

In [72]:
```
# declaring a object of Logistic regression class
clf4 = LogisticRegression()

# fit() function trains the model
# fitting the object with the training data
clf4.fit(X_train, y_train)

# predict() function predicts results from validation data
# predicting result using the trained data
y_pred4 = clf4.predict(X_test)

# confusion_matrix() gives the true_positives, false positives, true negatives, false nega
# making confusion matrix using predicted and given results in validation data
cm4=confusion_matrix(y_test,y_pred4)

# printing the confusion matrix
print(cm4)

# accuracy_score() is used to find the accuracy of the model
print(accuracy_score(y_test,y_pred4)*100)
```

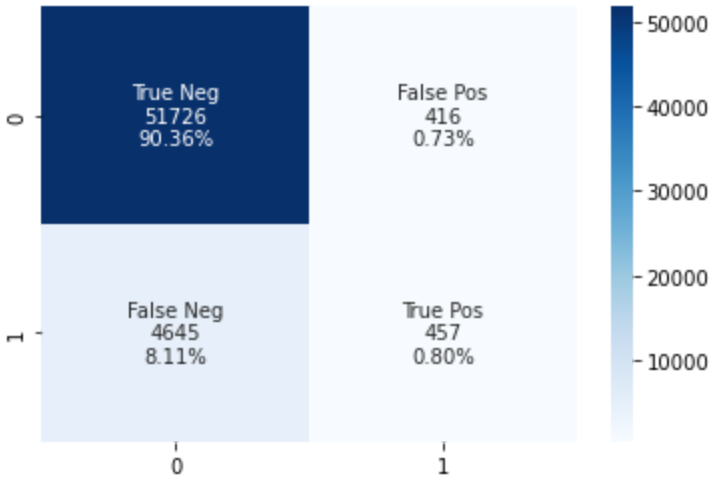
```
[[51726   416]
 [ 4645   457]]
389
```

In [73]:

```
group_names = ['True Neg','False Pos','False Neg','True Pos']
group_counts = ['{0:0.0f}'.format(value) for value in
                cm4.flatten()]
group_percentages = ['{0:.2%}'.format(value) for value in
                     cm4.flatten()/np.sum(cm4)]
labels = [f'{v1}\n{v2}\n{v3}' for v1, v2, v3 in
          zip(group_names,group_counts,group_percentages)]
labels = np.asarray(labels).reshape(2,2)
snb.heatmap(cm4, annot=labels, fmt='', cmap='Blues')
```

Out[73]:

```
<AxesSubplot:>
```



First: the code printed the confusion matrix which is compares the actual target values with those predicted by the KNN algorithm

-TN (True NoHeartDisease): 51726 (Values that actually havenot heart diseases)

-FP (False HeartDisease): 416 (represents the number of misclassified patients with the disease but actually they are healthy)

-TP (True HeartDisease): 457 (Number of patients which are truely predicted with heart disease)

-FN (False NoHeartDisease): 4645 (Number of patients misclassified as healthy but actually they are suffering from the disease)