Heart Disease Prediction

Overview

The primary aim of this project is to develop and evaluate machine learning models for predicting the presence or absence of heart disease based on various patient health metrics. The early and accurate prediction of heart disease is of paramount importance in healthcare, as it enables timely intervention, personalized treatment plans, and encourages preventive care. This predictive modeling approach can serve as a valuable tool for clinicians, assisting them in making more informed decisions and identifying at-risk individuals.

The dataset used consolidates information from two primary sources:

- UCI Machine Learning Repository - Heart Disease Dataset
- Kaggle - Heart Disease Dataset by Rasel Ahmed

Data Source and Acknowledgment

- Data was sourced from the UCI Machine Learning Repository and Kaggle.
- All patient data has been anonymized to ensure privacy and compliance with ethical data usage practices.

Kaggle Link: https://www.kaggle.com/datasets/data855/heart-disease/data
UCI Repository Link: https://archive.ics.uci.edu/dataset/45/heart+disease

Data Dictionary:

- age: age in years
- sex: sex (1 = male; 0 = female)
- cp: chest pain type
  - Value 1: typical angina
  - Value 2: atypical angina
  - Value 3: non-anginal pain
  - Value 4: asymptomatic
- trestbps: resting blood pressure (in mm Hg on admission to the hospital)
- chol: serum cholestoral in mg/dl
- fbs: (fasting blood sugar > 120 mg/dl) (1 = true; 0 = false)
- restecg: resting electrocardiographic results
  - Value 0: normal
  - Value 1: having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV)
  - Value 2: showing probable or definite left ventricular hypertrophy by Estes' criteria
- thalach: maximum heart rate achieved
- exang: exercise induced angina (1 = yes; 0 = no)
- oldpeak: ST depression induced by exercise relative to rest
- slope: the slope of the peak exercise ST segment
  - Value 1: upsloping
  - Value 2: flat
  - Value 3: downsloping
- ca: number of major vessels (0-3) colored by flourosopy
- thal: Thallium heart scan
  - Value 3: normal
  - Value 6: fixed defect
  - Value 7: reversable defect
- target (the lable):
  - 0 = no disease
  - 1 = disease

Libraries

In [ ]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline

import csv
import os
import pickle
import math

from scipy.stats import uniform
import optuna

import warnings
warnings.filterwarnings('ignore')

from sklearn.model_selection import train_test_split, RandomizedSearchCV, RepeatedStratifiedKFold, \
      GridSearchCV, cross_val_score, StratifiedKFold, KFold
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier, AdaBoostClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import GaussianNB, BernoulliNB
from sklearn.neural_network import MLPClassifier
from sklearn.preprocessing import LabelEncoder, MinMaxScaler
from sklearn.metrics import confusion_matrix, accuracy_score, precision_score,\
      recall_score, f1_score, roc_auc_score, ConfusionMatrixDisplay, roc_curve, auc, classification_report
```

Data

In this section, we will prepare data for the machine learning algorithms. This involves handling missing values, encoding categorical variables, and scaling numerical features to ensure all models perform optimally. Since the dataset is relatively clean, the primary focus is on encoding and scaling.

In [ ]:
```
# Loading of data
df = pd.read_csv('../Data/heart.csv')
df.head()
```

Out[ ]:

	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

In [4]:

```
df = df[df['ca'] < 4] #drop the wrong ca values
df = df[df['thal'] > 0] # drop the wong thal value
print(f'The length of the data now is {len(df)} instead of 303!')
```

```
The length of the data now is 296 instead of 303!
```

In [5]:

```
df = df.rename(
    columns = {'cp':'chest_pain_type',
               'trestbps':'resting_blood_pressure',
               'chol': 'cholesterol',
               'fbs': 'fasting_blood_sugar',
               'restecg' : 'resting_electrocardiogram',
               'thalach': 'max_heart_rate_achieved',
               'exang': 'exercise_induced_angina',
               'oldpeak': 'st_depression',
               'slope': 'st_slope',
               'ca':'num_major_vessels',
               'thal': 'Thallium_heart_scan'},
    errors="raise")
```

Exploratory Data Analysis

EDA is a crucial step to understand the data's characteristics, identify patterns, and visualize relationships between features. This helps in validating the data and informs the choice of algorithms.

In [6]:

```
df.shape
```

Out[6]:

```
(296, 14)
```

In [7]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 296 entries, 0 to 302
Data columns (total 14 columns):
 #   Column                     Non-Null Count  Dtype  
---  ------                     --------------  -----  
 0   age                        296 non-null    int64  
 1   sex                        296 non-null    int64  
 2   chest_pain_type            296 non-null    int64  
 3   resting_blood_pressure     296 non-null    int64  
 4   cholesterol                296 non-null    int64  
 5   fasting_blood_sugar        296 non-null    int64  
 6   resting_electrocardiogram  296 non-null    int64  
 7   max_heart_rate_achieved    296 non-null    int64  
 8   exercise_induced_angina    296 non-null    int64  
 9   st_depression              296 non-null    float64
 10  st_slope                   296 non-null    int64  
 11  num_major_vessels          296 non-null    int64  
 12  Thallium_heart_scan        296 non-null    int64  
 13  target                     296 non-null    int64  
dtypes: float64(1), int64(13)
memory usage: 34.7 KB
```

In [8]:

```
# numerical fearures 6
numerical_features = ['age', 'cholesterol', 'resting_blood_pressure', 'max_heart_rate_achieved', 'st_depression', 'num_major_vessels']

# categorical (binary)
bin_feats = ['sex', 'fasting_blood_sugar', 'exercise_induced_angina', 'target']

# caterorical (multi-)
nom_feats= ['chest_pain_type', 'resting_electrocardiogram', 'st_slope', 'Thallium_heart_scan']
categorical_features = nom_feats + bin_feats
```

In [9]:

```
df[numerical_features].describe().T
```

Out[9]:

	count	mean	std	min	25%	50%	75%	max
age	296.0	54.523649	9.059471	29.0	48.0	56.0	61.00	77.0
cholesterol	296.0	247.155405	51.977011	126.0	211.0	242.5	275.25	564.0
resting_blood_pressure	296.0	131.604730	17.726620	94.0	120.0	130.0	140.00	200.0
max_heart_rate_achieved	296.0	149.560811	22.970792	71.0	133.0	152.5	166.00	202.0
st_depression	296.0	1.059122	1.166474	0.0	0.0	0.8	1.65	6.2
num_major_vessels	296.0	0.679054	0.939726	0.0	0.0	0.0	1.00	3.0

In [10]:

```
# Check for null values
df.isna().sum()
```

Out[10]:

```
age                          0
sex                          0
chest_pain_type              0
resting_blood_pressure       0
cholesterol                  0
fasting_blood_sugar          0
resting_electrocardiogram    0
max_heart_rate_achieved      0
exercise_induced_angina      0
st_depression                0
st_slope                     0
num_major_vessels            0
Thallium_heart_scan          0
target                       0
dtype: int64
```

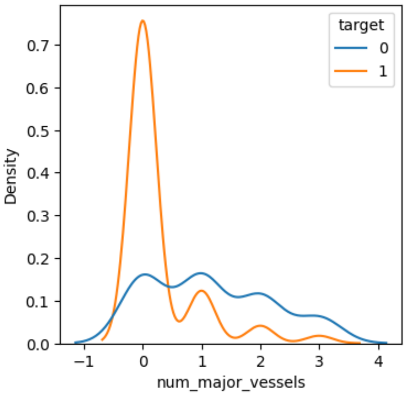
There seems to be no null values.

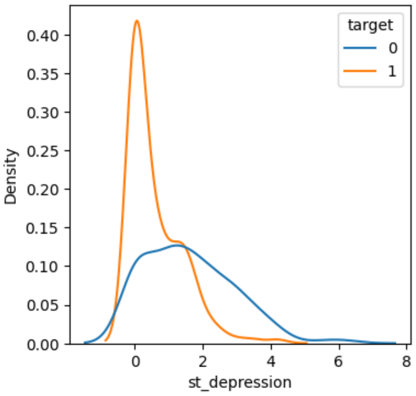
In [11]:

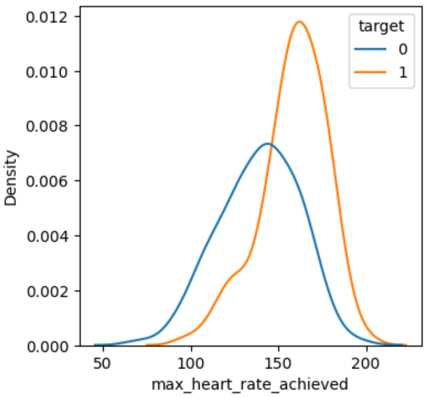
```
# check for duplicated records
df.duplicated().sum()
```

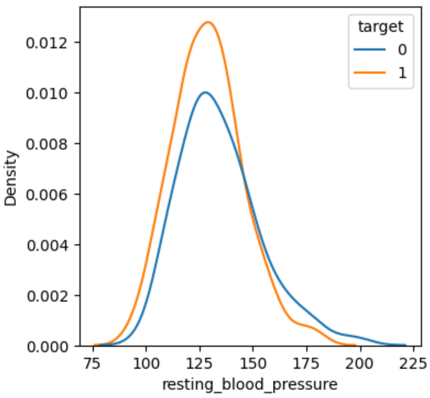
Out[11]: np.int64(0)

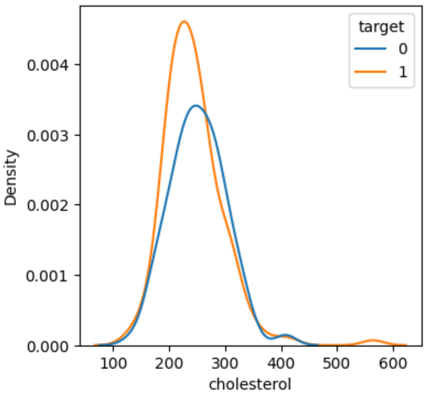
In [12]:
```python
# KDE plots
num_feat = numerical_features[::-1]
for feature in num_feat:
    plt.figure(figsize=(4,4))
    sns.kdeplot(data=df, x=feature, hue='target')
    plt.show()
```

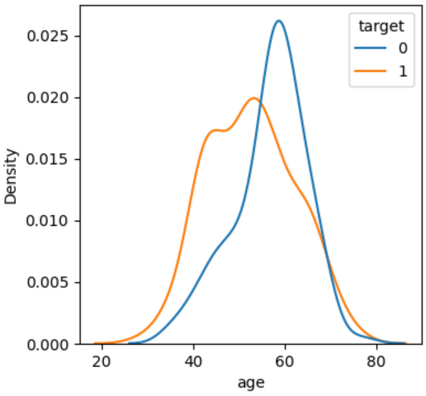








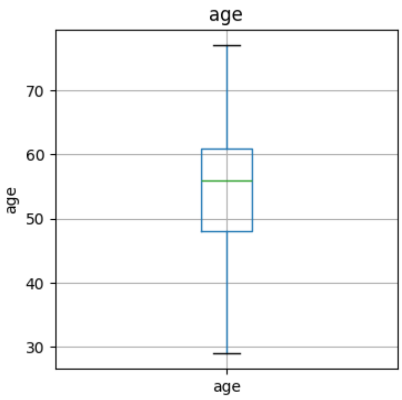


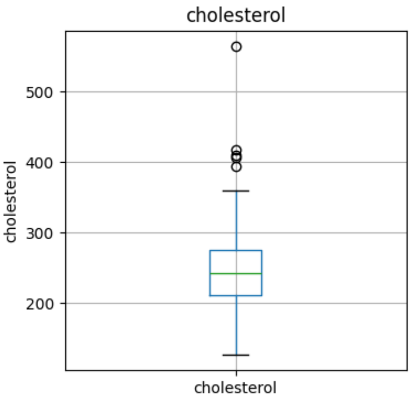


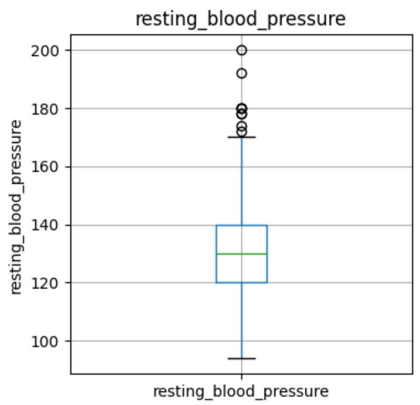
Few od the attributes can be observed to be positively skewed.

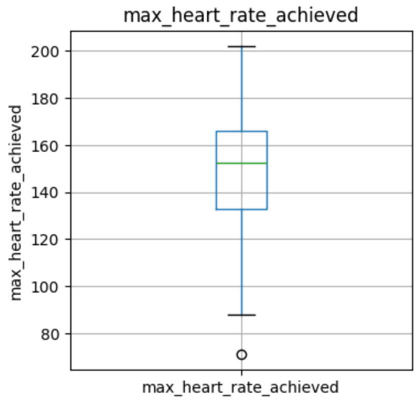
In [13]:

```
# Box plots
for feature in numerical_features:
  data = df.copy()

  if 0 in data[feature].unique():
    pass
  else:
    plt.figure(figsize=(4,4))
    data[feature] = data[feature]
    data.boxplot(column=feature)
    plt.ylabel(feature)
    plt.title(feature)
    plt.show()
```





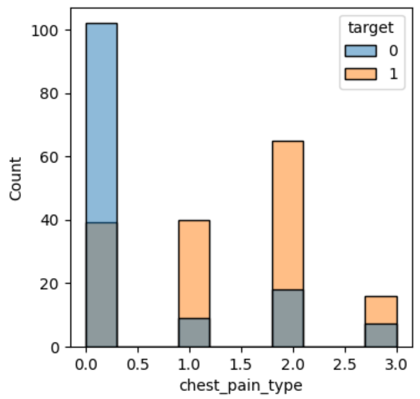


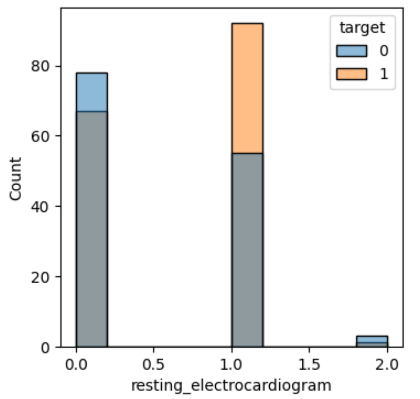


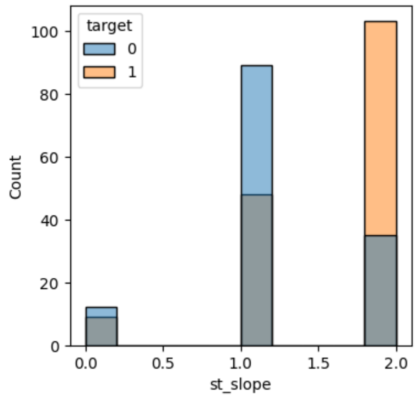
It can be observed that a few of the attributes contain outliers. As this is a medical dataset, I have chosen to not remove them as they may represent special cases or be not be an oulier at all.

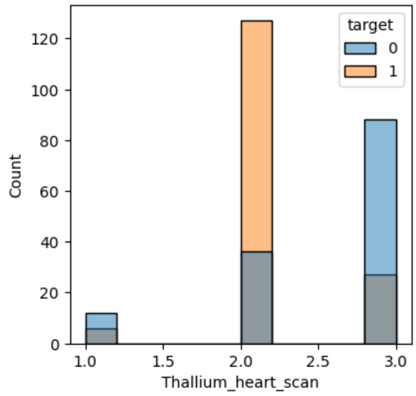
In [14]:

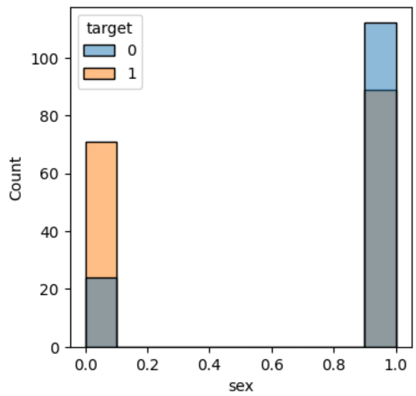
```
# bar plots
for feature in categorical_features:
    plt.figure(figsize=(4,4))
    sns.histplot(data=df, x=feature, hue='target')
    plt.show()
```

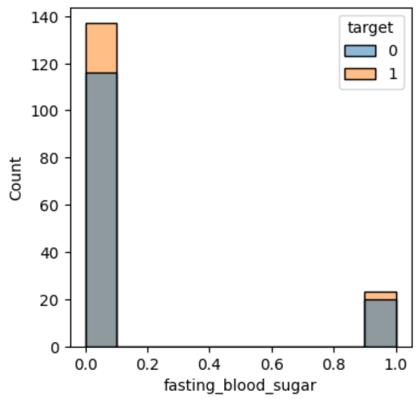


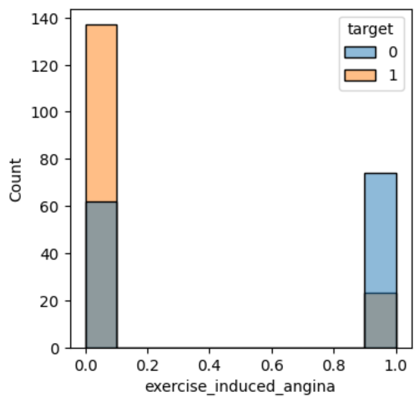


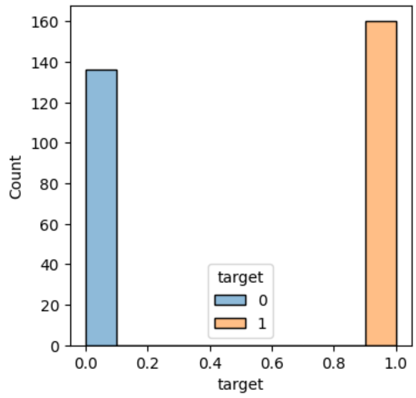

target
0
1
Count
0
20
40
60
80
100
0.0
0.5
1.0
1.5
2.0
st_slope


target
0
1
Count
0
20
40
60
80
100
120
1.0
1.5
2.0
2.5
3.0
Thallium_heart_scan


target
0
1
Count
0
20
40
60
80
100
0.0
0.2
0.4
0.6
0.8
1.0
sex

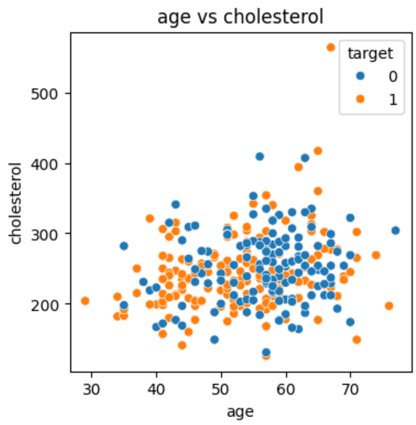

target
0
1
Count
0
20
40
60
80
100
120
140
0.0
0.2
0.4
0.6
0.8
1.0
fasting_blood_sugar

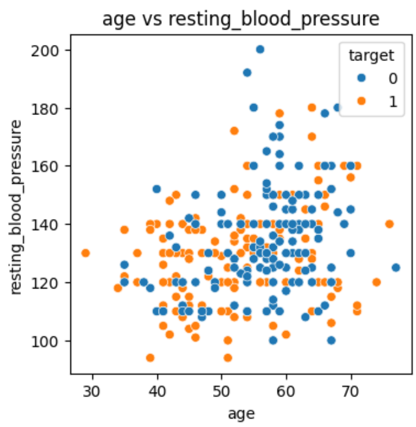

target
0
1
Count
0
20
40
60
80
100
120
140
0.0
0.2
0.4
0.6
0.8
1.0
exercise_induced_angina

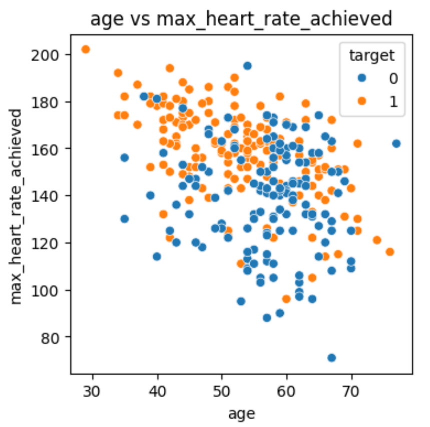


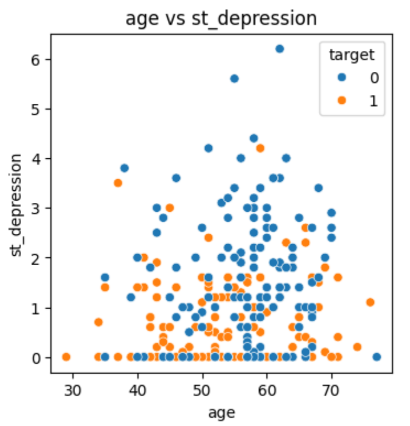
In [15]:

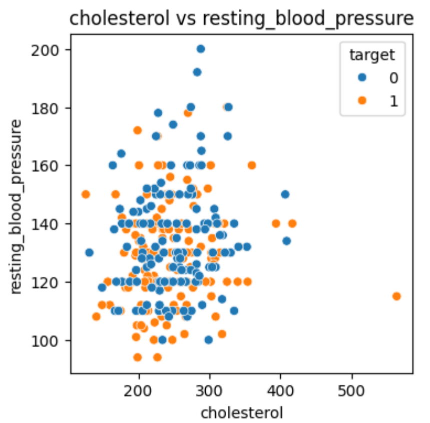
```
# scatter plot

def check_pair(pair, pair_dict):
    f1, f2 = pair
    # If f1 already has f2 recorded or vice versa → duplicate
    if f1 in pair_dict and f2 in pair_dict[f1]:
        return False
    if f2 in pair_dict and f1 in pair_dict[f2]:
        return False
    return True

def append_pair(pair, pair_dict):
    f1, f2 = pair
    pair_dict.setdefault(f1, []).append(f2)
    pair_dict.setdefault(f2, []).append(f1)

pair_dict = dict()

for f1 in ['age', 'cholesterol', 'resting_blood_pressure', 'max_heart_rate_achieved', 'st_depression']:
  for f2 in ['age', 'cholesterol', 'resting_blood_pressure', 'max_heart_rate_achieved', 'st_depression']:
    if f1 == f2:
      continue
    else:
      pair = (f1, f2)
      if check_pair(pair, pair_dict):
        append_pair(pair, pair_dict)
        plt.figure(figsize=(4,4))
        sns.scatterplot(data=df, x=f1, y=f2, hue='target')
        plt.title(f'{f1} vs {f2}')
        plt.show()
```

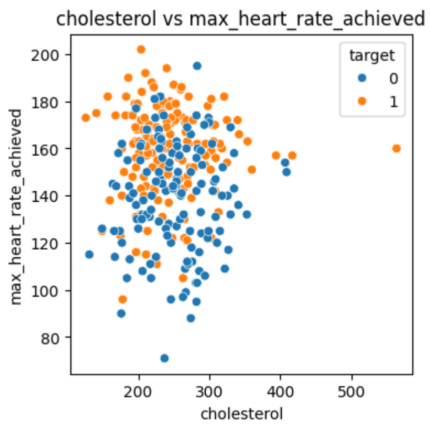


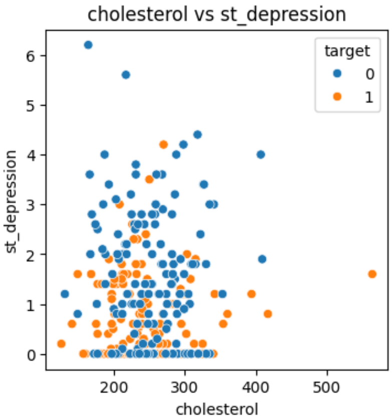


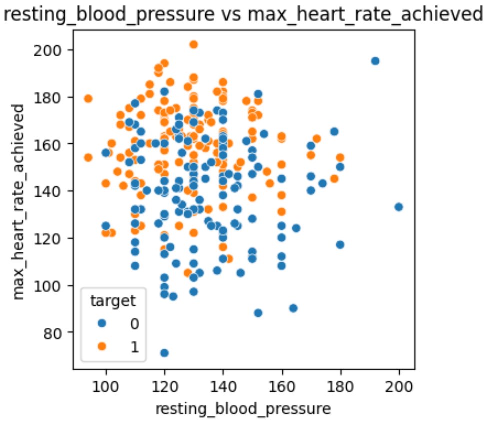

age vs max_heart_rate_achieved
max_heart_rate_achieved
age
target
0
1

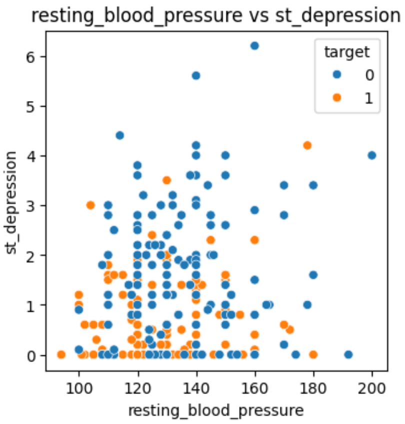

age vs st_depression
st_depression
age
target
0
1

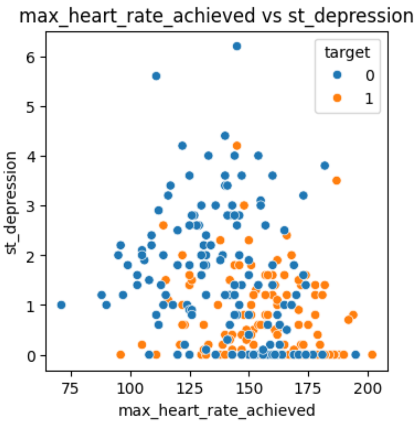

cholesterol vs resting_blood_pressure
resting_blood_pressure
cholesterol
target
0
1


cholesterol vs max_heart_rate_achieved
max_heart_rate_achieved
cholesterol
target
0
1



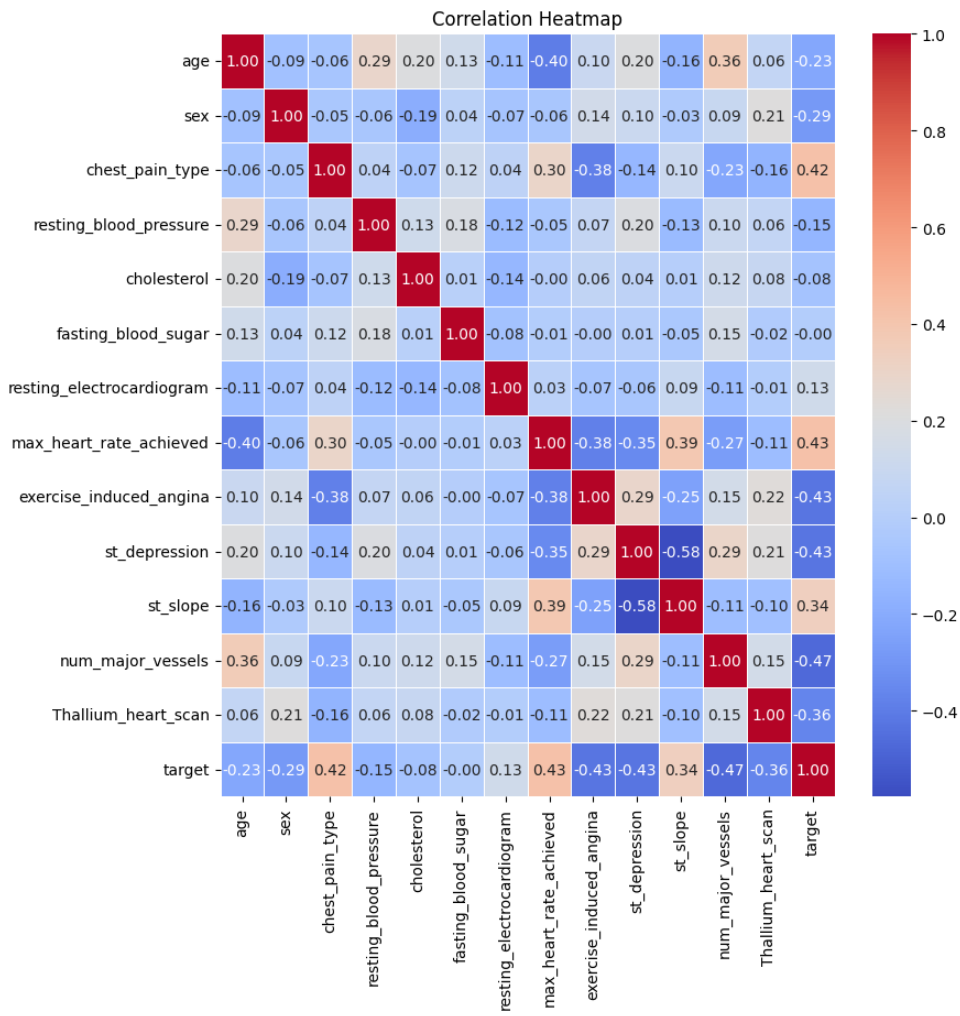






In [16]:

```
# Correlation heatmap
corr_matrix = df.corr()
plt.figure(figsize=(9,9))
sns.heatmap(corr_matrix, annot=True, cmap="coolwarm", fmt=".2f", linewidths=.5)
plt.title("Correlation Heatmap")
plt.show()
```



In [17]:

```
corr_matrix['target']
```

Out[17]:

```
age                         -0.225453
sex                         -0.285322
chest_pain_type              0.423425
resting_blood_pressure      -0.148922
cholesterol                 -0.076541
fasting_blood_sugar         -0.004680
resting_electrocardiogram    0.131716
max_heart_rate_achieved      0.426655
exercise_induced_angina     -0.425085
st_depression               -0.428804
st_slope                     0.337825
num_major_vessels           -0.467158
Thallium_heart_scan         -0.364399
target                       1.000000
Name: target, dtype: float64
```

In [18]:

```
# checking if dataset is misbalanced
df['target'].value_counts() / df.shape[0]
```

Out[18]:

```
target
1    0.540541
0    0.459459
Name: count, dtype: float64
```

In [19]:

```
df.columns
```

Out[19]:

```
Index(['age', 'sex', 'chest_pain_type', 'resting_blood_pressure',
       'cholesterol', 'fasting_blood_sugar', 'resting_electrocardiogram',
       'max_heart_rate_achieved', 'exercise_induced_angina', 'st_depression',
       'st_slope', 'num_major_vessels', 'Thallium_heart_scan', 'target'],
      dtype='object')
```

Model training

We will implement and evaluate several popular classification algorithms. The rationale for choosing these models is their proven effectiveness in classification tasks and their interpretability.

The following models are being compared for the classification task:

- Logistic Regression: A fundamental linear model that estimates the probability of a binary outcome using the logistic function. It serves as a strong baseline for classification problems due to its simplicity and interpretability.
- Decision Tree Classifier: A non-linear model that splits the data based on feature conditions, forming a tree-like structure of decisions. It is highly interpretable but can easily overfit without pruning or depth control.
- Random Forest Classifier: An ensemble of decision trees where each tree is trained on random subsets of data and features. It improves accuracy, generalization, and reduces overfitting compared to a single decision tree.
- Gradient Boosting Classifier: An ensemble technique that builds trees sequentially, where each tree learns from the errors of the previous one. It produces strong predictive performance and handles complex data patterns well.
- AdaBoost Classifier: An adaptive boosting algorithm that combines multiple weak learners, giving higher weights to misclassified samples in each round. It is effective for improving performance on difficult-to-classify cases.

- K-Nearest Neighbors (KNN): A distance-based model that assigns a class label based on the majority vote of its closest neighbors. Simple and effective, but sensitive to the choice of k and feature scaling.
- Support Vector Classifier (SVC): A model that finds the optimal hyperplane separating classes with maximum margin. With kernel functions, it can handle non-linear decision boundaries and is robust in high-dimensional spaces.
- Naïve Bayes (GaussianNB & BernoulliNB): Probabilistic classifiers based on Bayes' theorem. GaussianNB assumes continuous features follow a normal distribution, while BernoulliNB is suited for binary features. Both are fast and efficient.
- Multi-Layer Perceptron (MLP): A type of neural network consisting of multiple fully connected layers. It captures complex non-linear relationships but requires more data and tuning compared to simpler models.

Performance metrics evaluated: Accuracy, Precision, Recall, F1-score, ROC-AUC score, and Confusion Matrix.

Independent variable: Target
Dependent variable: ['age', 'sex', 'chest_pain_type', 'resting_blood_pressure', 'cholesterol', 'fasting_blood_sugar', 'resting_electrocardiogram', 'max_heart_rate_achieved', 'exercise_induced_angina', 'st_depression', 'st_slope', 'num_major_vessels', 'Thallium_heart_scan']

In [20]:
```
df.shape
```
Out[20]:
```
(296, 14)
```

In [21]:
```
df.head()
```
Out[21]:

	age	sex	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	resting_electrocardiogram	max_heart_rate_achieved	exercise_induced_angina	st_depr
0	63	1	3	145	233	1	0	150	0	
1	37	1	2	130	250	0	1	187	0	
2	41	0	1	130	204	0	0	172	0	
3	56	1	1	120	236	0	1	178	0	
4	57	0	0	120	354	0	1	163	1	

In [22]:
```
categorical_features
```
Out[22]:
```
['chest_pain_type',
 'resting_electrocardiogram',
 'st_slope',
 'Thallium_heart_scan',
 'sex',
 'fasting_blood_sugar',
 'exercise_induced_angina',
 'target']
```

In [ ]:
```
# label encoding
def label_encode_cat_features(data, cat_features):
    label_encoder = LabelEncoder()
    data_encoded = data.copy()

    for col in cat_features:
        data_encoded[col] = label_encoder.fit_transform(data[col])

    data = data_encoded
    return data

df = label_encode_cat_features(data, categorical_features)
```

In [24]:
```
y = df['target']
X = df.drop(['target'], axis=1)
```

In [25]:
```
y.shape, X.shape
```
Out[25]:
```
((296,), (296, 13))
```

In [26]:
```
seed = 42
# train test split
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.25, random_state=seed)
```

In [27]:
```
X_train.shape, X_test.shape
```
Out[27]:
```
((222, 13), (74, 13))
```

In [28]:
```
# standardizing the dataset
scaler = MinMaxScaler()
X_train=scaler.fit_transform(X_train)
X_test=scaler.transform(X_test)
```

In [29]:
```
def save_result_data(result_data, csv_file_path="training-log/model_result.csv", dir='training-log'):
    if os.path.exists(dir):
        with open(csv_file_path, 'a') as csvfile:
            csvwriter = csv.writer(csvfile)
            csvwriter.writerow(result_data)
    else:
        os.makedirs(dir, exist_ok=True)
        with open(csv_file_path, 'w') as csvfile:
            csvwriter = csv.writer(csvfile)
            csvwriter.writerow(['Name', 'Accuracy', 'Precision', 'Recall', 'F1 score', 'ROC_AUC Score'])
            csvwriter.writerow(result_data)

    csvfile.close()

def model_save(model,file_name, dir='model'):
    path = os.path.join(dir, file_name)

    if os.path.exists(dir):
        pass
    else:
        os.mkdir(dir)

    with open(path, 'wb') as file:
        pickle.dump(model, file)
```

In [30]:
```
def roc_auc_display(test_result, model_name):
    # print(test_result)
    plt.figure(figsize=(7,7))
    for name in model_name:
        fpr, tpr, _ = roc_curve(test_result['y_test'], test_result[name] )
```

```
        roc_auc = auc(fpr, tpr)
        plt.plot(fpr, tpr, label=f'{name} (AUC = {roc_auc:.2f})')

    plt.plot([0, 1], [0, 1], 'r--', label='Random Guess')
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title('ROC Curves for Two Models')
    plt.legend()
    plt.show()

def evaluate_model(model_list, model_name):
    pred_log = {'y_test': y_test}
    model_dict = {}
    results_list = []

    save_result_data(['New_Run', '---------', '---------', '---------','---------','---------'])

    for model, name in zip(model_list, model_name):
        # train & predict
        model_base = model
        model_base.fit(X_train, y_train)
        y_pred = model_base.predict(X_test)

        # save predictions and model
        pred_log[name] = y_pred
        model_dict[name] = model_base

        # compute metrics
        acc = accuracy_score(y_test, y_pred)
        prec = precision_score(y_test, y_pred)
        rec = recall_score(y_test, y_pred)
        f1 = f1_score(y_test, y_pred)
        roc = roc_auc_score(y_test, y_pred)
        cm = confusion_matrix(y_test, y_pred)

        # append to results list for DataFrame
        results_list.append({
            'Name': name,
            'Accuracy': acc,
            'Precision': prec,
            'Recall': rec,
            'F1 score': f1,
            'ROC_AUC': roc,
            'Confusion_Matrix': cm
        })

        result = [name, acc, prec, rec, f1, roc]
        save_result_data(result)

        file_name = name + ".pkl"
        model_save(model_base, file_name)

    # build DataFrame and print a rounded view for neat output
    results_df = pd.DataFrame(results_list)
    display_df = results_df.copy()
    numeric_cols = ['Accuracy', 'Precision', 'Recall', 'F1 score', 'ROC_AUC']
    display_df[numeric_cols] = display_df[numeric_cols].round(4)
    print(display_df.to_string(index=False))

    return pred_log, model_dict, results_df
```

In [ ]:

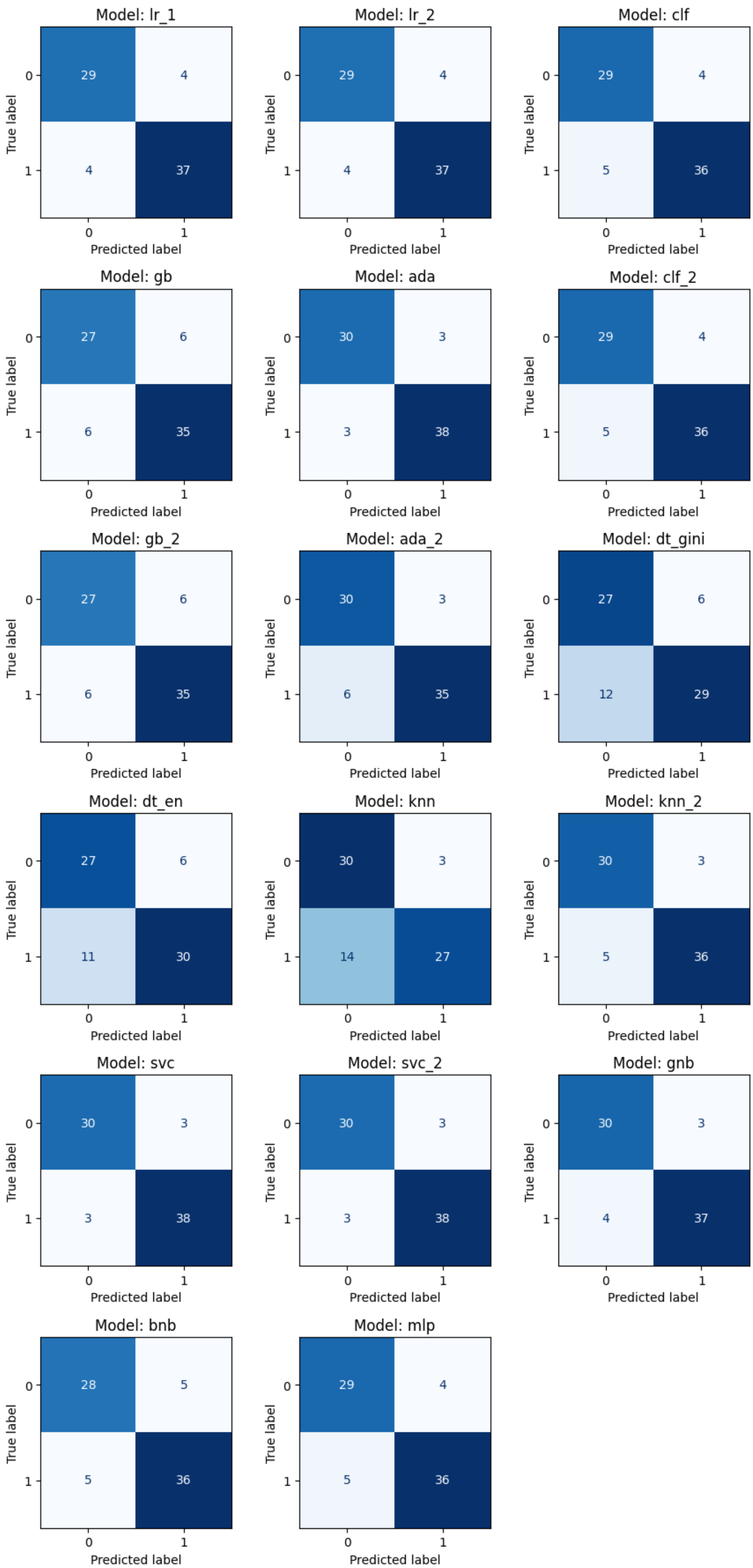
```
# Models
model_logistic_regression_1 = LogisticRegression()
model_logistic_regression_2 = LogisticRegression(solver='liblinear', random_state=seed)
model_clf = RandomForestClassifier(random_state=seed)
model_gb = GradientBoostingClassifier(random_state=seed)
model_ada = AdaBoostClassifier(random_state=seed)
model_clf_2 = RandomForestClassifier(n_estimators=100, random_state=seed)
model_gb_2 = GradientBoostingClassifier(n_estimators=100, random_state=seed)
model_ada_2 = AdaBoostClassifier(n_estimators=100, random_state=seed)
model_dt_gini = DecisionTreeClassifier(criterion='gini', random_state=seed)
model_dt_en = DecisionTreeClassifier(criterion='entropy', random_state=seed)
model_knn = KNeighborsClassifier(n_neighbors=2)
model_knn_2 = KNeighborsClassifier(n_neighbors=5)
model_svc = SVC()
model_svc_2 = SVC(probability=True, random_state=seed)
model_gnb = GaussianNB()
model_bnb = BernoulliNB()
model_mlp = MLPClassifier(hidden_layer_sizes=(50, 50), max_iter=100, random_state=seed)

model_list = [model_logistic_regression_1, model_logistic_regression_2, model_clf, model_gb, model_ada, model_clf_2,
              model_gb_2, model_ada_2, model_dt_gini, model_dt_en, model_knn, model_knn_2, model_svc, model_svc_2,
              model_gnb, model_bnb, model_mlp ]
model_name = ["lr_1", "lr_2", "clf", "gb", "ada", "clf_2", "gb_2", "ada_2", "dt_gini",
              "dt_en", "knn", "knn_2", "svc", "svc_2", "gnb", "bnb", "mlp"]

pred_log, model_dict, results_df = evaluate_model(model_list, model_name)
```

```
   Name  Accuracy  Precision  Recall  F1 score  ROC_AUC    Confusion_Matrix
   lr_1    0.8919     0.9024  0.9024    0.9024   0.8906  [[29, 4], [4, 37]]
   lr_2    0.8919     0.9024  0.9024    0.9024   0.8906  [[29, 4], [4, 37]]
    clf    0.8784     0.9000  0.8780    0.8889   0.8784  [[29, 4], [5, 36]]
     gb    0.8378     0.8537  0.8537    0.8537   0.8359  [[27, 6], [6, 35]]
    ada    0.9189     0.9268  0.9268    0.9268   0.9180  [[30, 3], [3, 38]]
  clf_2    0.8784     0.9000  0.8780    0.8889   0.8784  [[29, 4], [5, 36]]
   gb_2    0.8378     0.8537  0.8537    0.8537   0.8359  [[27, 6], [6, 35]]
  ada_2    0.8784     0.9211  0.8537    0.8861   0.8814  [[30, 3], [6, 35]]
dt_gini    0.7568     0.8286  0.7073    0.7632   0.7627 [[27, 6], [12, 29]]
  dt_en    0.7703     0.8333  0.7317    0.7792   0.7749 [[27, 6], [11, 30]]
    knn    0.7703     0.9000  0.6585    0.7606   0.7838 [[30, 3], [14, 27]]
  knn_2    0.8919     0.9231  0.8780    0.9000   0.8936  [[30, 3], [5, 36]]
    svc    0.9189     0.9268  0.9268    0.9268   0.9180  [[30, 3], [3, 38]]
  svc_2    0.9189     0.9268  0.9268    0.9268   0.9180  [[30, 3], [3, 38]]
    gnb    0.9054     0.9250  0.9024    0.9136   0.9058  [[30, 3], [4, 37]]
    bnb    0.8649     0.8780  0.8780    0.8780   0.8633  [[28, 5], [5, 36]]
    mlp    0.8784     0.9000  0.8780    0.8889   0.8784  [[29, 4], [5, 36]]
```

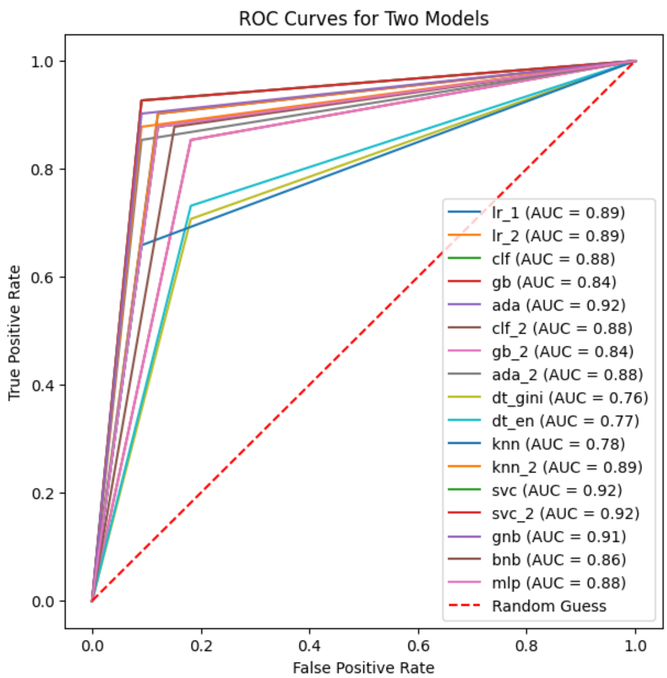
In [ ]:

```
# number of plots per row
n_cols = 3
n_models = len(results_df)
n_rows = math.ceil(n_models / n_cols)

fig, axes = plt.subplots(n_rows, n_cols, figsize=(9, 3 * n_rows))  # adjust width & height
axes = axes.flatten()  # flatten in case of multiple rows

for i, (_, row) in enumerate(results_df.iterrows()):
```

```
    name = row['Name']
    cm = row['Confusion_Matrix']

    disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=[0, 1])
    disp.plot(ax=axes[i], cmap="Blues", values_format="d", colorbar=False)
    axes[i].set_title(f'Model: {name}')

# Hiding any unused subplots if models < n_cols * n_rows
for j in range(i+1, len(axes)):
    fig.delaxes(axes[j])

plt.tight_layout()
plt.show()
```



In [ ]:
```
# ROC AUC Curve
roc_auc_display(pred_log, model_name)
```



Out of all the models tested, Logistic Regression, AdaBoost, Support Vector Classifier and Gaussian Naïve Bayes have shown the best performance. Moving forward, we will focus on these three models by applying cross-validation to ensure their robustness and performing hyperparameter tuning to optimize their predictive accuracy.

Hyperparameter Turning

In [34]:

```
lr = LogisticRegression(tol=1e-4, max_iter=1000, random_state=seed)

space = dict(C=uniform(loc=0, scale=5),
                     penalty=['l2', 'l1'],
                     solver= ['liblinear'])

search = RandomizedSearchCV(lr,
                         space,
                         random_state=seed,
                         cv = 5,
                         scoring='f1')

rand_search = search.fit(X_train, y_train)
print('Best Hyperparameters: %s' % rand_search.best_params_)

params = rand_search.best_params_
lr = LogisticRegression(**params)
lr.fit(X_train, y_train)
print(classification_report(y_test, lr.predict(X_test)))
```

```
Best Hyperparameters: {'C': np.float64(1.8727005942368125), 'penalty': 'l2', 'solver': 'liblinear'}
              precision    recall  f1-score   support

           0       0.85      0.88      0.87        33
           1       0.90      0.88      0.89        41

    accuracy                           0.88        74
   macro avg       0.88      0.88      0.88        74
weighted avg       0.88      0.88      0.88        74
```

In [ ]:

```
# Skip this

X, y = df.drop("target", axis=1), df["target"]

def objective(trial):
    model_name = trial.suggest_categorical("model", ["svc", "knn", "gb"])

    if model_name == "svc":
        params = {
            "C": trial.suggest_loguniform("C", 1e-3, 1e3),
            "gamma": trial.suggest_loguniform("gamma", 1e-4, 1e1),
            "kernel": trial.suggest_categorical("kernel", ["rbf", "poly", "sigmoid"])
        }
        model = SVC(**params)

    elif model_name == "knn":
        params = {
            "n_neighbors": trial.suggest_int("n_neighbors", 3, 50),
            "weights": trial.suggest_categorical("weights", ["uniform", "distance"]),
            "p": trial.suggest_int("p", 1, 2)  # 1=manhattan, 2=euclidean
        }
        model = KNeighborsClassifier(**params)

    elif model_name == "gb":
        params = {
            "n_estimators": trial.suggest_int("n_estimators", 100, 1000),
            "learning_rate": trial.suggest_loguniform("learning_rate", 1e-3, 0.3),
            "max_depth": trial.suggest_int("max_depth", 2, 10),
            "subsample": trial.suggest_uniform("subsample", 0.5, 1.0)
        }
        model = GradientBoostingClassifier(**params)

    # Cross-validation
    cv = StratifiedKFold(n_splits=5, shuffle=True, random_state=42)
    scores = cross_val_score(model, X, y, cv=cv, scoring="accuracy")
    return scores.mean()

# Run optimization
study = optuna.create_study(direction="maximize")
study.optimize(objective, n_trials=10)
```

```
print("Best Trial:")
print("  Value: ", study.best_trial.value)
print("  Params: ", study.best_trial.params)
```

In [37]:
```
# Logistic Regression
param_grid_lr = {
    'C': [0.01, 0.1, 1, 10, 100],
    'penalty': ['l1', 'l2', 'elasticnet', 'none'],
    'solver': ['saga']  # saga supports l1, l2, elasticnet, none
}
grid_lr = GridSearchCV(LogisticRegression(max_iter=5000), param_grid_lr, cv=5, scoring='f1')
grid_lr.fit(X_train, y_train)

# GaussianNB
param_grid_gnb = {
    'var_smoothing': np.logspace(-9, -1, 10)
}
grid_gnb = GridSearchCV(GaussianNB(), param_grid_gnb, cv=5, scoring='f1')
grid_gnb.fit(X_train, y_train)

# AdaBoost
param_grid_ada = {
    'n_estimators': [50, 100, 200, 300],
    'learning_rate': [0.001, 0.01, 0.1, 1]
}
grid_ada = GridSearchCV(AdaBoostClassifier(), param_grid_ada, cv=5, scoring='f1')
grid_ada.fit(X_train, y_train)

param_grid_svc = {
    "C": [0.001, 0.01, 0.1, 1, 10, 100, 1000],
    "gamma": [0.0001, 0.001, 0.01, 0.1, 1, 10],
    "kernel": ["rbf", "poly", "sigmoid"]
}
grid_svc = GridSearchCV(SVC(), param_grid_svc, cv=5, scoring='f1')
grid_svc.fit(X_train, y_train)

print("Best Logistic Regression params:", grid_lr.best_params_)
print("Best GaussianNB params:", grid_gnb.best_params_)
print("Best AdaBoost params:", grid_ada.best_params_)
print("Best Support Vector params:", grid_svc.best_params_)
```

```
Best Logistic Regression params: {'C': 1, 'penalty': 'l2', 'solver': 'saga'}
Best GaussianNB params: {'var_smoothing': np.float64(0.1)}
Best AdaBoost params: {'learning_rate': 0.01, 'n_estimators': 100}
Best Support Vector params: {'C': 0.01, 'gamma': 1, 'kernel': 'poly'}
```

In [38]:
```
print("Model: Grid LR\n",classification_report(y_test, grid_lr.predict(X_test), digits=4))
print("Model: Grid NB\n", classification_report(y_test, grid_gnb.predict(X_test), digits=4))
print("Model: Grid Adaboost\n", classification_report(y_test, grid_ada.predict(X_test), digits=4))
print("Model: Grid SVC\n", classification_report(y_test, grid_svc.predict(X_test), digits=4))
```

```
Model: Grid LR
               precision    recall  f1-score   support

           0     0.8788    0.8788    0.8788        33
           1     0.9024    0.9024    0.9024        41

    accuracy                         0.8919        74
   macro avg     0.8906    0.8906    0.8906        74
weighted avg     0.8919    0.8919    0.8919        74

Model: Grid NB
               precision    recall  f1-score   support

           0     0.8750    0.8485    0.8615        33
           1     0.8810    0.9024    0.8916        41

    accuracy                         0.8784        74
   macro avg     0.8780    0.8755    0.8766        74
weighted avg     0.8783    0.8784    0.8782        74

Model: Grid Adaboost
               precision    recall  f1-score   support

           0     0.9333    0.8485    0.8889        33
           1     0.8864    0.9512    0.9176        41

    accuracy                         0.9054        74
   macro avg     0.9098    0.8999    0.9033        74
weighted avg     0.9073    0.9054    0.9048        74

Model: Grid SVC
               precision    recall  f1-score   support

           0     0.9032    0.8485    0.8750        33
           1     0.8837    0.9268    0.9048        41

    accuracy                         0.8919        74
   macro avg     0.8935    0.8877    0.8899        74
weighted avg     0.8924    0.8919    0.8915        74
```

Apart from logistic regression, the other three models have experienced degradation in the performance metrics.

Cross validation

In [39]:
```
params = grid_lr.best_params_
lr = LogisticRegression(**params, max_iter=5000)
lr.fit(X_train, y_train)
print(classification_report(y_test, lr.predict(X_test), digits=4))
```

```
              precision    recall  f1-score   support

           0     0.8788    0.8788    0.8788        33
           1     0.9024    0.9024    0.9024        41

    accuracy                         0.8919        74
   macro avg     0.8906    0.8906    0.8906        74
weighted avg     0.8919    0.8919    0.8919        74
```

In [40]:
```
def perform_cross_validation(model_name, model_list, cv=None):
    for name, model in zip(model_name, model_list):
        cross_val_results = cross_val_score(model, X, y, cv=cv)
```

```
        print(f"\nCross-Validation Results of {name} (Accuracy):")
        for i, result in enumerate(cross_val_results, 1):
            print(f"  Fold {i}: {result * 100:.2f}%")

        print(f'Mean Accuracy {name}: {cross_val_results.mean()* 100:.2f}%')
```

In [41]:

```
num_folds = 5
kf = KFold(n_splits=num_folds, shuffle=True, random_state=seed)

cv_lr = LogisticRegression(**params, max_iter=5000)
cv_ada = AdaBoostClassifier(random_state=seed)
cv_gnb = GaussianNB()
cv_svc = SVC()

model_cv = [cv_lr, cv_ada, cv_gnb, cv_svc]
model_name = ['cv_lr', 'cv_ada', 'cv_gnb', 'cv_svc']
perform_cross_validation(model_name, model_cv, kf)
```

```
Cross-Validation Results of cv_lr (Accuracy):
  Fold 1: 91.67%
  Fold 2: 83.05%
  Fold 3: 69.49%
  Fold 4: 83.05%
  Fold 5: 83.05%
Mean Accuracy cv_lr: 82.06%

Cross-Validation Results of cv_ada (Accuracy):
  Fold 1: 86.67%
  Fold 2: 83.05%
  Fold 3: 81.36%
  Fold 4: 83.05%
  Fold 5: 77.97%
Mean Accuracy cv_ada: 82.42%

Cross-Validation Results of cv_gnb (Accuracy):
  Fold 1: 90.00%
  Fold 2: 86.44%
  Fold 3: 76.27%
  Fold 4: 84.75%
  Fold 5: 79.66%
Mean Accuracy cv_gnb: 83.42%

Cross-Validation Results of cv_svc (Accuracy):
  Fold 1: 71.67%
  Fold 2: 79.66%
  Fold 3: 55.93%
  Fold 4: 59.32%
  Fold 5: 62.71%
Mean Accuracy cv_svc: 65.86%
```

Explainability

In [42]:

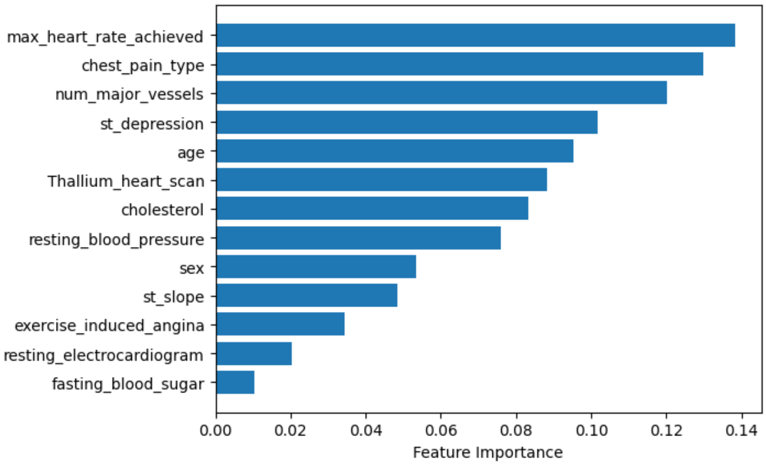
```
# Feature importance
print("Feature importance (Logistic Regression) (Coefficient and Odds Ratio):: ")
model_dict_reg = lr

# Coefficients and Odds Ratios
coefficients = model_dict_reg.coef_[0]
odds_ratios = np.exp(coefficients)


# Display feature importance using coefficients and odds ratios
feature_importance = pd.DataFrame({
    'Feature': X.columns,
    'Coefficient': coefficients,
    'Odds Ratio': odds_ratios
})
print(feature_importance.sort_values(by='Coefficient', ascending=False))
```

```
Feature importance (Logistic Regression) (Coefficient and Odds Ratio)::
                     Feature  Coefficient  Odds Ratio
2            chest_pain_type     1.665476    5.288190
7      max_heart_rate_achieved     1.148906    3.154738
10                  st_slope     0.968683    2.634473
6    resting_electrocardiogram     0.574723    1.776638
5        fasting_blood_sugar     0.205116    1.227668
0                        age    -0.387010    0.679084
4                cholesterol    -0.545959    0.579286
8      exercise_induced_angina    -0.926916    0.395772
3       resting_blood_pressure    -0.984107    0.373773
12       Thallium_heart_scan    -1.205090    0.299665
9              st_depression    -1.260475    0.283519
1                        sex    -1.510200    0.220866
11          num_major_vessels    -2.212351    0.109443
```

In [36]:

```
# Feature importance
print("Feature importance (Random Forest) (Coefficient and Odds Ratio):: ")
clf = model_dict['clf_2']
importances = clf.feature_importances_
feature_names = X.columns
sorted_idx = importances.argsort()

plt.barh(range(len(importances)), importances[sorted_idx])
plt.yticks(range(len(importances)), feature_names[sorted_idx])
plt.xlabel("Feature Importance")
plt.show()
```

```
Feature importance (Random Forest) (Coefficient and Odds Ratio)::
```



Conclusion from Feature Importance

- Most Influential Factors:
  - Max heart rate achieved and chest pain type are the strongest predictors. This suggests that exercise capacity and symptoms during exertion are critical indicators of heart disease risk.
  - Number of major vessels and ST depression also rank highly, highlighting the role of blood flow blockages and ECG abnormalities.
- Moderately Important Factors:
  - Age, Thallium heart scan results, cholesterol, and resting blood pressure contribute meaningfully, showing that traditional cardiovascular risk factors still hold weight.
- Less Influential Factors:
  - Sex, ST slope, exercise-induced angina, resting ECG, and fasting blood sugar have lower importance, suggesting they are less decisive in this dataset/model, though they still add some predictive value.

Potential Preventive Measures or Lifestyle Changes Based on Risk Factors

1. Chest Pain Type (Angina/Chest Discomfort)
   - Preventive Measures:
     - Early medical evaluation for recurring chest pain.
     - Regular cardiovascular check-ups.
     - Use of prescribed medications for hypertension, high cholesterol, or angina.
   - Lifestyle Changes:
     - Stress management (yoga, meditation, therapy).
     - Avoiding smoking and excessive alcohol intake.
     - Maintaining a heart-healthy diet (low sodium, high fiber, lean proteins).
2. ST Slope (Abnormal ECG indicating ischemia)
   - Preventive Measures:
     - Regular monitoring of heart electrical activity.
     - Timely interventions like exercise stress tests or echocardiography.
   - Lifestyle Changes:
     - Consistent moderate exercise tailored to tolerance.
     - Limiting high-fat and processed foods.
     - Compliance with medications (e.g., for blood pressure, cholesterol).
3. Resting Electrocardiogram (Abnormal Resting ECG)
   - Preventive Measures:
     - Routine ECG check-ups, especially for high-risk individuals.
     - Immediate evaluation of any abnormal heart rhythm or conduction issue.
   - Lifestyle Changes:
     - Reduce caffeine and stimulant intake.
     - Ensure adequate sleep and recovery.
     - Managing comorbidities (diabetes, hypertension).
4. Fasting Blood Sugar (Diabetes or Prediabetes)
   - Preventive Measures:
     - Regular blood sugar screening.
     - Early treatment of prediabetes with diet and exercise.
   - Lifestyle Changes:
     - Balanced diet (low in refined sugars, more whole grains).
     - Weight management and regular physical activity.
     - Consistent monitoring of blood glucose levels.
5. Max Heart Rate Achieved (Low values may suggest poor exercise capacity)
   - Preventive Measures:
     - Gradual and supervised exercise programs to improve cardiovascular fitness.
     - Stress tests to assess cardiac response.
   - Lifestyle Changes:
     - Engage in aerobic exercise (walking, swimming, cycling).
     - Avoid overexertion; follow a structured fitness plan approved by a doctor.
     - Regular monitoring during exercise.
6. Age (Non-modifiable risk factor)

- Preventive Measures:
  - More frequent screening as age increases.
  - Use of preventive medications if risk is high.
- Lifestyle Changes:
  - Maintain healthy habits throughout aging.
  - Social engagement and mental health care (reduces stress-related cardiac risks).
  - Prioritize preventive healthcare (vaccines, regular checkups).

Ethical Considerations in Using Predictive Models for Healthcare

1. Fairness and Bias
   - Models may reflect biases in training data (e.g., underrepresentation of certain age groups, genders, or ethnicities).
   - Risk of unfair treatment or misdiagnosis if predictions are skewed.
2. Transparency and Explainability
   - Patients and doctors should understand why the model predicts high risk.
   - Black-box predictions without explanation can reduce trust and hinder informed decisions.
3. Privacy and Data Security
   - Sensitive health data must be protected from misuse or breaches.
   - Consent is crucial when collecting and using patient data.
4. Over-Reliance on Models
   - Models should support, not replace, clinical judgment.
   - Ethical risk if doctors blindly follow predictions without considering patient context.
5. Psychological Impact
   - Labeling someone as “high risk” may cause unnecessary anxiety.
   - Communication should be careful, with emphasis on preventive steps.
6. Access and Equity
   - Predictive healthcare tools should be accessible to all, not just those in well-funded healthcare systems.
   - Risk of widening healthcare disparities if only some groups benefit.

Conclusions

This project successfully developed and evaluated several machine learning models for heart disease prediction. The Random Forest model emerged as the most effective classifier, demonstrating a high F1-score and AUC, which indicates its strong ability to balance precision and recall. In a medical context, high recall is particularly important to minimize false negatives (failing to identify a patient with heart disease), while maintaining a reasonable precision to avoid unnecessary anxiety or further testing. The findings validate the potential of machine learning in supporting clinical decision-making for early disease detection.

Future Work

To further improve and expand upon this project, the following avenues for future research and application are recommended:

1. Advanced Modeling: Explore more complex algorithms, such as XGBoost, LightGBM or deep learning models (e.g., neural networks), which can capture more intricate patterns in the data.

2. Feature Engineering: Create new features from existing ones. For example, a BMI feature can be calculated from height and weight (if available) to provide additional context.

3. Larger and More Diverse Datasets: The model's generalizability can be significantly improved by training on a larger, more diverse dataset that includes a wider range of patient demographics and medical history.

4. Model Interpretability: Use techniques like SHAP (SHapley Additive exPlanations) or LIME (Local Interpretable Model-agnostic Explanations) to provide insights into how the model arrives at its predictions. Understanding which features most influence a prediction can build trust and facilitate its adoption by healthcare professionals.

5. Deployment as a Clinical Tool: Integrate the best-performing model into a user-friendly application or a hospital's Electronic Health Record (EHR) system to provide real-time predictive scores for patients. This would require rigorous validation and adherence to medical device regulations.