Objective: The objective of this assignment is to perform binary classification on the hepatitis dataset using a Decision Tree classifier. Students will be required to read the dataset from a GitHub repository, build a Decision Tree model, and evaluate its performance using various metrics

```
import pandas as pd
import matplotlib.pyplot as plt
from sklearn import tree
import warnings
warnings.filterwarnings('ignore')
import seaborn as sns
import numpy as np
import plotly.express as px
```

1.Data Loading

```
url=
"https://raw.githubusercontent.com/rashakil-ds/Public-Datasets/main/
hepatitis.csv"
df = pd.read_csv(url)
df.head()
```

```
   Class  AGE  SEX  STEROID  ANTIVIRALS  FATIGUE  MALAISE  ANOREXIA  \
0      0   30    2      1.0           2        2        2         2
1      0   50    1      1.0           2        1        2         2
2      0   78    1      2.0           2        1        2         2
3      0   31    1      NaN           1        2        2         2
4      0   34    1      2.0           2        2        2         2

   LIVER BIG  LIVER FIRM  SPLEEN PALPABLE  SPIDERS  ASCITES
VARICES  \
0        1.0         2.0              2.0      2.0      2.0      2.0

1        1.0         2.0              2.0      2.0      2.0      2.0

2        2.0         2.0              2.0      2.0      2.0      2.0

3        2.0         2.0              2.0      2.0      2.0      2.0

4        2.0         2.0              2.0      2.0      2.0      2.0


   BILIRUBIN  ALK PHOSPHATE   SGOT  ALBUMIN  PROTIME  HISTOLOGY
0        1.0           85.0   18.0      4.0      NaN          1
1        0.9          135.0   42.0      3.5      NaN          1
2        0.7           96.0   32.0      4.0      NaN          1
3        0.7           46.0   52.0      4.0     80.0          1
4        1.0            NaN  200.0      4.0      NaN          1
```

```
df.describe().T

                 count        mean        std   min    25%   50%
75%  \
Class            154.0    0.207792   0.407051   0.0   0.00   0.0
0.00
AGE              154.0   41.246753  12.593344   7.0  32.00  39.0
50.00
SEX              154.0    1.103896   0.306121   1.0   1.00   1.0
1.00
STEROID          153.0    1.509804   0.501546   1.0   1.00   2.0
2.00
ANTIVIRALS       154.0    1.844156   0.363891   1.0   2.00   2.0
2.00
FATIGUE          154.0    1.350649   0.478730   1.0   1.00   1.0
2.00
MALAISE          154.0    1.603896   0.490682   1.0   1.00   2.0
2.00
ANOREXIA         154.0    1.792208   0.407051   1.0   2.00   2.0
2.00
LIVER BIG        145.0    1.827586   0.379049   1.0   2.00   2.0
2.00
LIVER FIRM       144.0    1.583333   0.494727   1.0   1.00   2.0
2.00
SPLEEN PALPABLE  150.0    1.800000   0.401340   1.0   2.00   2.0
2.00
SPIDERS          150.0    1.660000   0.475296   1.0   1.00   2.0
2.00
ASCITES          150.0    1.866667   0.341073   1.0   2.00   2.0
2.00
VARICES          150.0    1.880000   0.326050   1.0   2.00   2.0
2.00
BILIRUBIN        149.0    1.427517   1.212149   0.3   0.70   1.0
1.50
ALK PHOSPHATE    126.0  105.325397  51.508109  26.0  74.25  85.0
132.25
SGOT             151.0   85.894040  89.650890  14.0  31.50  58.0
100.50
ALBUMIN          139.0    3.817266   0.651523   2.1   3.40   4.0
4.20
PROTIME           88.0   61.852273  22.875244   0.0  46.00  61.0
76.25
HISTOLOGY        154.0    1.454545   0.499554   1.0   1.00   1.0
2.00

                   max
Class              1.0
AGE               78.0
SEX                2.0
STEROID            2.0
```

```
ANTIVIRALS           2.0
FATIGUE              2.0
MALAISE              2.0
ANOREXIA             2.0
LIVER BIG            2.0
LIVER FIRM           2.0
SPLEEN PALPABLE      2.0
SPIDERS              2.0
ASCITES              2.0
VARICES              2.0
BILIRUBIN            8.0
ALK PHOSPHATE      295.0
SGOT               648.0
ALBUMIN              6.4
PROTIME            100.0
HISTOLOGY            2.0
```

2.Data Preprocessing

```
#shape
df.shape
```

```
(154, 20)
```

```
df.info() #information
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 154 entries, 0 to 153
Data columns (total 20 columns):
 #   Column           Non-Null Count  Dtype  
---  ------           --------------  -----  
 0   Class            154 non-null    int64  
 1   AGE              154 non-null    int64  
 2   SEX              154 non-null    int64  
 3   STEROID          153 non-null    float64
 4   ANTIVIRALS       154 non-null    int64  
 5   FATIGUE          154 non-null    int64  
 6   MALAISE          154 non-null    int64  
 7   ANOREXIA         154 non-null    int64  
 8   LIVER BIG        145 non-null    float64
 9   LIVER FIRM       144 non-null    float64
 10  SPLEEN PALPABLE  150 non-null    float64
 11  SPIDERS          150 non-null    float64
 12  ASCITES          150 non-null    float64
 13  VARICES          150 non-null    float64
 14  BILIRUBIN        149 non-null    float64
 15  ALK PHOSPHATE    126 non-null    float64
 16  SGOT             151 non-null    float64
 17  ALBUMIN          139 non-null    float64
 18  PROTIME          88 non-null     float64
 19  HISTOLOGY        154 non-null    int64
dtypes: float64(12), int64(8)
memory usage: 24.2 KB
```

```
df.isnull().sum() #finding missing values
```

```
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
```

```
df.isnull().sum()/ df.shape[0]*100 #percentage of missing values
```

```
Class               0.000000
AGE                 0.000000
SEX                 0.000000
STEROID             0.649351
ANTIVIRALS          0.000000
FATIGUE             0.000000
MALAISE             0.000000
ANOREXIA            0.000000
LIVER BIG           5.844156
LIVER FIRM          6.493506
SPLEEN PALPABLE     2.597403
SPIDERS             2.597403
ASCITES             2.597403
VARICES             2.597403
BILIRUBIN           3.246753
ALK PHOSPHATE      18.181818
SGOT                1.948052
ALBUMIN             9.740260
```

```
PROTIME              42.857143
HISTOLOGY             0.000000
dtype: float64

#handling the missing value
df = df.drop('PROTIME', axis=1)
df

     Class  AGE  SEX  STEROID  ANTIVIRALS  FATIGUE  MALAISE  ANOREXIA  
\
0        0   30    2      1.0           2        2        2         2

1        0   50    1      1.0           2        1        2         2

2        0   78    1      2.0           2        1        2         2

3        0   31    1      NaN           1        2        2         2

4        0   34    1      2.0           2        2        2         2

..     ...  ...  ...      ...         ...      ...      ...       ...

149      1   46    1      2.0           2        1        1         1

150      0   44    1      2.0           2        1        2         2

151      0   61    1      1.0           2        1        1         2

152      0   53    2      1.0           2        1        2         2

153      1   43    1      2.0           2        1        2         2


     LIVER BIG  LIVER FIRM  SPLEEN PALPABLE  SPIDERS  ASCITES  VARICES  
\
0          1.0         2.0              2.0      2.0      2.0      2.0

1          1.0         2.0              2.0      2.0      2.0      2.0

2          2.0         2.0              2.0      2.0      2.0      2.0

3          2.0         2.0              2.0      2.0      2.0      2.0

4          2.0         2.0              2.0      2.0      2.0      2.0

..         ...         ...              ...      ...      ...      ...

149        2.0         2.0              2.0      1.0      1.0      1.0

150        2.0         1.0              2.0      2.0      2.0      2.0

151        1.0         1.0              2.0      1.0      2.0      2.0
```

```
152       2.0       2.0             1.0      1.0      2.0      1.0

153       2.0       2.0             1.0      1.0      1.0      2.0


     BILIRUBIN  ALK PHOSPHATE   SGOT  ALBUMIN  HISTOLOGY
0          1.0           85.0   18.0      4.0          1
1          0.9          135.0   42.0      3.5          1
2          0.7           96.0   32.0      4.0          1
3          0.7           46.0   52.0      4.0          1
4          1.0            NaN  200.0      4.0          1
..         ...            ...    ...      ...        ...
149        7.6            NaN  242.0      3.3          2
150        0.9          126.0  142.0      4.3          2
151        0.8           75.0   20.0      4.1          2
152        1.5           81.0   19.0      4.1          2
153        1.2          100.0   19.0      3.1          2

[154 rows x 19 columns]
```

```python
from sklearn.impute import KNNImputer
impute= KNNImputer()
for i in df.columns:
    df[i]= impute.fit_transform(df[[i]])
df
```

```
     Class   AGE  SEX   STEROID  ANTIVIRALS  FATIGUE  MALAISE
ANOREXIA  \
0      0.0  30.0  2.0  1.000000         2.0      2.0      2.0
2.0
1      0.0  50.0  1.0  1.000000         2.0      1.0      2.0
2.0
2      0.0  78.0  1.0  2.000000         2.0      1.0      2.0
2.0
3      0.0  31.0  1.0  1.509804         1.0      2.0      2.0
2.0
4      0.0  34.0  1.0  2.000000         2.0      2.0      2.0
2.0
..     ...   ...  ...       ...         ...      ...      ...       ..
.
149    1.0  46.0  1.0  2.000000         2.0      1.0      1.0
1.0
150    0.0  44.0  1.0  2.000000         2.0      1.0      2.0
2.0
151    0.0  61.0  1.0  1.000000         2.0      1.0      1.0
2.0
152    0.0  53.0  2.0  1.000000         2.0      1.0      2.0
2.0
153    1.0  43.0  1.0  2.000000         2.0      1.0      2.0
```

```
2.0

     LIVER BIG  LIVER FIRM  SPLEEN PALPABLE  SPIDERS  ASCITES  VARICES  \
0          1.0         2.0              2.0      2.0      2.0      2.0

1          1.0         2.0              2.0      2.0      2.0      2.0

2          2.0         2.0              2.0      2.0      2.0      2.0

3          2.0         2.0              2.0      2.0      2.0      2.0

4          2.0         2.0              2.0      2.0      2.0      2.0

..         ...         ...              ...      ...      ...      ...

149        2.0         2.0              2.0      1.0      1.0      1.0

150        2.0         1.0              2.0      2.0      2.0      2.0

151        1.0         1.0              2.0      1.0      2.0      2.0

152        2.0         2.0              1.0      1.0      2.0      1.0

153        2.0         2.0              1.0      1.0      1.0      2.0


     BILIRUBIN  ALK PHOSPHATE   SGOT  ALBUMIN  HISTOLOGY
0          1.0      85.000000   18.0      4.0        1.0
1          0.9     135.000000   42.0      3.5        1.0
2          0.7      96.000000   32.0      4.0        1.0
3          0.7      46.000000   52.0      4.0        1.0
4          1.0     105.325397  200.0      4.0        1.0
..         ...            ...    ...      ...        ...
149        7.6     105.325397  242.0      3.3        2.0
150        0.9     126.000000  142.0      4.3        2.0
151        0.8      75.000000   20.0      4.1        2.0
152        1.5      81.000000   19.0      4.1        2.0
153        1.2     100.000000   19.0      3.1        2.0

[154 rows x 19 columns]
```

```
df.duplicated().sum() #finding duplicates
```

```
0
```

```
df.isnull().sum()
```

```
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
HISTOLOGY          0
dtype: int64
```

```
df.nunique()
```

```
Class               2
AGE                49
SEX                 2
STEROID             3
ANTIVIRALS          2
FATIGUE             2
MALAISE             2
ANOREXIA            2
LIVER BIG           3
LIVER FIRM          3
SPLEEN PALPABLE     3
SPIDERS             3
ASCITES             3
VARICES             3
BILIRUBIN          35
ALK PHOSPHATE      84
SGOT               85
ALBUMIN            30
HISTOLOGY           2
dtype: int64
```

scaling

```
from sklearn.preprocessing import MinMaxScaler
scale = MinMaxScaler()
for j in df.columns:
    if df[j].nunique() > 1:
        df[j] = scale.fit_transform(df[[j]])

df
```

```
     Class       AGE  SEX   STEROID  ANTIVIRALS  FATIGUE  MALAISE
ANOREXIA  \
0      0.0  0.323944  1.0  0.000000         1.0      1.0      1.0
1.0
1      0.0  0.605634  0.0  0.000000         1.0      0.0      1.0
1.0
2      0.0  1.000000  0.0  1.000000         1.0      0.0      1.0
1.0
3      0.0  0.338028  0.0  0.509804         0.0      1.0      1.0
1.0
4      0.0  0.380282  0.0  1.000000         1.0      1.0      1.0
1.0
..     ...       ...  ...       ...         ...      ...      ...
...
149    1.0  0.549296  0.0  1.000000         1.0      0.0      0.0
0.0
150    0.0  0.521127  0.0  1.000000         1.0      0.0      1.0
1.0
151    0.0  0.760563  0.0  0.000000         1.0      0.0      0.0
1.0
152    0.0  0.647887  1.0  0.000000         1.0      0.0      1.0
1.0
153    1.0  0.507042  0.0  1.000000         1.0      0.0      1.0
1.0

     LIVER BIG  LIVER FIRM  SPLEEN PALPABLE  SPIDERS  ASCITES  VARICES
\
0          0.0         1.0              1.0      1.0      1.0      1.0

1          0.0         1.0              1.0      1.0      1.0      1.0

2          1.0         1.0              1.0      1.0      1.0      1.0

3          1.0         1.0              1.0      1.0      1.0      1.0

4          1.0         1.0              1.0      1.0      1.0      1.0

..         ...         ...              ...      ...      ...      ...

149        1.0         1.0              1.0      0.0      0.0      0.0

150        1.0         0.0              1.0      1.0      1.0      1.0

151        0.0         0.0              1.0      0.0      1.0      1.0

152        1.0         1.0              0.0      0.0      1.0      0.0

153        1.0         1.0              0.0      0.0      0.0      1.0


     BILIRUBIN  ALK PHOSPHATE      SGOT   ALBUMIN  HISTOLOGY
```

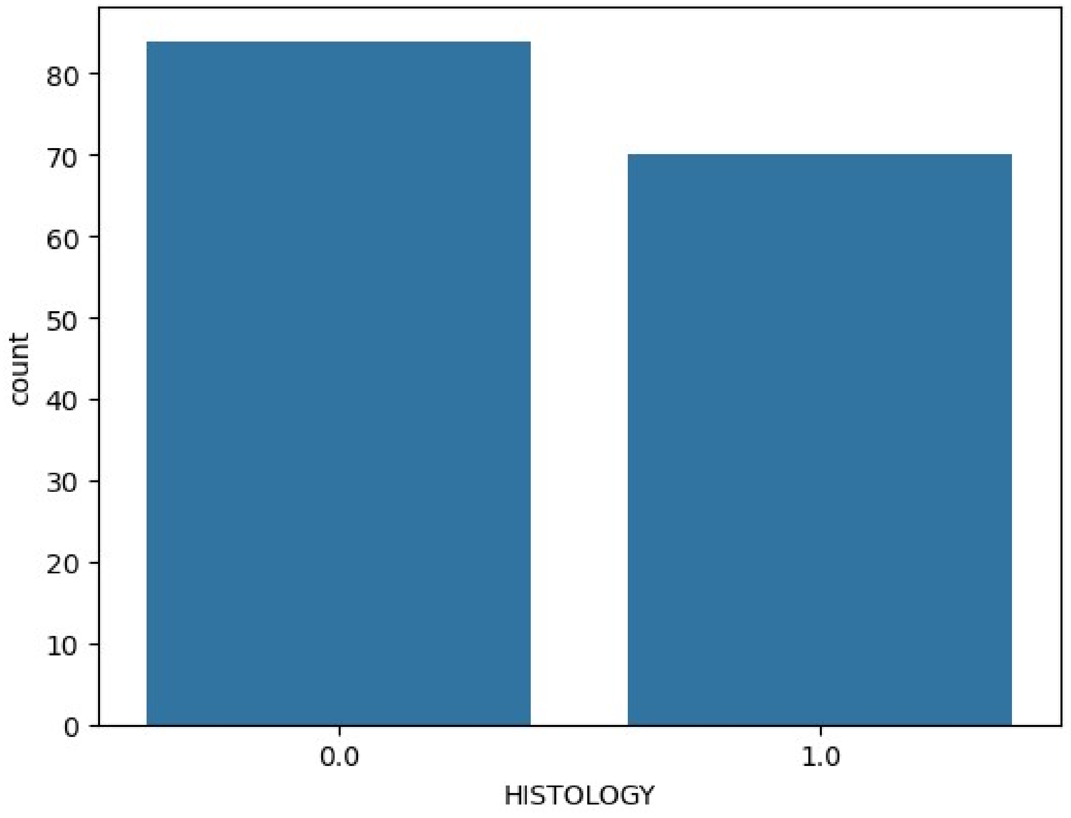
```
0     0.090909       0.219331  0.006309  0.441860        0.0
1     0.077922       0.405204  0.044164  0.325581        0.0
2     0.051948       0.260223  0.028391  0.441860        0.0
3     0.051948       0.074349  0.059937  0.441860        0.0
4     0.090909       0.294890  0.293375  0.441860        0.0
..         ...            ...       ...       ...        ...
149   0.948052       0.294890  0.359621  0.279070        1.0
150   0.077922       0.371747  0.201893  0.511628        1.0
151   0.064935       0.182156  0.009464  0.465116        1.0
152   0.155844       0.204461  0.007886  0.465116        1.0
153   0.116883       0.275093  0.007886  0.232558        1.0

[154 rows x 19 columns]
```

```
df.HISTOLOGY.value_counts()
```

```
0.0    84
1.0    70
Name: HISTOLOGY, dtype: int64
```

```
sns.countplot(x='HISTOLOGY', data=df)
```

```
<AxesSubplot:xlabel='HISTOLOGY', ylabel='count'>
```

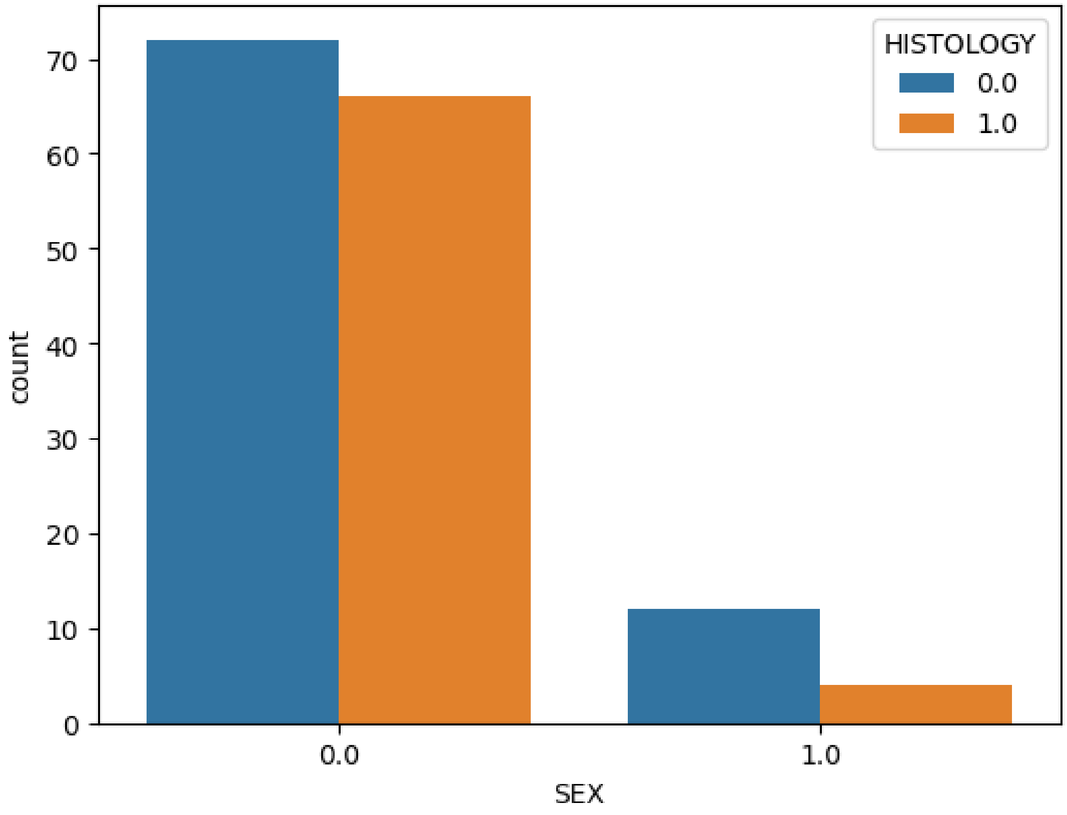


```
df.SEX.value_counts()
```

```
0.0    138
1.0     16
Name: SEX, dtype: int64
```

```
sns.countplot(x = 'SEX', data=df, hue='HISTOLOGY')
```

```
<AxesSubplot:xlabel='SEX', ylabel='count'>
```



```
#data spliting
x = df.drop(["HISTOLOGY"],axis = 1)
y = df["HISTOLOGY"]

x
```

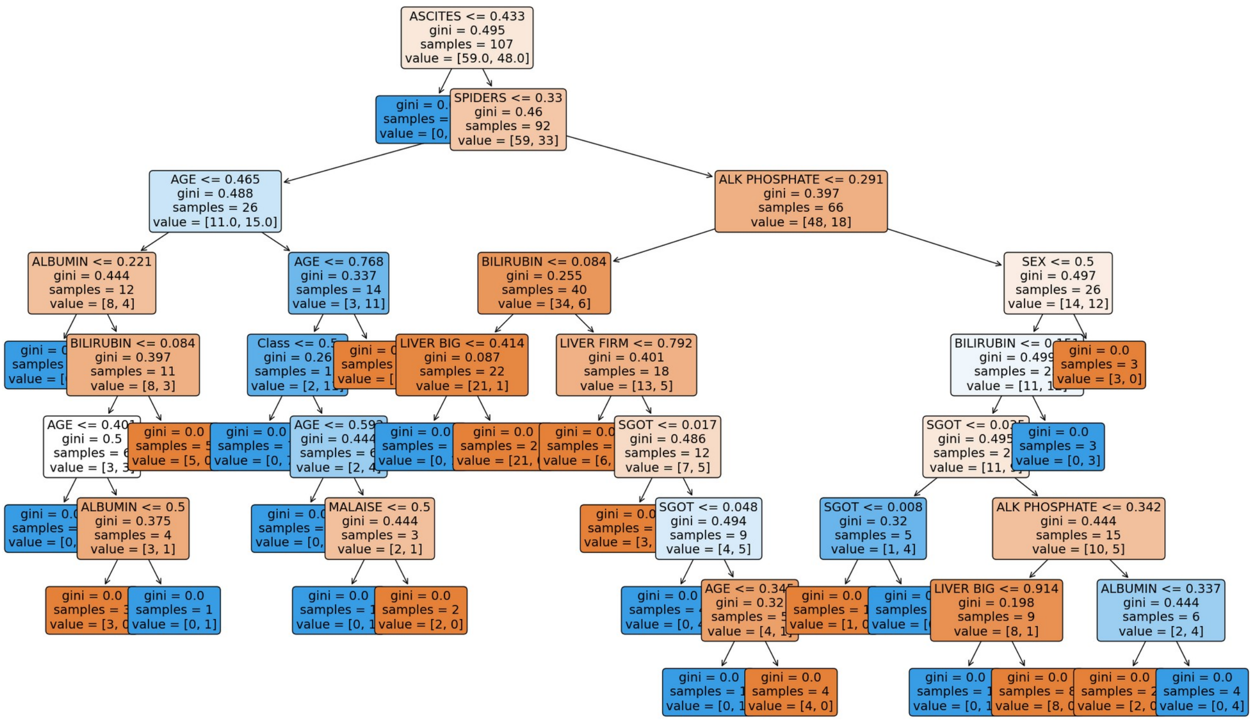
```
     Class       AGE  SEX   STEROID  ANTIVIRALS  FATIGUE  MALAISE
ANOREXIA  \
0      0.0  0.323944  1.0  0.000000         1.0      1.0      1.0
1.0
1      0.0  0.605634  0.0  0.000000         1.0      0.0      1.0
1.0
2      0.0  1.000000  0.0  1.000000         1.0      0.0      1.0
1.0
3      0.0  0.338028  0.0  0.509804         0.0      1.0      1.0
```

```
1.0
4      0.0  0.380282  0.0  1.000000         1.0      1.0      1.0
1.0
..     ...       ...  ...       ...         ...      ...      ...
...
149    1.0  0.549296  0.0  1.000000         1.0      0.0      0.0
0.0
150    0.0  0.521127  0.0  1.000000         1.0      0.0      1.0
1.0
151    0.0  0.760563  0.0  0.000000         1.0      0.0      0.0
1.0
152    0.0  0.647887  1.0  0.000000         1.0      0.0      1.0
1.0
153    1.0  0.507042  0.0  1.000000         1.0      0.0      1.0
1.0

     LIVER BIG  LIVER FIRM  SPLEEN PALPABLE  SPIDERS  ASCITES  VARICES
\
0          0.0         1.0              1.0      1.0      1.0      1.0

1          0.0         1.0              1.0      1.0      1.0      1.0

2          1.0         1.0              1.0      1.0      1.0      1.0

3          1.0         1.0              1.0      1.0      1.0      1.0

4          1.0         1.0              1.0      1.0      1.0      1.0

..         ...         ...              ...      ...      ...      ...

149        1.0         1.0              1.0      0.0      0.0      0.0

150        1.0         0.0              1.0      1.0      1.0      1.0

151        0.0         0.0              1.0      0.0      1.0      1.0

152        1.0         1.0              0.0      0.0      1.0      0.0

153        1.0         1.0              0.0      0.0      0.0      1.0


     BILIRUBIN  ALK PHOSPHATE      SGOT   ALBUMIN
0     0.090909       0.219331  0.006309  0.441860
1     0.077922       0.405204  0.044164  0.325581
2     0.051948       0.260223  0.028391  0.441860
3     0.051948       0.074349  0.059937  0.441860
4     0.090909       0.294890  0.293375  0.441860
..         ...            ...       ...       ...
149   0.948052       0.294890  0.359621  0.279070
150   0.077922       0.371747  0.201893  0.511628
```

```
151   0.064935       0.182156  0.009464  0.465116
152   0.155844       0.204461  0.007886  0.465116
153   0.116883       0.275093  0.007886  0.232558

[154 rows x 18 columns]

y

0      0.0
1      0.0
2      0.0
3      0.0
4      0.0
      ...
149    1.0
150    1.0
151    1.0
152    1.0
153    1.0
Name: HISTOLOGY, Length: 154, dtype: float64

from sklearn.model_selection import train_test_split
xtrain, xtest, ytrain, ytest = train_test_split(x,y, random_state=42,
train_size=.70)
xtrain.shape

(107, 18)
```

3.decision Tree Model

```
from sklearn.tree import DecisionTreeClassifier
dcls = DecisionTreeClassifier()
dcls.fit(xtrain, ytrain)

DecisionTreeClassifier()

plt.figure(figsize=(25,15))
tree.plot_tree(dcls, feature_names=x.columns, rounded=True,
filled=True, fontsize = 14)

[Text(0.37083333333333335, 0.9444444444444444, 'ASCITES <= 0.433\ngini
= 0.495\nsamples = 107\nvalue = [59.0, 48.0]'),
 Text(0.3375, 0.8333333333333334, 'gini = 0.0\nsamples = 15\nvalue =
[0, 15]'),
 Text(0.4041666666666667, 0.8333333333333334, 'SPIDERS <= 0.33\ngini =
0.46\nsamples = 92\nvalue = [59, 33]'),
 Text(0.16666666666666666, 0.7222222222222222, 'AGE <= 0.465\ngini =
0.488\nsamples = 26\nvalue = [11.0, 15.0]'),
 Text(0.06666666666666667, 0.6111111111111112, 'ALBUMIN <= 0.221\ngini
= 0.444\nsamples = 12\nvalue = [8, 4]'),
 Text(0.03333333333333333, 0.5, 'gini = 0.0\nsamples = 1\nvalue = [0,
1]'),
 Text(0.1, 0.5, 'BILIRUBIN <= 0.084\ngini = 0.397\nsamples = 11\nvalue
= [8, 3]'),
 Text(0.06666666666666667, 0.3888888888888889, 'AGE <= 0.401\ngini =
0.5\nsamples = 6\nvalue = [3, 3]'),
 Text(0.03333333333333333, 0.2777777777777778, 'gini = 0.0\nsamples =
2\nvalue = [0, 2]'),
 Text(0.1, 0.2777777777777778, 'ALBUMIN <= 0.5\ngini = 0.375\nsamples
= 4\nvalue = [3, 1]'),
 Text(0.06666666666666667, 0.16666666666666666, 'gini = 0.0\nsamples =
3\nvalue = [3, 0]'),
 Text(0.13333333333333333, 0.16666666666666666, 'gini = 0.0\nsamples =
1\nvalue = [0, 1]'),
 Text(0.13333333333333333, 0.3888888888888889, 'gini = 0.0\nsamples =
5\nvalue = [5, 0]'),
 Text(0.26666666666666666, 0.6111111111111112, 'AGE <= 0.768\ngini =
0.337\nsamples = 14\nvalue = [3, 11]'),
 Text(0.23333333333333334, 0.5, 'Class <= 0.5\ngini = 0.26\nsamples =
13\nvalue = [2, 11]'),
 Text(0.2, 0.3888888888888889, 'gini = 0.0\nsamples = 7\nvalue = [0,
7]'),
 Text(0.26666666666666666, 0.3888888888888889, 'AGE <= 0.592\ngini =
0.444\nsamples = 6\nvalue = [2, 4]'),
 Text(0.23333333333333334, 0.2777777777777778, 'gini = 0.0\nsamples =
3\nvalue = [0, 3]'),
 Text(0.3, 0.2777777777777778, 'MALAISE <= 0.5\ngini = 0.444\nsamples
= 3\nvalue = [2, 1]'),
 Text(0.26666666666666666, 0.16666666666666666, 'gini = 0.0\nsamples =
1\nvalue = [0, 1]'),
 Text(0.3333333333333333, 0.16666666666666666, 'gini = 0.0\nsamples =
2\nvalue = [2, 0]'),
 Text(0.3, 0.5, 'gini = 0.0\nsamples = 1\nvalue = [1, 0]'),
 Text(0.6416666666666667, 0.7222222222222222, 'ALK PHOSPHATE <= 0.291\
ngini = 0.397\nsamples = 66\nvalue = [48, 18]'),
 Text(0.43333333333333335, 0.6111111111111112, 'BILIRUBIN <= 0.084\
ngini = 0.255\nsamples = 40\nvalue = [34, 6]'),
 Text(0.36666666666666664, 0.5, 'LIVER BIG <= 0.414\ngini = 0.087\
nsamples = 22\nvalue = [21, 1]'),
 Text(0.3333333333333333, 0.3888888888888889, 'gini = 0.0\nsamples =
1\nvalue = [0, 1]'),
 Text(0.4, 0.3888888888888889, 'gini = 0.0\nsamples = 21\nvalue = [21,
0]'),
 Text(0.5, 0.5, 'LIVER FIRM <= 0.792\ngini = 0.401\nsamples = 18\
nvalue = [13, 5]'),
 Text(0.4666666666666667, 0.3888888888888889, 'gini = 0.0\nsamples =
6\nvalue = [6, 0]'),
 Text(0.5333333333333333, 0.3888888888888889, 'SGOT <= 0.017\ngini =
0.486\nsamples = 12\nvalue = [7, 5]'),
 Text(0.5, 0.2777777777777778, 'gini = 0.0\nsamples = 3\nvalue = [3,
0]'),
 Text(0.5666666666666667, 0.2777777777777778, 'SGOT <= 0.048\ngini =
0.494\nsamples = 9\nvalue = [4, 5]'),
 Text(0.5333333333333333, 0.16666666666666666, 'gini = 0.0\nsamples =
4\nvalue = [0, 4]'),
 Text(0.6, 0.16666666666666666, 'AGE <= 0.345\ngini = 0.32\nsamples =
5\nvalue = [4, 1]'),
 Text(0.5666666666666667, 0.05555555555555555, 'gini = 0.0\nsamples =
1\nvalue = [0, 1]'),
 Text(0.6333333333333333, 0.05555555555555555, 'gini = 0.0\nsamples =
4\nvalue = [4, 0]'),
 Text(0.85, 0.6111111111111112, 'SEX <= 0.5\ngini = 0.497\nsamples =
26\nvalue = [14, 12]'),
 Text(0.8166666666666667, 0.5, 'BILIRUBIN <= 0.151\ngini = 0.499\
nsamples = 23\nvalue = [11, 12]'),
 Text(0.7833333333333333, 0.3888888888888889, 'SGOT <= 0.035\ngini =
0.495\nsamples = 20\nvalue = [11, 9]'),
 Text(0.7, 0.2777777777777778, 'SGOT <= 0.008\ngini = 0.32\nsamples =
5\nvalue = [1, 4]'),
 Text(0.6666666666666666, 0.16666666666666666, 'gini = 0.0\nsamples =
1\nvalue = [1, 0]'),
 Text(0.7333333333333333, 0.16666666666666666, 'gini = 0.0\nsamples =
4\nvalue = [0, 4]'),
 Text(0.8666666666666667, 0.2777777777777778, 'ALK PHOSPHATE <= 0.342\
ngini = 0.444\nsamples = 15\nvalue = [10, 5]'),
 Text(0.8, 0.16666666666666666, 'LIVER BIG <= 0.914\ngini = 0.198\
nsamples = 9\nvalue = [8, 1]'),
 Text(0.7666666666666667, 0.05555555555555555, 'gini = 0.0\nsamples =
1\nvalue = [0, 1]'),
 Text(0.8333333333333334, 0.05555555555555555, 'gini = 0.0\nsamples =
8\nvalue = [8, 0]'),
 Text(0.9333333333333333, 0.16666666666666666, 'ALBUMIN <= 0.337\ngini
= 0.444\nsamples = 6\nvalue = [2, 4]'),
 Text(0.9, 0.05555555555555555, 'gini = 0.0\nsamples = 2\nvalue = [2,
0]'),
 Text(0.9666666666666667, 0.05555555555555555, 'gini = 0.0\nsamples =
4\nvalue = [0, 4]'),
 Text(0.85, 0.3888888888888889, 'gini = 0.0\nsamples = 3\nvalue = [0,
3]'),
 Text(0.8833333333333333, 0.5, 'gini = 0.0\nsamples = 3\nvalue = [3,
0]')]
```



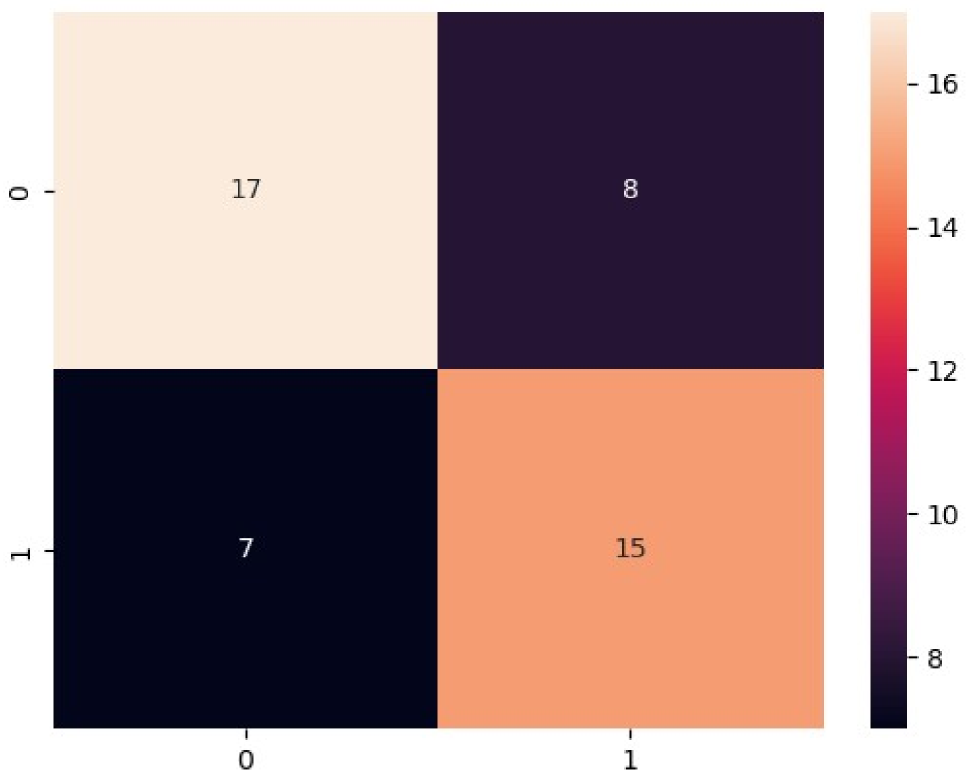
4. Model Evaluation:

```
predict = dcls.predict(xtrain)
predict

array([0., 0., 0., 0., 1., 1., 0., 1., 0., 0., 1., 0., 0., 0., 1., 1.,
0.,
       0., 0., 0., 0., 0., 1., 0., 0., 1., 1., 0., 1., 1., 0., 1., 1.,
0.,
       0., 1., 1., 0., 1., 1., 0., 0., 1., 1., 0., 0., 0., 0., 0., 1.,
0.,
       0., 0., 1., 1., 0., 1., 1., 1., 0., 0., 0., 1., 0., 0., 0., 0.,
1.,
       0., 1., 1., 0., 0., 1., 0., 1., 0., 1., 0., 1., 0., 1., 0., 0.,
1.,
       0., 0., 1., 1., 0., 1., 0., 0., 1., 1., 1., 1., 1., 0., 1., 1.,
0.,
       0., 1., 0., 1., 1.])

dcls.score(xtrain, ytrain)

1.0

predict2 = dcls.predict(xtest)
predict2
```

```
array([1., 1., 1., 1., 1., 0., 0., 0., 1., 0., 1., 1., 1., 0., 1., 1.,
1.,
       0., 0., 0., 0., 0., 1., 0., 0., 1., 1., 1., 0., 1., 1., 0., 0.,
1.,
       0., 1., 0., 0., 1., 0., 0., 0., 1., 0., 1., 0., 0.])

dcls.score(xtest, ytest)

0.6808510638297872
```

Confusion Matrix

```
from sklearn.metrics import classification_report, accuracy_score,
precision_score, recall_score, f1_score,
confusion_matrix,RocCurveDisplay

pred_test = dcls.predict(xtest)
pred_test

array([1., 1., 1., 1., 1., 0., 0., 0., 1., 0., 1., 1., 1., 0., 1., 1.,
1.,
       0., 0., 0., 0., 0., 1., 0., 0., 1., 1., 1., 0., 1., 1., 0., 0.,
1.,
       0., 1., 0., 0., 1., 0., 0., 0., 1., 0., 1., 0., 0.])

dcls.score(xtest, ytest)

0.6808510638297872

accuracy_score(ytest, dcls.predict(xtest))

0.6808510638297872

confusion_matrix(ytest, pred_test)

array([[17,  8],
       [ 7, 15]])

c_mat = confusion_matrix(ytest, dcls.predict(xtest))
c_mat

array([[17,  8],
       [ 7, 15]])

sns.heatmap(c_mat, annot=True )

<AxesSubplot:>
```



Precision

```
precision_score(ytest, dcls.predict(xtest))
```

```
0.6521739130434783
```

Recall

```
recall_score(ytest, dcls.predict(xtest))
```

```
0.6818181818181818
```

F1 Score

```
f1_score(ytest, dcls.predict(xtest))
```

```
0.6666666666666666
```

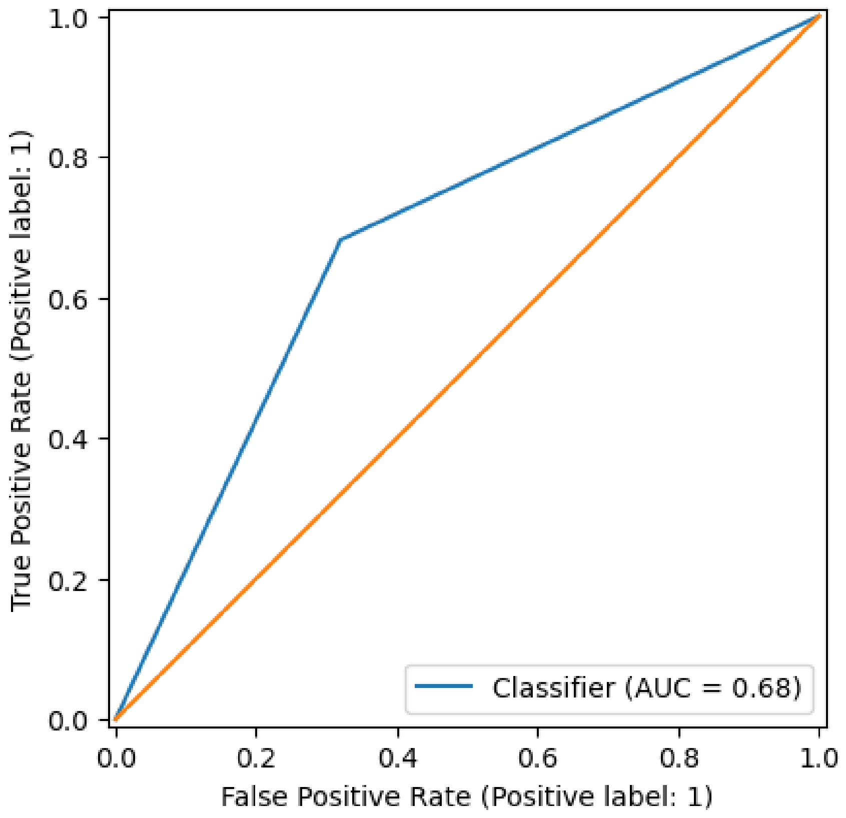
```
print(classification_report(ytest, dcls.predict(xtest)))
```

```
              precision    recall  f1-score   support

         0.0       0.71      0.68      0.69        25
         1.0       0.65      0.68      0.67        22

    accuracy                           0.68        47
```

```
   macro avg       0.68      0.68      0.68        47
weighted avg       0.68      0.68      0.68        47
```

AUC-ROC Score

```
RocCurveDisplay.from_predictions(ytest,dcls.predict(xtest))
plt.plot([0,1],[0,1])
plt.show()
```



```
#AUC= 68, which is above 50% so the model will work but not much
accurately
```