

Smart Bridge Assignment - 2

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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>

```
# Importing Required Libraries
```

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

▼ Task 1: Read the dataset and do data pre-processing

```
df = pd.read_csv('/content/drug200.csv') #Reading the data
print(df.head(),df.tail())
df.info()
```

	Age	Sex	BP	Cholesterol	Na_to_K	Drug		Age	Sex	BP	Cholesterol	Na_t
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						
195	56	F	LOW	HIGH	11.567	drugC						

```

196    16    M    LOW    HIGH    12.006    drugC
197    52    M    NORMAL    HIGH    9.894    drugX
198    23    M    NORMAL    NORMAL    14.020    drugX
199    40    F    LOW    NORMAL    11.349    drugX
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 200 entries, 0 to 199
Data columns (total 6 columns):
#   Column          Non-Null Count  Dtype
---  -
0   Age             200 non-null   int64
1   Sex             200 non-null   object
2   BP              200 non-null   object
3   Cholesterol     200 non-null   object
4   Na_to_K         200 non-null   float64
5   Drug            200 non-null   object
dtypes: float64(1), int64(1), object(4)
memory usage: 9.5+ KB

```

```
df['Drug'].value_counts()
```

```

DrugY      91
drugX      54
drugA      23
drugC      16
drugB      16
Name: Drug, dtype: int64

```

```
#Checking for null values
```

```
df.isnull().sum()
```

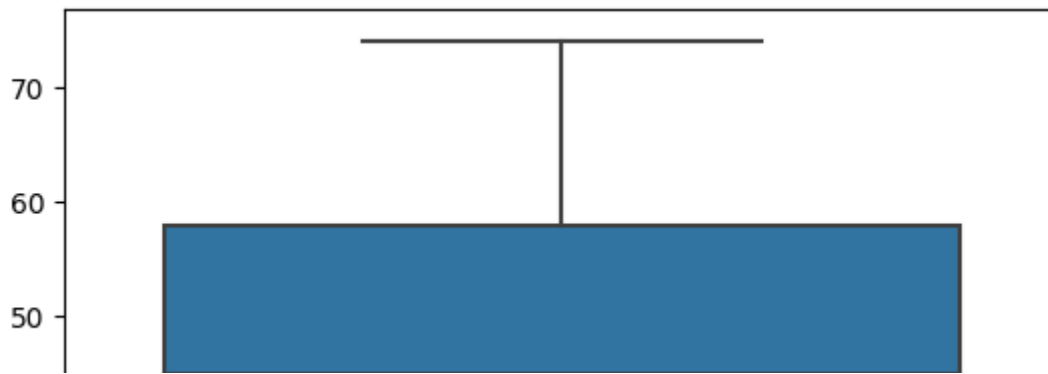
```

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

```

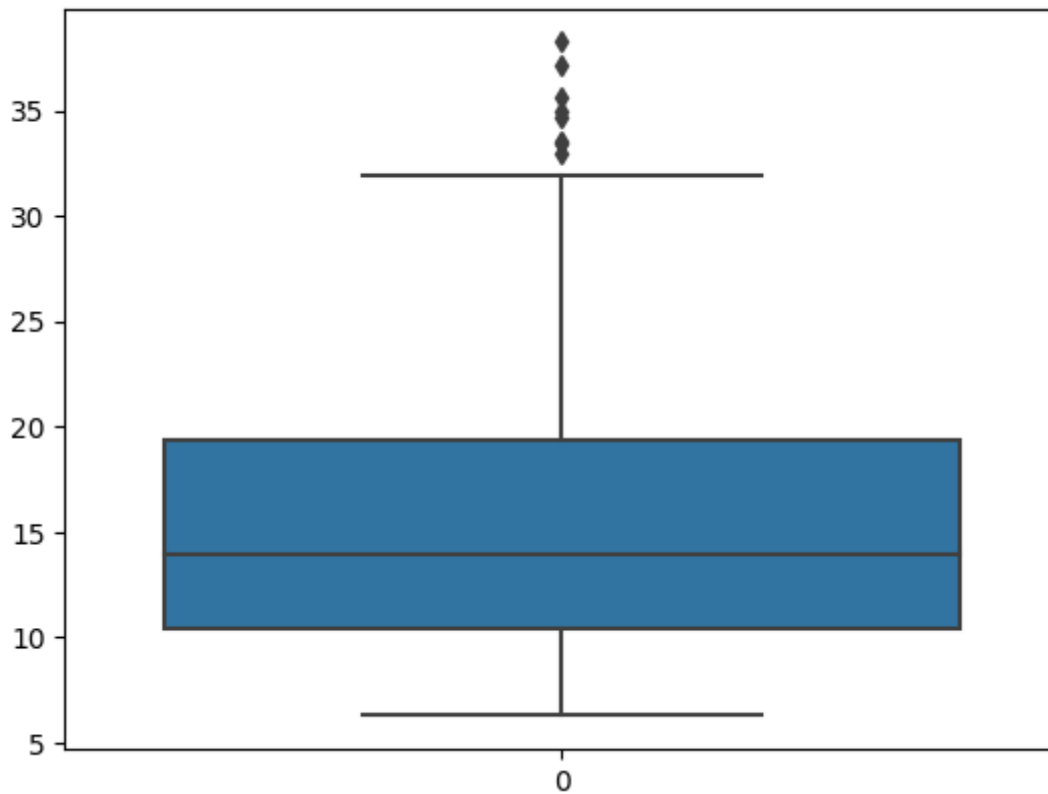
```
sns.boxplot(df['Age'])# no outliers
```

<Axes: >



```
sns.boxplot(df['Na_to_K'])# contains outliers
```

<Axes: >



```
# Na_to_K contains outliers
# Replacing outliers with medians
q1 = df.Na_to_K.quantile(0.25)
q3 = df.Na_to_K.quantile(0.75)

IQR = q3-q1
print('IQR is:\t',IQR)

UpperLimit = q3 + 1.5*IQR
print('Upper Limit is:\t',UpperLimit)
```

```
IQR is: 8.9345
Upper Limit is: 32.78175
```

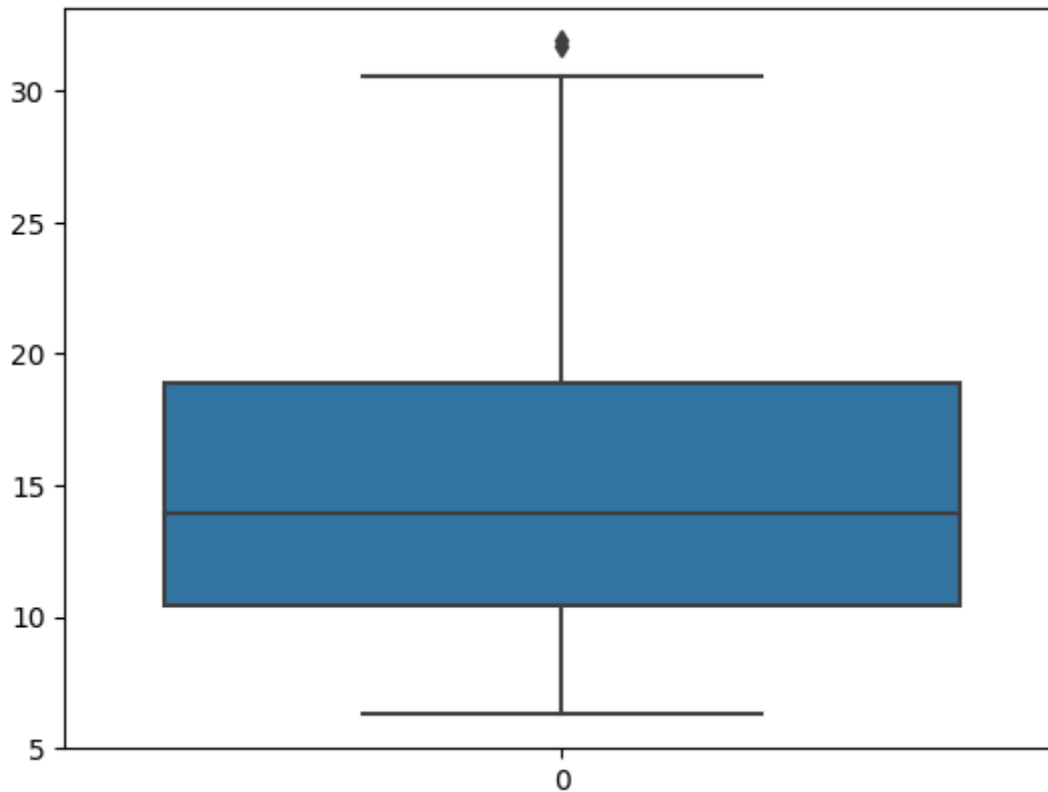
```
print(df['Na_to_K'].median())
```

```
13.9365
```

```
df['Na_to_K'] = np.where(df['Na_to_K']>UpperLimit,13.9365,df['Na_to_K'])
```

```
sns.boxplot(df['Na_to_K'])# Still contain outlier
```

```
<Axes: >
```



```
# Na_to_K contains outliers
```

```
q1 = df.Na_to_K.quantile(0.25)
```

```
q3 = df.Na_to_K.quantile(0.75)
```

```
IQR = q3-q1
```

```
print('IQR is:\t',IQR)
```

```
UpperLimit = q3 + 1.5*IQR
```

```
print('Upper Limit is:\t',UpperLimit)
```

```
print(df['Na_to_K'].median())
```

```
IQR is: 8.409000000000002
```

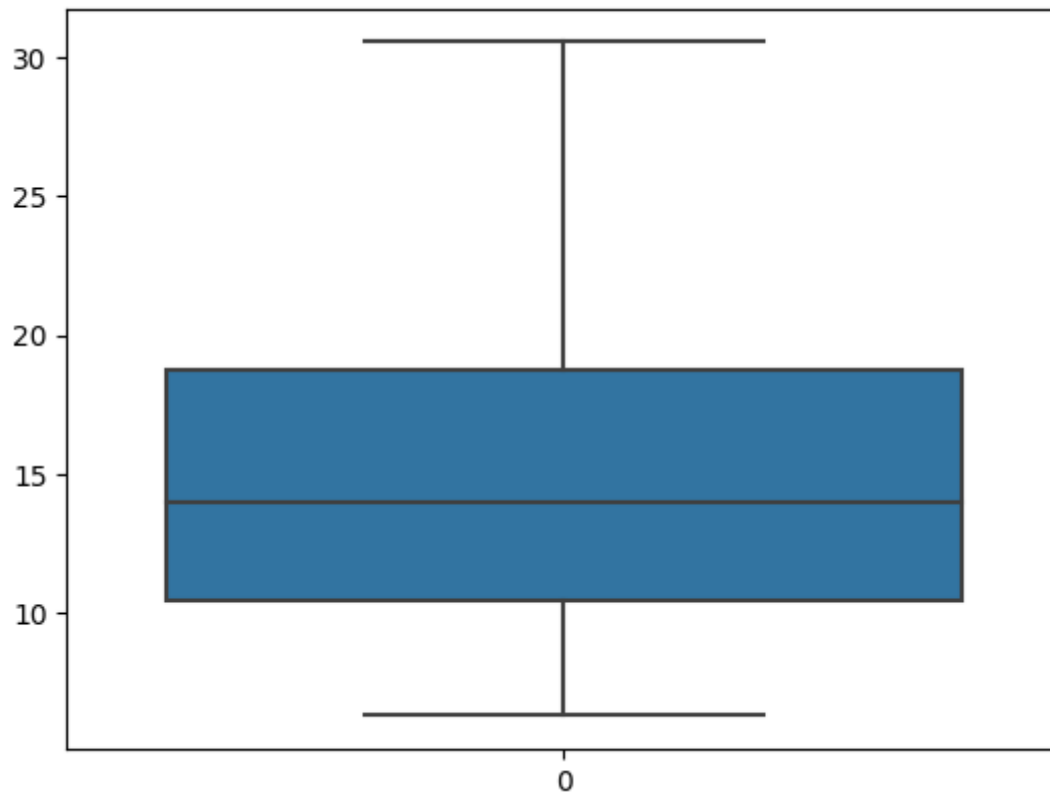
```
Upper Limit is: 31.468000000000004
```

```
13.93575
```

```
df['Na_to_K'] = np.where(df['Na_to_K']>UpperLimit,13.93575,df['Na_to_K'])
```

```
sns.boxplot(df['Na_to_K'])# Outlier handled successfully
```

<Axes: >



```
from sklearn.preprocessing import LabelEncoder, MinMaxScaler #library used for Encoding
```

```
le = LabelEncoder() #initialize the lib
# Convert categorical features to numerical labels
```

```
df['Sex'] = le.fit_transform(df['Sex'])
df['BP'] = le.fit_transform(df['BP'])
df['Cholesterol'] = le.fit_transform(df['Cholesterol'])
df['Drug'] = le.fit_transform(df['Drug'])
```

```
# Scale the numerical features
scaler = MinMaxScaler()
df[['Age', 'Na_to_K']] = scaler.fit_transform(df[['Age', 'Na_to_K']])
```

```
# Splitting the data
#x = df[['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K']]
x=df.drop(columns = ['Drug'],axis=1)
y = df['Drug']
y[0:5]
```

```
0    0
1    3
2    3
3    4
4    0
Name: Drug, dtype: int64
```

```
from sklearn.model_selection import train_test_split
```

```
xtrain,xtest,ytrain,ytest = train_test_split(x,y,test_size = 0.2,random_state=21)
print(xtrain.shape,xtest.shape,ytrain.shape,ytest.shape)
xtrain.head(),ytrain.head(),xtest.head(),ytest.head()
```

```
(160, 5) (40, 5) (160,) (40,)
(
      Age  Sex  BP  Cholesterol  Na_to_K
176  0.559322    1    0             1  0.171900
111  0.542373    0    2             1  0.017038
114  0.084746    0    2             1  0.123956
14   0.593220    0    2             0  0.264785
106  0.118644    1    2             0  0.233919,
176    1
111    4
114    4
14     4
106    4
Name: Drug, dtype: int64,
      Age  Sex  BP  Cholesterol  Na_to_K
144  0.406780    1    0             0  0.139718
9    0.474576    1    1             1  0.539076
17   0.474576    1    0             0  0.317009
20   0.711864    1    1             1  0.529199
45   0.864407    0    2             1  0.075641,
144    1
9      0
17     1
20     0
45     4
Name: Drug, dtype: int64)
```

Task 2: Build the ANN model with (input layer, min 3 hidden layers & output layer)

```
# ANN Model
```

```
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
```

```
model = Sequential()
model.add(Dense(64,input_dim=5,activation = 'relu')) #Adding Input layer with 4 neurons si
model.add(Dense(32,activation = 'relu')) #Adding 1st Hidden Layer with 32 neurons
model.add(Dense(26,activation = 'relu')) #Adding 2nd Hidden Layer with 26 neurons
model.add(Dense(18,activation = 'relu')) #Adding 3rd Hidden Layer with 18 neurons
model.add(Dense(12,activation = 'relu')) #Adding 4th Hidden Layer with 12 neurons
```

```
# Here it is multi class classification we softmax, if binary we use sigmoid
model.add(Dense(5,activation = 'softmax')) #Adding Ouput layer with 3 since we have 3 typ
```

```
# Here if it is softmax we use categorical_crossentropy and if it is sigmoid means we use  
  
# we mentioned metrics as accuracy so accuracy will also be printed at the time of output  
model.compile(optimizer='adam',loss='sparse_categorical_crossentropy',metrics = ['accuracy
```

```
model.summary()
```

```
Model: "sequential_1"
```

Layer (type)	Output Shape	Param #
dense_5 (Dense)	(None, 64)	384
dense_6 (Dense)	(None, 32)	2080
dense_7 (Dense)	(None, 26)	858
dense_8 (Dense)	(None, 18)	486
dense_9 (Dense)	(None, 12)	228
dense_10 (Dense)	(None, 5)	65
Total params: 4,101		
Trainable params: 4,101		
Non-trainable params: 0		

```
model.fit(xtrain, ytrain, epochs=56, batch_size=20,validation_data=(xtest, ytest))
```




```

8/8 [=====] - 0s 6ms/step - loss: 0.1138 - accuracy: 0.9
Epoch 43/56
8/8 [=====] - 0s 8ms/step - loss: 0.1173 - accuracy: 0.9
Epoch 44/56
8/8 [=====] - 0s 6ms/step - loss: 0.1279 - accuracy: 0.9
Epoch 45/56
8/8 [=====] - 0s 9ms/step - loss: 0.1655 - accuracy: 0.9
Epoch 46/56
8/8 [=====] - 0s 7ms/step - loss: 0.1648 - accuracy: 0.9
Epoch 47/56
8/8 [=====] - 0s 7ms/step - loss: 0.1766 - accuracy: 0.9
Epoch 48/56
8/8 [=====] - 0s 7ms/step - loss: 0.1163 - accuracy: 0.9
Epoch 49/56
8/8 [=====] - 0s 7ms/step - loss: 0.1109 - accuracy: 0.9
Epoch 50/56
8/8 [=====] - 0s 9ms/step - loss: 0.1106 - accuracy: 0.9
Epoch 51/56
8/8 [=====] - 0s 9ms/step - loss: 0.1007 - accuracy: 0.9
Epoch 52/56
8/8 [=====] - 0s 7ms/step - loss: 0.1059 - accuracy: 0.9
Epoch 53/56
8/8 [=====] - 0s 10ms/step - loss: 0.0963 - accuracy: 0.
Epoch 54/56
8/8 [=====] - 0s 9ms/step - loss: 0.0897 - accuracy: 0.9
Epoch 55/56
8/8 [=====] - 0s 7ms/step - loss: 0.1039 - accuracy: 0.9
Epoch 56/56
8/8 [=====] - 0s 10ms/step - loss: 0.1035 - accuracy: 0.
<keras.callbacks.History at 0x7f6003b15d50>

```

x.head()

	Age	Sex	BP	Cholesterol	Na_to_K	
0	0.135593	0	0	0	0.785464	
1	0.542373	1	1	0	0.280835	
2	0.542373	1	1	0	0.158237	
3	0.220339	0	2	0	0.062924	
4	0.779661	0	1	0	0.484547	

▼ Task 3: Test the model with random data

```

#here while predicting we should consider transformed values rather than original values
ypred = model.predict([[0.87,1,1,1,0.8249]])
print(ypred)

```

```

1/1 [=====] - 0s 97ms/step
[[1.0000000e+00 1.9125792e-15 1.7526185e-16 1.1560463e-12 9.9391274e-13]]

```



```
ypred = np.argmax(ypred)
ypred
```

```
0
```

```
output = ['DrugY', 'drugX', 'drugA', 'drugC', 'drugB']
output[ypred]
```

```
'DrugY'
```

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

```
2/2 [=====] - 0s 11ms/step - loss: 0.2022 - accuracy: 0.9006
Test accuracy: 89.9999761581421
```

