Heart

May 6, 2024

[1]:
```
#Imports library
```

[6]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
```

[8]:
```
# Read the CSV file into a DataFrame
heart_data=pd.read_csv("../Assignment/heart.csv")
```

[4]:
```
# What factors influence the likelihood of heart disease in patients according␣
 ↪to the dataset?
```

[10]:
```
#Print the first 5 rows of the dataset
heart_data.head()
```

[10]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

[ ]:
```

```

[5]:
```
#Print the last 5 rows of the dataset
heart_data.tail()
```

[5]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3	0
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3	0
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3	0
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3	0
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2	0

[6]:
```
#Number of rows and columns
heart_data.shape
```

[6]:
```
(303, 14)
```

[7]:
```
#Getting some info about the data
heart_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       303 non-null    int64  
 1   sex       303 non-null    int64  
 2   cp        303 non-null    int64  
 3   trestbps  303 non-null    int64  
 4   chol      303 non-null    int64  
 5   fbs       303 non-null    int64  
 6   restecg   303 non-null    int64  
 7   thalach   303 non-null    int64  
 8   exang     303 non-null    int64  
 9   oldpeak   303 non-null    float64
 10  slope     303 non-null    int64  
 11  ca        303 non-null    int64  
 12  thal      303 non-null    int64  
 13  target    303 non-null    int64  
dtypes: float64(1), int64(13)
memory usage: 33.3 KB
```

[8]:
```
#Checking for missing values
heart_data.isnull().sum()
#No missing values
```

[8]:
```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64
```

[9]:
```
#Get statistical measures about the data
heart_data.describe()
```

[9]:

	age	sex	cp	trestbps	chol	fbs
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.366337	0.683168	0.966997	131.623762	246.264026	0.148515
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000

	restecg	thalach	exang	oldpeak	slope	ca
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	0.528053	149.646865	0.326733	1.039604	1.399340	0.729373
std	0.525860	22.905161	0.469794	1.161075	0.616226	1.022606
min	0.000000	71.000000	0.000000	0.000000	0.000000	0.000000
25%	0.000000	133.500000	0.000000	0.000000	1.000000	0.000000
50%	1.000000	153.000000	0.000000	0.800000	1.000000	0.000000
75%	1.000000	166.000000	1.000000	1.600000	2.000000	1.000000
max	2.000000	202.000000	1.000000	6.200000	2.000000	4.000000

	thal	target
count	303.000000	303.000000
mean	2.313531	0.544554
std	0.612277	0.498835

```
min      0.000000    0.000000
25%      2.000000    0.000000
50%      2.000000    1.000000
75%      3.000000    1.000000
max      3.000000    1.000000
```

[10]:
```
#Checing the distribution of target variable
heart_data['target'].value_counts()
#1 have defects, 0 not present (Healthy)
```

[10]:
```
target
1    165
0    138
Name: count, dtype: int64
```

[14]:
```
#Split the features and Targets
X = heart_data.drop(columns='target', axis=1)
Y = heart_data['target']
```

[12]:
```
print (X)
```

```
     age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  \
0     63    1   3       145   233    1        0      150      0      2.3
1     37    1   2       130   250    0        1      187      0      3.5
2     41    0   1       130   204    0        0      172      0      1.4
3     56    1   1       120   236    0        1      178      0      0.8
4     57    0   0       120   354    0        1      163      1      0.6
..   ...  ...  ..       ...   ...  ...      ...      ...    ...      ...
298   57    0   0       140   241    0        1      123      1      0.2
299   45    1   3       110   264    0        1      132      0      1.2
300   68    1   0       144   193    1        1      141      0      3.4
301   57    1   0       130   131    0        1      115      1      1.2
302   57    0   1       130   236    0        0      174      0      0.0

     slope  ca  thal
0        0   0     1
1        0   0     2
2        2   0     2
3        2   0     2
4        2   0     2
..     ...  ..   ...
298      1   0     3
299      1   0     3
300      1   2     3
301      1   1     3
302      1   1     2
```

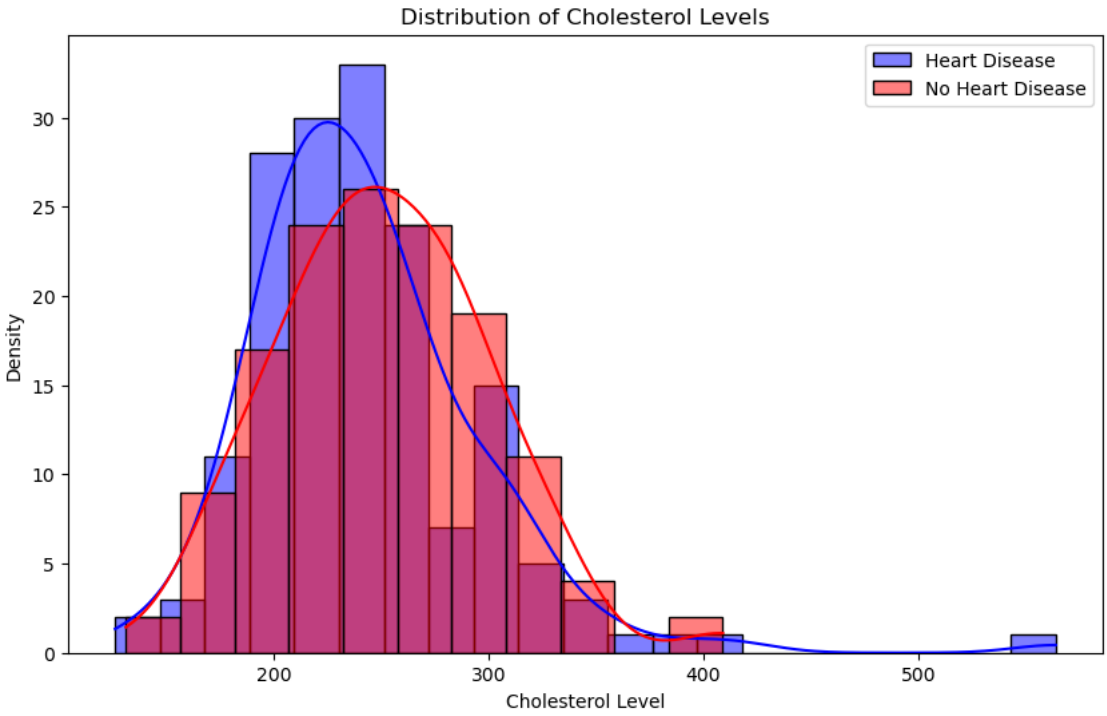
```
[303 rows x 13 columns]
```

[13]:
```
print(Y)
```

```
0      1
1      1
2      1
3      1
4      1
      ..
298    0
299    0
300    0
301    0
302    0
Name: target, Length: 303, dtype: int64
```

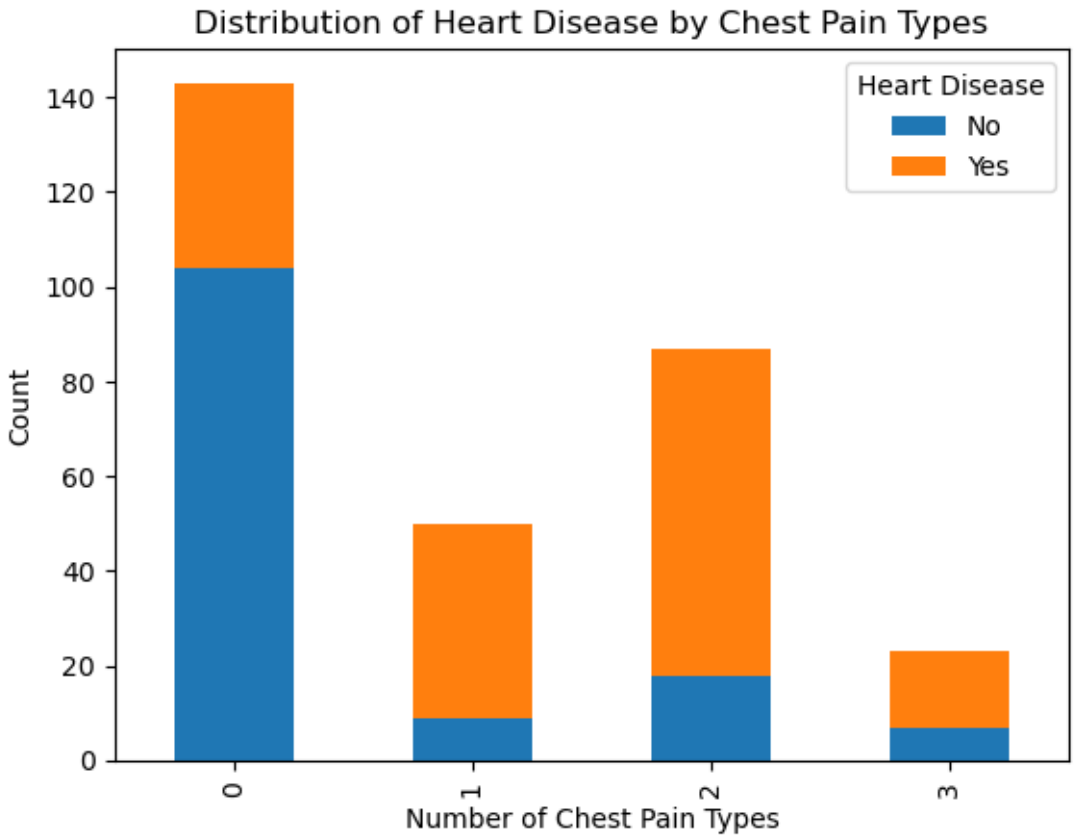
[6]:
```
# What is the distribution of cholesterol levels among patients with heart␣
 ↪disease, and how does it compare to those without heart disease? Please␣
 ↪visualize this using a histogram or a density plot.
```

[14]:
```
# Set up the figure and axis
plt.figure(figsize=(10, 6))

# Plot density plot for cholesterol levels of patients with heart disease
sns.histplot(heart_data[heart_data['target'] == 1]['chol'], color='blue',␣
 ↪label='Heart Disease', kde=True)

# Plot density plot for cholesterol levels of patients without heart disease
sns.histplot(heart_data[heart_data['target'] == 0]['chol'], color='red',␣
 ↪label='No Heart Disease', kde=True)

# Set labels and title
plt.xlabel('Cholesterol Level')
plt.ylabel('Density')
plt.title('Distribution of Cholesterol Levels')
plt.legend()

# Show the plot
plt.show()
```



[10]:
```
# Is there a relationship between the number of chest pain types experienced by␣
↪patients and the likelihood of heart disease?
```

[15]:
```
cross_tab = pd.crosstab(heart_data['cp'], heart_data['target'])
cross_tab.plot(kind='bar', stacked=True)
plt.xlabel('Number of Chest Pain Types')
plt.ylabel('Count')
plt.title('Distribution of Heart Disease by Chest Pain Types')
plt.legend(title='Heart Disease', labels=['No', 'Yes'])
plt.show()
```

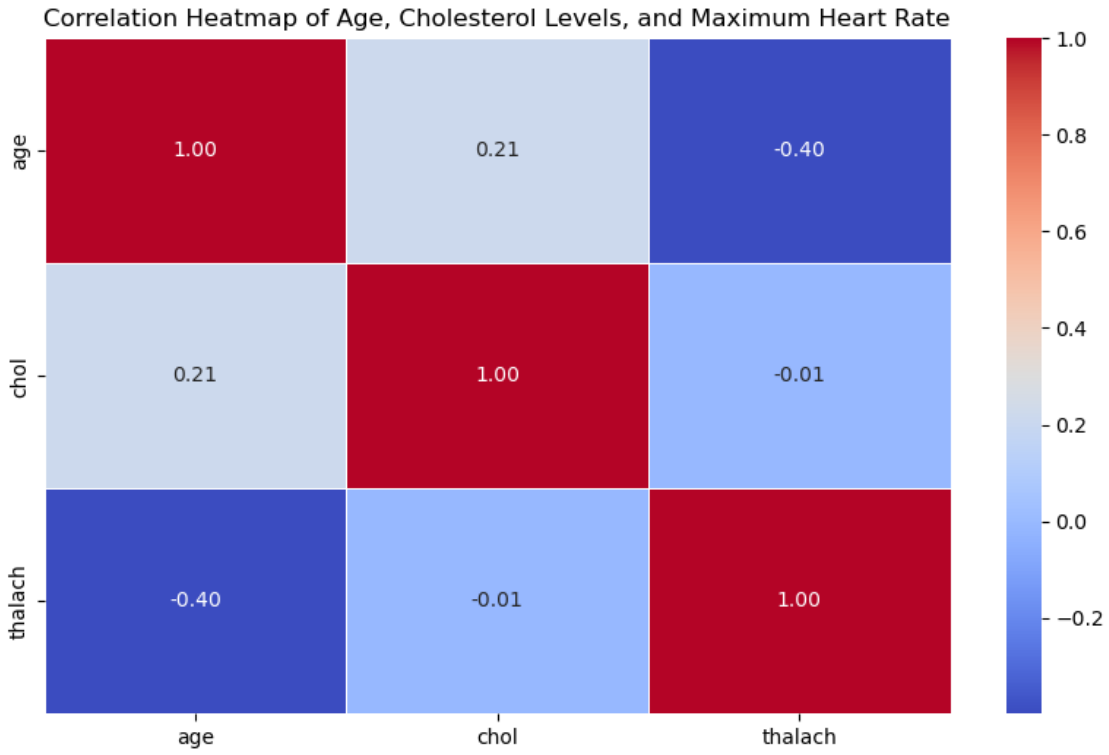


[8]:
```
# Can you use a heatmap to depict the correlation between different variables␣
↪in the dataset, such as age, cholesterol levels, and maximum heart rate␣
↪achieved?
```

[16]:
```
# Select the variables of interest
variables_of_interest = ['age', 'chol', 'thalach']

# Calculate the correlation matrix
correlation_matrix = heart_data[variables_of_interest].corr()
# Filter the correlation matrix to include only positive correlations
positive_correlation_matrix = correlation_matrix[correlation_matrix > 0]

# Find feature pairs with positive correlation
positive_correlation_features =␣
↪positive_correlation_matrix[positive_correlation_matrix < 1].stack().
↪reset_index()

# Rename the columns
positive_correlation_features.columns = ['Feature 1', 'Feature 2',␣
↪'Correlation']
```

```
# Filter out duplicate pairs and sort by correlation coefficient
positive_correlation_features = positive_correlation_features.
  ↪drop_duplicates(subset='Correlation', keep='first').
  ↪sort_values(by='Correlation', ascending=False)

# Print the features with positive correlation
print("Features with Positive Correlation:")
print(positive_correlation_features)

# Plot the heatmap
plt.figure(figsize=(10, 6))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt=".2f",␣
  ↪linewidths=0.5)
plt.title('Correlation Heatmap of Age, Cholesterol Levels, and Maximum Heart␣
  ↪Rate')
plt.show()
```

```
Features with Positive Correlation:
  Feature 1 Feature 2  Correlation
0       age      chol     0.213678
```



[12]:
```
# Model Implementation and Evaluation
```

[17]:
```
#Splitting the data into training data and Test data
```

[16]:
```
X_train, X_test, Y_train, Y_test= train_test_split(X, Y, test_size=0.2,␣
 ↪stratify=Y, random_state=2)
```

[18]:
```
#Check data
print(X.shape, X_train.shape, X_test.shape)
```

```
(303, 13) (242, 13) (61, 13)
```

[20]:
```
#Model Training
#Logistic Regression
```

[22]:
```
model= LogisticRegression()
```

[22]:
```
#Training the LogisticRegression model with the training data and Test data
```

[24]:
```
model.fit(X_train, Y_train)
```

```
/opt/conda/envs/anaconda-panel-2023.05-py310/lib/python3.11/site-
packages/sklearn/linear_model/_logistic.py:460: ConvergenceWarning: lbfgs failed
to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression
  n_iter_i = _check_optimize_result(
```

[24]:
```
LogisticRegression()
```

[24]:
```
#Model Evaluation
```

[25]:
```
#Accuracy on training data
X_train_prediction = model.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)
print('Accuracy on Training data: ', training_data_accuracy)
```

```
Accuracy on Training data:  0.8512396694214877
```

[26]:
```
#Accuracy on Test data
X_test_prediction = model.predict(X_test)
test_data_accuracy = accuracy_score(X_test_prediction, Y_test)
print('Accuracy on Training data: ', test_data_accuracy)
```

```
Accuracy on Training data:  0.819672131147541
```

[27]:
```
#Building a predictive system
```

[28]:
```
input_data  =(50,1,0,150,243,0,0,128,0,2.6,1,0,3)

#Change the input data to a numpy array
input_data_as_numpy_array=np.asarray(input_data)

#Reshape the numpy as we are predicting for only one instance
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

prediction = model.predict(input_data_reshaped)
print(prediction)

if (prediction[0]==0):
    print('The person does not have a Heart Disease')
else:
    print('The person has Heart Disease')
```

```
[0]
The person does not have a Heart Disease

/opt/conda/envs/anaconda-panel-2023.05-py310/lib/python3.11/site-
packages/sklearn/base.py:464: UserWarning: X does not have valid feature names,
but LogisticRegression was fitted with feature names
  warnings.warn(
```

[29]:
```
#Training the Random Forest model with the training data and test data
```

[30]:
```
from sklearn.metrics import precision_score, recall_score, f1_score

# Precision on training data
rf_training_precision = precision_score(Y_train, rf_train_predictions)

# Recall on training data
rf_training_recall = recall_score(Y_train, rf_train_predictions)

# F1-score on training data
rf_training_f1_score = f1_score(Y_train, rf_train_predictions)

print('Precision on Training data:', rf_training_precision)
print('Recall on Training data:', rf_training_recall)
print('F1-score on Training data:', rf_training_f1_score)

# Precision on test data
rf_test_precision = precision_score(Y_test, rf_test_predictions)

# Recall on test data
rf_test_recall = recall_score(Y_test, rf_test_predictions)
```

```
# F1-score on test data
rf_test_f1_score = f1_score(Y_test, rf_test_predictions)

print('Precision on Test data:', rf_test_precision)
print('Recall on Test data:', rf_test_recall)
print('F1-score on Test data:', rf_test_f1_score)
```

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
Cell In[30], line 4
      1 from sklearn.metrics import precision_score, recall_score, f1_score
      3 # Precision on training data
----> 4 rf_training_precision = precision_score(Y_train, rf_train_predictions)
      6 # Recall on training data
      7 rf_training_recall = recall_score(Y_train, rf_train_predictions)

NameError: name 'rf_train_predictions' is not defined
```

[ ]:
```
#Building a predictive system
```

[ ]:
```
import numpy as np

# Change the input data to a numpy array
input_data = (50, 1, 0, 150, 243, 0, 0, 128, 0, 2.6, 1, 0, 3)
input_data_as_numpy_array = np.asarray(input_data)

# Reshape the numpy array as we are predicting for only one instance
input_data_reshaped = input_data_as_numpy_array.reshape(1, -1)

# Predict using the trained model
prediction = rf_classifier.predict(input_data_reshaped)

# Print the prediction
if prediction[0] == 0:
    print('The person does not have heart disease.')
else:
    print('The person has heart disease.')
```

[ ]:
```
#Training the Support Vector Machine model with the training data and test data
```

[ ]:
```
from sklearn.svm import SVC
from sklearn.metrics import precision_score, recall_score, f1_score

# Initialize the Support Vector Machine Classifier
svm_classifier = SVC(kernel='linear', random_state=42)
```

```
# Train the classifier on the training data
svm_classifier.fit(X_train, Y_train)

# Make predictions on training data
svm_train_predictions = svm_classifier.predict(X_train)

# Make predictions on test data
svm_test_predictions = svm_classifier.predict(X_test)

# Precision on training data
svm_training_precision = precision_score(Y_train, svm_train_predictions)

# Recall on training data
svm_training_recall = recall_score(Y_train, svm_train_predictions)

# F1-score on training data
svm_training_f1_score = f1_score(Y_train, svm_train_predictions)

print('Precision on Training data:', svm_training_precision)
print('Recall on Training data:', svm_training_recall)
print('F1-score on Training data:', svm_training_f1_score)

# Precision on test data
svm_test_precision = precision_score(Y_test, svm_test_predictions)

# Recall on test data
svm_test_recall = recall_score(Y_test, svm_test_predictions)

# F1-score on test data
svm_test_f1_score = f1_score(Y_test, svm_test_predictions)

print('Precision on Test data:', svm_test_precision)
print('Recall on Test data:', svm_test_recall)
print('F1-score on Test data:', svm_test_f1_score)
```

[ ]:
```
#Training the K Nearest Neighbours model with the training data and test data
```

[ ]:
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import precision_score, recall_score, f1_score

# Initialize the K Nearest Neighbors Classifier
knn_classifier = KNeighborsClassifier(n_neighbors=5)

# Train the classifier on the training data
knn_classifier.fit(X_train, Y_train)
```

```
# Make predictions on training data
knn_train_predictions = knn_classifier.predict(X_train)

# Make predictions on test data
knn_test_predictions = knn_classifier.predict(X_test)

# Precision on training data
knn_training_precision = precision_score(Y_train, knn_train_predictions)

# Recall on training data
knn_training_recall = recall_score(Y_train, knn_train_predictions)

# F1-score on training data
knn_training_f1_score = f1_score(Y_train, knn_train_predictions)

print('Precision on Training data:', knn_training_precision)
print('Recall on Training data:', knn_training_recall)
print('F1-score on Training data:', knn_training_f1_score)

# Precision on test data
knn_test_precision = precision_score(Y_test, knn_test_predictions)

# Recall on test data
knn_test_recall = recall_score(Y_test, knn_test_predictions)

# F1-score on test data
knn_test_f1_score = f1_score(Y_test, knn_test_predictions)

print('Precision on Test data:', knn_test_precision)
print('Recall on Test data:', knn_test_recall)
print('F1-score on Test data:', knn_test_f1_score)
```

[ ]:
```
#Training the XG Boost model with the training data and test data
```

[ ]:
```
pip install xgboost
```

[71]:
```
import xgboost as xgb
from sklearn.metrics import precision_score, recall_score, f1_score

# Initialize the XGBoost Classifier
xgb_classifier = xgb.XGBClassifier()

# Train the classifier on the training data
xgb_classifier.fit(X_train, Y_train)

# Make predictions on training data
xgb_train_predictions = xgb_classifier.predict(X_train)
```

```
# Make predictions on test data
xgb_test_predictions = xgb_classifier.predict(X_test)

# Precision on training data
xgb_training_precision = precision_score(Y_train, xgb_train_predictions)

# Recall on training data
xgb_training_recall = recall_score(Y_train, xgb_train_predictions)

# F1-score on training data
xgb_training_f1_score = f1_score(Y_train, xgb_train_predictions)

print('Precision on Training data:', xgb_training_precision)
print('Recall on Training data:', xgb_training_recall)
print('F1-score on Training data:', xgb_training_f1_score)

# Precision on test data
xgb_test_precision = precision_score(Y_test, xgb_test_predictions)

# Recall on test data
xgb_test_recall = recall_score(Y_test, xgb_test_predictions)

# F1-score on test data
xgb_test_f1_score = f1_score(Y_test, xgb_test_predictions)

print('Precision on Test data:', xgb_test_precision)
print('Recall on Test data:', xgb_test_recall)
print('F1-score on Test data:', xgb_test_f1_score)
```

```
Precision on Training data: 1.0
Recall on Training data: 1.0
F1-score on Training data: 1.0
Precision on Test data: 0.78125
Recall on Test data: 0.7575757575757576
F1-score on Test data: 0.7692307692307692
```

[75]:
```
import numpy as np
from xgboost import XGBClassifier

# Assuming X_train and y_train are your training data
# Initialize and train the XGBoost model
xgb_classifier = XGBClassifier()
xgb_classifier.fit(X_train, Y_train)

# Define the input data
input_data = np.array([(50, 1, 0, 150, 243, 0, 0, 128, 0, 2.6, 1, 0, 3)])
```

```
# Reshape the input data as we are predicting for only one instance
input_data_reshaped = input_data.reshape(1, -1)

# Make predictions using the trained model
prediction = xgb_classifier.predict(input_data_reshaped)

# Print the prediction
if prediction[0] == 0:
    print('The person does not have heart disease.')
else:
    print('The person has heart disease.')
```

```
The person does not have heart disease.
```

[32]:
```
from sklearn.metrics import accuracy_score
from sklearn.ensemble import RandomForestClassifier
from xgboost import XGBClassifier

# Initialize and train Random Forest Classifier
rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)
rf_classifier.fit(X_train, Y_train)

# Make predictions using Random Forest
rf_test_predictions = rf_classifier.predict(X_test)

# Calculate accuracy for Random Forest
rf_test_accuracy = accuracy_score(Y_test, rf_test_predictions)

print('Random Forest - Test Accuracy:', rf_test_accuracy)

# Initialize and train XGBoost Classifier
xgb_classifier = XGBClassifier()
xgb_classifier.fit(X_train, Y_train)

# Make predictions using XGBoost
xgb_test_predictions = xgb_classifier.predict(X_test)

# Calculate accuracy for XGBoost
xgb_test_accuracy = accuracy_score(Y_test, xgb_test_predictions)

print('XGBoost - Test Accuracy:', xgb_test_accuracy)

# Compare accuracies and select the best model
if rf_test_accuracy > xgb_test_accuracy:
    print('Random Forest is the best-performing model.')
elif rf_test_accuracy < xgb_test_accuracy:
```

```
    print('XGBoost is the best-performing model.')
else:
    print('Both Random Forest and XGBoost have the same accuracy.')
```

```
Random Forest - Test Accuracy: 0.8032786885245902
XGBoost - Test Accuracy: 0.7540983606557377
Random Forest is the best-performing model.
```

[38]:
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score

# Assuming X and y are your features and target variable respectively
# 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)

# Initialize the Random Forest Classifier
rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)

# Train the classifier on the training data
rf_classifier.fit(X_train, Y_train)

# Make predictions on the test data
Y_pred = rf_classifier.predict(X_test)

# Calculate accuracy
accuracy = accuracy_score(Y_test, Y_pred)
print('Accuracy:', accuracy)
```

```
Accuracy: 0.8360655737704918
```

[46]:
```
import numpy as np
from sklearn.ensemble import RandomForestClassifier

# Assuming X_train and y_train are your training data
# Initialize the Random Forest Classifier
rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)

# Train the classifier on the training data
rf_classifier.fit(X_train, Y_train)

# Input data
input_data = np.array([[50, 1, 0, 150, 243, 0, 0, 128, 0, 2.6, 1, 0, 3]])

# Make prediction using the trained Random Forest model
prediction = rf_classifier.predict(input_data)
```

```
# Print prediction
if prediction[0] == 0:
    print('The person does not have Heart Disease')
else:
    print('The person has Heart Disease')
```

```
The person does not have Heart Disease

/opt/conda/envs/anaconda-panel-2023.05-py310/lib/python3.11/site-
packages/sklearn/base.py:464: UserWarning: X does not have valid feature names,
but RandomForestClassifier was fitted with feature names
  warnings.warn(
```

[ ]: