

PRACTICA 23

```
In [2]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.tree import DecisionTreeClassifier
from sklearn import metrics
from sklearn.model_selection import train_test_split
import warnings
warnings.filterwarnings('ignore')
```

```
In [3]: drugs = pd.read_csv('C:/Users/Isaac/Desktop/IHD/EBAC DT/M23 DS/drugs.csv')
drugs
```

Out[3]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
0	23	F	HIGH	HIGH	25.355	drugY
1	47	M	LOW	HIGH	13.093	drugC
2	47	M	LOW	HIGH	10.114	drugC
3	28	F	NORMAL	HIGH	7.798	drugX
4	61	F	LOW	HIGH	18.043	drugY

```
In [4]: # definimos características para los pronósticos
feature_cols = ['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K']

# definimos valores para 'x' y 'y'
X = drugs[feature_cols].values
y = drugs.Drug
```

Convertir las variables predictoras cualitativas de esta base a una escala numérica mediante la instrucción `preprocessing.LabelEncoder()`

```
In [5]: from sklearn import preprocessing

cod_sex = preprocessing.LabelEncoder()
cod_sex.fit(['F', 'M'])
X[:,1] = cod_sex.transform(X[:,1])

cod_bp = preprocessing.LabelEncoder()
cod_bp.fit(['HIGH', 'LOW', 'NORMAL'])
X[:,2] = cod_bp.transform(X[:,2])

cod_chol = preprocessing.LabelEncoder()
cod_chol.fit(['HIGH', 'NORMAL'])
X[:,3] = cod_chol.transform(X[:,3])
```

```
In [6]: # creamos grupos de entrenamiento y prueba

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.3, random_state = 1)
```

```
In [7]: # objeto de clasificación del árbol de decisión

clf = DecisionTreeClassifier()

# entrenamos el modelo

clf.fit(X_train, y_train)
```

Out[7]:

DecisionTreeClassifier

DecisionTreeClassifier()

```
In [8]: # realizamos predicciones

clf_pred = clf.predict(X_test)
```

```
In [10]: # Matriz de Conficion

from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, clf_pred)
cm
```

```
Out[10]: array([[ 4,  0,  0,  0,  0],
                [ 2,  4,  0,  0,  0],
                [ 0,  0,  4,  0,  0],
                [ 0,  0,  0, 19,  0],
                [ 0,  0,  0,  0, 27]], dtype=int64)
```

ESTADISTICAS DE DESEMPEÑO

```
In [11]: from sklearn.metrics import classification_report
print(classification_report(y_test, clf_pred))
```

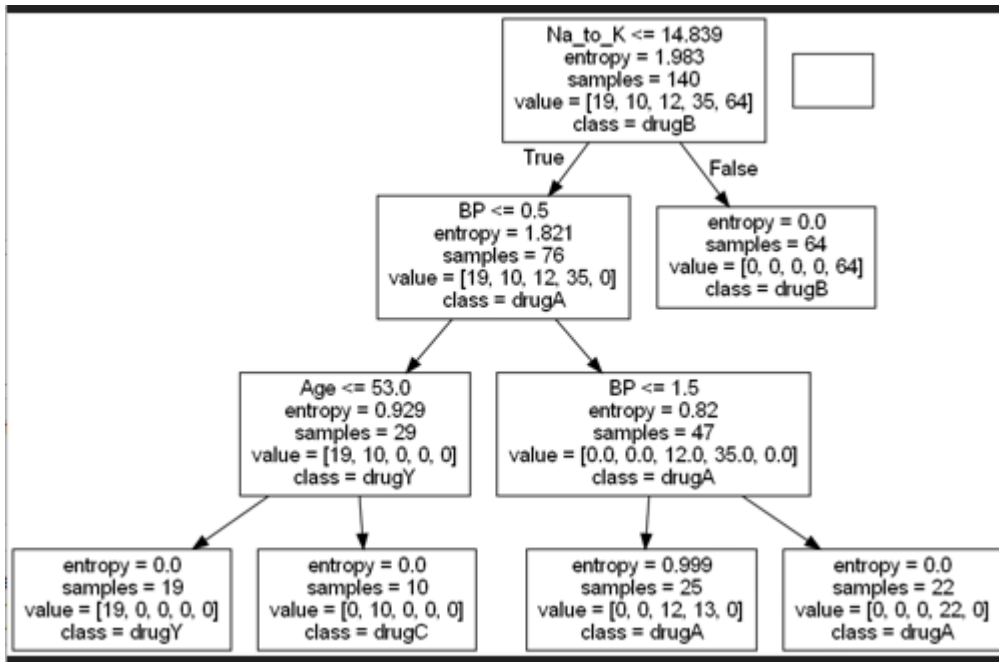
	precision	recall	f1-score	support
drugA	0.67	1.00	0.80	4
drugB	1.00	0.67	0.80	6
drugC	1.00	1.00	1.00	4
drugX	1.00	1.00	1.00	19
drugY	1.00	1.00	1.00	27
accuracy			0.97	60
macro avg	0.93	0.93	0.92	60
weighted avg	0.98	0.97	0.97	60

ARBOL DE DECISION (REGLAS)

```
In [13]: dot_data = tree.export_graphviz(clf, out_file = None, feature_names = feature_cols, class_names = ['drugY','drugC','drugX','drugA','drugB'],
# creamos la grafica de Arbol
graph = pydotplus.graph_from_dot_data(dot_data)
```

```
In [14]: # creacion del Arbol en formato png
```

```
graph.write_png('drug.png')
image = Image.open('drug.png')
image.show()
```



utilizando entropy

```
In [16]: clf = DecisionTreeClassifier(criterion = 'entropy', max_depth = 3)
         clf.fit(X_train, y_train)
         clf_pred = clf.predict(X_test)
```

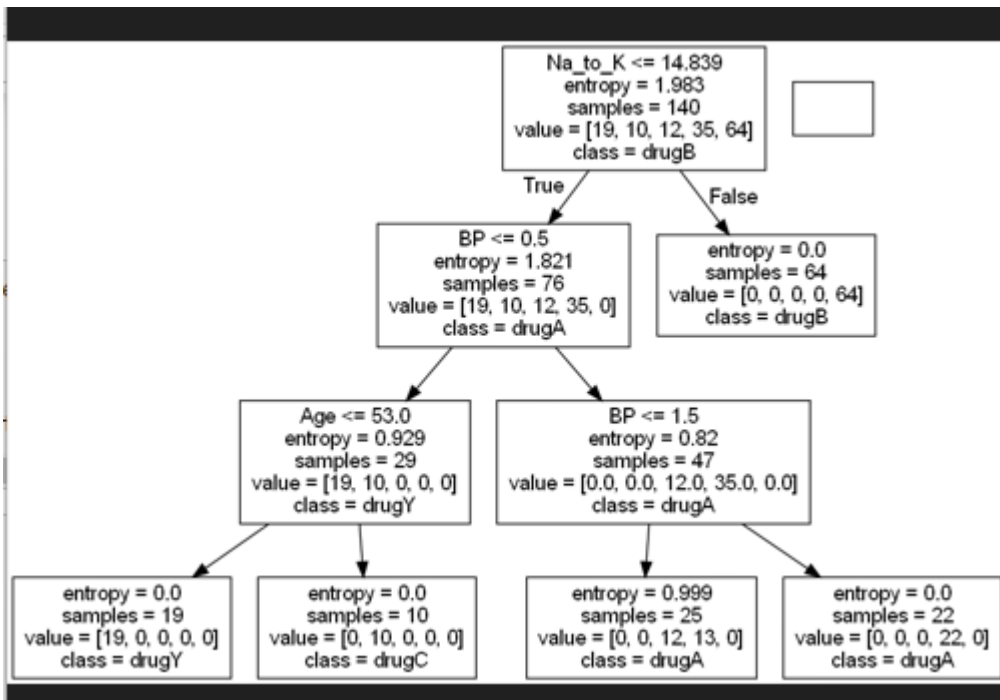
```
In [18]: from sklearn.metrics import classification_report
         print(classification_report(y_test, clf_pred))
```

	precision	recall	f1-score	support
drugA	0.67	1.00	0.80	4
drugB	1.00	0.67	0.80	6
drugC	0.00	0.00	0.00	4
drugX	0.83	1.00	0.90	19
drugY	1.00	1.00	1.00	27
accuracy			0.90	60
macro avg	0.70	0.73	0.70	60
weighted avg	0.86	0.90	0.87	60

```
In [19]: dot_data = tree.export_graphviz(clf, out_file = None, feature_names = feature_cols, class_names = ['drugY', 'drugC', 'drugX', 'drugA', 'drugB'])
         # creamos la grafica de Arbol
         graph = pydotplus.graph_from_dot_data(dot_data)
```

```
In [27]: # creacion del Arbol en formato png
```

```
graph.write_png('Drug.png')
image = Image.open('Drug.png')
image.show()
```



¿Qué medicamento recomendaría utilizar para un paciente con los siguientes datos?

Age	Sex	BP	Cholesterol	Na_to_K
50	F	HIGH	NORMAL	15.302

```

In [21]: # Predicción con nuevos valores específicos
new_data = {'Age': 50, 'Sex': 'F', 'BP': 'HIGH', 'Cholesterol': 'NORMAL', 'Na_to_K': 15.302}
new_data['Sex'] = cod_sex.transform([new_data['Sex']])[0]
new_data['BP'] = cod_bp.transform([new_data['BP']])[0]
new_data['Cholesterol'] = cod_chol.transform([new_data['Cholesterol']])[0]

In [26]: new_data_array = np.array([[new_data['Age'], new_data['Sex'], new_data['BP'], new_data['Cholesterol'], new_data['Na_to_K']]])
new_data_array

Out[26]: array([[50.    ,  0.    ,  0.    ,  1.    , 15.302]])

In [25]: # Realizamos la predicción
pred_drug = clf.predict(new_data_array)
print("La predicción para el nuevo dato es:", predicted_drug[0])

La predicción para el nuevo dato es: drugY
  
```

*** El medicamento que se recomendaría al paciente con los datos dados, sería Drug Y**