Heart Disease Prediction

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Objective: Create a predictive model and visualize risk factors for heart disease based on historical patient data. What risk factors in terms of demographics, health conditions can we detect to anticipate heart disease?

Summary of Report

Why is this important?

- This is important because heart disease is the leading cause of death worldwide. However, with the power of data science and machine learning, we can create models to predict heart disease and identify risk factors like age, sex, health conditions, blood information, etc. so that we can use preventive care to minimize the effects of heart disease.
- This topic is motivating because it combines healthcare and data science - two fields with the power to impact millions of lives. By addressing challenges in current diagnostic methods, it opens avenues for more inclusive healthcare.
- I am not the first to do this, because one of the most promising uses of technology is for medicine purposes and is a field that will continue to be researched. Also, since heart disease is so deadly, this will be a priority because of how much it will improve life expectancy and create a healthier population

Relation to Course Content

- I will use all the Python that we have learned in class
- Statistical analysis with Python and visualizations to find potential trends and correlations
- Pandas to handle all our data, including cleaning, one-hot encoding, analyzing, preparing for models
- Matplotlib and seaborn to visualize and analyze data
- Scikit-learn to create and test predictive models

Changes from project proposal

- I will only be using one of the datasets rather than both like proposed. There is already some overlap between the two and the dataset I am using already has 12 attributes, 11 of them being health features and the last one being the dependent variable (heart disease). I feel that this is enough information to go off of for the project
- I will also not be implementing a database. The dataset is simple and relatively small enough and does not require the features of a database. I did the lab instead.

Dataset

- UCI Machine Learning contains raw patient data and heart disease data
  - https://archive.ics.uci.edu/dataset/45/heart+disease
- Kaggle contains user-cleaned and compiled dataset from these from UCI Machine Learning which is the dataset I will be working off of.
  - https://www.kaggle.com/datasets/fedesoriano/heart-failure-prediction/data contains cleaned UCI data which makes working with the data much easier

Methods used

- To clean, encode, create statistic analyses, and prepare for modeling, I used the Pandas package and read the data into a Pandas dataframe. This made it easy with its built-in functions to find any outliers, missing values, perform one-hot encoding, and get general statistics for each of the columns.
- To visualize the data, I used the Matplotlib package along with Seaborn to visualize the data.
  - For our categorical data, I used a bar plot to get the distribution of the categorical data and count plots to plot each categorical value vs prevalence of heart disease.
  - For our numerical data, I used a box plot to visualize the distrbution of our quantitative data based on whether the patients had heart disease or not. Additionally, I used a histogram with a line to visualize this distribution in a more intuitive way.
- To create a predictive model, I used scikit-learn, two of its models, and some of its metrics to create, test, and view how successful it was. I used an 80/20 train/test split. I used all 11 columns, with the categorical variables split using one-hot encoding, as independent variables and heart disease and the dependent variable.
  - The first model I used was logistic regression. The weighted f-score was 0.88 which is very good.
  - The second model I used was random forest classification. The weighted f-score was even better at 0.89.
    - Using this model, I was able to use its feature importances to find the greatest risks of heart disease in order from most to least impactful on the model.
  - In particular, both models were slightly better at correctly predicting heart disease compared to predicting no heart disease.

Results

- The results verified the analyses I made in the project. Every single one of the variables I analyzed made a strong impact on my model, which is why it performed so well.
- Some limitations of the model are that there is a small chance for either a false positive or a false negative. In particular, a false negative might lead to the patient believing they don't have heart disease and make unhealthy life choices. The model should not be the only thing doctors or patients use to determine heart disease.
- After analyzing the dataset, knowing your health status on these conditions will help predict heart disease and allow you to make lifestyle changes and receive medical advice to minimize the effects of heart disease.
- Many of these can be done at home, like measuring maximum heart rate, blood pressure, or identifying chest pain. However, some of these require going to the doctor or s pecialized, like measuring cholesterol or taking an ECG, which is why good medical infrastructure is important in reducing what is worldwide human's greatest killer today.
- More research has and will continue to be done on more efficient ways to predict heart disease as well as preventing and mitigating heart disease.

In [1]:
```
import zipfile
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, confusion_matrix
```

1. Import data from heart.csv

Dataset is from https://www.kaggle.com/datasets/fedesoriano/heart-failure-prediction.

- We will use Kaggle commands to download the library, zipfile to unzip the file, and pandas to read the csv into df.

In [2]:
```
!kaggle datasets download fedesoriano/heart-failure-prediction
with zipfile.ZipFile("heart-failure-prediction.zip","r") as zip_ref:
    zip_ref.extractall("heart-failure-prediction")
```

```
Dataset URL: https://www.kaggle.com/datasets/fedesoriano/heart-failure-prediction
License(s): ODbL-1.0
heart-failure-prediction.zip: Skipping, found more recently modified local copy (use --force to force download)
```

In [3]:
```
df = pd.read_csv("heart-failure-prediction/heart.csv")
df.head()
```

Out[3]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up	0
1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat	1
2	37	M	ATA	130	283	0	ST	98	N	0.0	Up	0
3	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat	1
4	54	M	NAP	150	195	0	Normal	122	N	0.0	Up	0

- We use pandas functions to get structure of dataset before we start working

In [4]:
```
df.columns
```

Out[4]:
```
Index(['Age', 'Sex', 'ChestPainType', 'RestingBP', 'Cholesterol', 'FastingBS',
       'RestingECG', 'MaxHR', 'ExerciseAngina', 'Oldpeak', 'ST_Slope',
       'HeartDisease'],
      dtype='object')
```

In [5]:
```
df.dtypes
```

Out[5]:
```
Age                 int64
Sex                object
ChestPainType      object
RestingBP           int64
Cholesterol         int64
FastingBS           int64
RestingECG         object
MaxHR               int64
ExerciseAngina     object
Oldpeak           float64
ST_Slope           object
HeartDisease        int64
dtype: object
```

In [6]:
```
df.describe()
```

Out[6]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
count	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000
mean	53.510893	132.396514	198.799564	0.233115	136.809368	0.887364	0.553377
std	9.432617	18.514154	109.384145	0.423046	25.460334	1.066570	0.497414
min	28.000000	0.000000	0.000000	0.000000	60.000000	-2.600000	0.000000
25%	47.000000	120.000000	173.250000	0.000000	120.000000	0.000000	0.000000
50%	54.000000	130.000000	223.000000	0.000000	138.000000	0.600000	1.000000
75%	60.000000	140.000000	267.000000	0.000000	156.000000	1.500000	1.000000
max	77.000000	200.000000	603.000000	1.000000	202.000000	6.200000	1.000000

2. Make sure data is clean before we start analyzing it

- This looks for any missing values in our dataframe.

In [7]:
```
df.isna().sum()
```

Out[7]:
```
Age               0
Sex               0
ChestPainType     0
RestingBP         0
Cholesterol       0
FastingBS         0
RestingECG        0
MaxHR             0
ExerciseAngina    0
Oldpeak           0
ST_Slope          0
HeartDisease      0
dtype: int64
```

- This checks for any identical rows in our dataframe.

In [8]:
```
print(df.duplicated().sum())
```

```
0
```

- This gets the unique values for our categorical data

In [9]:
```
col_cat = ["Sex", "ChestPainType", "FastingBS", "RestingECG", "ExerciseAngina", "ST_Slope"]
for col in col_cat:
    print(f"Unique values in {col}:")
    print(df[col].value_counts())
    print('\n')
```

```
Unique values in Sex:
Sex
M    725
F    193
Name: count, dtype: int64


Unique values in ChestPainType:
ChestPainType
ASY    496
NAP    203
ATA    173
TA      46
Name: count, dtype: int64


Unique values in FastingBS:
FastingBS
0    704
1    214
Name: count, dtype: int64


Unique values in RestingECG:
RestingECG
Normal    552
LVH       188
ST        178
Name: count, dtype: int64


Unique values in ExerciseAngina:
ExerciseAngina
N    547
Y    371
Name: count, dtype: int64


Unique values in ST_Slope:
ST_Slope
Flat    460
Up      395
Down     63
Name: count, dtype: int64
```

In [10]:
```
df.describe()
```

Out[10]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
count	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000
mean	53.510893	132.396514	198.799564	0.233115	136.809368	0.887364	0.553377
std	9.432617	18.514154	109.384145	0.423046	25.460334	1.066570	0.497414
min	28.000000	0.000000	0.000000	0.000000	60.000000	-2.600000	0.000000
25%	47.000000	120.000000	173.250000	0.000000	120.000000	0.000000	0.000000
50%	54.000000	130.000000	223.000000	0.000000	138.000000	0.600000	1.000000
75%	60.000000	140.000000	267.000000	0.000000	156.000000	1.500000	1.000000
max	77.000000	200.000000	603.000000	1.000000	202.000000	6.200000	1.000000

- There are outliers for Cholesterol and RestingBP, with values of 0 which is not possible.

In [11]:
```
df.loc[df['RestingBP'] == 0]
```

Out[11]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
449	55	M	NAP	0	0	0	Normal	155	N	1.5	Flat	1

- This row is the only person missing RestingBP and is also missing Cholesterol, so it should not affect our dataset too much if we remove them.

In [12]:
```
df = df[df['RestingBP'] != 0]
df.loc[df['Cholesterol'] == 0]
```

Out[12]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
293	65	M	ASY	115	0	0	Normal	93	Y	0.0	Flat	1
294	32	M	TA	95	0	1	Normal	127	N	0.7	Up	1
295	61	M	ASY	105	0	1	Normal	110	Y	1.5	Up	1
296	50	M	ASY	145	0	1	Normal	139	Y	0.7	Flat	1
297	57	M	ASY	110	0	1	ST	131	Y	1.4	Up	1
...	...	...	...	...	...	...	...	...	...	...	...	...
514	43	M	ASY	122	0	0	Normal	120	N	0.5	Up	1
515	63	M	NAP	130	0	1	ST	160	N	3.0	Flat	0
518	48	M	NAP	102	0	1	ST	110	Y	1.0	Down	1
535	56	M	ASY	130	0	0	LVH	122	Y	1.0	Flat	1
536	62	M	NAP	133	0	1	ST	119	Y	1.2	Flat	1

171 rows × 12 columns

- There are a lot of missing Cholesterol values so we will impute the value with the median.

In [13]:
```
df['Cholesterol'] = df['Cholesterol'].replace(0, df['Cholesterol'].median())
df['Cholesterol'].describe()
```

Out[13]:
```
count    917.000000
mean     240.600872
std       54.009298
min       85.000000
25%      214.000000
50%      223.000000
75%      267.000000
max      603.000000
Name: Cholesterol, dtype: float64
```

3. Visualize dataset

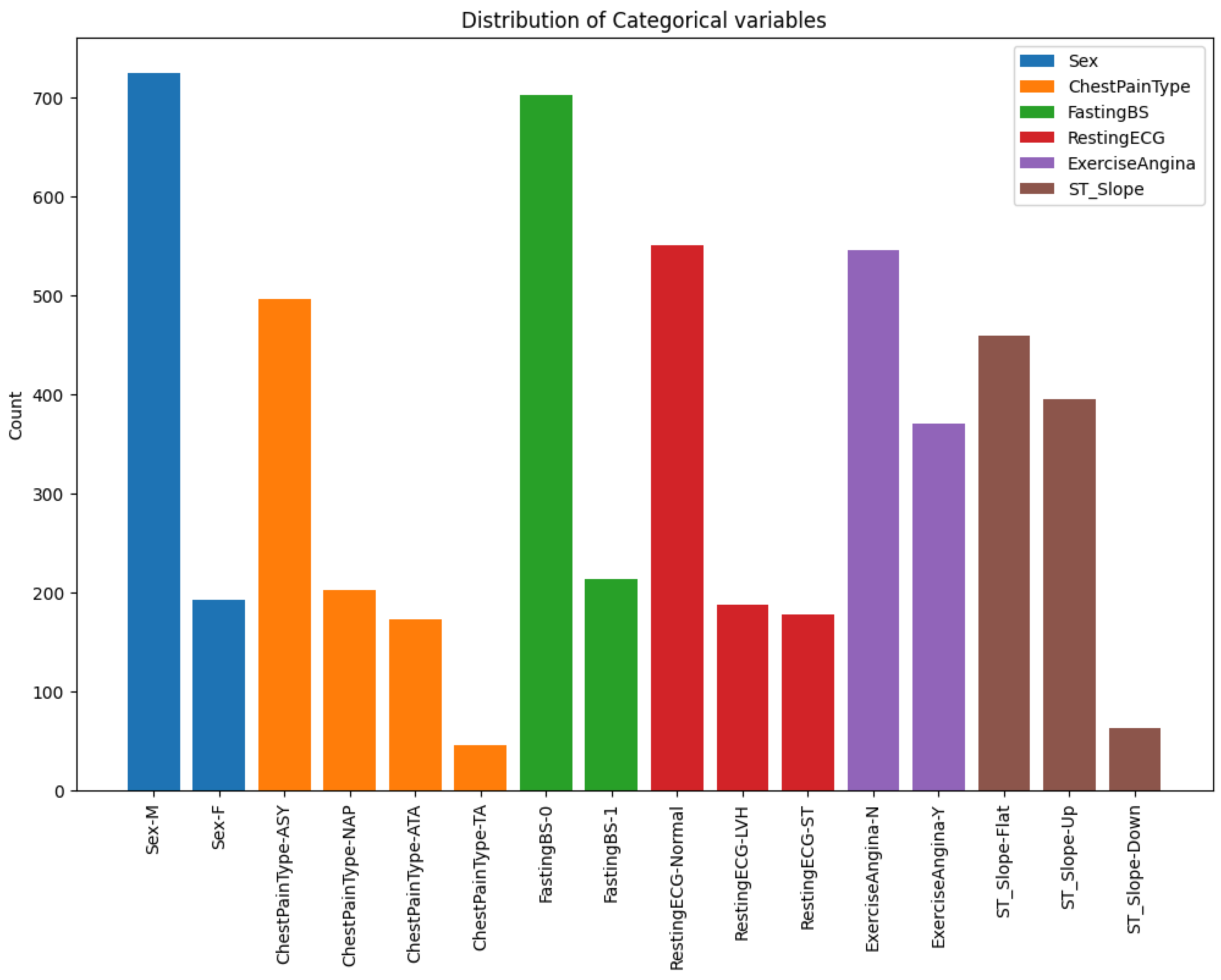
Explanation of variables

Source: https://archive.ics.uci.edu/dataset/45/heart+disease

- Categorical variables
  - `Sex`
    - `M` : male
    - `F` : female
  - `ChestPainType`
    - `ATA` : atypical angina (chest pain that doesn't follow typical pattern)
    - `NAP` : non-anginal pain (pain not related to heart)
    - `ASY` : asymptomatic (no pain)
    - `TA` : typical angina (chest pain typically related to heart issues)
  - `FastingBS` (fasting blood sugar)
    - `0` : normal (below 120 mg/dl)
    - `1` : abnormal (above 120mg/dl)
  - `RestingECG` (electrocardiogram results)
    - `Normal`
    - `ST` : ST-T wave abnormality (changes in segments of ECG waves)
    - `LVH` : left ventricular hypertrophy (enlargement of heart's left ventricle)
  - `ExerciseAngina` (chest pain during exercise)
    - `Y` : yes
    - `N` : no
  - `ST_Slope` (slope of ST segment in ECG)
    - `Up` : up-sloping ST segment (generally normal)
    - `Flat` : flat ST segment (potential indicator of heart disease)
    - `Down` : down-sloping ST segment (potential indicator of heart disease)
  - `HeartDisease`
    - `0` : no heart disease
    - `1` : heart disease
- Numerical variables
  - `Age`
    - Represents the age of the patient in years.
  - `RestingBP`
    - Resting Blood Pressure, measured in mm Hg (millimeters of mercury).
    - Indicates the blood pressure of the patient while at rest. High blood pressure can be a risk factor for heart disease.
  - `Cholesterol`
    - Total cholesterol level in mg/dL (milligrams per deciliter).
    - Abnormal cholesterol levels (high or low) can be indicative of heart health issues.
  - `MaxHR`
    - Maximum heart rate achieved during exercise, measured in beats per minute (bpm).
    - Lower maximum heart rate values can indicate heart disease, while higher maximum heart rate can indicate physical fitness.
  - `Oldpeak`
    - ECG ST depression induced by exercise relative to rest, measured in mm.
    - Higher values might suggest underlying cardiac problems or reduced blood flow.

- From this information alone, we might want to look at correlations between demographics (age, sex) and the other variables.
- We should also look at how each of these variables correlate with heart disease prevalence.

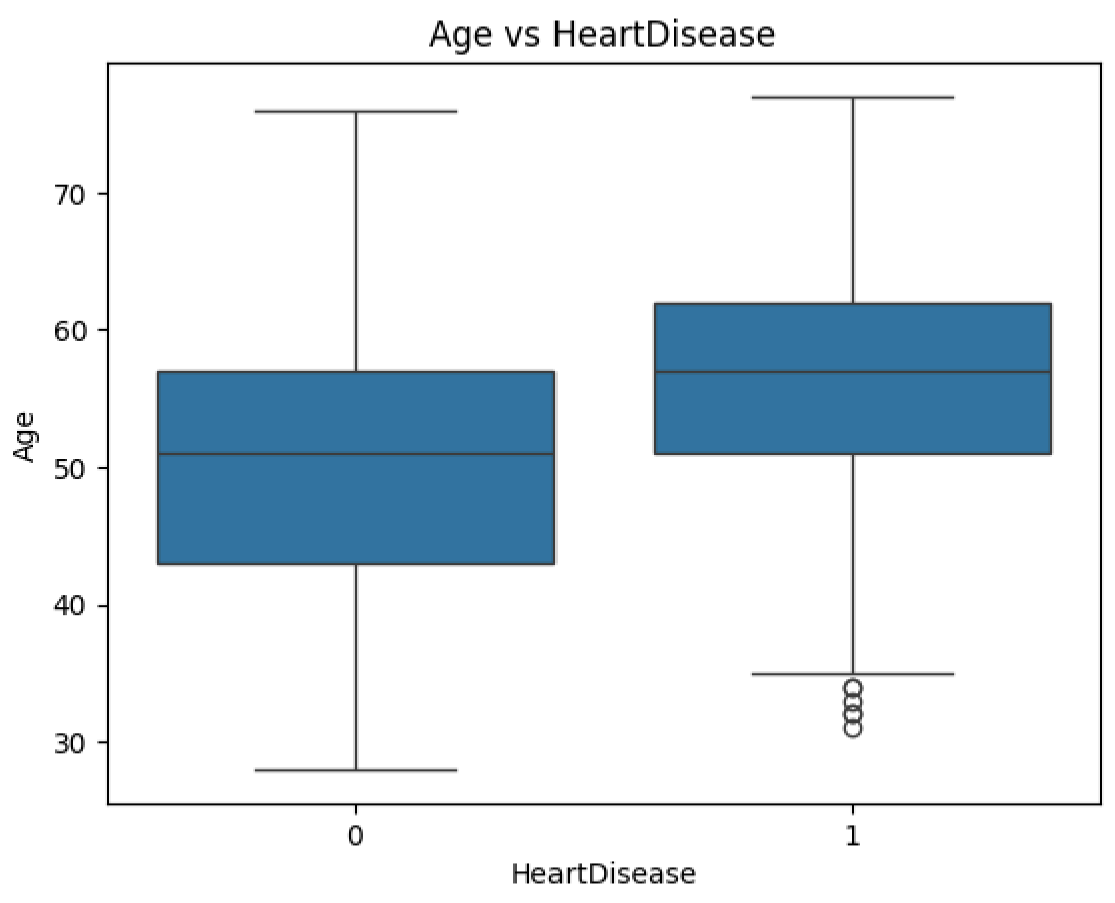
In [14]:
```python
# Plot distribution of categorical variables with barplots
counts = {col: df[col].value_counts() for col in col_cat}
plt.figure(figsize=(12, 8))
for i, (col, count) in enumerate(counts.items(), 1):
    plt.bar([f"{col}-{index}" for index in count.index], count.values, label=col)
plt.xticks(rotation=90)
plt.ylabel("Count")
plt.title("Distribution of Categorical variables")
plt.legend()
plt.show()
```

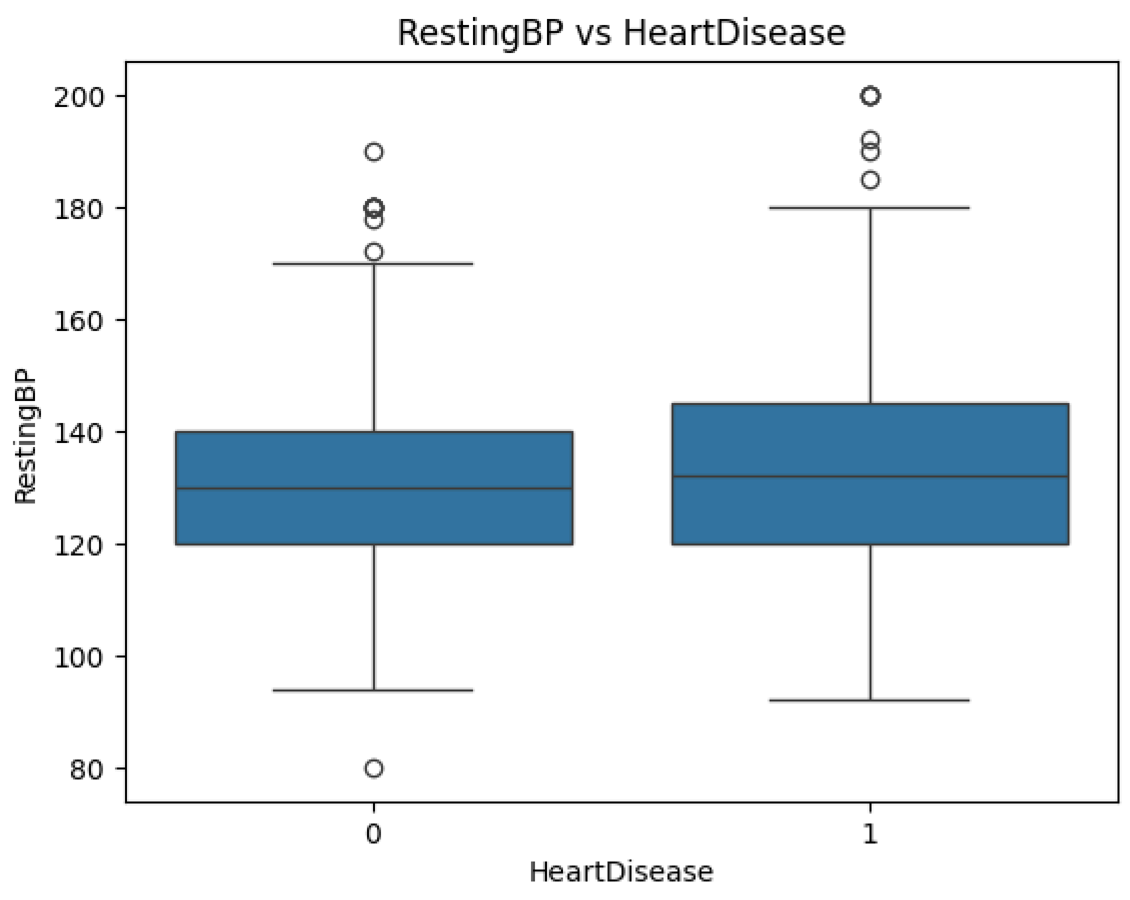


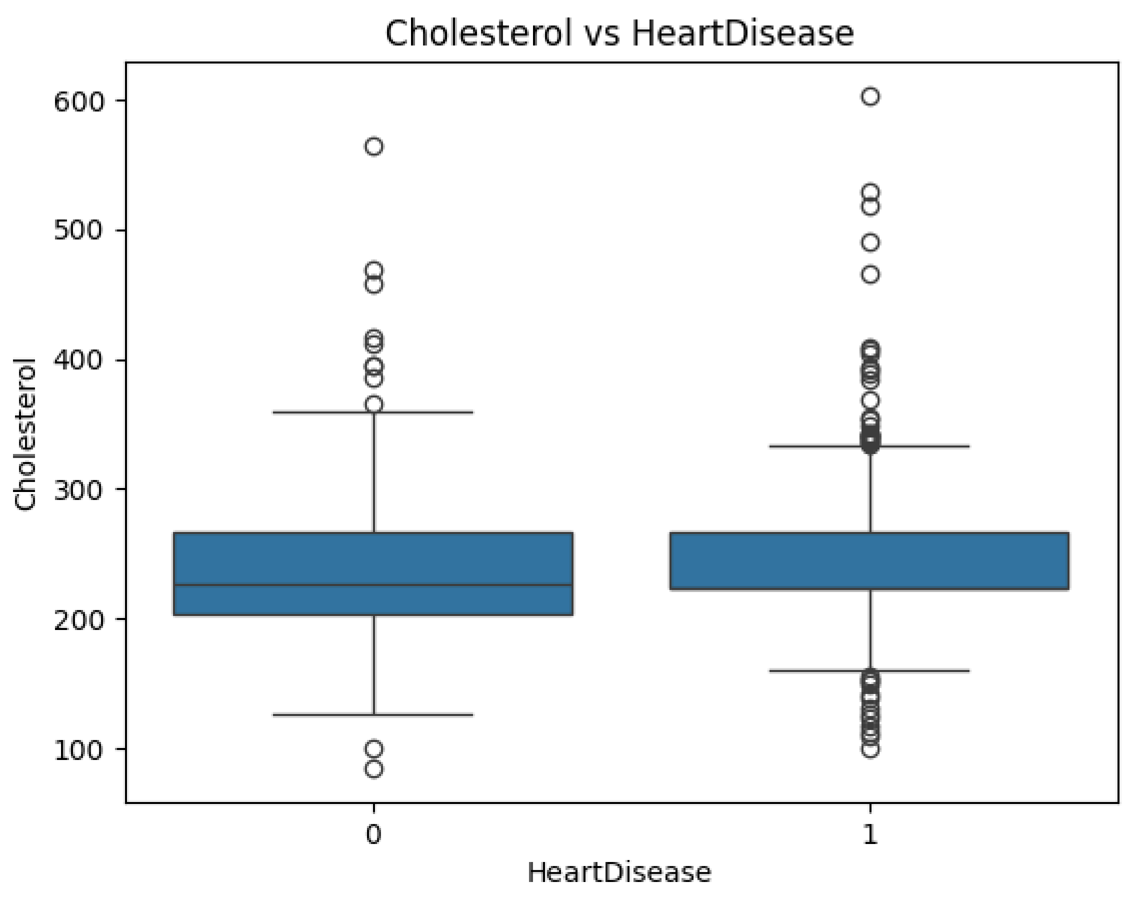
- This dataset seems to be dominated by males. For chest pain, fasting blood sugar, resting ecg, and exercise angina, the majority of patients seem to be normal. However, many patients seem to have a flat st slope which is an indicator of heart disease.

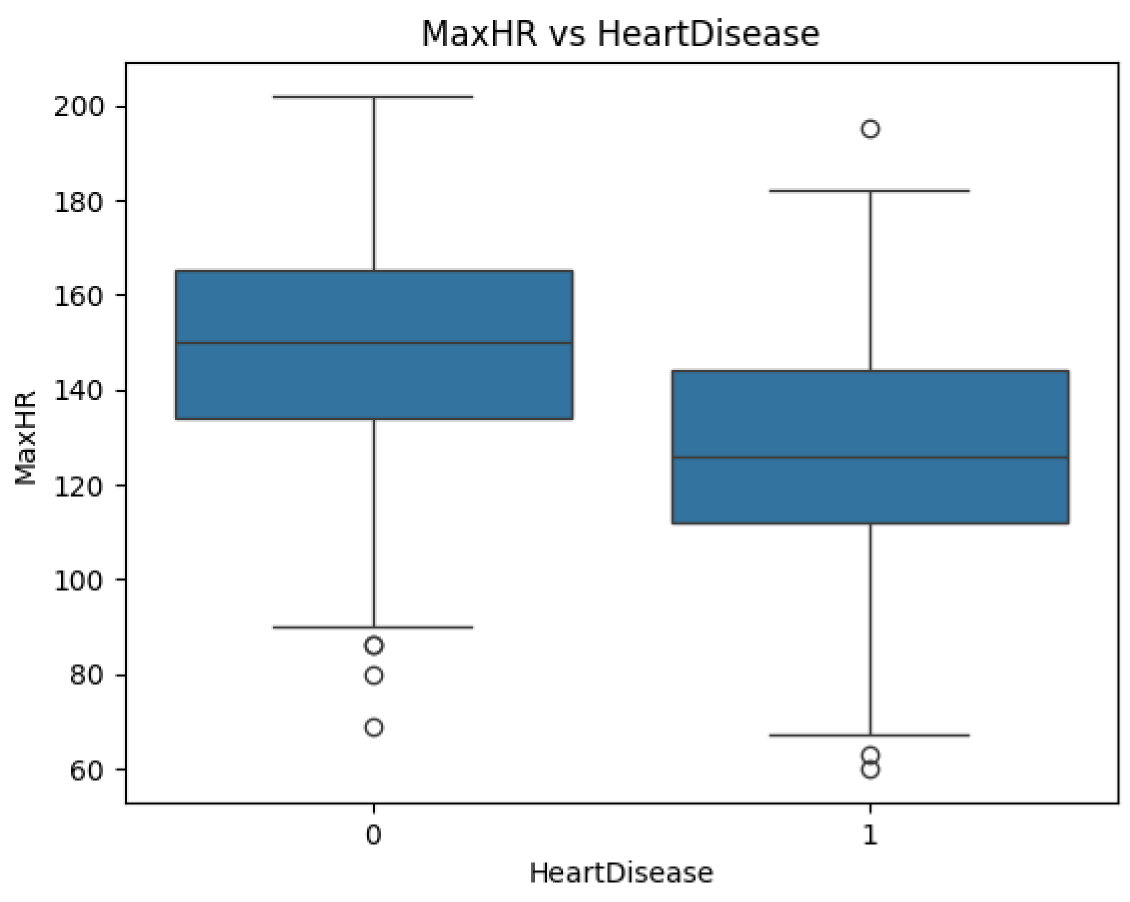
Visualize numerical variables vs heart disease using box plots

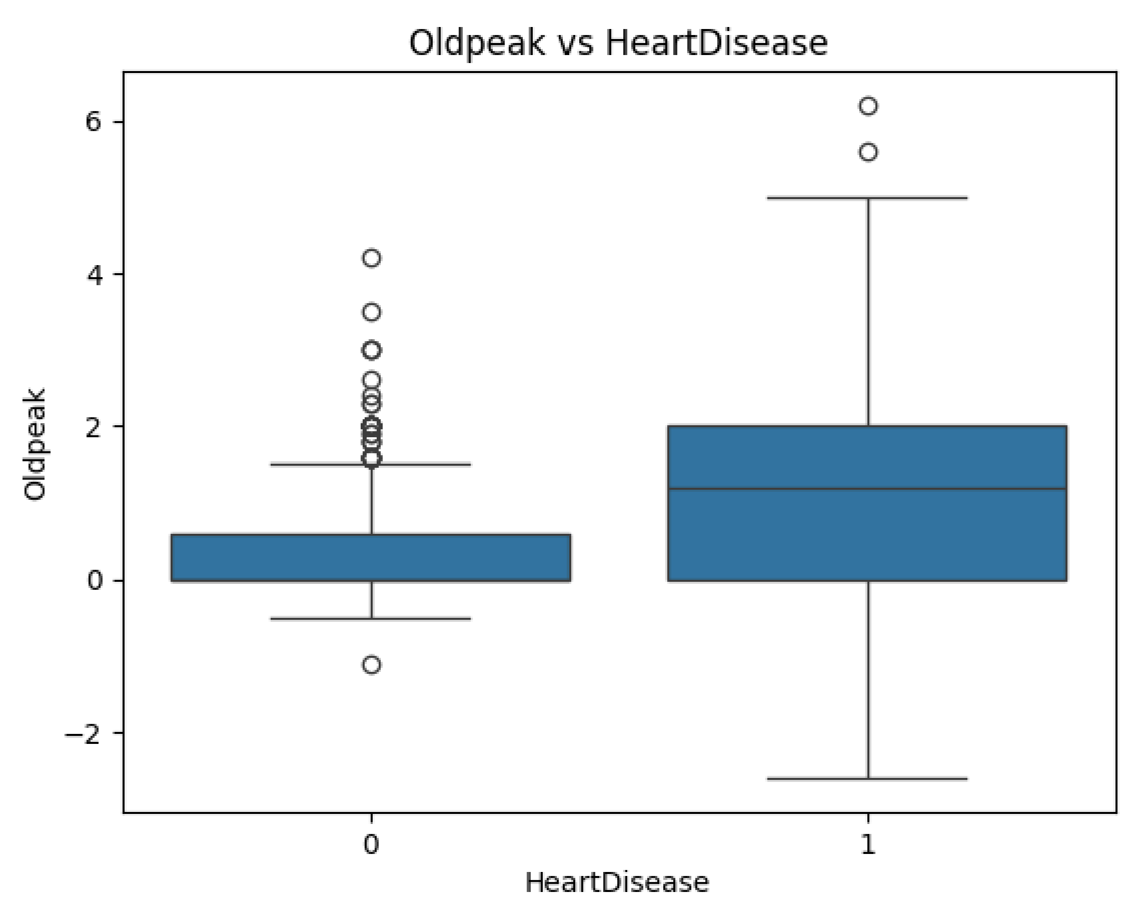
In [15]:
```
col_num = ['Age', 'RestingBP', 'Cholesterol', 'MaxHR', 'Oldpeak']

for i, column in enumerate(col_num, 1):
    sns.boxplot(x='HeartDisease', y=column, data=df)
    plt.title(f'{column} vs HeartDisease')
    plt.show()
```











```
In [16]: # Get distribution of each categorical value with pandas
         for col in col_num:
             print(f'{col} vs HeartDisease')
             print(df.groupby('HeartDisease')[col].describe())
             print('\n')
```

```
Age vs HeartDisease
              count       mean       std   min   25%   50%   75%   max
HeartDisease
0             410.0  50.551220  9.444915  28.0  43.0  51.0  57.0  76.0
1             507.0  55.901381  8.735583  31.0  51.0  57.0  62.0  77.0


RestingBP vs HeartDisease
              count        mean        std   min    25%    50%    75%    max
HeartDisease
0             410.0  130.180488  16.499585  80.0  120.0  130.0  140.0  190.0
1             507.0  134.449704  18.928797  92.0  120.0  132.0  145.0  200.0


Cholesterol vs HeartDisease
              count        mean        std    min    25%    50%     75%    max
HeartDisease
0             410.0  238.000000  54.130197   85.0  204.0  227.0  266.75  564.0
1             507.0  242.704142  53.872885  100.0  223.0  223.0  267.00  603.0


MaxHR vs HeartDisease
              count        mean        std   min    25%    50%    75%    max
HeartDisease
0             410.0  148.151220  23.288067  69.0  134.0  150.0  165.0  202.0
1             507.0  127.601578  23.378376  60.0  112.0  126.0  144.0  195.0


Oldpeak vs HeartDisease
              count      mean       std  min  25%  50%  75%  max
HeartDisease
0             410.0  0.408049  0.699709 -1.1  0.0  0.0  0.6  4.2
1             507.0  1.273767  1.152966 -2.6  0.0  1.2  2.0  6.2
```

For these boxplots and their respective statistics, we can make several analyses:

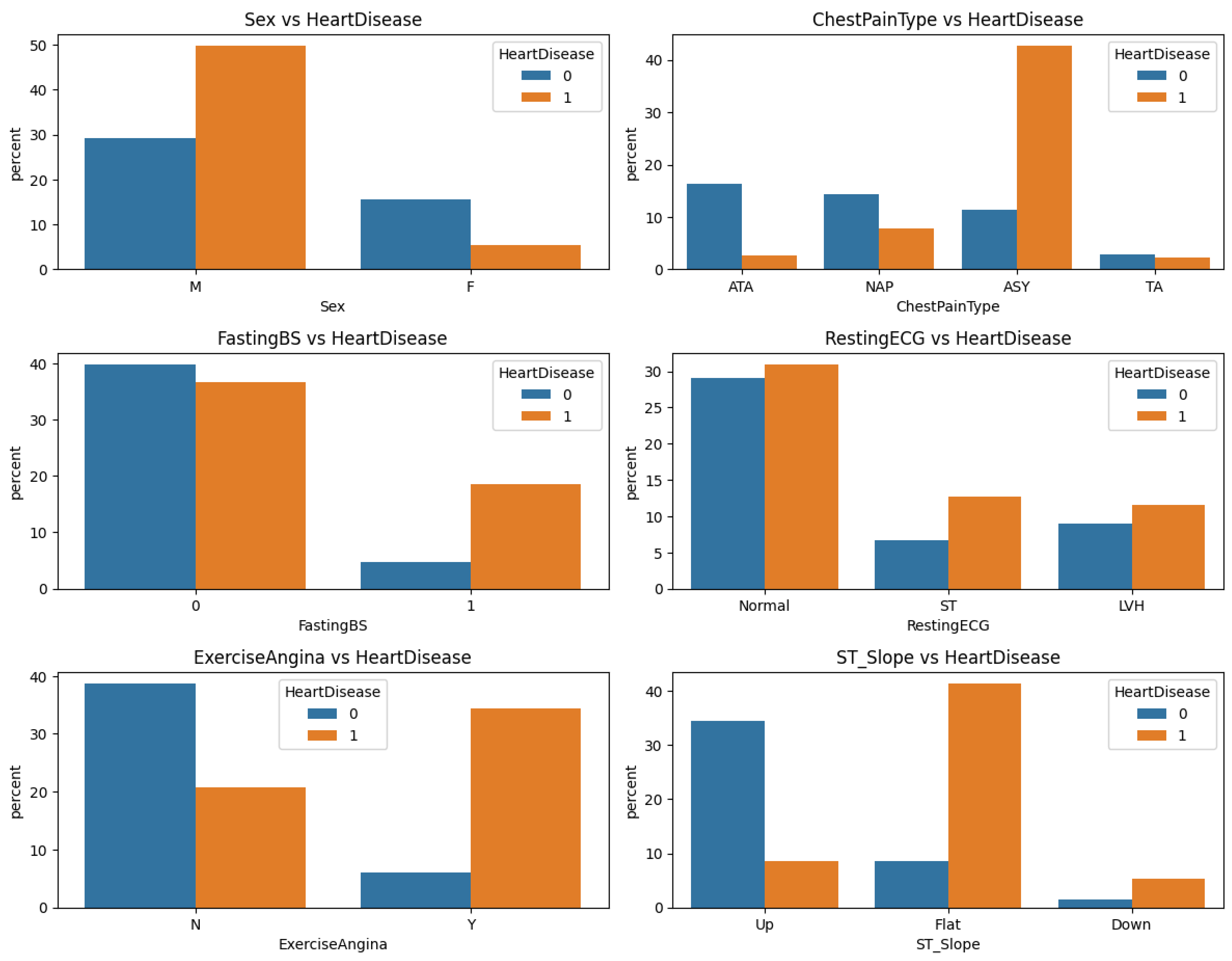
- Age:
    - The age graph for those with heart disease is shifted right compared to those without heart disease.
    - The mean and median are both higher in those with heart disease than those without.
    - High positive correlation
- RestingBP:
    - The resting blood pressure of those with heart disease is slightly higher across the range, with slightly higher min, quartiles, and max.
    - Example: median of those with heart disease is 132 compared to 130
    - Low positive correlation
- Cholesterol:
    - The cholesterol levels of those with heart disease is higher in the lower and upper ranges of the dataset than those without.
        - We imputed a lot of these values so the range of values will be much closer to the median.
    - The median cholesterol level of those with heart disease (223) is slightly lower than the median of those without heart disease (227) yet the mean is higher and the min and max are higher. The distribution data for those with heart disease is skewed right.
    - Moderate positive correlation
- MaxHR:
    - The max heart rate of those with heart disease is visibly and consistently lower than those without
    - The median max heart rate of those with heart disease is 24 lower and the mean is 21 lower. This trend is seen across the entire dataset
    - High negative correlation
- OldPeak:
    - The distribution of values of those with heart disease is much more spread out than those without heart disease.
    - The standard deviation of those with heart disease (1.15) is much greater than those without (0.70).
    - The mean and median are also higher for those with heart disease compared to those without.
    - Moderate positive correlation on high values and low negative correlation on low values

Conclusion: all the numerical variables have some correlation with heart disease, with some being very strong predictors of heart disease.

Visualizing categorical variables vs heart disease using count plot

```
In [17]: plt.figure(figsize=(12, 12))
```

```python
# Plotting categorical columns with HeartDisease
for i, column in enumerate(col_cat, 1):
    plt.subplot(4, 2, i)
    sns.countplot(x=column, hue='HeartDisease', data=df, stat='percent')
    plt.title(f'{column} vs HeartDisease')
    plt.tight_layout()

plt.show()
```



In [18]:
```python
# Calculate proportions within each category
for column in col_cat:
    print(f"Proportions of HeartDisease in each category of {column}:")
    crosstab = pd.crosstab(df[column], df['HeartDisease'], margins=True, margins_name="Total")
    crosstab_percent = crosstab.div(crosstab.sum(axis=1), axis=0) * 100
    print(crosstab_percent)
    print("\n")
```

```
Proportions of HeartDisease in each category of Sex:
HeartDisease          0          1  Total
Sex
F             37.046632  12.953368   50.0
M             18.439227  31.560773   50.0
Total         22.355507  27.644493   50.0


Proportions of HeartDisease in each category of ChestPainType:
HeartDisease           0          1  Total
ChestPainType
ASY            10.483871  39.516129   50.0
ATA            43.063584   6.936416   50.0
NAP            32.425743  17.574257   50.0
TA             28.260870  21.739130   50.0
Total          22.355507  27.644493   50.0


Proportions of HeartDisease in each category of FastingBS:
HeartDisease          0          1  Total
FastingBS
0             26.031294  23.968706   50.0
1             10.280374  39.719626   50.0
Total         22.355507  27.644493   50.0


Proportions of HeartDisease in each category of RestingECG:
HeartDisease          0          1  Total
RestingECG
LVH           21.808511  28.191489   50.0
Normal        24.228675  25.771325   50.0
ST            17.134831  32.865169   50.0
Total         22.355507  27.644493   50.0


Proportions of HeartDisease in each category of ExerciseAngina:
HeartDisease            0          1  Total
ExerciseAngina
N               32.509158  17.490842   50.0
Y                7.412399  42.587601   50.0
Total           22.355507  27.644493   50.0


Proportions of HeartDisease in each category of ST_Slope:
HeartDisease          0          1  Total
ST_Slope
Down          11.111111  38.888889   50.0
Flat           8.605664  41.394336   50.0
Up            40.126582   9.873418   50.0
Total         22.355507  27.644493   50.0
```

Analysis of categorical variables

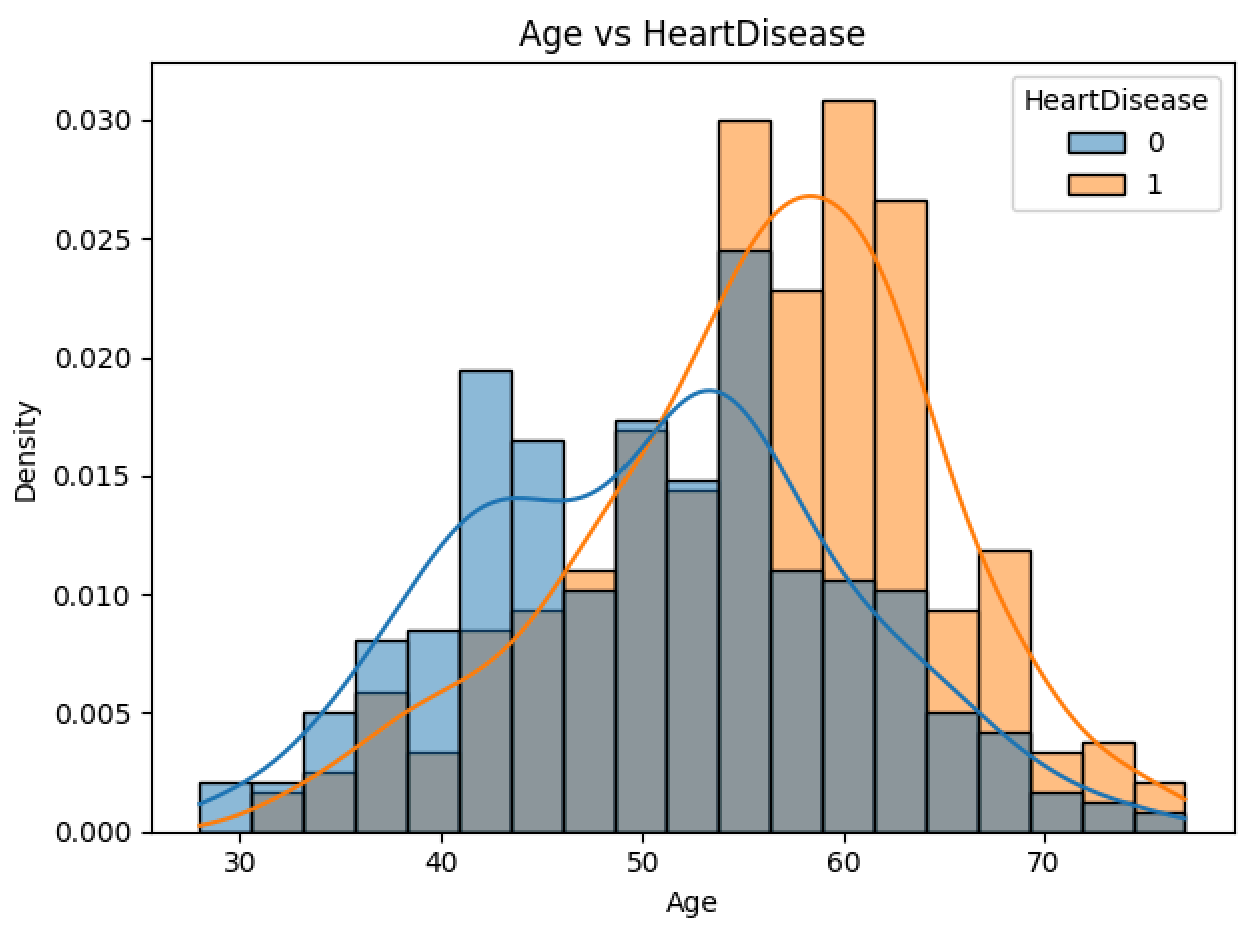
- Sex:
    - Males are much more likely to have heart disease (32%) compared to females (13%).
- ChestPainType:
    - Patients with any type of chest pain (ATA, NAP, TA) are less likely to have heart disease.
    - Interestingly, patients without any chest pain (ASY) are almost four times as likely to have heart disease (40%) than not (10%). Additionally, 79% of patients with heart disease have no heart pain.
- FastingBS:
    - Having normal fasting blood sugar is not very indicative of heart disease.
    - Having elevated fasting blood sugar is very indicative of heart disease.
- Resting ECG:
    - Normal ECG is not very indicative of heart disease but any abnormal ECG is slightly more likely to result in heart disease.
- Exercise Angina:
    - Having angina during exercise is a very strong indicator of heart disease, with 43% of people who have angina and heart disease as compared to 17% of people without angina having heart disease.
- ST Slope:
    - Up-sloping ST (normal) is highly correlated with no heart disease, while flat and down-sloping ST is very highly correlated with heart disease.

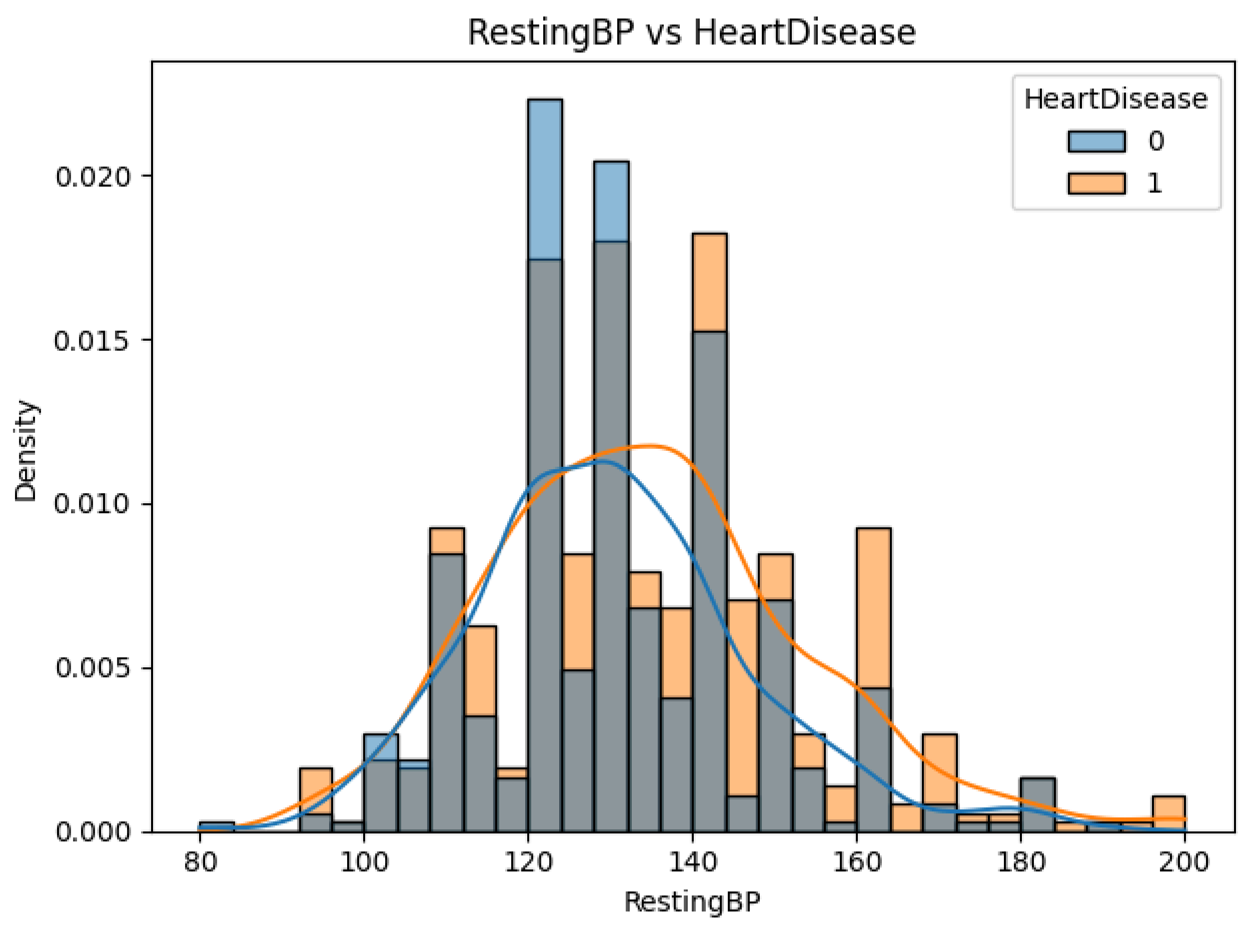
Conclusion: All the categorical variables are predictors of heart disease in some way. Some categorical variables are much better predictors of heart disease than others.

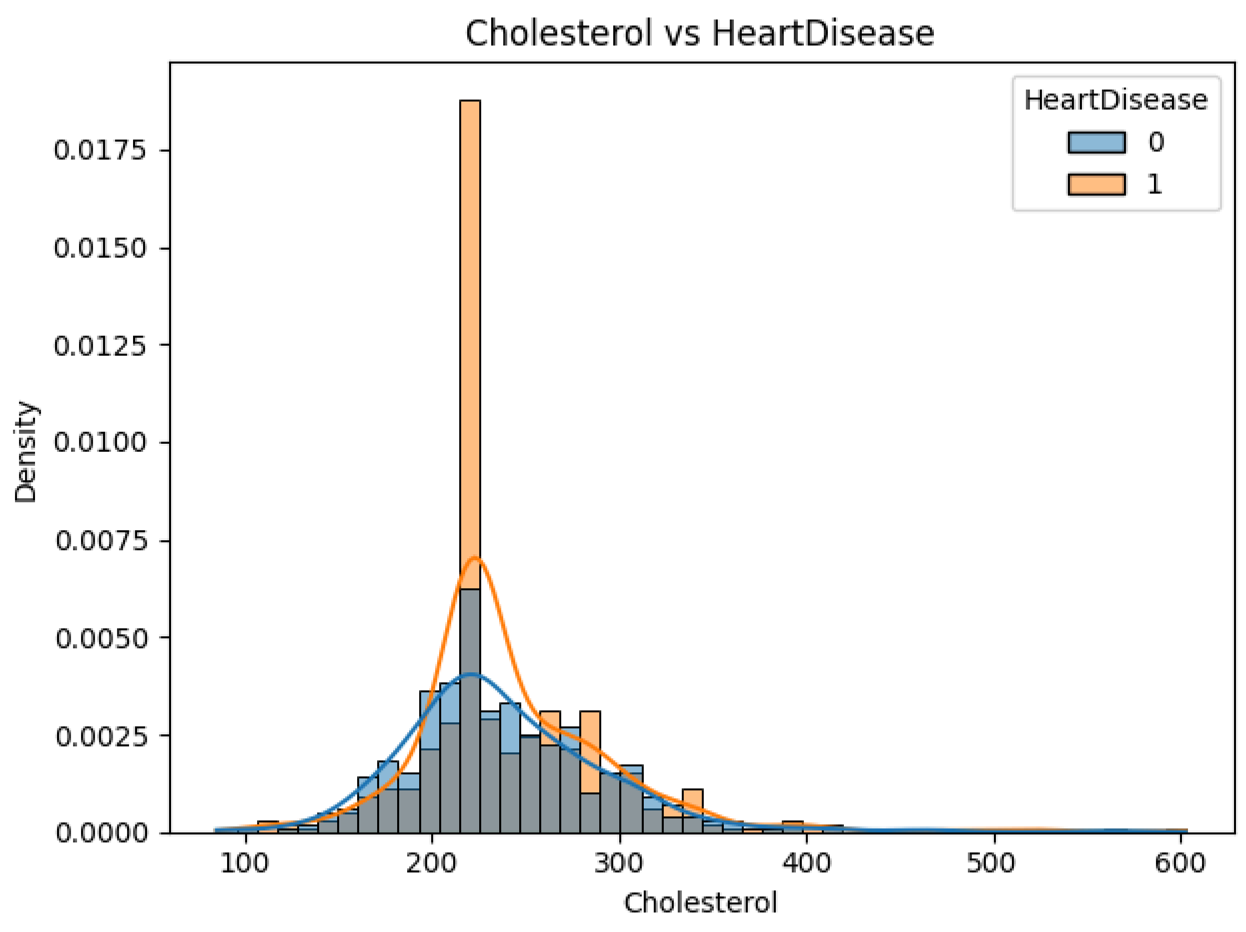
Some more visualization of the numerical variables using histogram and line

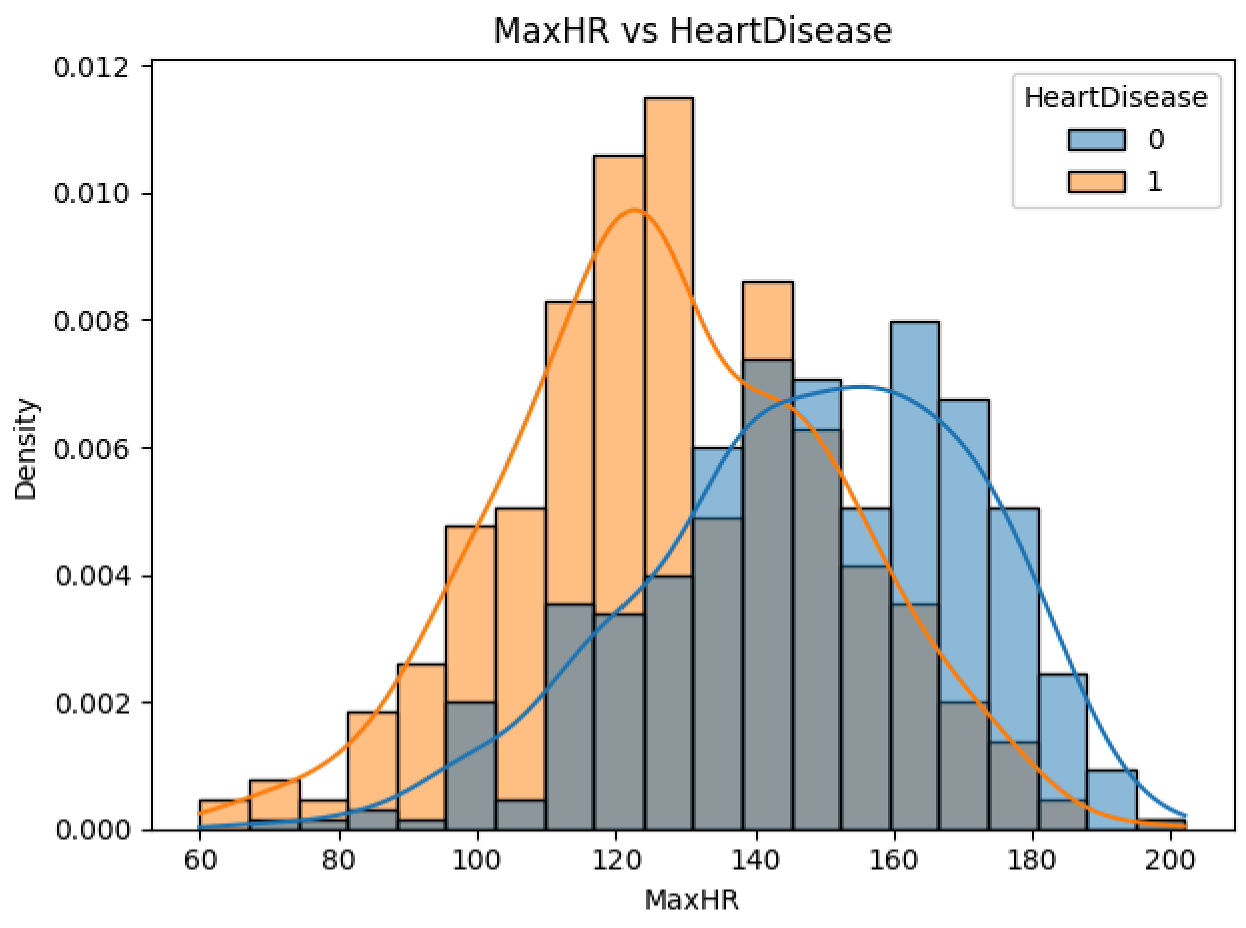
- Reinforces previous conclusions we made about numerical variables
    - Age is shifted right for heart disease compared to those without
    - Resting BP is skewed to the right for heart disease compared to those without
    - Cholesterol is also skewed to the right for heart disease but slightly compared to those without
    - Max heart rate is significantly shifted right for heart disease compared to those without
    - Old peak is mostly skewed right for heart disease but has greater variance leading to more extreme minimum values, compared to those without

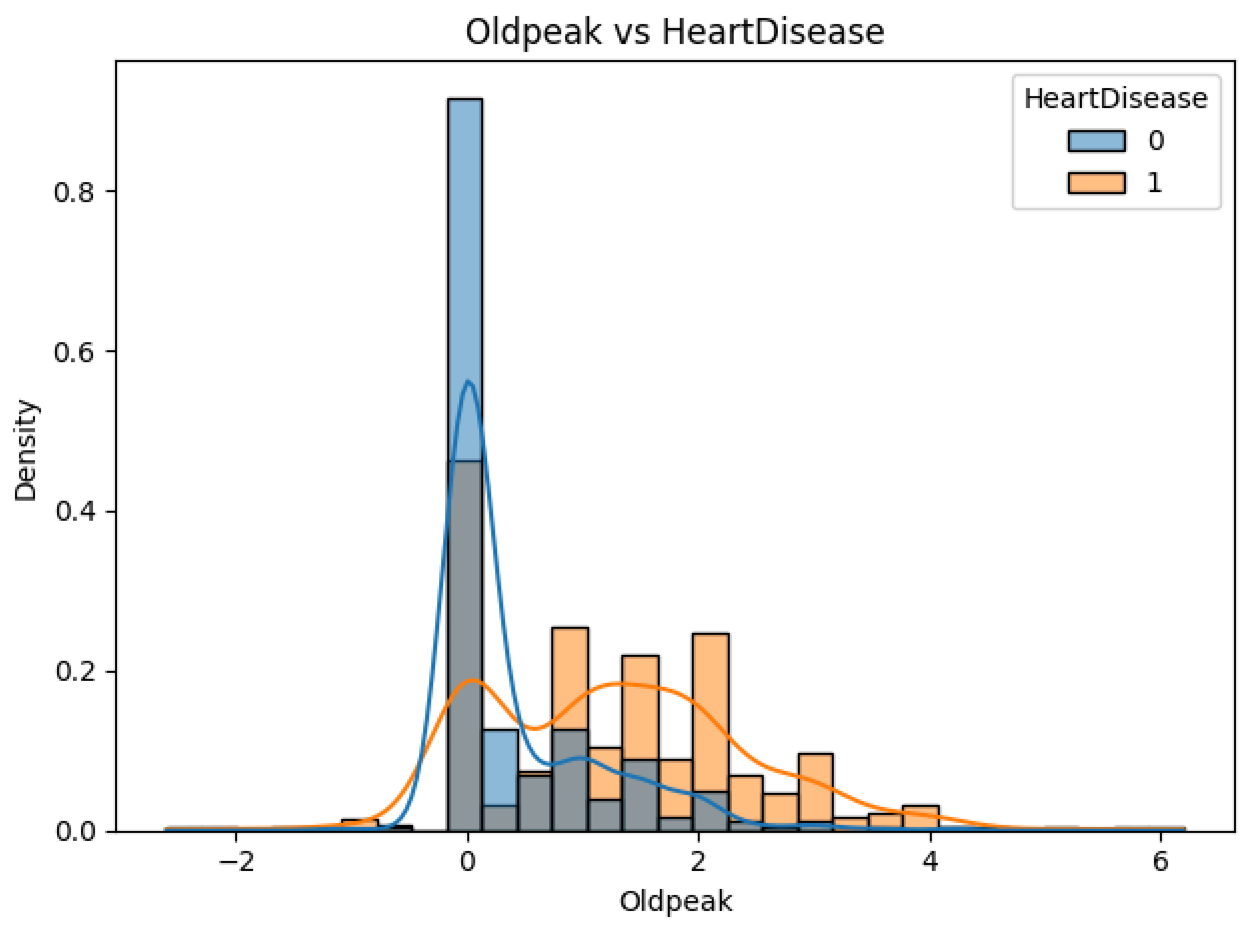
In [19]:
```
# Plotting numerical columns with HeartDisease using histograms
for i, column in enumerate(col_num, len(col_cat) + 1):
    sns.histplot(data=df, x=column, hue='HeartDisease', kde=True, multiple='layer' , stat='density')
    plt.title(f'{column} vs HeartDisease')
    plt.tight_layout()
    plt.show()
```











4. Creating a predictive model for heart disease

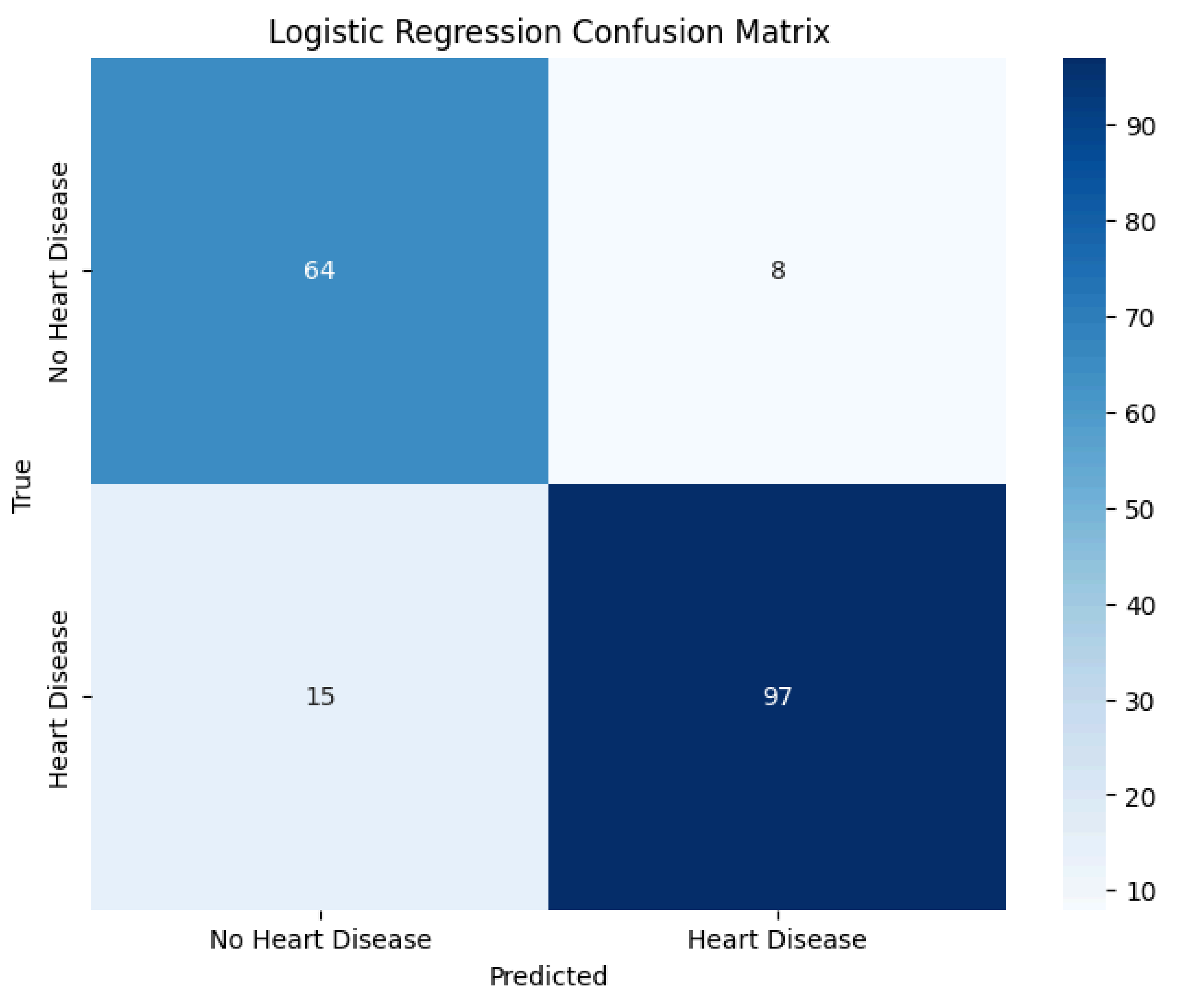
- We will use the scikit-learn package and its logistics regression and random forest classification models to create a model to predict heart disease.

In [20]:
```
# Prepare data
df_encoded = pd.get_dummies(df, columns=col_cat, dtype='int', drop_first=True)
```

We will use a logistic regression model because our dependent variable is discrete

In [21]:
```
# Define variables
X = df_encoded.drop("HeartDisease", axis=1)
y = df_encoded["HeartDisease"]

# 80/20 train/test split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Logistic regression model
log_reg = LogisticRegression(max_iter=10000)
log_reg.fit(X_train, y_train)
y_pred_log = log_reg.predict(X_test)

# Results
print("Logistic Regression Classification Report:\n" + classification_report(y_test, y_pred_log))
cm_log = confusion_matrix(y_test, y_pred_log)

# Plot classification matrix
plt.figure(figsize=(8, 6))
sns.heatmap(cm_log, annot=True, fmt='d', cmap='Blues', xticklabels=['No Heart Disease', 'Heart Disease'], yticklabels=['No Heart Disease', 'Heart Disease'])
plt.xlabel('Predicted')
plt.ylabel('True')
plt.title('Logistic Regression Confusion Matrix')
plt.show()
```

```
Logistic Regression Classification Report:
              precision    recall  f1-score   support

           0       0.81      0.89      0.85        72
           1       0.92      0.87      0.89       112

    accuracy                           0.88       184
   macro avg       0.87      0.88      0.87       184
weighted avg       0.88      0.88      0.88       184
```

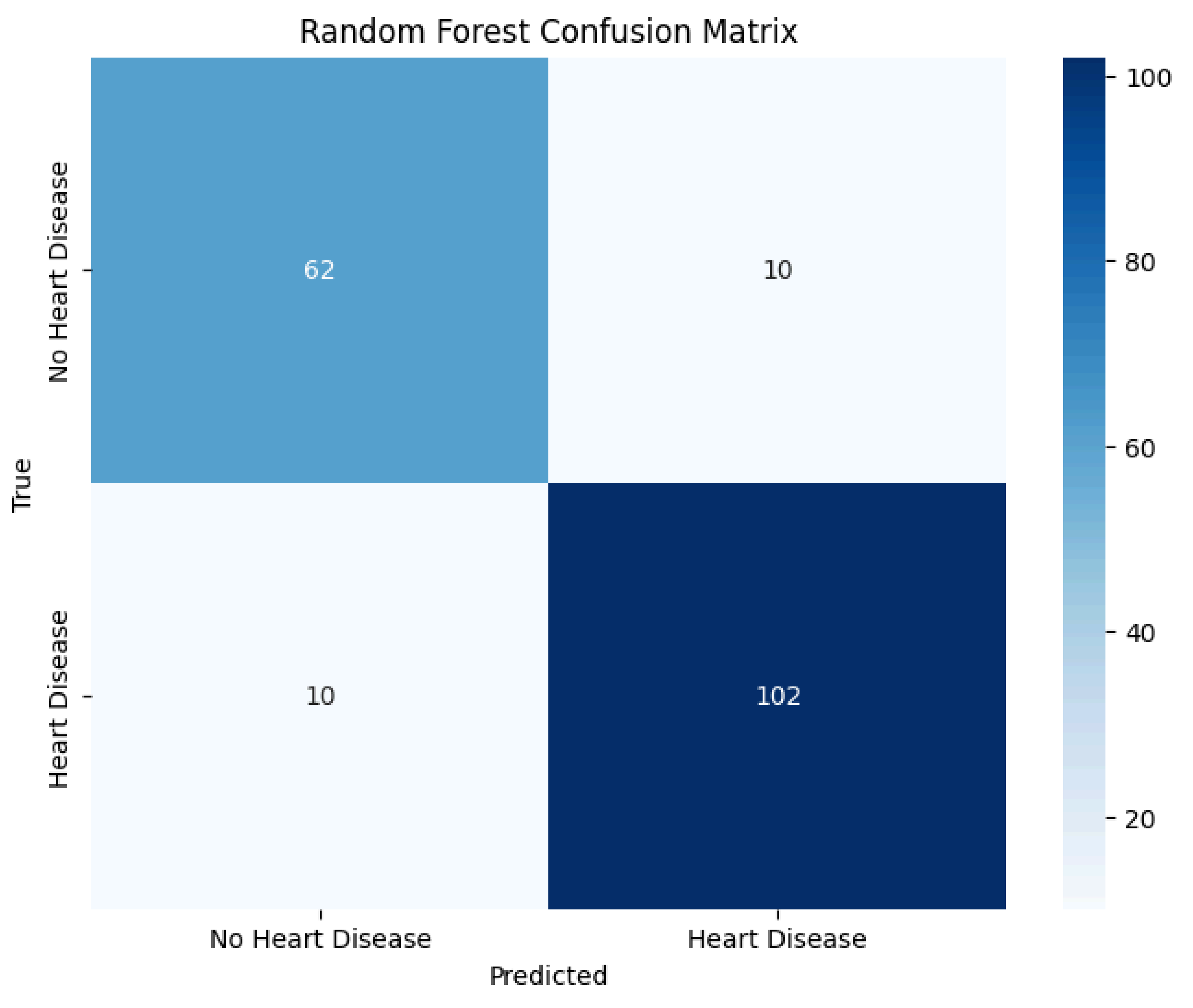


Results of logistic regression

- Logistic regression model has high precision and recall, which means the model can correctly predict and identify heart disease cases respectively.
    - The model correctly predicted no heart disease 81% of the time and correctly identified no heart disease 89% of the time.
    - The model correctly predicted heart disease 92% of the time and correctly identified heart disease 87% of the time.
- The model works slightly better for predicting heart disease than predicting no heart disease, with an f1_score of 0.89 vs 0.85 respectively.

In [22]:
```python
# Random Forest model
rf_clf = RandomForestClassifier(random_state=42)
rf_clf.fit(X_train, y_train)
y_pred_rf = rf_clf.predict(X_test)

# Results
print("Random Forest Classification Report:\n" + classification_report(y_test, y_pred_rf))
cm_rf = confusion_matrix(y_test, y_pred_rf)

# Plot classification matrix
plt.figure(figsize=(8, 6))
sns.heatmap(cm_rf, annot=True, fmt='d', cmap='Blues', xticklabels=['No Heart Disease', 'Heart Disease'], yticklabels=['No Heart Disease', 'Heart Disease'])
plt.xlabel('Predicted')
plt.ylabel('True')
plt.title('Random Forest Confusion Matrix')
plt.show()
```

```
Random Forest Classification Report:
              precision    recall  f1-score   support

           0       0.86      0.86      0.86        72
           1       0.91      0.91      0.91       112

    accuracy                           0.89       184
   macro avg       0.89      0.89      0.89       184
weighted avg       0.89      0.89      0.89       184
```

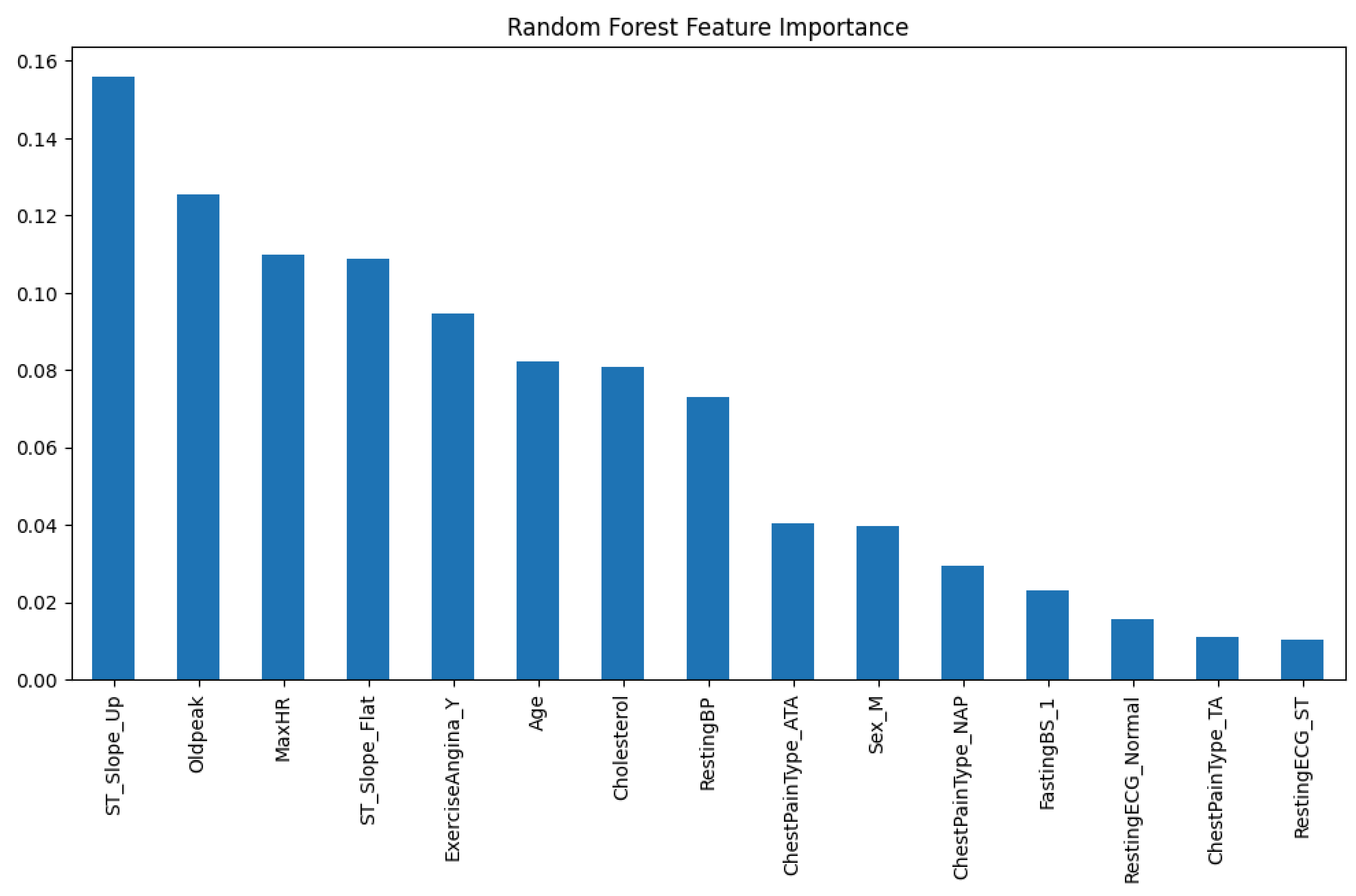


Results of random forest

- The random forest model had even greater success than the logistic regression model.
    - The model correctly predicted no heart disease 86% of the time and correctly identified no heart disease 86% of the time.
    - The model correctly predicted heart disease 91% of the time and correctly identified heart disease 91% of the time.
- Again, the model performs better predicting heart disease as compared to predicting no heart disease.

Using the Random Forest model, we will identify the greatest risk factors for heart disease

In [23]:
```python
# Random Forest model Feature Importance
feature_importance = pd.Series(rf_clf.feature_importances_, index=X.columns).sort_values(ascending=False)

# Plot feature importance
plt.figure(figsize=(12, 6))
feature_importance.plot(kind='bar')
plt.title("Random Forest Feature Importance")
plt.show()

# Identify greatest risk factors
risk_factors = feature_importance.head(10)
print("Top Risk Factors for Heart Disease:")
print(risk_factors)
```



```
Top Risk Factors for Heart Disease:
ST_Slope_Up          0.155878
Oldpeak              0.125577
MaxHR                0.109860
ST_Slope_Flat        0.108732
ExerciseAngina_Y     0.094666
Age                  0.082255
Cholesterol          0.080939
RestingBP            0.072965
ChestPainType_ATA    0.040452
Sex_M                0.039695
dtype: float64
```

Using our data visualization analysis as well as the feature importance analysis, we can identify the top 5 following risk factors:

- Existence of ST slope up is the greatest risk factor for heart disease according to our model.
- Old peak is the second greatest risk factor, and extreme values will increase your risk of heart disease.
- Having a low max heart rate is the third greatest risk factor for heart disease.
- Existence of ST slope flat is the fourth greatest risk factor.
- Having angina during exercise is the fifth greatest risk factor.

5. Conclusion

- After analyzing the dataset, knowing your health status on these conditions will help predict heart disease and allow you to make lifestyle changes and receive medical advice to minimize the effects of heart disease.
- Many of these can be done at home, like measuring maximum heart rate, blood pressure, or identifying chest pain. However, some of these require going to the doctor or specialized tests, like measuring cholesterol or taking an ECG, which is why good medical infrastructure is important in reducing what is worldwide human's greatest killer today.
- More research has and will continue to be done on more efficient ways to predict heart disease as well as preventing and mitigating heart disease.