ML LAB 6

Name: Soumyadeep Ganguly

Reg No: 24MDT0082

In [1]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

In [2]:

```
df = pd.read_csv("liver_patient.csv")
df.head()
```

Out[2]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Proti
0	65	Female	0.7	0.1	187	16	18	
1	62	Male	10.9	5.5	699	64	100	
2	62	Male	7.3	4.1	490	60	68	
3	58	Male	1.0	0.4	182	14	20	
4	72	Male	3.9	2.0	195	27	59	

In [3]:

```
df.drop(['Age','Gender'],axis=1,inplace=True)
```

In [4]:

```
from sklearn.preprocessing import MinMaxScaler

mms = MinMaxScaler(feature_range=(0,1))
data = mms.fit_transform(df)
cols = df.columns[:]
```

```
df = pd.DataFrame(data=data, columns=cols)
df.head(4)
```

Out[4]:

	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin
0	0.004021	0.000000	0.060576	0.003015	0.001626	0.594203	0.521739
1	0.140751	0.275510	0.310699	0.027136	0.018296	0.695652	0.500000
2	0.092493	0.204082	0.208598	0.025126	0.011791	0.623188	0.521739
3	0.008043	0.015306	0.058134	0.002010	0.002033	0.594203	0.543478

In [5]:

```
d = df.values
d
```

Out[5]:

```
array([[0.00402145, 0.        , 0.06057645, ..., 0.52173913, 0.24      ,
        1.        ],
       [0.14075067, 0.2755102 , 0.31069858, ..., 0.5       , 0.176     ,
        1.        ],
       [0.0924933 , 0.20408163, 0.20859795, ..., 0.52173913, 0.236     ,
        1.        ],
       ...,
       [0.00536193, 0.00510204, 0.0889106 , ..., 0.5       , 0.28      ,
        1.        ],
       [0.01206434, 0.02040816, 0.05911089, ..., 0.54347826, 0.28      ,
        1.        ],
       [0.0080429 , 0.01020408, 0.07474353, ..., 0.76086957, 0.48      ,
        0.        ]], shape=(583, 9))
```

In [6]:

```
x = d[:,:-1]
y = d[:,-1]
```

In [7]:

```
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test = train_test_split(x, y, test_size=0.2, random_state=0)
```

In [9]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
```

```
l_reg = LogisticRegression()
l_reg.fit(x_train,y_train)
```

Out[9]:

```
▾ LogisticRegression
LogisticRegression()
```

In [10]:

```
y_pred = l_reg.predict(x_train)
acc_lr = accuracy_score(y_pred, y_train)
acc_lr
```

Out[10]:

```
0.7253218884120172
```

K-Fold Cross Validation

In [11]:

```
from sklearn.model_selection import KFold, cross_val_score

k_f_val = KFold(n_splits=5, shuffle=True, random_state=0)
results = cross_val_score(l_reg, x_train, y_train, scoring='accuracy', cv=k_f_val)
results
```

Out[11]:

```
array([0.81914894, 0.72043011, 0.74193548, 0.70967742, 0.6344086 ])
```

In [12]:

```
np.mean(results)
```

Out[12]:

```
np.float64(0.7251201098146878)
```

Stratified K-Fold Cross Validation

In [13]:

```
from sklearn.model_selection import StratifiedKFold

skf_val = StratifiedKFold(n_splits=5, shuffle=True, random_state=0)

results_skf = cross_val_score(l_reg, x_train, y_train, scoring='accuracy', cv=skf_val)
results_skf
```

Out[13]:
```
array([0.72340426, 0.72043011, 0.72043011, 0.7311828 , 0.7311828 ])
```

In [14]:
```
results_skf.mean()
```

Out[14]:
```
np.float64(0.7253260123541525)
```

Performance Measures

In [15]:
```
y_pred_test = l_reg.predict(x_test)
accuracy_score(y_pred_test, y_test)
```

Out[15]:
```
0.6666666666666666
```

In [16]:
```
from sklearn.metrics import confusion_matrix, precision_score, recall_score, f1_score, ConfusionMatrixDisplay
cm = confusion_matrix(y_test, y_pred_test)
cm
```

Out[16]:
```
array([[ 0, 39],
       [ 0, 78]])
```

In [17]:
```
ps = precision_score(y_test, y_pred_test)
ps
```

Out[17]:
```
0.6666666666666666
```

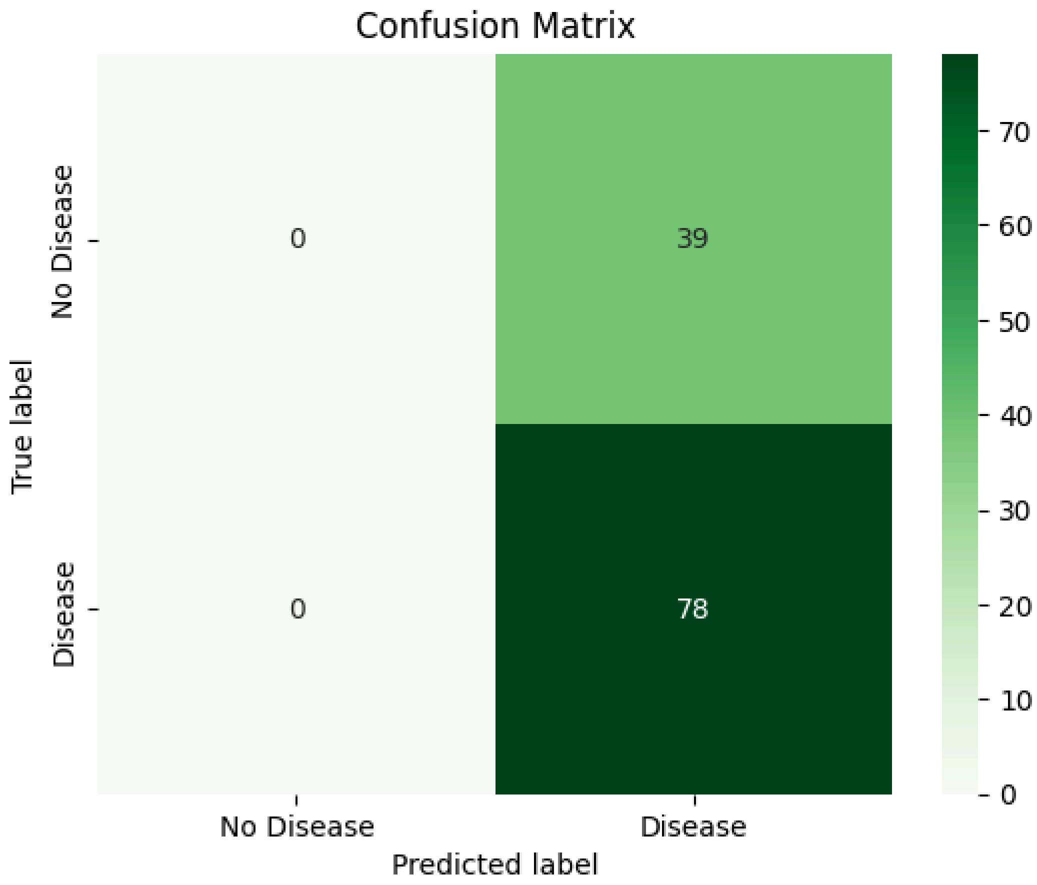
In [18]:
```
rs = recall_score(y_test, y_pred_test)
rs
```

Out[18]:
```
1.0
```

In [19]:
```
f1s = f1_score(y_test, y_pred_test)
f1s
```

Out[19]:
```
0.8
```

In [20]:
```
import seaborn as sns
sns.heatmap(cm, annot=True, fmt='d', cmap='Greens', xticklabels=['No Disease', 'Disease'], yticklabels=['No Disease', 'Disease
plt.xlabel('Predicted label')
plt.ylabel('True label')
plt.title('Confusion Matrix')
plt.show()
```



Decision Tree - logistic Regression

In [21]:
```
from sklearn.tree import DecisionTreeClassifier, plot_tree
dtc = DecisionTreeClassifier()
dtc.fit(x_train, y_train)
```

Out[21]:

```
▾ DecisionTreeClassifier
DecisionTreeClassifier()
```

In [23]:

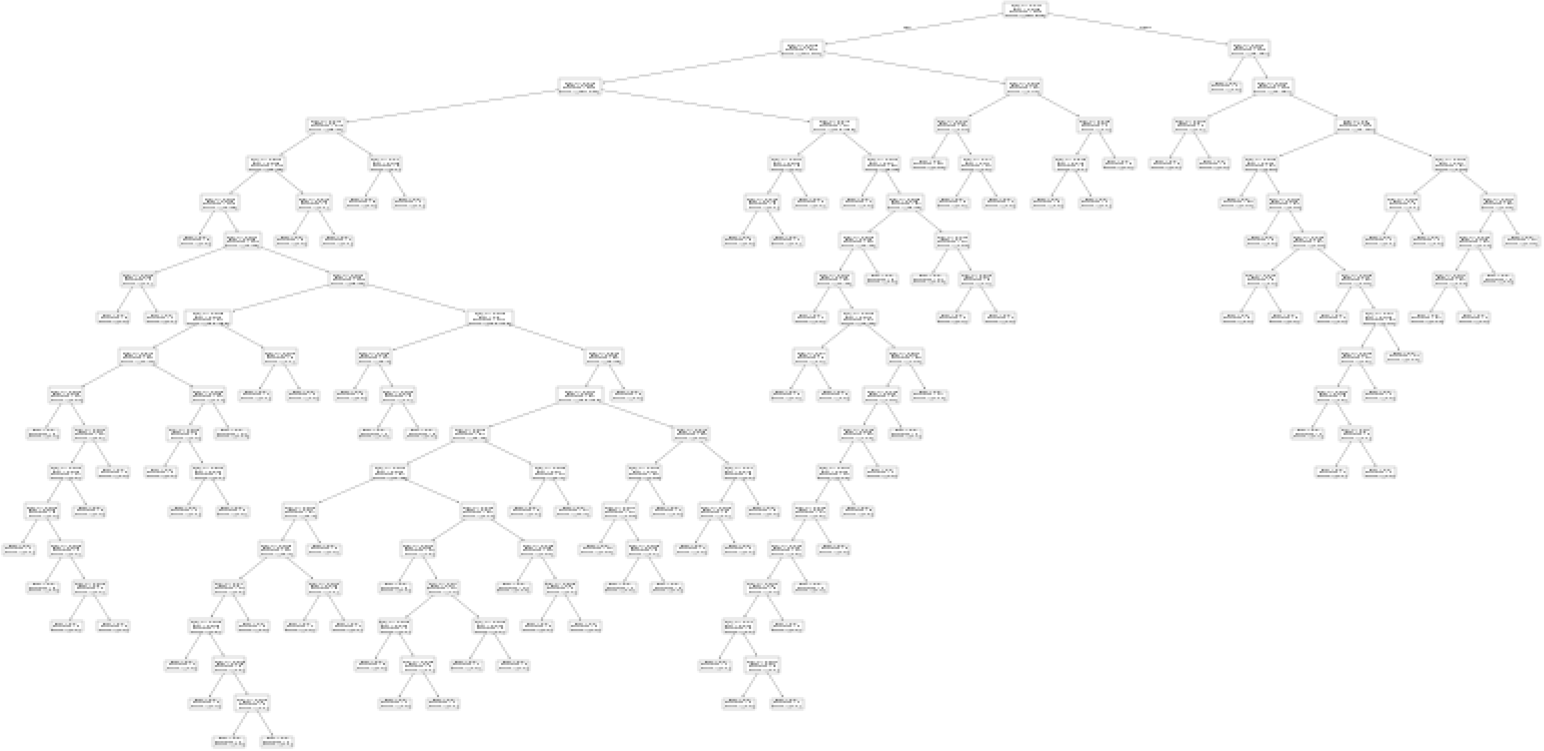
```
pred = dtc.predict(x_test)
accuracy_score(pred, y_test)
```

Out[23]:

```
0.6495726495726496
```

In [24]:

```
plt.figure(figsize=(100,50), dpi=10)
plot_tree(dtc)
plt.show()
```



Decision Tree - Linear Regression

In [25]:
```
df2 = pd.read_csv("Book1.csv")
df2.head()
```

Out[25]:

	price	area	bedrooms	bathrooms	stories	parking	furnishingstatus
0	13300000	7420	4	2	3	2	furnished
1	12250000	8960	4	4	4	3	furnished
2	12250000	9960	3	2	2	2	semi-furnished
3	12215000	7500	4	2	2	3	furnished
4	11410000	7420	4	1	2	2	furnished

In [26]:
```
df2.drop(['furnishingstatus'], axis=1, inplace=True)
```

In [27]:
```
mms = MinMaxScaler(feature_range=(0,1))
d = mms.fit_transform(df2)
cols = df2.columns[:]
df2 = pd.DataFrame(data=d, columns=cols)
df2.head(4)
```

Out[27]:

	price	area	bedrooms	bathrooms	stories	parking
0	1.000000	0.356777	0.50	0.333333	0.666667	0.666667
1	0.880096	0.469597	0.50	1.000000	1.000000	1.000000
2	0.880096	0.542857	0.25	0.333333	0.333333	0.666667
3	0.876099	0.362637	0.50	0.333333	0.333333	1.000000

In [28]:

```
x = df2.values[:,1:]
y = df2.values[:,1]
x_train,x_test,y_train,y_test = train_test_split(x,y,test_size=0.2,random_state=0)
```

In [29]:

```
from sklearn.tree import DecisionTreeRegressor
from sklearn.metrics import mean_squared_error

dtc_linreg = DecisionTreeRegressor()
dtc_linreg.fit(x_train, y_train)
```

Out[29]:

```
▾ DecisionTreeRegressor  i ?

DecisionTreeRegressor()
```

In [30]:

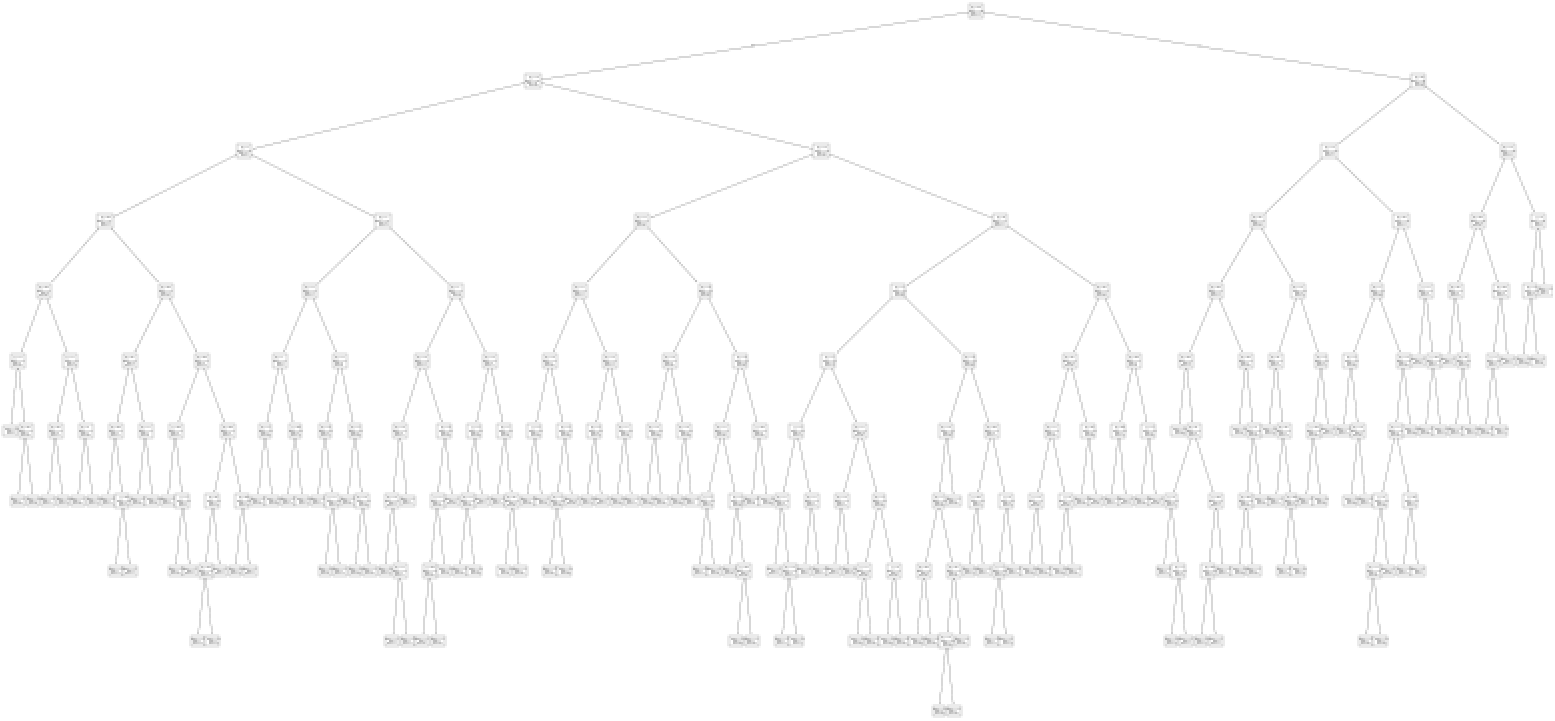
```
pred = dtc_linreg.predict(x_test)
mean_squared_error(pred, y_test)
```

Out[30]:

```
0.0006450250506514239
```

In [31]:

```
plt.figure(figsize=(100,50), dpi=10)
plot_tree(dtc_linreg)
plt.show()
```



Hyperparameter Tuning: Grid Search

In [32]:
```
from sklearn.model_selection import GridSearchCV
```

In [33]:
```
df = pd.read_csv('liver_patient.csv')
df.head(4)
```

Out[33]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Proti
0	65	Female	0.7	0.1	187	16	18	
1	62	Male	10.9	5.5	699	64	100	
2	62	Male	7.3	4.1	490	60	68	
3	58	Male	1.0	0.4	182	14	20	

In [34]:

```
df.drop('Gender', axis=1, inplace=True)
```

In [35]:

```
mms = MinMaxScaler()
x = mms.fit_transform(df)
X = x[:, 0:9]
Y = x[:, 9]
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, random_state=42)
```

In [36]:

```
param_grid = {
 'max_depth': [3, 5, 10],
 'min_samples_leaf': [1, 5, 10, 20]
 }
```

In [37]:

```
dt_model = DecisionTreeClassifier(random_state=0)
grid_search = GridSearchCV(estimator=dt_model, param_grid=param_grid, cv=5, scoring='accuracy', n_jobs=-1)
grid_search.fit(X_train, Y_train)
best_params = grid_search.best_params_
best_model = grid_search.best_estimator_
Y_pred = best_model.predict(X_test)
accuracy = accuracy_score(Y_test, Y_pred)
print("Best Parameters:", best_params)
print("Best Cross-validation Accuracy:", grid_search.best_score_)
print("Test Accuracy:", accuracy)
```

```
Best Parameters: {'max_depth': 3, 'min_samples_leaf': 1}
Best Cross-validation Accuracy: 0.6759780370624571
Test Accuracy: 0.717948717948718
```

In [ ]: