Heart-Well Data Analysis Report

Introduction

Heart-Well as a company has decided to integrate medical expertise and cutting-edge technology to contribute towards prevention of sudden cardiac arrests.We,As Data Scientists have been tasked to identify and predict patients who potentially could be subject to sudden cardiac arrest. This report showcases our proficiency in importing libraries, manipulating data frames, and employing advanced analytical techniques, all tailored to the unique challenges posed by cardiac health. Through meticulous data exploration and innovative feature engineering, we have uncovered key predictors influencing sudden cardiac arrests risk, empowering us to develop robust prediction models. This report is a deeper exploration of our data-driven journey and the transformative impact it may yield on patient outcomes.

The following Python packages and libraries are required in order to run the code in this project:

In [5]:
```
# Import necessary libraries
import math
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import bs4
import sklearn
from scipy.stats import zscore
import warnings
from sklearn.linear_model import LinearRegression, LogisticRegression
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.pipeline import Pipeline, make_pipeline
from sklearn.compose import ColumnTransformer
from sklearn.compose import make_column_selector as selector
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import cross_val_score, train_test_split, Grid
from sklearn.tree import DecisionTreeClassifier
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassi
from sklearn.metrics import confusion_matrix, accuracy_score, precision_sco
from sklearn import set_config
set_config(display='diagram')
warnings.filterwarnings("ignore")
```

In [7]:
```
# Load the data into a DataFrame
heartwell_df = pd.read_csv("/Users/trishla/Downloads/SuddenCardiacArrest.cs
heartwell_df.head()
```

Out[7]:

	PatientName	Age	Sex	ECG-Resting	ST-Slope	BloodPressure-Resting	HeartRate-Max	ChestPainType	Cho
0	Patient 1	40	M	Normal	Up	140	172	ATA	
1	Patient 2	49	F	Normal	Flat	160	156	NAP	
2	Patient 3	37	M	ST	Up	130	98	ATA	
3	Patient 4	48	F	Normal	Flat	138	108	ASY	
4	Patient 5	54	M	Normal	Up	150	122	NAP	

Removed identifiable features to preserve privacy.

Exploratory Data Analysis

Removed identifiable features

In [8]:
```
heartwell_df = heartwell_df.drop(columns="PatientName")
heartwell_df.head()
```

Out[8]:

	Age	Sex	ECG-Resting	ST-Slope	BloodPressure-Resting	HeartRate-Max	ChestPainType	Cholesterol	Bloo
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 [9]:
```
heartwell_df.shape
```

Out[9]:
```
(1221, 12)
```

Data Types

In [10]:
```
heartwell_df.dtypes
```

Out[10]:
```
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

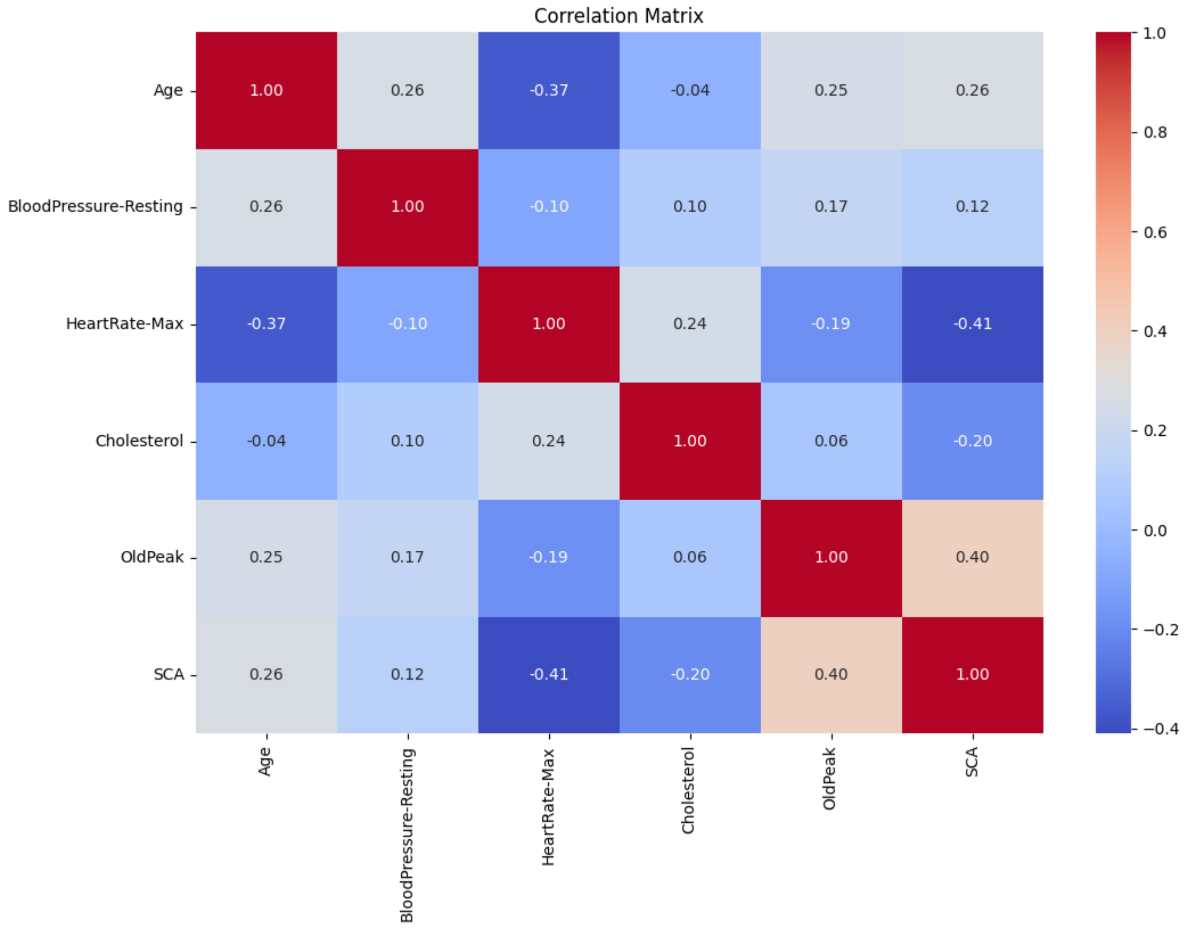
In [11]:
```
heartwell_df.describe()
```

Out[11]:

	Age	BloodPressure-Resting	HeartRate-Max	Cholesterol	OldPeak	SCA
count	1221.000000	1221.000000	1221.000000	1221.000000	1221.000000	1221.000000
mean	53.741196	132.221130	139.985258	210.684685	0.925143	0.529894
std	9.341351	18.286927	25.443021	100.425185	1.092282	0.499310
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

Correlation plot

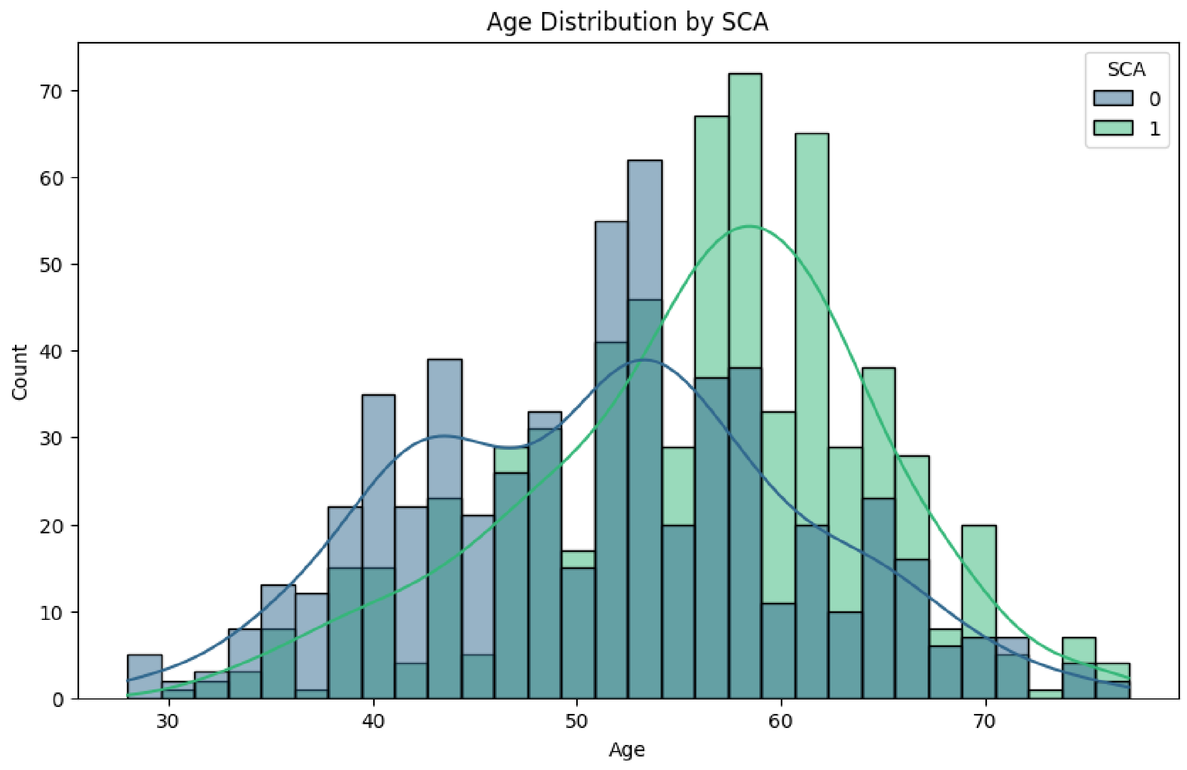
In [12]:
```
plt.figure(figsize=(12,8))
sns.heatmap(heartwell_df.corr(numeric_only=True), annot=True, cmap='coolwarr
plt.title("Correlation Matrix")
plt.show()
```

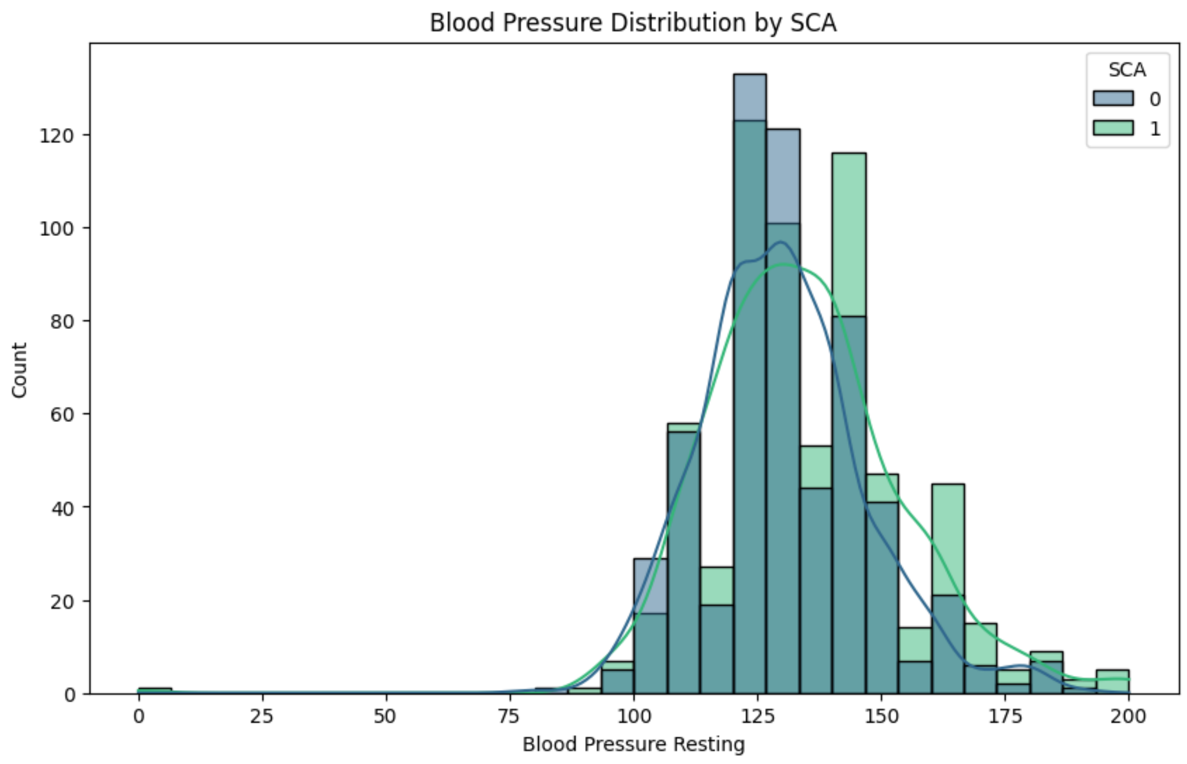


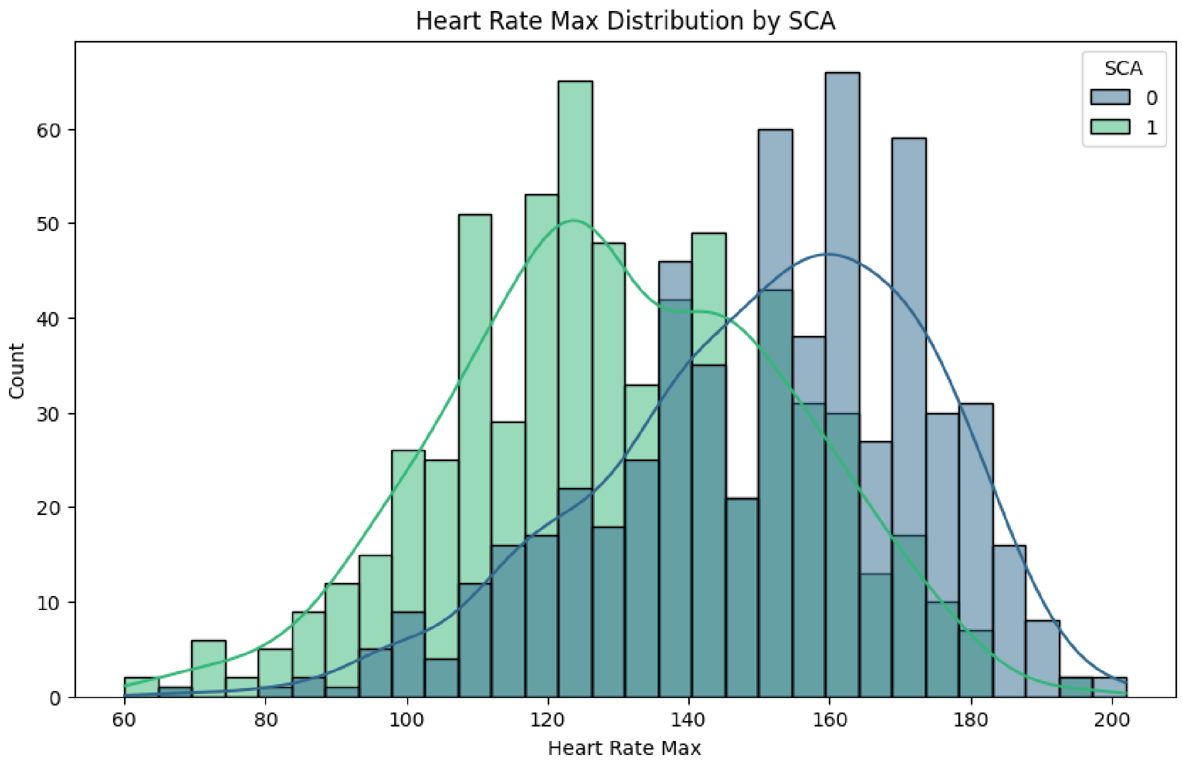
Data Distribution (Feature vs Target Variable)

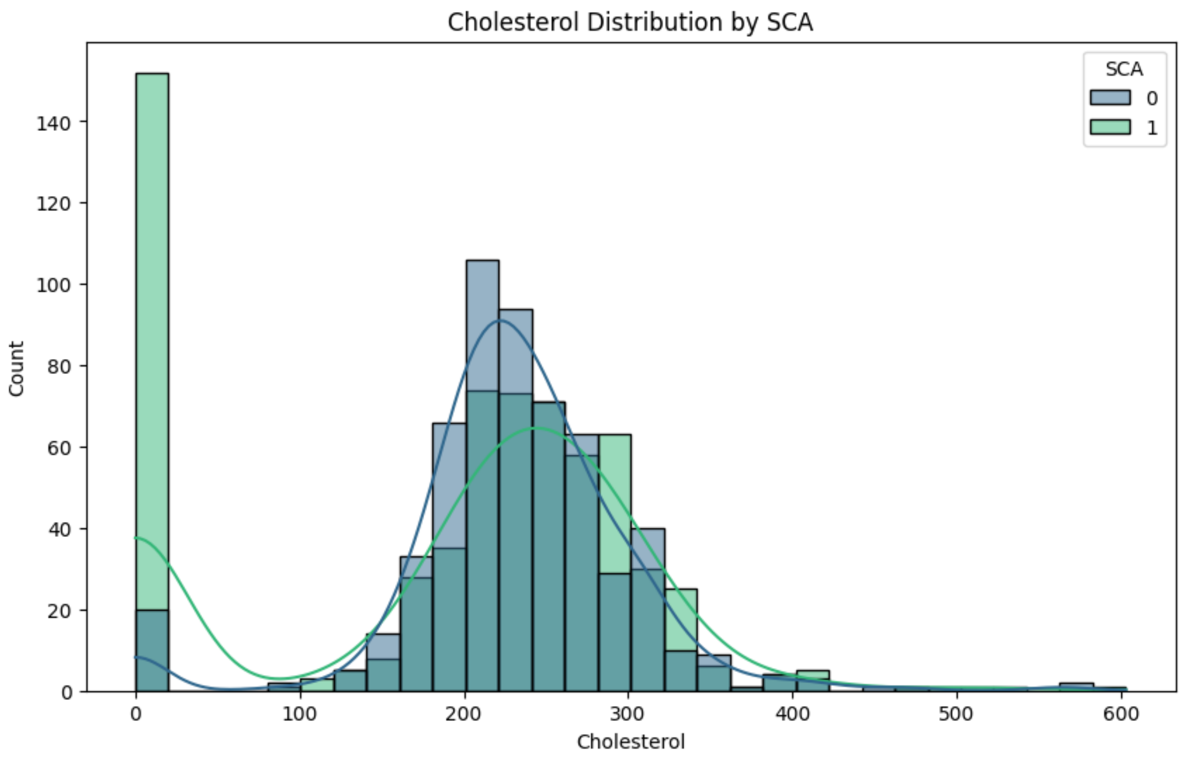
In [13]:
```
# Age vs SCA
plt.figure(figsize=(10, 6))
sns.histplot(x='Age', hue='SCA', data=heartwell_df, bins=30, kde=True, pale
plt.title('Age Distribution by SCA')
plt.xlabel('Age')
plt.ylabel('Count')
plt.show()

# Blood Pressure vs SCA
plt.figure(figsize=(10, 6))
sns.histplot(x='BloodPressure-Resting', hue='SCA', data=heartwell_df, bins=
plt.title('Blood Pressure Distribution by SCA')
plt.xlabel('Blood Pressure Resting')
plt.ylabel('Count')
plt.show()

# Heart Rate Max vs SCA
plt.figure(figsize=(10, 6))
sns.histplot(x='HeartRate-Max', hue='SCA', data=heartwell_df, bins=30, kde=
plt.title('Heart Rate Max Distribution by SCA')
plt.xlabel('Heart Rate Max')
plt.ylabel('Count')
plt.show()

# Cholesterol vs SCA
plt.figure(figsize=(10, 6))
sns.histplot(x='Cholesterol', hue='SCA', data=heartwell_df, bins=30, kde=Tru
plt.title('Cholesterol Distribution by SCA')
plt.xlabel('Cholesterol')
plt.ylabel('Count')
plt.show()
```

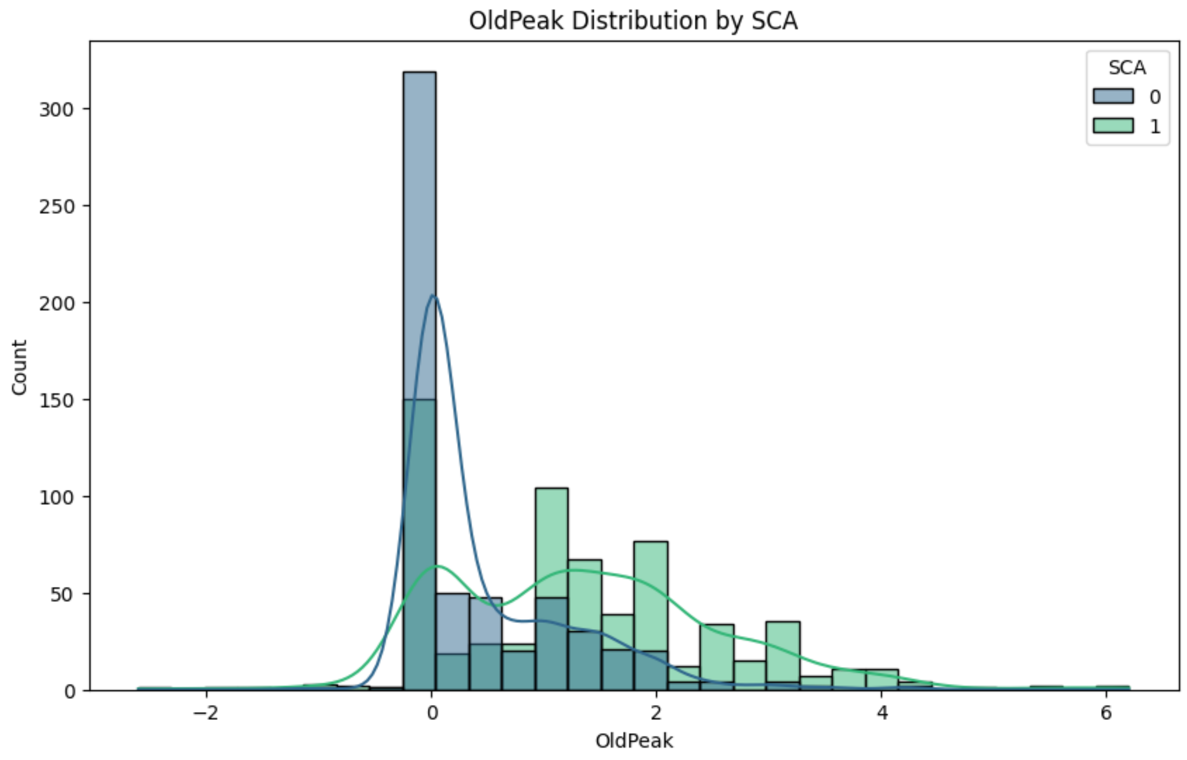
```
# OldPeak vs SCA
plt.figure(figsize=(10, 6))
sns.histplot(x='OldPeak', hue='SCA', data=heartwell_df, bins=30, kde=True, p
plt.title('OldPeak Distribution by SCA')
plt.xlabel('OldPeak')
plt.ylabel('Count')
plt.show()
```






Heart Rate Max Distribution by SCA
SCA
0
1
Count
Heart Rate Max
0
10
20
30
40
50
60
60
80
100
120
140
160
180
200


Cholesterol Distribution by SCA
SCA
0
1
Count
Cholesterol
0
20
40
60
80
100
120
140
0
100
200
300
400
500
600



Data Pre-Processing and Wrangling

Missing Values

In [14]:
```
heartwell_df.isnull().sum()
```

Out[14]:
```
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
```

Missing values imputation

In [15]:
```
print("No imputation of missing values required since there are no missing v
```

```
No imputation of missing values required since there are no missing values
in data to affect our models
```

Duplicate Data

In [16]:
```
duplicate_rows = heartwell_df.duplicated().sum()
#duplicate_rows
print(f"The number of duplicated rows in our data is {duplicate_rows}")
```

```
The number of duplicated rows in our data is 303
```

In [17]:
```
heartwell_df = heartwell_df.drop_duplicates()
```

In [18]:
```
duplicate_rows = heartwell_df.duplicated().sum()
duplicate_rows
```

Out[18]:
```
0
```

In [19]:
```
print("We have removed the duplicated records")
```

```
We have removed the duplicated records
```

Feature Engineering

Added AgeGroup category column based on age range.

In [20]:
```
# Define age ranges and corresponding labels
bins = [19,39,59,79,99]
labels = ['19-39','40-59','60-79','80-99']

# Create the 'AgeGroup' column
heartwell_df['AgeGroup'] = pd.cut(heartwell_df['Age'], bins=bins, labels=lal
heartwell_df.head(5)
```

Out[20]:

	Age	Sex	ECG-Resting	ST-Slope	BloodPressure-Resting	HeartRate-Max	ChestPainType	Cholesterol	Bloo
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	

Calculate the risk based on Age, Blood Pressure-Resting, Cholesterol, and Max Heart Rate

In [21]:
```
# The formula for risk calculation can be adjusted based on specific require

heartwell_df["risk"]= heartwell_df["Age"]/(heartwell_df["BloodPressure-Resti
heartwell_df.head(5)
```

Out[21]:

	Age	Sex	ECG-Resting	ST-Slope	BloodPressure-Resting	HeartRate-Max	ChestPainType	Cholesterol	Bloo
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 [22]:
```
# Calculated Z-scores for numerical features
z_scores = zscore(heartwell_df.select_dtypes(include=np.number))
z_scores
```

Out[22]:

	Age	BloodPressure-Resting	HeartRate-Max	Cholesterol	OldPeak	SCA	risk
0	-1.433140	0.410909	1.382928	0.825070	-0.832432	-1.113115	-1.081028
1	-0.478484	1.491752	0.754157	-0.171961	0.105664	0.898380	-0.503071
2	-1.751359	-0.129513	-1.525138	0.770188	-0.832432	-1.113115	-0.976116
3	-0.584556	0.302825	-1.132156	0.139040	0.574711	0.898380	-0.403427
4	0.051881	0.951331	-0.581981	-0.034755	-0.832432	-1.113115	-0.201110
...	...	...	...	...	...	...	...
913	-0.902775	-1.210356	-0.188999	0.596393	0.293283	0.898380	-0.679814
914	1.536902	0.627078	0.164684	-0.053049	2.357094	0.898380	0.276317
915	0.370100	-0.129513	-0.857069	-0.620168	0.293283	0.898380	0.443715
916	0.370100	-0.129513	1.461525	0.340275	-0.832432	0.898380	-0.381773
917	-1.645286	0.302825	1.422226	-0.217696	-0.832432	-1.113115	-0.872442

918 rows × 7 columns

In [23]:
```
# Set a threshold for Z score to catch the outliers
threshold = 3
outliers = np.abs(z_scores) > threshold
outliers
```

Out[23]:

	Age	BloodPressure-Resting	HeartRate-Max	Cholesterol	OldPeak	SCA	risk
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

918 rows × 7 columns

In [24]:
```
# Removed outliers
df_no_outliers = heartwell_df[~outliers.any(axis=1)]
df_no_outliers
```

Out[24]:

	Age	Sex	ECG-Resting	ST-Slope	BloodPressure-Resting	HeartRate-Max	ChestPainType	Cholesterol	Bl
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	264	
914	68	M	Normal	Flat	144	141	ASY	193	
915	57	M	Normal	Flat	130	115	ASY	131	
916	57	F	LVH	Flat	130	174	ATA	236	
917	38	M	Normal	Up	138	173	NAP	175	

891 rows × 14 columns

Categorical Data Encoding

In [25]:
```
# Categorical Data Encoding:One-Hot Encoding on multiple columns to converts
df_encoded = pd.get_dummies(df_no_outliers, columns=['Sex','ECG-Resting','S
df_encoded.head()
```

Out[25]:

	Age	BloodPressure-Resting	HeartRate-Max	Cholesterol	OldPeak	SCA	risk	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 × 27 columns

Feature Scaling

In [26]:
```
# Feature Scaling: Standard Scaling (Z-score normalization),Standard scaling

# Initialize the StandardScaler
scaler = StandardScaler()

## Fit and transform the selected features
```

```
df_encoded[['Age', 'BloodPressure-Resting', 'Cholesterol', 'OldPeak']] = sca
    df_encoded[['Age', 'BloodPressure-Resting', 'Cholesterol', 'OldPeak']])

df_encoded
```

Out[26]:

	Age	BloodPressure-Resting	HeartRate-Max	Cholesterol	OldPeak	SCA	risk	Sex_F
0	-1.420081	0.460473	172	0.842348	-0.861509	0	0.066556	False
1	-0.466902	1.629032	156	-0.186787	0.132540	1	0.098790	True
2	-1.737808	-0.123807	98	0.785698	-0.861509	0	0.072407	False
3	-0.572811	0.343617	108	0.134228	0.629564	1	0.104348	True
4	0.062642	1.044752	122	-0.045163	-0.861509	0	0.115632	False
...	...	...	...	...	...	...	...	...
913	-0.890537	-1.292366	132	0.606308	0.331350	1	0.088933	False
914	1.545365	0.694185	141	-0.064046	2.518258	1	0.142259	False
915	0.380368	-0.123807	115	-0.649425	0.331350	1	0.151596	False
916	0.380368	-0.123807	174	0.341943	-0.861509	1	0.105556	True
917	-1.631899	0.343617	173	-0.233995	-0.861509	0	0.078189	False

891 rows × 27 columns

Build Functions.

In [27]:
```
# Function for evaluating the model
def evaluate_model(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='coolwarm')
    plt.title('Confusion Matrix')
    plt.show()
```

Models Building

Decision Tree

In [28]:
```
X = df_encoded.drop("SCA", axis=1)
y = df_encoded["SCA"]
```

In [29]:
```
# splitting 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 [30]:
```
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 [31]:
```
#Initialize the Decision Tree classifier
dt_model = DecisionTreeClassifier(random_state=42)

#Train the Decision Tree model on the training data
dt_model.fit(X_train, y_train)
dt_model
```

Out[31]:
```
▾ DecisionTreeClassifier
DecisionTreeClassifier(random_state=42)
```

Random Forest

In [32]:
```
# Initialize the Random Forest classifier
rf_model = RandomForestClassifier(random_state=42)

# Train the Random Forest model on the training data
rf_model.fit(X_train, y_train)
```

Out[32]:
```
▾ RandomForestClassifier
RandomForestClassifier(random_state=42)
```

Support Vector Machine

In [33]:
```
# Initialize the SVM classifier
svm_model = SVC(random_state=42)

# Train the Support Vector Machine model on the training data
svm_model.fit(X_train, y_train)
```

Out[33]:
```
▾ SVC
SVC(random_state=42)
```

K Nearest Neighbors

In [34]:
```
#Initialize the KNeighborsClassifier
knn_model = KNeighborsClassifier(n_neighbors=5)

# Train the model on the training data
knn_model.fit(X_train, y_train)
```

```
Out[34]: ▾ KNeighborsClassifier
         KNeighborsClassifier()
```

Gradient Boosting

```
In [35]: # Initialize the Gradient Boosting classifier
         gb_model = GradientBoostingClassifier(random_state=42)

         # Train the model on the training data
         gb_model.fit(X_train, y_train)
```

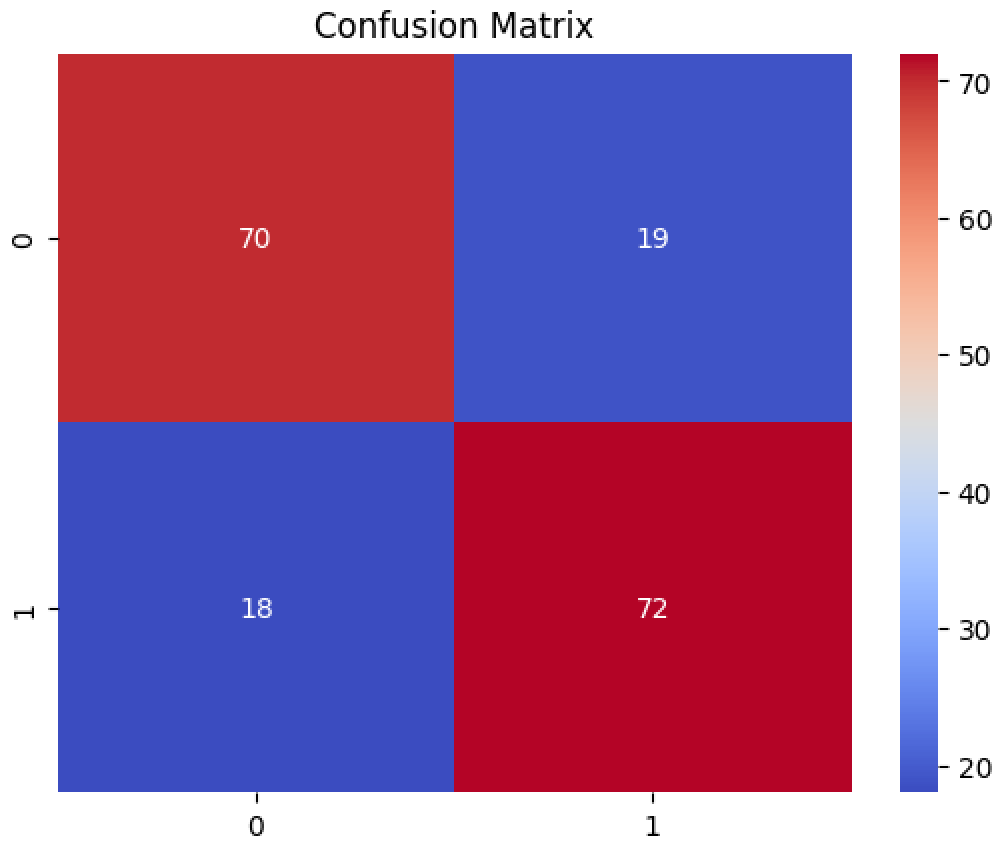
```
Out[35]: ▾          GradientBoostingClassifier
         GradientBoostingClassifier(random_state=42)
```

Models Evaluation and Comparisions

Decision Tree Evaluation

```
In [36]: # Make predictions on the test data
         evaluate_model(dt_model, X_test, y_test, average='weighted')
```

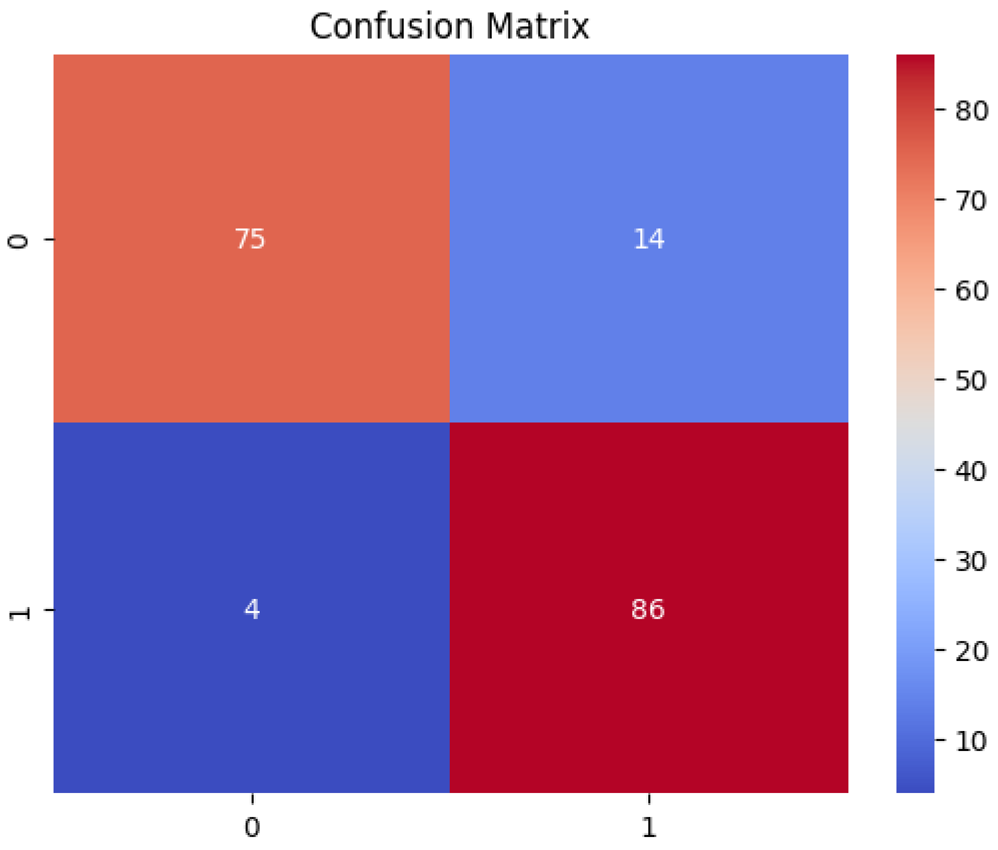
```
Accuracy: 0.79
Precision: 0.79
Recall: 0.79
F1-score: 0.79
DecisionTreeClassifier Cross-Validation Accuracy: 0.75
```



Random Forest Evaluation

In [37]:
```
# Make predictions on the test data
evaluate_model(rf_model, X_test, y_test)
```

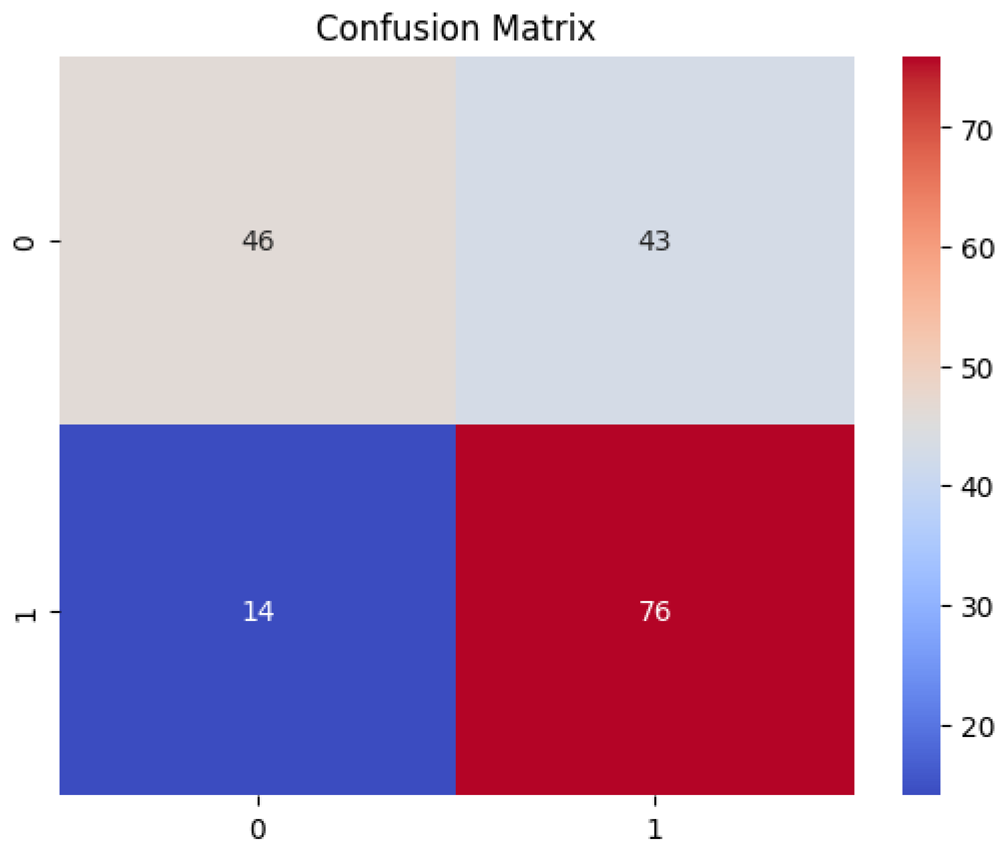
```
Accuracy: 0.90
Precision: 0.90
Recall: 0.90
F1-score: 0.90
RandomForestClassifier Cross-Validation Accuracy: 0.82
```



Support Vector Machine Evaluation

In [38]:
```
# Make predictions on the test data
evaluate_model(svm_model, X_test, y_test)
```

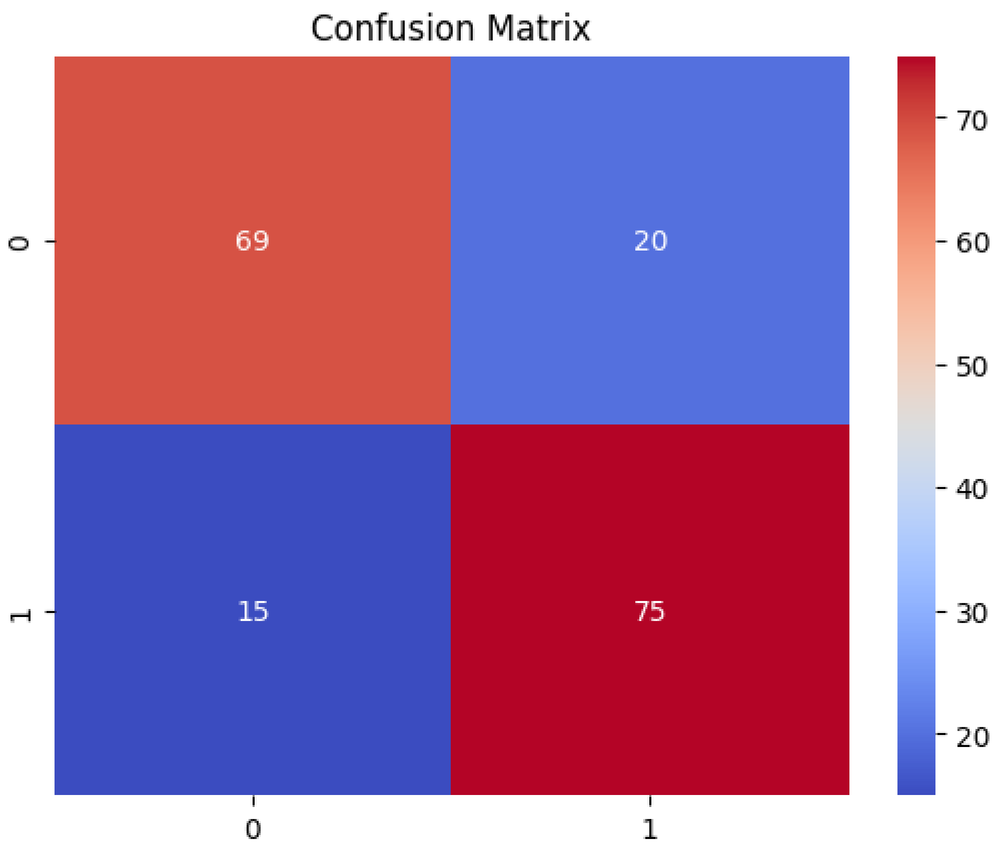
```
Accuracy: 0.68
Precision: 0.70
Recall: 0.68
F1-score: 0.67
SVC Cross-Validation Accuracy: 0.68
```



K-Nearest Neighbors Evaluation

In [39]:
```
# Make predictions on the test data
evaluate_model(knn_model, X_test, y_test)
```

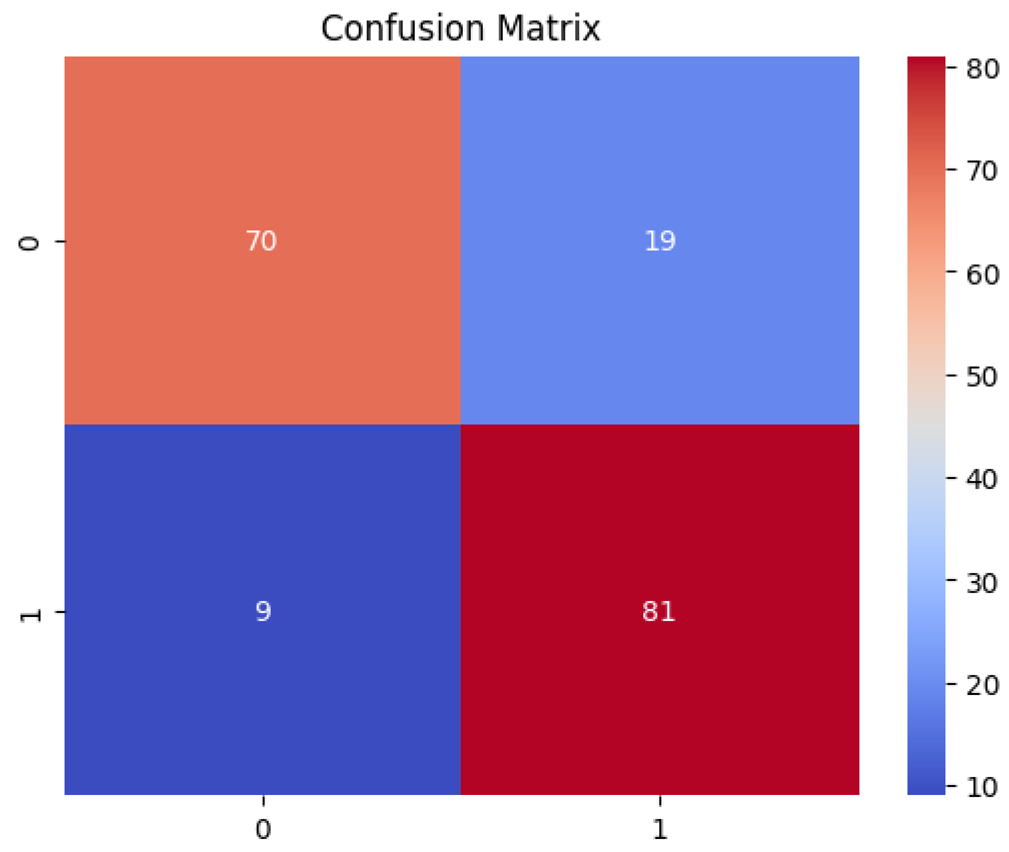
```
Accuracy: 0.80
Precision: 0.81
Recall: 0.80
F1-score: 0.80
KNeighborsClassifier Cross-Validation Accuracy: nan
```



Gradient Boosting Evaluation

```
In [40]: # Make predictions on the test data
         evaluate_model(gb_model, X_test, y_test)
```

```
Accuracy: 0.84
Precision: 0.85
Recall: 0.84
F1-score: 0.84
GradientBoostingClassifier Cross-Validation Accuracy: 0.81
```


Confusion Matrix
70
19
9
81
0
1
0
1
80
70
60
50
40
30
20
10