

HEALTHCARE ANALYSIS ON HEART DISEASE DATA

```
# IMPORTING DATA AND EXPLORING DATA

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

from pylab import rcParams
rcParams['figure.figsize'] = (6, 4)
sns.set_style('whitegrid')

from sklearn.metrics import accuracy_score, classification_report,
confusion_matrix

import warnings
warnings.filterwarnings('ignore')

hd = pd.read_csv(r"C:\ProgramData\MySQL\MySQL Server 8.0\Uploads\Heart_new2.csv")

hd.head()

   HeartDisease    BMI  Smoking  AlcoholDrinking  Stroke
PhysicalHealth \
0            No  16.60      Yes                  No      No          3
1            No  20.34      No                   No     Yes          0
2            No  26.58      Yes                  No      No         20
3            No  24.21      No                   No      No          0
4            No  23.71      No                   No      No         28

   MentalHealth  DiffWalking      Sex AgeCategory    Race Diabetic \
0            30           No  Female  55-59  White    Yes
1             0           No  Female  80 or older  White    No
2            30           No   Male  65-69  White    Yes
3             0           No  Female  75-79  White    No
4             0           Yes  Female  40-44  White    No

   PhysicalActivity  GenHealth  SleepTime Asthma KidneyDisease
SkinCancer
```

```

0      Yes  Very good      5      Yes      No
Yes
1      Yes  Very good      7      No      No
No
2      Yes      Fair      8      Yes      No
No
3      No       Good      6      No      No
Yes
4      Yes  Very good      8      No      No
No

```

```
hd.info()
```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4500 entries, 0 to 4499
Data columns (total 18 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   HeartDisease    4500 non-null    object 
 1   BMI              4500 non-null    float64
 2   Smoking          4500 non-null    object 
 3   AlcoholDrinking 4500 non-null    object 
 4   Stroke           4500 non-null    object 
 5   PhysicalHealth   4500 non-null    int64  
 6   MentalHealth     4500 non-null    int64  
 7   DiffWalking      4500 non-null    object 
 8   Sex              4500 non-null    object 
 9   AgeCategory      4500 non-null    object 
 10  Race             4500 non-null    object 
 11  Diabetic         4500 non-null    object 
 12  PhysicalActivity 4500 non-null    object 
 13  GenHealth        4500 non-null    object 
 14  SleepTime        4500 non-null    int64  
 15  Asthma           4500 non-null    object 
 16  KidneyDisease   4500 non-null    object 
 17  SkinCancer       4500 non-null    object 
dtypes: float64(1), int64(3), object(14)
memory usage: 632.9+ KB

```

```
hd.shape
```

```
(4500, 18)
```

```
hd.columns
```

```

Index(['HeartDisease', 'BMI', 'Smoking', 'AlcoholDrinking', 'Stroke',
       'PhysicalHealth', 'MentalHealth', 'DiffWalking', 'Sex',
       'AgeCategory',
       'Race', 'Diabetic', 'PhysicalActivity', 'GenHealth',
       'SleepTime',

```

```

'Asthma', 'KidneyDisease', 'SkinCancer'],
dtype='object')

type(hd)
pandas.core.frame.DataFrame

hd.isnull().sum()

HeartDisease      0
BMI               0
Smoking           0
AlcoholDrinking   0
Stroke            0
PhysicalHealth    0
MentalHealth      0
DiffWalking        0
Sex               0
AgeCategory       0
Race              0
Diabetic          0
PhysicalActivity  0
GenHealth          0
SleepTime          0
Asthma            0
KidneyDisease     0
SkinCancer         0
dtype: int64

hd.head()

   HeartDisease      BMI  Smoking  AlcoholDrinking  Stroke
PhysicalHealth \
0           No    16.60      Yes                No      No          3
1           No    20.34      No                  No      Yes          0
2           No    26.58      Yes                No      No         20
3           No    24.21      No                  No      No          0
4           No    23.71      No                  No      No         28

   MentalHealth  DiffWalking  Sex  AgeCategory  Race  Diabetic \
0            30          No  Female    55-59  White    Yes
1             0          No  Female  80 or older  White    No
2            30          No   Male    65-69  White    Yes
3             0          No  Female    75-79  White    No
4             0          Yes Female   40-44  White    No

```

	PhysicalActivity	GenHealth	SleepTime	Asthma	KidneyDisease
SkinCancer					
0	Yes	Very good	5	Yes	No
Yes					
1	Yes	Very good	7	No	No
No					
2	Yes	Fair	8	Yes	No
No					
3	No	Good	6	No	No
Yes					
4	Yes	Very good	8	No	No
No					

EDA (Exploratory Data Analysis)

Using Data Visualization

1.age: Patients age in years

2.sex : Female or male (1-Male,0-Female)

3.cp :Chest pain (1- Typical Angina, 2-Atypical Angina,3-Non- anginal pain, 4-Asymptomatic)

4.trestbp: Resting BloodPressure

5.chol :Cholestrol

6.fbs : Fasting Blood Sugar(>120 mg/dl, 1-True, 0 - False)

7.restecg : Resting electrocardiographic measurement (0 = normal, 1 = having ST-T wave abnormality, 2 = showing probable or definite left ventricular hypertrophy by Estes' criteria)

8.thalach :The person's maximum heart rate achieved

9.exang : Exercise induced angina (1 = yes; 0 = no)

10.oldpeak: ST depression induced by exercise relative to rest ('ST' relates to positions on the ECG plot. See more here)

11.slope : the slope of the peak exercise ST segment (Value 1: upsloping, Value 2: flat, Value 3: downsloping)

12.ca :The number of major vessels (0-3)

13.thal : A blood disorder called thalassemia (3 = normal; 6 = fixed defect; 7 = reversable defect)

14.target : Heart disease (0 = no, 1 = yes)

```
hd.describe()
```

```

          BMI  PhysicalHealth  MentalHealth  SleepTime
count  4500.000000  4500.000000  4500.000000  4500.000000
mean   29.340040    4.105111    4.439778    7.043333
std    6.676625    8.573743    8.593363    1.595765
min   12.480000    0.000000    0.000000    1.000000
25%  24.687500    0.000000    0.000000    6.000000
50%  28.250000    0.000000    0.000000    7.000000
75%  33.000000    3.000000    5.000000    8.000000
max   75.820000   30.000000   30.000000   20.000000

pd.set_option('display.float_format','{:,.2f}'.format)

hd.describe()

          BMI  PhysicalHealth  MentalHealth  SleepTime
count  4500.00        4500.00        4500.00        4500.00
mean   29.34         4.11         4.44         7.04
std    6.68          8.57         8.59         1.60
min   12.48          0.00          0.00         1.00
25%  24.69          0.00          0.00         6.00
50%  28.25          0.00          0.00         7.00
75%  33.00          3.00          5.00         8.00
max   75.82         30.00         30.00        20.00

hd['HeartDisease'].value_counts()

HeartDisease
No      4017
Yes     483
Name: count, dtype: int64

hd.shape
(4500, 18)

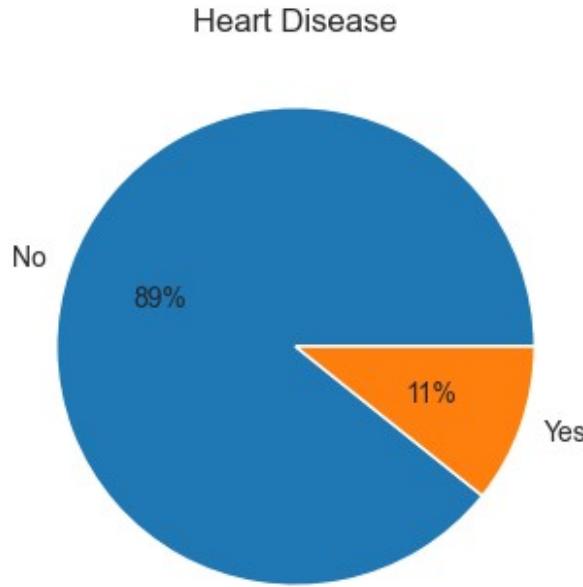
hd['HeartDisease'].value_counts()/hd.shape[0]*100

HeartDisease
No      89.27
Yes     10.73
Name: count, dtype: float64

# percentage of positive and negative heart diseases
labels = hd['HeartDisease'].value_counts().index
values = hd['HeartDisease'].value_counts().values

plt.pie(values, labels=labels, autopct='%.1f%%')
plt.title('Heart Disease')
plt.show()

```



Histogram plot for all feature

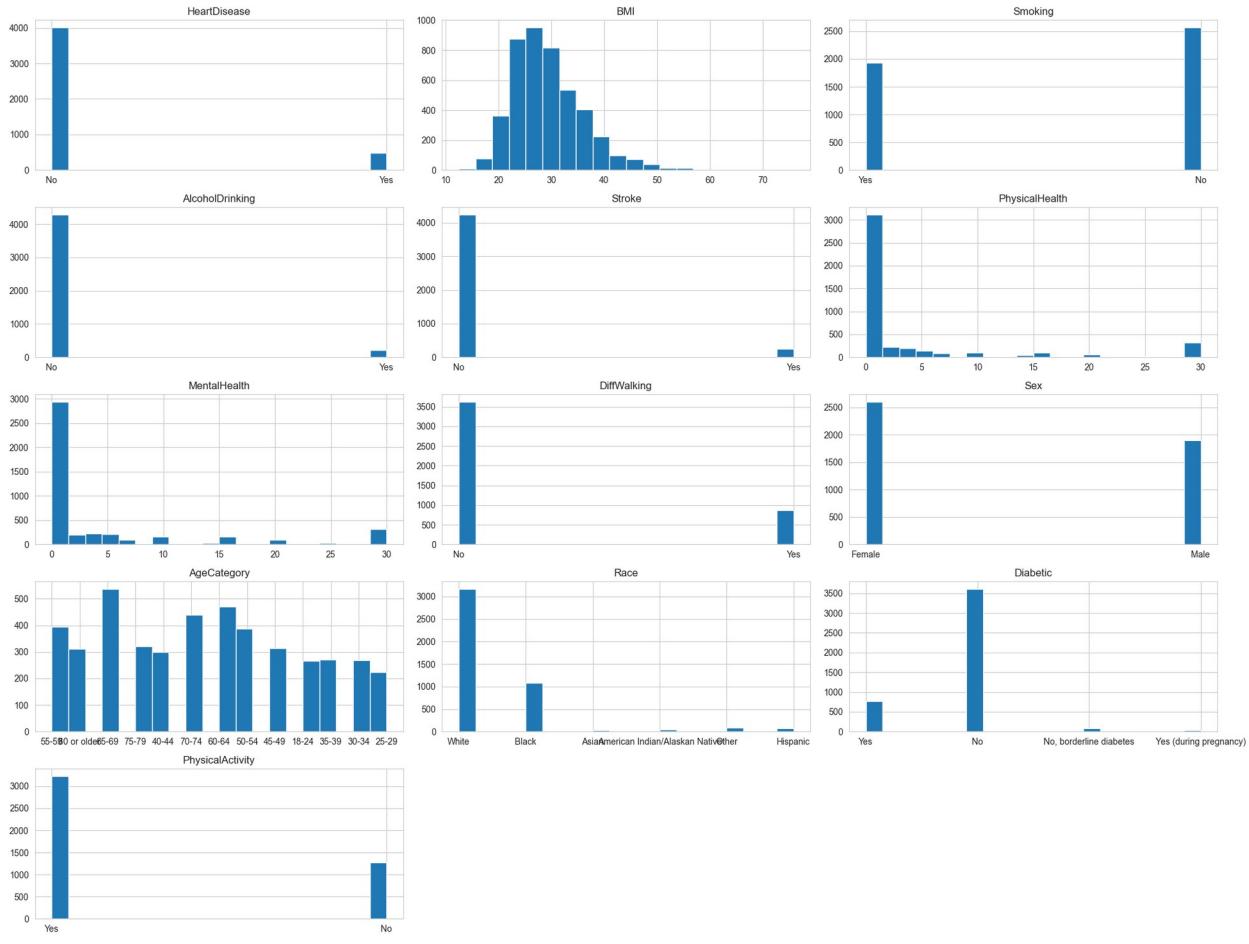
```
import itertools
import math
import matplotlib.pyplot as plt
import itertools

col = hd.columns[:13]
plt.figure(figsize=(20, 15))

length = len(col)
rows = math.ceil(length / 3)

for j, i in enumerate(col):
    plt.subplot(rows, 3, j + 1)
    hd[i].hist(bins=20)
    plt.title(i)

plt.tight_layout()
plt.show()
```



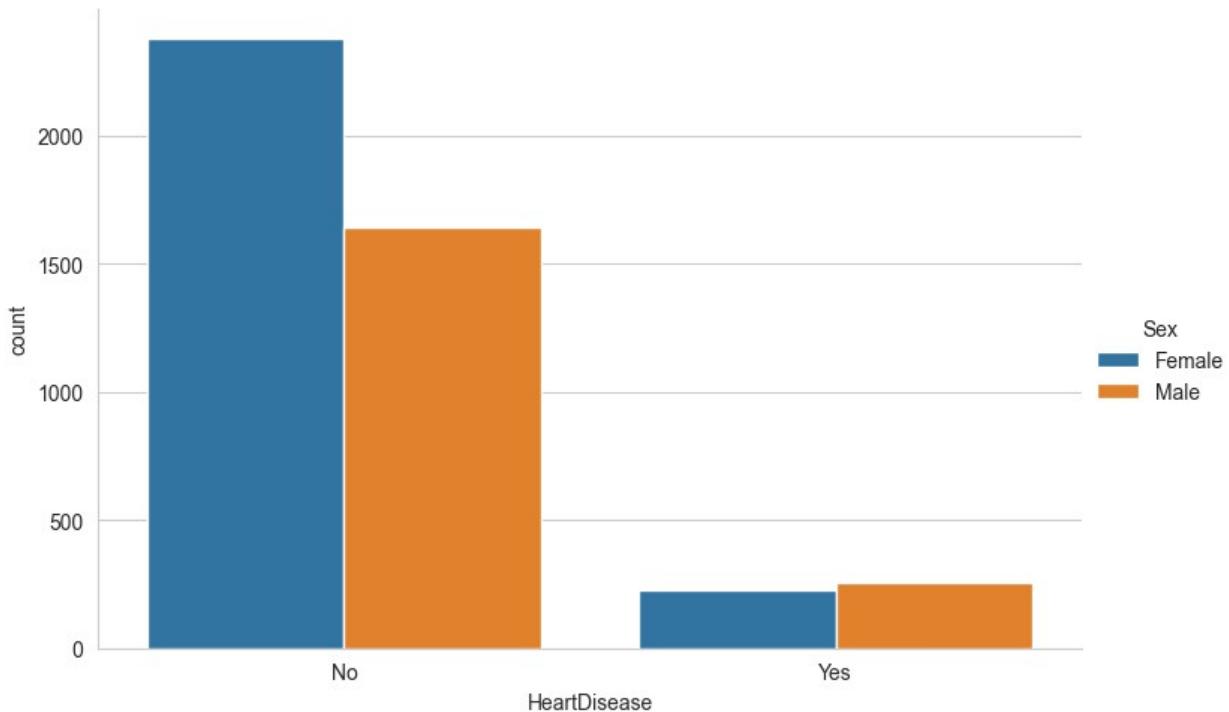
```

import seaborn as sns
import matplotlib.pyplot as plt

sns.catplot(
    x='HeartDisease',
    data=hd,
    hue='Sex',
    kind='count',
    height=5,
    aspect=1.5
)

plt.show()

```



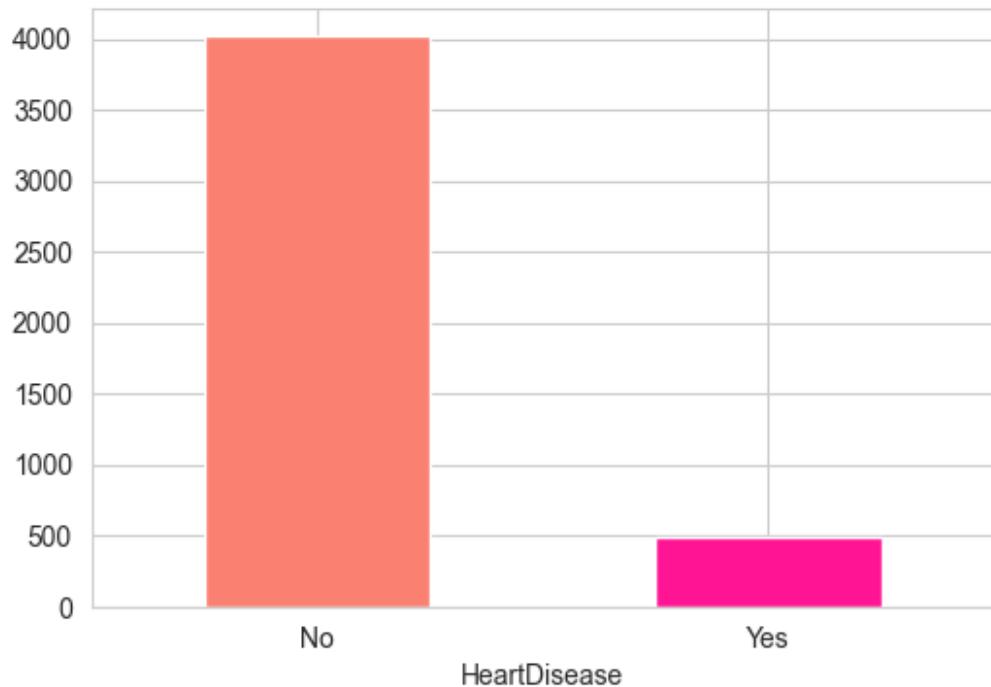
```
hd.rename(columns={'Sex': 'sex'}, inplace=True)
hd['sex'].value_counts()

sex
Female    2604
Male      1896
Name: count, dtype: int64
```

From the above Histogram plots we can conclude Age, Cholesterol, Resting blood pressure and person's maximum heart rate achieved plays major role in detection of Heart Disease.

From the another plot we can conclude that number of men are majorly having Heart disease than compared to females. And also men are more healthier than females

```
hd['HeartDisease'].value_counts().plot(kind='bar', color=["salmon", "deeppink"])
plt.xticks(rotation=0)
plt.show()
```



```
# Possibility of having Heart Disease
#Creating a Function for unique values in data
categorical_values = []
for column in hd.columns:
    print('=====')
    print(f'{column} : {hd[column].unique()}')
    if len(hd[column].unique()) <= 10:
        categorical_values.append(column)

=====
HeartDisease : ['No' 'Yes']
=====
BMI : [16.6 20.34 26.58 ... 25.52 37.02 54.75]
=====
Smoking : ['Yes' 'No']
=====
AlcoholDrinking : ['No' 'Yes']
=====
Stroke : ['No' 'Yes']
=====
PhysicalHealth : [ 3  0 20 28  6 15  5 30  7  1  2 21  4 10 14 18  8
25 16 29 27 17 24 12
23 26 22 19  9 13]
=====
MentalHealth : [30  0  2  5 15  8  4  3 10 14 20  1  7 24  9 28 16 12
6 25 17 18 21 29
22 13 23 27]
=====
```

```
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']
=====
SleepTime : [ 5 7 8 6 12 4 9 10 15 3 2 1 16 18 14 20 11]
=====
Asthma : ['Yes' 'No']
=====
KidneyDisease : ['No' 'Yes']
=====
SkinCancer : ['Yes' 'No']

import seaborn as sns
import matplotlib.pyplot as plt

plt.figure(figsize=(12, 12))

for i, column in enumerate(categorical_values, 1):
    plt.subplot(3, 3, i)
    sns.barplot(data=hd, x=column, y='target')
    plt.ylabel('Possibility to have heart disease')
    plt.xlabel(column)

plt.tight_layout()
plt.show()

-----
-----
ValueError                                Traceback (most recent call
last)
Cell In[31], line 8
      6 for i, column in enumerate(categorical_values, 1):
      7     plt.subplot(3, 3, i)
----> 8     sns.barplot(data=hd, x=column, y='target')
      9     plt.ylabel('Possibility to have heart disease')
```

```
10     plt.xlabel(column)

File c:\Users\kumara swamy\AppData\Local\Programs\Python\Python313\
Lib\site-packages\seaborn\categorical.py:2341, in barplot(data, x, y,
hue, order, hue_order, estimator, errorbar, n_boot, seed, units,
weights, orient, color, palette, saturation, fill, hue_norm, width,
dodge, gap, log_scale, native_scale, formatter, legend, capsizer,
err_kws, ci, errcolor, errwidth, ax, **kwargs)
2338 if estimator is len:
2339     estimator = "size"
-> 2341 p = _CategoricalAggPlotter(
2342     data=data,
2343     variables=dict(x=x, y=y, hue=hue, units=units,
weight=weights),
2344     order=order,
2345     orient=orient,
2346     color=color,
2347     legend=legend,
2348 )
2350 if ax is None:
2351     ax = plt.gca()

File c:\Users\kumara swamy\AppData\Local\Programs\Python\Python313\
Lib\site-packages\seaborn\categorical.py:67, in
_CategoricalPlotter.__init__(self, data, variables, order, orient,
require_numeric, color, legend)
56 def __init__(
57     self,
58     data=None,
(...):
64     legend="auto",
65 ):
---> 67     super().__init__(data=data, variables=variables)
69     # This method takes care of some bookkeeping that is
necessary because the
70     # original categorical plots (prior to the 2021 refactor)
had some rules that
71     # don't fit exactly into VectorPlotter logic. It may be
wise to have a second
(...):
76     # default VectorPlotter rules. If we do decide to make
orient part of the
77     # _base variable assignment, we'll want to figure out how
to express that.
78     if self.input_format == "wide" and orient in ["h", "y"]:

File c:\Users\kumara swamy\AppData\Local\Programs\Python\Python313\
Lib\site-packages\seaborn\_base.py:634, in
VectorPlotter.__init__(self, data, variables)
629 # var_ordered is relevant only for categorical axis variables,
```

```
and may
  630 # be better handled by an internal axis information object
that tracks
  631 # such information and is set up by the scale_* methods. The
analogous
  632 # information for numeric axes would be information about log
scales.
  633 self._var_ordered = {"x": False, "y": False} # alt., used
DefaultDict
--> 634 self.assign_variables(data, variables)
  636 # TODO Lots of tests assume that these are called to
initialize the
  637 # mappings to default values on class initialization. I'd
prefer to
  638 # move away from that and only have a mapping when explicitly
called.
  639 for var in ["hue", "size", "style"]:

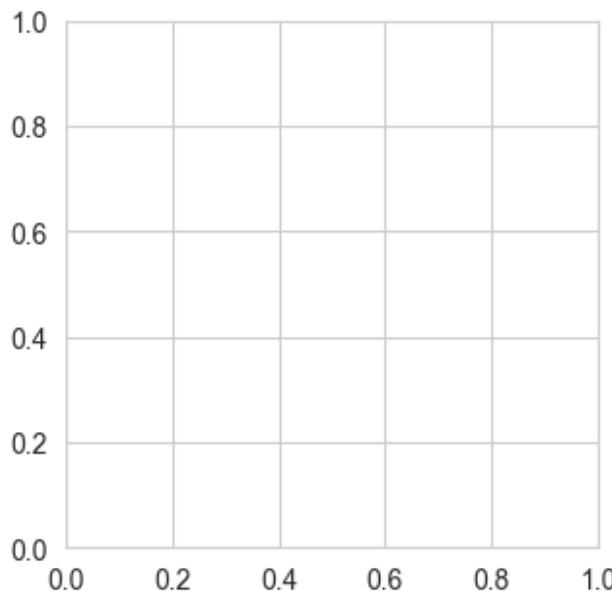
File c:\Users\kumara swamy\AppData\Local\Programs\Python\Python313\
Lib\site-packages\seaborn\_base.py:679, in
VectorPlotter.assign_variables(self, data, variables)
  674 else:
  675     # When dealing with long-form input, use the newer
PlotData
  676     # object (internal but introduced for the objects
interface)
  677     # to centralize / standardize data consumption logic.
  678     self.input_format = "long"
--> 679     plot_data = PlotData(data, variables)
  680     frame = plot_data.frame
  681     names = plot_data.names

File c:\Users\kumara swamy\AppData\Local\Programs\Python\Python313\
Lib\site-packages\seaborn\_core\data.py:58, in PlotData.__init__(self,
data, variables)
  51 def __init__(
  52     self,
  53     data: DataSource,
  54     variables: dict[str, VariableSpec],
  55 ):
  57     data = handle_data_source(data)
--> 58     frame, names, ids = self._assign_variables(data,
variables)
  60     self.frame = frame
  61     self.names = names

File c:\Users\kumara swamy\AppData\Local\Programs\Python\Python313\
Lib\site-packages\seaborn\_core\data.py:232, in
PlotData._assign_variables(self, data, variables)
  230     else:
```

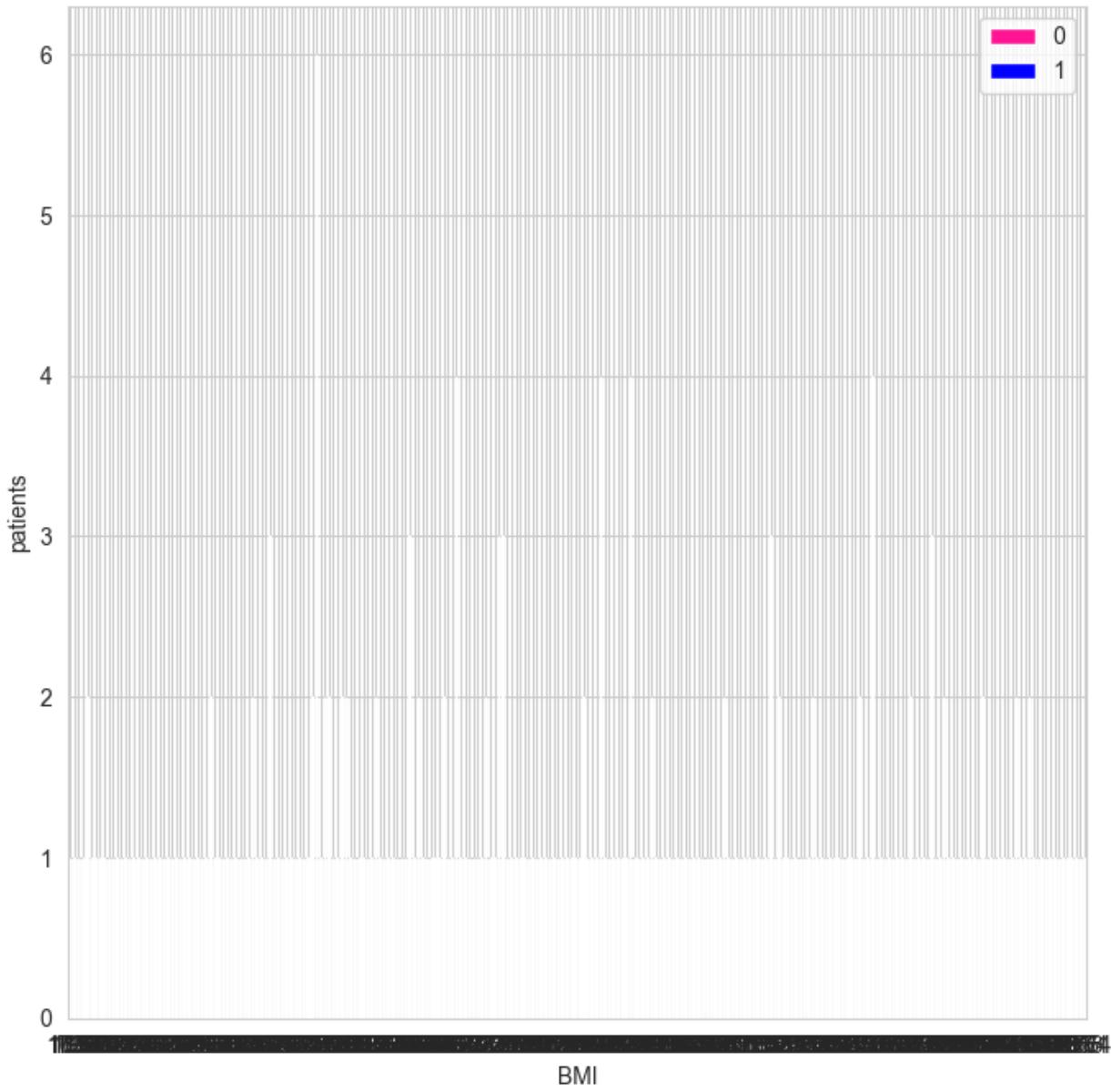
```
231         err += "An entry with this name does not appear in  
`data`."  
--> 232     raise ValueError(err)  
234 else:  
235  
236     # Otherwise, assume the value somehow represents data  
237  
238     # Ignore empty data structures  
239     if isinstance(val, Sized) and len(val) == 0:
```

ValueError: Could not interpret value `smoking` for `x`. An entry with this name does not appear in `data`.



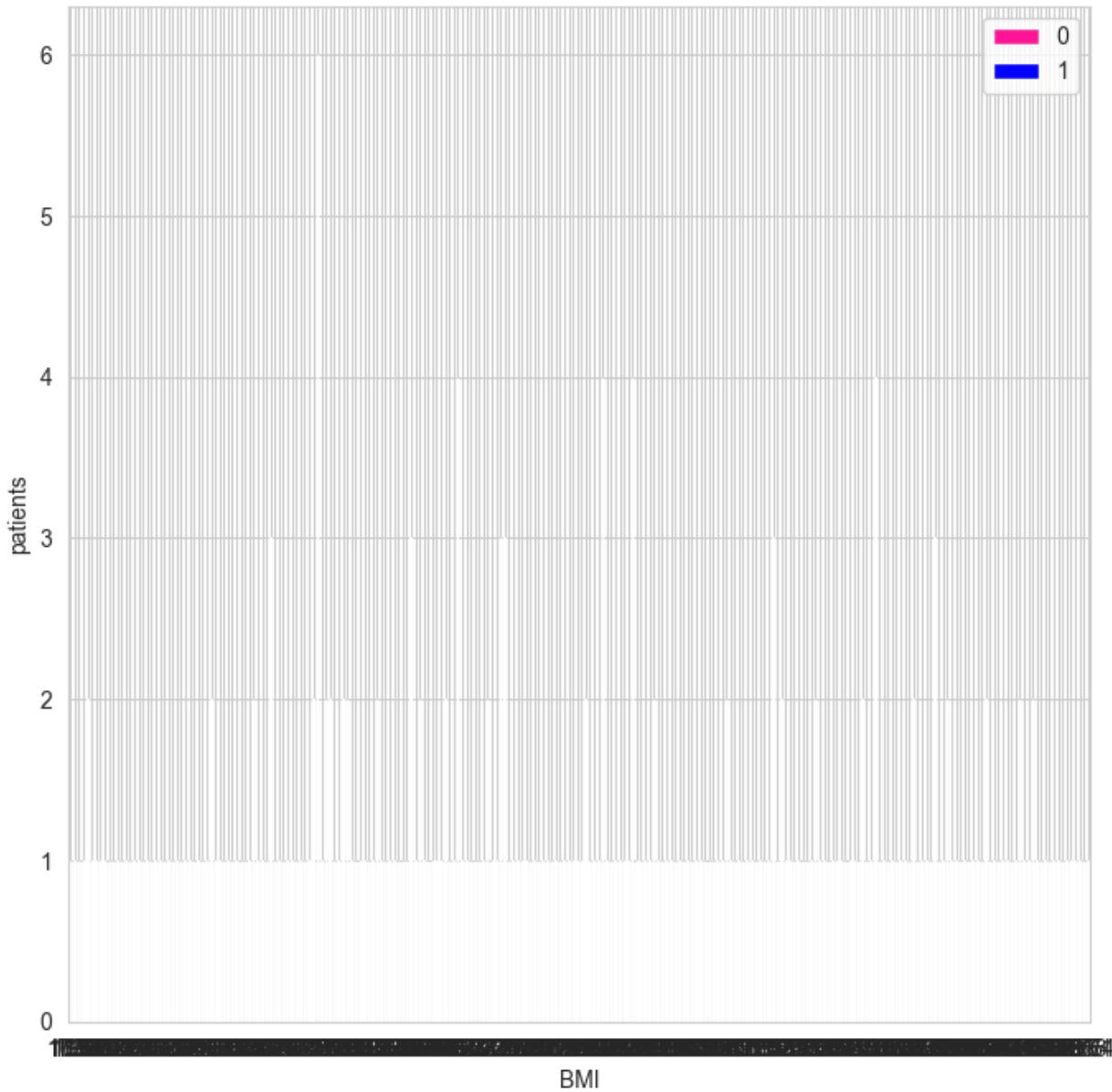
The possibility of having Heart Disease can be judged from the above barplots.

```
pd.crosstab(hd['BMI'][::15], hd['target']).plot(  
    kind="bar",  
    figsize=(8, 8),  
    color=["deeppink", "blue"]  
)  
  
plt.ylabel("patients")  
plt.xticks(rotation=0)  
plt.legend(['0', '1'])  
plt.show()
```



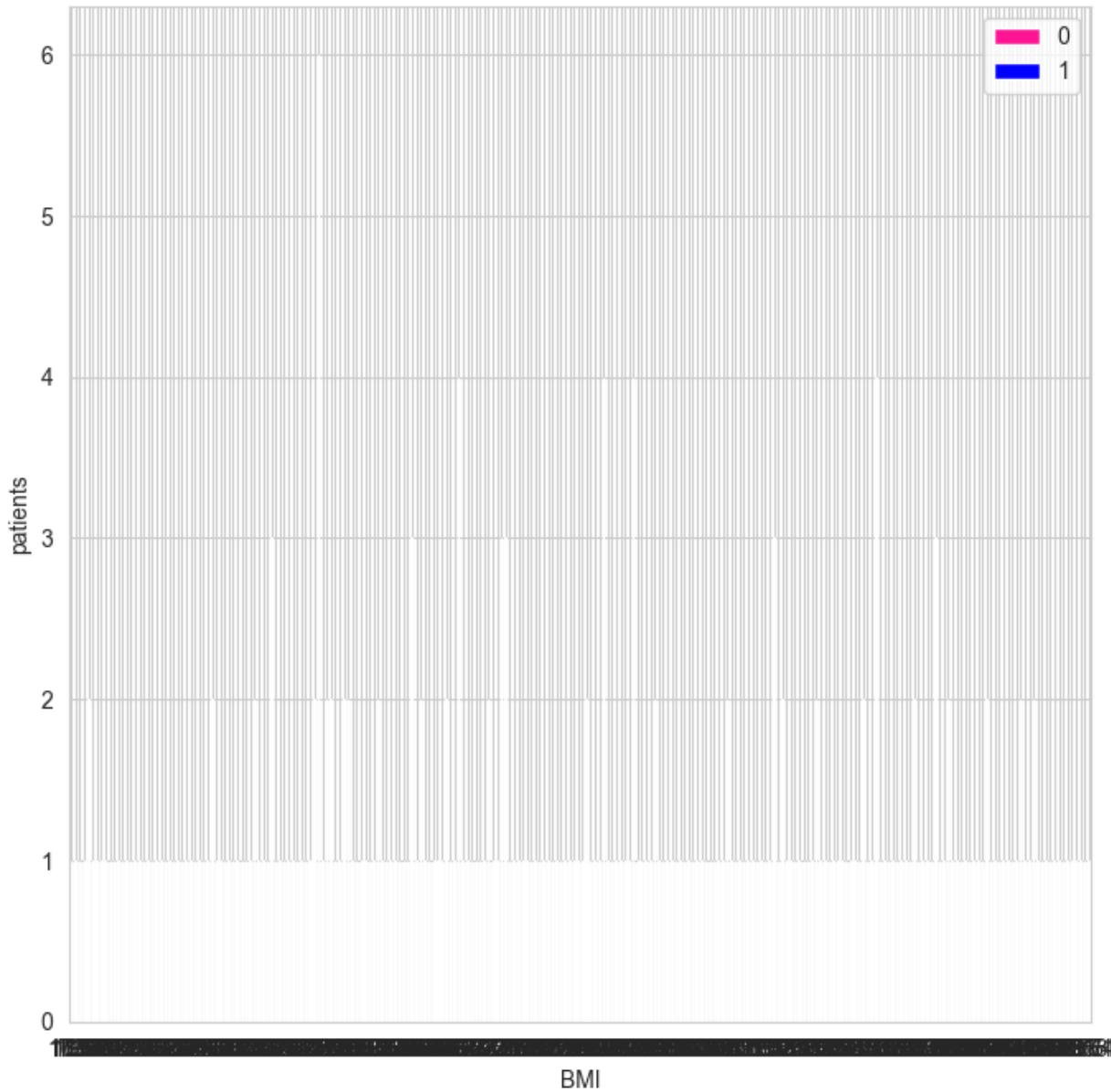
```
pd.crosstab(hd['BMI'][::15], hd['target']).plot(
    kind="bar",
    figsize=(8, 8),
    color=["deeppink", "blue"]
)

plt.ylabel("patients")
plt.xticks(rotation=0)
plt.legend(['0', '1'])
plt.show()
```

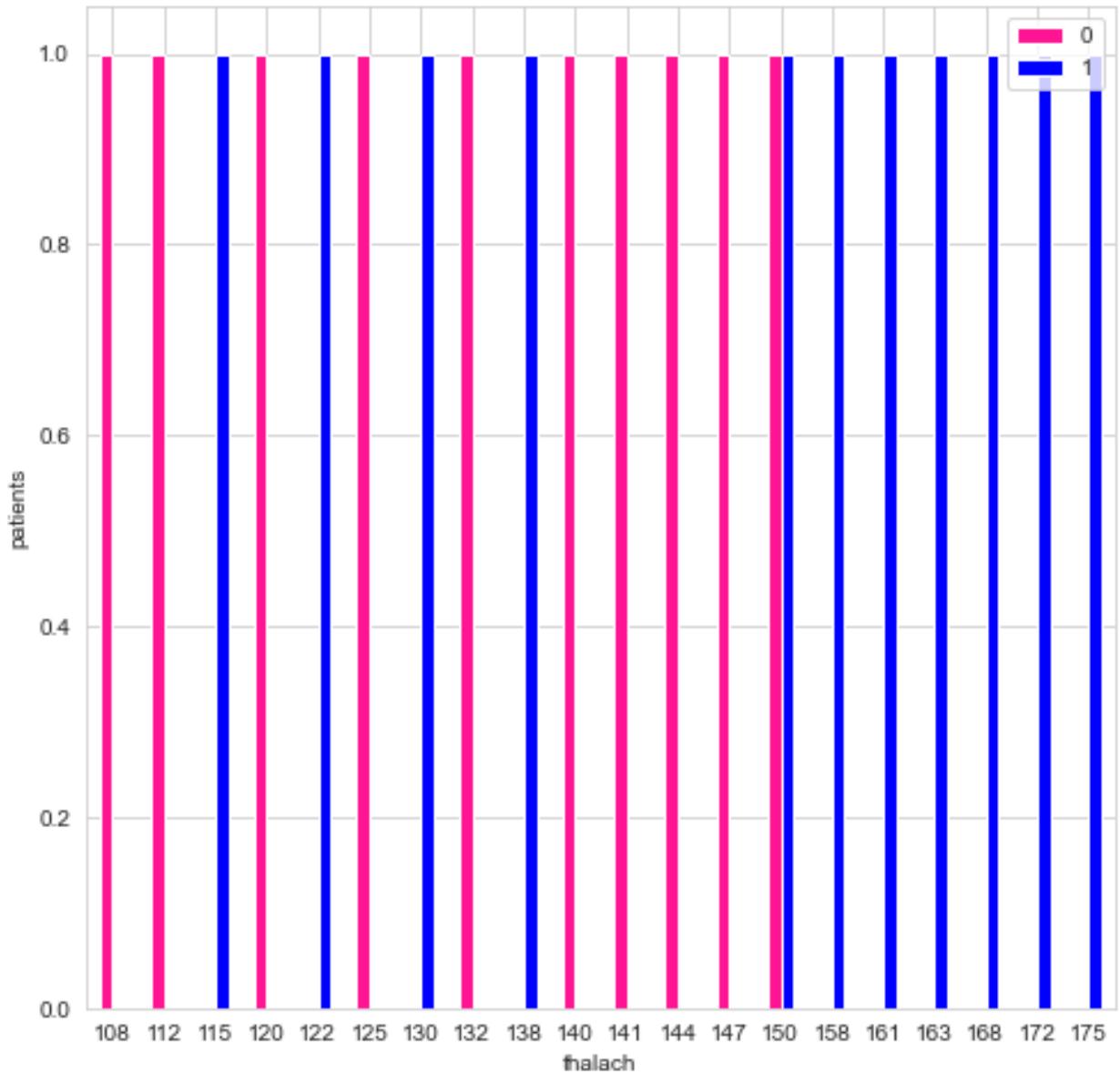


The above graph tells us that patients with Type 3 chest pain have heart disease. and very few Patients with 1 type chest pain have heart disease

```
pd.crosstab(hd['BMI'][::15], hd['target']).plot(  
    kind="bar",  
    figsize=(8, 8),  
    color=["deeppink", "blue"]  
)  
  
plt.ylabel("patients")  
plt.xticks(rotation=0)  
plt.legend(['0', '1'])  
plt.show()
```



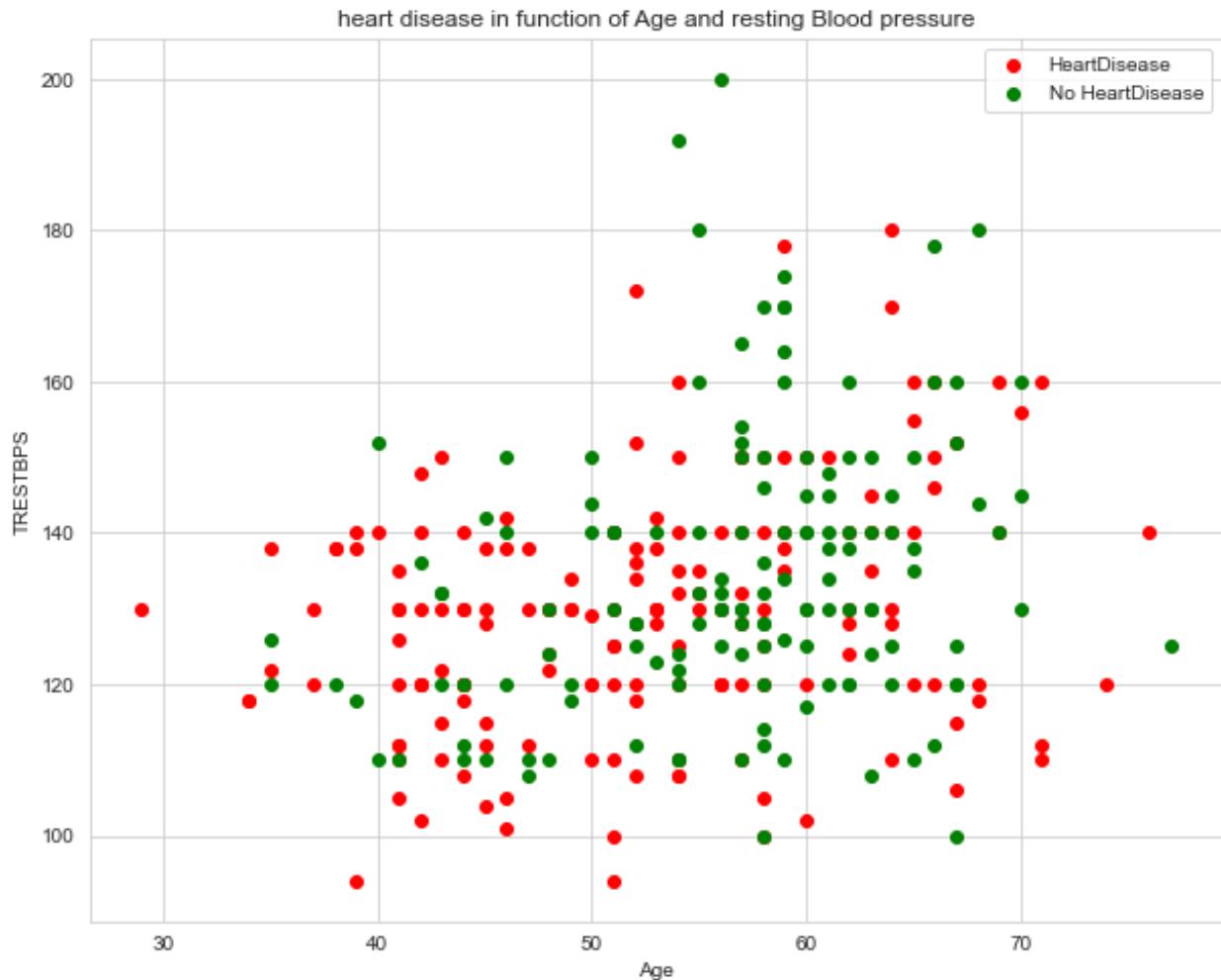
```
# Comparing maximum heart rate with target
pd.crosstab(hd.thalach[::-15],hd.target).plot(kind="bar",figsize=(8,8),
color=["deeppink","blue"])
plt.ylabel("patients");
plt.xticks(rotation=0);
plt.legend(['0', '1']);
```



```
# FINDING Heart Disease PEOPLE WITH restingBloodPressure AND AGE  
USING SCATTER PLOT
```

```
plt.figure(figsize=(10,8))  
plt.scatter(hd.age[hd.target==1],hd.trestbps[hd.target==1],color="Red")  
  
plt.scatter(hd.age[hd.target==0],hd.trestbps[hd.target==0],color="Green")  
  
plt.title("heart disease in function of Age and resting Blood  
pressure")  
plt.xlabel("Age")
```

```
plt.ylabel("TRESTBPS")
plt.legend(["HeartDisease", "No HeartDisease"]);
```

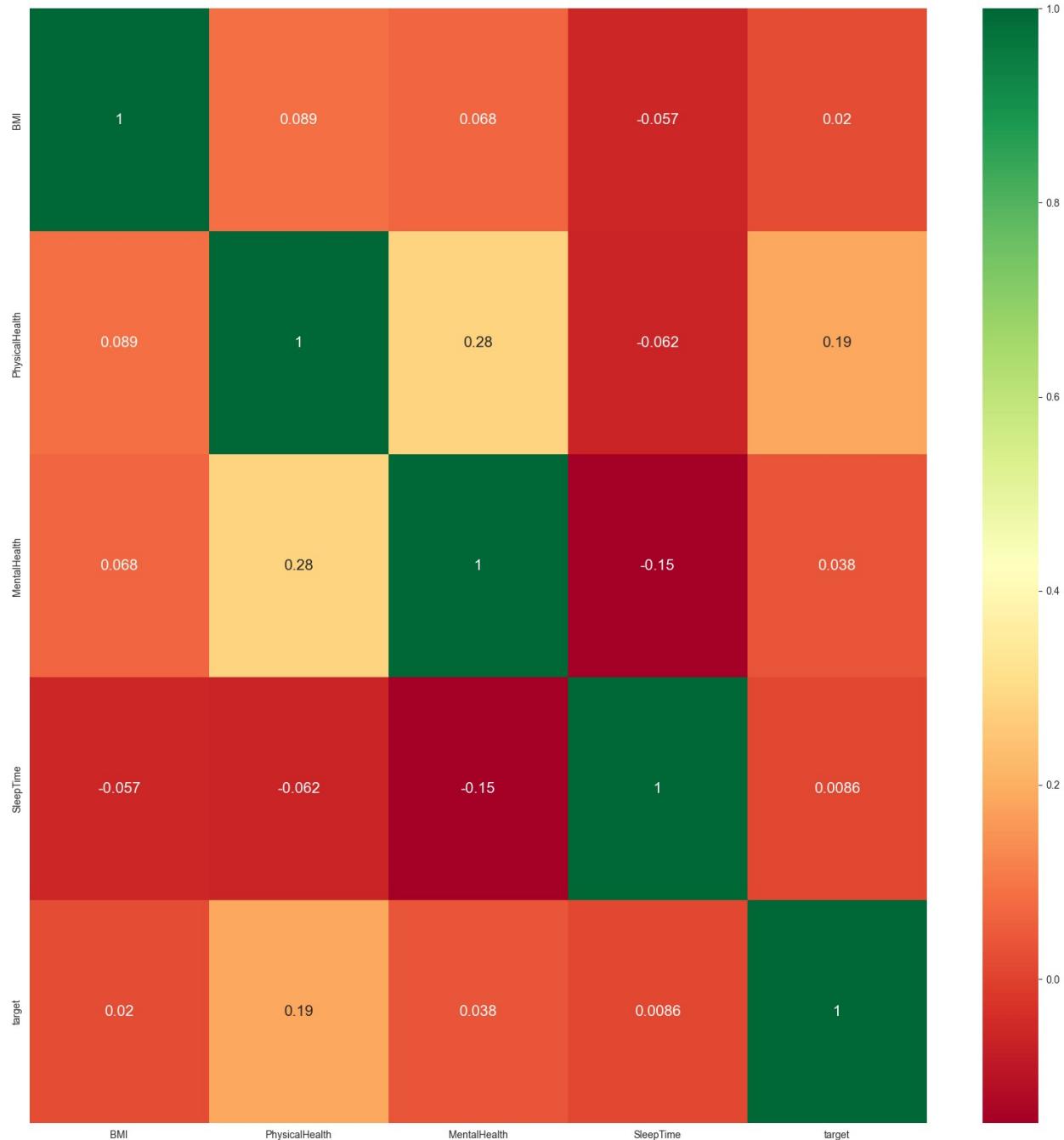


```
import seaborn as sns
import matplotlib.pyplot as plt

numeric_hd = hd.select_dtypes(include=['int64', 'float64'])

corr_matrix = numeric_hd.corr()

plt.figure(figsize=(20, 20))
sns.heatmap(
    corr_matrix,
    annot=True,
    cmap="RdYlGn",
    annot_kws={"size": 15}
)
plt.show()
```



OBSERVATION

1. Major features for having Heart disease are : Resting blood pressure, Cholesterol, Chest pain and Maximum Heart rates achieved.
2. The data is not balanced.
3. From the another plot we can conclude that number of men are majorly having Heart disease than compared to females. And also men are more healthier than females.

4. The graph tells us that patients with Type 3 chest pain have heart disease and very few Patients with 1 type chest pain can have heart disease.

```
# creating a copy of dataset
heart = hd.copy()

heart.shape

(4500, 19)

heart = heart.rename(columns={'condition':'target'})
heart.head()

   HeartDisease    BMI Smoking AlcoholDrinking Stroke PhysicalHealth \
0           No 16.60      Yes            No      No             3
1           No 20.34      No            No     Yes             0
2           No 26.58      Yes            No      No            20
3           No 24.21      No            No      No             0
4           No 23.71      No            No      No            28

   MentalHealth DiffWalking   sex AgeCategory   Race Diabetic \
0          30        No Female  55-59 White    Yes
1           0        No Female 80 or older White   No
2          30        No  Male  65-69 White    Yes
3           0        No Female  75-79 White   No
4           0       Yes Female 40-44 White   No

   PhysicalActivity GenHealth SleepTime Asthma KidneyDisease
SkinCancer \
0           Yes  Very good      5     Yes      No
Yes
1           Yes  Very good      7     No      No
No
2           Yes       Fair      8     Yes      No
No
3           No        Good      6     No      No
Yes
4           Yes  Very good      8     No      No
No

   target
0      0
1      0
2      0
3      0
4      0
```

Lets divide our data set and use training dataset for model training, and test dataset is to evaluate model performance

```
from sklearn.model_selection import train_test_split

x= heart.drop(columns= 'target')
y= heart.target

x_train, x_test, y_train, y_test= train_test_split(x, y, test_size=0.25, random_state=42)
print('X_train size: {}, X_test size: {}'.format(x_train.shape, x_test.shape))

X_train size: (3375, 18), X_test size: (1125, 18)
```

feature scaling

```
X = hd.drop('target', axis=1)
y = hd['target']

X_encoded = pd.get_dummies(X, drop_first=True)
from sklearn.model_selection import train_test_split

x_train, x_test, y_train, y_test = train_test_split(
    X_encoded, y, test_size=0.2, random_state=42
)
from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()
x_train_scaler = scaler.fit_transform(x_train)
x_test_scaler = scaler.transform(x_test)
```

Linear regression

```
from sklearn.linear_model import LinearRegression
lr_clf= LinearRegression()
lr_clf.fit(x_train_scaler, y_train)
y_pred_lr= lr_clf.predict(x_test_scaler)
lr_clf.score(x_test_scaler,y_test)

0.5377610331681861
```

LinearRegression is not the suitable model

LOGISTIC REGRESSION

```
from sklearn.linear_model import LogisticRegression

logr_clf= LogisticRegression()
logr_clf.fit(x_train_scaler, y_train)
y_pred_lor= logr_clf.predict(x_test_scaler)
logr_clf.score(x_test_scaler,y_test)

1.0

print('Classification Report\n', classification_report(y_test,
y_pred_lor))
print('Accuracy: {}%'.format(round((accuracy_score(y_test,
y_pred_lor)*100),2)))

Classification Report
precision    recall   f1-score   support
          0       1.00     1.00      1.00      814
          1       1.00     1.00      1.00      86

accuracy                           1.00      900
macro avg                         1.00     1.00      1.00      900
weighted avg                      1.00     1.00      1.00      900

Accuracy: 100.0%

cm = confusion_matrix(y_test, y_pred_lor)
cm

array([[814,    0],
       [  0,  86]])
```

Decision Tree classifier

```
dt_clf= LogisticRegression()
dt_clf.fit(x_train_scaler, y_train)
y_pred_dct= dt_clf.predict(x_test_scaler)
dt_clf.score(x_test_scaler,y_test)

1.0

print('Classification Report\n', classification_report(y_test,
y_pred_dct))
print('Accuracy: {}%'.format(round((accuracy_score(y_test,
y_pred_dct)*100),2)))
```

```

Classification Report
precision    recall   f1-score   support
          0       1.00      1.00      1.00      814
          1       1.00      1.00      1.00       86

accuracy                           1.00      900
macro avg       1.00      1.00      1.00      900
weighted avg     1.00      1.00      1.00      900

Accuracy: 100.0%
cm = confusion_matrix(y_test, y_pred_dct)
cm
array([[814,    0],
       [  0,  86]])

```

Random Forest

```

from sklearn.ensemble import RandomForestClassifier

rf_clf= LogisticRegression()
rf_clf.fit(x_train_scaler, y_train)
y_pred_rfc= rf_clf.predict(x_test_scaler)
rf_clf.score(x_test_scaler,y_test)

1.0

print('Classification Report\n', classification_report(y_test,
y_pred_rfc))
print('Accuracy: {}%'.format(round((accuracy_score(y_test,
y_pred_rfc)*100),2)))

Classification Report
precision    recall   f1-score   support
          0       1.00      1.00      1.00      814
          1       1.00      1.00      1.00       86

accuracy                           1.00      900
macro avg       1.00      1.00      1.00      900
weighted avg     1.00      1.00      1.00      900

Accuracy: 100.0%

cm = confusion_matrix(y_test, y_pred_rfc)
cm

```

```
array([[814,    0],
       [  0,   86]])
```

SVC

```
from sklearn.svm import SVC

svc_clf= LogisticRegression()
svc_clf.fit(x_train_scaler, y_train)
y_pred_svc= svc_clf.predict(x_test_scaler)
svc_clf.score(x_test_scaler,y_test)

1.0

print('Classification Report\n', classification_report(y_test,
y_pred_svc))
print('Accuracy: {}%'.format(round((accuracy_score(y_test,
y_pred_svc)*100),2)))

Classification Report
      precision    recall  f1-score   support
          0       1.00     1.00     1.00      814
          1       1.00     1.00     1.00      86

   accuracy         1.00      1.00      1.00      900
  macro avg       1.00     1.00     1.00      900
weighted avg       1.00     1.00     1.00      900

Accuracy: 100.0%

cm = confusion_matrix(y_test, y_pred_svc)
cm

array([[814,    0],
       [  0,   86]])
```

```
import pickle

filename = 'Healthcare_Analysis_on_Heart_Disease.pkl'
pickle.dump(rf_clf, open(filename, 'wb'))
```