# **ASSESSMENT 2**

# Build an ANN model for Drug classification.

This project aims to analyze the relationship between various medical parameters and drug effectiveness. The dataset consists of patient information, including age, sex, blood pressure levels (BP), cholesterol levels, sodium-to-potassium ratio (Na\_to\_K), drug type, and corresponding labels. The goal is to develop a model that can accurately predict the class or category of a given drug based on its features.

### Import the libraries

### In [1]:

```
import pandas as pd
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras import Sequential
from tensorflow.keras.layers import Flatten,Dense
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.model_selection import train_test_split
import numpy as np
import seaborn as sb
import matplotlib.pyplot as mp
```

#### Load the dataset

```
In [2]:
```

```
dataset = pd.read_csv('drug.csv')
```

#### Glimpse of the dataset

## In [3]:

```
dataset.head()
```

### Out[3]:

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

# **Data Preprocessing**

### Check for total no. of rows and column

```
In [4]:
```

```
dataset.shape
```

# Out[4]:

(200, 6)

Total number of rows are 200 Total number of columns are 6

# **Check for missing values**

## In [5]:

```
dataset.isnull().sum()
```

# Out[5]:

Age	0
Sex	0
BP	0
Cholesterol	0
Na_to_K	0
Drug	0
dtype: int64	

### **Check for dataset information**

# In [6]:

```
dataset.info
```

# Out[6]:

<box< th=""><th colspan="2"><pre><bound dataframe.inf="" drug<="" method="" pre=""></bound></pre></th><th>ne.info of</th><th>Age S</th><th>ex</th><th>BP Cholesterol</th><th>Na_to_K</th></box<>	<pre><bound dataframe.inf="" drug<="" method="" pre=""></bound></pre>		ne.info of	Age S	ex	BP Cholesterol	Na_to_K	
0	23	F	HIGH	HIGH	25.355	DrugY		
1	47	М	LOW	HIGH	13.093	drugC		
2	47	Μ	LOW	HIGH	10.114	drugC		
3	28	F	NORMAL	HIGH	7.798	drugX		
4	61	F	LOW	HIGH	18.043	DrugY		
	• • •		• • •	• • •	• • •			
195	56	F	LOW	HIGH	11.567	drugC		
196	16	Μ	LOW	HIGH	12.006	drugC		
197	52	Μ	NORMAL	HIGH	9.894	drugX		
198	23	Μ	NORMAL	NORMAL	14.020	drugX		
199	40	F	LOW	NORMAL	11.349	drugX		
196 197 198	16 52 23	M M M	LOW NORMAL NORMAL	HIGH HIGH NORMAL	12.006 9.894 14.020	drugC drugX drugX		

[200 rows x 6 columns]>

# Check for statistical info

# In [7]:

dataset.describe

# Out[7]:

<box< th=""><th>und me</th><th>thod</th><th>NDFrame.</th><th>describe of</th><th>Age</th><th>Sex</th><th>BP Cholesterol</th><th>Na_to_</th></box<>	und me	thod	NDFrame.	describe of	Age	Sex	BP Cholesterol	Na_to_
K	Drug							
0	23	F	HIGH	HIGH	25.355	DrugY		
1	47	Μ	LOW	HIGH	13.093	drugC		
2	47	Μ	LOW	HIGH	10.114	drugC		
3	28	F	NORMAL	HIGH	7.798	drugX		
4	61	F	LOW	HIGH	18.043	DrugY		
• •	• • •	• •	• • •	• • •	• • •	• • •		
195	56	F	LOW	HIGH	11.567	drugC		
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197	52	Μ	NORMAL	HIGH	9.894	drugX		
198	23	Μ	NORMAL	NORMAL	14.020	drugX		
199	40	F	LOW	NORMAL	11.349	drugX		

[200 rows  $x \in columns$ ]>

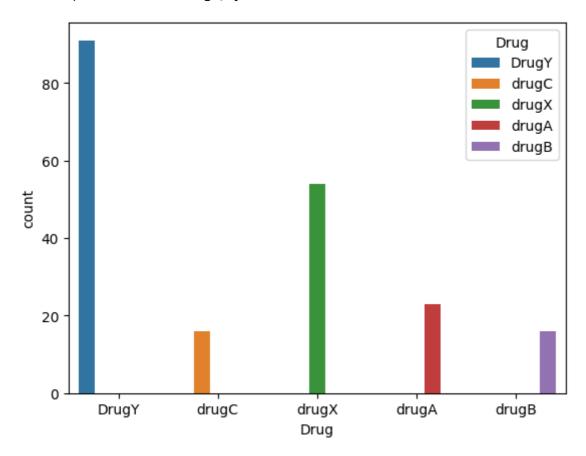
# Let's Visualize in the Graph forms

# In [8]:

```
sb.countplot(x='Drug',data=dataset,hue='Drug')
```

# Out[8]:

<AxesSubplot: xlabel='Drug', ylabel='count'>



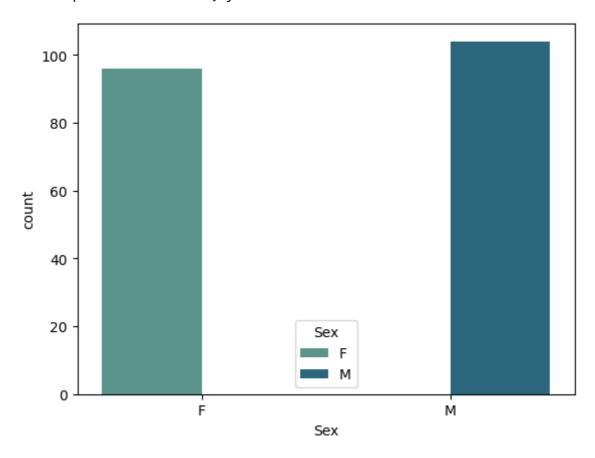
Consumption of Drug Y is more and Drug B is less compare to all

# In [9]:

sb.countplot(x='Sex',data=dataset,palette='crest',hue='Sex')

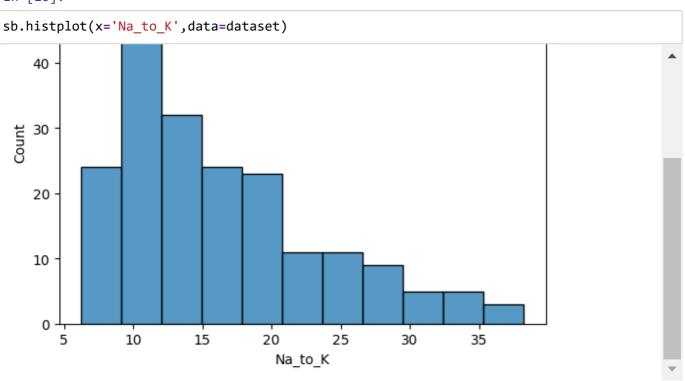
# Out[9]:

<AxesSubplot: xlabel='Sex', ylabel='count'>



Male Drug's consumption is more compare to Female

In [10]:



### Segregate the data into train & test

```
In [11]:
```

```
X = dataset.drop(columns = ['Drug'],axis=1)
Y = dataset['Drug']
```

Drug column is the output(target) column in this dataset.

```
In [12]:
```

```
Y_class = len(np.unique(Y))
print(Y_class)
```

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The above code snippet will fetch the count of unique class value of the target column.

### Convert the Categorical data into interger data

```
In [13]:
```

```
X = pd.get_dummies(X,columns=['Sex','BP','Cholesterol'],drop_first = True)
LE = LabelEncoder()
Y = LE.fit_transform(Y)
```

**get\_dummies** is a pandas function which will convert the one-hot encoding categorical value into numeric value

Labelencoder will assign a numeric value to a category value.

```
In [14]:
```

```
X_train, X_test, Y_train, Y_test = train_test_split (X,Y,test_size=0.3,random_state=2)
```

In the above code snippet, I have divide the dataset into train and test

### **Feature Scaling**

```
In [15]:
```

```
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.fit_transform(X_test)
```

StandardScaler is used for scaling the numeric values

### In [16]:

```
Y_train = keras.utils.to_categorical(Y_train)
Y_test = keras.utils.to_categorical(Y_test)
```

the to\_categorical() function from the Keras library to convert the target variable arrays Y\_train and Y\_test into one-hot encoded arrays.

#### create a ANN model

### In [17]:

```
model = Sequential()
model.add(Dense(48, input_dim=6, activation='relu'))
model.add(Dense(36, activation='relu'))
model.add(Dense(24, activation='relu'))
model.add(Dense(12, activation='relu'))
output_layer = Dense(Y_class,activation='softmax')
model.add(output_layer)
```

### In [19]:

```
model.summary()
```

### Model: "sequential"

Layer (type)	Output Shape	Param #
dense (Dense)	(None, 48)	336
dense_1 (Dense)	(None, 36)	1764
dense_2 (Dense)	(None, 24)	888
dense_3 (Dense)	(None, 12)	300
dense_4 (Dense)	(None, 5)	65

Total params: 3,353 Trainable params: 3,353 Non-trainable params: 0

### compile the model

### In [18]:

```
model.compile(loss='categorical_crossentropy', optimizer='adam', metrics=['accuracy'])
```

### train the model

In [19]:

model.fit(X\_train,Y\_train,epochs=48,batch\_size=6)

```
Epoch 1/48
racy: 0.2929
Epoch 2/48
racy: 0.4214
Epoch 3/48
racy: 0.6429
Epoch 4/48
racy: 0.6643
Epoch 5/48
racy: 0.6714
Epoch 6/48
racy: 0.7500
Epoch 7/48
24/24 [============= ] - 0s 1ms/step - loss: 0.5144 - accu
racy: 0.8071
Epoch 8/48
racy: 0.9286
Epoch 9/48
racy: 0.9786
Epoch 10/48
racy: 0.9786
Epoch 11/48
racy: 0.9857
Epoch 12/48
racy: 0.9786
Epoch 13/48
racy: 0.9929
Epoch 14/48
racy: 0.9857
Epoch 15/48
racy: 0.9929
Epoch 16/48
racy: 0.9929
Epoch 17/48
racy: 0.9929
Epoch 18/48
racy: 1.0000
Epoch 19/48
racy: 0.9929
Epoch 20/48
racy: 1.0000
Epoch 21/48
```

```
racy: 1.0000
Epoch 22/48
racy: 1.0000
Epoch 23/48
racy: 1.0000
Epoch 24/48
racy: 1.0000
Epoch 25/48
racy: 1.0000
Epoch 26/48
24/24 [============= ] - 0s 1ms/step - loss: 0.0202 - accu
racy: 1.0000
Epoch 27/48
racy: 1.0000
Epoch 28/48
racy: 1.0000
Epoch 29/48
racy: 1.0000
Epoch 30/48
racy: 1.0000
Epoch 31/48
racy: 1.0000
Epoch 32/48
24/24 [============ ] - 0s 1ms/step - loss: 0.0137 - accu
racy: 1.0000
Epoch 33/48
racy: 1.0000
Epoch 34/48
racy: 1.0000
Epoch 35/48
racy: 1.0000
Epoch 36/48
racy: 1.0000
Epoch 37/48
racy: 1.0000
Epoch 38/48
racy: 1.0000
Epoch 39/48
racy: 1.0000
Epoch 40/48
racy: 1.0000
Epoch 41/48
```

```
racy: 1.0000
Epoch 42/48
24/24 [=========== ] - 0s 1ms/step - loss: 0.0084 - accu
racy: 1.0000
Epoch 43/48
24/24 [=============== ] - Os 1ms/step - loss: 0.0153 - accu
racy: 0.9929
Epoch 44/48
24/24 [============== ] - Os 1ms/step - loss: 0.0059 - accu
racy: 1.0000
Epoch 45/48
racy: 1.0000
Epoch 46/48
racy: 1.0000
Epoch 47/48
racy: 1.0000
Epoch 48/48
24/24 [=========== ] - Os 1ms/step - loss: 0.0047 - accu
racy: 1.0000
Out[19]:
```

<keras.callbacks.History at 0x12f6ca780d0>

#### evaluate the model on the test set

### In [20]:

```
test_loss, test_acc = model.evaluate(X_test, Y_test)
print('Test accuracy:', test_acc * 100)
```

2/2 [=========== ] - 0s 5ms/step - loss: 0.3741 - accura

cy: 0.8833

Test accuracy: 88.33333253860474