

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")
```

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	1221.000000
mean	53.741196	132.221130	139.985258	210.684685	0.925143	0.529815
std	9.341351	18.286927	25.443021	100.425185	1.092282	0.499815
min	28.000000	0.000000	60.000000	0.000000	-2.600000	0.000000
25%	47.000000	120.000000	122.000000	188.000000	0.000000	0.000000
50%	54.000000	130.000000	141.000000	228.000000	0.600000	1.000000
75%	60.000000	140.000000	160.000000	269.000000	1.600000	1.000000
max	77.000000	200.000000	202.000000	603.000000	6.200000	1.000000

Understanding the data

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

```
Out [ ]: SCA
1      647
0      574
Name: count, 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)}.

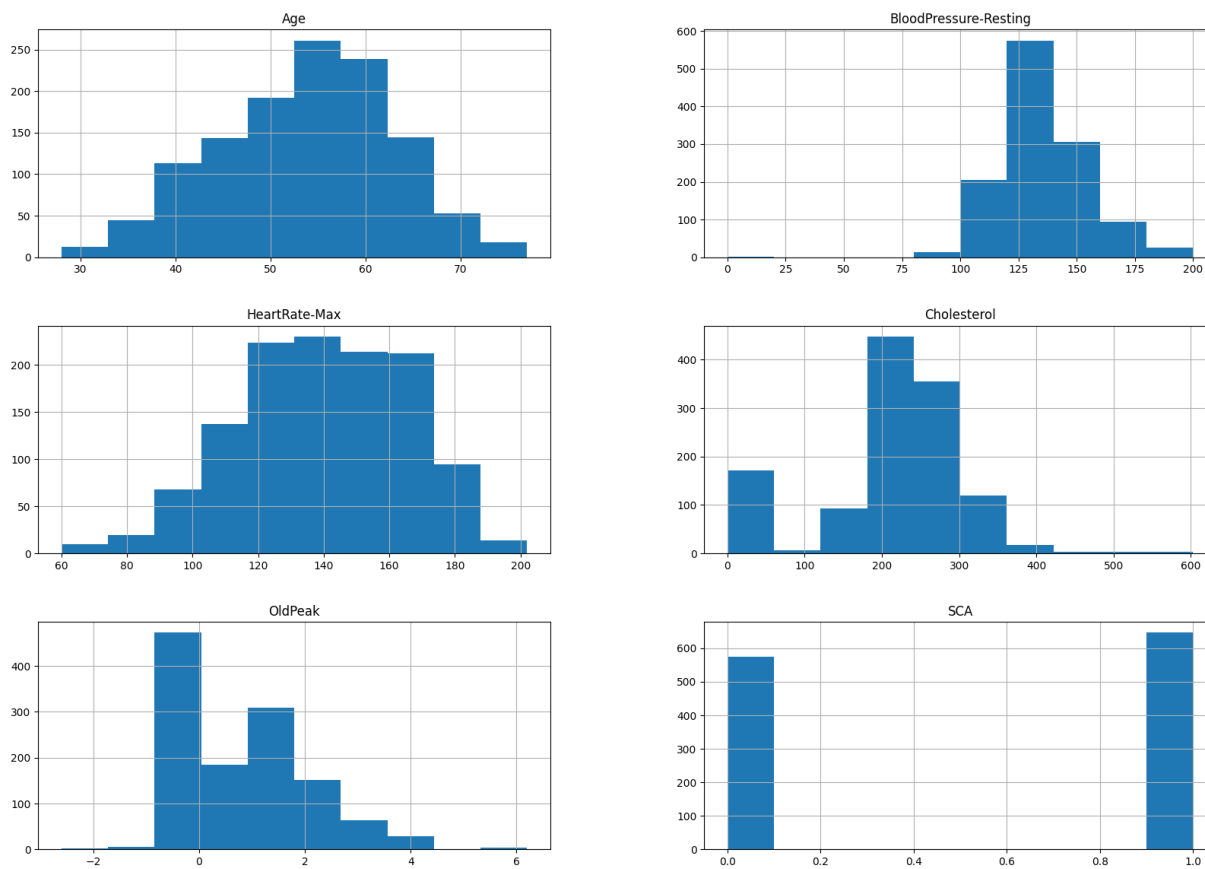
Categorical features: {', '.join(categorical_columns)}.
''')
```

There are 1221 observations and 11 features.

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

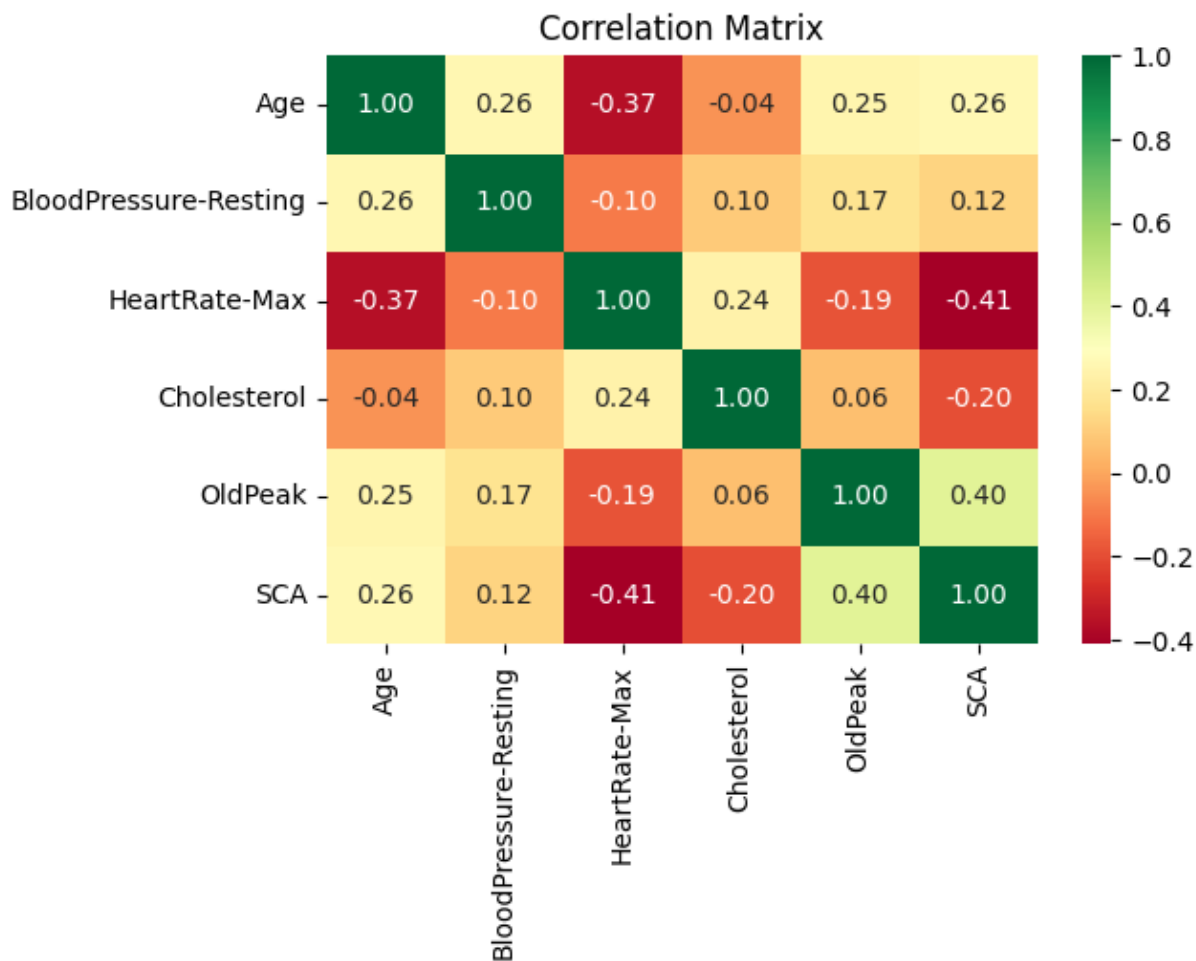
Categorical features: Sex, ECG-Resting, ST-Slope, ChestPainType, BloodSugar-Fasting, ExerciseAngina.

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



Correlation Plots for numerical data

```
In [ ]: plt.figure(figsize=(6,4))
sns.heatmap(heart_data[['Age', 'BloodPressure-Resting', 'HeartRate-Max', 'Cholesterol', 'OldPeak', 'SCA']])
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[ ]: Sex
M      931
F      290
Name: count, dtype: int64
```

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

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

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

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

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

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

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

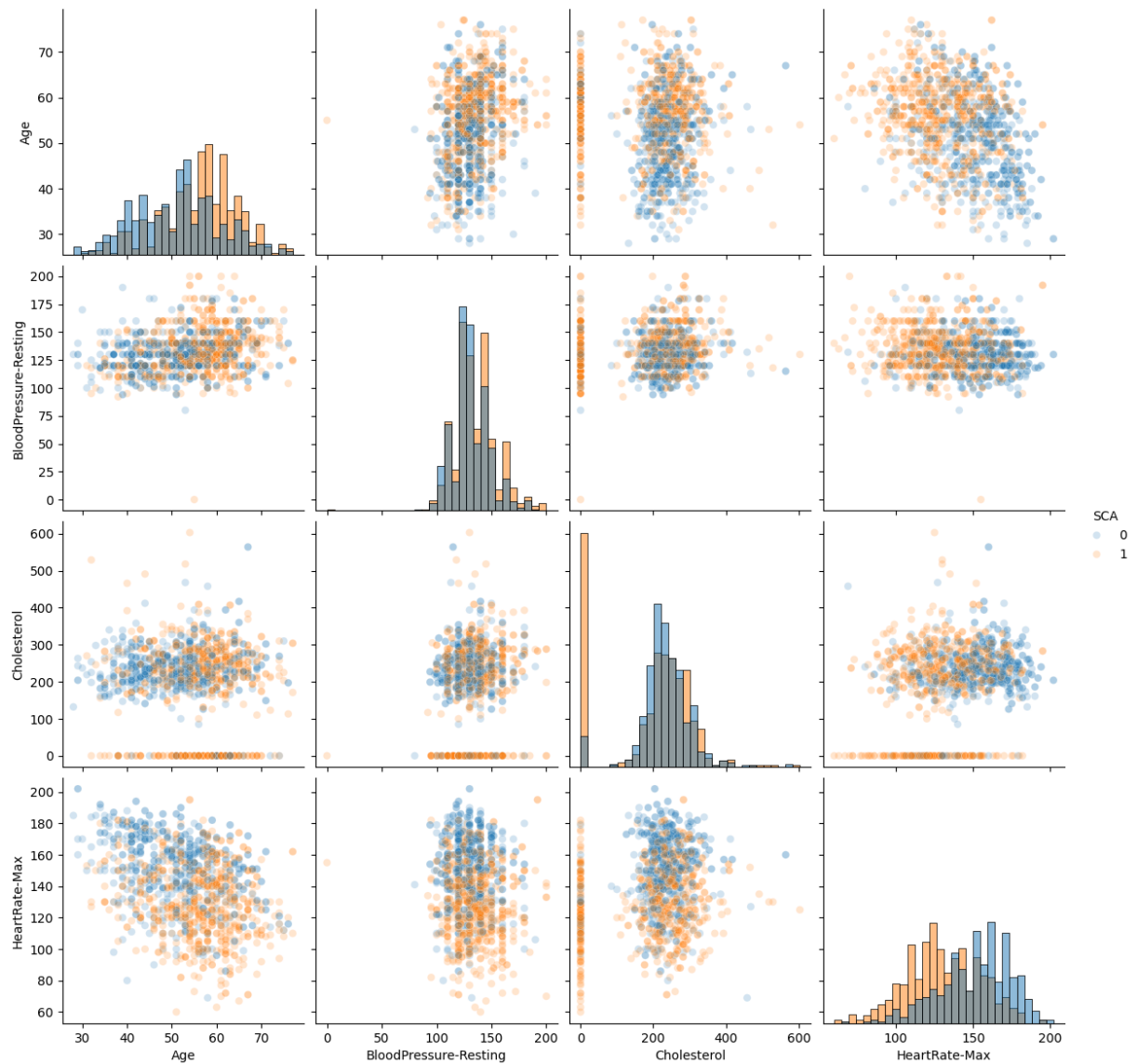
```
Out[ ]: BloodSugar-Fasting
Normal    962
High      259
Name: count, dtype: int64
```

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

```
Out[ ]: ExerciseAngina
N      751
Y      470
Name: count, 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) & (heart_data['Cholesterol'] != 0)]
heart_data
```

```
Out[ ]:
```

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

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:

- $\text{Risk} = \text{Age} / (\text{BloodPressure-Resting} + \text{Cholesterol} + \text{HeartRate-Max})$

```
In [ ]: heart_data['HeartRisk'] = heart_data['Age'] / (heart_data['BloodPressure-Resting'] + heart_data['Cholesterol'] + heart_data['HeartRate-Max'])
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	HeartRisk
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 x 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 x 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	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
...
913	45	M	Normal	Flat	110	132	TA	258
914	68	M	Normal	Flat	144	141	ASY	192
915	57	M	Normal	Flat	130	115	ASY	116
916	57	F	LVH	Flat	130	174	ATA	259
917	38	M	Normal	Up	138	173	NAP	116

738 rows x 13 columns

Categorical Data Encoding

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

Out []:

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

5 rows x 23 columns

Feature Scaling

```
In [ ]: scaler = StandardScaler()
df_encoded[['Age', 'BloodPressure-Resting', 'Cholesterol', 'OldPeak', 'HeartRate-Max']] = scaler.fit_transform(df_encoded[['Age', 'BloodPressure-Resting', 'Cholesterol', 'OldPeak', 'HeartRate-Max']])
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 x 23 columns

Model Building and Evaluations

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(scores):.2f}')
    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, ran
```

```
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
DecisionTreeClassifier(random_state=142)
```

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

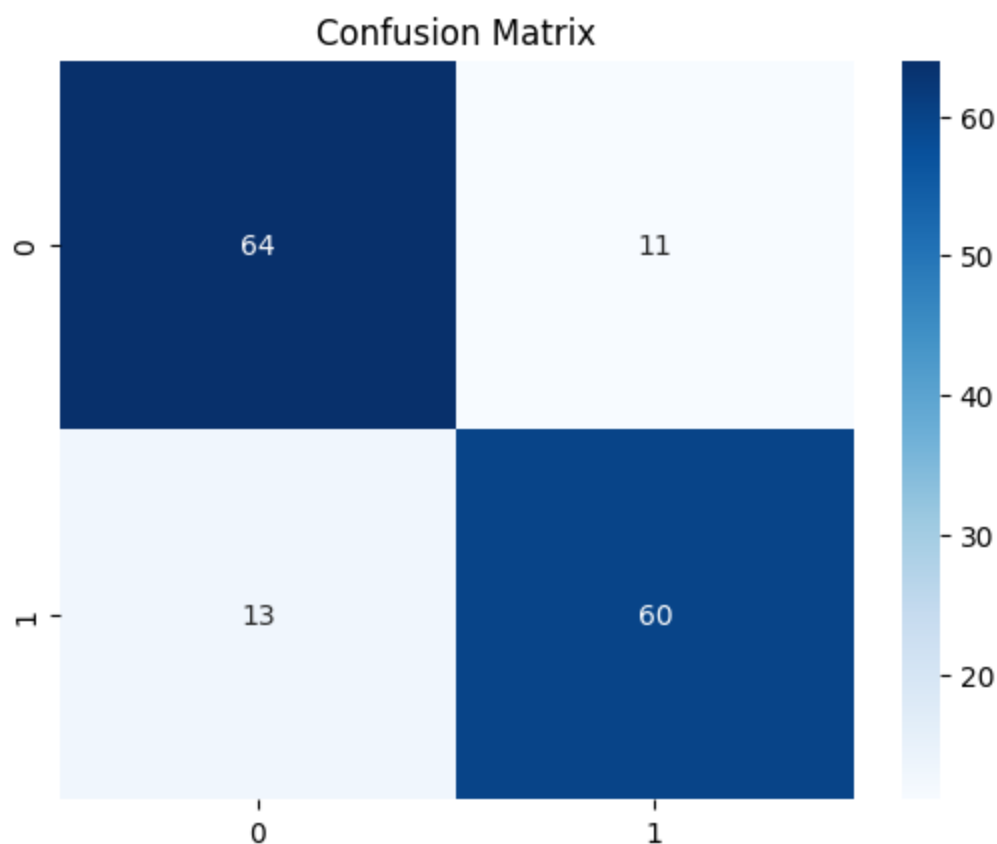
Accuracy: 0.84

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)
```

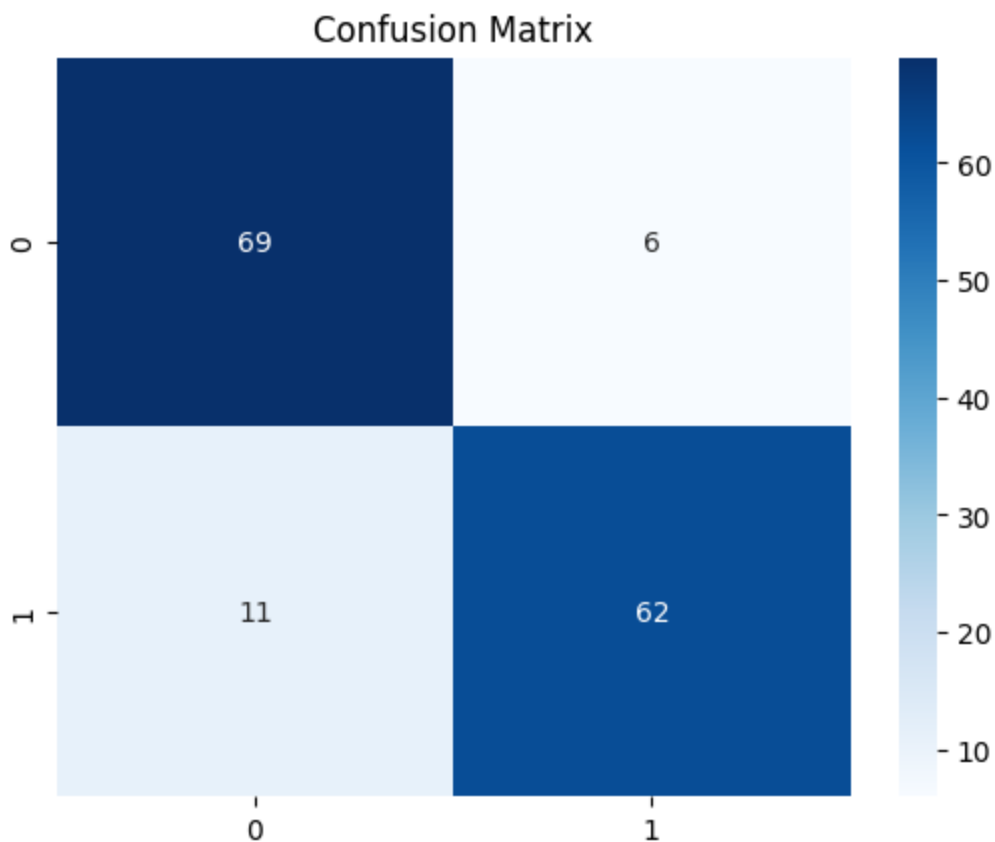
Accuracy: 0.89

Precision: 0.89

Recall: 0.89

F1-score: 0.88

RandomForestClassifier Cross-Validation Accuracy: 0.86



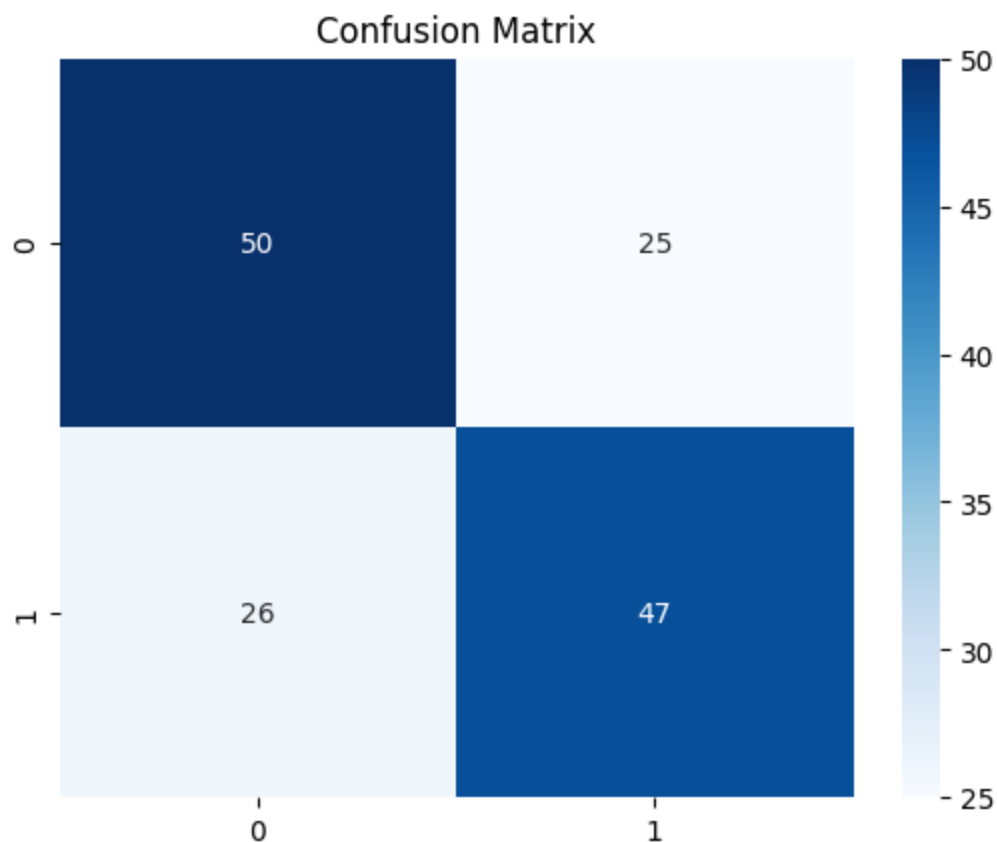
Support Vector Machine

```
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



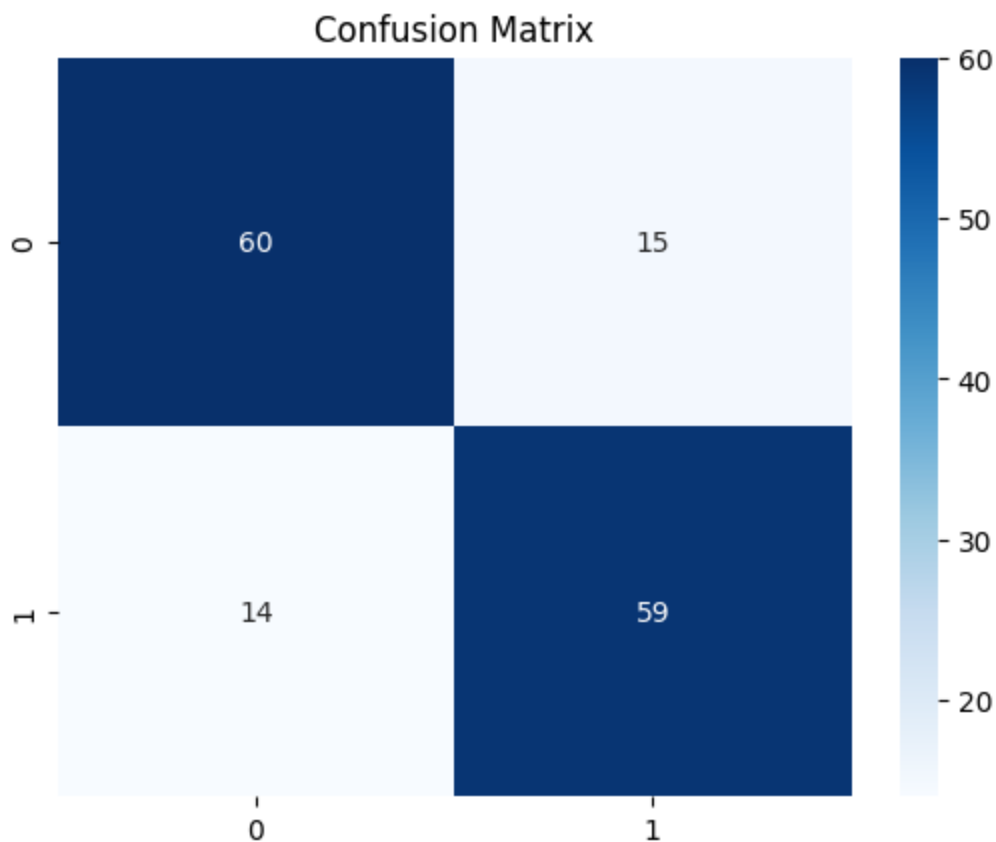
K-Nearest Neighbors

```
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
GradientBoostingClassifier(random_state=42)
```

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

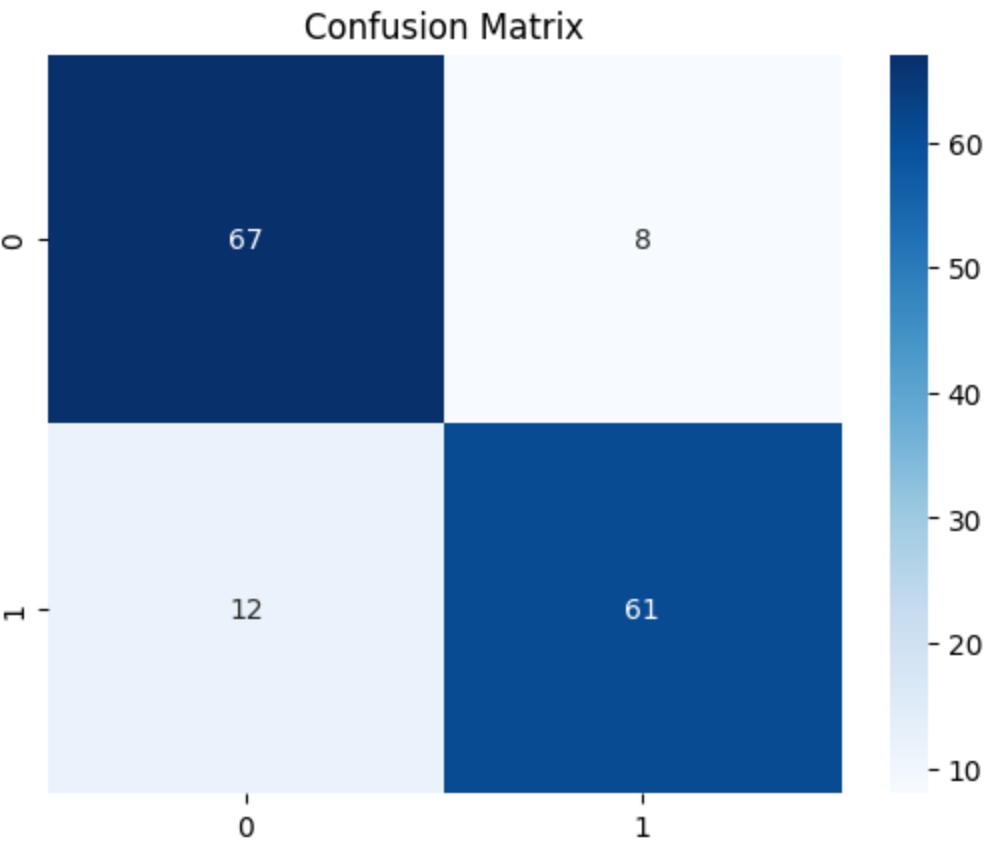
Accuracy: 0.86

Precision: 0.87

Recall: 0.86

F1-score: 0.86

GradientBoostingClassifier Cross-Validation Accuracy: 0.85



```
In [ ]:
```