```
!pip install seaborn
```

```
Requirement already satisfied: seaborn in /opt/anaconda3/lib/python3.12/site-packages (0.13.2)
Requirement already satisfied: numpy!=1.24.0,>=1.20 in /opt/anaconda3/lib/python3.12/site-packages (from seaborn) (1.26.4)
Requirement already satisfied: pandas>=1.2 in /opt/anaconda3/lib/python3.12/site-packages (from seaborn) (2.2.2)
Requirement already satisfied: matplotlib!=3.6.1,>=3.4 in /opt/anaconda3/lib/python3.12/site-packages (from seaborn) (3.8.4)
Requirement already satisfied: contourpy>=1.0.1 in /opt/anaconda3/lib/python3.12/site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.2.0)
Requirement already satisfied: cycler>=0.10 in /opt/anaconda3/lib/python3.12/site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (0.11.0)
Requirement already satisfied: fonttools>=4.22.0 in /opt/anaconda3/lib/python3.12/site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (4.51.0)
Requirement already satisfied: kiwisolver>=1.3.1 in /opt/anaconda3/lib/python3.12/site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.4.4)
Requirement already satisfied: packaging>=20.0 in /opt/anaconda3/lib/python3.12/site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (23.2)
Requirement already satisfied: pillow>=8 in /opt/anaconda3/lib/python3.12/site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (10.3.0)
Requirement already satisfied: pyparsing>=2.3.1 in /opt/anaconda3/lib/python3.12/site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (3.0.9)
Requirement already satisfied: python-dateutil>=2.7 in /opt/anaconda3/lib/python3.12/site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (2.9.0.p
Requirement already satisfied: pytz>=2020.1 in /opt/anaconda3/lib/python3.12/site-packages (from pandas>=1.2->seaborn) (2024.1)
Requirement already satisfied: tzdata>=2022.7 in /opt/anaconda3/lib/python3.12/site-packages (from pandas>=1.2->seaborn) (2023.3)
Requirement already satisfied: six>=1.5 in /opt/anaconda3/lib/python3.12/site-packages (from python-dateutil>=2.7->matplotlib!=3.6.1,>=3.4->seaborn
```

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from matplotlib.pyplot import figure
import seaborn as sn
```

```
data = pd.read_csv("/Users/kavanamanvi/Desktop/PML/Final Project/heart.csv")
```

```
data.head()
```

	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

Data Information

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 12 columns):
 #   Column          Non-Null Count  Dtype
---  ------          --------------  -----
 0   Age             918 non-null    int64
 1   Sex             918 non-null    object
 2   ChestPainType   918 non-null    object
 3   RestingBP       918 non-null    int64
 4   Cholesterol     918 non-null    int64
 5   FastingBS       918 non-null    int64
 6   RestingECG      918 non-null    object
 7   MaxHR           918 non-null    int64
 8   ExerciseAngina  918 non-null    object
 9   Oldpeak         918 non-null    float64
 10  ST_Slope        918 non-null    object
 11  HeartDisease    918 non-null    int64
dtypes: float64(1), int64(6), object(5)
memory usage: 86.2+ KB
```

Check for None values in features

```
data.isna().sum()
```

```
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
```

Comment

1. There are no None values/empty values

Data Description

```
data.describe().T
```

	count	mean	std	min	25%	50%	75%	max
Age	918.0	53.510893	9.432617	28.0	47.00	54.0	60.0	77.0
RestingBP	918.0	132.396514	18.514154	0.0	120.00	130.0	140.0	200.0
Cholesterol	918.0	198.799564	109.384145	0.0	173.25	223.0	267.0	603.0
FastingBS	918.0	0.233115	0.423046	0.0	0.00	0.0	0.0	1.0
MaxHR	918.0	136.809368	25.460334	60.0	120.00	138.0	156.0	202.0
Oldpeak	918.0	0.887364	1.066570	-2.6	0.00	0.6	1.5	6.2
HeartDisease	918.0	0.553377	0.497414	0.0	0.00	1.0	1.0	1.0

```
data.describe(include=['O']).T
```

	count	unique	top	freq
Sex	918	2	M	725
ChestPainType	918	4	ASY	496
RestingECG	918	3	Normal	552
ExerciseAngina	918	2	N	547
ST_Slope	918	3	Flat	460

Exploratory Data Analysis

Check for correlation

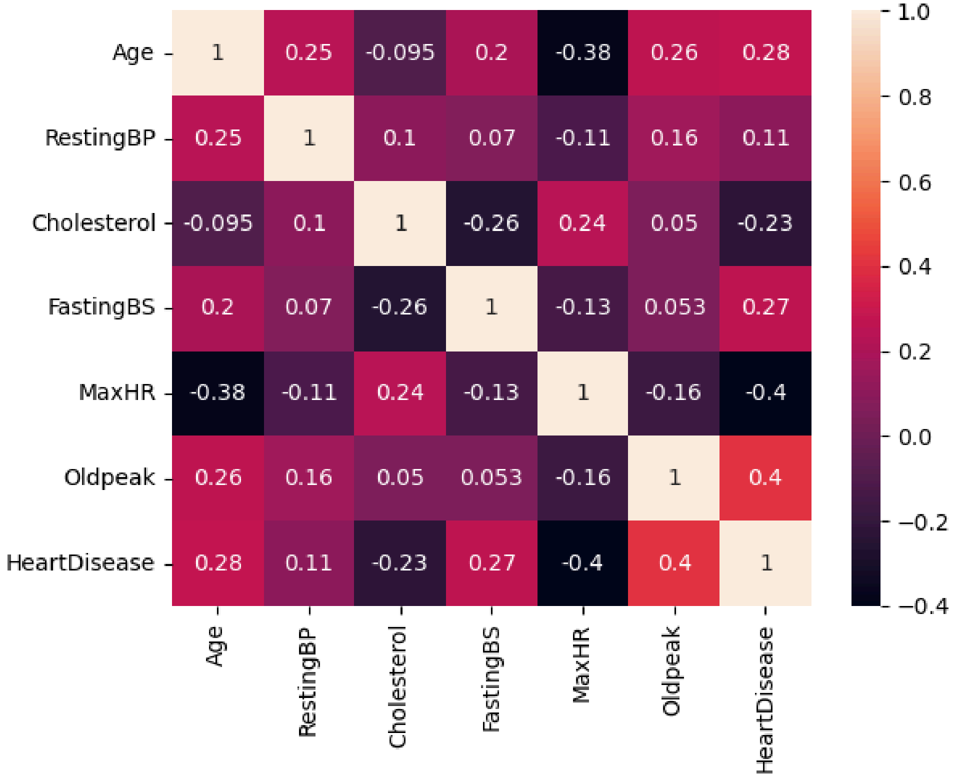
```
correlation_data = data.drop(columns = ["Sex", "ChestPainType", "RestingECG", "ExerciseAngina", "ST_Slope"]).corr()
```

```
correlation_data
```

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisease
Age	1.000000	0.254399	-0.095282	0.198039	-0.382045	0.258612	0.282039
RestingBP	0.254399	1.000000	0.100893	0.070193	-0.112135	0.164803	0.107589
Cholesterol	-0.095282	0.100893	1.000000	-0.260974	0.235792	0.050148	-0.232741
FastingBS	0.198039	0.070193	-0.260974	1.000000	-0.131438	0.052698	0.267291
MaxHR	-0.382045	-0.112135	0.235792	-0.131438	1.000000	-0.160691	-0.400421
Oldpeak	0.258612	0.164803	0.050148	0.052698	-0.160691	1.000000	0.403951
HeartDisease	0.282039	0.107589	-0.232741	0.267291	-0.400421	0.403951	1.000000

```
sn.heatmap(correlation_data, annot=True)
```

<Axes: >



Comments on Correlation

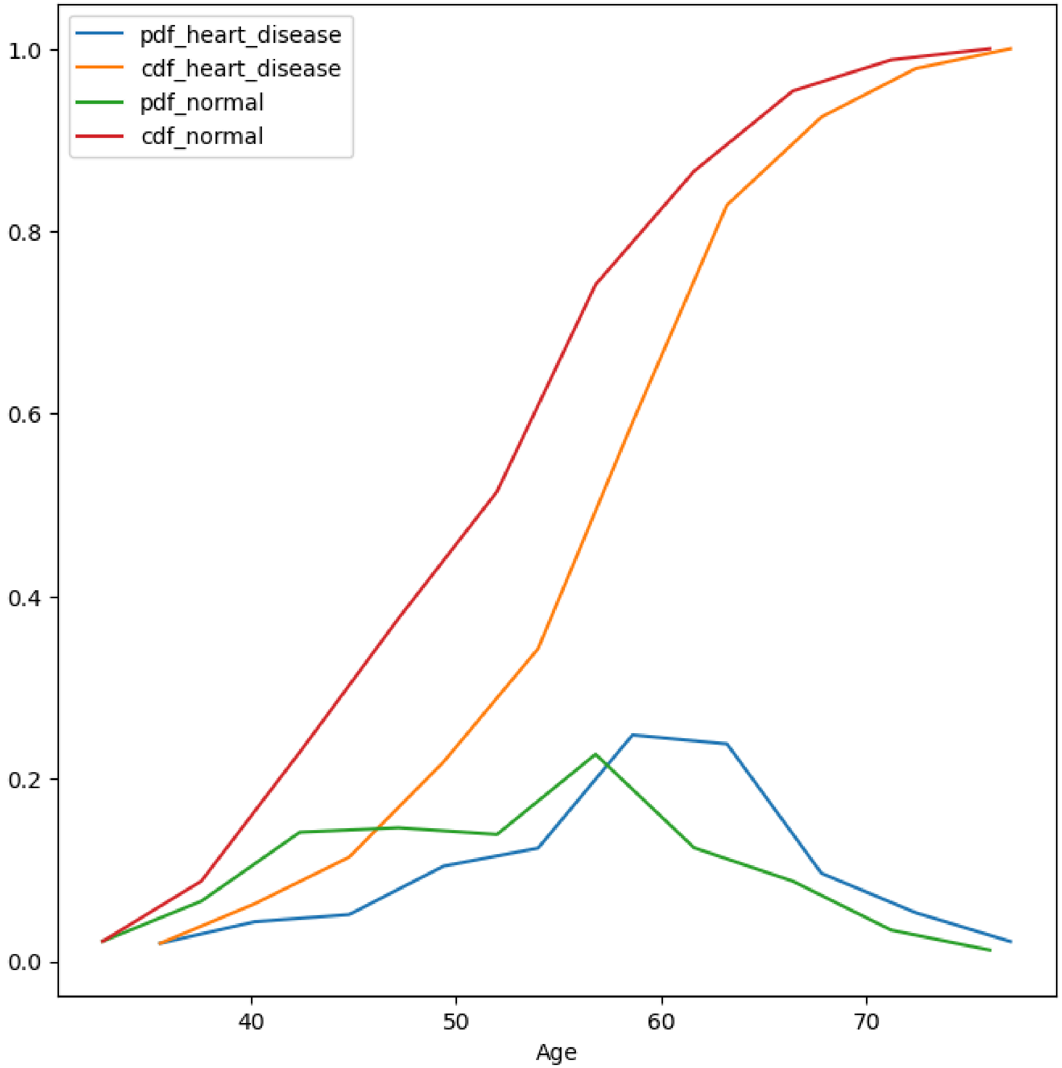
1. From the correaltion matrix and heatmap correlation table, there are no features that are correlated with each other.
2. There is no need to drop any feature/column from the data

How "Age' Feature is effecting Heart Failure?

Or Is Age is perfect predictor of Heart Failure?

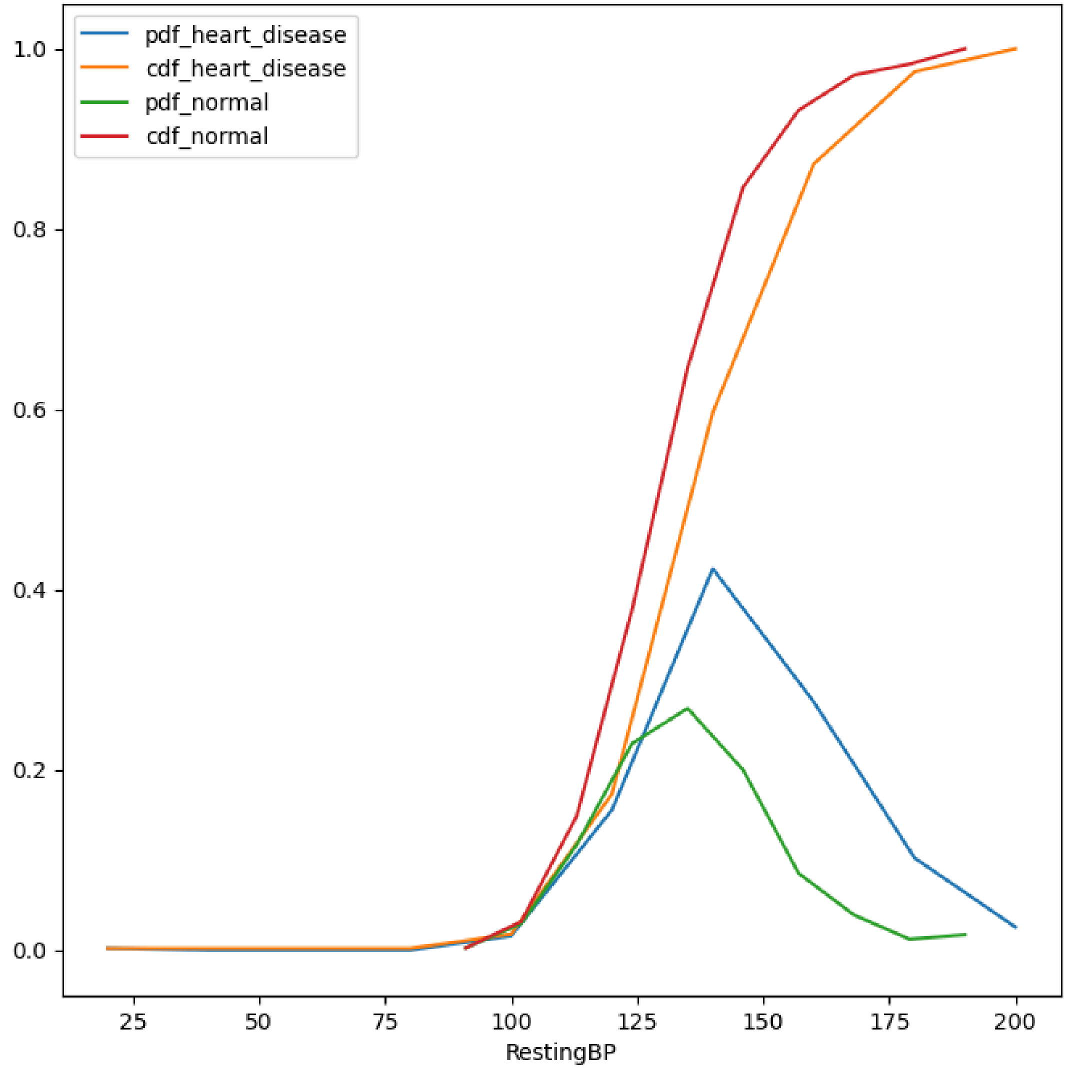
```
def pdf_cdf_graph(feature_name):

    heart_disease = data[data["HeartDisease"]==1]
    normal = data[data["HeartDisease"]==0]

    counts1, bin_edges1 = np.histogram(heart_disease[feature_name], bins=10, density=True)
    counts2, bin_edges2 = np.histogram(normal[feature_name], bins=10, density=True)

    pdf_heart_disease = counts1/sum(counts1)
    pdf_normal = counts2/sum(counts2)

    cdf_heart_disease = np.cumsum(pdf_heart_disease)
    cdf_normal = np.cumsum(pdf_normal)

    figure(figsize=(8,8))
    plt.plot(bin_edges1[1:], pdf_heart_disease, label = "pdf_heart_disease")
    plt.plot(bin_edges1[1:], cdf_heart_disease, label = "cdf_heart_disease")

    plt.plot(bin_edges2[1:], pdf_normal, label = "pdf_normal")
    plt.plot(bin_edges2[1:], cdf_normal, label = "cdf_normal")

    plt.legend(loc = "upper left")

    plt.xlabel(feature_name)
    plt.show()
```

```
pdf_cdf_graph("Age")
```



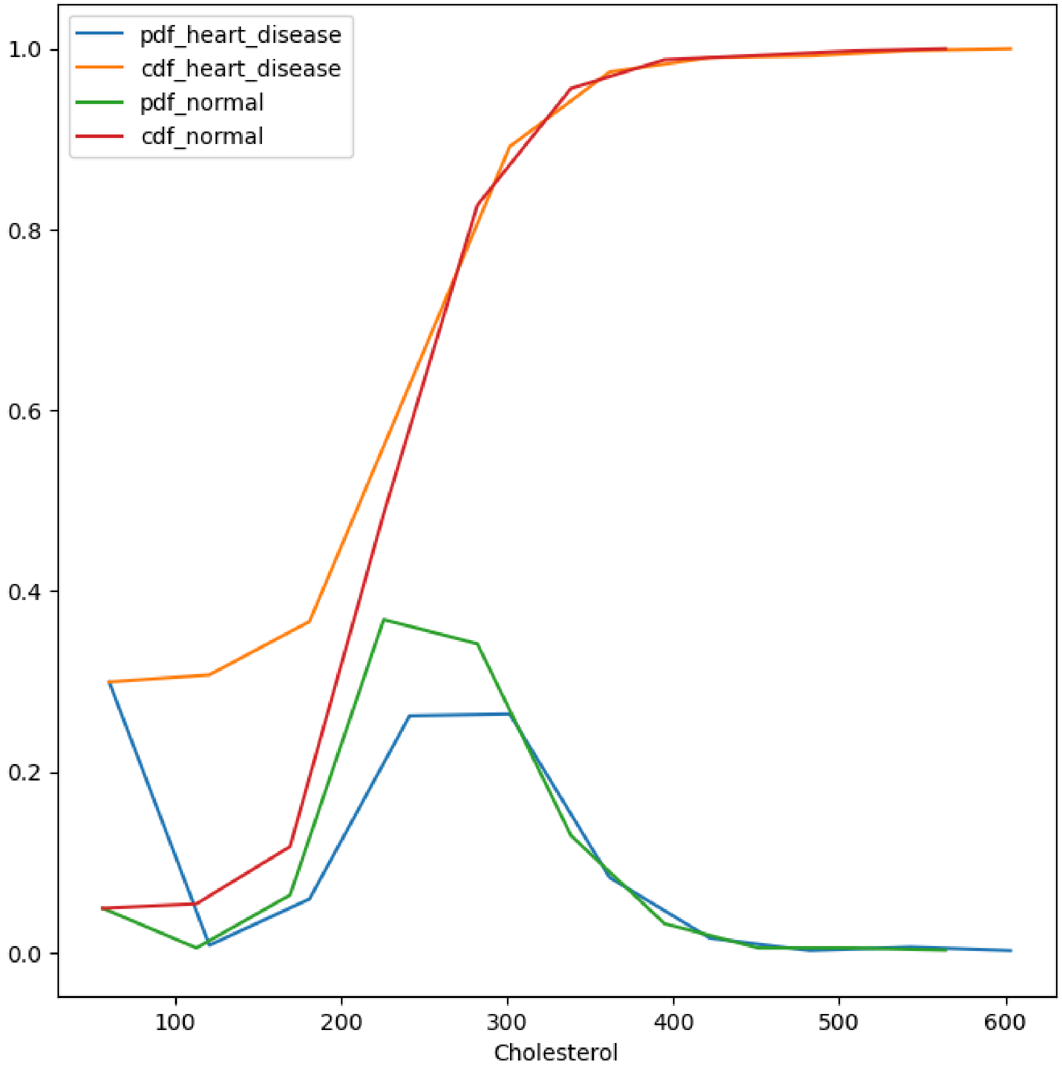
How RestingBP is impacting traget varibale

```
pdf_cdf_graph("RestingBP")
```



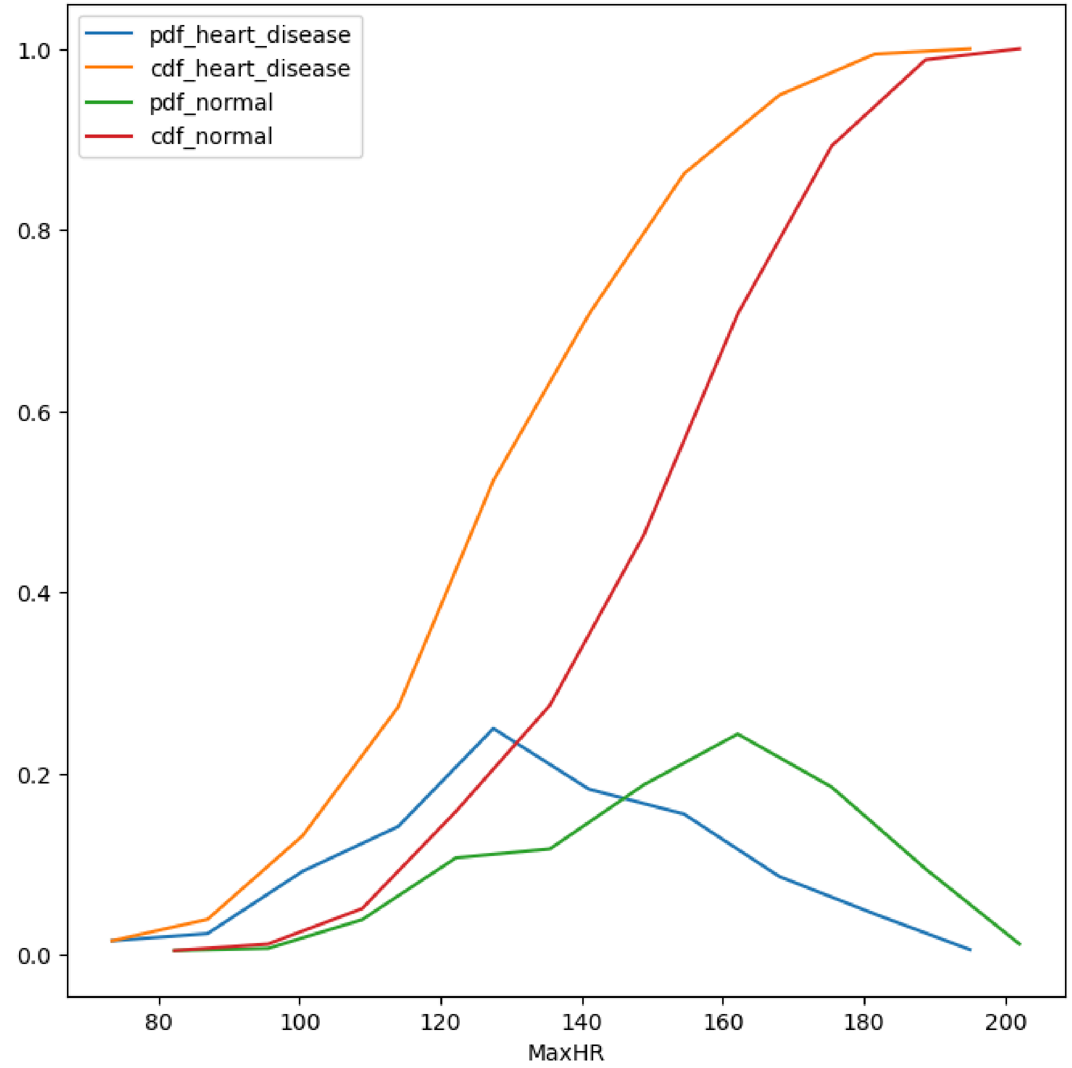
How Cholestrol is impacting target variable

```
pdf_cdf_graph("Cholesterol")
```



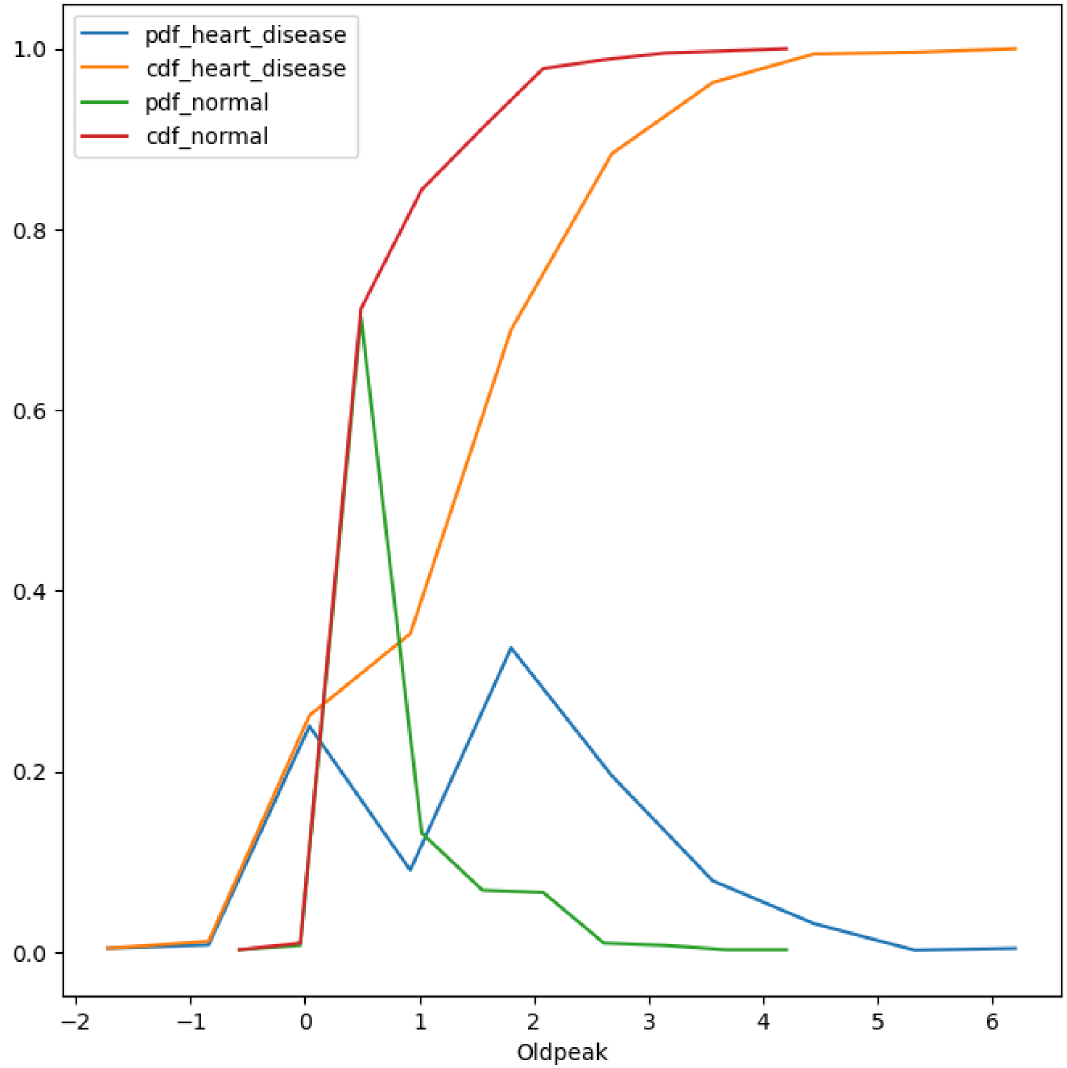
How MaxHR can differentiating traget variable

```
pdf_cdf_graph("MaxHR")
```



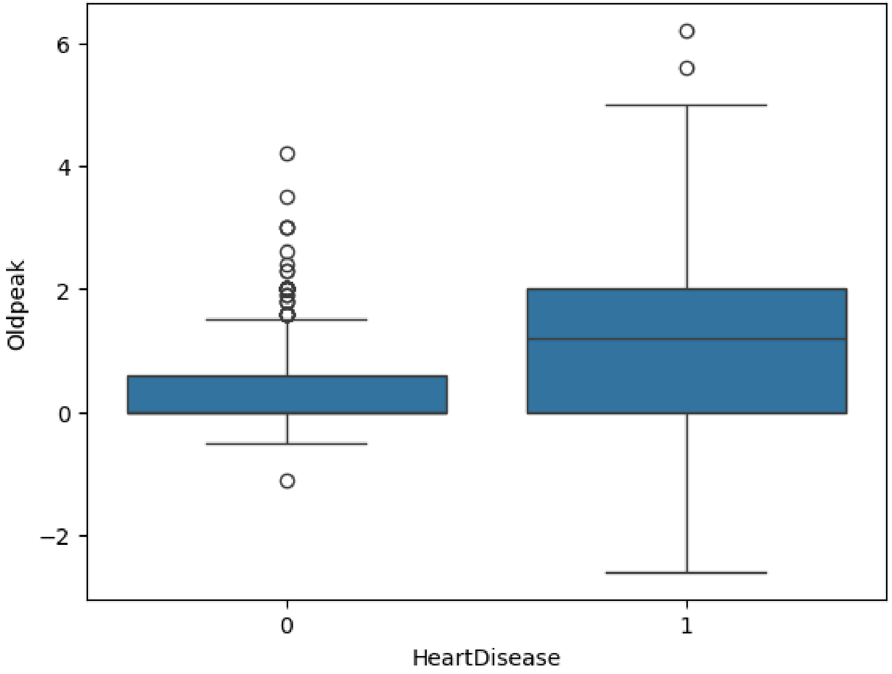
How Oldpeak is differentiating target variable?

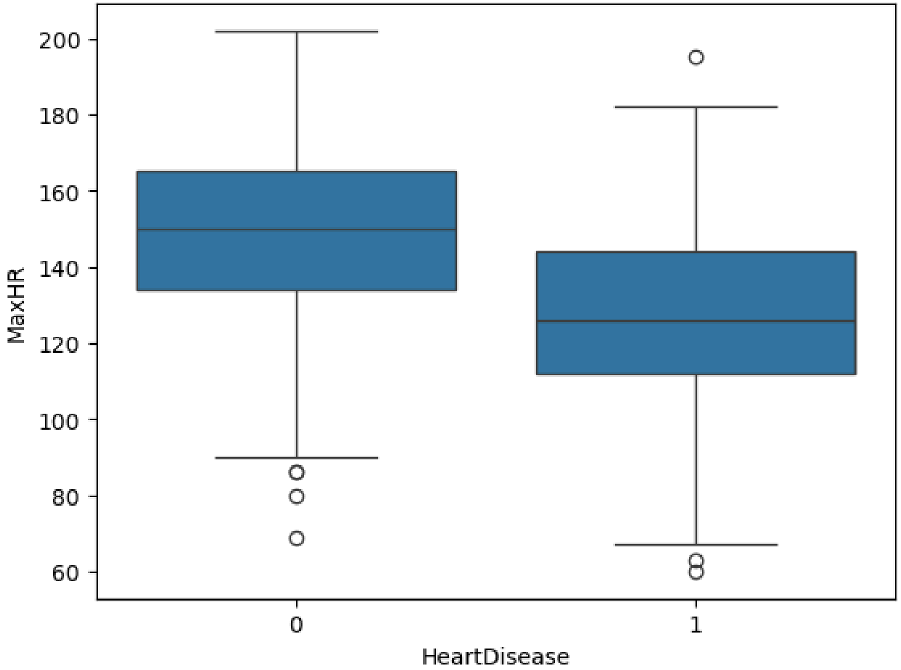
```
pdf_cdf_graph("Oldpeak")
```

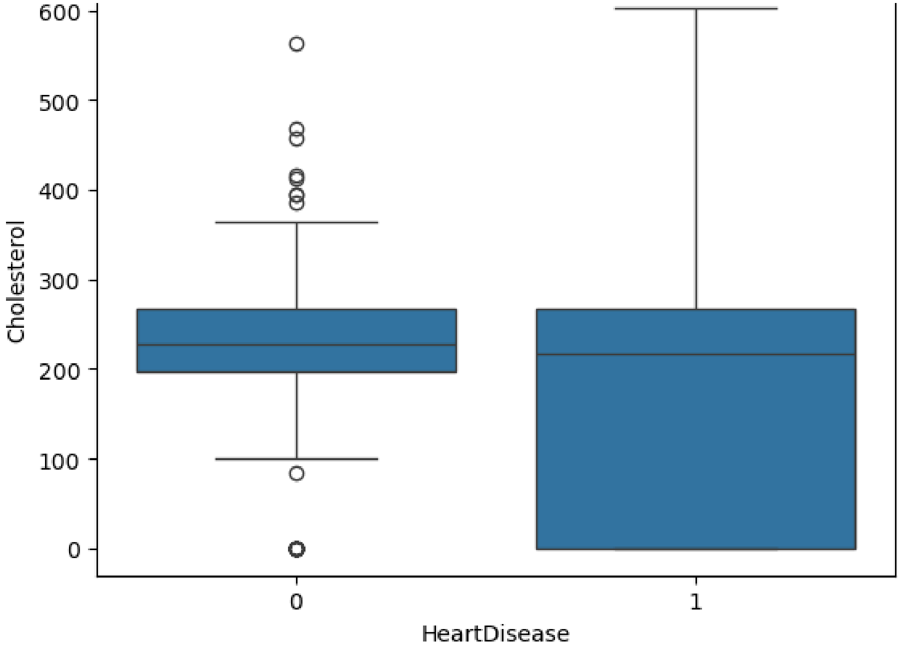


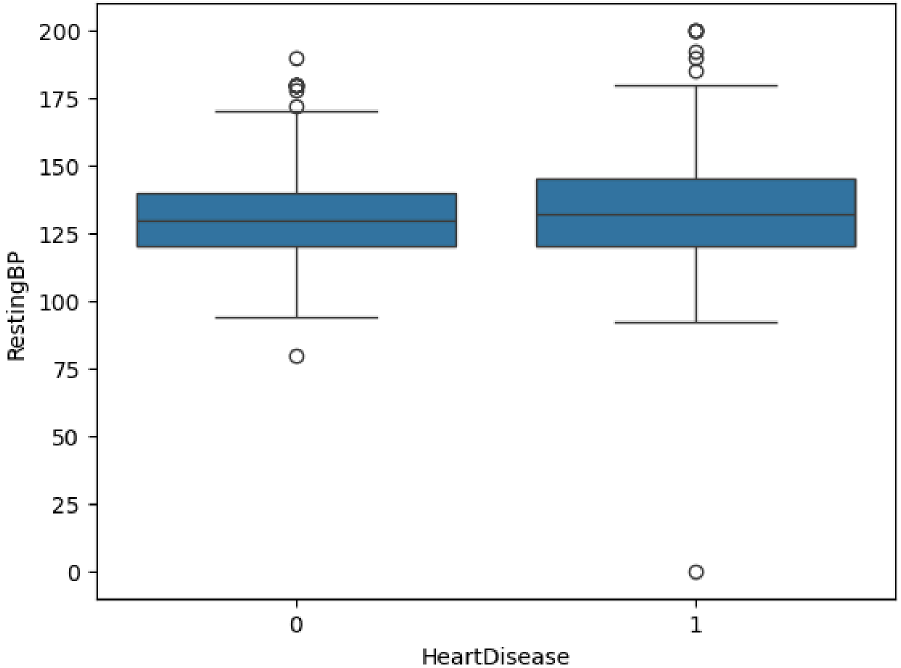

```
numerical_features = ["Oldpeak", "MaxHR", "Cholesterol", "RestingBP", "Age"]
```

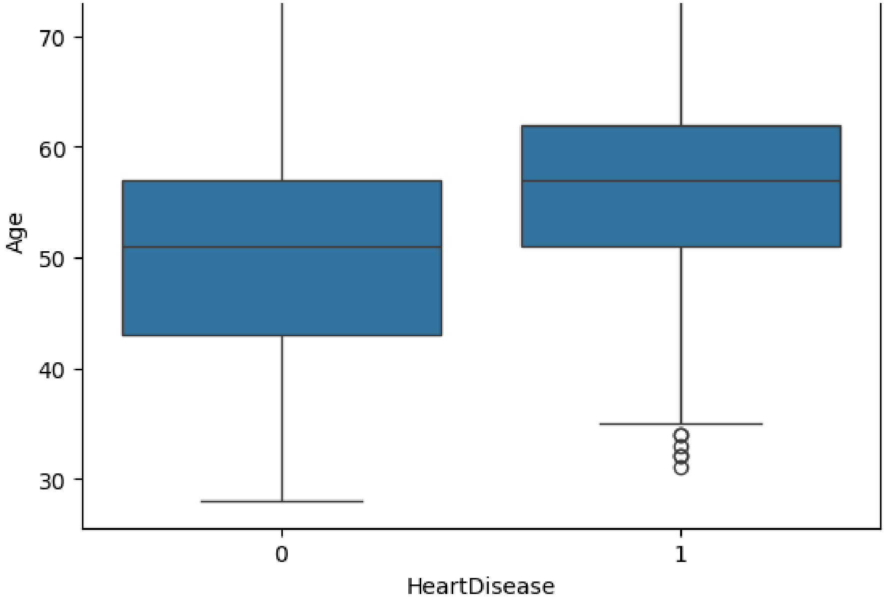
```
for feature in numerical_features:

    sn.boxplot(x = "HeartDisease", y=feature, data=data)
    plt.show()
```


6
4
2
0
−2
Oldpeak
0
1
HeartDisease


200
180
160
140
120
100
80
60
MaxHR
0
1
HeartDisease


600
500
400
300
200
100
0
Cholesterol
0
1
HeartDisease


200
175
150
125
100
75
50
25
0
RestingBP
0
1
HeartDisease



70
60
50
40
30
Age
0
1
HeartDisease

Comments on numerical feature analysis

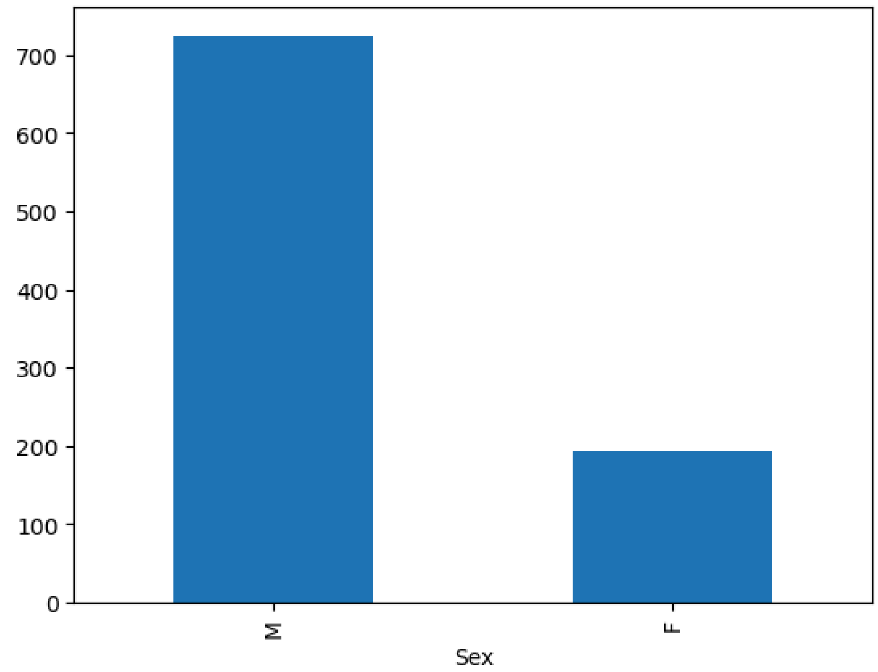
1. All the numeircal features doesn't show much impact on target variable.
2. All the pdf and cdf graphs of all numericla features doesn't show much variation in differentiating target variable.
3. These numerical features pdfs and cdfs grpahs overlaps between heart disease and normal traget variable.
4. But from data description from kaggle, all these numerical features are important in differentiating target variable.
5. From Box cox plot also most of data differentiating Heart Disease and Normal are over laped.
6. In general, from data description, these fetaures should differentiate the target varibale and the reason for not shoing differnce is due to some noise in the data

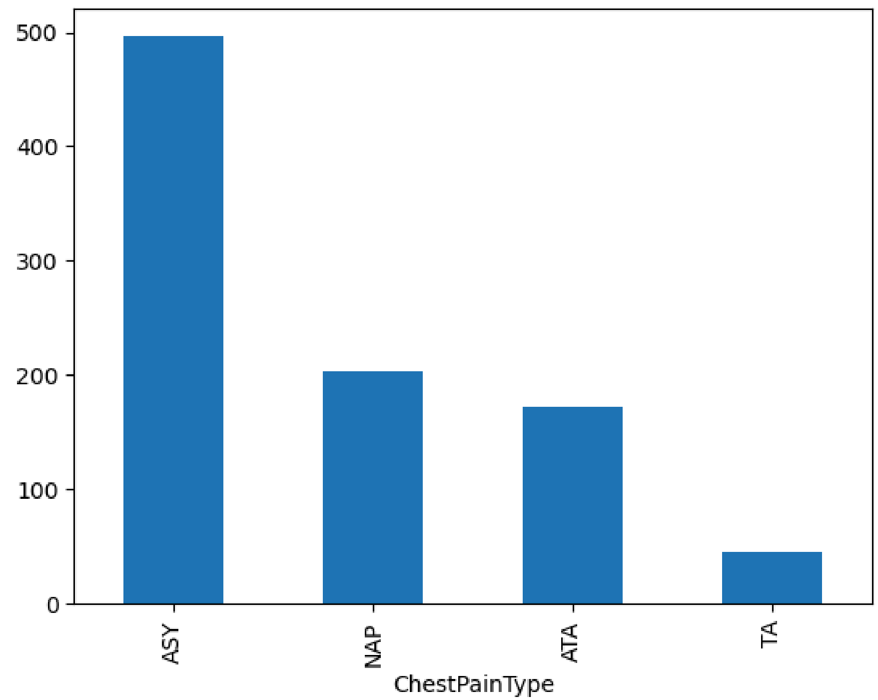
Analysis on categorical variables

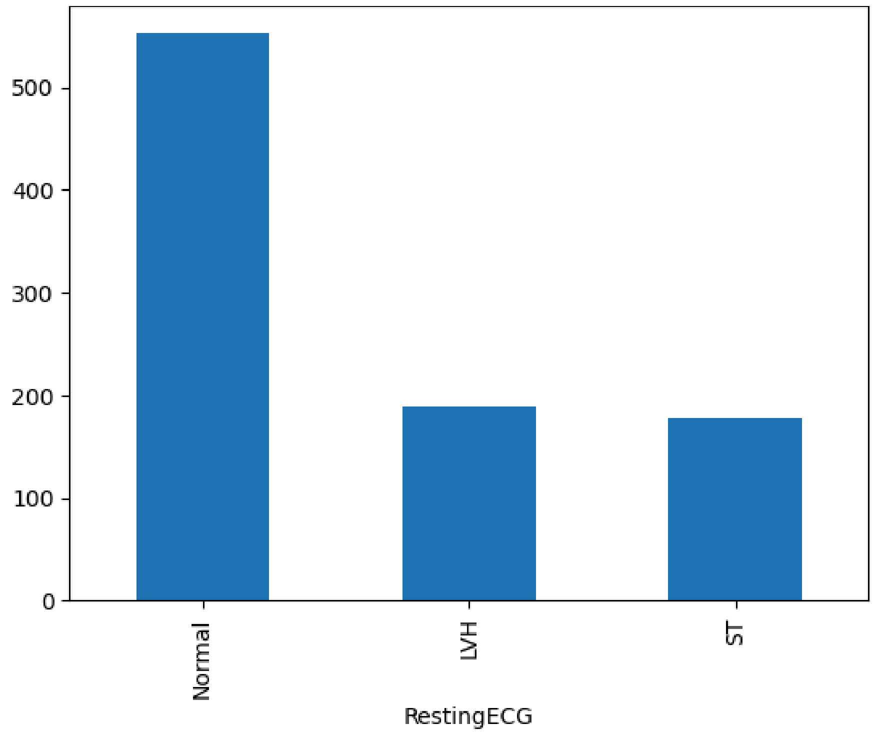
```
categorical_features = list(data.describe(include=['O']).columns)
```

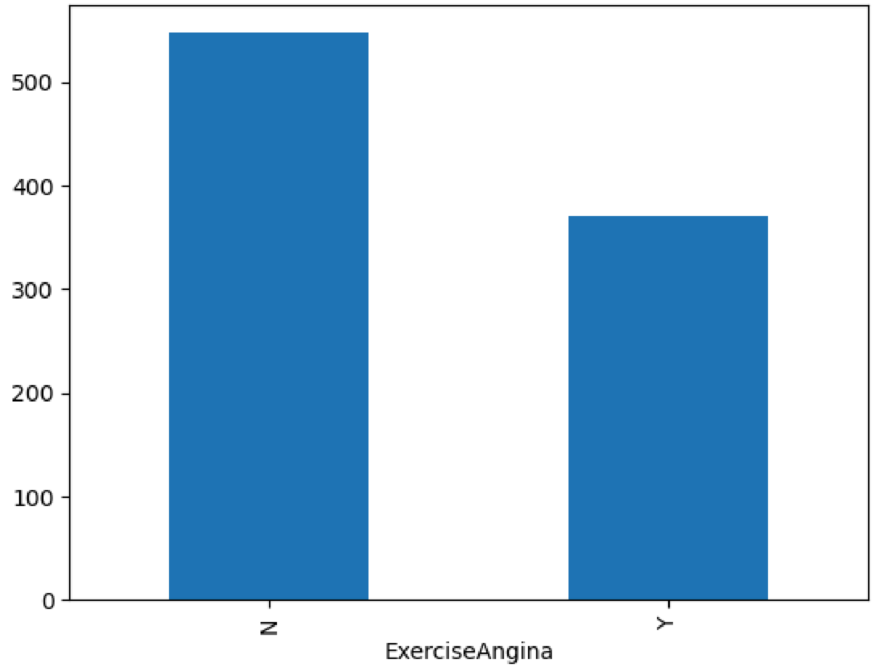
```
categorical_features.append("FastingBS")
```

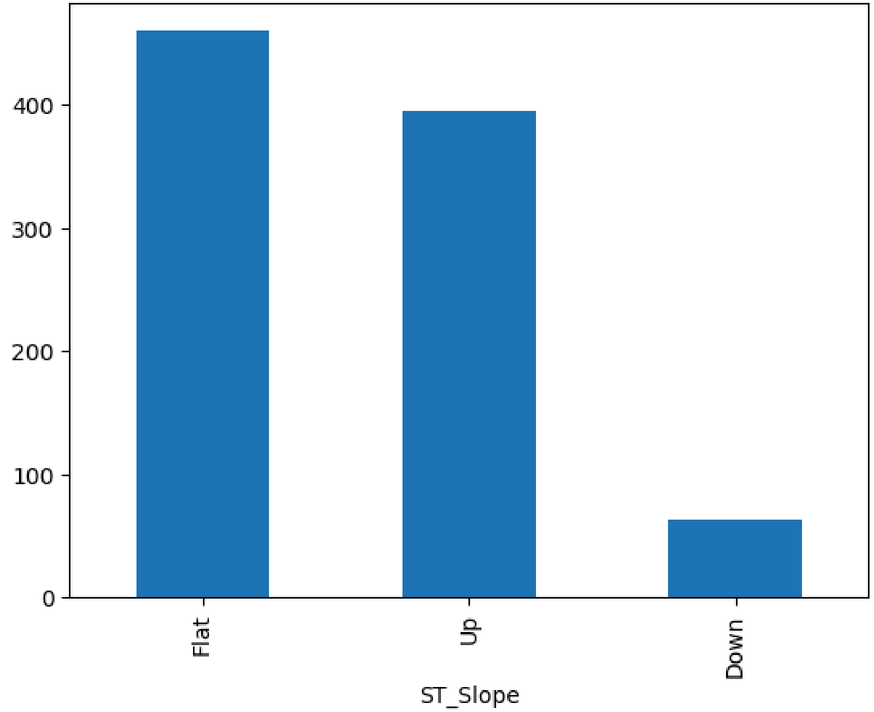
```
for cat_features in categorical_features:
    data[cat_features].value_counts().plot(kind = 'bar')
    plt.show()
```

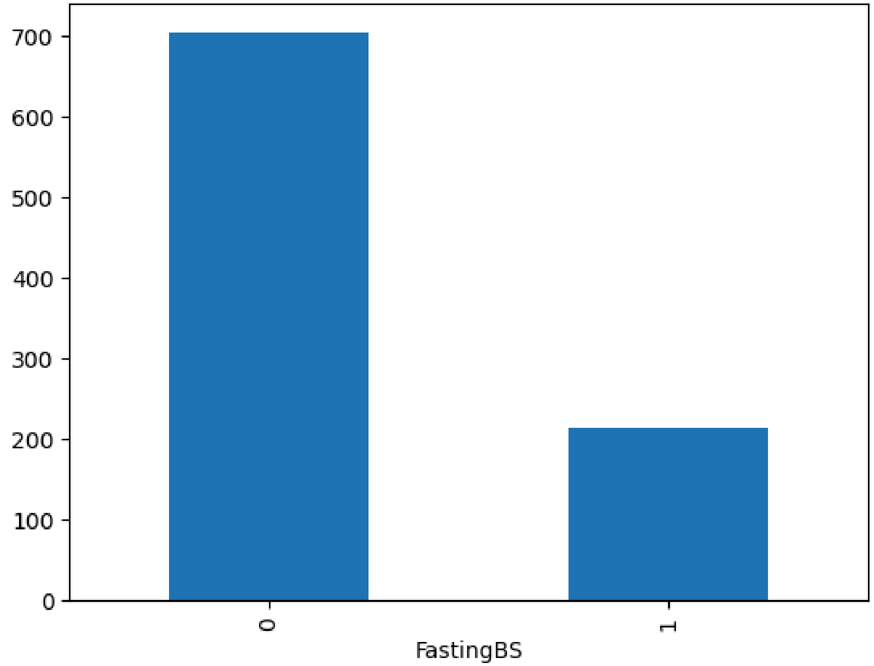

700
600
500
400
300
200
100
0
M
F
Sex


500
400
300
200
100
0
ASY
NAP
ATA
TA
ChestPainType


500
400
300
200
100
0
Normal
LVH
ST
RestingECG


500
400
300
200
100
0
N
Y
ExerciseAngina


400
300
200
100
0
Flat
Up
Down
ST_Slope


700
600
500
400
300
200
100
0
0
1
FastingBS

Comment on Bar plot

1. From bar plot on categorical fetaures, catogrical class values are not well balanced.
2. In "sex" feature, male(70%) data dominates female(30%).
3. In ST_Slope, Flat class domintaes Down class major scale.
4. In ExcerciseAngina, No class are more in number than yes class.
5. For RestingECVG feature, Normal dominates ST class.
6. ChestPainType, ASY dominates TA.

```
for feature in categorical_features:
    print(data.groupby([feature, "HeartDisease"])["HeartDisease"].count())
```

```
Sex  HeartDisease
F    0               143
     1                50
M    0               267
     1               458
Name: HeartDisease, dtype: int64
ChestPainType  HeartDisease
ASY            0               104
               1               392
ATA            0               149
               1                24
NAP            0               131
               1                72
TA             0                26
               1                20
Name: HeartDisease, dtype: int64
RestingECG  HeartDisease
LVH         0                82
            1               106
Normal      0               267
            1               285
ST          0                61
            1               117
Name: HeartDisease, dtype: int64
ExerciseAngina  HeartDisease
N               0               355
                1               192
Y               0                55
                1               316
Name: HeartDisease, dtype: int64
ST_Slope  HeartDisease
Down      0                14
          1                49
```

```
Flat      0               79
          1              381
Up        0              317
          1               78
Name: HeartDisease, dtype: int64
FastingBS  HeartDisease
0          0               366
           1               338
1          0                44
           1               170
Name: HeartDisease, dtype: int64
```

Encoding Feature and standardising numerical values

```
from sklearn.preprocessing import OneHotEncoder
from sklearn.preprocessing import StandardScaler
```

```
one_hot_en = OneHotEncoder(sparse_output=False)
std_scale = StandardScaler()
```

```
en_data = one_hot_en.fit_transform(data[categorical_features[:-1]])
std_data = std_scale.fit_transform(data[numerical_features])
```

```
en_df = pd.DataFrame(en_data,
                     columns=one_hot_en.get_feature_names_out(categorical_features[:-1]))
```

```
std_df = pd.DataFrame(std_data, columns=numerical_features)
```

```
final_df = pd.concat([en_df, std_df, data["FastingBS"], data["HeartDisease"]], axis=1)
```

```
final_df
```

	Sex_F	Sex_M	ChestPainType_ASY	ChestPainType_ATA	ChestPainType_NAP	ChestPainType_TA	RestingECG_LVH	RestingECG_Normal	RestingECG_ST	Exerc:
0	0.0	1.0	0.0	1.0	0.0	0.0	0.0	1.0	0.0	
1	1.0	0.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	
2	0.0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	1.0	
3	1.0	0.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	
4	0.0	1.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	
...	...	...	...	...	...	...	...	...	...	
913	0.0	1.0	0.0	0.0	0.0	1.0	0.0	1.0	0.0	
914	0.0	1.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	
915	0.0	1.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	
916	1.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0	
917	0.0	1.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	

918 rows × 21 columns

SVM

```
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.preprocessing import StandardScaler
```

```
# Separate features and target
X = final_df.drop('HeartDisease', axis=1)
y = final_df['HeartDisease']
```

```
# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

```
# Create and train the SVM model
svm_model = SVC(kernel='linear', random_state=42)
svm_model.fit(X_train, y_train)
```

```
SVC
SVC(kernel='linear', random_state=42)
```

```
# Make predictions on the test set
y_pred = svm_model.predict(X_test)
```

```
# Evaluate the model
print("Confusion Matrix:")
print(confusion_matrix(y_test, y_pred))
print("\nClassification Report:")
print(classification_report(y_test, y_pred))
```

```
Confusion Matrix:
[[67 10]
 [17 90]]

Classification Report:
              precision    recall  f1-score   support

           0       0.80      0.87      0.83        77
           1       0.90      0.84      0.87       107

    accuracy                           0.85       184
   macro avg       0.85      0.86      0.85       184
weighted avg       0.86      0.85      0.85       184
```

SVM: Grid Search to find optimal parameters

```
from sklearn.model_selection import GridSearchCV
```

```
param_grid = {
    'C': [0.1, 1, 10, 100],
    'gamma': [1, 0.1, 0.01, 0.001],
    'kernel': ['rbf', 'linear','poly','sigmoid']
}
```

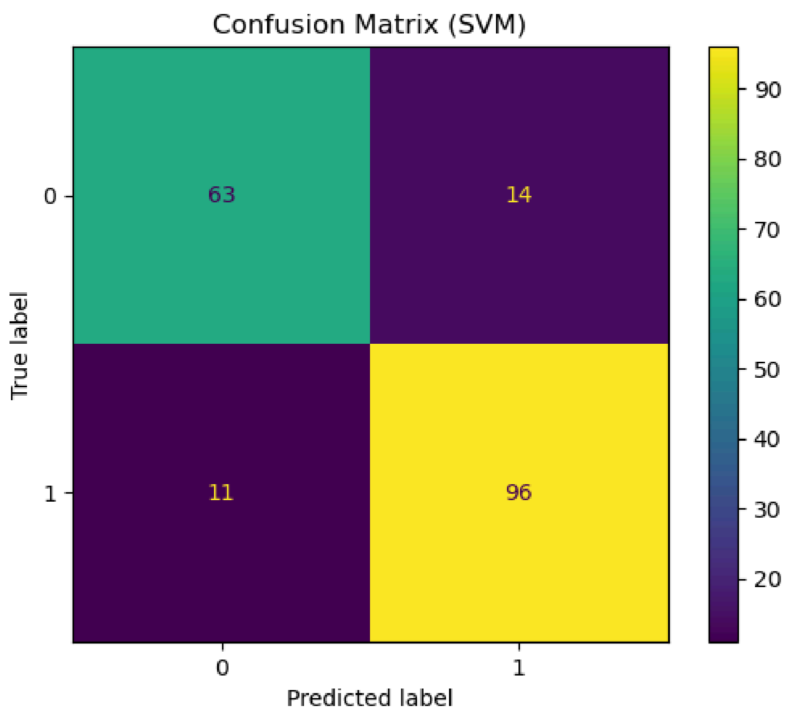
```
svm_grid_search = GridSearchCV(SVC(), param_grid, cv=5)
svm_grid_search.fit(X_train, y_train)
```

```
▸ GridSearchCV
  ▸ estimator: SVC
    ▸ SVC
```

```
print("Best parameters:", svm_grid_search.best_params_)
svm_best_model = svm_grid_search.best_estimator_
```

```
Best parameters: {'C': 1, 'gamma': 0.1, 'kernel': 'rbf'}
```

```
from sklearn.metrics import ConfusionMatrixDisplay

ConfusionMatrixDisplay.from_estimator(svm_best_model, X_test, y_test)
plt.title("Confusion Matrix (SVM)")
plt.show()
```



```
# Evaluate on the training data
y_train_pred = svm_best_model.predict(X_train)
print("\nClassification Report with Best Model (Training Data):")
print(classification_report(y_train, y_train_pred))
```

```
Classification Report with Best Model (Training Data):
              precision    recall  f1-score   support

           0       0.92      0.85      0.89       333
           1       0.88      0.94      0.91       401

    accuracy                           0.90       734
   macro avg       0.90      0.90      0.90       734
weighted avg       0.90      0.90      0.90       734
```

```
# Evaluate on the test data
y_pred = svm_best_model.predict(X_test)
print("\nClassification Report with Best Model (Test Data):")
print(classification_report(y_test, y_pred))
```

```
Classification Report with Best Model (Test Data):
              precision    recall  f1-score   support

           0       0.85      0.82      0.83        77
           1       0.87      0.90      0.88       107

    accuracy                           0.86       184
   macro avg       0.86      0.86      0.86       184
weighted avg       0.86      0.86      0.86       184
```

Descision Tree

```
data_df=data
data_df
```

	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
...	...	...	...	...	...	...	...	...	...	...	...	...
913	45	M	TA	110	264	0	Normal	132	N	1.2	Flat	1
914	68	M	ASY	144	193	1	Normal	141	N	3.4	Flat	1
915	57	M	ASY	130	131	0	Normal	115	Y	1.2	Flat	1
916	57	F	ATA	130	236	0	LVH	174	N	0.0	Flat	1
917	38	M	NAP	138	175	0	Normal	173	N	0.0	Up	0

918 rows × 12 columns

```
from sklearn.preprocessing import LabelEncoder
```

```
# Preprocessing
le = LabelEncoder()
categorical_columns = ['Sex', 'ChestPainType', 'RestingECG', 'ExerciseAngina', 'ST_Slope']
for col in categorical_columns:
    data_df[col] = le.fit_transform(data_df[col])
```

```
# Separate features and target
X_tree = data_df.drop('HeartDisease', axis=1)
y_tree = data_df['HeartDisease']
```

```
# Split the data into training and testing sets
X_train_tree, X_test_tree, y_train_tree, y_test_tree = train_test_split(X_tree, y_tree, test_size=0.2, random_state=42)
```

```
from sklearn.tree import DecisionTreeClassifier
from sklearn.preprocessing import LabelEncoder
```

```
# Create and train the decision tree classifier
dt_classifier = DecisionTreeClassifier(random_state=42)
```

```
dt_classifier.fit(X_train_tree, y_train_tree)
```

```
DecisionTreeClassifier
DecisionTreeClassifier(random_state=42)
```

```
# Make predictions on the test set
y_pred = dt_classifier.predict(X_test_tree)
```

```
from sklearn.metrics import accuracy_score, classification_report
```

```
# Evaluate the model
accuracy = accuracy_score(y_test_tree, y_pred)
print(f"Accuracy: {accuracy:.2f}")
```

```
Accuracy: 0.78
```

```
# Print the classification report
print("\nClassification Report:")
print(classification_report(y_test_tree, y_pred))
```

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

           0       0.70      0.83      0.76        77
           1       0.86      0.75      0.80       107

    accuracy                           0.78       184
   macro avg       0.78      0.79      0.78       184
weighted avg       0.79      0.78      0.78       184
```

```
# Feature importance
feature_importance = pd.DataFrame({'feature': X_tree.columns, 'importance': dt_classifier.feature_importances_})
feature_importance = feature_importance.sort_values('importance', ascending=False)
print("\nFeature Importance:")
print(feature_importance)
```

```
Feature Importance:
```

```
            feature  importance
10         ST_Slope    0.404613
7             MaxHR    0.107363
4       Cholesterol    0.107085
0               Age    0.099090
9           Oldpeak    0.071004
2     ChestPainType    0.058537
3         RestingBP    0.037457
1               Sex    0.035152
8    ExerciseAngina    0.030485
5         FastingBS    0.028976
6        RestingECG    0.020238
```

Find best model: Decision Tree

```
# Define parameter grid
param_grid = {
    'criterion': ['gini', 'entropy'],
    'max_depth': [None, 1,2,3,4,5, 10, 15, 20],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4],
    'max_features': ['sqrt', 'log2', None],
    'class_weight': [None, 'balanced']
}
```

```
# Create a decision tree classifier
dt = DecisionTreeClassifier(random_state=42)
```

```
# Perform grid search
dt_grid_search = GridSearchCV(estimator=dt, param_grid=param_grid, cv=5, n_jobs=-1, verbose=0)
dt_grid_search.fit(X_train_tree, y_train_tree)
```

```
▸ GridSearchCV
▸ estimator: DecisionTreeClassifier
    ▸ DecisionTreeClassifier
```

```
# Get the best model
dt_best_model = dt_grid_search.best_estimator_
```

```
# Make predictions on the test set
y_pred = dt_best_model.predict(X_test_tree)
```

```
# Print results
print("Best parameters:", dt_grid_search.best_params_)
```

```
Best parameters: {'class_weight': None, 'criterion': 'gini', 'max_depth': 4, 'max_features': None, 'min_samples_leaf': 4, 'min_samples_split': 2}
```

```
print("\nAccuracy:", accuracy_score(y_test_tree, y_pred))
```

```

Accuracy: 0.875
```

```
# Generate predictions for the training set
y_train_pred = dt_best_model.predict(X_train_tree)

# Print classification reports
print("\nClassification Report - Training Set:")
print(classification_report(y_train_tree, y_train_pred))
```

```

Classification Report - Training Set:
              precision    recall  f1-score   support

           0       0.91      0.80      0.85       333
           1       0.85      0.94      0.89       401

    accuracy                           0.87       734
   macro avg       0.88      0.87      0.87       734
weighted avg       0.88      0.87      0.87       734

```

```
# Generate predictions for the test set
y_test_pred = dt_best_model.predict(X_test_tree)

print("\nClassification Report - Test Set:")
print(classification_report(y_test_tree, y_test_pred))
```

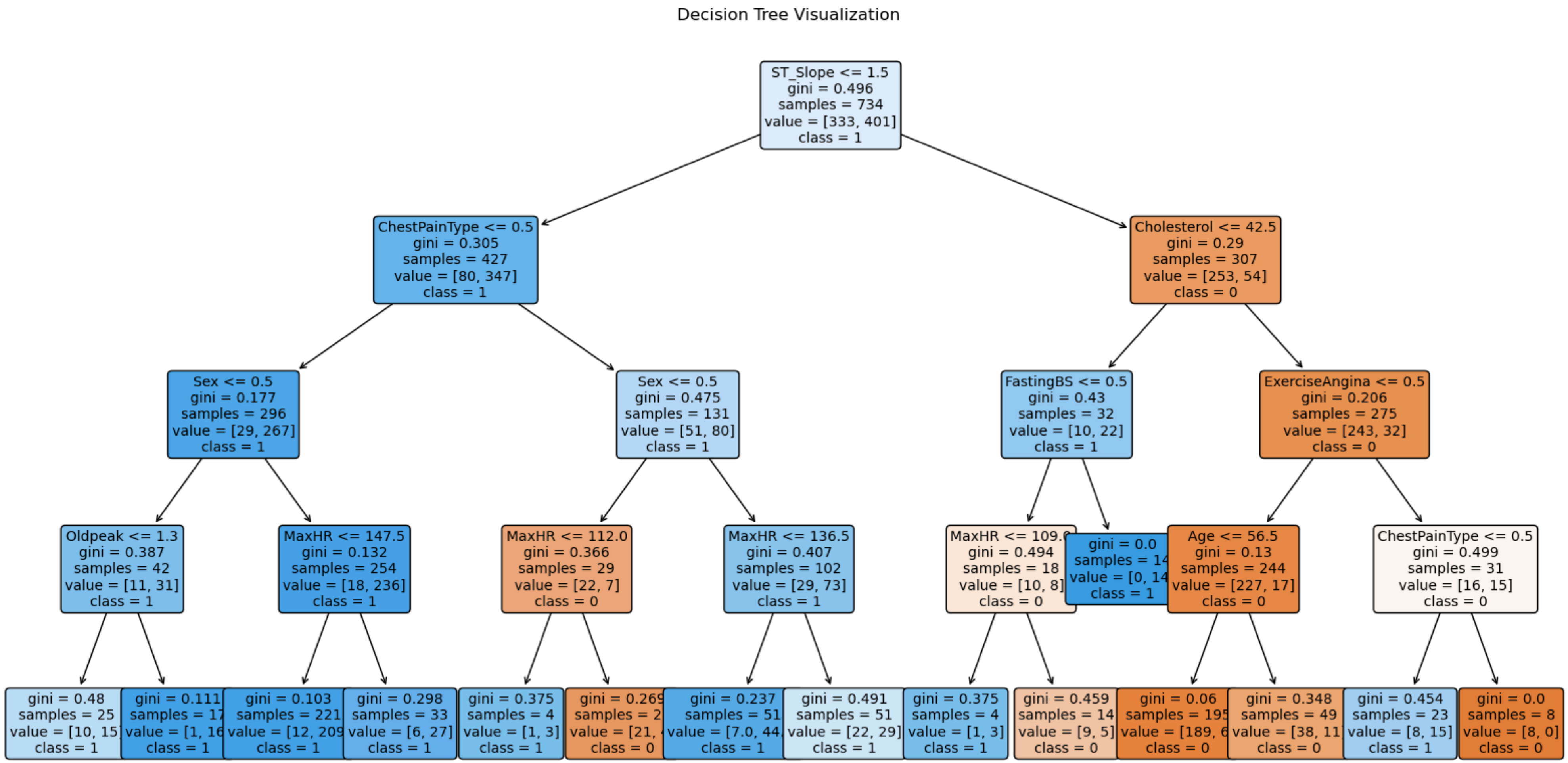
```

Classification Report - Test Set:
              precision    recall  f1-score   support

           0       0.85      0.86      0.85        77
           1       0.90      0.89      0.89       107

    accuracy                           0.88       184
```

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

```
# Feature importance
feature_importance = pd.DataFrame({'feature': X_tree.columns, 'importance': dt_best_model.feature_importances_})
feature_importance = feature_importance.sort_values('importance', ascending=False)
print("\nFeature Importance:")
print(feature_importance)
```

```
Feature Importance:
           feature  importance
10        ST_Slope    0.643433
2    ChestPainType    0.090923
4      Cholesterol    0.083084
1              Sex    0.056825
8   ExerciseAngina    0.041931
7            MaxHR    0.038682
5        FastingBS    0.021597
0              Age    0.013058
9          Oldpeak    0.010466
3        RestingBP    0.000000
6       RestingECG    0.000000
```

```
from sklearn.tree import plot_tree
import matplotlib.pyplot as plt

# Create a plot for the decision tree
plt.figure(figsize=(20, 10))  # Adjust the figure size as needed
plot_tree(
    dt_best_model,
    feature_names=X_train_tree.columns,  # Replace with actual feature names if available
    class_names=[str(cls) for cls in dt_best_model.classes_],  # Replace with actual class names if available
    filled=True,
    rounded=True,
    fontsize=10
)

plt.title("Decision Tree Visualization")
plt.show()
```



Random Forest : Bagging

```
from sklearn.ensemble import RandomForestClassifier
```

```
# Bagging: Random Forest
rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)
```

```
rf_classifier.fit(X_train_tree, y_train_tree)
rf_predictions = rf_classifier.predict(X_test_tree)
```

```
print("Random Forest (Bagging) Results:")
print("Accuracy:", accuracy_score(y_test_tree, rf_predictions))
```

```
Random Forest (Bagging) Results:
Accuracy: 0.8804347826086957
```

```
# Predictions for the training set
rf_train_predictions = rf_classifier.predict(X_train_tree)

# Classification report for training data
print("\nClassification Report - Training Set:")
print(classification_report(y_train_tree, rf_train_predictions))
```

```
Classification Report - Training Set:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       333
           1       1.00      1.00      1.00       401

    accuracy                           1.00       734
   macro avg       1.00      1.00      1.00       734
weighted avg       1.00      1.00      1.00       734
```

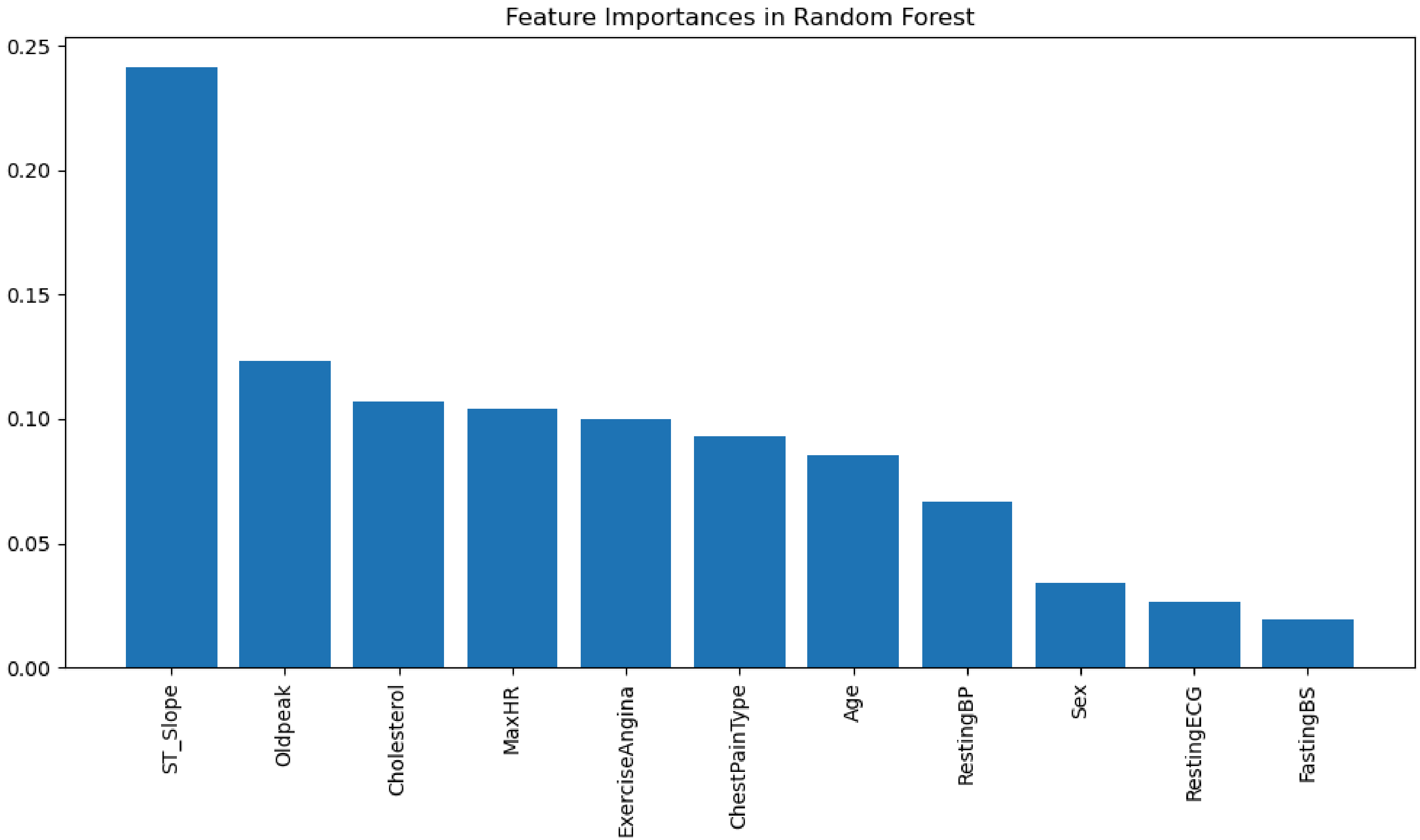
```
# Predictions for the test set
rf_test_predictions = rf_classifier.predict(X_test_tree)

# Classification report for test data
print("\nClassification Report - Test Set:")
print(classification_report(y_test_tree, rf_test_predictions))
```

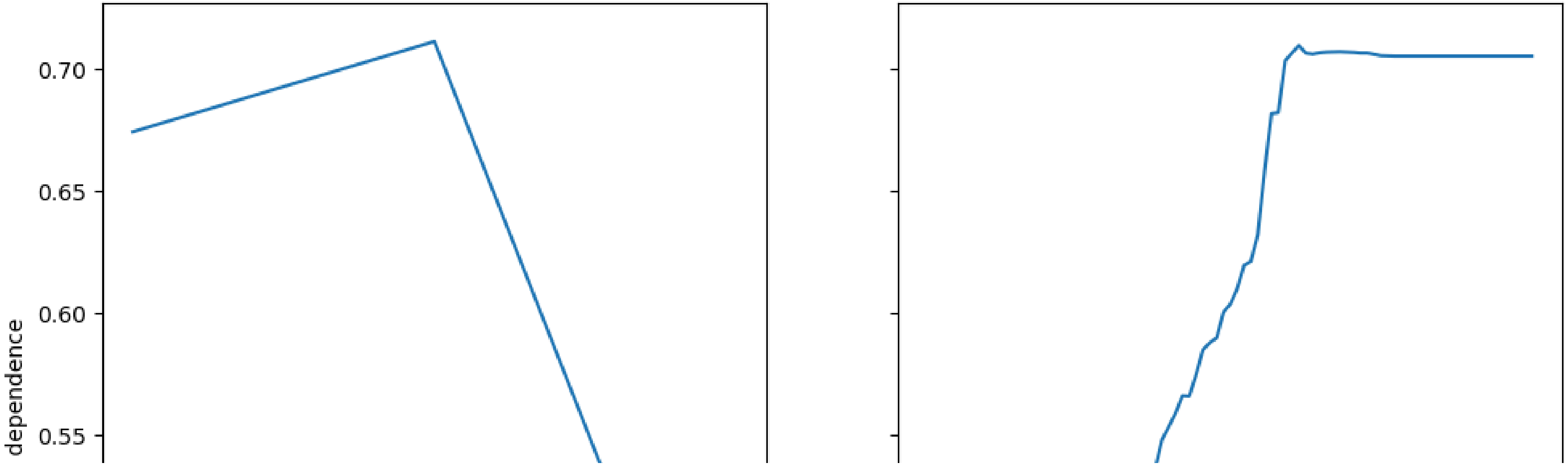
```
Classification Report - Test Set:
              precision    recall  f1-score   support

           0       0.86      0.86      0.86        77
           1       0.90      0.90      0.90       107

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

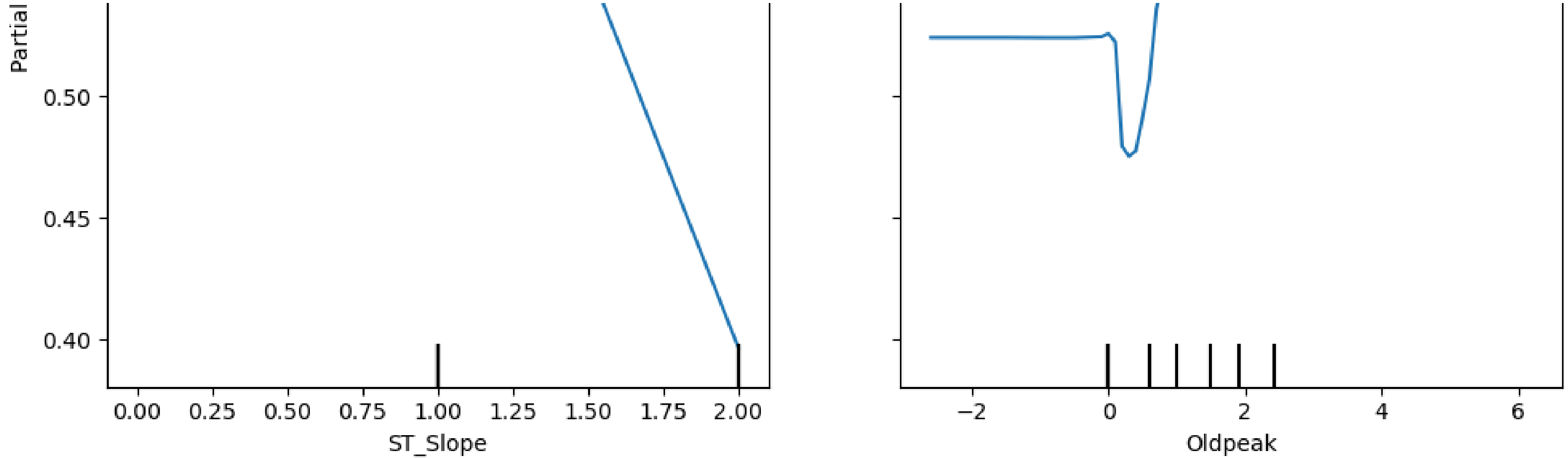
```
# Feature importance for Random Forest
feature_importance_rf = pd.DataFrame({'feature': X_tree.columns, 'importance': rf_classifier.feature_importances_})
print("\nTop 5 important features (Random Forest):")
print(feature_importance_rf.sort_values('importance', ascending=False).head())
```

```
Top 5 important features (Random Forest):
           feature  importance
10        ST_Slope    0.241312
9          Oldpeak    0.123073
4      Cholesterol    0.107227
7            MaxHR    0.103848
8   ExerciseAngina    0.100046
```

```
import matplotlib.pyplot as plt
import numpy as np
from sklearn.inspection import PartialDependenceDisplay

# Extract feature names
feature_names = X_train_tree.columns  # Assuming X_train_tree is a DataFrame

# Plot feature importances
plt.figure(figsize=(10, 6))
importances = rf_classifier.feature_importances_
indices = np.argsort(importances)[::-1]

plt.title("Feature Importances in Random Forest")
plt.bar(range(X_train_tree.shape[1]), importances[indices])
plt.xticks(range(X_train_tree.shape[1]), feature_names[indices], rotation=90)
plt.tight_layout()
plt.show()

# Plot partial dependence for top two features
fig, ax = plt.subplots(figsize=(10, 6))
PartialDependenceDisplay.from_estimator(
    rf_classifier,
    X_train_tree,
    features=[indices[0], indices[1]],  # Indices of top 2 features
    feature_names=feature_names,
    ax=ax
)
plt.tight_layout()
plt.show()
```


Feature Importances in Random Forest
0.25
0.20
0.15
0.10
0.05
0.00
ST_Slope
Oldpeak
Cholesterol
MaxHR
ExerciseAngina
ChestPainType
Age
RestingBP
Sex
RestingECG
FastingBS


0.70
0.65
0.60
0.55
dependence



1. A bar plot of feature importances, showing which features the Random Forest model considers most important for classification.
2. A partial dependence plot for the two most important features, illustrating how these features affect the model's predictions.

GradientBoosting/: Boosting

```
from sklearn.ensemble import GradientBoostingClassifier
```

```
# Boosting: Gradient Boosting
gb_classifier = GradientBoostingClassifier(n_estimators=100, learning_rate=0.1, random_state=42)
gb_classifier.fit(X_train_tree, y_train_tree)
gb_predictions = gb_classifier.predict(X_test_tree)
```

```
print("\nGradient Boosting Results:")
print("Accuracy:", accuracy_score(y_test, gb_predictions))
```

```
Gradient Boosting Results:
Accuracy: 0.875
```

```
# Predictions for the training set
gb_train_predictions = gb_classifier.predict(X_train_tree)

# Classification report for the training set
```

```
print("\nClassification Report - Training Set:")
print(classification_report(y_train, gb_train_predictions))
```

```
Classification Report - Training Set:
              precision    recall  f1-score   support

           0       0.94      0.93      0.93       333
           1       0.94      0.95      0.95       401

    accuracy                           0.94       734
   macro avg       0.94      0.94      0.94       734
weighted avg       0.94      0.94      0.94       734
```

```
# Predictions for the test set
gb_test_predictions = gb_classifier.predict(X_test_tree)

# Classification report for the test set
print("\nClassification Report - Test Set:")
print(classification_report(y_test, gb_test_predictions))
```

```
Classification Report - Test Set:
              precision    recall  f1-score   support

           0       0.82      0.90      0.86        77
           1       0.92      0.86      0.89       107

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

```
# Feature importance for Gradient Boosting
feature_importance_gb = pd.DataFrame({'feature': X_tree.columns, 'importance': gb_classifier.feature_importances_})
print("\nTop 5 important features (Gradient Boosting):")
print(feature_importance_gb.sort_values('importance', ascending=False).head())
```

```
Top 5 important features (Gradient Boosting):
           feature  importance
10        ST_Slope    0.474190
9          Oldpeak    0.093711
4      Cholesterol    0.088439
2    ChestPainType    0.083655
8   ExerciseAngina    0.062131
```

```
import matplotlib.pyplot as plt
import numpy as np
from sklearn.inspection import PartialDependenceDisplay

# Assuming X_train_tree is a DataFrame with named columns
feature_names = X_train_tree.columns.tolist()

# Plot feature importances
plt.figure(figsize=(10, 6))
importances = gb_classifier.feature_importances_
indices = np.argsort(importances)[::-1]
plt.title("Feature Importances in Gradient Boosting")
plt.bar(range(len(feature_names)), importances[indices])
plt.xticks(range(len(feature_names)), [feature_names[i] for i in indices], rotation=90)
plt.tight_layout()
plt.show()

# Plot partial dependence for top two features
fig, ax = plt.subplots(figsize=(10, 6))
PartialDependenceDisplay.from_estimator(gb_classifier, X_train_tree,
                                        features=[feature_names[indices[0]], feature_names[indices[1]]],
                                        feature_names=feature_names, ax=ax)
plt.tight_layout()
plt.show()
```