## Importing Libraries

In [ ]:
```
#importing basic modules
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

#importing modules required model building
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, classification_report
from sklearn.preprocessing import LabelEncoder, OneHotEncoder
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import cross_val_score, StratifiedKFold
from sklearn.metrics import confusion_matrix, precision_score, recall_score,
from scipy.stats import zscore

#importing models
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.neighbors import KNeighborsClassifier

#importing system modules to avoid warnings
import warnings
warnings.filterwarnings("ignore")
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, cal
l drive.mount("/content/drive", force_remount=True).
```

## Loading the Data

In [ ]:
```
heart_data = pd.read_csv('SuddenCardiacArrest.csv')
```

In [ ]:
```
heart_data.head(5)
```

Out[ ]:

| | PatientName | Age | Sex | ECG-Resting | ST-Slope | BloodPressure-Resting | HeartRate-Max | ChestPainTyp |
|---|---|---|---|---|---|---|---|---|
| **0** | Patient 1 | 40 | M | Normal | Up | 140 | 172 | AT |
| **1** | Patient 2 | 49 | F | Normal | Flat | 160 | 156 | NA |
| **2** | Patient 3 | 37 | M | ST | Up | 130 | 98 | AT |
| **3** | Patient 4 | 48 | F | Normal | Flat | 138 | 108 | AS |
| **4** | Patient 5 | 54 | M | Normal | Up | 150 | 122 | NA |

# EDA

## Removing identifiable features:

- Patient Name was the only identifiable feature

In [ ]:
```
heart_data = heart_data.drop('PatientName', axis = 1)
heart_data.head(5)
```

Out[ ]:

| | Age | Sex | ECG-Resting | ST-Slope | BloodPressure-Resting | HeartRate-Max | ChestPainType | Cholesterol |
|---|---|---|---|---|---|---|---|---|
| **0** | 40 | M | Normal | Up | 140 | 172 | ATA | 289 |
| **1** | 49 | F | Normal | Flat | 160 | 156 | NAP | 180 |
| **2** | 37 | M | ST | Up | 130 | 98 | ATA | 283 |
| **3** | 48 | F | Normal | Flat | 138 | 108 | ASY | 214 |
| **4** | 54 | M | Normal | Up | 150 | 122 | NAP | 195 |

## Data Dimensions

In [ ]:
```
heart_data.shape
```

Out[ ]:
```
(1221, 12)
```

## Data Types

In [ ]:
```
heart_data.dtypes
```

Out[ ]:
```
Age                       int64
Sex                      object
ECG-Resting              object
ST-Slope                 object
BloodPressure-Resting     int64
HeartRate-Max             int64
ChestPainType            object
Cholesterol               int64
BloodSugar-Fasting       object
ExerciseAngina           object
OldPeak                 float64
SCA                       int64
dtype: object
```

## Summary Statistics

In [ ]:
```
heart_data.describe()
```

Out[ ]:

| | Age | BloodPressure-Resting | HeartRate-Max | Cholesterol | OldPeak | S |
|---|---|---|---|---|---|---|
| **count** | 1221.000000 | 1221.000000 | 1221.000000 | 1221.000000 | 1221.000000 | 1221.000( |
| **mean** | 53.741196 | 132.221130 | 139.985258 | 210.684685 | 0.925143 | 0.5298 |
| **std** | 9.341351 | 18.286927 | 25.443021 | 100.425185 | 1.092282 | 0.499: |
| **min** | 28.000000 | 0.000000 | 60.000000 | 0.000000 | -2.600000 | 0.000( |
| **25%** | 47.000000 | 120.000000 | 122.000000 | 188.000000 | 0.000000 | 0.000( |
| **50%** | 54.000000 | 130.000000 | 141.000000 | 228.000000 | 0.600000 | 1.000( |
| **75%** | 60.000000 | 140.000000 | 160.000000 | 269.000000 | 1.600000 | 1.000( |
| **max** | 77.000000 | 200.000000 | 202.000000 | 603.000000 | 6.200000 | 1.000( |

## Understanding the data

In [ ]:
```
target_column = 'SCA'
heart_data[target_column].value_counts()
```

Out[ ]:
```
1    647
0    574
Name: SCA, dtype: int64
```

In [ ]:
```
features = heart_data.drop(columns='SCA')
features.head()
```

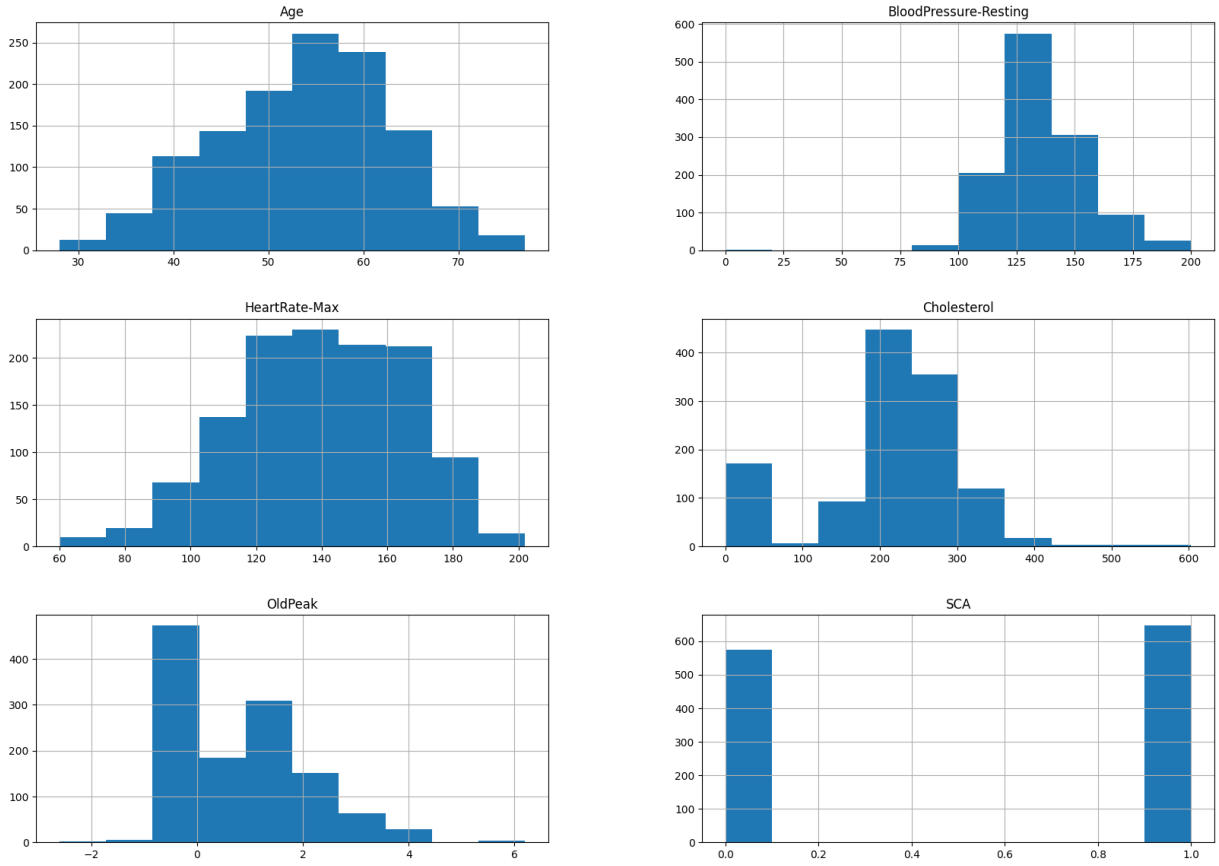
Out[ ]:

| | Age | Sex | ECG-Resting | ST-Slope | BloodPressure-Resting | HeartRate-Max | ChestPainType | Cholesterol |
|---|---|---|---|---|---|---|---|---|
| **0** | 40 | M | Normal | Up | 140 | 172 | ATA | 289 |
| **1** | 49 | F | Normal | Flat | 160 | 156 | NAP | 180 |
| **2** | 37 | M | ST | Up | 130 | 98 | ATA | 283 |
| **3** | 48 | F | Normal | Flat | 138 | 108 | ASY | 214 |
| **4** | 54 | M | Normal | Up | 150 | 122 | NAP | 195 |

In [ ]:
```
numeric_columns = features.select_dtypes(include=np.number).columns.values
categorical_columns = features.drop(columns=numeric_columns).columns.values

print(f'''
There are {features.shape[0]} observations and {features.shape[1]} features.

Numeric features: {', '.join(numeric_columns)}.

Categorical features: {', '.join(categorical_columns)}.
''')
```

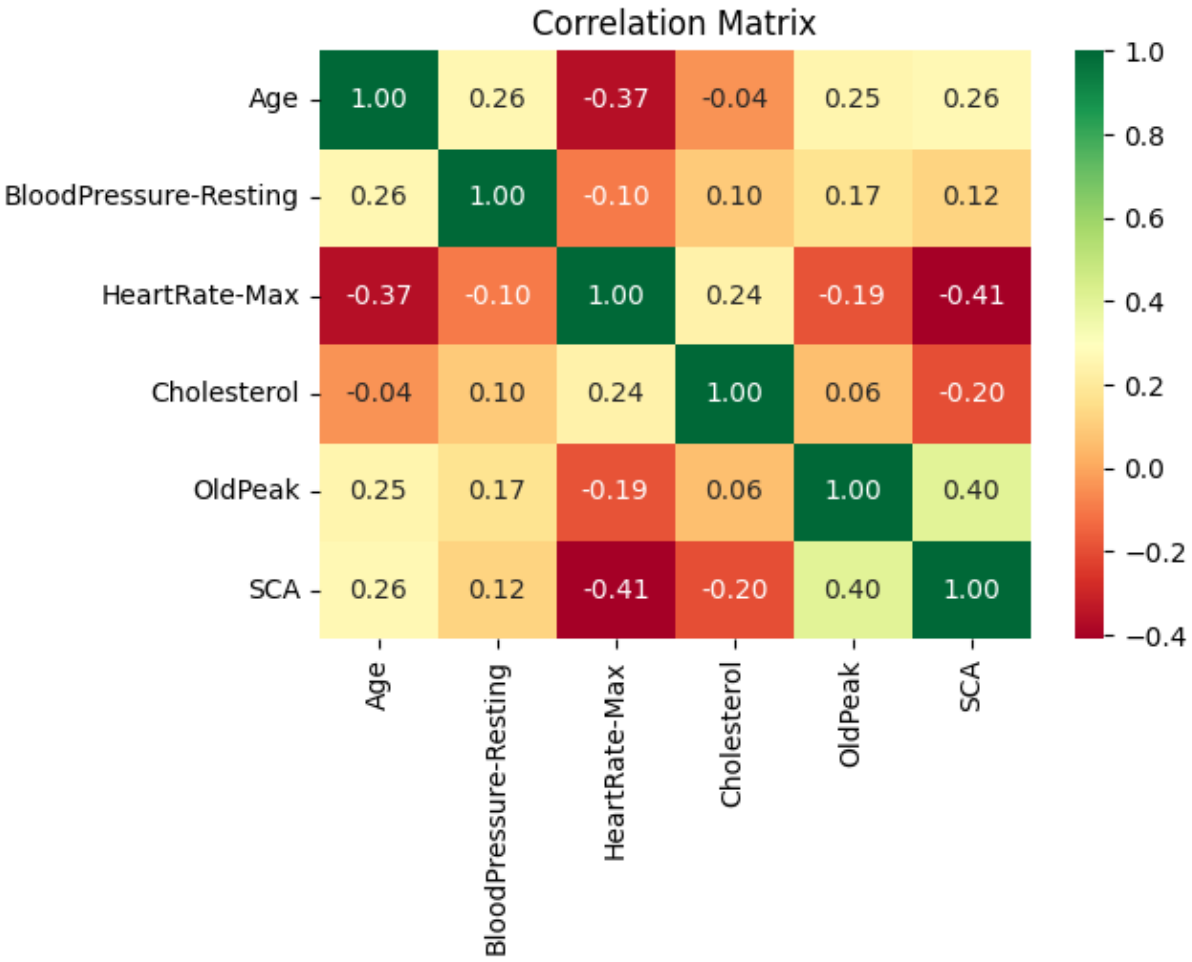
```
There are 1221 observations and 11 features.

Numeric features: Age, BloodPressure-Resting, HeartRate-Max, Cholesterol, Ol
dPeak.

Categorical features: Sex, ECG-Resting, ST-Slope, ChestPainType, BloodSugar-
Fasting, ExerciseAngina.
```

In [ ]:
```
heart_data.hist(figsize=(20, 14));
```




## Correlation Plots for numerical data

In [ ]:
```
plt.figure(figsize=(6,4))
sns.heatmap(heart_data.corr(), annot=True, cmap='RdYlGn', fmt=".2f")
plt.title("Correlation Matrix")
plt.show()
```




For categorical variables, we check the distribution by taking the count of each category/group

In [ ]:
```
heart_data['Sex'].value_counts()
```

Out[ ]:
```
M    931
F    290
Name: Sex, dtype: int64
```

In [ ]:
```
heart_data['ECG-Resting'].value_counts()
```

Out[ ]:
```
Normal    703
LVH       336
ST        182
Name: ECG-Resting, dtype: int64
```

In [ ]:
```
heart_data['ST-Slope'].value_counts()
```

Out[ ]:
```
Flat    600
Up      537
Down     84
Name: ST-Slope, dtype: int64
```

In [ ]:
```
heart_data['ChestPainType'].value_counts()
```

Out[ ]:
```
ASY    640
NAP    289
ATA    223
TA      69
Name: ChestPainType, dtype: int64
```

In [ ]:
```
heart_data['BloodSugar-Fasting'].value_counts()
```

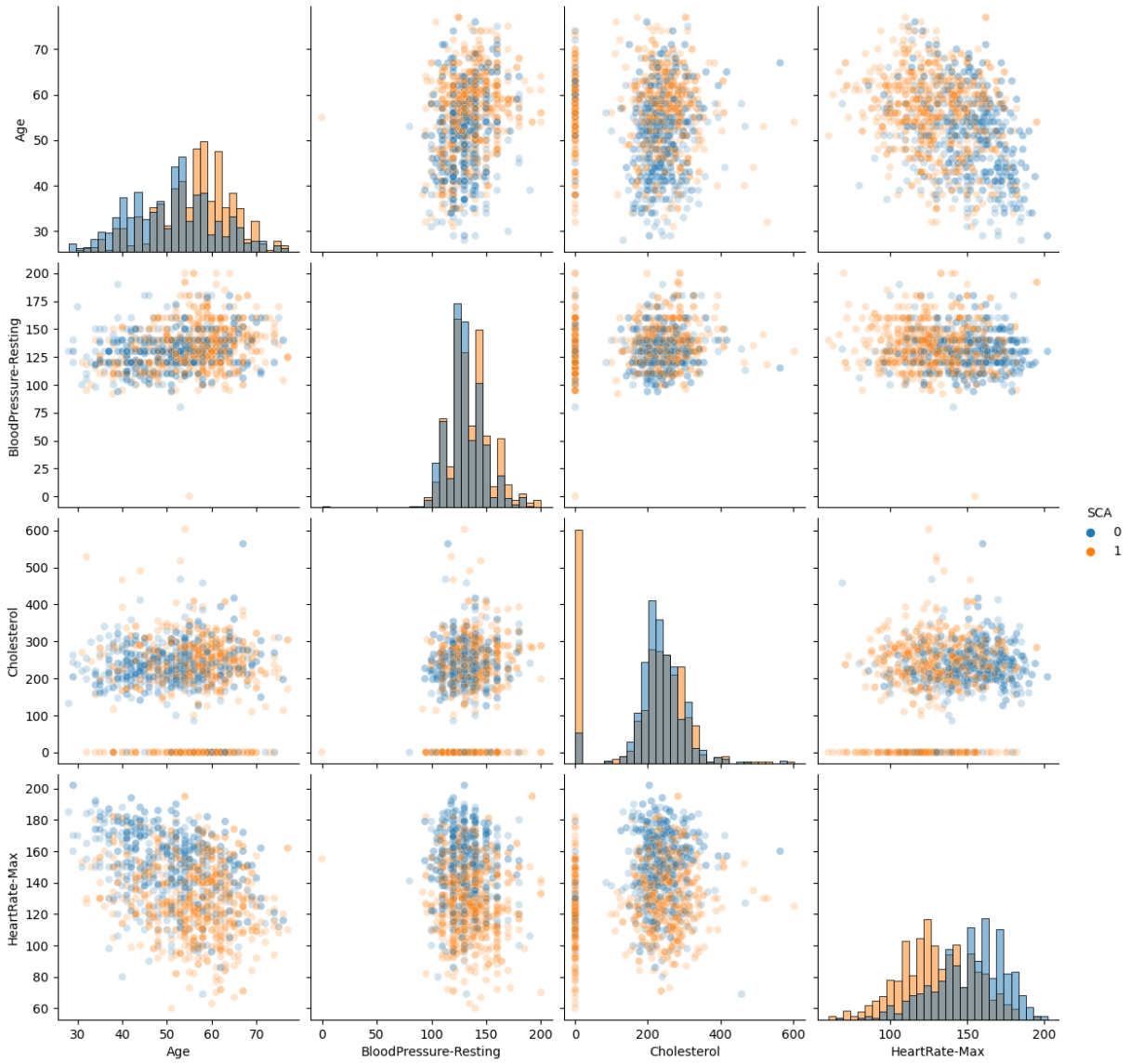
Out[ ]:
```
Normal    962
High      259
Name: BloodSugar-Fasting, dtype: int64
```

In [ ]:
```
heart_data['ExerciseAngina'].value_counts()
```

Out[ ]:
```
N    751
Y    470
Name: ExerciseAngina, dtype: int64
```

## Plotting the data against target variable for inspection

In [ ]:
```
columns = ['Age', 'BloodPressure-Resting', 'Cholesterol','HeartRate-Max']
sns.pairplot(data=heart_data, vars=columns,
             hue=target_column, plot_kws={'alpha': 0.2},
             height=3, diag_kind='hist', diag_kws={'bins': 30});
```




# Data Preprocessing and Wrangling

## Missing values

In [ ]:
```
heart_data.isnull().sum()
```

Out[ ]:
```
Age                     0
Sex                     0
ECG-Resting             0
ST-Slope                0
BloodPressure-Resting   0
HeartRate-Max           0
ChestPainType           0
Cholesterol             0
BloodSugar-Fasting      0
ExerciseAngina          0
OldPeak                 0
SCA                     0
dtype: int64
```

There are no null values to be handled. **But, there are some rows that have either Resting BP or Cholesterol set to 0. We are removing those rows for cleaner data**

In [ ]:
```
heart_data = heart_data.loc[(heart_data['BloodPressure-Resting'] != 0) & (he

heart_data
```

Out[ ]:

| | Age | Sex | ECG-Resting | ST-Slope | BloodPressure-Resting | HeartRate-Max | ChestPainType | Cholest |
|---|---|---|---|---|---|---|---|---|
| **0** | 40 | M | Normal | Up | 140 | 172 | ATA | |
| **1** | 49 | F | Normal | Flat | 160 | 156 | NAP | |
| **2** | 37 | M | ST | Up | 130 | 98 | ATA | |
| **3** | 48 | F | Normal | Flat | 138 | 108 | ASY | |
| **4** | 54 | M | Normal | Up | 150 | 122 | NAP | |
| **...** | ... | ... | ... | ... | ... | ... | ... | |
| **1216** | 45 | M | Normal | Flat | 110 | 132 | TA | |
| **1217** | 68 | M | Normal | Flat | 144 | 141 | ASY | |
| **1218** | 57 | M | Normal | Flat | 130 | 115 | ASY | |
| **1219** | 57 | F | LVH | Flat | 130 | 174 | ATA | |
| **1220** | 38 | M | Normal | Up | 138 | 173 | NAP | |

1049 rows × 12 columns

## Duplicate Data

In [ ]:
```
duplicate_rows = heart_data.duplicated().sum()
print("There are", duplicate_rows, "duplicate rows")
```

```
There are 303 duplicate rows
```

In [ ]:
```
# Removing duplicate rows
heart_data = heart_data.drop_duplicates()

#Checking once again
duplicate_rows = heart_data.duplicated().sum()
print("After removing, there are", duplicate_rows, "duplicate rows")
```

```
After removing, there are 0 duplicate rows
```

## Feature Engineering

Adding a new column 'HeartRisk' which is calculated using Age, Resting BP, Max Heart Rate and Cholesterol using the formula below:

- Risk = Age/(BloodPressure-Resting + Cholesterol + HeartRate-Max)

In [ ]:
```
heart_data['HeartRisk'] = heart_data['Age']/(heart_data['BloodPressure-Resti
heart_data.head()
```

Out[ ]:

| | Age | Sex | ECG-Resting | ST-Slope | BloodPressure-Resting | HeartRate-Max | ChestPainType | Cholesterol |
|---|---|---|---|---|---|---|---|---|
| **0** | 40 | M | Normal | Up | 140 | 172 | ATA | 289 |
| **1** | 49 | F | Normal | Flat | 160 | 156 | NAP | 180 |
| **2** | 37 | M | ST | Up | 130 | 98 | ATA | 283 |
| **3** | 48 | F | Normal | Flat | 138 | 108 | ASY | 214 |
| **4** | 54 | M | Normal | Up | 150 | 122 | NAP | 195 |

## Outliers

In [ ]:
```
# Calculate Z-scores for numerical features
z_scores = zscore(heart_data.select_dtypes(include=np.number))
z_scores
```

Out[ ]:

| | Age | BloodPressure-Resting | HeartRate-Max | Cholesterol | OldPeak | SCA | Heart |
|---|---|---|---|---|---|---|---|
| **0** | -1.356073 | 0.403980 | 1.296470 | 0.750494 | -0.840942 | -0.955416 | -1.58 |
| **1** | -0.408656 | 1.561980 | 0.643613 | -1.093405 | 0.091771 | 1.046664 | -0.21 |
| **2** | -1.671879 | -0.175019 | -1.722993 | 0.648995 | -0.840942 | -0.955416 | -1.33 |
| **3** | -0.513925 | 0.288180 | -1.314958 | -0.518244 | 0.558127 | 1.046664 | 0.02 |
| **4** | 0.117686 | 0.982980 | -0.743708 | -0.839657 | -0.840942 | -0.955416 | 0.50 |
| **...** | ... | ... | ... | ... | ... | ... | |
| **913** | -0.829731 | -1.333019 | -0.335672 | 0.327582 | 0.278313 | 1.046664 | -0.63 |
| **914** | 1.591446 | 0.635580 | 0.031560 | -0.873490 | 2.330281 | 1.046664 | 1.63 |
| **915** | 0.433492 | -0.175019 | -1.029333 | -1.922314 | 0.278313 | 1.046664 | 2.03 |
| **916** | 0.433492 | -0.175019 | 1.378077 | -0.146081 | -0.840942 | 1.046664 | 0.07 |
| **917** | -1.566610 | 0.288180 | 1.337274 | -1.177987 | -0.840942 | -0.955416 | -1.09 |

746 rows × 7 columns

In [ ]:
```
threshold = 4
outliers = np.abs(z_scores) > threshold
outliers
```

Out[ ]:

| | Age | BloodPressure-Resting | HeartRate-Max | Cholesterol | OldPeak | SCA | HeartRisk |
|---|---|---|---|---|---|---|---|
| **0** | False | False | False | False | False | False | False |
| **1** | False | False | False | False | False | False | False |
| **2** | False | False | False | False | False | False | False |
| **3** | False | False | False | False | False | False | False |
| **4** | False | False | False | False | False | False | False |
| **...** | ... | ... | ... | ... | ... | ... | ... |
| **913** | False | False | False | False | False | False | False |
| **914** | False | False | False | False | False | False | False |
| **915** | False | False | False | False | False | False | False |
| **916** | False | False | False | False | False | False | False |
| **917** | False | False | False | False | False | False | False |

746 rows × 7 columns

In [ ]:
```
# Remove outliers or handle them as needed
df_no_outliers = heart_data[~outliers.any(axis=1)]
df_no_outliers
```

Out[ ]:

| | Age | Sex | ECG-Resting | ST-Slope | BloodPressure-Resting | HeartRate-Max | ChestPainType | Choleste |
|---|---|---|---|---|---|---|---|---|
| **0** | 40 | M | Normal | Up | 140 | 172 | ATA | 2 |
| **1** | 49 | F | Normal | Flat | 160 | 156 | NAP | 1 |
| **2** | 37 | M | ST | Up | 130 | 98 | ATA | 2 |
| **3** | 48 | F | Normal | Flat | 138 | 108 | ASY | 2 |
| **4** | 54 | M | Normal | Up | 150 | 122 | NAP | 1 |
| **...** | ... | ... | ... | ... | ... | ... | ... | |
| **913** | 45 | M | Normal | Flat | 110 | 132 | TA | 2 |
| **914** | 68 | M | Normal | Flat | 144 | 141 | ASY | 1 |
| **915** | 57 | M | Normal | Flat | 130 | 115 | ASY | 1 |
| **916** | 57 | F | LVH | Flat | 130 | 174 | ATA | 2 |
| **917** | 38 | M | Normal | Up | 138 | 173 | NAP | 1 |

738 rows × 13 columns

## Categorical Data Encoding

In [ ]:
```
df_encoded = pd.get_dummies(df_no_outliers, columns=['Sex','ECG-Resting','ST
df_encoded.head()
```

Out[ ]:

| | Age | BloodPressure-Resting | HeartRate-Max | Cholesterol | OldPeak | SCA | HeartRisk | Sex_F | S |
|---|---|---|---|---|---|---|---|---|---|
| **0** | 40 | 140 | 172 | 289 | 0.0 | 0 | 0.066556 | 0 | |
| **1** | 49 | 160 | 156 | 180 | 1.0 | 1 | 0.098790 | 1 | |
| **2** | 37 | 130 | 98 | 283 | 0.0 | 0 | 0.072407 | 0 | |
| **3** | 48 | 138 | 108 | 214 | 1.5 | 1 | 0.104348 | 1 | |
| **4** | 54 | 150 | 122 | 195 | 0.0 | 0 | 0.115632 | 0 | |

5 rows × 23 columns

## Feature Scaling

In [ ]:
```
scaler = StandardScaler()
df_encoded[['Age', 'BloodPressure-Resting', 'Cholesterol', 'OldPeak', 'Heart
```

```
    df_encoded[['Age', 'BloodPressure-Resting', 'Cholesterol', 'OldPeak', 'H

df_encoded
```

Out[ ]:

| | Age | BloodPressure-Resting | HeartRate-Max | Cholesterol | OldPeak | SCA | HeartRisk |
|---|---|---|---|---|---|---|---|
| **0** | -1.359533 | 0.402577 | 172 | 0.856427 | -0.853378 | 0 | -1.631185 |
| **1** | -0.407702 | 1.560419 | 156 | -1.170842 | 0.108579 | 1 | -0.222797 |
| **2** | -1.676810 | -0.176343 | 98 | 0.744834 | -0.853378 | 0 | -1.375531 |
| **3** | -0.513461 | 0.286793 | 108 | -0.538483 | 0.589557 | 1 | 0.020021 |
| **4** | 0.121093 | 0.981498 | 122 | -0.891860 | -0.853378 | 0 | 0.513034 |
| **...** | ... | ... | ... | ... | ... | ... | ... |
| **913** | -0.830738 | -1.334185 | 132 | 0.391457 | 0.300970 | 1 | -0.653490 |
| **914** | 1.601718 | 0.634146 | 141 | -0.929058 | 2.417273 | 1 | 1.676448 |
| **915** | 0.438369 | -0.176343 | 115 | -2.082184 | 0.300970 | 1 | 2.084370 |
| **916** | 0.438369 | -0.176343 | 174 | -0.129310 | -0.853378 | 1 | 0.072789 |
| **917** | -1.571051 | 0.286793 | 173 | -1.263836 | -0.853378 | 0 | -1.122893 |

738 rows × 23 columns

# Model Building and Evalauations

## Evaluation module

In [ ]:

```
def evaluate(model, x_test, y_test, average='weighted'):
    y_pred = model.predict(x_test)
    acc = accuracy_score(y_test, y_pred)
    precision = precision_score(y_test, y_pred, average=average)
    recall = recall_score(y_test, y_pred, average=average)
    f1 = f1_score(y_test, y_pred, average=average)
    scores = cross_val_score(model, x, y, cv=5, scoring='accuracy')
    print(f'Accuracy: {acc:.2f}')
    print(f'Precision: {precision:.2f}')
    print(f'Recall: {recall:.2f}')
    print(f'F1-score: {f1:.2f}')
    print(f"{type(model).__name__} Cross-Validation Accuracy: {np.mean(score
    cm = confusion_matrix(y_test, y_pred)
    sns.heatmap(cm, annot=True, fmt='d', cmap='Blues')
    plt.title('Confusion Matrix')
    plt.show()
```

## Preparing the data for models

In [ ]:
```
x = df_encoded.drop("SCA", axis=1)
y = df_encoded["SCA"]
```

In [ ]:
```
# Split data into training and testing sets
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2, rar
```

In [ ]:
```
x_train = np.array(x_train)
x_test = np.array(x_test)
y_train = np.array(y_train)
y_test = np.array(y_test)
```

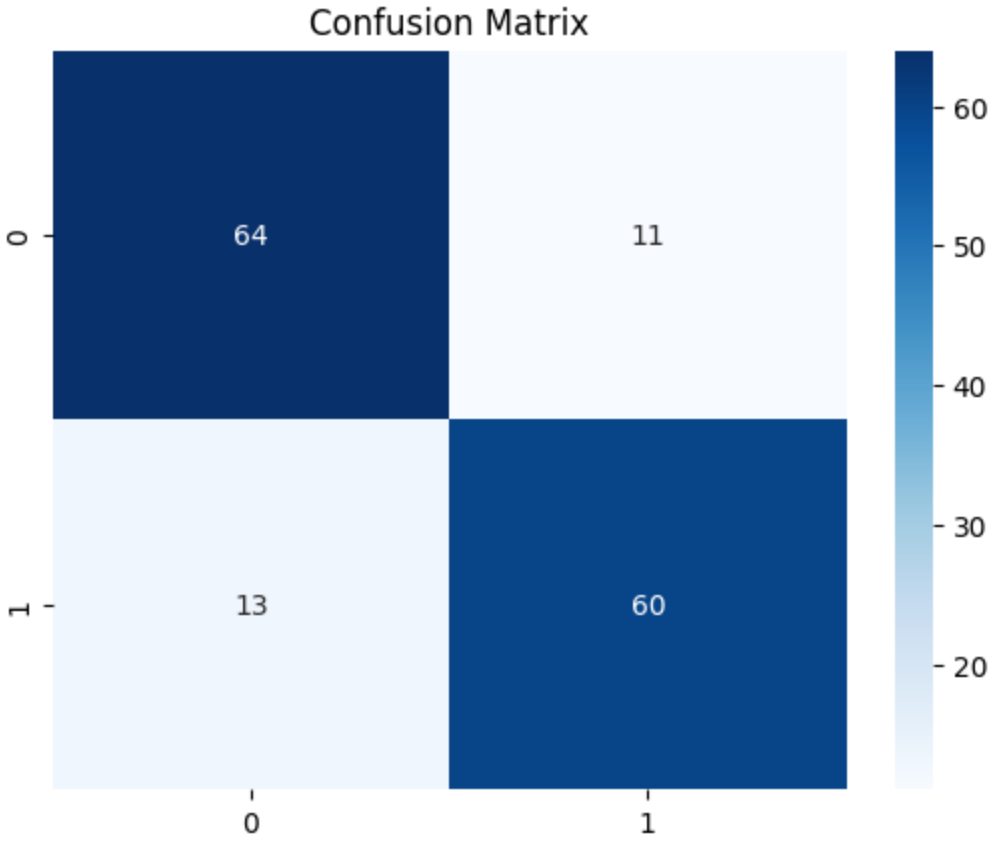
## Decision Tree Model

In [ ]:
```
decision_tree = DecisionTreeClassifier(random_state=142)
decision_tree.fit(x_train, y_train)
decision_tree
```

Out[ ]:
```
DecisionTreeClassifier(random_state=142)
```

In [ ]:
```
evaluate(decision_tree, x_test, y_test, average='weighted')
```

```
Accuracy: 0.84
Precision: 0.84
Recall: 0.84
F1-score: 0.84
DecisionTreeClassifier Cross-Validation Accuracy: 0.78
```



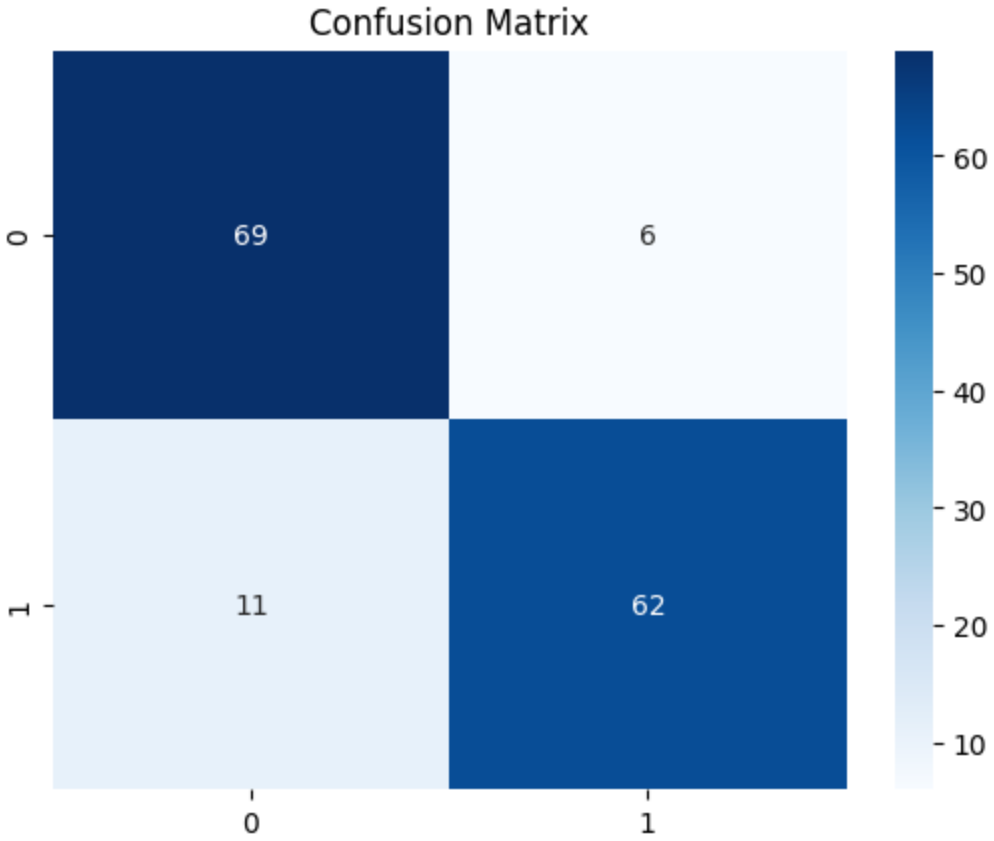

## Random Forest

In [ ]:
```
random_forest = RandomForestClassifier(random_state=42)
random_forest.fit(x_train, y_train)
```

Out[ ]:
```
RandomForestClassifier
RandomForestClassifier(random_state=42)
```

In [ ]:
```
evaluate(random_forest, x_test, y_test)
```

```
Accuracy: 0.89
Precision: 0.89
Recall: 0.89
F1-score: 0.88
RandomForestClassifier Cross-Validation Accuracy: 0.86
```



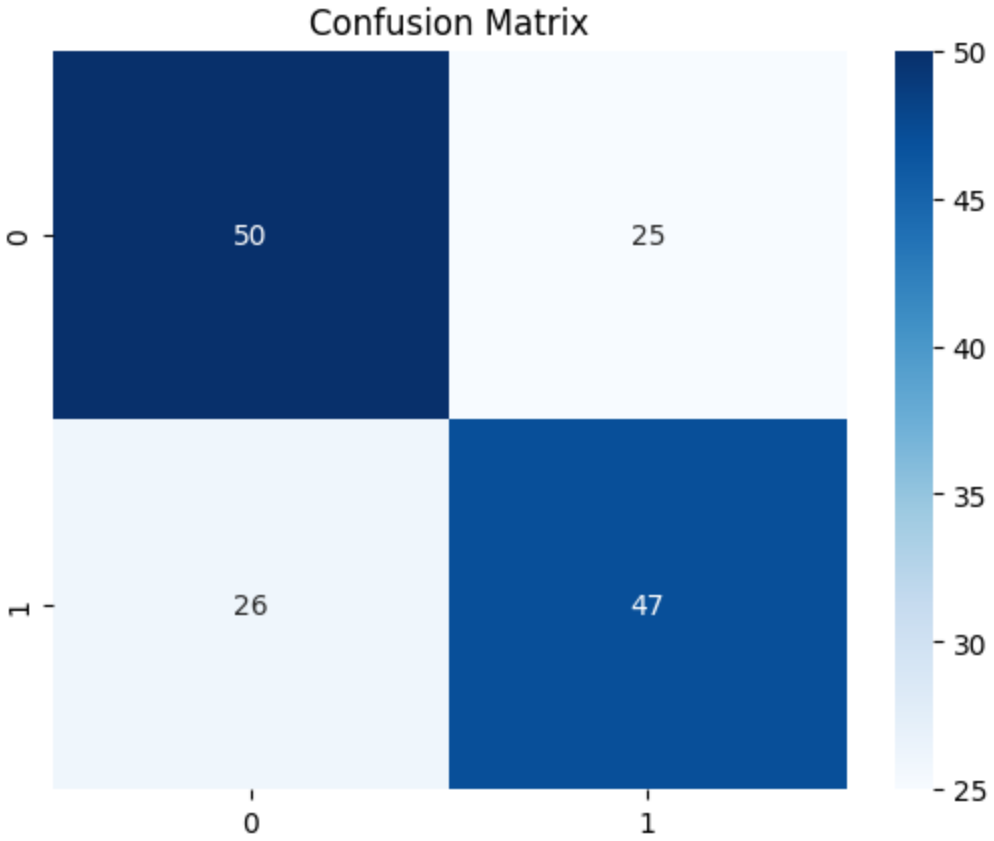

## Support Vector Machine

In [ ]:
```
svm = SVC(random_state=42)
svm.fit(x_train, y_train)
```

Out[ ]:
```
SVC
SVC(random_state=42)
```

In [ ]:
```
evaluate(svm, x_test, y_test)
```

```
Accuracy: 0.66
Precision: 0.66
Recall: 0.66
F1-score: 0.66
SVC Cross-Validation Accuracy: 0.67
```



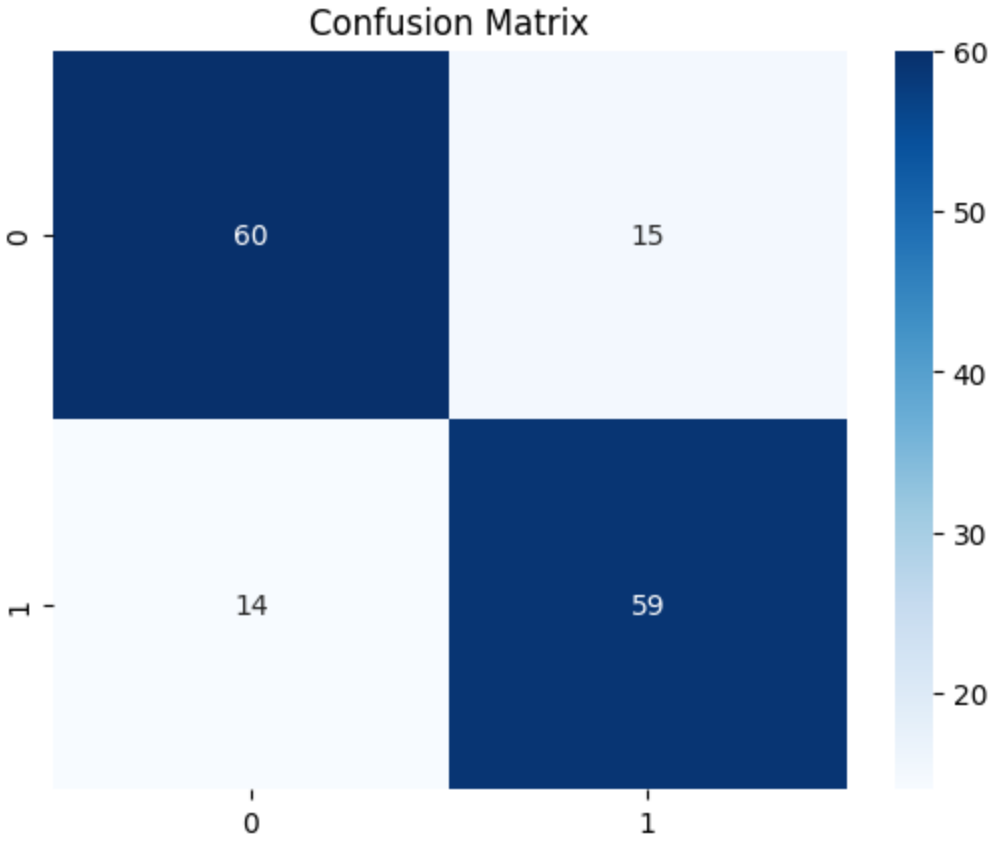

## K-Nearest Neighbors

In [ ]:
```
knn = KNeighborsClassifier(n_neighbors=5)
knn.fit(x_train, y_train)
```

Out[ ]:
```
▾ KNeighborsClassifier
KNeighborsClassifier()
```

In [ ]:
```
evaluate(knn, x_test, y_test)
```

```
Accuracy: 0.80
Precision: 0.80
Recall: 0.80
F1-score: 0.80
KNeighborsClassifier Cross-Validation Accuracy: 0.79
```



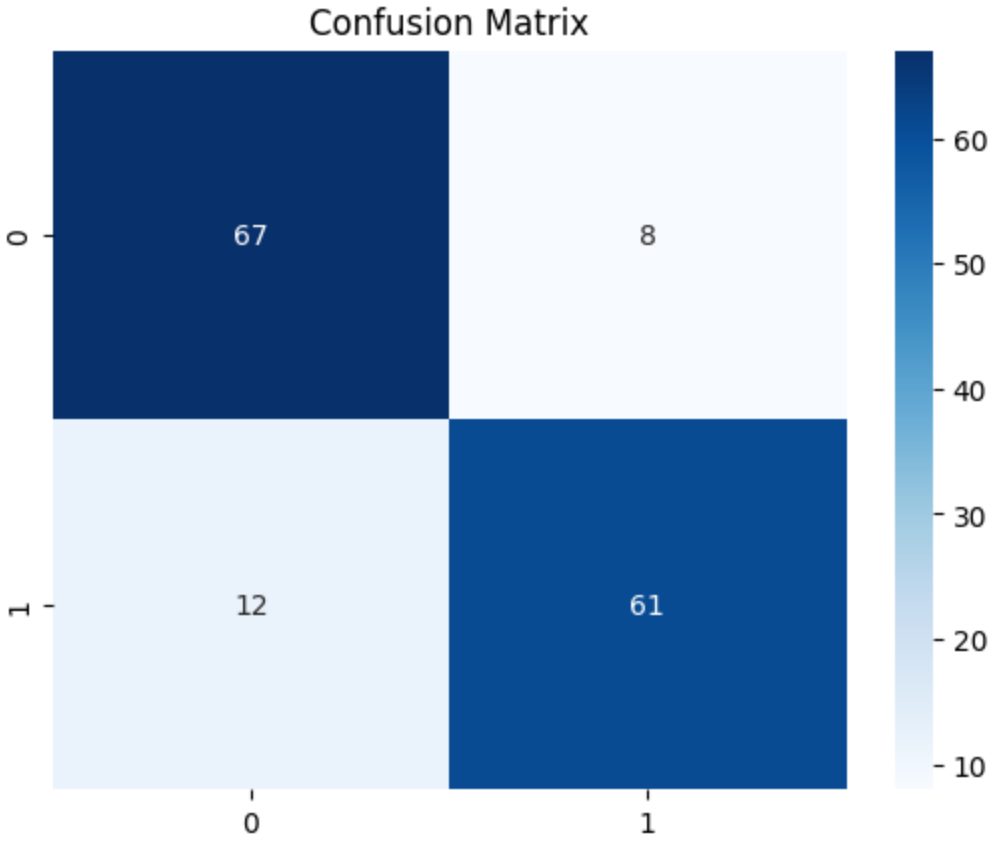

## Gradient Boost

In [ ]:
```
gradient_boost = GradientBoostingClassifier(random_state=42)
gradient_boost.fit(x_train, y_train)
```

Out[ ]:
```
GradientBoostingClassifier(random_state=42)
```

In [ ]:
```
evaluate(gradient_boost, x_test, y_test)
```

```
Accuracy: 0.86
Precision: 0.87
Recall: 0.86
F1-score: 0.86
GradientBoostingClassifier Cross-Validation Accuracy: 0.85
```




In [ ]: