

# THYROID DISEASE CLASSIFICATION USING ML

## MILESTONE 1: Data Collection & Preparation

### Activity 1: Collect the dataset

- ⇒ There are many popular open sources for collecting the data. Eg: kaggle.com, UCI repository, etc.
- ⇒ In this project, we have used drug200.csv data. This data is downloaded from kaggle.com. Please refer to the link given below to download the dataset.
- ⇒ Link: <https://www.kaggle.com/prathamtripathi/drug-classification>.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	Age	Sex	BP	Cholesterol	Na_to_K	Drug														
2		23 F	HIGH	HIGH	25.355	DrugY														
3		47 M	LOW	HIGH	13.093	drugC														
4		47 M	LOW	HIGH	10.114	drugC														
5		28 F	NORMAL	HIGH	7.798	drugX														
6		61 F	LOW	HIGH	18.043	DrugY														
7		22 F	NORMAL	HIGH	8.607	drugX														
8		49 F	NORMAL	HIGH	16.275	DrugY														
9		41 M	LOW	HIGH	11.037	drugC														
10		60 M	NORMAL	HIGH	15.171	DrugY														
11		43 M	LOW	NORMAL	19.368	DrugY														
12		47 F	LOW	HIGH	11.767	drugC														
13		34 F	HIGH	NORMAL	19.199	DrugY														
14		43 M	LOW	HIGH	15.376	DrugY														
15		74 F	LOW	HIGH	20.942	DrugY														
16		50 F	NORMAL	HIGH	12.703	drugX														
17		16 F	HIGH	NORMAL	15.516	DrugY														
18		69 M	LOW	NORMAL	11.455	drugX														
19		43 M	HIGH	HIGH	13.972	drugA														
20		23 M	LOW	HIGH	7.298	drugC														

### Activity 1.1: Importing the libraries

Import the necessary libraries as shown in the image

```
Importing the Libraries

[1] import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import matplotlib.pyplot as plt
from sklearn.metrics import accuracy_score, classification_report
```

## Activity 1.2: Read the Dataset

- ⇒ Our dataset format might be in .csv, excel files, .txt, .json, etc. We can read the dataset with the help of pandas.
- ⇒ In pandas, we have a function called `read_csv()` to read the dataset. As a parameter, we have to give the directory of the csv file

### Read the Dataset

```
[ ] drug = pd.read_csv('drug200.csv')
```

```
drug.head()
```

	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

```
[ ] drug.shape
```

```
(200, 6)
```

## Activity2: Data Pre-processing

As we have understood how the data is, let's pre-process the collected data. The download data set is not suitable for training the machine learning model as it might have so much randomness so we need to clean the dataset properly in order to fetch good results. This activity includes the following steps.

- Handling missing values
- Descriptive analysis
- Splitting the dataset as x and y
- Handling Categorical Values
- Splitting dataset into training and test set

**Note:** These are the general steps of pre-processing the data before using it for machine learning. Depending on the condition of your dataset, you may or may not have to go through all these steps.

## Activity 2.1: Checking for null values

- ⇒ For checking the null values, `data.isnull()` function is used. To sum those null values we use the `.sum()` function to it. From the below image we found that

there are no null values present in our dataset. So we can skip handling the missing values step.

#### Data Pre-processing

```
[ ] drug.describe()
```

	Age	Na_to_K
count	200.000000	200.000000
mean	44.315000	16.084485
std	16.544315	7.223956
min	15.000000	6.269000
25%	31.000000	10.445500
50%	45.000000	13.936500
75%	58.000000	19.380000
max	74.000000	38.247000

#### 1. Checking for null values

```
[ ] drug.isnull().sum()
```

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

```
[ ] drug.columns
```

```
Index(['Age', 'Sex', 'BP', 'Cholesterol', 'Na_to_K', 'Drug'], dtype='object')
```

No Null Values

⇒ NO null values, stop the checking for null values.

### Activity 2.2: Splitting the data x and y

⇒ Splitting the data x and y

#### 2. Splitting the data x and y

```
✓ [12] x_drug = drug.iloc[:, 0:5].values
15 x_drug[0]
```

```
array([23, 'F', 'HIGH', 'HIGH', 25.355], dtype=object)
```

```
✓ [13] y_drug = drug.iloc[:, 5].values
18 y_drug[0]
```

```
'DrugY'
```

```
x_drug
[60, 'M', 'HIGH', 'NORMAL', 8.621],
[74, 'M', 'HIGH', 'NORMAL', 15.436],
[39, 'M', 'HIGH', 'HIGH', 9.664],
[61, 'M', 'NORMAL', 'HIGH', 9.443],
[37, 'F', 'LOW', 'NORMAL', 12.006],
[26, 'F', 'HIGH', 'NORMAL', 12.307],
[61, 'F', 'LOW', 'NORMAL', 7.34],
[22, 'M', 'LOW', 'HIGH', 8.151],
[49, 'M', 'HIGH', 'NORMAL', 8.7],
[68, 'M', 'HIGH', 'HIGH', 11.009],
[55, 'M', 'NORMAL', 'NORMAL', 7.261],
[72, 'F', 'LOW', 'NORMAL', 14.642],
[37, 'M', 'LOW', 'NORMAL', 16.724],
[49, 'M', 'LOW', 'HIGH', 10.537],
[31, 'M', 'HIGH', 'NORMAL', 11.227],
[53, 'M', 'LOW', 'HIGH', 22.963],
[59, 'F', 'LOW', 'HIGH', 10.444],
[34, 'F', 'LOW', 'NORMAL', 12.923],
[30, 'F', 'NORMAL', 'HIGH', 10.443],
[57, 'F', 'HIGH', 'NORMAL', 9.945],
[43, 'M', 'NORMAL', 'NORMAL', 12.859],
[21, 'F', 'HIGH', 'NORMAL', 28.632],
[16, 'M', 'HIGH', 'NORMAL', 19.007],
[38, 'M', 'LOW', 'HIGH', 18.295],
[58, 'F', 'LOW', 'HIGH', 26.645],
[57, 'F', 'NORMAL', 'HIGH', 14.216],
[39, 'F', 'NORMAL', 'NORMAL', 17.225],
[41, 'F', 'LOW', 'NORMAL', 18.739],
[42, 'M', 'HIGH', 'NORMAL', 12.766],
[73, 'F', 'HIGH', 'HIGH', 18.348],
[48, 'M', 'HIGH', 'NORMAL', 10.446],
[25, 'M', 'NORMAL', 'HIGH', 19.011],
[39, 'M', 'NORMAL', 'HIGH', 15.969],
[67, 'F', 'NORMAL', 'HIGH', 15.891],
[22, 'F', 'HIGH', 'NORMAL', 22.818],
[59, 'F', 'NORMAL', 'HIGH', 13.884],
[20, 'F', 'LOW', 'NORMAL', 11.686],
[36, 'F', 'HIGH', 'NORMAL', 15.49],
[18, 'F', 'HIGH', 'HIGH', 37.188],
[57, 'F', 'NORMAL', 'NORMAL', 25.893],
[70, 'M', 'HIGH', 'HIGH', 9.849],
[47, 'M', 'HIGH', 'HIGH', 10.403],
[65, 'M', 'HIGH', 'NORMAL', 34.997],
[64, 'M', 'HIGH', 'NORMAL', 20.932],
[58, 'M', 'HIGH', 'HIGH', 18.991],
[23, 'M', 'HIGH', 'HIGH', 8.011],
[72, 'M', 'LOW', 'HIGH', 16.31],
[72, 'M', 'LOW', 'HIGH', 6.769],
[46, 'F', 'HIGH', 'HIGH', 34.686],
[56, 'F', 'LOW', 'HIGH', 11.567],
[16, 'M', 'LOW', 'HIGH', 12.006],
[52, 'M', 'NORMAL', 'HIGH', 9.894],
[23, 'M', 'NORMAL', 'NORMAL', 14.02],
[40, 'F', 'LOW', 'NORMAL', 11.349]], dtype=object)
```

### Activity 2.3: Handling Categorical Values

- ⇒ As we can see our dataset has categorical data we must convert the categorical data to integer encoding or binary encoding.
- ⇒ To convert the categorical features into numerical features we use encoding techniques. There are several techniques but in our project we are using OneHotEncoder and ColumnTransformer.
  - In our project, categorical features are x and y values.
  - Here, applying Ordinal Encoding on x values.

## ONE HOT ENCODING

Handling Categorical Values

```
[ ] from sklearn.preprocessing import OneHotEncoder
    from sklearn.compose import ColumnTransformer

[ ] oneHotEncoderDrugs = ColumnTransformer(transformers=[('OneHot', OneHotEncoder(), [1,2,3]), remainder='passthrough'])

[ ] x_drug = oneHotEncoderDrugs.fit_transform(x_drug)

[ ] x_drug

array([[1.0, 0.0, 1.0, ..., 0.0, 23, 25.355],
       [0.0, 1.0, 0.0, ..., 0.0, 47, 13.093],
       [0.0, 1.0, 0.0, ..., 0.0, 47, 10.114],
       ...,
       [0.0, 1.0, 0.0, ..., 0.0, 52, 9.894],
       [0.0, 1.0, 0.0, ..., 1.0, 23, 14.02],
       [1.0, 0.0, 0.0, ..., 1.0, 40, 11.349]], dtype=object)
```

```
[ ] from sklearn.preprocessing import StandardScaler
```

```
scalerDrug = StandardScaler()
x_drug = scalerDrug.fit_transform(x_drug)
x_drug

array([[ 1.040833, -1.040833, 1.26388393, ..., -0.97043679,
        -1.29159102, 1.28652212],
       [-0.96076892, 0.96076892, -0.79121189, ..., -0.97043679,
        0.16269866, -0.4151454 ],
       [-0.96076892, 0.96076892, -0.79121189, ..., -0.97043679,
        0.16269866, -0.82855818],
       ...,
       [-0.96076892, 0.96076892, -0.79121189, ..., -0.97043679,
        0.46567567, -0.85908883],
       [-0.96076892, 0.96076892, -0.79121189, ..., 1.03046381,
        -1.29159102, -0.28650033],
       [ 1.040833, -1.040833, -0.79121189, ..., 1.03046381,
        -0.26146916, -0.6571702 ]])
```

## Activity 2.4: Splitting data into train and test

- ⇒ Now let's split the Dataset into train and test sets.
- ⇒ **Changes:** first split the dataset into x and y and then split the data set.
- ⇒ Here x and y variables are created. On x variable, data is passed with dropping the target variable. And my target variable is passed. For splitting training and testing data we are using the `train_test_split()` function from sklearn. As parameters, we are passing x, y, test\_size, random\_state.

## Splitting data into train and test

```
[ ] from sklearn.model_selection import train_test_split

[ ] x_drug_train, x_drug_test, y_drug_train, y_drug_test = train_test_split(x_drug, y_drug, test_size = 0.25, random_state=0)

[ ] x_drug_train

array([[ 1.040833, -1.040833, -0.79121189, ..., -0.97043679,
        -0.988614, 0.4982762 ],
       [ 1.040833, -1.040833, 1.26388393, ..., 1.03046381,
        0.52627108, -0.49813326],
       [ 1.040833, -1.040833, 1.26388393, ..., -0.97043679,
        -1.59456803, 2.92865486],
       ...,
       [ 1.040833, -1.040833, -0.79121189, ..., -0.97043679,
        -0.26146916, -0.83008471],
       [-0.96076892, 0.96076892, -0.79121189, ..., -0.97043679,
        1.43520212, -0.80399408],
       [ 1.040833, -1.040833, -0.79121189, ..., 1.03046381,
        -0.32206457, 0.15827576]])
```