```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model selection import train test split
from sklearn.preprocessing import LabelEncoder
from sklearn import tree
import random
path = 'drug.csv'
data = pd.read csv(path)
print('data')
print(data)
data
     Age Sex
                  BP Cholesterol
                                   Na to K
                                             Drug
0
                                    25.355
      23
                HIGH
                                            drugY
           F
                             HIGH
      47
                 LOW
1
           М
                             HIGH
                                    13.093
                                            drugC
2
      47
                 LOW
                                    10.114
           М
                             HIGH
                                            drugC
3
           F
              NORMAL
      28
                             HIGH
                                       NaN
                                            drugX
4
      61
           F
                                    18.043
                 LOW
                             HIGH
                                            drugY
      56
                                    11.567
195
           F
                 LOW
                             HIGH
                                            drugC
                                    12.006
196
      16
           М
                 LOW
                             HIGH
                                            drugC
197
      52
              NORMAL
           М
                             HIGH
                                     9.894
                                            drugX
198
      23
           М
              NORMAL
                              NaN
                                    14.020
                                            drugX
199
      40
           F
                           NORMAL
                                    11.349
                 LOW
                                            drugX
[200 rows x 6 columns]
missing values = data.isnull().sum()
print("Missing values in each column in data:")
print(missing values)
Missing values in each column in data:
               0
Age
Sex
               0
BP
               2
               2
Cholesterol
               1
Na to K
               0
Drug
dtype: int64
data = data.dropna()
print('data after removing missing values')
print(data)
data after removing missing values
                  BP Cholesterol
                                   Na to K
     Age Sex
                                             Drug
0
      23
           F
                HIGH
                             HIGH
                                    25.355
                                            drugY
1
      47
           М
                 LOW
                                    13.093
                             HIGH
                                            druaC
2
      47
           М
                 LOW
                             HIGH
                                    10.114
                                            drugC
```

```
4
      61
           F
                 LOW
                                    18.043
                             HIGH
                                             drugY
5
           F
                                     8.607
      22
              NORMAL
                             HIGH
                                             drugX
                              . . .
194
      46
          F
                HIGH
                             HIGH
                                    34.686
                                             druaY
195
      56
           F
                 LOW
                             HIGH
                                    11.567
                                             drugC
196
      16
                 LOW
                                    12.006
                                             drugC
           М
                             HIGH
197
      52
           М
              NORMAL
                                    9.894
                                             drugX
                             HIGH
199
      40
           F
                 LOW
                           NORMAL
                                    11.349 drugX
[195 rows x 6 columns]
def categorize features(data):
    categorical features =
data.select dtypes(include=['object']).columns.tolist()
    numerical features =
data.select dtypes(include=[np.number]).columns.tolist()
    return categorical features, numerical features
categorical, numerical = categorize features(data)
print("Categorical Features:", categorical)
Categorical Features: ['Sex', 'BP', 'Cholesterol', 'Drug']
# the features and targets are separated
num of cols = data.shape[1]
X = data.iloc[:, 0:num_of_cols - 1]
y = data.iloc[:, num of cols - 1:num of cols]
print("features")
print(X)
print("----
print("targets")
print(y)
features
     Age Sex
                   BP Cholesterol
                                   Na to K
                                    25.355
0
      23
           F
                HIGH
                             HIGH
1
      47
           М
                 LOW
                             HIGH
                                    13.093
2
      47
           Μ
                 LOW
                             HIGH
                                    10.114
4
      61
                 LOW
                                    18.043
           F
                             HIGH
5
      22
           F
              NORMAL
                                     8.607
                             HIGH
. .
     . . .
                  . . .
                              . . .
          . .
                                    34.686
194
      46
          F
                HIGH
                             HIGH
195
      56
           F
                 LOW
                             HIGH
                                    11.567
196
      16
                 LOW
                                    12,006
           М
                             HIGH
197
      52
           М
              NORMAL
                             HIGH
                                     9.894
                           NORMAL
                                    11.349
199
      40
           F
                 LOW
[195 rows x 5 columns]
```

```
targets
      Drug
0
     druaY
1
     drugC
2
     drugC
4
    drugY
5
    drugX
194 drugY
195 drugC
196 drugC
197 drugX
199 drugX
[195 rows x 1 columns]
# First experiment
print('First experiment')
print('----')
# Generate a list of 5 unique random numbers
random numbers = random.sample(range(1, 101), 5)
print('random numbers: ', random numbers)
print()
highest = [0,0,0]
count = 1
for random seed in random numbers:
    # the data is shuffled and split into training and testing sets
    X_train, X_test, y_train, y_test = train_test_split(X, y,
shuffle=True, test size=0.30, random state=random seed)
    # categorical features are encoded
    categorical columns X = categorical[:-1]
    label encoder X = LabelEncoder()
    for i in range(len(categorical columns X)):
        X_train[categorical_columns_X[i]] =
label encoder X.fit transform(X train[categorical columns X[i]])
        X test[categorical columns X[i]] =
label encoder X.transform(X test[categorical columns X[i]])
    # categorical targets are encoded
    categorical columns y = categorical[-1:]
    label encoder y = LabelEncoder()
    y train[categorical columns y[0]] =
label encoder y.fit transform(y train[categorical columns y[0]])
    y test[categorical columns y[0]] =
label encoder y.transform(y test[categorical columns y[0]])
```

```
maxD = random.randint(2, 4)
   model = tree.DecisionTreeClassifier(criterion="entropy",
max depth=maxD)
   model.fit(X_train, y_train)
   y pred = model.predict(X test)
   print('Experiment #'+str(count)+':')
   accuracy = model.score(X test, y test)
   print("Accuracy: ", accuracy)
   print("Tree depth:", model.tree .max depth)
   print("Total number of nodes:", model.tree .node count)
   count+=1
   if highest[0] < accuracy:</pre>
       highest = [accuracy, model.tree_.max_depth,
model.tree .node count]
   elif highest[0] == accuracy:
       if highest[1] < model.tree .max depth:</pre>
           highest = [accuracy, model.tree .max depth,
model.tree .node count]
   print()
   print("-" * 50)
   print()
First experiment
------
random numbers: [95, 46, 55, 20, 88]
Experiment #1:
Accuracy: 1.0
Tree depth: 4
Total number of nodes: 11
  _____
Experiment #2:
Accuracy: 0.864406779661017
Tree depth: 2
Total number of nodes: 5
Experiment #3:
Accuracy: 0.9830508474576272
Tree depth: 4
Total number of nodes: 11
Experiment #4:
Accuracy: 0.8305084745762712
```

```
Tree depth: 2
Total number of nodes: 5
Experiment #5:
Accuracy: 0.8983050847457628
Tree depth: 3
Total number of nodes: 9
print('The highest overall performance')
print("Accuracy: ", highest[0])
print("Tree depth:", highest[1])
print("Total number of nodes:", highest[2])
The highest overall performance
Accuracy: 1.0
Tree depth: 4
Total number of nodes: 11
# Second experiment
print('Second experiment')
print('----')
# categorical features are encoded
categorical_columns_X = categorical[:-1]
label encoder X = LabelEncoder()
for i in range(len(categorical columns X)):
   X[categorical_columns_X[i]] =
label encoder X.fit transform(X[categorical columns X[i]])
print("X after encoding")
print(X)
# categorical targets are encoded
categorical_columns_y = categorical[-1:]
label encoder y = LabelEncoder()
y[categorical columns y[0]] =
label encoder y.fit transform(y[categorical columns y[0]])
print()
print("y after encoding")
print(y)
Second experiment
X after encoding
```

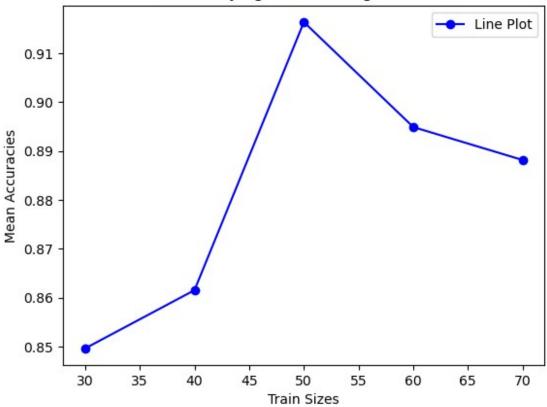
```
Age Sex BP
                   Cholesterol Na to K
0
      23
            0
                                25.355
                0
                             0
1
      47
            1
                1
                             0
                                 13.093
2
      47
            1
                1
                             0
                                 10.114
4
      61
            0
                1
                             0
                                 18.043
5
      22
            0
                2
                             0
                                  8,607
     . . .
               . .
                                     . . .
194
      46
            0
                0
                                 34.686
                             0
      56
            0
195
                1
                             0
                                 11.567
196
      16
            1 1
                             0
                                 12.006
                2
            1
                                  9.894
197
      52
                             0
            0
                1
                             1
199
      40
                                 11.349
[195 rows x 5 columns]
y after encoding
     Drug
        4
1
        2
2
        2
4
        4
5
        3
194
        4
        2
195
        2
196
        3
197
199
        3
[195 rows x 1 columns]
print('Second experiment')
print('----')
trainSizes = [30, 40, 50, 60, 70]
means accuracy = []
means nodes = []
for trainSize in trainSizes:
    print('train size:', trainSize)
    # Generate a list of 5 unique random numbers
    random numbers = random.sample(range(1, 101), 5)
    print('random numbers: ', random numbers)
    print()
    accuracies = []
    sizes = []
    for random seed in random numbers:
        # the data is shuffled and split into training and testing
sets
        X_train, X_test, y_train, y_test = train_test_split(X, y,
shuffle=True, train_size=(trainSize/100), random_state=random_seed)
```

```
maxD = random.randint(2, 4)
       model = tree.DecisionTreeClassifier(criterion="entropy",
max depth=maxD)
       model.fit(X train, y train)
       y pred = model.predict(X test)
       accuracy = model.score(X_test, y_test)
       size = model.tree .node count
       accuracies.append(accuracy)
       sizes.append(size)
   print('Mean, Maximum, and Minimum accuracy')
   print('----')
   mean acc = sum(accuracies)/len(accuracies)
   maximum acc = max(accuracies)
   minimum acc = min(accuracies)
   print('Mean: ', mean_acc)
   print('Maximum: ', maximum_acc)
   print('Minimum: ', minimum_acc)
   means accuracy.append(mean acc)
   print('Mean, Maximum, and Minimum tree size')
   print('-----')
   mean node = sum(sizes)/len(sizes)
   maximum node = max(sizes)
   minimum_node = min(sizes)
   print('Mean: ', mean_node)
   print('Maximum: ', maximum_node)
print('Minimum: ', minimum_node)
   means nodes.append(mean node)
   print()
   print('-'*70)
   print()
Second experiment
------
train size: 30
random numbers: [29, 71, 24, 93, 16]
Mean, Maximum, and Minimum accuracy
-----
Mean: 0.8496350364963503
Maximum: 0.8978102189781022
Minimum: 0.7956204379562044
Mean, Maximum, and Minimum tree size
-----
Mean: 6.6
Maximum: 9
Minimum: 5
```

```
train size: 40
random_numbers: [29, 48, 70, 80, 52]
Mean, Maximum, and Minimum accuracy
Mean: 0.8615384615384615
Maximum: 0.9914529914529915
Minimum: 0.811965811965812
Mean, Maximum, and Minimum tree size
Mean: 6.2
Maximum: 11
Minimum: 5
train size: 50
random_numbers: [32, 50, 100, 58, 71]
Mean, Maximum, and Minimum accuracy
Mean: 0.9163265306122449
Maximum: 1.0
Minimum: 0.8571428571428571
Mean, Maximum, and Minimum tree size
Mean: 8.2
Maximum: 11
Minimum: 5
train size: 60
random_numbers: [1, 39, 19, 8, 82]
Mean, Maximum, and Minimum accuracy
Mean: 0.8948717948717949
Maximum: 0.9743589743589743
Minimum: 0.8589743589743589
Mean, Maximum, and Minimum tree size
Mean: 8.6
Maximum: 11
Minimum: 5
```

```
train size: 70
random numbers: [67, 1, 43, 47, 100]
Mean, Maximum, and Minimum accuracy
Mean: 0.8881355932203391
Maximum: 1.0
Minimum: 0.7966101694915254
Mean, Maximum, and Minimum tree size
Mean: 7.4
Maximum: 11
Minimum: 5
plt.plot(trainSizes, means accuracy, marker='o', linestyle='-',
color='b', label='Line Plot')
plt.xlabel('Train Sizes')
plt.ylabel('Mean Accuracies')
plt.title('Accuracy against Training Set Size')
plt.legend()
plt.show()
```

Accuracy against Training Set Size



```
plt.plot(trainSizes,means_nodes, marker='o', linestyle='-', color='b',
label='Line Plot')
plt.xlabel('Train Sizes')
plt.ylabel('Number of Nodes')
plt.title('Number of Nodes in Final Tree against Training Set Size')
plt.legend()
plt.show()
```

