## Question

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. Dataset Link: https://www.kaggle.com/datasets/prathamtripathi/drug-classification

Task 1: Read the dataset and do data pre-processing Task 2: Build the ANN model with (input layer, min 3 hidden layers & output layer) Task 3: Test the model with random data

```
In [4]:
          import pandas as pd
          import numpy as np
          import matplotlib.pyplot as plt
          import seaborn as sns
In [6]:
          df = pd.read csv('drug200.csv')
Out[6]:
             Age
                  Sex
                            BP Cholesterol Na_to_K
                                                     Drug
           0
               23
                          HIGH
                                     HIGH
                                             25.355 DrugY
               47
                           LOW
                                     HIGH
                                             13 093
                    M
                                                    druaC
           2
               47
                    M
                           LOW
                                     HIGH
                                             10.114 drugC
               28
                       NORMAL
                                     HIGH
                                              7.798
                                                    drugX
                    F
                                             18.043 DrugY
                           LOW
                                     HIGH
           4
               61
         195
                    F
                           LOW
               56
                                     HIGH
                                             11.567
                                                   drugC
                                             12.006
                           LOW
                                     HIGH
         196
               16
                    M
                                                    druaC
         197
               52
                    М
                      NORMAL
                                     HIGH
                                              9.894
                                                    drugX
         198
               23
                       NORMAL
                                  NORMAL
                                             14.020 drugX
                                             11.349 drugX
         199
               40
                           LOW
                                  NORMAL
```

200 rows × 6 columns

47

М

LOW

HIGH

13.093 drugC

```
In [7]: df.head()
Out[7]: Age Sex BP Cholesterol Na_to_K Drug
```

t[7]:		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

```
drugC
                                       HIGH
                                              12.006
          196
                16
                     Μ
                           LOW
                                                      drugC
          197
                     Μ
                        NORMAL
                                       HIGH
                                               9.894
                52
                                                      drugX
                        NORMAL
                                     NORMAL
          198
                23
                     Μ
                                              14.020
                                                      drugX
                     F
                                     NORMAL
                                              11.349 drugX
         199
                40
                           LOW
          [200 rows x 6 columns]>
In [16]:
          df.shape
Out[16]: (200, 6)
In [13]:
          df.describe
                                                                BP Cholesterol Na_to_K
Out[13]: <bound method NDFrame.describe of
                                                                                           Drug
                                                  Age Sex
                                              25.355 DrugY
                    F
                          HIGH
                23
                                       HIGH
                                              13.093
                     Μ
                           LOW
         1
                47
                                       HIGH
                                                      drugC
         2
                47
                     Μ
                           LOW
                                       HIGH
                                              10.114
                                                      drugC
                        NORMAL
                    F
         3
                28
                                       HIGH
                                               7.798
                                                      drugX
                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
                23
                        NORMAL
                                     NORMAL
                                              14.020
          198
                     Μ
                                                      drugX
                                              11.349 drugX
         199
                40
                     F
                           LOW
                                     NORMAL
          [200 rows x 6 columns]>
In [32]:
          sns.countplot(x='Drug',data=df,hue='Drug')
Out[32]: <AxesSubplot:xlabel='Drug', ylabel='count'>
                                                     Drug
                                                     DrugY
            80
                                                      drugC
                                                      drugX
                                                      drugA
            60
                                                      drugB
           40
            20
```

```
In [33]:
          X=df.iloc[:,0:5]
          Y=df['Drug']
In [34]:
          Y_class=len(np.unique(Y))
          print(Y_class)
```

5

2

3

4

195

47

28 F

61

56

F

F

LOW

LOW

LOW

NORMAL

HIGH

HIGH

HIGH

HIGH

10.114 drugC

drugX

DrugY

7.798

18.043

11.567

```
In [35]:
```

Out[35]:

DrugY

drugC

drugX

Drug

drugA

drugB

	Age	Sex	BP	Cholesterol	Na_to_K
0	23	F	HIGH	HIGH	25.355

```
F NORMAL
               61
                          LOW
                                    HIGH
                                           18.043
         195
               56
                          LOW
                                    HIGH
                                           11.567
         196
                         LOW
                                    HIGH
                                           12.006
               16
                                            9.894
         197
               52
                   M NORMAL
                                    HIGH
         198
               23
                    M NORMAL
                                 NORMAL
                                           14.020
                                 NORMAL
         200 rows × 5 columns
In [21]:
Out[21]: 0
                DrugY
                 drugC
                drugC
         3
                 drugX
         4
                DrugY
         195
                drugC
         196
                drugC
         197
                drugX
         198
                 drugX
         199
                 drugX
         Name: Drug, Length: 200, dtype: object
In [36]:
          from sklearn.preprocessing import LabelEncoder
          X=pd.get dummies(X,columns=['Sex','BP','Cholesterol'],drop_first = True)
          Le=LabelEncoder()
          Y=Le.fit transform(Y)
In [37]:
          from sklearn.model_selection import train_test_split
          X_train,X_test,Y_train,Y_test=train_test_split(X,Y,test_size=0.4,random_state=10)
In [38]:
          from sklearn.preprocessing import StandardScaler
          sc=StandardScaler()
          X train=sc.fit transform(X train)
          X_test=sc.fit_transform(X_test)
In [39]:
          from tensorflow import keras
          Y_train=keras.utils.to_categorical(Y_train)
          Y_test=keras.utils.to_categorical(Y_test)
In [40]:
          from tensorflow.keras.models import Sequential
          from tensorflow.keras.layers import Dense
          mod=Sequential()
          mod.add(Dense(48,input_dim=6, activation='relu'))
          mod.add(Dense(36,activation='relu'))
          mod.add(Dense(24,activation='relu'))
          mod.add(Dense(12,activation='relu'))
          mod.add(Dense(Y_class,activation='softmax'))
In [42]:
          mod.compile(loss='categorical_crossentropy',optimizer='adam',metrics=['accuracy'])
In [43]:
          mod.fit(X_train,Y_train,epochs=48,batch_size=6)
         Epoch 1/48
```

20/20 [================= ] - 0s 4ms/step - loss: 1.4643 - accuracy: 0.5667

LOW

LOW

47

Epoch 2/48

Epoch 3/48

3 28 M

HIGH

HIGH

HIGH

13.093

10.114

7.798

```
Epoch 4/48
20/20 [============= ] - 0s 4ms/step - loss: 1.1402 - accuracy: 0.7500
Epoch 5/48
      20/20 [==
Epoch 6/48
      ========] - Os 4ms/step - loss: 0.7377 - accuracy: 0.7417
20/20 [====
Epoch 7/48
Epoch 8/48
Epoch 9/48
Epoch 10/48
Epoch 11/48
Epoch 12/48
Epoch 13/48
Epoch 14/48
20/20 [=====
    Epoch 15/48
    20/20 [=====
Epoch 16/48
20/20 [============] - 0s 4ms/step - loss: 0.1604 - accuracy: 0.9750
Epoch 17/48
Epoch 18/48
20/20 [============= ] - 0s 8ms/step - loss: 0.1041 - accuracy: 0.9833
Epoch 19/48
Epoch 20/48
20/20 [======
    Epoch 21/48
20/20 [============] - 0s 4ms/step - loss: 0.0545 - accuracy: 1.0000
Epoch 22/48
Epoch 23/48
20/20 [=====
    Epoch 24/48
Fnoch 25/48
20/20 [============ ] - 0s 4ms/step - loss: 0.0330 - accuracy: 1.0000
Epoch 26/48
Epoch 27/48
Epoch 28/48
20/20 [=====
    Epoch 29/48
20/20 [=====
    Epoch 30/48
Epoch 31/48
Epoch 32/48
Epoch 33/48
Epoch 34/48
Epoch 35/48
Epoch 36/48
Epoch 37/48
Epoch 38/48
20/20 [=====
    Epoch 39/48
Epoch 40/48
Epoch 41/48
Epoch 42/48
Epoch 43/48
20/20 [=====
   Epoch 44/48
20/20 [============= ] - 0s 4ms/step - loss: 0.0041 - accuracy: 1.0000
```

```
Epoch 45/48
     Epoch 46/48
     Epoch 47/48
                  ========] - Os 6ms/step - loss: 0.0035 - accuracy: 1.0000
     20/20 [=====
     Epoch 48/48
     Out[43]: <keras.callbacks.History at 0x1cda2b3a0d0>
In [46]:
     test loss,test acc=mod.evaluate(X test,Y test)
     print('Test Accuracy:',test_acc*100)
     Test Accuracy: 85.00000238418579
In [51]:
     pred = mod.predict(X_test[:1])
     1/1 [======] - 0s 20ms/step
In [52]:
Out[52]: array([[9.9998724e-01, 5.9284008e-07, 1.0111640e-06, 1.1128964e-05,
         6.6235086e-12]], dtype=float32)
In [ ]:
```

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