#### **Decision Tree Classification on Hepatitis Dataset**

```
In [1]: import pandas as pd
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import confusion_matrix, precision_score, recall_score, f1_score, refrom sklearn.metrics import classification_report
```

# **Data Loading**

### Out[2]:

	Class	AGE	SEX	STEROID	ANTIVIRALS	FATIGUE	MALAISE	ANOREXIA	LIVER BIG		SPLEEN PALPABLE	SF
0	0	30	2	1.0	2	2	2	2	1.0	2.0	2.0	
1	0	50	1	1.0	2	1	2	2	1.0	2.0	2.0	
2	0	78	1	2.0	2	1	2	2	2.0	2.0	2.0	
3	0	31	1	NaN	1	2	2	2	2.0	2.0	2.0	
4	0	34	1	2.0	2	2	2	2	2.0	2.0	2.0	

# In [3]: df.isnull().sum()

```
Out[3]: Class
                             0
        AGE
                             0
        SEX
                             0
        STEROID
                             1
        ANTIVIRALS
                             0
        FATIGUE
                             0
        MALAISE
                             0
        ANOREXIA
                             0
        LIVER BIG
                             9
                            10
        LIVER FIRM
        SPLEEN PALPABLE
                             4
        SPIDERS
                             4
        ASCITES
                             4
        VARICES
                             4
        BILIRUBIN
                             5
                            28
        ALK PHOSPHATE
        SGOT
                             3
        ALBUMIN
                            15
        PROTIME
                            66
        HISTOLOGY
                             0
        dtype: int64
```

# Check the missing values

```
In [4]: | missing_values = df.isnull().sum()
        print(missing_values)
         Class
         AGE
                              0
                              0
         SEX
        STEROID
                              1
        ANTIVIRALS
                              0
        FATIGUE
                              0
        MALAISE
                              0
        ANOREXIA
                              0
         LIVER BIG
                              9
         LIVER FIRM
                             10
         SPLEEN PALPABLE
                              4
         SPIDERS
                              4
         ASCITES
                              4
         VARICES
                              4
        BILIRUBIN
                              5
        ALK PHOSPHATE
                             28
        SGOT
                             3
                             15
         ALBUMIN
        PROTIME
                             66
        HISTOLOGY
                              0
        dtype: int64
In [5]: df.dropna(inplace = True)
         Split the dataset into features (X) and Target Variable (y)
In [6]: X = df.drop('Class', axis = 1)
        y = df['Class']
```

```
Convert the target variable to binary(1 for positive, 0 for negative)
```

```
In [7]: y = y.apply(lambda x: 1 if x == 1 else 0)
```

#### **Decision Tree Model**

# Split the dataset into training and testing sets

```
In [8]: X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42
```

#### **Build a Decision Tree classifier**

```
In [9]: clf = DecisionTreeClassifier()
```

Train the model on the training set

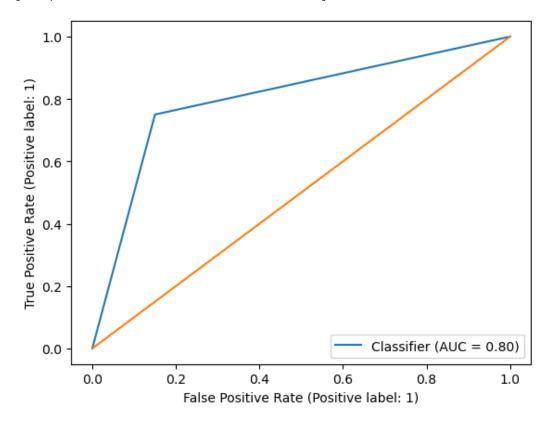
```
In [10]: clf.fit(X_train, y_train)
Out[10]:
          ▼ DecisionTreeClassifier
          DecisionTreeClassifier()
         Make predictions on the testing set
In [11]: | clf.score(X_test, y_test)
Out[11]: 0.83333333333333334
         Evaluate the model
In [12]: y_pred = clf.predict(X_test)
         Evaluate the model using various matrics
In [13]: conf_matrix = confusion_matrix(y_test, y_pred)
         prec_score = precision_score(y_test, y_pred)
         rec_score = recall_score(y_test, y_pred)
         f1 = f1_score(y_test, y_pred)
         roc_auc = roc_auc_score(y_test, y_pred)
         Print the evaluate results
In [14]: print('Confusion Matrix:\n', conf matrix)
         print('Precision Score: ', prec_score)
         print('Recall Score: ', rec_score)
         print('F1 Score: ', f1)
         print('AUC-ROC Score: ', roc_auc)
         Confusion Matrix:
          [[17 3]
          [ 1 3]]
         Precision Score: 0.5
         Recall Score: 0.75
```

#### **Classifier for AUC**

F1 Score: 0.6 AUC-ROC Score: 0.8

```
In [15]: from sklearn.metrics import RocCurveDisplay
    import matplotlib.pyplot as plt
    RocCurveDisplay.from_predictions(y_test, y_pred)
    plt.plot([0,1],[0,1])
```

Out[15]: [<matplotlib.lines.Line2D at 0x2068a6a1510>]



## **Results and Analysis**

### **Summary of Evaluation Metrics**

The model exhibits a decent performance with a Precision of 0.5, indicating a balanced prediction of positive outcomes. A Recall of 0.75 suggests that the model captures a substantial portion of the actual positive cases. The F1 Score of 0.6 signifies a reasonable balance between Precision and Recall. An AUC-ROC Score of 0.8 indicates a good ability to discriminate between positive and negative instances.

# Strengths and Weaknesses of the Decision Tree Model:

**Strengths:** Decision trees are interpretable and suitable for simple decision-making scenarios. They handle both numerical and categorical data well. Decision trees provide insights into feature importance.

**Weaknesses:** The model may be sensitive to noisy data and prone to overfitting. Decision trees might not capture complex relationships in the data as effectively as more sophisticated models. They may struggle with class imbalances.

**Recommendations:** Consider tuning hyperparameters to potentially improve model performance. Explore ensemble methods or alternative algorithms to address weaknesses. Evaluate the model's performance on different subsets of the data to ensure robustness.