## Al Assignment 2.

## Building an ANN model for Drug classification.

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```
In [1]:
          # Importing Libraries
          import numpy as np
          import pandas as pd
          import matplotlib.pyplot as plt
          import seaborn as sns
In [2]:
          import tensorflow as tf
          from tensorflow import keras
          from keras.layers import Dense,BatchNormalization,Dropout
          from sklearn.model_selection import train_test_split
          from sklearn.metrics import accuracy_score
In [4]:
          # Loading the dataset
          from google.colab import files
          uploaded = files.upload()
         Choose Files No file chosen
                                              Upload widget is only available when the cell has been
        executed in the current browser session. Please rerun this cell to enable.
         Saving drug200.csv to drug200.csv
```

## Reading the Dataset.

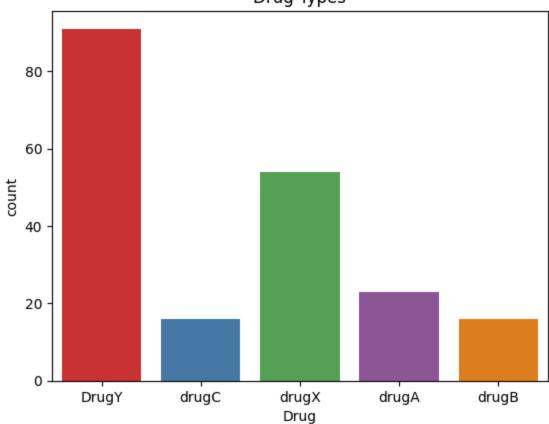
```
In [6]:
    df = pd.read_csv('drug200.csv')
    df.head()
```

Out[6]:		Age	Sex	ВР	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

```
In [10]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
         RangeIndex: 200 entries, 0 to 199
         Data columns (total 6 columns):
               Column
                            Non-Null Count Dtype
                            -----
          0
                            200 non-null
                                            int64
               Age
          1
              Sex
                            200 non-null
                                            object
              BP
                            200 non-null
                                            object
          3
              Cholesterol 200 non-null
                                            object
                            200 non-null
                                            float64
              Na_to_K
          5
              Drug
                            200 non-null
                                            obiect
         dtypes: float64(1), int64(1), object(4)
         memory usage: 9.5+ KB
In [13]:
          df.isnull().sum()
                         0
         Age
Out[13]:
         Sex
                         0
         ΒP
                         0
         Cholesterol
                         0
                         0
         Na_to_K
         Drug
                         0
         dtype: int64
In [15]:
          df.duplicated().sum()
Out[15]:
In [16]:
          df['Drug'].unique()
          array(['DrugY', 'drugC', 'drugX', 'drugA', 'drugB'], dtype=object)
Out[16]:
In [27]:
          sns.countplot(x=df['Drug'], palette = "Set1")
          plt.title('Drug Types');
          <ipython-input-27-ba7d2a90dba2>:1: FutureWarning:
         Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0.
         Assign the `x` variable to `hue` and set `legend=False` for the same effect.
            sns.countplot(x=df['Drug'], palette = "Set1")
```





# Preprocessing.

```
In [28]: X=df.drop(columns='Drug')
    y=df['Drug']
```

In [29]: X=pd.get\_dummies(X,dtype=float,drop\_first=True)
X

Out[29]:		Age	Na_to_K	Sex_M	BP_LOW	BP_NORMAL	${\bf Cholesterol\_NORMAL}$
	0	23	25.355	0.0	0.0	0.0	0.0
	1	47	13.093	1.0	1.0	0.0	0.0
	2	47	10.114	1.0	1.0	0.0	0.0
	3	28	7.798	0.0	0.0	1.0	0.0
	4	61	18.043	0.0	1.0	0.0	0.0
	•••		•••				
	195	56	11.567	0.0	1.0	0.0	0.0
	196	16	12.006	1.0	1.0	0.0	0.0
	197	52	9.894	1.0	0.0	1.0	0.0
	198	23	14.020	1.0	0.0	1.0	1.0

	Age	Na_to_K	Sex_M	BP_LOW	BP_NORMAL	Cholesterol_NORMAL
199	40	11.349	0.0	1.0	0.0	1.0

200 rows × 6 columns

In [30]:

```
sns.distplot(df['Age']);
```

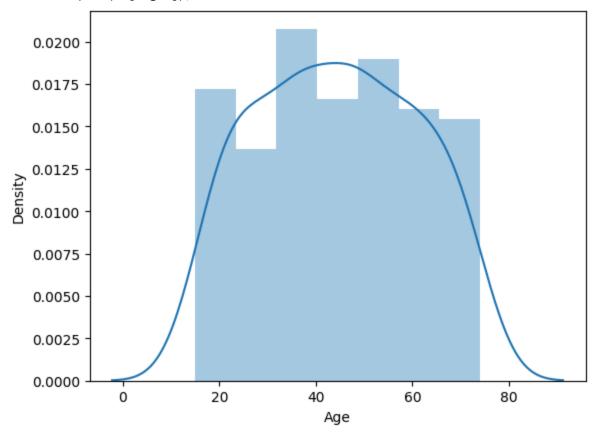
<ipython-input-30-3cd339c99e47>:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

sns.distplot(df['Age']);



In [31]:

```
sns.distplot(df['Na_to_K'])
```

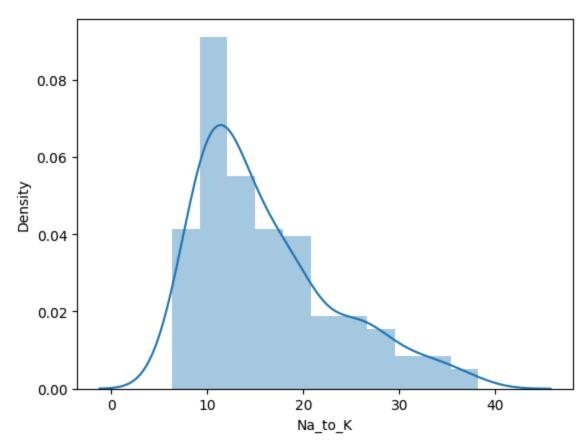
<ipython-input-31-bf7533b30019>:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

```
sns.distplot(df['Na_to_K'])
Out[31]: <Axes: xlabel='Na_to_K', ylabel='Density'>
```



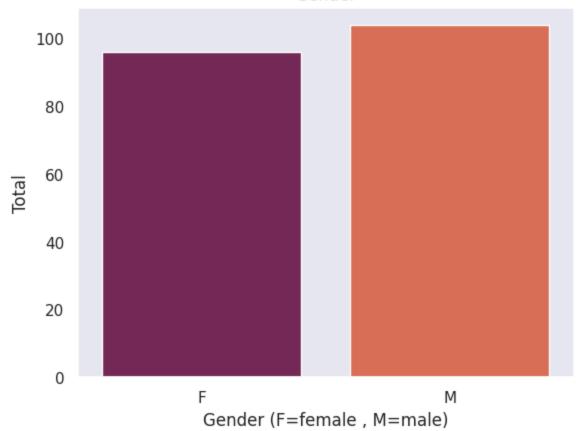
```
sns.set_theme(style="dark")
sns.countplot(data=df ,x= df['Sex'] , palette='rocket')
plt.xlabel('Gender (F=female , M=male)')
plt.ylabel('Total')
plt.title('Gender');
```

<ipython-input-32-2d15fd91a2c3>:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

```
sns.countplot(data=df ,x= df['Sex'] , palette='rocket')
```

#### Gender

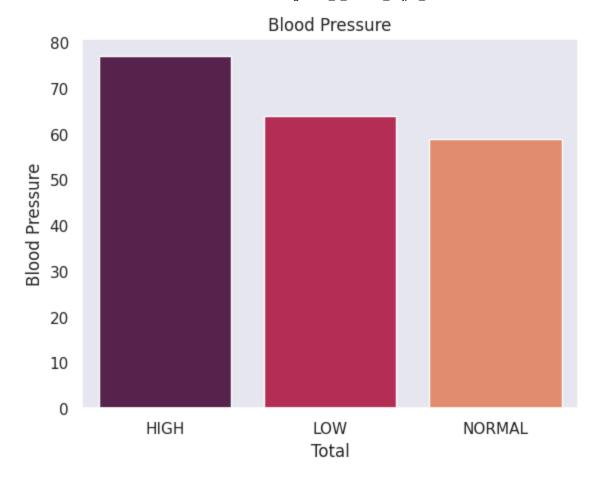


```
In [33]:
    sns.countplot( data=df, x=df['BP'], palette="rocket")
    plt.ylabel('Blood Pressure')
    plt.xlabel('Total')
    plt.title('Blood Pressure');
```

<ipython-input-33-f353d9e00834>:1: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effect.

sns.countplot( data=df, x=df['BP'], palette="rocket")



## **Building ANN Model.**

```
In [41]:
          from sklearn.preprocessing import StandardScaler
          X = df.drop('Drug', axis=1).values
          y = pd.get_dummies(df['Drug']).values # One-hot encode the target variable
          # Splitting the dataset into the Training set and Test set
          X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=4
In [52]:
          # Feature Scaling
          scaler = StandardScaler()
          X_train = scaler.fit_transform(X_train)
          X_test = scaler.transform(X_test)
In [53]:
          # Build the Neural Network Model
          model = tf.keras.models.Sequential([
              tf.keras.layers.Dense(128, activation='relu', input_shape=(X_train.shape[1],)),
              tf.keras.layers.Dense(64, activation='relu'),
              tf.keras.layers.Dense(32, activation='relu'),
              tf.keras.layers.Dense(y_train.shape[1], activation='softmax') # Output Layer
          ])
In [46]:
          # Compile the Model
          model.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['accuracy'])
```

```
# Train the Model
model.fit(X_train, y_train, batch_size=32, epochs=25, validation_split=0.1)

# Evaluate the Model
loss, accuracy = model.evaluate(X_test, y_test)
print(f'Test Loss: {loss}, Test Accuracy: {accuracy}')
```

```
Epoch 1/25
val_loss: 0.1764 - val_accuracy: 0.9375
Epoch 2/25
5/5 [============ - - 0s 22ms/step - loss: 0.1867 - accuracy: 0.9792 -
val_loss: 0.1512 - val_accuracy: 1.0000
val_loss: 0.1286 - val_accuracy: 0.9375
Epoch 4/25
5/5 [===========] - 0s 28ms/step - loss: 0.1462 - accuracy: 0.9792 -
val_loss: 0.1196 - val_accuracy: 0.9375
Epoch 5/25
5/5 [================== ] - 0s 21ms/step - loss: 0.1312 - accuracy: 0.9722 -
val_loss: 0.1080 - val_accuracy: 0.9375
val_loss: 0.0922 - val_accuracy: 0.9375
5/5 [============ - - 0s 20ms/step - loss: 0.1015 - accuracy: 0.9861 -
val_loss: 0.0820 - val_accuracy: 0.9375
Epoch 8/25
5/5 [============ - - 0s 21ms/step - loss: 0.0918 - accuracy: 0.9861 -
val_loss: 0.0750 - val_accuracy: 0.9375
Epoch 9/25
5/5 [=========== - - 0s 29ms/step - loss: 0.0859 - accuracy: 0.9722 -
val_loss: 0.0693 - val_accuracy: 0.9375
Epoch 10/25
5/5 [============ - - 0s 31ms/step - loss: 0.0813 - accuracy: 0.9583 -
val_loss: 0.0662 - val_accuracy: 0.9375
Epoch 11/25
val_loss: 0.0604 - val_accuracy: 0.9375
Epoch 12/25
val_loss: 0.0545 - val_accuracy: 0.9375
Epoch 13/25
5/5 [============ - - 0s 20ms/step - loss: 0.0613 - accuracy: 0.9722 -
val_loss: 0.0504 - val_accuracy: 0.9375
val_loss: 0.0474 - val_accuracy: 0.9375
Epoch 15/25
val loss: 0.0447 - val accuracy: 0.9375
Epoch 16/25
val_loss: 0.0393 - val_accuracy: 0.9375
Epoch 17/25
5/5 [=========== - os 20ms/step - loss: 0.0482 - accuracy: 0.9653 -
val_loss: 0.0375 - val_accuracy: 0.9375
Epoch 18/25
```

```
5/5 [=================== ] - 0s 17ms/step - loss: 0.0477 - accuracy: 0.9444 -
val_loss: 0.0382 - val_accuracy: 0.9375
Epoch 19/25
5/5 [============ - - 0s 19ms/step - loss: 0.0436 - accuracy: 0.9861 -
val_loss: 0.0387 - val_accuracy: 0.9375
Epoch 20/25
val_loss: 0.0369 - val_accuracy: 0.9375
Epoch 21/25
val_loss: 0.0333 - val_accuracy: 0.9375
Epoch 22/25
val_loss: 0.0319 - val_accuracy: 0.9375
Epoch 23/25
5/5 [================ ] - 0s 19ms/step - loss: 0.0378 - accuracy: 0.9444 -
val_loss: 0.0278 - val_accuracy: 0.9375
Epoch 24/25
5/5 [============ - - 0s 17ms/step - loss: 0.0358 - accuracy: 0.9792 -
val_loss: 0.0324 - val_accuracy: 0.9375
Epoch 25/25
5/5 [============ - - 0s 21ms/step - loss: 0.0398 - accuracy: 0.9375 -
val_loss: 0.0309 - val_accuracy: 0.9375
Test Loss: 0.030085628852248192, Test Accuracy: 0.9750000238418579
```

### Testing model with random data.

```
In [45]:
         # Generating random input data
         num_samples = 5
          # Generating random data of the same shape as input features
          random input = np.random.rand(num samples, X train.shape[1])
          # Scaling the random input data
          random_input_scaled = scaler.transform(random_input)
          # Predicting using the trained model
          predictions = model.predict(random_input_scaled)
          # Decode one-hot encoded predictions to get the predicted drug
          predicted drugs = [np.argmax(pred) for pred in predictions]
          # Mapping predicted drug index to actual drug name
          drug_mapping = {0: 'drugA', 1: 'drugB', 2: 'drugC', 3: 'drugX', 4: 'drugY'}
          predicted_drugs_names = [drug_mapping[pred] for pred in predicted_drugs]
          # Displaying the random input and predicted drugs
          print("Random Input Data:")
          print(random_input)
         print("\nPredicted Drugs:")
         print(predicted drugs names)
         Random Input Data:
         [[0.75014702 0.21788608 0.2416202 0.57287512 0.84810747]
          [0.80696005 0.94628087 0.47614017 0.0406879 0.83551932]
          [0.85600118 0.01422557 0.86672845 0.98778917 0.19111268]
```

[0.29004582 0.22753831 0.95762639 0.14957082 0.10376679]
[0.85872801 0.38564201 0.41468926 0.84889413 0.65737201]]

Predicted Drugs:
['drugA', 'drugA', 'drugC', 'drugA']

In []: