```
from google.colab import drive
drive.mount('/content/gdrive')

file_path = '/content/gdrive/MyDrive/heart_failure data.csv'
```

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

```
import pandas as pd
data= pd.read_csv(file_path)
data.head(5)
```

	age	anaemia	creatinine_phosphokinase	diabetes	ejection_fraction	high_blood_pressure	platelets	serum_creatinine	serum_sodium
0	75.0	0	582	0	20	1	265000.00	1.9	130
1	55.0	0	7861	0	38	0	263358.03	1.1	136
2	65.0	0	146	0	20	0	162000.00	1.3	129
3	50.0	1	111	0	20	0	210000.00	1.9	137
4	65.0	1	160	1	20	0	327000.00	2.7	116

Step 1: Problem Definition

Define the objective clearly. Understand the business problem or the research question you're trying to answer. This ensures the analysis is aligned with the goal.

Our objective is to understand what is causing a Death Event. By understanding what causes a Death Event it may help put a focus and emphasis on that specific issue. Understanding what causes Death Events can ultimately help reduce the number of Death Events.

Define the type of task you want to perform: Regression/ Classification/Clustering and why?

We will perform a classification analysis to determine how the independent variables serum creatinine, platelets, ejection fraction, serum sodium, and creatinine phosphokinase, impact the dependent variable Death Event. We are doing this to determine what events determine the change of a death event.

Step 2: Exploratory Data Analysis (EDA)

```
#summary statistics
data.info()
data.describe()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 299 entries, 0 to 298
Data columns (total 13 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   age                       299 non-null    float64
 1   anaemia                   299 non-null    int64  
 2   creatinine_phosphokinase  299 non-null    int64  
 3   diabetes                  299 non-null    int64  
 4   ejection_fraction         299 non-null    int64  
 5   high_blood_pressure       299 non-null    int64  
 6   platelets                 299 non-null    float64
 7   serum_creatinine          299 non-null    float64
 8   serum_sodium              299 non-null    int64  
 9   sex                       299 non-null    int64  
 10  smoking                   299 non-null    int64  
 11  time                      299 non-null    int64  
 12  DEATH_EVENT               299 non-null    int64  
dtypes: float64(3), int64(10)
memory usage: 30.5 KB
```

	age	anaemia	creatinine_phosphokinase	diabetes	ejection_fraction	high_blood_pressure	platelets	serum_creatini
count	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000
mean	60.833893	0.431438	581.839465	0.418060	38.083612	0.351171	263358.029264	1.393
std	11.894809	0.496107	970.287881	0.494067	11.834841	0.478136	97804.236869	1.034
min	40.000000	0.000000	23.000000	0.000000	14.000000	0.000000	25100.000000	0.500
25%	51.000000	0.000000	116.500000	0.000000	30.000000	0.000000	212500.000000	0.900
50%	60.000000	0.000000	250.000000	0.000000	38.000000	0.000000	262000.000000	1.100
75%	70.000000	1.000000	582.000000	1.000000	45.000000	1.000000	303500.000000	1.400
max	95.000000	1.000000	7861.000000	1.000000	80.000000	1.000000	850000.000000	9.400

```
data.shape
```

```
(299, 13)
```

```
# Import necessary libraries
data = pd.read_csv(file_path)

# Display basic information about the dataset
print("Dataset Info:")
print(data.info())
print("\nSummary Statistics:")
print(data.describe())


import matplotlib.pyplot as plt
```

```
Dataset Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 299 entries, 0 to 298
Data columns (total 13 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   age                       299 non-null    float64
 1   anaemia                   299 non-null    int64  
 2   creatinine_phosphokinase  299 non-null    int64  
 3   diabetes                  299 non-null    int64  
 4   ejection_fraction         299 non-null    int64  
 5   high_blood_pressure       299 non-null    int64  
 6   platelets                 299 non-null    float64
 7   serum_creatinine          299 non-null    float64
 8   serum_sodium              299 non-null    int64  
 9   sex                       299 non-null    int64  
 10  smoking                   299 non-null    int64  
 11  time                      299 non-null    int64  
 12  DEATH_EVENT               299 non-null    int64  
dtypes: float64(3), int64(10)
memory usage: 30.5 KB
None

Summary Statistics:
              age     anaemia  creatinine_phosphokinase    diabetes  \
count  299.000000  299.000000                299.000000  299.000000   
mean    60.833893    0.431438                581.839465    0.418060   
```

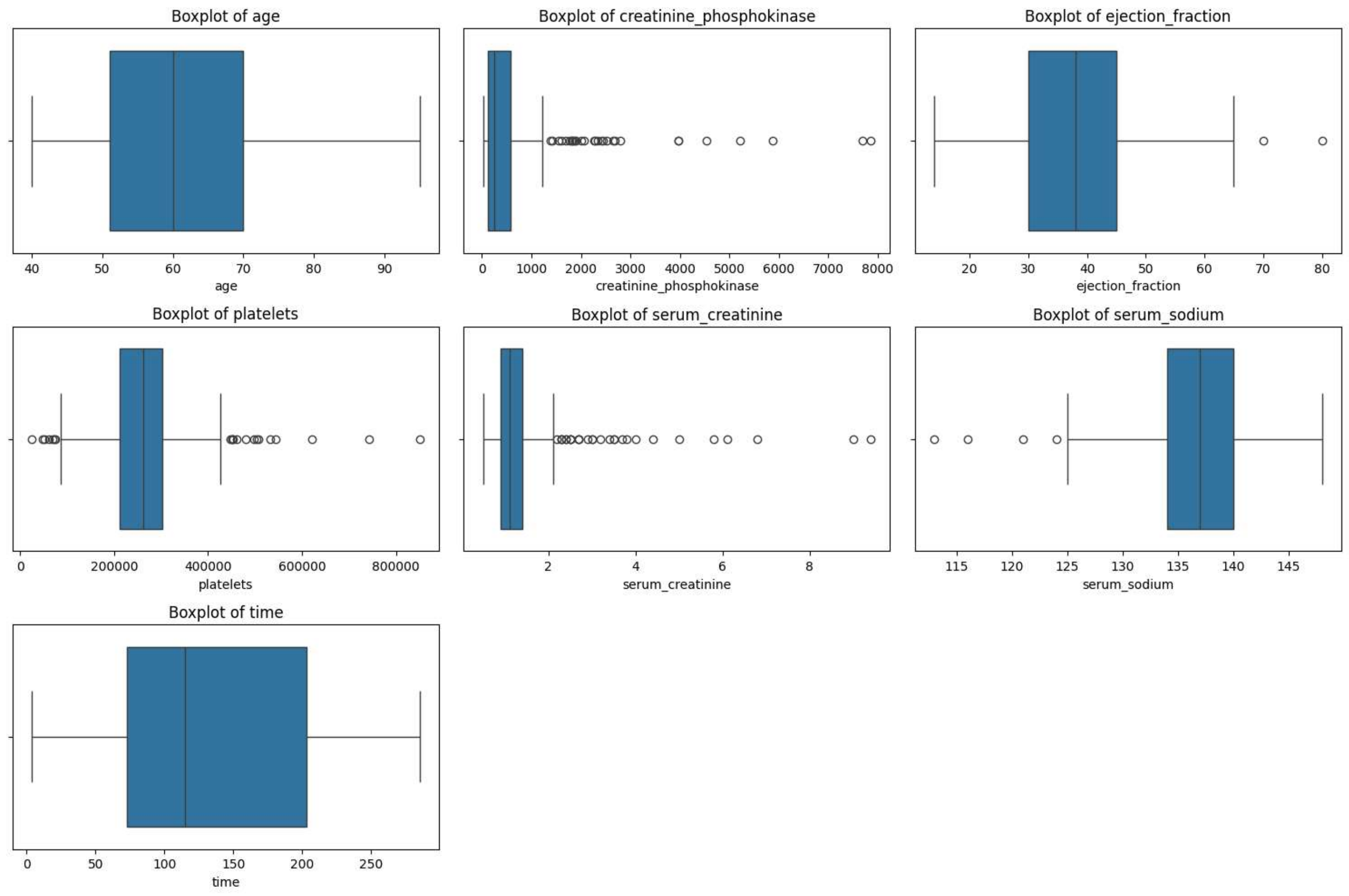
```
std     11.894809    0.496107               970.287881    0.494067
min     40.000000    0.000000                23.000000    0.000000
25%     51.000000    0.000000               116.500000    0.000000
50%     60.000000    0.000000               250.000000    0.000000
75%     70.000000    1.000000               582.000000    1.000000
max     95.000000    1.000000              7861.000000    1.000000

       ejection_fraction  high_blood_pressure      platelets  \
count         299.000000           299.000000     299.000000
mean           38.083612             0.351171  263358.029264
std            11.834841             0.478136   97804.236869
min            14.000000             0.000000   25100.000000
25%            30.000000             0.000000  212500.000000
50%            38.000000             0.000000  262000.000000
75%            45.000000             1.000000  303500.000000
max            80.000000             1.000000  850000.000000

       serum_creatinine  serum_sodium         sex    smoking        time  \
count         299.00000    299.000000  299.000000  299.00000  299.000000
mean            1.39388    136.625418    0.648829    0.32107  130.260870
std             1.03451      4.412477    0.478136    0.46767   77.614208
min             0.50000    113.000000    0.000000    0.00000    4.000000
25%             0.90000    134.000000    0.000000    0.00000   73.000000
50%             1.10000    137.000000    1.000000    0.00000  115.000000
75%             1.40000    140.000000    1.000000    1.00000  203.000000
max             9.40000    148.000000    1.000000    1.00000  285.000000

       DEATH_EVENT
count    299.00000
mean       0.32107
std        0.46767
```

Double-click (or enter) to edit

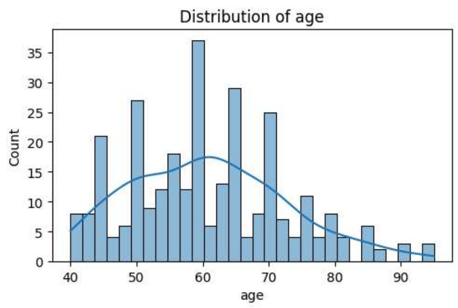
```
# Detect Missing Values
missing_values = data.isnull().sum()
print("\nMissing Values in Each Column:")
print(missing_values)
```

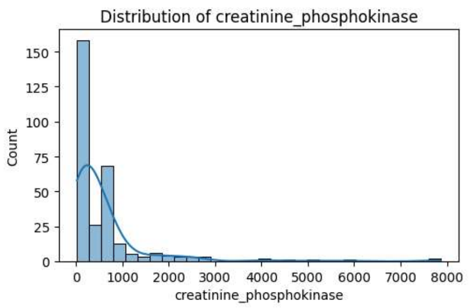
```
Missing Values in Each Column:
age                         0
anaemia                     0
creatinine_phosphokinase    0
diabetes                    0
ejection_fraction           0
high_blood_pressure         0
platelets                   0
serum_creatinine            0
serum_sodium                0
sex                         0
smoking                     0
time                        0
DEATH_EVENT                 0
dtype: int64
```

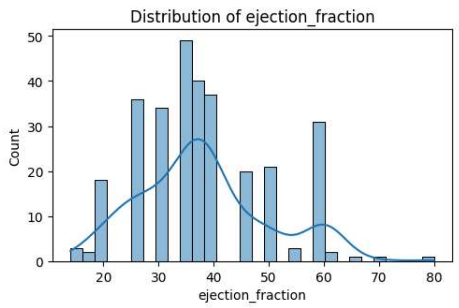
```
# Detect Outliers Using Boxplots for Numerical Features
numerical_features = ['age', 'creatinine_phosphokinase', 'ejection_fraction',
                      'platelets', 'serum_creatinine', 'serum_sodium', 'time']
import matplotlib.pyplot as plt
plt.figure(figsize=(15, 10))
for i, feature in enumerate(numerical_features, 1):
    plt.subplot(3, 3, i)
    sns.boxplot(x=data[feature])
    plt.title(f"Boxplot of {feature}")
plt.xlabel(feature)
plt.tight_layout()
plt.show()
```

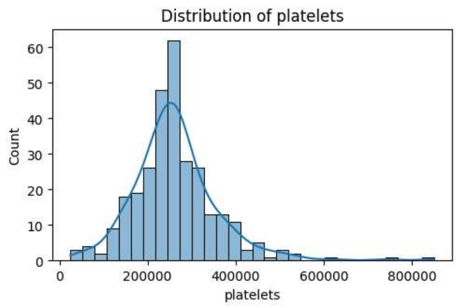


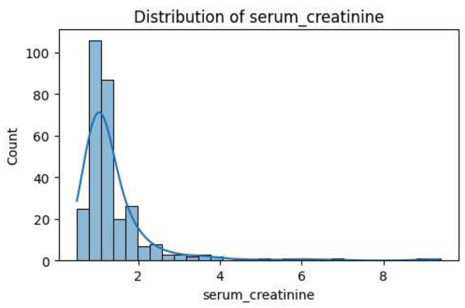
```
# Visualize Distributions of Numerical Features
plt.figure(figsize=(15, 10))
for i, feature in enumerate(numerical_features, 1):
    plt.subplot(3, 3, i)
    sns.histplot(data[feature], bins=30, kde=True)
    plt.title(f"Distribution of {feature}")
    plt.xlabel(feature)
plt.tight_layout()
plt.show()

# Visualize Counts of Categorical Features
categorical_features = ['anaemia', 'diabetes', 'high_blood_pressure', 'sex', 'smoking', 'DEATH_EVENT']
plt.figure(figsize=(15, 10))
for i, feature in enumerate(categorical_features[:-1], 1):  # Exclude DEATH_EVENT for now
    plt.subplot(3, 2, i)
    sns.countplot(x=data[feature])
    plt.title(f"Countplot of {feature}")
    plt.xlabel(feature)
plt.tight_layout()
plt.show()
```

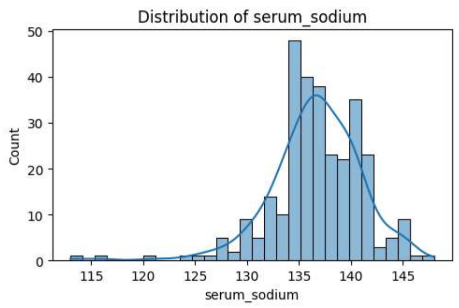

Distribution of age
Count
age

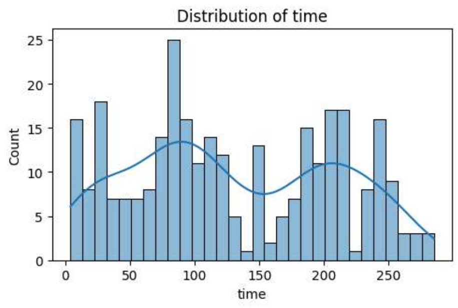

Distribution of creatinine_phosphokinase
Count
creatinine_phosphokinase

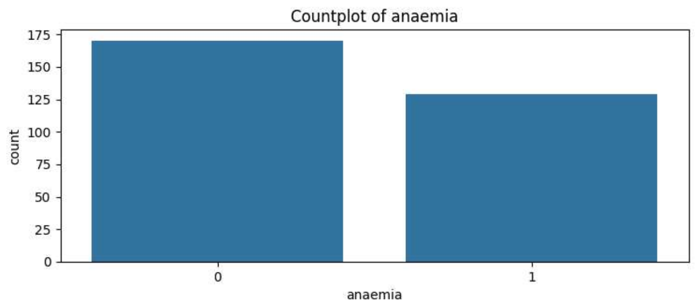

Distribution of ejection_fraction
Count
ejection_fraction

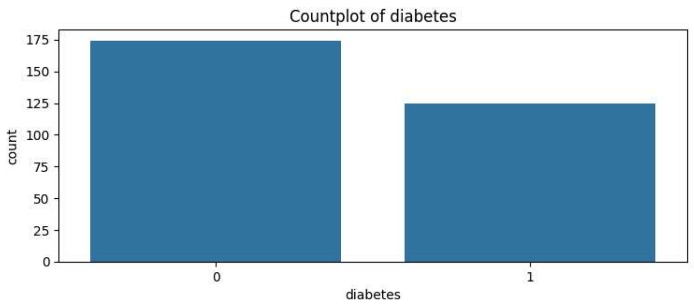

Distribution of platelets
Count
platelets

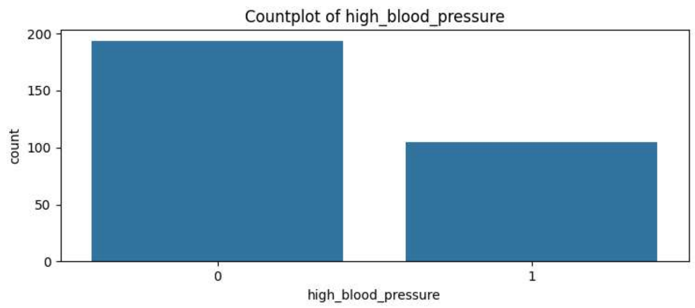

Distribution of serum_creatinine
Count
serum_creatinine

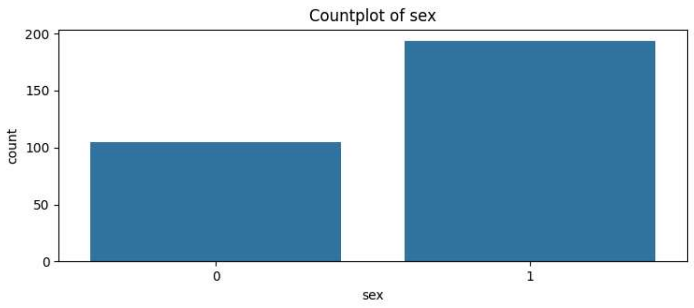

Distribution of serum_sodium
Count
serum_sodium

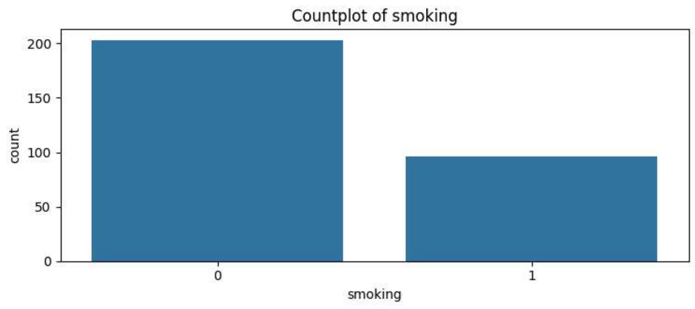

Distribution of time
Count
time


Countplot of anaemia
count
anaemia


Countplot of diabetes
count
diabetes


Countplot of high_blood_pressure
count
high_blood_pressure


Countplot of sex
count
sex


Countplot of smoking
count
smoking

feature selection:

```
#hypotheses for futher analysis
```

Null Hypothesis (H_0): There is no significant relationship between the categories (features such as age, anaemia, creatinine phosphokinase, diabetes, etc.) and the likelihood of a Death Event.

Alternative Hypothesis (H_1): At least one of the categories (features) significantly impacts the likelihood of a Death Event.

Feature Classification:

age: Numerical Continuous

anaemia: Categorical Nominal

creatinine_phosphokinase: Numerical Continuous

diabetes: Categorical Nominal

ejection_fraction: Numerical Discrete

high_blood_pressure: Categorical Nominal

platelets: Numerical Continuous

serum_creatinine: Numerical Continuous

serum_sodium: Numerical Continuous

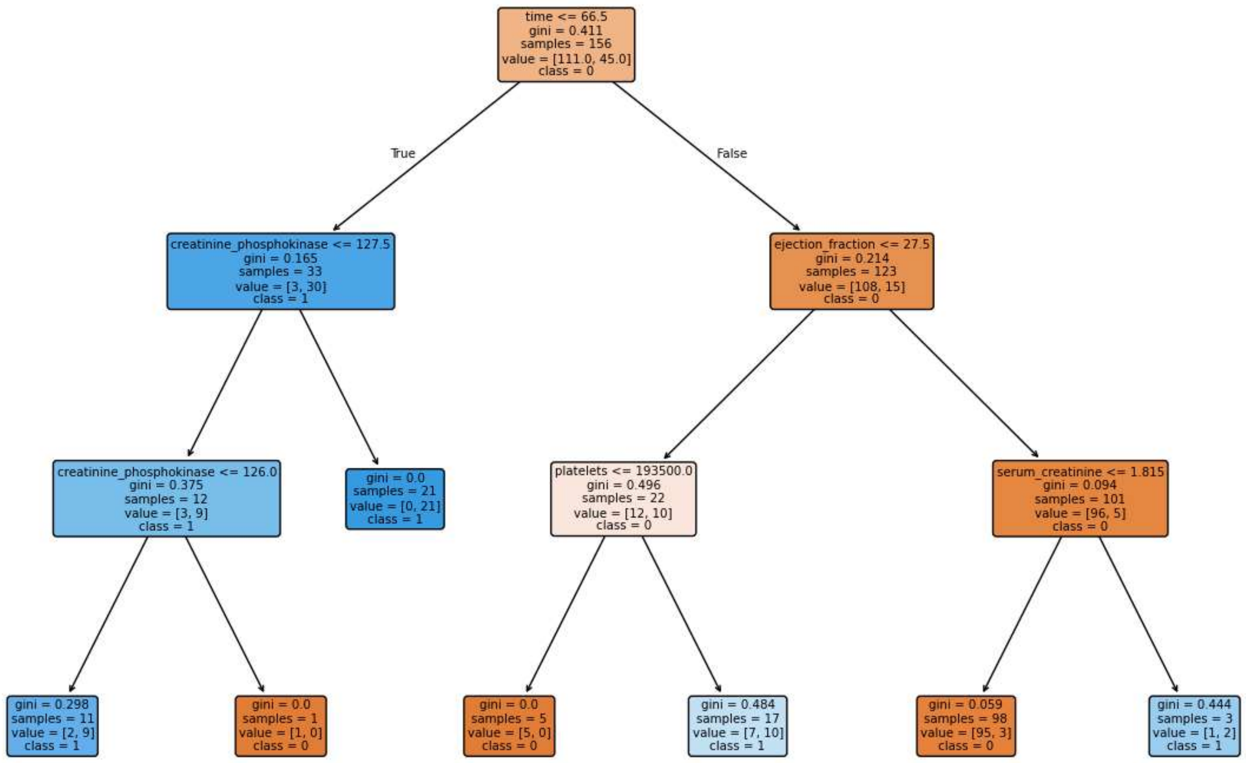
sex: Categorical Nominal

smoking: Categorical Nominal

time: Numerical Time Series

DEATH_EVENT: Categorical Nominal

```
import pandas as pd
from sklearn.tree import DecisionTreeClassifier
from sklearn import tree
import matplotlib.pyplot as plt

# Fit decision tree classifier
clf = DecisionTreeClassifier(max_depth=3)
clf = clf.fit(X_train, y_train)

feature_names = X_train.columns
# Convert class names to strings
class_names = [str(cls) for cls in clf.classes_]

# Plot the decision tree
plt.figure(figsize=(15, 10))
tree.plot_tree(clf,
               filled=True,
               feature_names=feature_names,
              class_names=class_names,  # Use the converted class names
              rounded=True)
plt.show()
```



If time ≤ 67.5, the samples are sent to the left branch. If time > 67.5, the samples are sent to the right branch.

Left branch 1: If ejection fraction ≤ 72.5, the samples are further split into the next level. If ejection fraction > 72.5, only one patient is classified, with no death event (class 0).

Left branch 2: If creatinine phosphokinase ≤ 109.5, the samples are split further. If creatinine phosphokinase > 109.5, there is a strong majority of no death events (class 0)

Right branch 1: If serum creatinine ≤ 1.815, the majority of patients experience no death events (class 0). If serum creatinine > 1.815, there's a higher proportion of death events, leading to further splits.

Right branch 2: If platelets ≤ 90,000, the data splits again based on serum sodium. If platelets > 90,000, the model predicts no death events (class 0) with very high confidence (low Gini index of 0.093).

Right branch 3: If serum sodium ≤ 132.5, the risk of a death event (class 1) is high. If serum sodium > 132.5, the risk of a death event is lower.

Step 3: Data Preprocessing

```
# Load the dataset
data = pd.read_csv(file_path)

# 1. Detect Missing Values
print("Missing Values in Each Column:")
missing_values = data.isnull().sum()
print(missing_values)
```

```
Missing Values in Each Column:
age                         0
anaemia                     0
creatinine_phosphokinase    0
diabetes                    0
ejection_fraction           0
high_blood_pressure         0
platelets                   0
serum_creatinine            0
serum_sodium                0
sex                         0
smoking                     0
time                        0
DEATH_EVENT                 0
dtype: int64
```

```
# 2. Handle Duplicates
duplicates = data.duplicated().sum()
print(f"\nNumber of duplicate rows: {duplicates}")

# If duplicates exist, remove them
data = data.drop_duplicates()
```

```

Number of duplicate rows: 0
```

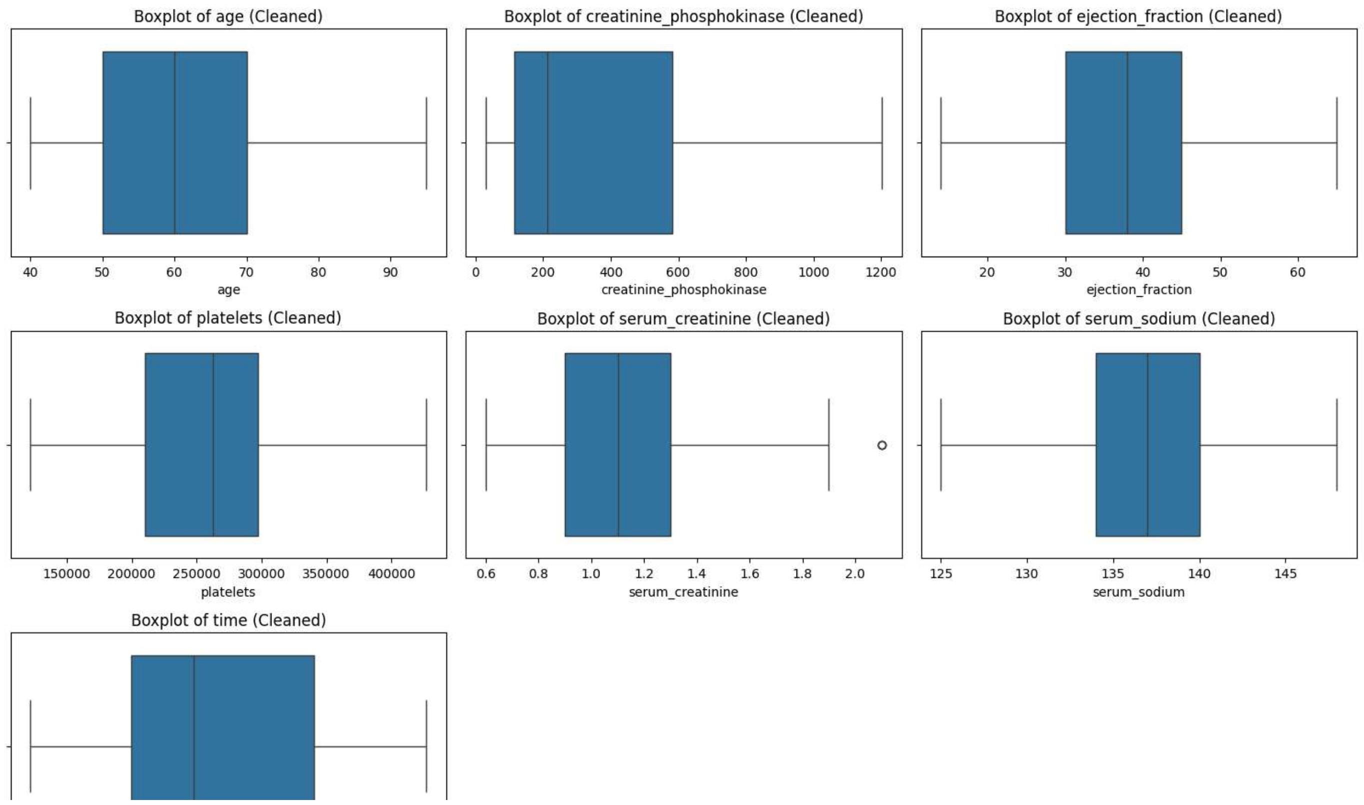
```
# 3. Detect and Handle Outliers
# Use IQR to filter out outliers in numerical features
numerical_features = ['age', 'creatinine_phosphokinase', 'ejection_fraction',
                      'platelets', 'serum_creatinine', 'serum_sodium', 'time']

for feature in numerical_features:
    Q1 = data[feature].quantile(0.25)
    Q3 = data[feature].quantile(0.75)
    IQR = Q3 - Q1
    lower_bound = Q1 - 1.5 * IQR
    upper_bound = Q3 + 1.5 * IQR

    # Filter out outliers
    outliers_removed = data[(data[feature] >= lower_bound) & (data[feature] <= upper_bound)]

    print(f"\nFeature: {feature}")
    print(f"Outliers removed: {len(data) - len(outliers_removed)}")

    # Update the dataset by removing outliers
    data = outliers_removed
```

```

Feature: age
Outliers removed: 0

Feature: creatinine_phosphokinase
Outliers removed: 29

Feature: ejection_fraction
Outliers removed: 2

Feature: platelets
Outliers removed: 18

Feature: serum_creatinine
Outliers removed: 23

Feature: serum_sodium
Outliers removed: 3

Feature: time
Outliers removed: 0
```

```
# 4. Check for Erroneous Data (e.g., negative values where not applicable)
for feature in numerical_features:
    if (data[feature] < 0).any():
        print(f"Erroneous data found in {feature}")

# Display cleaned dataset info
print("\nCleaned Dataset Info:")
print(data.info())
```

```
# Visualize to confirm cleaning process
plt.figure(figsize=(15, 10))
for i, feature in enumerate(numerical_features, 1):
    plt.subplot(3, 3, i)
    sns.boxplot(x=data[feature])
    plt.title(f"Boxplot of {feature} (Cleaned)")
plt.tight_layout()
plt.show()
```

```
Cleaned Dataset Info:
<class 'pandas.core.frame.DataFrame'>
Index: 224 entries, 0 to 298
Data columns (total 13 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   age                       224 non-null    float64
 1   anaemia                   224 non-null    int64  
 2   creatinine_phosphokinase  224 non-null    int64  
 3   diabetes                  224 non-null    int64  
 4   ejection_fraction         224 non-null    int64  
 5   high_blood_pressure       224 non-null    int64  
 6   platelets                 224 non-null    float64
 7   serum_creatinine          224 non-null    float64
 8   serum_sodium              224 non-null    int64  
 9   sex                       224 non-null    int64  
 10  smoking                   224 non-null    int64  
 11  time                      224 non-null    int64  
 12  DEATH_EVENT               224 non-null    int64  
dtypes: float64(3), int64(10)
memory usage: 24.5 KB
None
```



```
# Feature Engineering: Create new features or variables that may improve the model
# Example: Create a feature for age group
data['age_group'] = pd.cut(data['age'], bins=[0, 50, 70, 100], labels=['young', 'middle_aged', 'old'])

# Encode the new feature
age_group_encoded = pd.get_dummies(data['age_group'], drop_first=True)

# Concatenate with the original dataset
data = pd.concat([data.drop(columns=['age_group']), age_group_encoded], axis=1)

print("Feature Engineered Data:")
print(data.head())
```

```
Feature Engineered Data:
    age  anaemia  creatinine_phosphokinase  diabetes  ejection_fraction  \
   0  75.0        0                       582         0                 20
   2  65.0        0                       146         0                 20
   3  50.0        1                       111         0                 20
   5  90.0        1                        47         0                 40
   6  75.0        1                       246         0                 15

      high_blood_pressure  platelets  serum_creatinine  serum_sodium  sex  \
   0                    1   265000.0               1.9           130    1
   2                    0   162000.0               1.3           129    1
   3                    0   210000.0               1.9           137    1
   5                    1   204000.0               2.1           132    1
   6                    0   127000.0               1.2           137    1

      smoking  time  DEATH_EVENT  middle_aged    old
   0        0     4            1        False   True
   2        1     7            1         True  False
   3        0     7            1        False  False
   5        1     8            1        False   True
   6        0    10            1        False   True
```

Step 4: Feature Selection

```
from sklearn.model_selection import train_test_split

# Define features
X = data.drop(['DEATH_EVENT'],axis=1)
y = data['DEATH_EVENT']
```

Step 5: Modeling

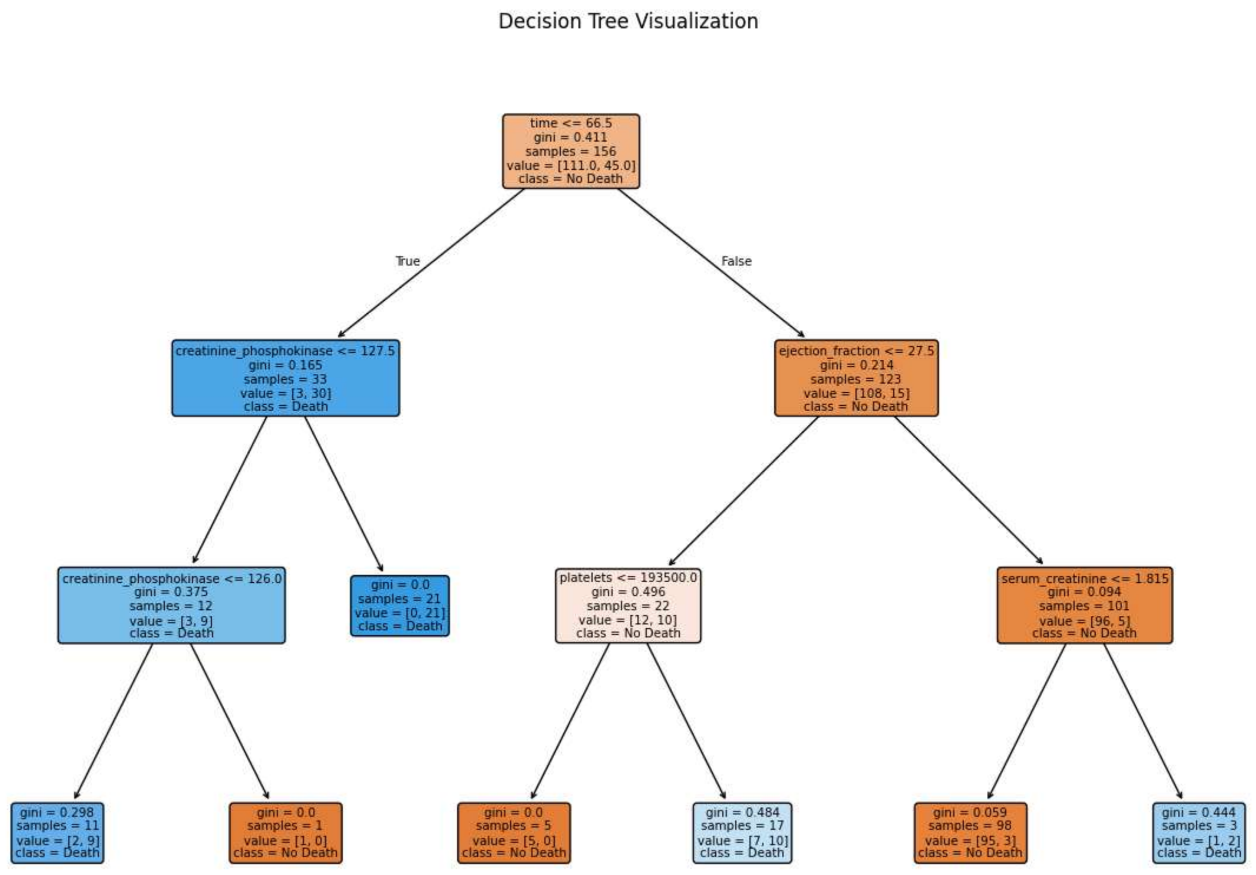
```
# Split the data: 70% training, 30% testing
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)

# Show the shape of the resulting datasets
print(f"X_train shape: {X_train.shape}, y_train shape: {y_train.shape}")
print(f"X_test shape: {X_test.shape}, y_test shape: {y_test.shape}")
```

```
X_train shape: (156, 14), y_train shape: (156,)
X_test shape: (68, 14), y_test shape: (68,)
```

```
# Train a Decision Tree Classifier
clf = DecisionTreeClassifier(max_depth=3, random_state=42)
clf.fit(X_train, y_train)
```

```
DecisionTreeClassifier
DecisionTreeClassifier(max_depth=3, random_state=42)
```

```
from sklearn.tree import DecisionTreeClassifier, plot_tree
import matplotlib.pyplot as plt
# Visualize the Decision Tree
plt.figure(figsize=(15, 10))
plot_tree(clf, filled=True, feature_names=X.columns, class_names=['No Death', 'Death'], rounded=True)
plt.title("Decision Tree Visualization")
plt.show()
```



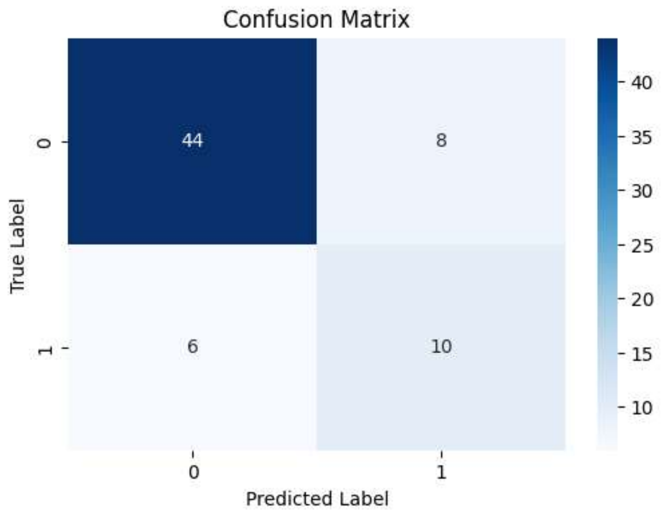
```
from sklearn.metrics import classification_report, accuracy_score
# Predict on test data
y_pred = clf.predict(X_test)

# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
print(f"Model Accuracy: {accuracy:.2f}")

# Classification report
print("\nClassification Report:")
print(classification_report(y_test, y_pred))
```

```
Model Accuracy: 0.79

Classification Report:
              precision    recall  f1-score   support

           0       0.88      0.85      0.86        52
           1       0.56      0.62      0.59        16

    accuracy                           0.79        68
   macro avg       0.72      0.74      0.73        68
weighted avg       0.80      0.79      0.80        68
```

Step 6: Model Evaluation

Confusion Matrix

```
#Confusion Matrix
from sklearn.metrics import confusion_matrix
import seaborn as sns
y_pred = clf.predict(X_test)
# Compute the confusion matrix
cm = confusion_matrix(y_test, y_pred)

# Create a heatmap to display the binary confusion matrix
plt.figure(figsize=(6, 4))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues')

# Add labels and title
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix')

# Show the plot
plt.show()
```



Accuracy Matrix

```
#Accuracy Metric
from sklearn.metrics import accuracy_score

# Calculate accuracy score
accuracy = accuracy_score(y_test, y_pred)
print(f"Model Accuracy: {accuracy:.2f}")
```

```
Model Accuracy: 0.79
```

ROC-AUC

```
#ROC-AUC
from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt
y_pred = clf.predict(X_test)
fpr, tpr, thresholds = roc_curve(y_test,y_pred)
roc_auc= auc(fpr, tpr)

plt.figure()
plt.plot(fpr, tpr, color= 'darkorange', lw=2, label='ROC curve (area= %0.2f)' %roc_auc)
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC)')
plt.legend(loc="lower right")
plt.show()
```