In [1]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
import matplotlib.pyplot as plt
import plotly.express as px
```

In [2]:
```
url = 'https://raw.githubusercontent.com/rashakil-ds/Public-Datasets/main/hepa
```

In [3]:
```
df = pd.read_csv(url)
```

In [4]:
```
df.head()
```

Out[4]:

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

In [5]:
```
df.describe() # summary statistics of the dataset
```

Out[5]:

	Class	AGE	SEX	STEROID	ANTIVIRALS	FATIGUE	MALAISE	AN
count	154.000000	154.000000	154.000000	153.000000	154.000000	154.000000	154.000000	15
mean	0.207792	41.246753	1.103896	1.509804	1.844156	1.350649	1.603896	
std	0.407051	12.593344	0.306121	0.501546	0.363891	0.478730	0.490682	
min	0.000000	7.000000	1.000000	1.000000	1.000000	1.000000	1.000000	
25%	0.000000	32.000000	1.000000	1.000000	2.000000	1.000000	1.000000	
50%	0.000000	39.000000	1.000000	2.000000	2.000000	1.000000	2.000000	
75%	0.000000	50.000000	1.000000	2.000000	2.000000	2.000000	2.000000	
max	1.000000	78.000000	2.000000	2.000000	2.000000	2.000000	2.000000	

Data Preprocessing

1. Handle any missing values appropriately

In [6]:
```
df.isnull().sum()
```

Out[6]:
```
Class               0
AGE                 0
SEX                 0
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
ALBUMIN            15
PROTIME            66
HISTOLOGY           0
dtype: int64
```

In [7]:
```
columns_to_fill = df[['STEROID', 'LIVER BIG', 'LIVER FIRM', 'SPLEEN PALPABLE',
                      'SPIDERS', 'ASCITES', 'VARICES', 'BILIRUBIN', 'ALK PHOSP
                      'SGOT','ALBUMIN', 'PROTIME']]
#print(columns_to_fill)

# Fill null values with the mean of each respective column
for column in columns_to_fill:
    column_mean = df[column].mean()
    df[column].fillna(column_mean, inplace=True)
```

In [8]:
```
df.isnull().sum()
```

Out[8]:
```
Class              0
AGE                0
SEX                0
STEROID            0
ANTIVIRALS         0
FATIGUE            0
MALAISE            0
ANOREXIA           0
LIVER BIG          0
LIVER FIRM         0
SPLEEN PALPABLE    0
SPIDERS            0
ASCITES            0
VARICES            0
BILIRUBIN          0
ALK PHOSPHATE      0
SGOT               0
ALBUMIN            0
PROTIME            0
HISTOLOGY          0
dtype: int64
```

In [9]:
```
df.head()
```

Out[9]:

	Class	AGE	SEX	STEROID	ANTIVIRALS	FATIGUE	MALAISE	ANOREXIA	LIVER BIG	LIVER FIRM	P
0	0	30	2	1.000000	2	2	2	2	1.0	2.0	
1	0	50	1	1.000000	2	1	2	2	1.0	2.0	
2	0	78	1	2.000000	2	1	2	2	2.0	2.0	
3	0	31	1	1.509804	1	2	2	2	2.0	2.0	
4	0	34	1	2.000000	2	2	2	2	2.0	2.0	

Scaling

Normalization

In [10]:
```
from sklearn.preprocessing import MinMaxScaler
```

In [11]:
```
scaler = MinMaxScaler()
```

In [12]:
```
columns_to_normalize = df.columns[1:]
```

In [13]:
```
df[columns_to_normalize] = scaler.fit_transform(df[columns_to_normalize])
```

In [14]:
```
df.head()
```

Out[14]:

	Class	AGE	SEX	STEROID	ANTIVIRALS	FATIGUE	MALAISE	ANOREXIA	LIVER BIG	LIVER FIRM
0	0	0.323944	1.0	0.000000	1.0	1.0	1.0	1.0	0.0	1.0
1	0	0.605634	0.0	0.000000	1.0	0.0	1.0	1.0	0.0	1.0
2	0	1.000000	0.0	1.000000	1.0	0.0	1.0	1.0	1.0	1.0
3	0	0.338028	0.0	0.509804	0.0	1.0	1.0	1.0	1.0	1.0
4	0	0.380282	0.0	1.000000	1.0	1.0	1.0	1.0	1.0	1.0

2. Split the dataset

In [15]:
```
x = df.drop('Class', axis = 1)
y = df[['Class']]
```

In [16]:
```
x.head()
```

Out[16]:

	AGE	SEX	STEROID	ANTIVIRALS	FATIGUE	MALAISE	ANOREXIA	LIVER BIG	LIVER FIRM	SP PALP
0	0.323944	1.0	0.000000	1.0	1.0	1.0	1.0	0.0	1.0	
1	0.605634	0.0	0.000000	1.0	0.0	1.0	1.0	0.0	1.0	
2	1.000000	0.0	1.000000	1.0	0.0	1.0	1.0	1.0	1.0	
3	0.338028	0.0	0.509804	0.0	1.0	1.0	1.0	1.0	1.0	
4	0.380282	0.0	1.000000	1.0	1.0	1.0	1.0	1.0	1.0	

In [17]:
```
x.shape
```

Out[17]:
```
(154, 19)
```

In [18]:
```
y.head()
```

Out[18]:

	Class
0	0
1	0
2	0
3	0
4	0

In [19]:
```
y.shape
```

Out[19]: (154, 1)

Decision Tree Model

1. Split the dataset into training (70%) and testing sets

In [20]:
```
from sklearn.model_selection import train_test_split
```

In [21]:
```
x_train, x_test, y_train, y_test = train_test_split(x, y, train_size = .70)
```

In [22]:
```
x_train.shape
```

Out[22]: (107, 19)

In [23]:
```
x_test.shape
```

Out[23]: (47, 19)

In [24]:
```
y_test.shape
```

Out[24]: (47, 1)

In [25]:
```
y_train.shape
```

Out[25]: (107, 1)

In [26]:
```
x_train.head()
```

Out[26]:

	AGE	SEX	STEROID	ANTIVIRALS	FATIGUE	MALAISE	ANOREXIA	LIVER BIG	LIVER FIRM	PA
43	0.690141	0.0	0.0	1.0	0.0	1.0	1.0	1.0	1.0	
116	0.605634	0.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
50	0.450704	0.0	0.0	1.0	1.0	1.0	1.0	1.0	1.0	
27	0.718310	1.0	1.0	1.0	0.0	1.0	1.0	1.0	0.0	
82	0.845070	1.0	0.0	1.0	0.0	0.0	1.0	1.0	1.0	

In [27]:
```
x_test.head()
```

Out[27]:

	AGE	SEX	STEROID	ANTIVIRALS	FATIGUE	MALAISE	ANOREXIA	LIVER BIG	LIVER FIRM
17	0.464789	0.0	0.0	1.0	0.0	1.0	1.0	1.000000	0.000000
137	0.563380	0.0	1.0	1.0	0.0	0.0	1.0	1.000000	0.000000
12	0.478873	0.0	1.0	0.0	0.0	1.0	1.0	1.000000	0.000000
36	0.225352	0.0	1.0	1.0	0.0	0.0	0.0	1.000000	1.000000
140	0.661972	0.0	0.0	1.0	0.0	0.0	1.0	0.827586	0.583333

2.Building a Decision Tree classifier

In [28]:
```
from sklearn.tree import DecisionTreeClassifier
```

In [29]:
```
dt = DecisionTreeClassifier()
```

3. Train the model

In [30]:
```
dt.fit(x_train, y_train)
```

Out[30]:

DecisionTreeClassifier

DecisionTreeClassifier()

In [31]:
```
pred_tain = dt.predict(x_train) # training result
pred_tain
```

Out[31]:
```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0,
       0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0,
       0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1,
       0, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1],
      dtype=int64)
```

In [32]:
```
y_train.head()
```

Out[32]:

	Class
43	0
116	0
50	0
27	0
82	0

In [33]:
```
y_train['Predicted_tain_value'] = dt.predict(x_train)
```

In [34]:
```
y_train.head()
```

Out[34]:

	Class	Predicted_tain_value
43	0	0
116	0	0
50	0	0
27	0	0
82	0	0

In [35]:
```
y_train.drop('Predicted_tain_value', axis = 1, inplace = True)
```

In [36]:
```
y_train.head()
```

Out[36]:

	Class
43	0
116	0
50	0
27	0
82	0

In [37]:
```
dt.score(x_train, y_train)
```

Out[37]:
```
1.0
```

Model Evaluation

1. Make predictions on the testing set

In [38]:
```
pred_test = dt.predict(x_test)
pred_test
```

Out[38]:
```
array([0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 0, 0,
       0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1,
       0, 1, 0], dtype=int64)
```

In [39]:
```
y_test.head()
```

Out[39]:

	Class
17	0
137	1
12	0
36	0
140	1

In [40]:
```
y_test['predicted_test_value'] = dt.predict(x_test)
```

In [41]:
```
y_test.head()
```

Out[41]:

	Class	predicted_test_value
17	0	0
137	1	0
12	0	0
36	0	0
140	1	1

In [42]:
```
y_test.drop('predicted_test_value', axis = 1, inplace = True)
```

In [43]:
```
y_test.head()
```

Out[43]:

	Class
17	0
137	1
12	0
36	0
140	1

In [44]:
```
dt.score(x_test, y_test)
```

Out[44]:
```
0.8297872340425532
```

2. Confusion Matrix

In [45]:
```
from sklearn.metrics import classification_report, accuracy_score, precision_s
```

In [46]:
```
accuracy_score(y_test, pred_test) # actual y and predicted y
```

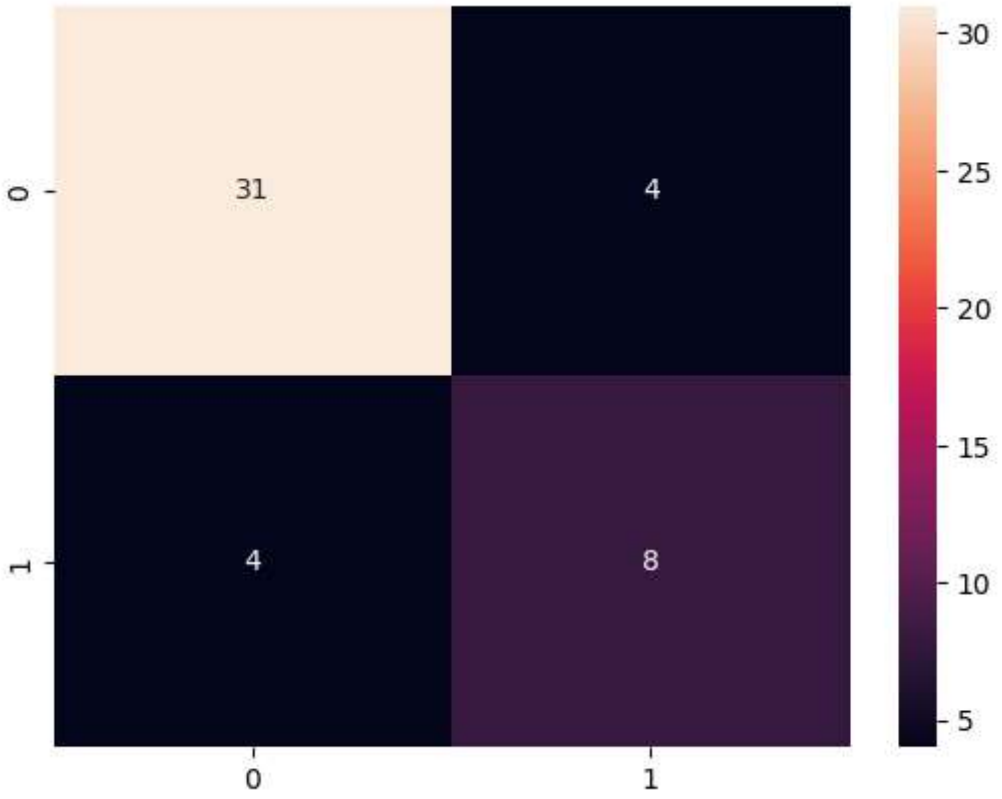
Out[46]:
```
0.8297872340425532
```

In [47]:
```
cm = confusion_matrix (y_test, pred_test)
cm
```

Out[47]:
```
array([[31,  4],
       [ 4,  8]], dtype=int64)
```

In [48]:
```
sns.heatmap(cm, annot=True)
```

Out[48]: <Axes: >



3. Precision

In [49]:
```
precision_score(y_test, pred_test)
```

Out[49]: 0.6666666666666666

4. Recall

In [50]:
```
recall_score (y_test, pred_test)
```

Out[50]: 0.6666666666666666

5. f1_score

In [51]:
```
f1_score (y_test, pred_test)
```

Out[51]: 0.6666666666666666

6. AUC_ROC

In [52]:
```
auc_roc = roc_auc_score(y_test, pred_test)
```

In [53]:
```
auc_roc
```

Out[53]:
```
0.7761904761904761
```

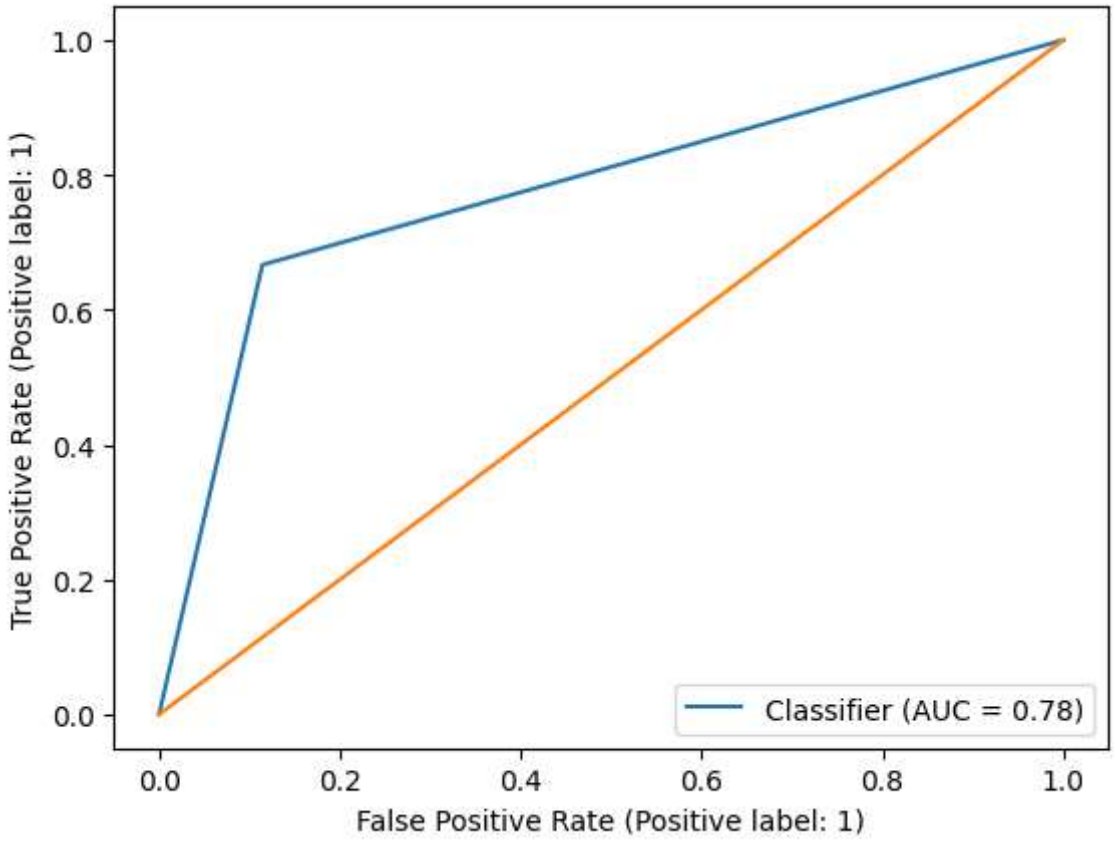
In [54]:
```
print(classification_report(y_test, pred_test))
```

```
              precision    recall  f1-score   support

           0       0.89      0.89      0.89        35
           1       0.67      0.67      0.67        12

    accuracy                           0.83        47
   macro avg       0.78      0.78      0.78        47
weighted avg       0.83      0.83      0.83        47
```

In [55]:
```
RocCurveDisplay.from_predictions(y_test, pred_test)
plt.plot([0,1], [0,1])
plt.show()
```



Results and Analysis

1. Summarize the results obtained from the evaluation metrics.

Confusion Matrix:

True Positive (TP): 31 whic is correctly identified. True Negative (TN): 8 whic is also correctly identified. False Positive (FP): 4 didn't get the expected answer and the answer is wrong. False Negative (FN): 4 which is predicted false answer.

Precision (Positive Predictive Value): Precision is the ratio of correctly predicted positive observations to the total predicted positives. Using this (TP / (TP + FP)) we can get Precision score.

Recall (Sensitivity or True Positive Rate): Recall is the ratio of correctly predicted positive observations to the all observations in the actual class and the formula for Recall is = (TP / (TP + FN)).

F1 Score: The F1 score is the weighted average of precision and recall, where 1 is the best and 0 is the worst. It is calculated = 2 * (Precision * Recall) / (Precision + Recall).

AUC-ROC Score:

The AUC-ROC score represents the area under the Receiver Operating Characteristic (ROC) curve. It measures the ability of the model to distinguish between positive and negative cases.

2. Discuss the strengths and weaknesses of the Decision Tree model for this dataset.

Strengths of the Decision Tree Model

Decision Trees are interpretable and easy to understand, making them useful for providing insights into the factors influencing the predictions.Decision Trees can handle both numerical and categorical data without the need for extensive data preprocessing.They are non-parametric and can capture complex relationships in the data. Decision tree helps us for training and testing the dataset and also predict th values. To get good accuracy decission tree works quite fine.

Weaknesses of the Decision Tree Model:

Prone to Overfitting: Decision Trees may overfit the training data, capturing noise in the dataset and resulting in poor generalization to new data.

Instability: Small changes in the data can lead to different tree structures, impacting the model's stability.

Limited Expressiveness: A single decision tree may not capture highly complex relationships in the data compared to more advanced models.