In [1]:

```
!wget https://raw.githubusercontent.com/keerthy456/Machine-Learning-Final-Project-Vakkalagadda-Keerthi/main/h
eart_disease.csv
```

```
--2022-04-28 00:04:25--  https://raw.githubusercontent.com/keerthy456/Machine-Learning-Final-Project-Vakkalag
adda-Keerthi/main/heart_disease.csv
Resolving raw.githubusercontent.com (raw.githubusercontent.com)... 185.199.108.133, 185.199.109.133, 185.199.
110.133, ...
Connecting to raw.githubusercontent.com (raw.githubusercontent.com)|185.199.108.133|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 25189554 (24M) [text/plain]
Saving to: ‘heart_disease.csv.2’

heart_disease.csv.2 100%[===================>]  24.02M   133MB/s    in 0.2s

2022-04-28 00:04:26 (133 MB/s) - ‘heart_disease.csv.2’ saved [25189554/25189554]
```

In [ ]:

```
pip install dython
```

In [4]:

```
import numpy as np
import pandas as pd
from dython.nominal import associations
import os
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns
```

In [5]:

```
heart_df = pd.read_csv('heart_disease.csv')
```

In [6]:

```
heart_df.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
```

In [23]:
```
heart_df.isnull()
```

Out[23]:

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	PhysicalHealth	MentalHealth	DiffWalking	Sex	AgeCategory	Race	I
0	False	False	False	False	False	False	False	False	False	False	False	
1	False	False	False	False	False	False	False	False	False	False	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	
...	...	...	...	...	...	...	...	...	...	...	...	
319790	False	False	False	False	False	False	False	False	False	False	False	
319791	False	False	False	False	False	False	False	False	False	False	False	
319792	False	False	False	False	False	False	False	False	False	False	False	
319793	False	False	False	False	False	False	False	False	False	False	False	
319794	False	False	False	False	False	False	False	False	False	False	False	

319795 rows × 18 columns

Target Variable Analysis

In [7]:
```
heart_df['HeartDisease'].value_counts()
```

Out[7]:
```
No     292422
Yes     27373
Name: HeartDisease, dtype: int64
```

In [8]:
```
numeric_features = heart_df.select_dtypes(include=[np.number])
```

In [9]:
```
numerical_df = heart_df[['BMI', 'PhysicalHealth', 'MentalHealth', 'SleepTime', 'HeartDisease']]
```

In [10]:
```
categorical_features= [col for col in heart_df.columns if heart_df[col].dtypes == 'object']
```

In [11]:
```
for feature in categorical_features:
    print(feature, ":", heart_df[feature].unique())
    print()
```

```
HeartDisease : ['No' 'Yes']

Smoking : ['Yes' 'No']

AlcoholDrinking : ['No' 'Yes']

Stroke : ['No' 'Yes']

DiffWalking : ['No' 'Yes']

Sex : ['Female' 'Male']

AgeCategory : ['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']

Race : ['White' 'Black' 'Asian' 'American Indian/Alaskan Native' 'Other'
 'Hispanic']

Diabetic : ['Yes' 'No' 'No, borderline diabetes' 'Yes (during pregnancy)']

PhysicalActivity : ['Yes' 'No']

GenHealth : ['Very good' 'Fair' 'Good' 'Poor' 'Excellent']

Asthma : ['Yes' 'No']

KidneyDisease : ['No' 'Yes']

SkinCancer : ['Yes' 'No']
```

Zero Null values are detected in dataset

In [168]:

```
heart_df[heart_df.isnull().any(axis=1)]
```

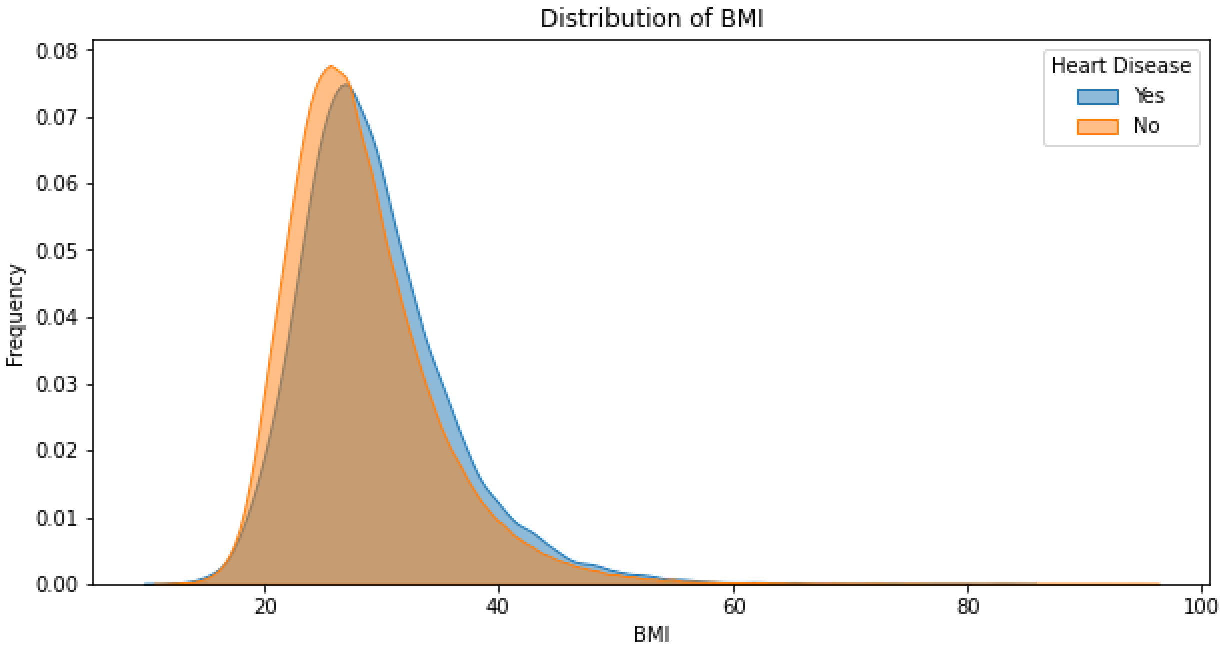
Out[168]:

HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	PhysicalHealth	MentalHealth	DiffWalking	Sex	AgeCategory	Race	Diabetic

Distribution of Numerical Features

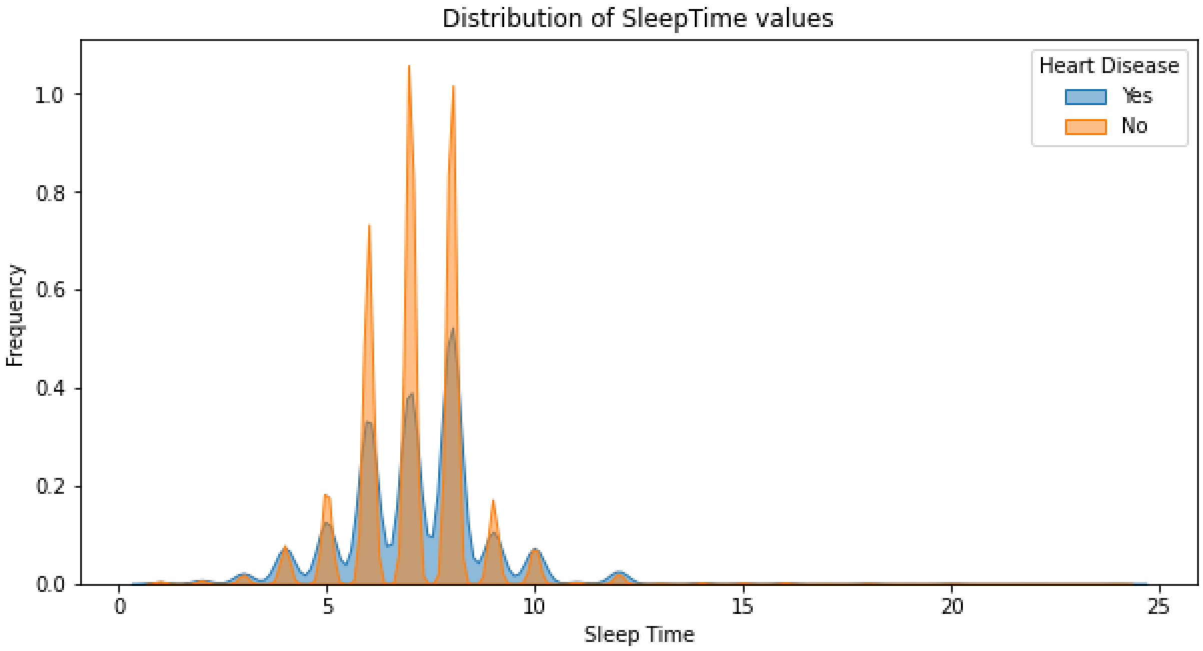
In [175]:

```
fig, axes = plt.subplots(figsize = (10,5))
sns.kdeplot(heart_df[heart_df["HeartDisease"]=='Yes']["BMI"], alpha=0.5,shade = True, label="Yes", ax = axes)
sns.kdeplot(heart_df[heart_df["HeartDisease"]=='No']["BMI"], alpha=0.5,shade = True, label="No", ax = axes)
plt.title('Distribution of BMI')
axes.set_xlabel("BMI")
axes.set_ylabel("Frequency")
axes.legend(title='Heart Disease')
plt.show()
```



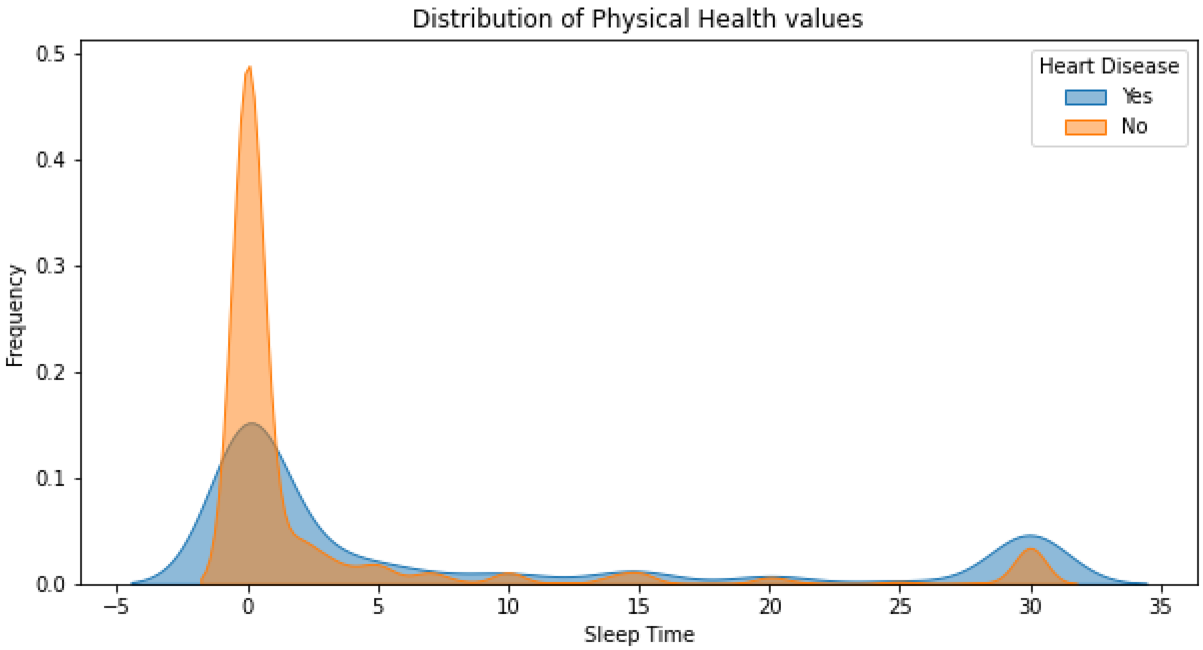
In [174]:

```
fig, axes = plt.subplots(figsize = (10,5))
sns.kdeplot(heart_df[heart_df["HeartDisease"]=='Yes']["SleepTime"], alpha=0.5,shade = True, label="Yes", ax = axes)
sns.kdeplot(heart_df[heart_df["HeartDisease"]=='No']["SleepTime"], alpha=0.5,shade = True, label="No", ax = axes)
plt.title('Distribution of SleepTime values')
axes.set_xlabel("Sleep Time")
axes.set_ylabel("Frequency")
axes.legend(title='Heart Disease')
plt.show()
```



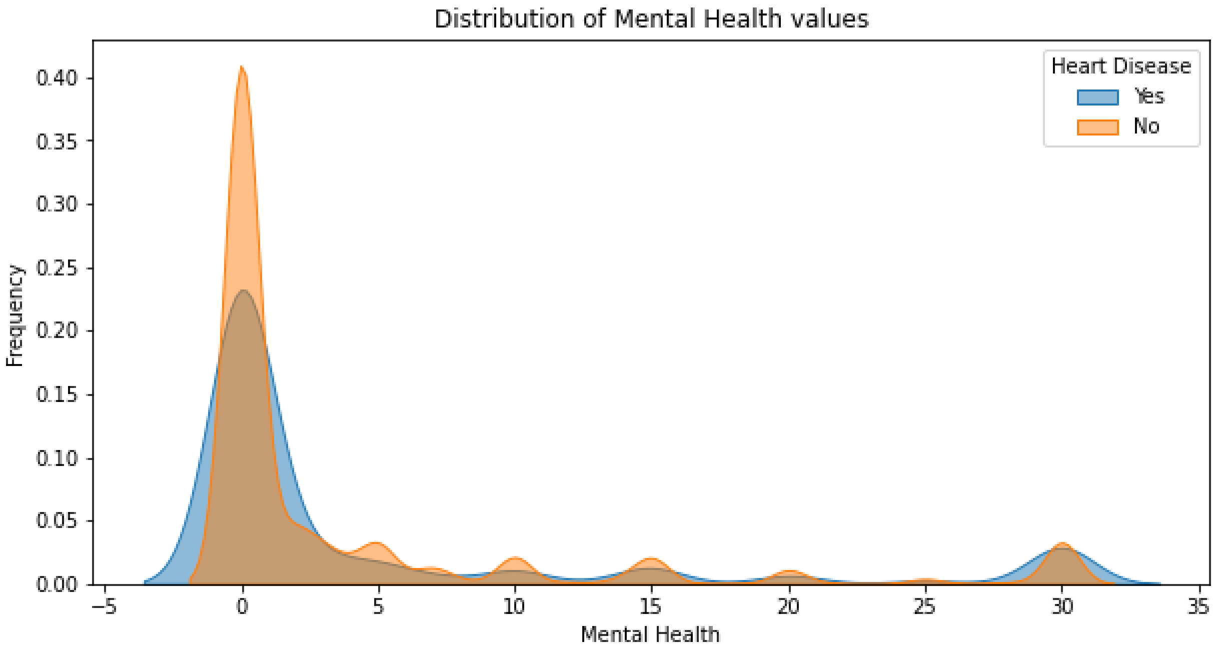
In [173]:

```
fig, axes = plt.subplots(figsize = (10,5))
sns.kdeplot(heart_df[heart_df["HeartDisease"]=='Yes']["PhysicalHealth"], alpha=0.5,shade = True, label="Yes",
ax = axes)
sns.kdeplot(heart_df[heart_df["HeartDisease"]=='No']["PhysicalHealth"], alpha=0.5,shade = True, label="No", a
x = axes)
plt.title('Distribution of Physical Health values')
axes.set_xlabel("Sleep Time")
axes.set_ylabel("Frequency")
axes.legend(title='Heart Disease')
plt.show()
```



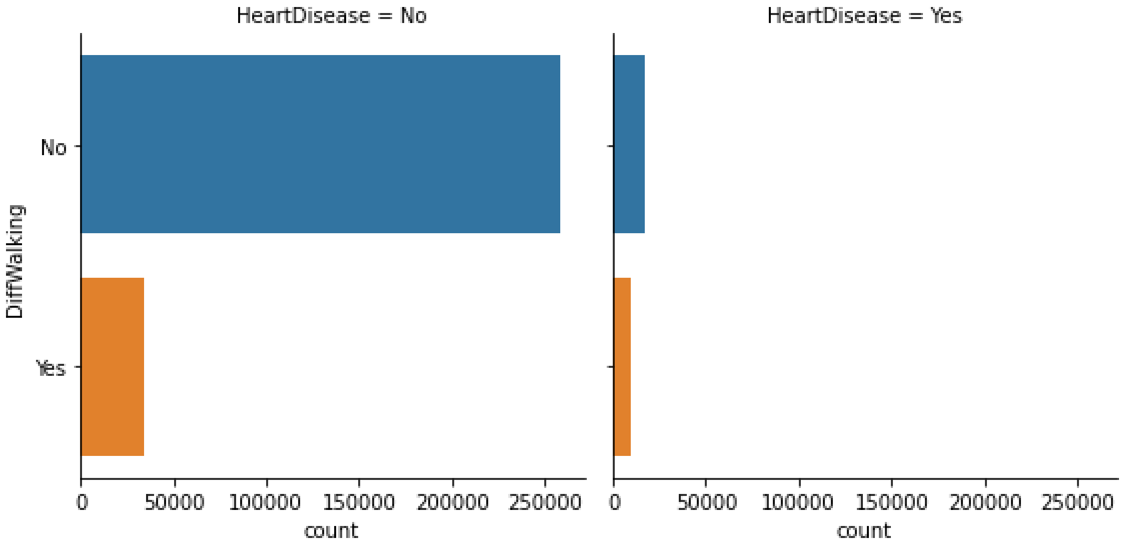
In [172]:

```
fig, axes = plt.subplots(figsize = (10,5))
sns.kdeplot(heart_df[heart_df["HeartDisease"]=='Yes']["MentalHealth"], alpha=0.5,shade = True,  label="Yes", ax = axes)
sns.kdeplot(heart_df[heart_df["HeartDisease"]=='No']["MentalHealth"], alpha=0.5,shade = True, label="No", ax = axes)
plt.title('Distribution of Mental Health values')
axes.set_xlabel("Mental Health")
axes.set_ylabel("Frequency")
axes.legend(title='Heart Disease')
plt.show()
```



```
In [16]: sns.catplot( y= 'DiffWalking' , col = 'HeartDisease',kind= 'count', data=heart_df, height = 4)
```

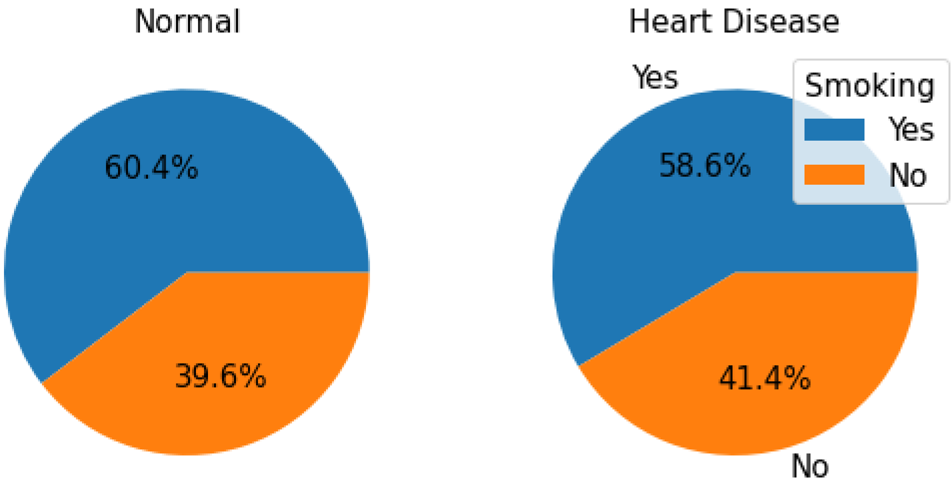
```
Out[16]: <seaborn.axisgrid.FacetGrid at 0x7fae01a9f3d0>
```

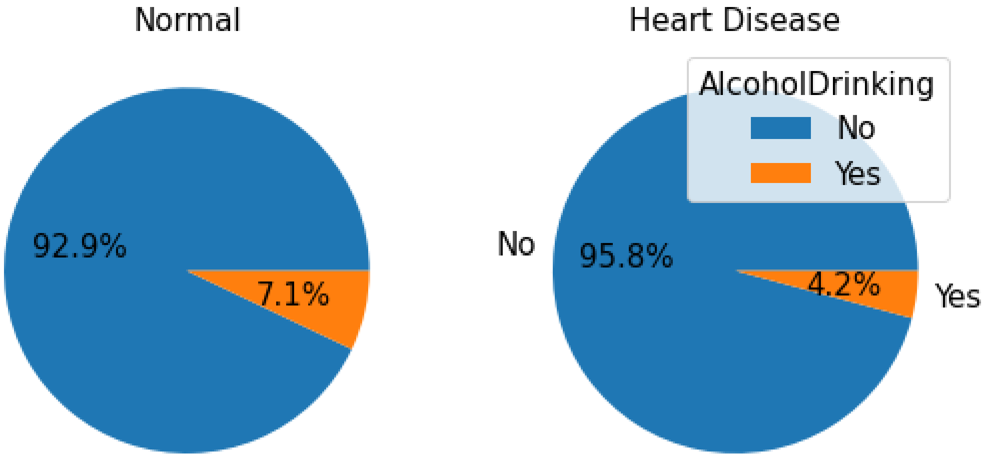


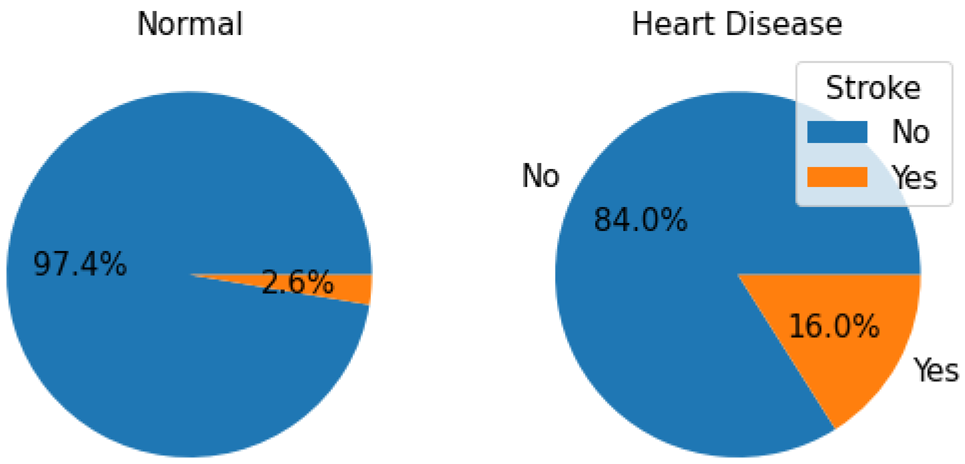
Analyzing Distribution of people with Heart Disease on differet features

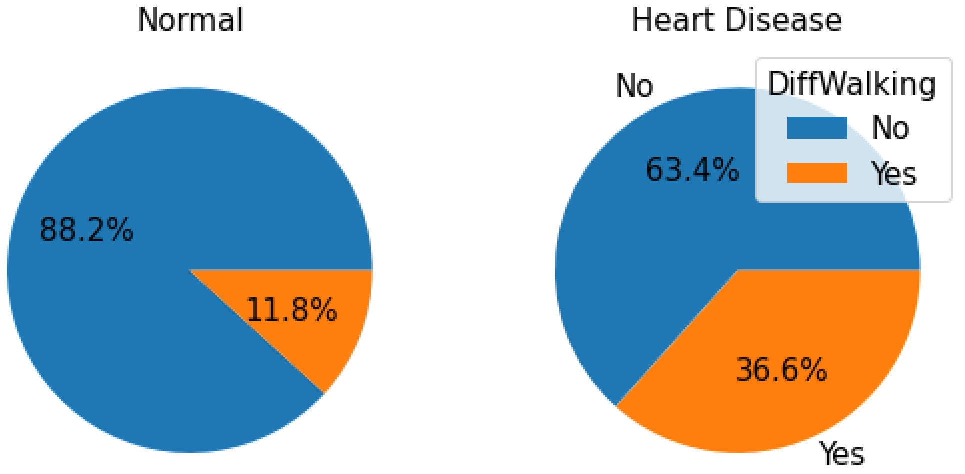
In [43]:

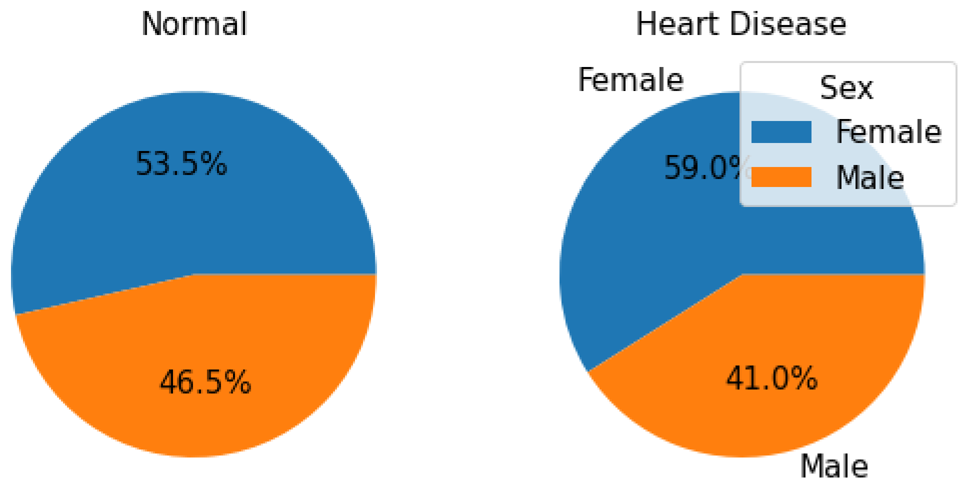
```
for feature in categorical_features:
  if (not(feature in ['Race', 'AgeCategory', 'Diabetic', 'HeartDisease'])):
    fig,axes = plt.subplots(1,2,figsize=(9,8))
    labels = heart_df[feature].unique()
    textprops = {"fontsize":15}

    axes[0].pie(heart_df[heart_df.HeartDisease=="No"][feature].value_counts(),autopct='%1.1f%%',textprops =textprops)
    axes[0].set_title('Normal',fontsize=15)
    axes[1].pie(heart_df[heart_df.HeartDisease=="Yes"][feature].value_counts() , labels = labels, autopct='%1.1f%%',textprops =textprops)
    axes[1].set_title('Heart Disease',fontsize=15)

    plt.legend(title = feature, fontsize=15, title_fontsize=15)
    plt.show()
```

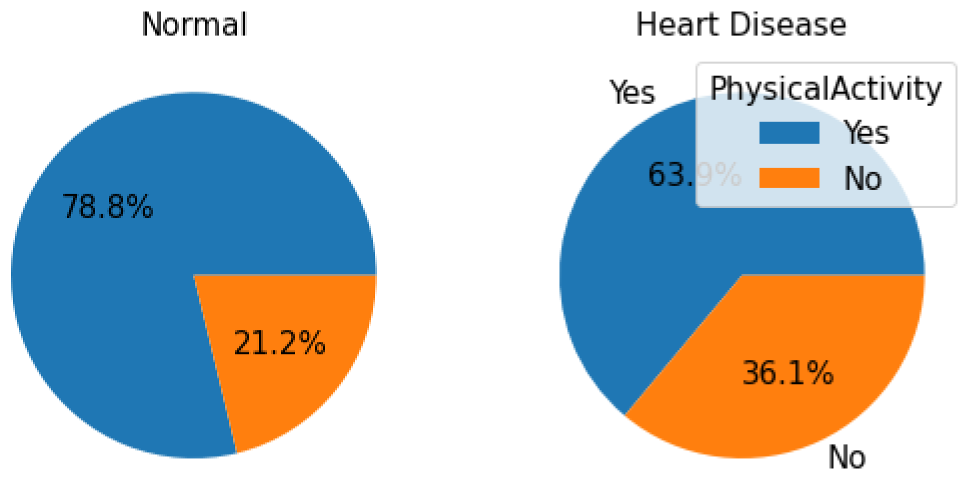

Normal
60.4%
39.6%
Heart Disease
Yes
58.6%
41.4%
No
Smoking
🟦 Yes
🟧 No

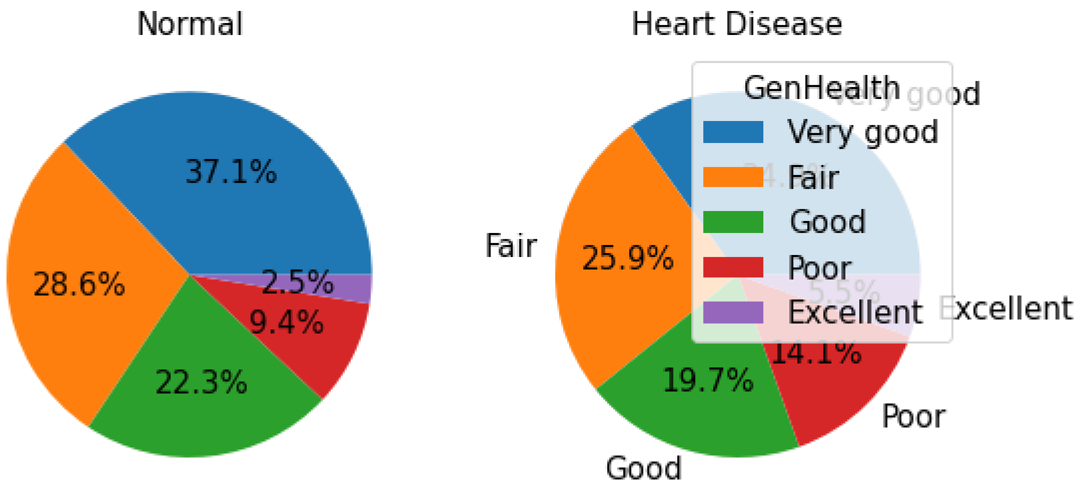

Normal
92.9%
7.1%
Heart Disease
AlcoholDrinking
🟦 No
🟧 Yes
No
95.8%
4.2%
Yes

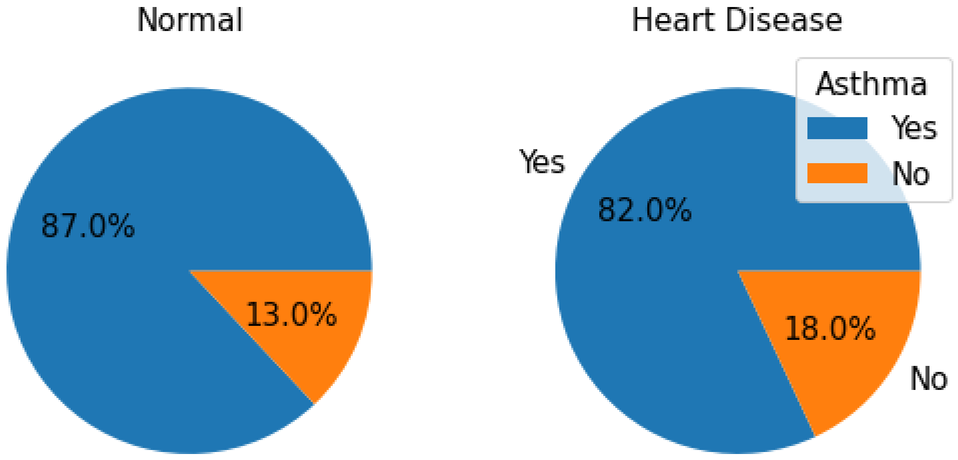

Normal
97.4%
2.6%
Heart Disease
Stroke
No
Yes
No
84.0%
16.0%
Yes

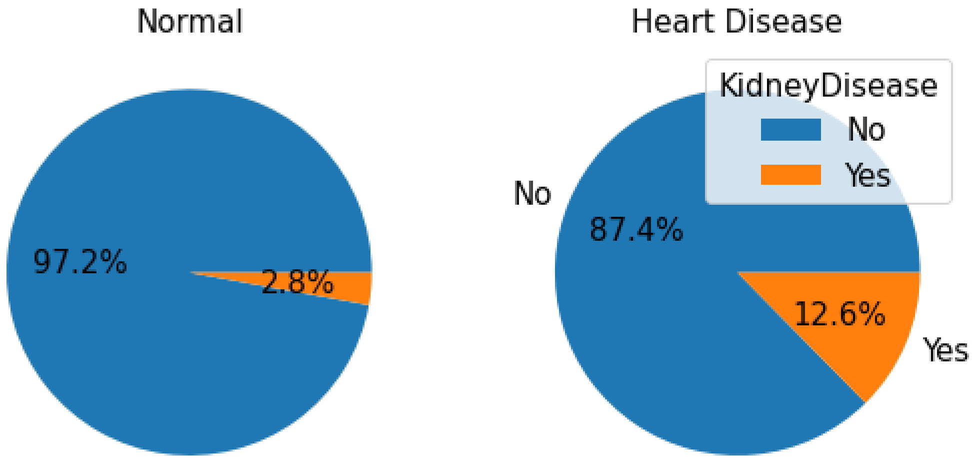

Normal
88.2%
11.8%
Heart Disease
DiffWalking
No
Yes
No
63.4%
36.6%
Yes

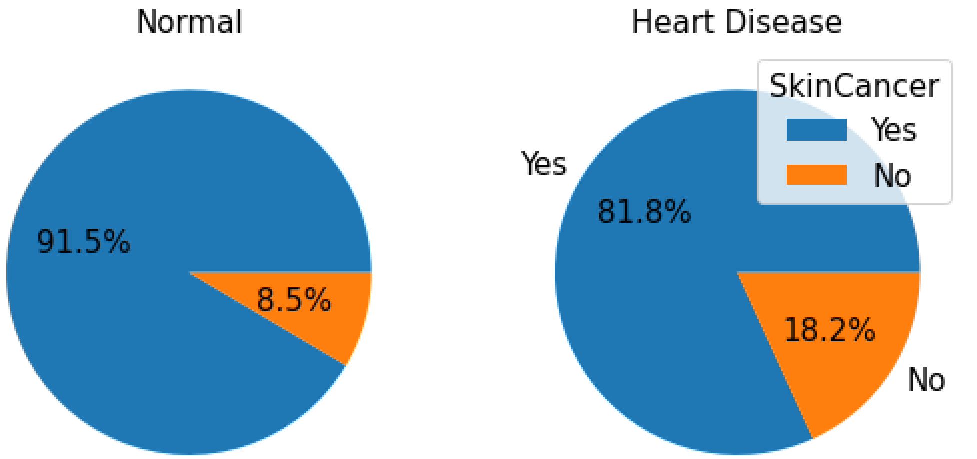

Normal
53.5%
46.5%
Heart Disease
Female
59.0%
41.0%
Male
Sex
🟦 Female
🟧 Male


Normal
78.8%
21.2%
Heart Disease
Yes
63.9%
36.1%
No
PhysicalActivity
🟦 Yes
🟧 No


Normal
37.1%
28.6%
2.5%
9.4%
22.3%
Heart Disease
GenHealth
🟦 Very good
🟧 Fair
🟩 Good
🟥 Poor
🟪 Excellent
Very good
Fair
25.9%
5.5%
Excellent
14.1%
19.7%
Poor
Good

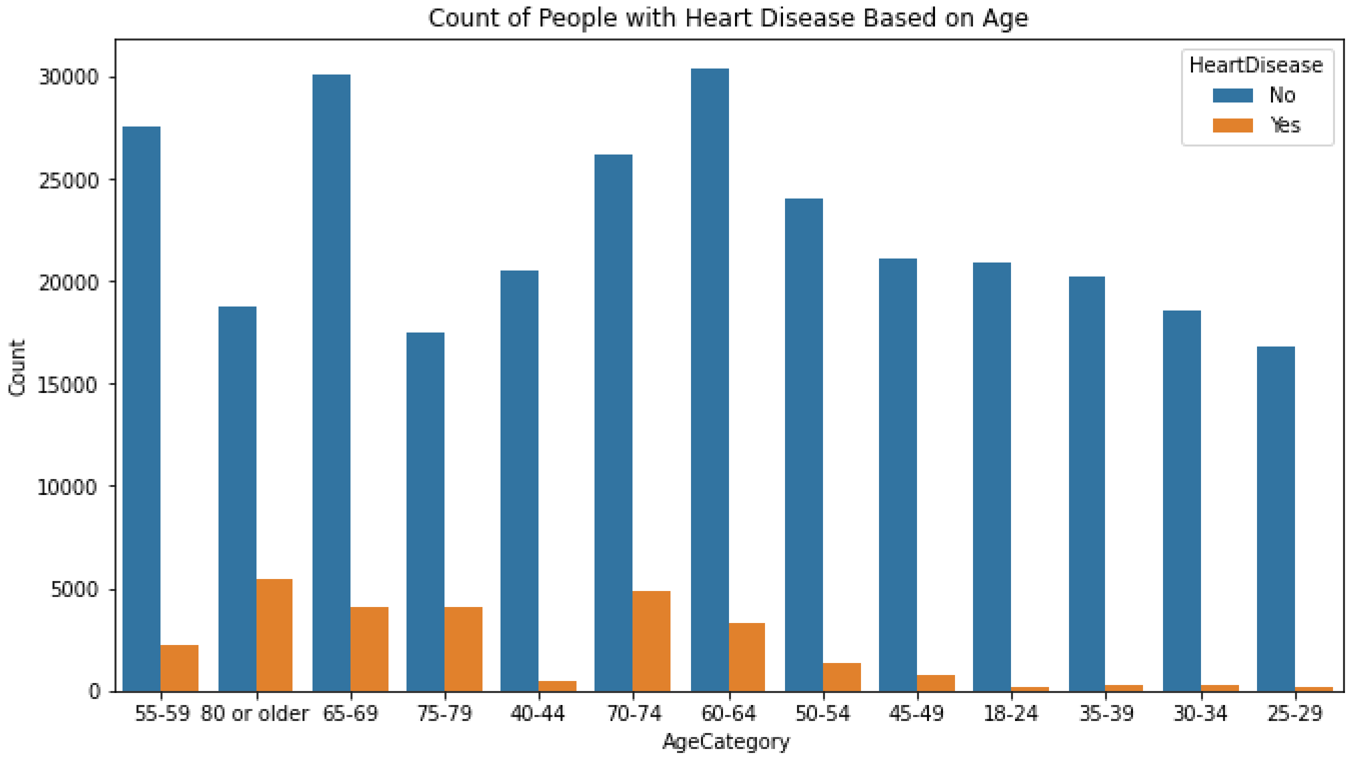

Normal
87.0%
13.0%
Heart Disease
Asthma
🟦 Yes
🟧 No
Yes
82.0%
18.0%
No


Normal
97.2%
2.8%
Heart Disease
KidneyDisease
No
Yes
No
87.4%
12.6%
Yes


Normal
91.5%
8.5%
Heart Disease
SkinCancer
Yes
No
Yes
81.8%
18.2%
No

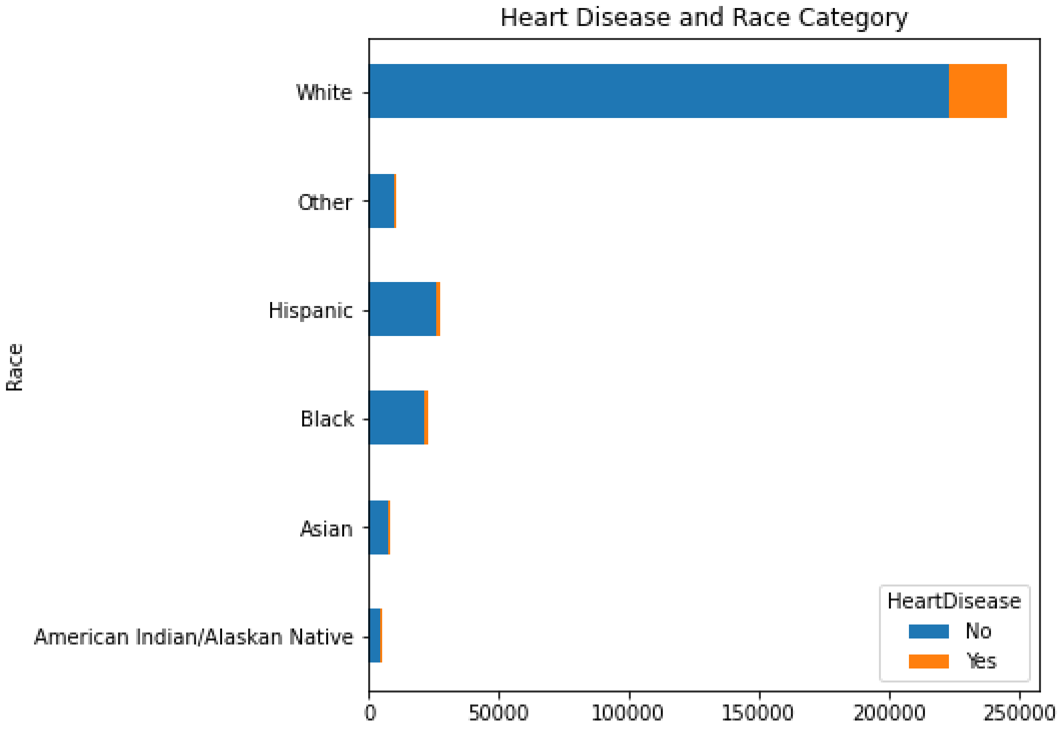
In [176]:

```
plt.figure(figsize = (11,6))
sns.countplot(x = heart_df['AgeCategory'], hue = 'HeartDisease', data = heart_df)
plt.title("Count of People with Heart Disease Based on Age")
plt.ylabel('Count')
plt.show()
```

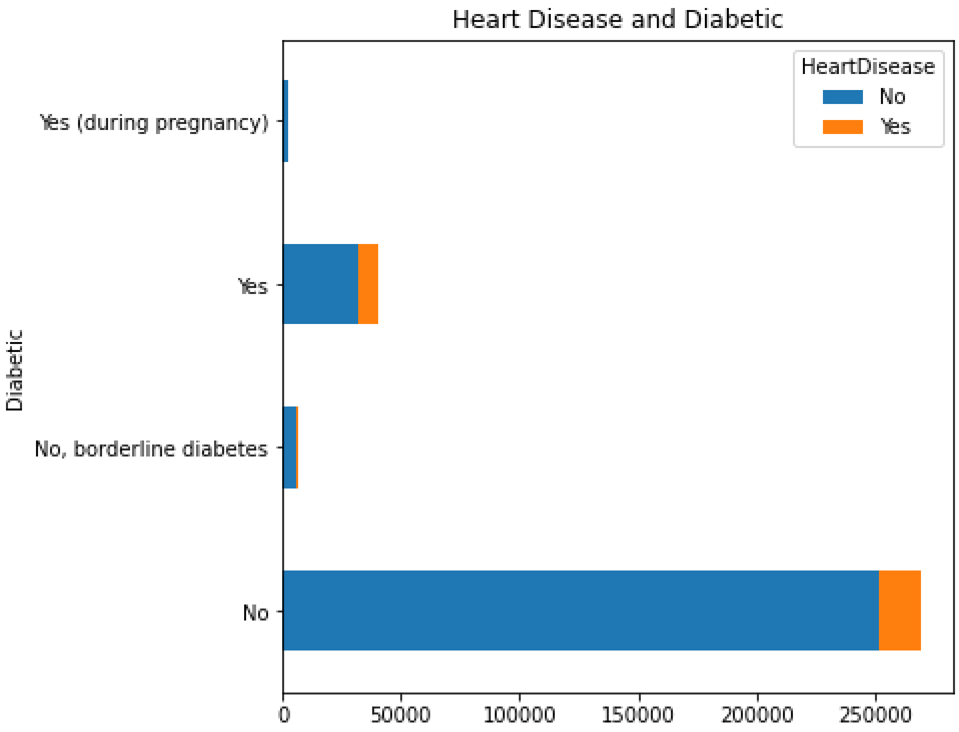


In [177]:

```
age_h=pd.DataFrame(pd.crosstab(heart_df["Race"],heart_df["HeartDisease"])).reset_index()
ax=age_h.plot(x="Race",kind='barh', stacked=True, title='Heart Disease and Race Category',figsize=(6,6))
```



```
In [178]: age_h=pd.DataFrame(pd.crosstab(heart_df["Diabetic"],heart_df["HeartDisease"])).reset_index()
          ax=age_h.plot(x="Diabetic",kind='barh', stacked=True, title='Heart Disease and Diabetic',figsize=(6,6))
```



Aggregate Relationship

In [164]:

```
r = heart_df.groupby(['HeartDisease','Stroke'])[['BMI']].aggregate(['median','min','mean'])
r
```

Out[164]:

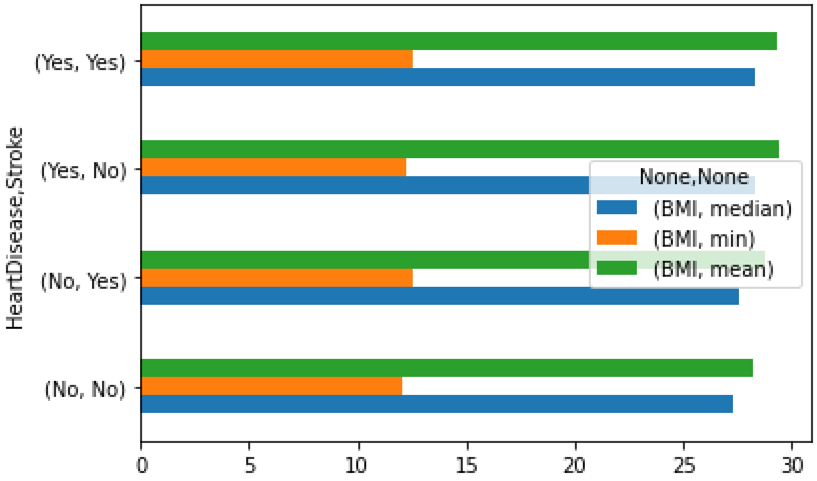
		BMI		
		median	min	mean
HeartDisease	Stroke			
No	No	27.25	12.02	28.210930
	Yes	27.60	12.53	28.733646
Yes	No	28.34	12.21	29.410951
	Yes	28.34	12.48	29.352581

In [165]:

```
r.plot(kind='barh')
```

Out[165]:

```
<AxesSubplot:ylabel='HeartDisease,Stroke'>
```



from the above plot people with BMI value Higher than '28' has high probablity of getting a heart disease and stroke.

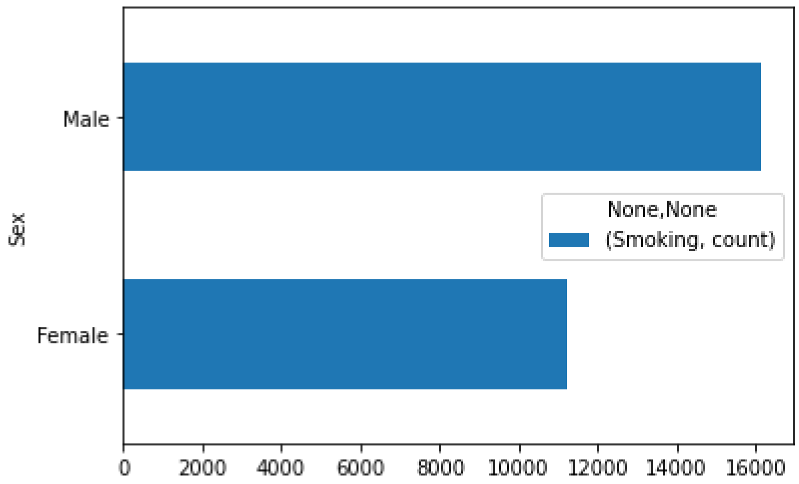
In [219]:
```
r1 = heart_df[heart_df["HeartDisease"]=='Yes'].groupby(['Sex'])[['Smoking']].aggregate(['count'])
r1
```

Out[219]:

	Smoking
	count
Sex	
Female	11234
Male	16139

In [221]:
```
r1.plot(kind='barh')
```

Out[221]:
```
<AxesSubplot:ylabel='Sex'>
```

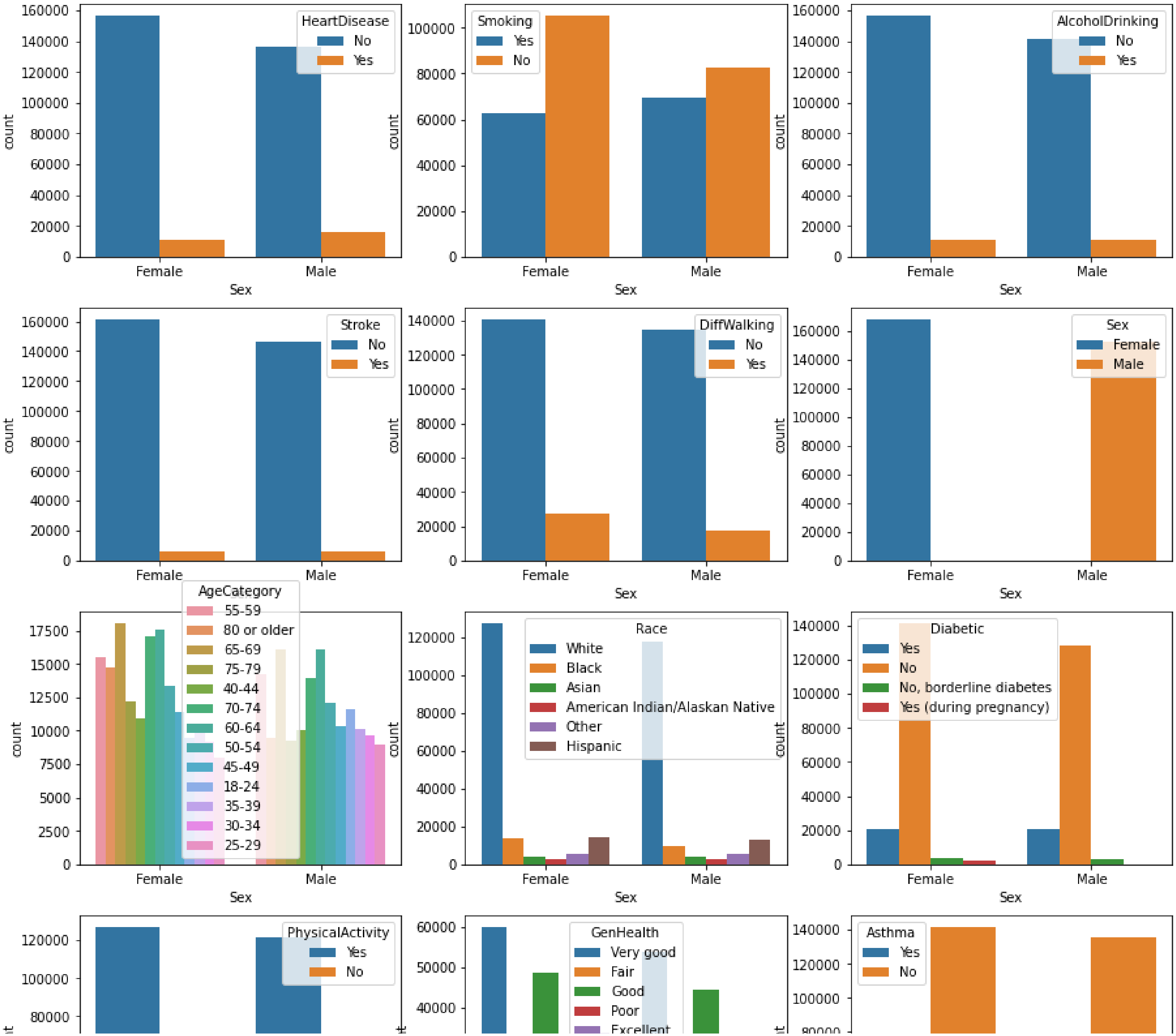


From the results male adults who have heart disease smoke more than female peers.

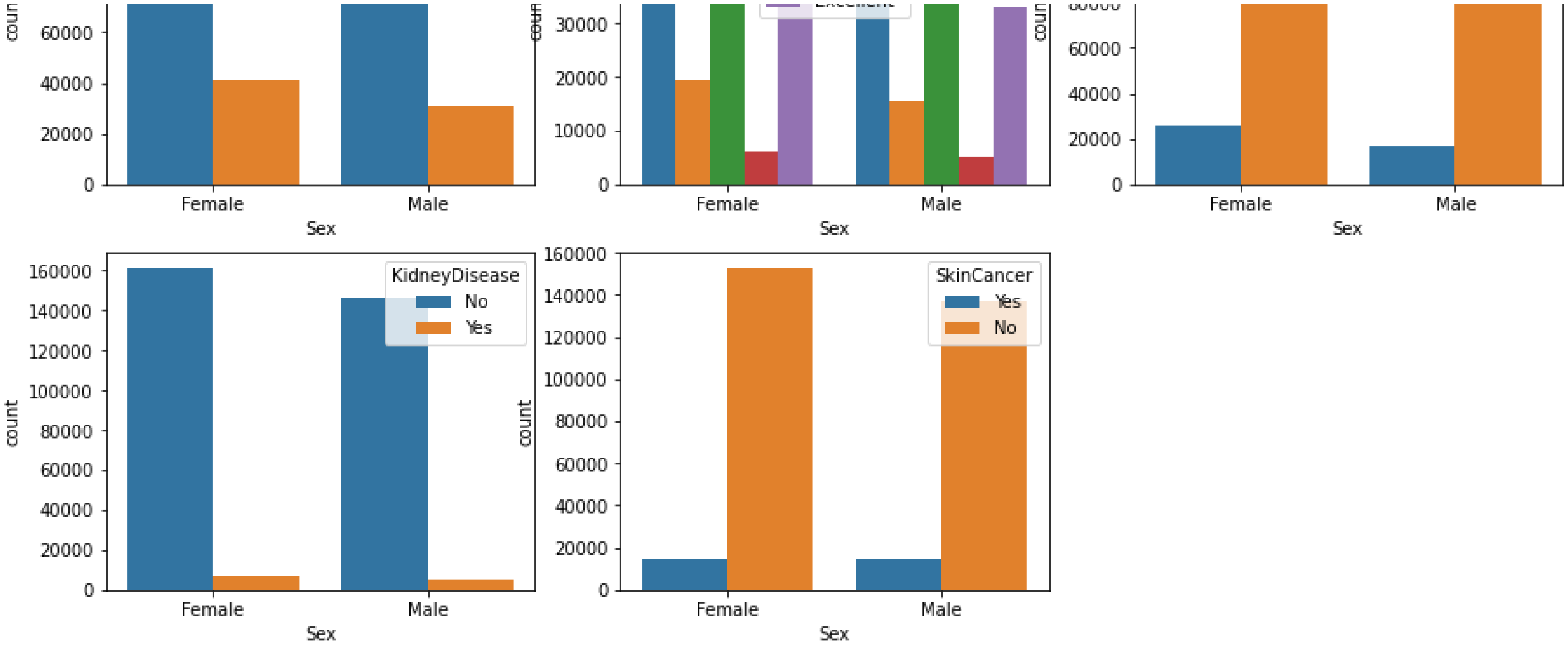
Analyzing the Distribution of Categorical variables depending on gender

In [21]:

```
size = 1
plt.figure(figsize = (15,25))
for feature in categorical_features:
    plt.subplot(6,3,size)
    sns.countplot(x = 'Sex',hue = heart_df[feature] , data = heart_df)
    size = size+1
```



160000
140000
120000
100000
80000
60000
40000
20000
0
count
Female
Male
Sex
HeartDisease
No
Yes
100000
80000
60000
40000
20000
0
count
Female
Male
Sex
Smoking
Yes
No
160000
140000
120000
100000
80000
60000
40000
20000
0
count
Female
Male
Sex
AlcoholDrinking
No
Yes
160000
140000
120000
100000
80000
60000
40000
20000
0
count
Female
Male
Stroke
No
Yes
140000
120000
100000
80000
60000
40000
20000
0
count
Female
Male
Sex
DiffWalking
No
Yes
160000
140000
120000
100000
80000
60000
40000
20000
0
count
Female
Male
Sex
Sex
Female
Male
17500
15000
12500
10000
7500
5000
2500
0
count
Female
Male
Sex
AgeCategory
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
120000
100000
80000
60000
40000
20000
0
count
Female
Male
Sex
Race
White
Black
Asian
American Indian/Alaskan Native
Other
Hispanic
140000
120000
100000
80000
60000
40000
20000
0
count
Female
Male
Sex
Diabetic
Yes
No
No, borderline diabetes
Yes (during pregnancy)
120000
100000
80000
PhysicalActivity
Yes
No
60000
50000
40000
GenHealth
Very good
Fair
Good
Poor
Excellent
140000
120000
100000
80000
Asthma
Yes
No



Summary

My conclusions after performing basic data analysis on dataset for predicting responsible key-features for having "Heart Disease" are:

The adults whose age is greater than or euqal to 80 have higher chances of getting a heart disease. In overall Dataset, most people who are diagnosed with heart disease are smokers and in that, percentage of male adults is high. White and Black people seem to have higher chance of getting heart disease. I did not see any relationship between heart disease and people who are Heavy drinkers/ asthma patients. Diabetic adults seem to have more chances of getting heart disease. However, the dataset is highly unbalanced and because of this some conculsions/plots needed to be further investiged and I'm hoping that by applying sampling techinques on dataset we can achieve noticable relationships between some features.