Heart Disease Risk Analysis

March 19, 2025

1 Heart Disease Risk Analysis Using EDA and Machine Learning

1.1 Step 1: Understanding the Data

[10]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import MinMaxScaler, StandardScaler
from scipy.stats import ttest_ind
from scipy.stats import chi2_contingency
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, precision_score, recall_score,␣
 ↪f1_score, classification_report
from sklearn.model_selection import GridSearchCV
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, precision_score, recall_score,␣
 ↪f1_score
from sklearn.model_selection import cross_val_score
import shap
```

[11]:

```
#data loading
df = pd.read_csv(r'C:\Users\User\Downloads\HeartDiseaseTrain-Test.csv')
```

[14]:

```
#exploring the dataset
df.head()
```

[14]:

```
   age     sex chest_pain_type  resting_blood_pressure  cholestoral  \
0   52    Male  Typical angina                     125          212
1   53    Male  Typical angina                     140          203
2   70    Male  Typical angina                     145          174
3   61    Male  Typical angina                     148          203
4   62  Female  Typical angina                     138          294
```

```
      fasting_blood_sugar               rest_ecg  Max_heart_rate  \
0    Lower than 120 mg/ml  ST-T wave abnormality             168
1  Greater than 120 mg/ml                 Normal             155
2    Lower than 120 mg/ml  ST-T wave abnormality             125
3    Lower than 120 mg/ml  ST-T wave abnormality             161
4  Greater than 120 mg/ml  ST-T wave abnormality             106

  exercise_induced_angina  oldpeak        slope vessels_colored_by_flourosopy  \
0                      No      1.0  Downsloping                           Two
1                     Yes      3.1    Upsloping                          Zero
2                     Yes      2.6    Upsloping                          Zero
3                      No      0.0  Downsloping                           One
4                      No      1.9         Flat                         Three

         thalassemia  target
0  Reversable Defect       0
1  Reversable Defect       0
2  Reversable Defect       0
3  Reversable Defect       0
4       Fixed Defect       0
```

[16]:

```
df.rename(columns={'cholestoral': 'cholesterol'}, inplace=True)
```

[18]:

```
# datatypes
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1025 entries, 0 to 1024
Data columns (total 14 columns):
 #   Column                         Non-Null Count  Dtype
---  ------                         --------------  -----
 0   age                            1025 non-null   int64
 1   sex                            1025 non-null   object
 2   chest_pain_type                1025 non-null   object
 3   resting_blood_pressure         1025 non-null   int64
 4   cholesterol                    1025 non-null   int64
 5   fasting_blood_sugar            1025 non-null   object
 6   rest_ecg                       1025 non-null   object
 7   Max_heart_rate                 1025 non-null   int64
 8   exercise_induced_angina        1025 non-null   object
 9   oldpeak                        1025 non-null   float64
 10  slope                          1025 non-null   object
 11  vessels_colored_by_flourosopy  1025 non-null   object
 12  thalassemia                    1025 non-null   object
 13  target                         1025 non-null   int64
dtypes: float64(1), int64(5), object(8)
memory usage: 112.2+ KB
```

[20]:
```
# Summary statistics for numeric columns
df.describe()
```

[20]:
```
                age  resting_blood_pressure  cholesterol  Max_heart_rate  \
count  1025.000000             1025.000000   1025.00000     1025.000000   
mean     54.434146              131.611707    246.00000      149.114146   
std       9.072290               17.516718     51.59251       23.005724   
min      29.000000               94.000000    126.00000       71.000000   
25%      48.000000              120.000000    211.00000      132.000000   
50%      56.000000              130.000000    240.00000      152.000000   
75%      61.000000              140.000000    275.00000      166.000000   
max      77.000000              200.000000    564.00000      202.000000   

           oldpeak       target  
count  1025.000000  1025.000000  
mean      1.071512     0.513171  
std       1.175053     0.500070  
min       0.000000     0.000000  
25%       0.000000     0.000000  
50%       0.800000     1.000000  
75%       1.800000     1.000000  
max       6.200000     1.000000  
```

[22]:
```
#identify missing data
df.isnull().sum()
```

[22]:
```
age                             0
sex                             0
chest_pain_type                 0
resting_blood_pressure          0
cholesterol                     0
fasting_blood_sugar             0
rest_ecg                        0
Max_heart_rate                  0
exercise_induced_angina         0
oldpeak                         0
slope                           0
vessels_colored_by_flourosopy   0
thalassemia                     0
target                          0
dtype: int64
```

[24]:
```
#identify duplicates &  Check number of duplicates
df.duplicated().sum()
```

[24]:
```
723
```

[26]:

```
# Identify categorical columns
categorical_cols = df.select_dtypes(include=['object', 'category']).columns.
 ↪tolist()
print("Categorical Columns:", categorical_cols)
```

```
Categorical Columns: ['sex', 'chest_pain_type', 'fasting_blood_sugar',
'rest_ecg', 'exercise_induced_angina', 'slope', 'vessels_colored_by_flourosopy',
'thalassemia']
```

[28]:

```
# Check which columns exist in the dataset
valid_categorical_cols = [col for col in categorical_cols if col in df.columns]
print("Valid columns for Label Encoding:", valid_categorical_cols)
```

```
Valid columns for Label Encoding: ['sex', 'chest_pain_type',
'fasting_blood_sugar', 'rest_ecg', 'exercise_induced_angina', 'slope',
'vessels_colored_by_flourosopy', 'thalassemia']
```

[30]:

```
# Apply Label Encoding to existing categorical columns
label_encoder = LabelEncoder()
for col in valid_categorical_cols:
    df[col] = label_encoder.fit_transform(df[col])
```

[32]:

```
# Verify encoding
print(df.head())
```

```
   age  sex  chest_pain_type  resting_blood_pressure  cholesterol  \
0   52    1                3                     125          212
1   53    1                3                     140          203
2   70    1                3                     145          174
3   61    1                3                     148          203
4   62    0                3                     138          294

   fasting_blood_sugar  rest_ecg  Max_heart_rate  exercise_induced_angina  \
0                    1         2             168                        0
1                    0         1             155                        1
2                    1         2             125                        1
3                    1         2             161                        0
4                    0         2             106                        0

   oldpeak  slope  vessels_colored_by_flourosopy  thalassemia  target
0      1.0      0                              3            3       0
1      3.1      2                              4            3       0
2      2.6      2                              4            3       0
3      0.0      0                              1            3       0
4      1.9      1                              2            0       0
```

2 Normalization

[35]:
```
# Identify numerical columns (integers & floats) excluding the target
numerical_cols = df.select_dtypes(include=['int64', 'float64']).columns.tolist()
numerical_cols.remove('target')
```

[37]:
```
# Apply Min-Max Normalization
scaler = MinMaxScaler()
df_normalized = df.copy()
df_normalized[numerical_cols] = scaler.fit_transform(df[numerical_cols])
```

[39]:
```
# Apply Min-Max Normalization
scaler = MinMaxScaler()
df_normalized = df.copy()
df_normalized[numerical_cols] = scaler.fit_transform(df[numerical_cols])
```

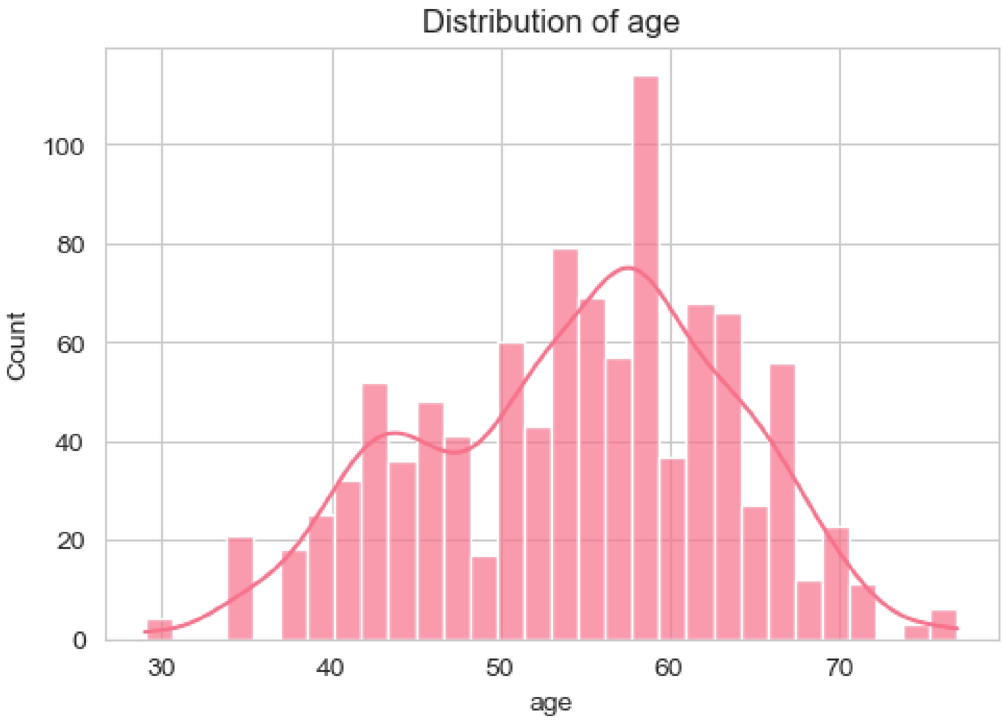
[41]:
```
# Display results
print(df_normalized.head())  # Normalized dataset
```

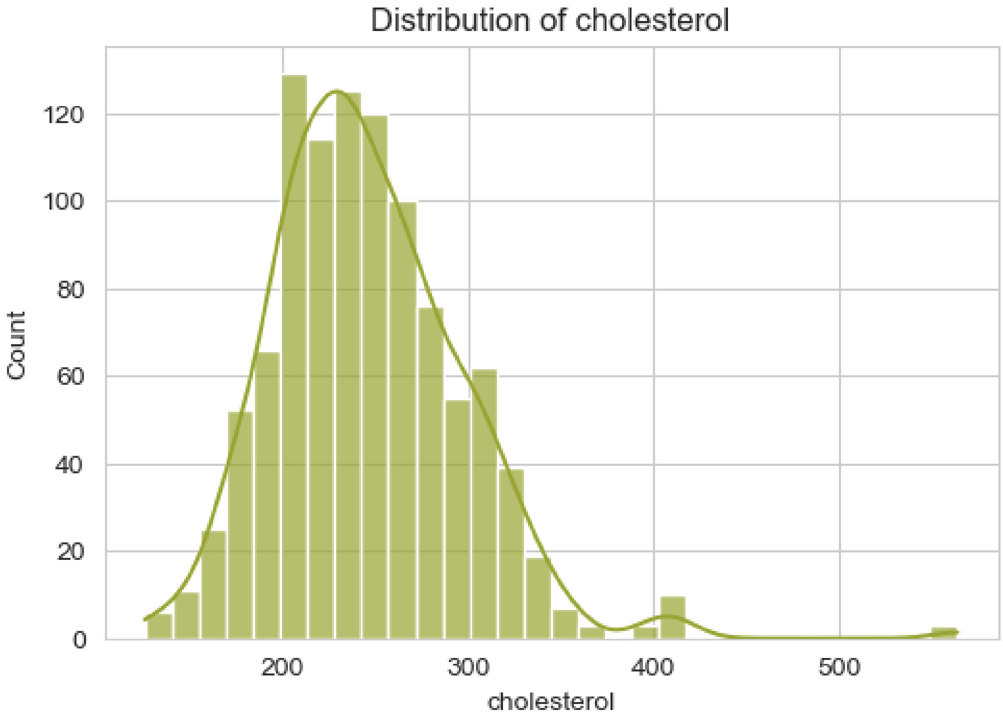
```
        age  sex  chest_pain_type  resting_blood_pressure  cholesterol  \
0  0.479167    1                3                0.292453     0.196347
1  0.500000    1                3                0.433962     0.175799
2  0.854167    1                3                0.481132     0.109589
3  0.666667    1                3                0.509434     0.175799
4  0.687500    0                3                0.415094     0.383562

   fasting_blood_sugar  rest_ecg  Max_heart_rate  exercise_induced_angina  \
0                    1         2        0.740458                        0
1                    0         1        0.641221                        1
2                    1         2        0.412214                        1
3                    1         2        0.687023                        0
4                    0         2        0.267176                        0

    oldpeak  slope  vessels_colored_by_flourosopy  thalassemia  target
0  0.161290      0                              3            3       0
1  0.500000      2                              4            3       0
2  0.419355      2                              4            3       0
3  0.000000      0                              1            3       0
4  0.306452      1                              2            0       0
```

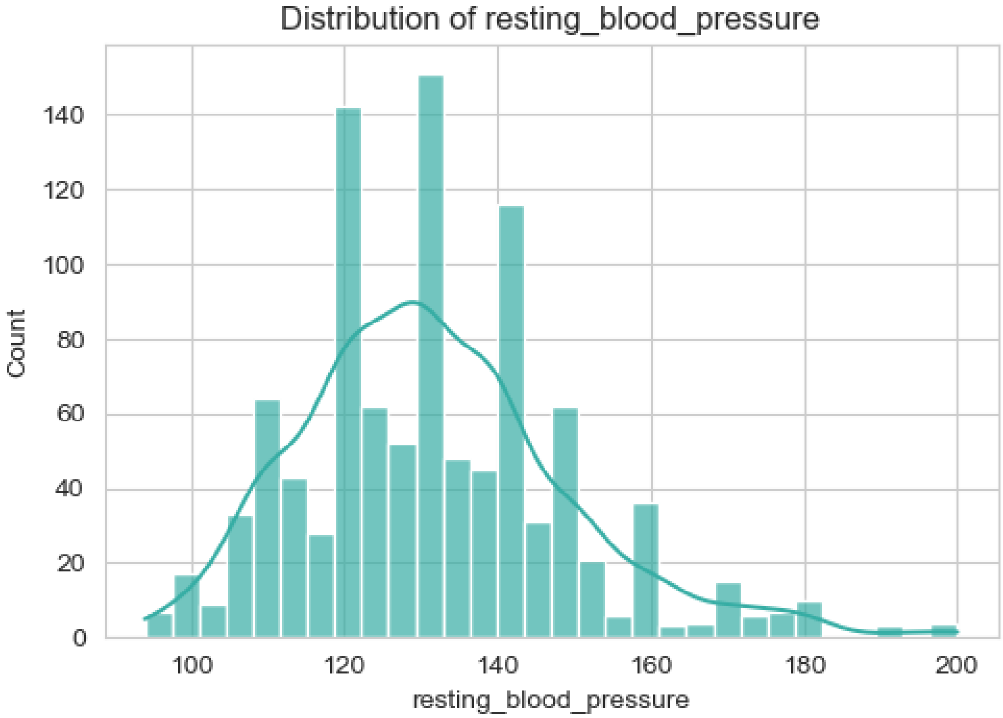
3 EXPLORATORY ANALYSIS

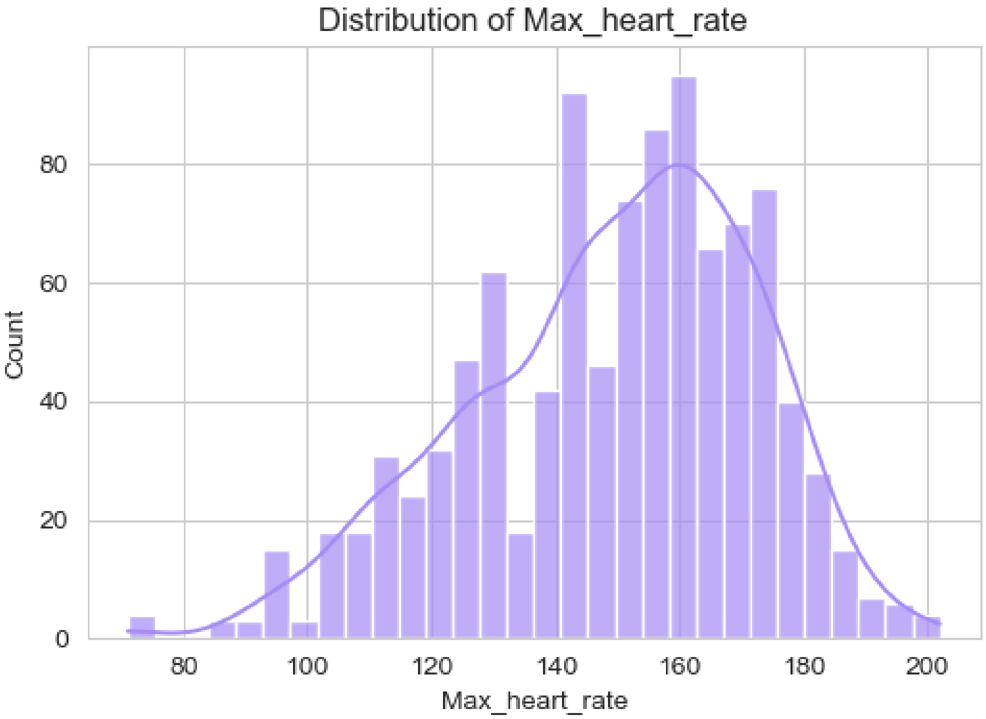
[44]:
```
# Define numerical columns first
num_cols = ['age', 'cholesterol', 'resting_blood_pressure', 'Max_heart_rate']

# Generates unique colors
palette = sns.color_palette("husl", len(num_cols))
```

```
# Set a nice background
sns.set_style("whitegrid")

# Loop through numerical columns and plot distributions
for col, color in zip(num_cols, palette):
    if col in df.columns:
        plt.figure(figsize=(6, 4))
        sns.histplot(df[col], bins=30, kde=True, color=color, alpha=0.7)
        plt.title(f"Distribution of {col}")
        plt.show()
```



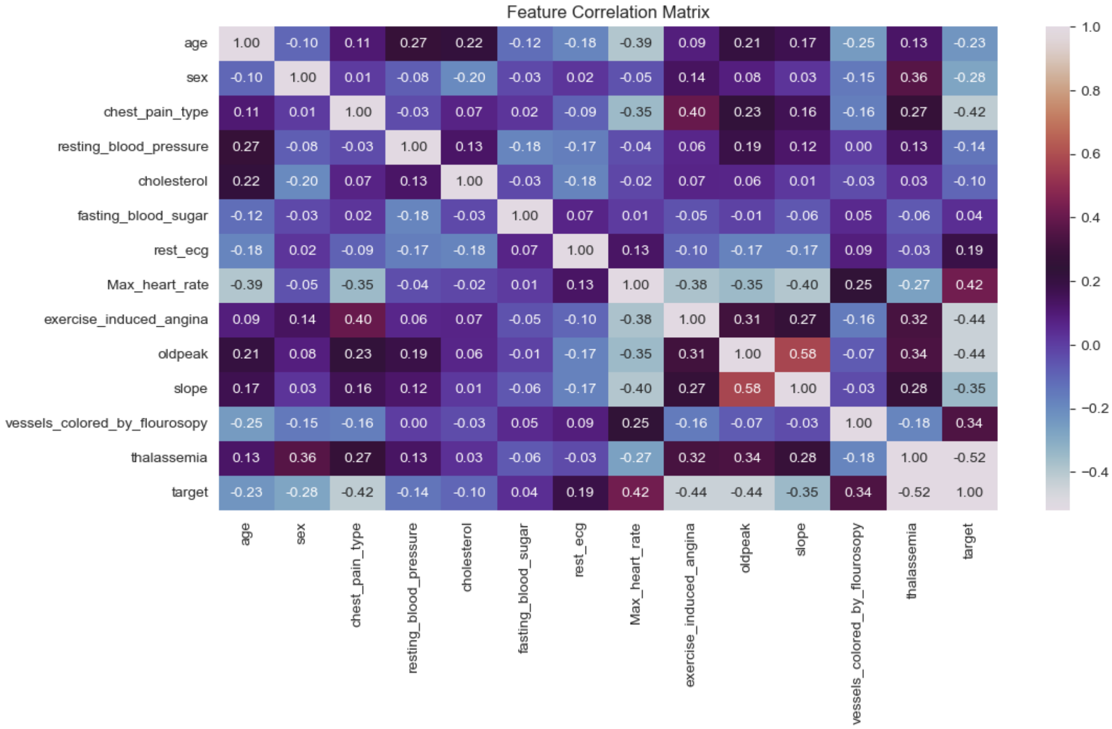

Distribution of cholesterol
Count
0
20
40
60
80
100
120
200
300
400
500
cholesterol


Distribution of resting_blood_pressure
Count
0
20
40
60
80
100
120
140
100
120
140
160
180
200
resting_blood_pressure



[46]:

```
#Bivariate Analysis - Relationship with Heart Disease
plt.figure(figsize=(12, 6))
sns.heatmap(df.corr(), annot=True, cmap="twilight", fmt=".2f")
plt.title("Feature Correlation Matrix")
plt.show()
```

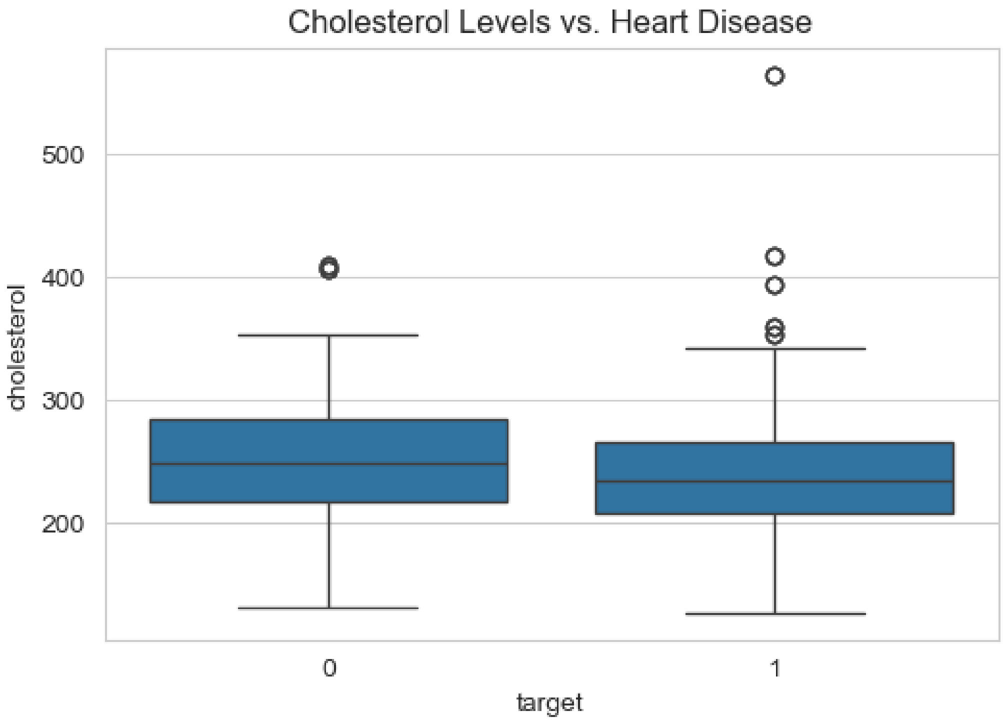


Feature Correlation Matrix

	age	sex	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_ecg	Max_heart_rate	exercise_induced_angina	oldpeak	slope	vessels_colored_by_flourosopy	thalassemia	target
age	1.00	-0.10	0.11	0.27	0.22	-0.12	-0.18	-0.39	0.09	0.21	0.17	-0.25	0.13	-0.23
sex	-0.10	1.00	0.01	-0.08	-0.20	-0.03	0.02	-0.05	0.14	0.08	0.03	-0.15	0.36	-0.28
chest_pain_type	0.11	0.01	1.00	-0.03	0.07	0.02	-0.09	-0.35	0.40	0.23	0.16	-0.16	0.27	-0.42
resting_blood_pressure	0.27	-0.08	-0.03	1.00	0.13	-0.18	-0.17	-0.04	0.06	0.19	0.12	0.00	0.13	-0.14
cholesterol	0.22	-0.20	0.07	0.13	1.00	-0.03	-0.18	-0.02	0.07	0.06	0.01	-0.03	0.03	-0.10
fasting_blood_sugar	-0.12	-0.03	0.02	-0.18	-0.03	1.00	0.07	0.01	-0.05	-0.01	-0.06	0.05	-0.06	0.04
rest_ecg	-0.18	0.02	-0.09	-0.17	-0.18	0.07	1.00	0.13	-0.10	-0.17	-0.17	0.09	-0.03	0.19
Max_heart_rate	-0.39	-0.05	-0.35	-0.04	-0.02	0.01	0.13	1.00	-0.38	-0.35	-0.40	0.25	-0.27	0.42
exercise_induced_angina	0.09	0.14	0.40	0.06	0.07	-0.05	-0.10	-0.38	1.00	0.31	0.27	-0.16	0.32	-0.44
oldpeak	0.21	0.08	0.23	0.19	0.06	-0.01	-0.17	-0.35	0.31	1.00	0.58	-0.07	0.34	-0.44
slope	0.17	0.03	0.16	0.12	0.01	-0.06	-0.17	-0.40	0.27	0.58	1.00	-0.03	0.28	-0.35
vessels_colored_by_flourosopy	-0.25	-0.15	-0.16	0.00	-0.03	0.05	0.09	0.25	-0.16	-0.07	-0.03	1.00	-0.18	0.34
thalassemia	0.13	0.36	0.27	0.13	0.03	-0.06	-0.03	-0.27	0.32	0.34	0.28	-0.18	1.00	-0.52
target	-0.23	-0.28	-0.42	-0.14	-0.10	0.04	0.19	0.42	-0.44	-0.44	-0.35	0.34	-0.52	1.00

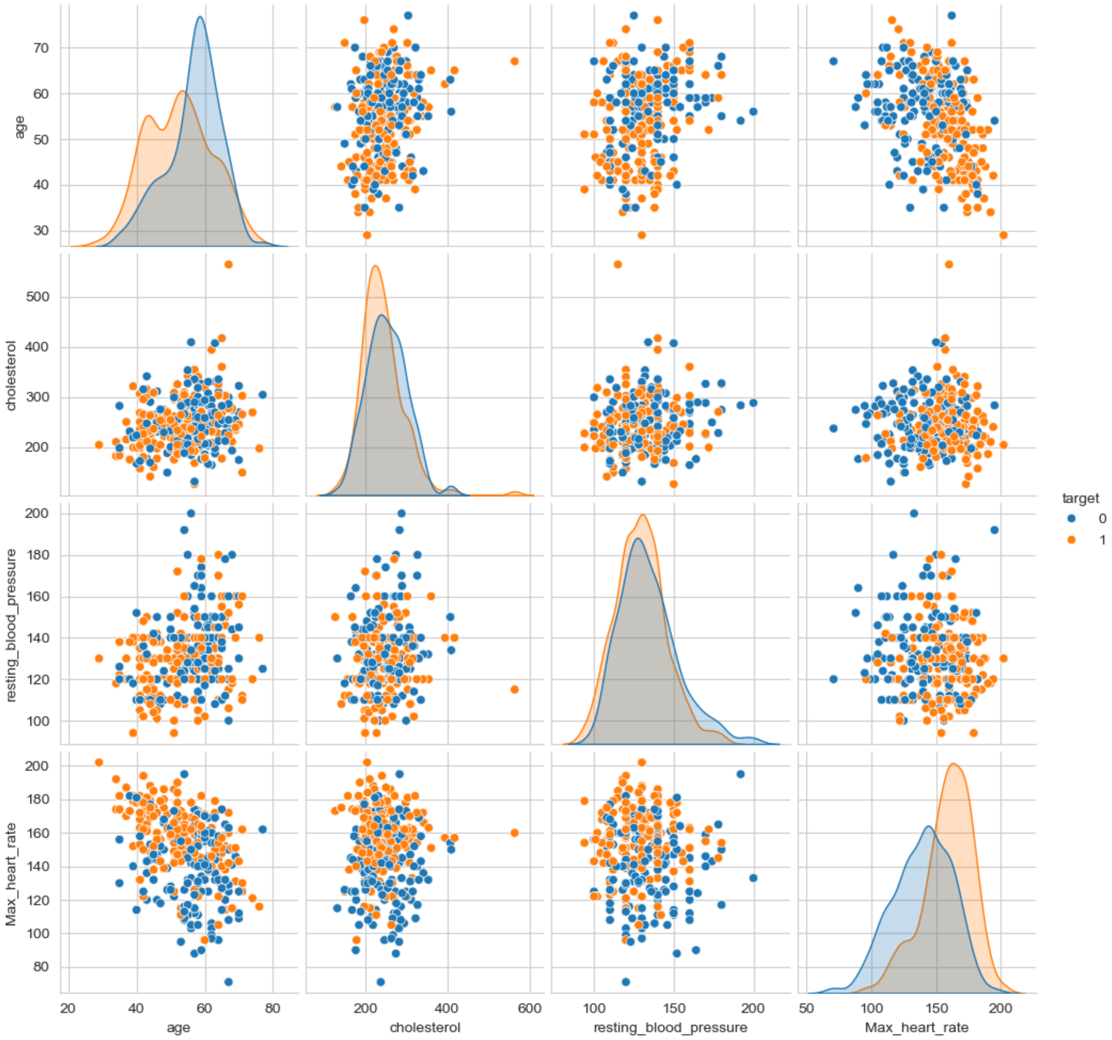
[48]:

```
# Boxplot of cholesterol levels by heart disease status
plt.figure(figsize=(6, 4))
sns.boxplot(x=df['target'], y=df['cholesterol'])
plt.title("Cholesterol Levels vs. Heart Disease")
plt.show()
```



[50]:

```
#  Multivariate Analysis - Pair Plot
sns.pairplot(df, hue="target", vars=['age', 'cholesterol',␣
 ↪'resting_blood_pressure', 'Max_heart_rate'])
plt.show()
```


age
cholesterol
resting_blood_pressure
Max_heart_rate
target
● 0
● 1
70
60
50
40
30
500
400
300
200
200
180
160
140
120
100
200
180
160
140
120
100
80
20
40
60
80
200
400
600
100
150
200
50
100
150
200

4 Hypothesis Testing

5 Test if Cholesterol Levels Differ Between Heart Disease and No Heart Disease Patients

5.1 Hypothesis:

5.2 Null (H): No difference in cholesterol levels between patients with and without heart disease.

5.3 Alternative (H): Cholesterol levels significantly differ between the two groups.

[53]:

```python
# Step 1: Remove duplicate column (keep only one 'cholesterol')
df = df.loc[:, ~df.columns.duplicated()]

# Step 2: Ensure 'cholesterol' is a single column
df['cholesterol'] = pd.to_numeric(df['cholesterol'], errors='coerce')

print("Successfully fixed 'cholesterol' column and converted to numeric.")
```

```
Successfully fixed 'cholesterol' column and converted to numeric.
```

[56]:

```python
# Grouping by heart disease presence
heart_disease = df[df['target'] == 1]['cholesterol']
no_heart_disease = df[df['target'] == 0]['cholesterol']

# Perform t-test
t_stat, p_value = ttest_ind(heart_disease, no_heart_disease, equal_var=False)
print(f"T-statistic: {t_stat}, P-value: {p_value}")

if p_value < 0.05:
    print("Cholesterol levels are significantly different between groups.")
else:
    print("No significant difference in cholesterol levels.")
```

```
T-statistic: -3.219133918272536, P-value: 0.0013262409956772104
Cholesterol levels are significantly different between groups.
```

6 Test if Sex is Associated with Heart Disease (Chi-Square Test)

6.1 Hypothesis:

6.2 H : Sex is not related to heart disease.

6.3 H : Sex is significantly associated with heart disease.

[59]:

```
# Creating a contingency table
contingency_table = pd.crosstab(df['sex'], df['target'])

# Perform Chi-Square Test
chi2, p_value, _, _ = chi2_contingency(contingency_table)
print(f"Chi-Square Statistic: {chi2}, P-value: {p_value}")


if p_value < 0.05:
    print("Sex and heart disease are significantly associated.")
else:
    print("No significant association between sex and heart disease.")
```

```
Chi-Square Statistic: 78.86305133922973, P-value: 6.656820681726434e-19
Sex and heart disease are significantly associated.
```

7 Test if Blood Pressure is Higher in Patients with Heart Disease

7.1 Hypothesis:

7.2 H : No difference in resting blood pressure between groups.

7.3 H : Patients with heart disease have significantly higher blood pressure

[62]:

```
# Grouping by heart disease presence
bp_heart_disease = df[df['target'] == 1]['resting_blood_pressure']
bp_no_heart_disease = df[df['target'] == 0]['resting_blood_pressure']

# Perform t-test
t_stat, p_value = ttest_ind(bp_heart_disease, bp_no_heart_disease,␣
 ↪equal_var=False)
print(f"T-statistic: {t_stat}, P-value: {p_value}")


if p_value < 0.05:
    print("Blood pressure is significantly different in heart disease patients.
 ↪")
else:
    print("No significant difference in blood pressure levels.")
```

```
T-statistic: -4.465214972380933, P-value: 8.922491860767991e-06
Blood pressure is significantly different in heart disease patients.
```

8 Model Building

[65]:
```
#split data before training
X = df.drop(columns=['target'])  # Features
y = df['target']  # Target variable

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
 ↪random_state=42)
```

[67]:
```
#Standardize data (important for KNN & Logistic Regression)
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

8.1 Train Models

[70]:
```
# Initialize models
models = {
    "Logistic Regression": LogisticRegression(),
    "Decision Tree": DecisionTreeClassifier(),
    "K-Nearest Neighbors": KNeighborsClassifier(n_neighbors=5)
}
```

[72]:
```
#Train & Evaluate Models
for name, model in models.items():
    model.fit(X_train, y_train)  # Train
    y_pred = model.predict(X_test)  # Predict
     # Calculate metrics
    accuracy = accuracy_score(y_test, y_pred)
    precision = precision_score(y_test, y_pred)
    recall = recall_score(y_test, y_pred)
    f1 = f1_score(y_test, y_pred)
    print(f" {name} Performance:")
    print(f"   - Accuracy: {accuracy:.4f}")
    print(f"   - Precision: {precision:.4f}")
    print(f"   - Recall: {recall:.4f}")
    print(f"   - F1-score: {f1:.4f}")
    print("-" * 40)
```

```
 Logistic Regression Performance:
   - Accuracy: 0.7951
   - Precision: 0.7699
   - Recall: 0.8447
   - F1-score: 0.8056
----------------------------------------
 Decision Tree Performance:
   - Accuracy: 0.9854
   - Precision: 1.0000
   - Recall: 0.9709
   - F1-score: 0.9852
----------------------------------------
 K-Nearest Neighbors Performance:
   - Accuracy: 0.8244
   - Precision: 0.7965
   - Recall: 0.8738
   - F1-score: 0.8333
----------------------------------------
```

9 Hyperparameter Tuning

9.1 Decision Tree Hyperparameter Tuning

9.1.1 max_depth (controls the depth of the tree)

9.1.2 min_samples_split (minimum samples needed to split a node)

9.1.3 min_samples_leaf (minimum samples in a leaf)

[76]:

```
# Define hyperparameter grids
dt_params = {
    'max_depth': [3, 5, 10, None],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 5]
}
```

9.2 KNN Hyperparameter Tuning

9.2.1 n_neighbors (number of nearest neighbors)

9.2.2 weights (uniform vs. distance)

9.2.3 metric (euclidean, manhattan)

[79]:

```
knn_params = {
    'n_neighbors': [3, 5, 7, 9, 11],
    'weights': ['uniform', 'distance'],
    'metric': ['euclidean', 'manhattan']
}
```

[81]:

```
# Initialize models
dt = DecisionTreeClassifier(random_state=42)
knn = KNeighborsClassifier()
```

[83]:

```
# Grid search with cross-validation
dt_grid = GridSearchCV(dt, dt_params, cv=5, scoring='accuracy', n_jobs=-1)
knn_grid = GridSearchCV(knn, knn_params, cv=5, scoring='accuracy', n_jobs=-1)
```

[85]:

```
# Fit models
dt_grid.fit(X_train, y_train)
knn_grid.fit(X_train, y_train)
```

[85]:

```
GridSearchCV(cv=5, estimator=KNeighborsClassifier(), n_jobs=-1,
             param_grid={'metric': ['euclidean', 'manhattan'],
                         'n_neighbors': [3, 5, 7, 9, 11],
                         'weights': ['uniform', 'distance']},
             scoring='accuracy')
```

[86]:

```
# Best models
best_dt = dt_grid.best_estimator_
best_knn = knn_grid.best_estimator_
```

[87]:

```
# Print best parameters
print("Best Decision Tree Parameters:", dt_grid.best_params_)
print("Best KNN Parameters:", knn_grid.best_params_)
```

```
Best Decision Tree Parameters: {'max_depth': None, 'min_samples_leaf': 1,
'min_samples_split': 2}
Best KNN Parameters: {'metric': 'euclidean', 'n_neighbors': 5, 'weights':
'distance'}
```

9.3 Evaluate Tuned Models

let's train the optimized models and compare their accuracy, precision, recall, and F1-score.

[92]:

```
# Train optimized Decision Tree
best_dt.fit(X_train, y_train)
y_pred_dt = best_dt.predict(X_test)
```

[94]:

```
# Train optimized KNN
best_knn.fit(X_train, y_train)
y_pred_knn = best_knn.predict(X_test)
```

[96]:

```
# Function to evaluate model
def evaluate_model(y_true, y_pred, model_name):
    accuracy = accuracy_score(y_true, y_pred)
    precision = precision_score(y_true, y_pred)
    recall = recall_score(y_true, y_pred)
    f1 = f1_score(y_true, y_pred)

    print(f" {model_name} Performance:")
    print(f"   - Accuracy: {accuracy:.4f}")
    print(f"   - Precision: {precision:.4f}")
    print(f"   - Recall: {recall:.4f}")
    print(f"   - F1-score: {f1:.4f}")
    print("-" * 40)
```

[98]:

```
# Evaluate models
evaluate_model(y_test, y_pred_dt, "Tuned Decision Tree")
evaluate_model(y_test, y_pred_knn, "Tuned KNN")
```

```
  Tuned Decision Tree Performance:
    - Accuracy: 0.9854
    - Precision: 1.0000
    - Recall: 0.9709
    - F1-score: 0.9852
----------------------------------------
  Tuned KNN Performance:
    - Accuracy: 1.0000
    - Precision: 1.0000
    - Recall: 1.0000
    - F1-score: 1.0000
----------------------------------------
```

9.4 Cross-Validation

Instead of relying only on one train-test split, let's use Stratified K-Fold Cross-Validation to ensure stable results.

[101]:

```
# 10-fold Cross-validation
cv_scores_dt = cross_val_score(best_dt, X, y, cv=10, scoring='accuracy')
cv_scores_knn = cross_val_score(best_knn, X, y, cv=10, scoring='accuracy')

print(f"  Decision Tree Cross-Validation Accuracy: {cv_scores_dt.mean():.4f} ±␣
 ↪{cv_scores_dt.std():.4f}")
print(f"  KNN Cross-Validation Accuracy: {cv_scores_knn.mean():.4f} ±␣
 ↪{cv_scores_knn.std():.4f}")
```

```
  Decision Tree Cross-Validation Accuracy: 0.9912 ± 0.0134
  KNN Cross-Validation Accuracy: 0.9942 ± 0.0117
```

9.5 Check for Data Leakage

Feature Importance (Decision Tree)

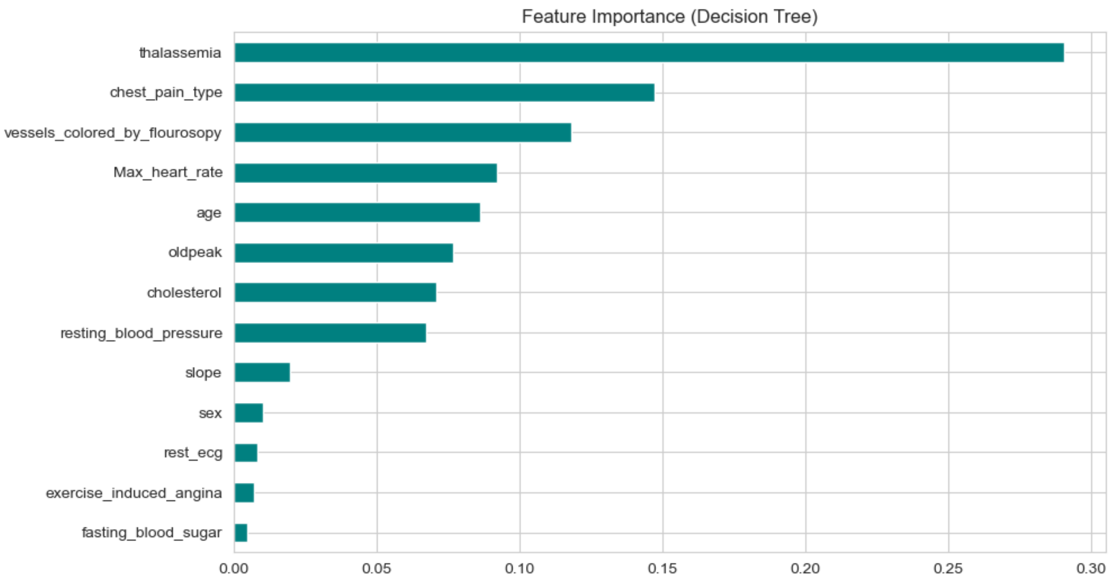
If some features have extremely high importance, they might be leaking target information.

[104]:

```
# Get feature importances
feat_importances = pd.Series(best_dt.feature_importances_, index=X.columns)
```

[106]:

```
# Plot
plt.figure(figsize=(10, 6))
feat_importances.sort_values().plot(kind="barh", color="teal")
plt.title("Feature Importance (Decision Tree)")
plt.show()
```



# Objective of SHAP Analysis ## Identify which features (like age, cholesterol, blood pressure, etc.) most influence the model's prediction. ## Determine whether features increase or decrease heart disease risk. ## Provide interpretable insights to make the model's decision-making transparent.

[109]:
```
#Train a Machine Learning Model
#Before applying SHAP, ensure that the KNN classifier is properly trained:
knn.fit(X_train, y_train)
```

[109]:
```
KNeighborsClassifier()
```

[111]:
```
df.columns
```

[111]:
```
Index(['age', 'sex', 'chest_pain_type', 'resting_blood_pressure',
       'cholesterol', 'fasting_blood_sugar', 'rest_ecg', 'Max_heart_rate',
       'exercise_induced_angina', 'oldpeak', 'slope',
       'vessels_colored_by_flourosopy', 'thalassemia', 'target'],
      dtype='object')
```

[199]:
```
feature_names = [ 'cholesterol','age']
```

9.6 Define the SHAP Explainer

9.6.1 SHAP has different explainers, but since KNN doesn't have a direct SHAP integration, we use KernelExplainer:

[116]:

```
# Select a small subset of training data for efficient computation
sample_data = X_train[:100]

# Define SHAP Explainer
explainer = shap.KernelExplainer(knn.predict_proba, sample_data)
```

[173]:

```
# Generate SHAP values for a test sample
shap_values = explainer.shap_values(X_test)
```

```
  0%|          | 0/205 [00:00<?, ?it/s]
```

[175]:

```
# Check if SHAP values are in multi-class format (list of arrays)
if isinstance(shap_values, list) and len(shap_values) > 1:
    class_index = 1
    shap_values = shap_values[class_index]
# Print shape for verification
print("SHAP values shape after fix:", len(shap_values), len(shap_values[0]))
```

```
SHAP values shape after fix: 205 13
```

[177]:

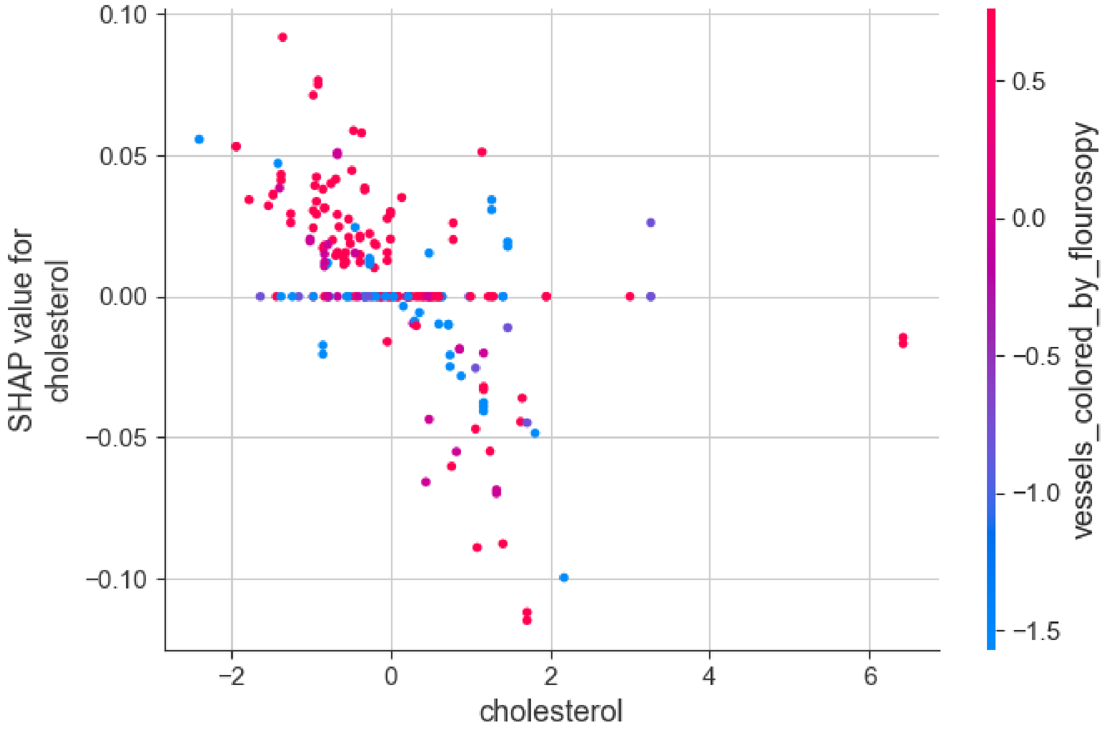
```
# Print shape for verification
print("SHAP values shape after fix:", len(shap_values), len(shap_values[0]))
```

```
SHAP values shape after fix: 205 13
```

[179]:

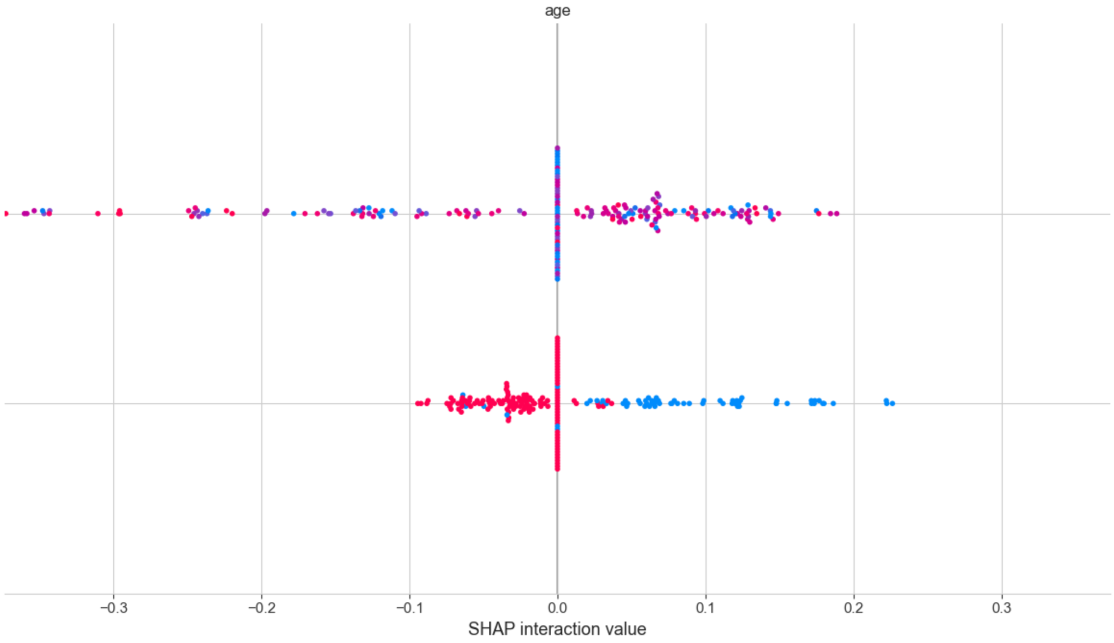
```
# Select SHAP values for one class
shap_values_class1 = shap_values[:, :, 1]

print("Fixed SHAP values shape:", shap_values_class1.shape)

#  plot
shap.dependence_plot("cholesterol", shap_values_class1, X_test,␣
 ↪feature_names=feature_names)
```

```
Fixed SHAP values shape: (205, 13)
```



[201]:
```
shap.summary_plot(shap_values, X_test, feature_names=feature_names)
```

```
<Figure size 640x480 with 0 Axes>
```



10 Heart Disease Risk Analysis

10.1 The objective of the project was to analyze heart disease risk key factors using machine learning model. The dataset used is teh UCI Heart Disease Dataset, which contains key health indicators such as cholesterol levels, blood pressure, and age. The workflow consist the following steos.

10.1.1 1. Data Preprocessing: Handling missing values, feature scaling, and encoding categorical variables.

10.1.2 2. Exploratory Data Analysis (EDA): Understanding feature distributions, correlations, and key risk indicators.

10.1.3 3. Model Training & Evaluation: Training multiple machine learning models, selecting the best-performing one using metrics like accuracy, precision, and recall.

10.1.4 4. Feature Importance Analysis: Using SHAP to interpret the model's predictions and understand which features contribute most to heart disease risk.

10.1.5 5. Visualization & Insights: Generating SHAP plots and other visualizations to make the results interpretable.

This analysis helps in understanding the most critical factors influencing heart disease, providing a foundation for further healthcare-related predictive modeling and decision-making.

[ ]:

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