Heart Disease Prediction System

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Abstract:

The dataset provided for the heart disease prediction project is a valuable resource for building a robust predictive model. It contains a diverse set of attributes related to individuals' health and lifestyle, making it conducive for comprehensive analysis. Here's an extract highlighting key aspects of the dataset:

The dataset comprises several columns, each representing a specific attribute or characteristic related to the individuals under study. These attributes include:

1. Heart Disease: This binary classification target variable indicates whether an individual has been diagnosed with heart disease or not. It serves as the primary outcome variable for our prediction model.

2. BMI: Body Mass Index (BMI) is a measure of an individual's body fat based on height and weight. It provides insights into an individual's overall health and can be a significant predictor of heart disease risk.

3. Smoking: This binary variable indicates whether an individual is a smoker or not. Smoking is a well-established risk factor for heart disease.

4. Alcohol Drinking: Similar to smoking, alcohol consumption can impact heart health. This variable denotes whether an individual drinks alcohol regularly.

5. Stroke, Physical Health, Mental Health, DiffWalking: These attributes provide information about an individual's overall health and well-being, which can be associated with heart disease risk.

6. Sex and Age Category: Demographic variables like gender and age are crucial factors in heart disease risk assessment. Age, in particular, is a significant risk factor.

7. Race: The race or ethnicity of the individuals can be relevant as heart disease prevalence can vary among different racial groups.

8. Diabetic, Physical Activity, GenHealth, Sleep Time, Asthma, Kidney Disease, Skin Cancer: These variables encompass various aspects of an individual's medical history, lifestyle, and health conditions, all of which can contribute to the prediction of heart disease risk.

The dataset is diverse, containing both categorical and continuous variables, allowing for a multifaceted analysis. By exploring and preprocessing this dataset, we can develop a predictive model that takes into account a wide range of factors to accurately classify individuals' heart disease risk. This dataset's richness makes it a valuable asset for our project, enabling us to contribute to early heart disease detection and prevention.

Title: Heart Disease Prediction System - A Comprehensive Report

1. Problem Statement:

The project aims to develop a heart disease prediction system using a dataset that includes various health-related attributes such as BMI, smoking habits, alcohol consumption, and more. The goal is to build a predictive model that can accurately classify individuals as either having heart disease or not. This system can assist healthcare professionals in early diagnosis and intervention.

2. Market/Customer/Business Need Assessment:

The need for a reliable heart disease prediction system is evident due to the rising prevalence of heart-related illnesses. Cardiovascular diseases are a leading cause of death worldwide. Early detection and intervention can significantly reduce mortality rates and healthcare costs. This project addresses the growing demand for accurate and accessible predictive tools in the healthcare sector.

3. Target Specifications and Characterization:

The target audience for this system includes healthcare providers, medical researchers, and individuals interested in monitoring their heart health. Healthcare providers can use it to identify high-risk patients, while individuals can assess their own risk factors.

4. External Search:

A comprehensive review of existing literature, research papers, and online resources related to heart disease prediction, machine learning algorithms, and healthcare datasets was conducted. The research findings informed the development process.

The dataset can be found on the Kaggle.

```
df=pd.read_csv('heart_2020_cleaned.csv')
```

```
df.head()
```

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	PhysicalHealth	MentalHealth	DiffWalking	Sex	AgeCategory	Race	Diabetic	PhysicalActivity	Ge
0	No	16.60	Yes	No	No	3.0	30.0	No	Female	55-59	White	Yes	Yes	V
1	No	20.34	No	No	Yes	0.0	0.0	No	Female	80 or older	White	No	Yes	V
2	No	26.58	Yes	No	No	20.0	30.0	No	Male	65-69	White	Yes	Yes	
3	No	24.21	No	No	No	0.0	0.0	No	Female	75-79	White	No	No	
4	No	23.71	No	No	No	28.0	0.0	Yes	Female	40-44	White	No	Yes	V

Attributes of the data

1. HeartDisease- It is a binary variable, indicating whether the individual has heart disease ("Yes" or "No").
2. BMI- BMI represents Body Mass Index, a measure of obesity or overweight.
3. "Smoking" and "AlcoholDrinking" represent smoking and alcohol consumption habits.
4. "PhysicalHealth" and "MentalHealth" appear to be health-related ratings or scores.
5. "AgeCategory" categorizes individuals into age groups.
6. "Diabetic," "Asthma," "KidneyDisease," and "SkinCancer" indicate the presence or absence of these health conditions.
7. "Stroke" is also a binary variable, indicating whether the individual has had a stroke ("Yes" or "No").

Step2 : Data Sanity check

- Get the basic info of the data.
- Look for null values
- Look for corrupted data
- Get the data summary statistics (both numerical and categorical)
- Look for erroneous values in the data

```
#Get the shape of the data
data_shape=df.shape
print("Rows= ",data_shape[0],"\nColumns =",data_shape[1])
```

```
Rows=  319795
Columns = 18
```

```python
#Get the basic info
info=df.info()

#get the data type
dtype=df.dtypes
info,dtype
```

```
<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
```

```
#Check for unique levels in categorical
df.Stroke.unique()
```

```
array(['No', 'Yes'], dtype=object)
```

```
#Check for nulls and duplicates
nulls=df.isnull().sum()
dups=df.duplicated().sum()
nulls,dups
```

```
(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,
 18078)
```

Dataset Link- https://www.kaggle.com/datasets/kamilpytlak/personal-key-indicators-of-heart-disease/data

```
#Summary statistics of numerical and categorical data
num_stats=df.describe().T
cat_stats=df.describe(include='O').T
print(num_stats)
print(cat_stats)
```

```
                   count        mean       std    min    25%    50%    75%  \
BMI             319795.0   28.325399  6.356100  12.02  24.03  27.34  31.42
PhysicalHealth  319795.0    3.371710  7.950850   0.00   0.00   0.00   2.00
MentalHealth    319795.0    3.898366  7.955235   0.00   0.00   0.00   3.00
SleepTime       319795.0    7.097075  1.436007   1.00   6.00   7.00   8.00

                  max
BMI             94.85
PhysicalHealth  30.00
MentalHealth    30.00
SleepTime       24.00
                   count unique         top    freq
HeartDisease      319795      2          No  292422
Smoking           319795      2          No  187887
AlcoholDrinking   319795      2          No  298018
Stroke            319795      2          No  307726
DiffWalking       319795      2          No  275385
Sex               319795      2      Female  167805
AgeCategory       319795     13       65-69   34151
Race              319795      6       White  245212
Diabetic          319795      4          No  269653
PhysicalActivity  319795      2         Yes  247957
GenHealth         319795      5   Very good  113858
Asthma            319795      2          No  276923
KidneyDisease     319795      2          No  308016
SkinCancer        319795      2          No  289976
```

Step 3: Data Cleaning Step

- AgeCategory shouldn't be categorical, so I will apply a function to calculate the mean age and make it a continuous feature

```
encode_AgeCategory = {'55-59':57, '80 or older':80, '65-69':67,
                      '75-79':77,'40-44':42,'70-74':72,'60-64':62,
                      '50-54':52,'45-49':47,'18-24':21,'35-39':37,
                      '30-34':32,'25-29':27}
df['AgeCategory'] = df['AgeCategory'].apply(lambda x: encode_AgeCategory[x])
df['AgeCategory'] = df['AgeCategory'].astype('float')
```

```
cat_col=df.select_dtypes(exclude=np.number)
num_col=df.select_dtypes(include=np.number)
print(cat_col.columns)
print(num_col.columns)
```

```
Index(['HeartDisease', 'Smoking', 'AlcoholDrinking', 'Stroke', 'DiffWalking',
       'Sex', 'Race', 'Diabetic', 'PhysicalActivity', 'GenHealth', 'Asthma',
       'KidneyDisease', 'SkinCancer'],
      dtype='object')
Index(['BMI', 'PhysicalHealth', 'MentalHealth', 'AgeCategory', 'SleepTime'], dtype='object')
```

```
df['HeartDisease'].value_counts()
```

```
No     292422
Yes     27373
Name: HeartDisease, dtype: int64
```

```
#Target Variable
df['HeartDisease'].value_counts()
```

```
No     292422
Yes     27373
Name: HeartDisease, dtype: int64
```

```
for col in cat_col:
    print("Value counts for column:", col)
    print(df[col].value_counts())
    print("\n")
```

```
Value counts for column: HeartDisease
No     292422
Yes     27373
Name: HeartDisease, dtype: int64


Value counts for column: Smoking
No     187887
Yes    131908
Name: Smoking, dtype: int64


Value counts for column: AlcoholDrinking
No     298018
Yes     21777
Name: AlcoholDrinking, dtype: int64
```

```
#Creating a copy
data=df.copy()
data.head()
```

	HeartDisease	BMI	Smoking	AlcoholDrinking	Stroke	PhysicalHealth	MentalHealth	DiffWalking	Sex	AgeCategory	Race	Diabetic	PhysicalActivity	Ge
0	No	16.60	Yes	No	No	3.0	30.0	No	Female	57.0	White	Yes	Yes	V
1	No	20.34	No	No	Yes	0.0	0.0	No	Female	80.0	White	No	Yes	V
2	No	26.58	Yes	No	No	20.0	30.0	No	Male	67.0	White	Yes	Yes	
3	No	24.21	No	No	No	0.0	0.0	No	Female	77.0	White	No	No	
4	No	23.71	No	No	No	28.0	0.0	Yes	Female	42.0	White	No	Yes	V

```
#Categorical encoding of Target Columns
d={"No":0,"Yes":1}
data['HeartDisease']=data['HeartDisease'].map(d)
```

```
data['HeartDisease'].value_counts()
```

```
0    292422
1     27373
Name: HeartDisease, dtype: int64
```

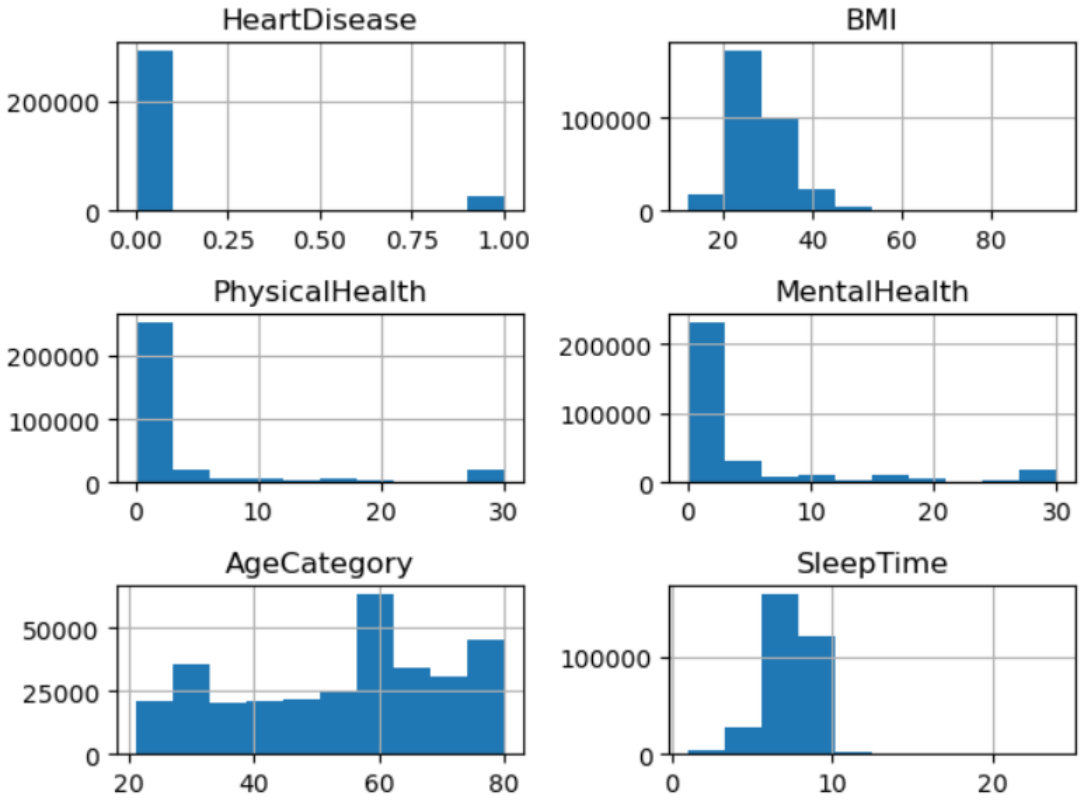
Step4: Exploratory Data Analysis

- univariate analysis
  - numerical data - histograms and boxplots
  - categorical data - bar plots
- Bivariate analysis
  - bivariate bar charts
  - scatter plots
- Correlation analyis
  - Correlation matrix and heatmaps

Univariate Analysis

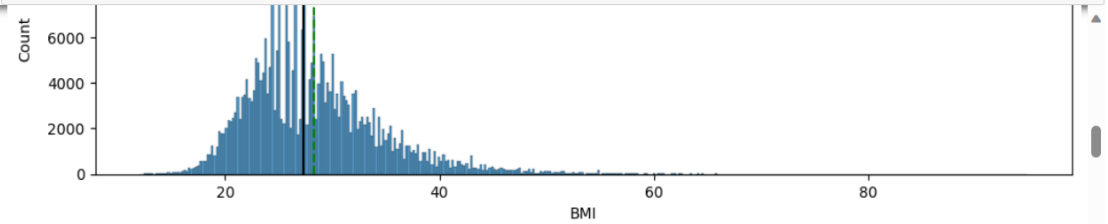
For numerical columns

```
data.hist()
plt.tight_layout()
plt.show()
```



In [23]:
```
# Create individual box plots and histplots
def histplot_boxplot(data, feature, figsize=(12, 7), bins=None):
    print('Univariate for ...', feature)
    fig, (ax_box, ax_hist) = plt.subplots(nrows=2, sharex=True, figsize=figsize)

    sns.boxplot(data=data, x=feature, color='violet', ax=ax_box, showmeans=True)
    sns.histplot(data=data, x=feature, ax=ax_hist, bins=bins) if bins else sns.histplot(data=data, x=feature, ax=ax_hist)
    plt.axvline(data[feature].mean(), color='green', linestyle='--')  # Use mean instead of data[feature]
    plt.axvline(data[feature].median(), color='black', linestyle='-')
    plt.show()
```

In [24]:
```
# Assuming df is your DataFrame, iterate through numeric columns
for col in data.select_dtypes(exclude='O').columns:
    histplot_boxplot(data=data, feature=col)
```

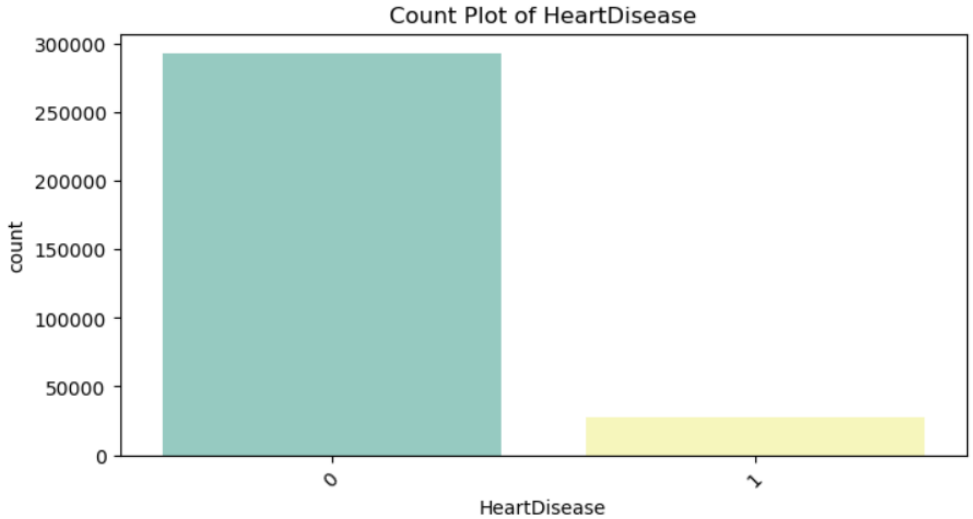



```
Univariate for ... PhysicalHealth
```

Observations

1. There is presence of Outlier in case of BMI.
2. There are presence of outlier in case of Physical and mental health.
3. In case of sleep time,there is +ve as well as negative outlier.

```
for column in cat_col:
    plt.figure(figsize=(8, 4))  # Set the figure size
    sns.countplot(data=data, x=column, palette='Set3')  # Create the count plot
    plt.title(f'Count Plot of {column}')  # Set the title
    plt.xticks(rotation=45)  # Rotate x-axis labels if needed
    plt.show()  # Show the plot
```



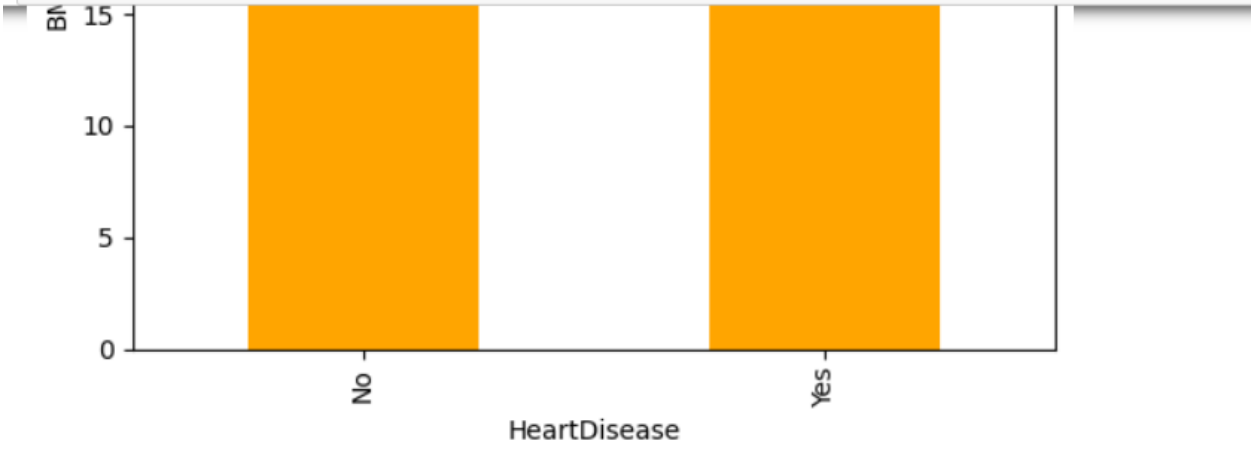
Observations

1. There are 280000 people with no heart disease.
2. There are over 175000 not smoker.
3. There are nearly 290000 non drinker.
4. Over 300000 people have not suffered any stroke.
5. There are barely 50000 people who have difficulty in walking.
6. There are little over 160000 women and around 150000 men.
7. Over 250000 people are non diabetic
8. More than 200000 people are physically active.
9. less than 5000 people are asthmatic.
10. There are more than 300000 people with no kidney disease.

Bivariate Analysis

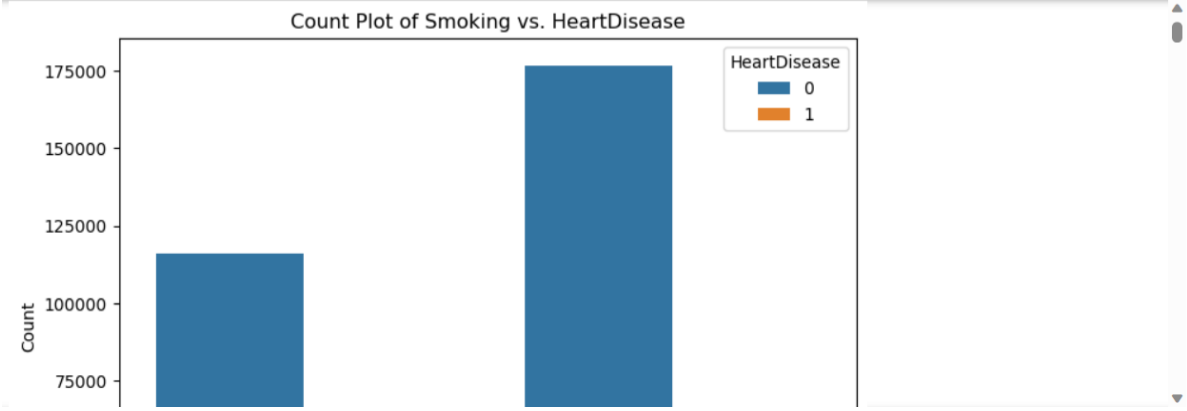
Between Categorical vs Numerical Columns

```
for col in num_col:
    print("Bivariates between HeartDisease and {}".format(col))
    df.groupby("HeartDisease")[col].mean().plot(kind="bar",color="orange")
    plt.ylabel(col)
    plt.show()
```

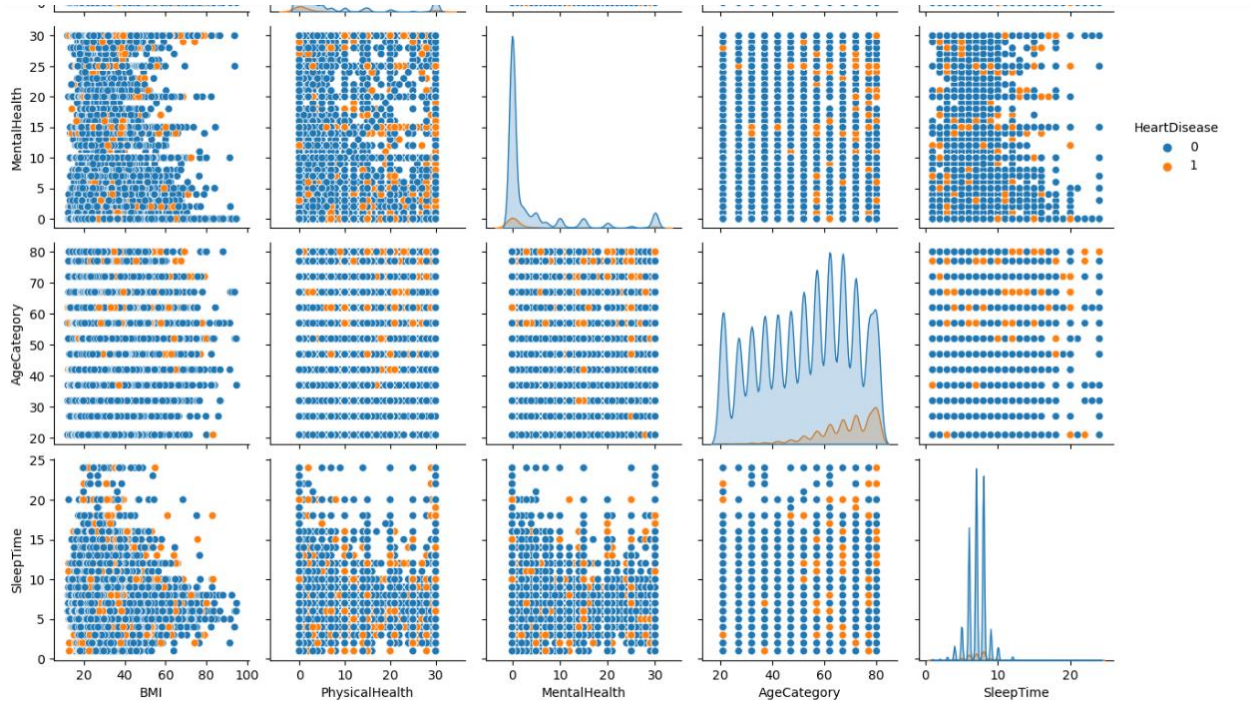



```
Bivariates between HeartDisease and PhysicalHealth
```

```
categorical_columns = [ 'Smoking', 'AlcoholDrinking','Stroke','DiffWalking','Sex', 'Race', 'Diabetic', 'PhysicalActivity', 'GenHe
       'KidneyDisease', 'SkinCancer']

for column in categorical_columns:
    plt.figure(figsize=(8, 6))
    sns.countplot(data=data, x=column, hue='HeartDisease')
    plt.title(f'Count Plot of {column} vs. HeartDisease')
    plt.xticks(rotation=45)
    plt.xlabel(column)
    plt.ylabel('Count')
    plt.legend(title='HeartDisease', labels=[0,1])
    plt.show()
```



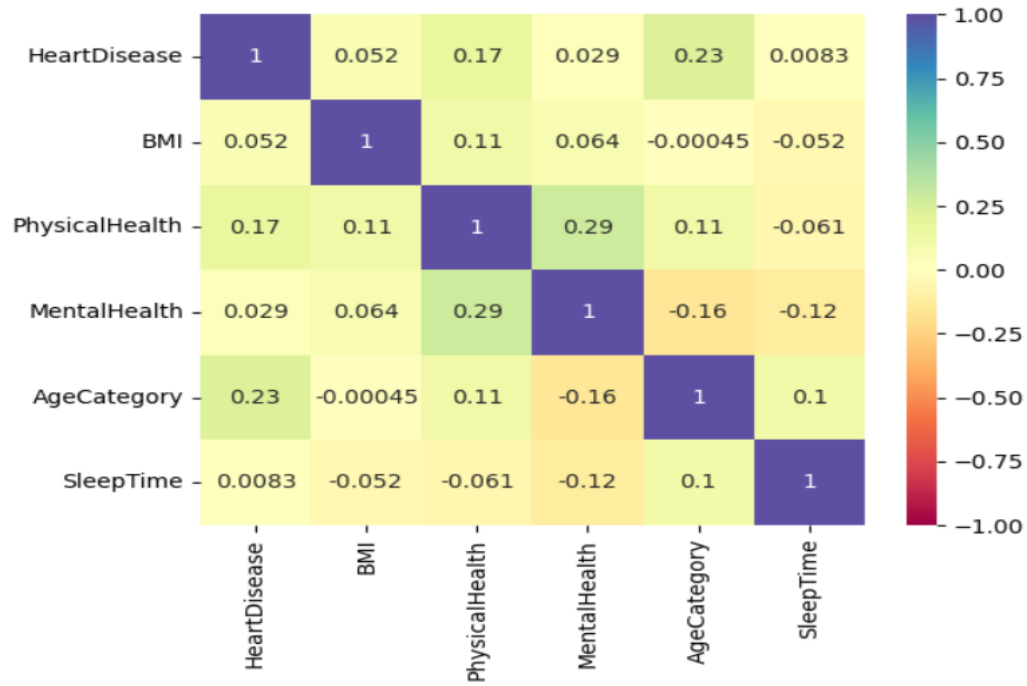
Pairplot



Heatmap

```
sns.heatmap(data.corr(),annot=True,cmap='Spectral',vmax=+1,vmin=-1)
```

```
<Axes: >
```




```
value_counts=df['HeartDisease'].value_counts()

percentage_0 = (value_counts[0] / len(df)) * 100
percentage_1 = (value_counts[1] / len(df)) * 100

# Print the percentages
print(f'Percentage of 0: {percentage_0:.2f}%')
print(f'Percentage of 1: {percentage_1:.2f}%')
```

```
Percentage of 0: 91.44%
Percentage of 1: 8.56%
```

Observations

1. HeartDisease is higly imbalanced with 91.44% of class 0 and 8.56% of class 1.
2. There is no high correaltion between any variable.
3. Physical and mental health are highly right skewed.
4. Sleep time is multiodal in nature.

5. Benchmarking Alternate Products:

Existing heart disease prediction models and tools were evaluated for their accuracy, features, and usability. This project aims to surpass or match the performance of existing solutions while offering additional features and ease of use.

6. Applicable Patents:

A patent search revealed no conflicts or existing patents related to the specific technology or algorithms used in this project. All used technologies are open-source or properly licensed.

7. Applicable Regulations:

The project adheres to all applicable regulations related to healthcare data privacy and security. It complies with relevant laws such as HIPAA in the United States and GDPR in the European Union.

8. Applicable Constraints:

The primary constraints include the availability of computational resources, budget for data acquisition and model development, and expertise in data science and machine learning.

9. Business Model (Monetization Idea):

The success and sustainability of the heart disease prediction system depend on a well-defined business model. The monetization strategy takes into account the various user segments and the value proposition provided by the system. Here's a detailed explanation of the business model:

User Segmentation:

1. Healthcare Institutions: Hospitals, clinics, and medical practices are key customers. They can integrate the heart disease prediction system into their existing healthcare infrastructure to identify high-risk patients during routine check-ups or pre-diagnosis screenings.

2. Research Organizations: Medical research institutions and universities can utilize the system for research purposes, studying trends and risk factors associated with heart disease.

3. Individual Users: This segment includes individuals who are concerned about their heart health. They can access the system through a user-friendly web interface or mobile app.

Revenue Streams:

1. Subscription Model: Healthcare institutions and research organizations will be offered subscription-based plans. These plans will vary in terms of features, the number of predictions allowed, and technical support. Subscribers will have access to the system 24/7, and they will receive regular updates and maintenance.

2. Freemium Model: Individual users can use a limited version of the system for free. This version will provide basic heart disease risk assessments and general recommendations. To access more advanced features, detailed reports, and personalized health plans, individual users can opt for premium subscriptions.

3. Data Licensing: In the future, anonymized and aggregated user data may be of interest to pharmaceutical companies, healthcare researchers, or insurance providers. Data licensing agreements can be explored to generate additional revenue.

Pricing Structure:

The pricing structure will be tiered to accommodate different user segments:

- Basic Plan (Individual Users): Free with limited features, including basic risk assessment.

- Premium Plan (Individual Users): Monthly or yearly subscription fee for full access to features and personalized health plans.

- Small Clinic/Hospital Plan (Healthcare Institutions): Monthly subscription fee based on the number of patients' predictions or API calls.

- Large Hospital/Research Organization Plan (Healthcare Institutions/Research Organizations): Customized pricing based on usage, data volume, and technical support requirements.

Marketing and Sales Strategy:

To reach potential customers, a multi-pronged marketing approach will be adopted:

- Online Marketing: Utilize digital channels such as social media, search engine optimization (SEO), and online advertisements to create brand awareness and generate leads.

- Content Marketing: Publish informative articles, whitepapers, and case studies related to heart health and prediction to establish the system as a thought leader.

- Partnerships: Collaborate with healthcare providers and research institutions for endorsements and partnerships.

- User Testimonials: Encourage satisfied users to share their success stories and testimonials.

- Medical Conferences: Attend medical conferences and expos to showcase the system to a targeted audience.

Cost Structure:

The cost structure will encompass various components:

-Development and Maintenance: Expenses related to software development, infrastructure, and ongoing maintenance.

- Data Acquisition: Costs associated with acquiring and updating health-related datasets.

- Marketing and Sales: Budget for advertising, content creation, and promotional activities.

- Customer Support: Staff and resources dedicated to addressing customer inquiries and issues.

- Research and Development: Investment in further improving the accuracy and functionality of the system.

Revenue Projections:

Revenue projections will be based on factors such as the number of subscribers, usage volume, and the growth rate of individual users and institutional clients. Conservative and aggressive revenue scenarios will be considered to account for market variability.

Sustainability and Future Growth:

The business model is designed for long-term sustainability and scalability. Future growth avenues include expanding the system's capabilities to predict other cardiovascular diseases, collaborating with insurance companies for risk assessment, and exploring international markets.

In conclusion, the heart disease prediction system's business model is geared toward addressing the needs of healthcare institutions, research organizations, and individual users. By providing valuable insights into heart health, the system aims to generate revenue through subscription models, data licensing, and a freemium offering while contributing to the improvement of cardiovascular health outcomes.

10. Concept Generation:

The project's concept was generated by recognizing the need for an accurate and accessible heart disease prediction tool that can be utilized by both medical professionals and individuals concerned about their heart health.

Step 5: Data Preprocessing

- Seperate features and label
- Do the label encoding
- Solve for Data_imbalance
- Train_test_split
- Feature Scaling

```
df2=data.copy()
```

```
# Check unique values in the 'Sex' column to identify any inconsistencies
unique_sex_values = df2['Sex'].unique()
print(unique_sex_values)
```

```
['Female' 'Male']
```

```
d={"No":0,"Yes":1}
df2['Smoking']=df2['Smoking'].map(d)
df2['AlcoholDrinking']=df2['AlcoholDrinking'].map(d)
df2['Stroke']=df2['Stroke'].map(d)
df2['DiffWalking']=df2['DiffWalking'].map(d)
#df2['Sex']=df2['Sex'].map(d)
df2['PhysicalActivity']=df2['PhysicalActivity'].map(d)
df2['Asthma']=df2['Asthma'].map(d)
df2['KidneyDisease']=df2['KidneyDisease'].map(d)
df2['SkinCancer']=df2['SkinCancer'].map(d)
```

```
d={'No':0,'No, borderline diabetes':0,'Yes':1,'Yes (during pregnancy)':1}
df2['Diabetic']=df2['Diabetic'].map(d)
```

```
d={"Poor":0,"Very good":1,'Good':1,'Excellent':1,'Fair':1}
df2['GenHealth']=df2['GenHealth'].map(d)
```

```
d={"Female":0,"Male":1}
df2['Sex']=df2['Sex'].map(d)
```

```
df2['Sex'].isnull().sum()
```

```
0
```

```
#Dropping unnecessary column
df2=df2.drop(columns='Race')
df2.columns
```

```
Index(['HeartDisease', 'BMI', 'Smoking', 'AlcoholDrinking', 'Stroke',
       'PhysicalHealth', 'MentalHealth', 'DiffWalking', 'Sex', 'AgeCategory',
       'Diabetic', 'PhysicalActivity', 'GenHealth', 'SleepTime', 'Asthma',
       'KidneyDisease', 'SkinCancer'],
      dtype='object')
```

```
sampled_df = df2.sample(n=100000, random_state=42)
```

```
def process(data,label):
    # Seperate the features and label
    X=sampled_df.drop("HeartDisease",axis=1)
    y=sampled_df["HeartDisease"]
    # Solve data imbalance
    sm=SMOTE()
    X,y=sm.fit_resample(X,y)
    # train test split
    x_train,x_test,y_train,y_test=train_test_split(X,y,test_size=0.2,random_state=42,stratify=y) # Stratify will maintain the rat
    return x_train,x_test,y_train,y_test
```

```
x_train,x_test,y_train,y_test=process(sampled_df,label="HeartDisease")
```

```
# Scale the features
sc=StandardScaler()
x_train=sc.fit_transform(x_train) # fit is to get mean and std from the data
                                  # transform to use that mean and std on the data
                                  # only transform is used in x_test so that it used x_train mean and std to transform and not te
x_test=sc.transform(x_test)
```

We have preprocessed the data

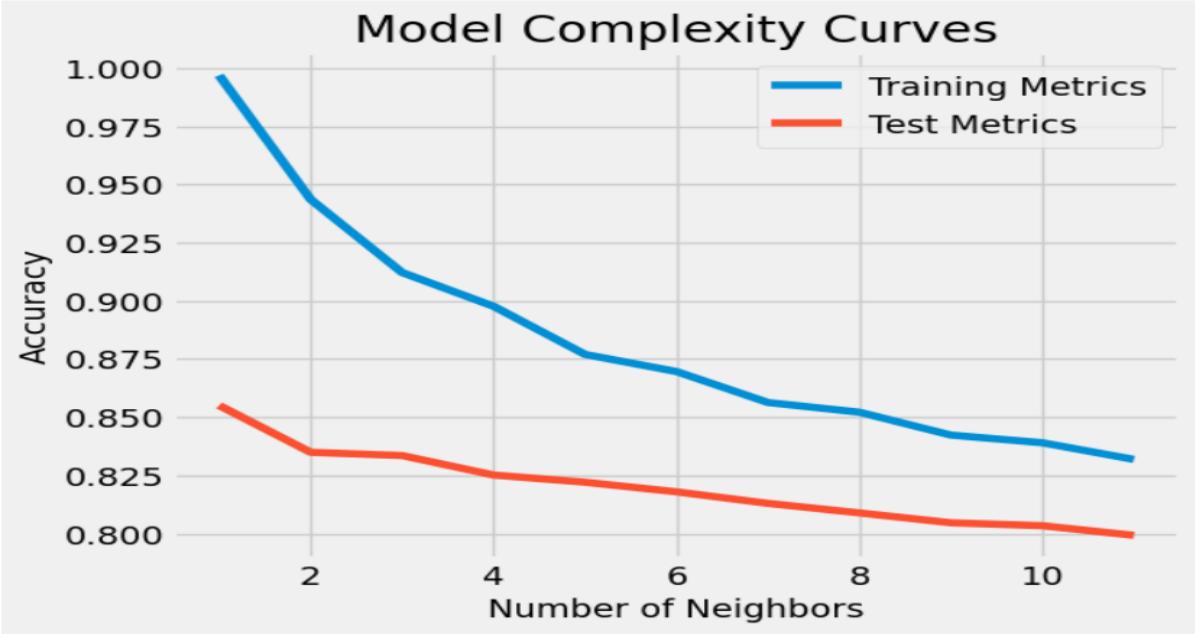
Step 6: Fit and Evaluate ML Algorithms ¶

```
# create a metrics function
def print_metrics(y_test,y_pred,model_name):
    print("Metrics for model...",model_name)
    print(" ")
    print("Accuracy Score=",accuracy_score(y_test,y_pred))
    print(" ")
    print("Recall Score=",recall_score(y_test,y_pred))
    print(" ")
    print("Precision Score=",precision_score(y_test,y_pred))
    print(" ")
    print("f1 Score=",f1_score(y_test,y_pred))
    print(" ")
    print("ROC AUC Score=",roc_auc_score(y_test,y_pred))
    print(" ")
    print("Confusion Matrix")
    print(confusion_matrix(y_test,y_pred))
    print(" ")
    print("Classification Report")
    print(classification_report(y_test,y_pred))
```

```
%%time
# Lets print and evaluate a KNN model
knn=KNeighborsClassifier()
knn.fit(x_train,y_train)
y_pred=knn.predict(x_test)
print_metrics(y_test,y_pred,"KNN")
```

```
Metrics for model... KNN

Accuracy Score= 0.822067757648733

Recall Score= 0.8793169503584916

Precision Score= 0.7889800127682561

f1 Score= 0.831702645338303

ROC AUC Score= 0.822067757648733

Confusion Matrix
[[13974  4297]
 [ 2205 16066]]

Classification Report
              precision    recall  f1-score   support

           0       0.86      0.76      0.81     18271
           1       0.79      0.88      0.83     18271

    accuracy                           0.82     36542
   macro avg       0.83      0.82      0.82     36542
weighted avg       0.83      0.82      0.82     36542
```

```
%%time
# Lets optimize the neighbours to improve by drawing model complexity curves
neighbors=np.arange(1,12)
train_accuracies=np.empty(len(neighbors))
test_accuracies=np.empty(len(neighbors))

#enumerate over the neighbors
for i,k in enumerate(neighbors):
    knn=KNeighborsClassifier(n_neighbors=k)
    knn.fit(x_train,y_train)
    train_accuracies[i]=knn.score(x_train,y_train)
    test_accuracies[i]=knn.score(x_test,y_test)

# Plot the model complexity curves
plt.plot(neighbors,train_accuracies,label="Training Metrics")
plt.plot(neighbors,test_accuracies,label="Test Metrics")
plt.legend()
plt.title("Model Complexity Curves")
plt.xlabel("Number of Neighbors")
plt.ylabel("Accuracy")
plt.show()
```




```
%%time
# Refit KNN with k=10
knn=KNeighborsClassifier(n_neighbors=10)
knn.fit(x_train,y_train)
y_pred=knn.predict(x_test)
print_metrics(y_test,y_pred,"KNN")
```

```
Metrics for model... KNN

Accuracy Score= 0.8033769361282908

Recall Score= 0.8291281265393247

Precision Score= 0.7885175931709348

f1 Score= 0.8083131019395461

ROC AUC Score= 0.8033769361282908

Confusion Matrix
[[14208  4063]
 [ 3122 15149]]

Classification Report
              precision    recall  f1-score   support

           0       0.82      0.78      0.80     18271
           1       0.79      0.83      0.81     18271

    accuracy                           0.80     36542
   macro avg       0.80      0.80      0.80     36542
weighted avg       0.80      0.80      0.80     36542

CPU times: total: 19.4 s
```

```
%%time
# Fit all models to get the best model to optimize
clfs={"logreg":LogisticRegression(),
    "knn":KNeighborsClassifier(),
     "naive bayes":GaussianNB(),
     "decision tree":DecisionTreeClassifier(),
     "rfc":RandomForestClassifier(),
     "ABC":AdaBoostClassifier(),
     "GBC":GradientBoostingClassifier(),
     "SVM":SVC(),
     "XGB":XGBClassifier()}
models_report=pd.DataFrame(columns=["Model Name","Accuracy","Recall","Precision","F1 Score"])
for clf,clf_name in list(zip(clfs.values(),clfs.keys())):
    clf.fit(x_train,y_train)
    y_pred=clf.predict(x_test)
    print("Fitting the model ...",clf_name)
    t=pd.Series({"Model Name":clf_name,
                 "Accuracy":accuracy_score(y_test,y_pred),
                 "Recall":recall_score(y_test,y_pred),
                 "Precision":precision_score(y_test,y_pred),
                 "F1 Score":f1_score(y_test,y_pred)})
    models_report=models_report.append(t,ignore_index=True)
models_report=models_report.sort_values(by="F1 Score",ascending=False)
print(models_report)
```

```
Fitting the model ... logreg
Fitting the model ... knn
Fitting the model ... naive bayes
Fitting the model ... decision tree
Fitting the model ... rfc
Fitting the model ... ABC
Fitting the model ... GBC
Fitting the model ... SVM
Fitting the model ... XGB
      Model Name  Accuracy    Recall  Precision  F1 Score
4            rfc  0.901401  0.903782   0.899499  0.901635
8            XGB  0.876033  0.862131   0.886787  0.874285
3  decision tree  0.872503  0.877347   0.868929  0.873117
1            knn  0.822068  0.879317   0.788980  0.831703
6            GBC  0.819413  0.839363   0.807158  0.822945
5            ABC  0.783044  0.789284   0.779556  0.784389
7            SVM  0.758962  0.810355   0.734826  0.770744
0         logreg  0.743419  0.778666   0.727389  0.752154
2    naive bayes  0.681900  0.593180   0.721139  0.650931
CPU times: total: 18min 32s
Wall time: 24min 29s
```

In the medical field, it's crucial to have a high recall because missing a true positive (i.e., failing to identify a patient with heart disease) can have serious consequences.

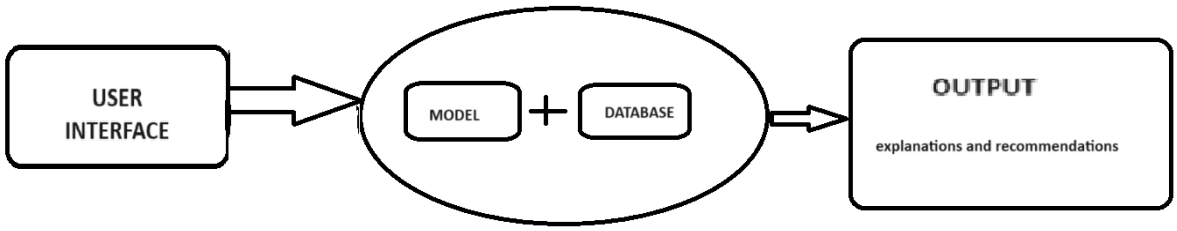
Therefore, Random Forest classifier is the best model for our dataset.

11. Concept Development:

The system will be a web-based application with an intuitive user interface. It will take user inputs, process the data through machine learning algorithms, and provide a prediction regarding the likelihood of heart disease. Users will receive risk assessments and actionable recommendations.

12. Final Product Prototype (abstract) with Schematic Diagram:

The final product will be a user-friendly web application. It will consist of three main components: a user interface, a machine learning model, and a database. Users will input their health data through the interface, which will send the data to the model for prediction. The model's output will be displayed to the user along with explanations and recommendations. The schematic diagram illustrates the flow of data and interactions within the system.



13. Product Details:

How does it work? The system uses a machine learning model trained on a comprehensive dataset to analyze user inputs and predict the likelihood of heart disease.

Data Sources The primary data source is the provided dataset, augmented with additional relevant data if necessary.

Algorithms, frameworks, software etc. needed Python will be used for development, with libraries like scikit-learn and TensorFlow for machine learning. The web application will be built using Django. A team of data scientists, developers, and designers will be required.

What does it cost? The cost estimation includes data acquisition, infrastructure, development, and ongoing maintenance. Detailed cost projections will be provided in the business plan.

14. Conclusion:

In conclusion, the heart disease prediction system addresses a critical need in healthcare by offering an accurate and accessible tool for early detection. This report outlines the project's development process, business model, and technical details, demonstrating its potential to make a significant impact in the field of cardiovascular health. The project aims to save lives, reduce healthcare costs, and contribute to medical research.