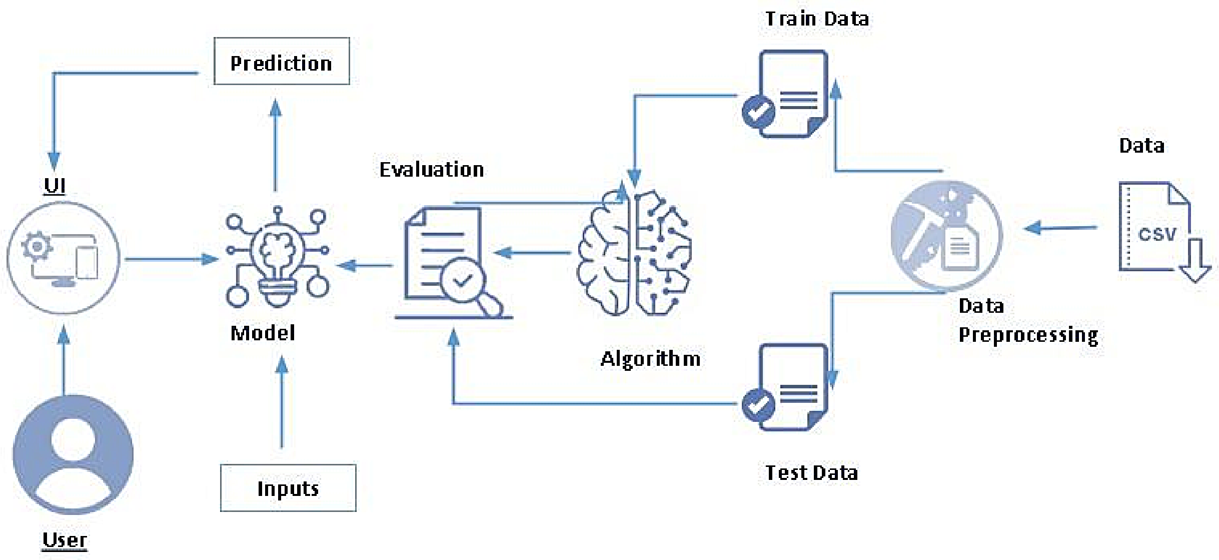
Drug Classification Using Machine Learning

Nowadays our lifestyle has been changing. Per family, at least one person has Motorcycles or cars, etc. In the same way, we all have health issues. An earlier generation has proved “Health is Wealth”. But, for our generation, this slogan is quite challenging.
We have completely moved with hybrid veggies, junk foods, etc. Due to these foods, we are not getting sufficient nutrition and suffering from health issues. To overcome this, we are consulting doctors and taking some drugs as medicines. In this project, we have some characteristics of the patients as a dataset. The target variable of this dataset is Drugs. The drug names are confidential. So, those names are replaced as DrugX, DrugY, DrugA , DrugB, and DrugC . By consulting a doctor each time, you have to pay a doctor fee and additional charges. For saving money and time, you can use this web application to predict your drug type. The main purpose of the Drug Classification system is to predict the suitable drug type confidently for the patients based on their characteristics. The main problem here is not just the feature sets and target sets but also the approach that is taken in solving these types of problems.
We will be using classification algorithms such as Decision tree, Random forest, KNN, and xgboost. We will train and test the data with these algorithms. From this best model is selected and saved in pkl format. We will be doing flask integration and IBM deployment.

TECHNICAL ARCHITECTURE:



Project Objectives

By the end of this project:

- You'll be able to understand the problem to classify if it is a regression or a classification kind of problem.
- You will be able to know how to pre-process/clean the data using different data preprocessing techniques.
- You will be able to analyze or get insights into data through visualization.
- Applying different algorithms according to the dataset and based on visualization.
- You will be able to know how to build a web application using the Flask framework

Project Flow

Project Flow:

- The user interacts with the UI to enter the input.
- Entered input is analyzed by the model which is integrated.
- Once the model analyses the input the prediction is showcased on the UI

To accomplish this, we have to complete all the activities listed below,

- Data collection
  - Collect the dataset or create the dataset
- Visualizing and analyzing data
  - Univariate analysis
  - Bivariate analysis
  - Multivariate analysis
  - Descriptive analysis
- Data pre-processing
  - Checking for null values
  - Handling outlier

    - Handling categorical data
    - Splitting data into train and test
- Model building
    - Import the model building libraries
    - Initializing the model
    - Training and testing the model
    - Evaluating the performance of the model
    - Save the model
- Application Building
    - Create an HTML file
    - Build python code

Pre-Requisites

In order to develop this project we need to install the following software/packages:

Step 1: Anaconda Navigator

Anaconda Navigator is a free and open-source distribution of the Python and R programming languages for data science and machine learning-related applications. It can be installed on Windows, Linux, and macOS.Conda is an open-source, cross-platform, package management system. Anaconda comes with great tools like JupyterLab, Jupyter Notebook, QtConsole, Spyder, Glueviz, Orange, Rstudio, Visual Studio Code.

For this project, we will be using a Jupyter notebook and Spyder

To install the Anaconda navigator and to know how to use Jupyter Notebook & Spyder using Anaconda watch the video

Step 2: Python packages

To build Machine learning models you must require the following packages

- Sklearn: Scikit-learn is a library in Python that provides many unsupervised and supervised learning algorithms.
- NumPy: NumPy is a Python package that stands for 'Numerical Python. It is the core library for scientific computing, which contains a powerful n-dimensional array of object
- Pandas: pandas is a fast, powerful, flexible, and easy-to-use open-source data analysis and manipulation tool, built on top of the Python programming language.
- Matplotlib: It provides an object-oriented API for embedding plots into applications using

general-purpose GUI toolkits

Step 3: Flask - Web framework used for building Web applications.

Watch the video below to learn how to install packages.

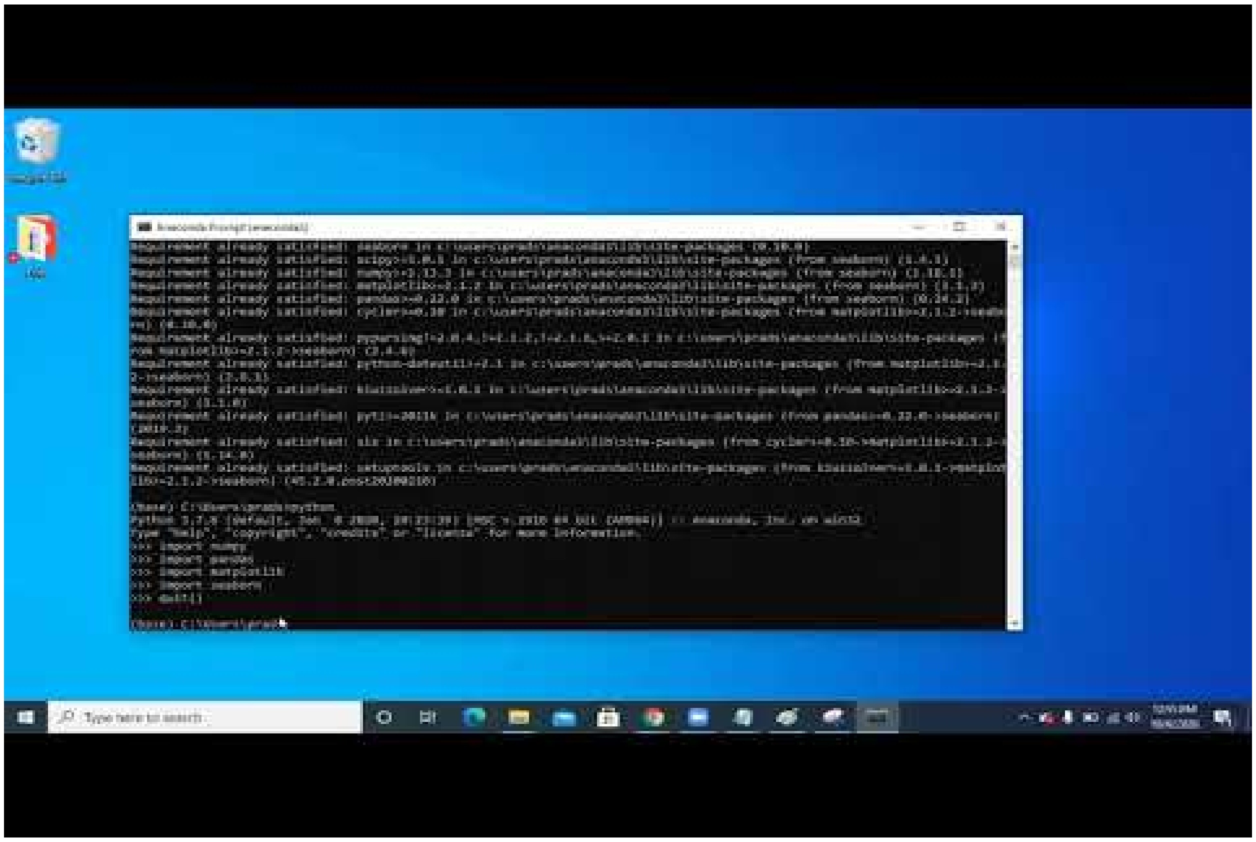
If you are using anaconda navigator, follow the below steps to download the required packages:

Open anaconda prompt as administrator

- Type **“pip install numpy ”** and click enter
- Type **“pip install pandas ”** and click enter
- Type **“pip install scikit-learn”** and click enter.
- Type **”pip install matplotlib”** and click enter.
- Type **”pip install scipy"** and click enter.
- Type **”pip install pickle-mixin”** and click enter.
- Type **”pip install seaborn”** and click enter.

- Type **“pip install Flask ”** and click enter.

If you are using Pycharm IDE, you can install the packages through the command prompt and follow the same syntax as above.



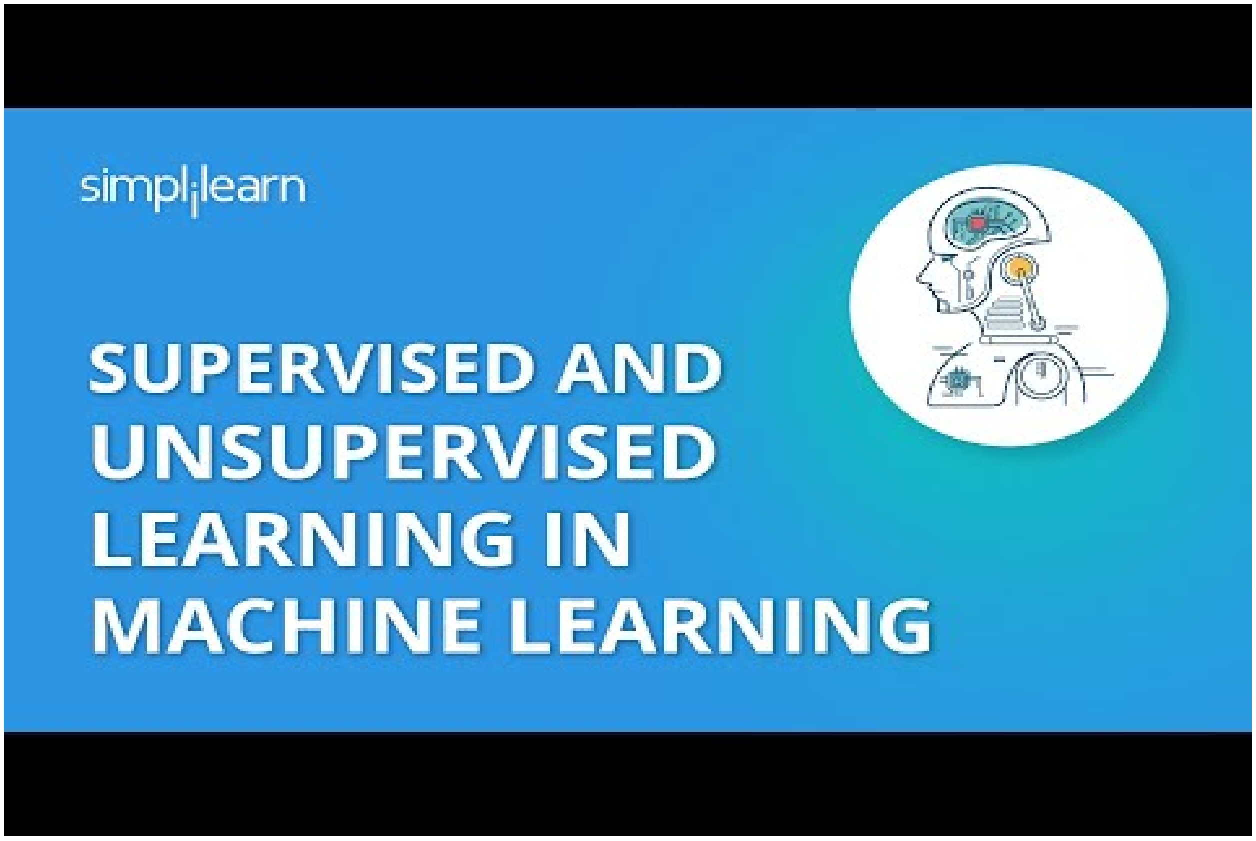
```
Requirement already satisfied: seaborn in c:\users\prads\anaconda3\lib\site-packages (0.10.0)
Requirement already satisfied: scipy>=1.0.1 in c:\users\prads\anaconda3\lib\site-packages (from seaborn) (1.4.1)
Requirement already satisfied: numpy>=1.13.3 in c:\users\prads\anaconda3\lib\site-packages (from seaborn) (1.18.1)
Requirement already satisfied: matplotlib>=2.1.2 in c:\users\prads\anaconda3\lib\site-packages (from seaborn) (3.1.3)
Requirement already satisfied: pandas>=0.22.0 in c:\users\prads\anaconda3\lib\site-packages (from seaborn) (0.24.2)
Requirement already satisfied: cycler>=0.10 in c:\users\prads\anaconda3\lib\site-packages (from matplotlib>=2.1.2->seabo
rn) (0.10.0)
Requirement already satisfied: pyparsing!=2.0.4,!=2.1.2,!=2.1.6,>=2.0.1 in c:\users\prads\anaconda3\lib\site-packages (f
rom matplotlib>=2.1.2->seaborn) (2.4.6)
Requirement already satisfied: python-dateutil>=2.1 in c:\users\prads\anaconda3\lib\site-packages (from matplotlib>=2.1.
2->seaborn) (2.8.1)
Requirement already satisfied: kiwisolver>=1.0.1 in c:\users\prads\anaconda3\lib\site-packages (from matplotlib>=2.1.2->
seaborn) (1.1.0)
Requirement already satisfied: pytz>=2011k in c:\users\prads\anaconda3\lib\site-packages (from pandas>=0.22.0->seaborn)
(2019.3)
Requirement already satisfied: six in c:\users\prads\anaconda3\lib\site-packages (from cycler>=0.10->matplotlib>=2.1.2->
seaborn) (1.14.0)
Requirement already satisfied: setuptools in c:\users\prads\anaconda3\lib\site-packages (from kiwisolver>=1.0.1->matplot
lib>=2.1.2->seaborn) (45.2.0.post20200210)

(base) C:\Users\prads>python
Python 3.7.6 (default, Jan  8 2020, 20:23:39) [MSC v.1916 64 bit (AMD64)] :: Anaconda, Inc. on win32
Type "help", "copyright", "credits" or "license" for more information.
>>> import numpy
>>> import pandas
>>> import matplotlib
>>> import seaborn
>>> quit()

(base) C:\Users\prads>
```

Prior Knowledge

One should have knowledge of the following Concepts

Please refer to the videos below to gain sufficient required knowledge to complete the project.

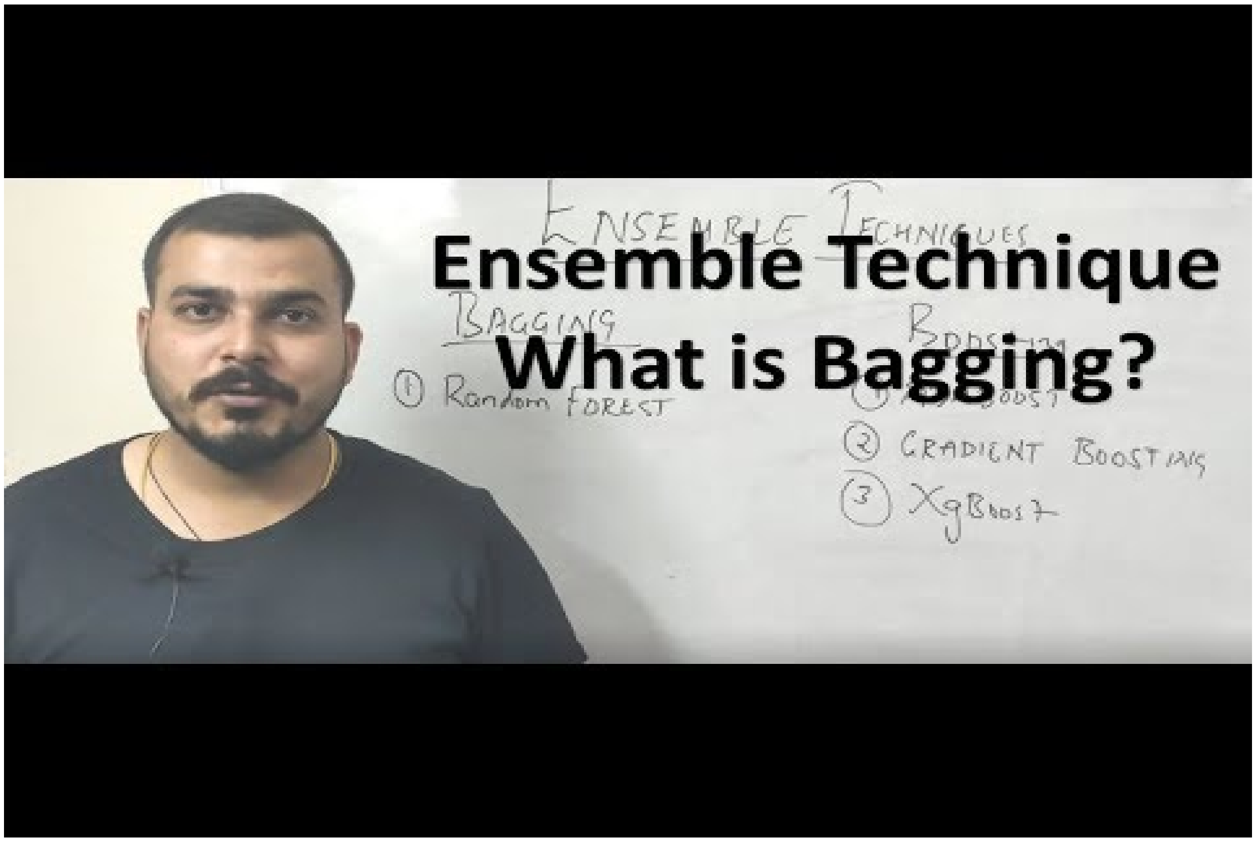
- **Supervised and unsupervised learning:**



- **Regression Classification and Clustering :**

- **Random Forest Classifier:**

- **Ensemble Technique:**



- **Decision Tree Classifier:**

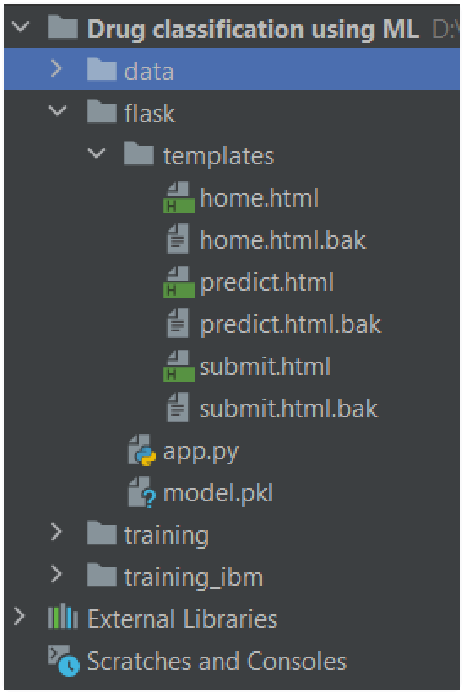
- **KNN**: Refer the link
- **Xgboost**: Refer the link
- **Evaluation metrics:** Refer the link

- **Flask:**

Let's start building the project.

Project Structure

Create a Project folder that contains files as shown below



```
Drug classification using ML  D:
  data
  flask
    templates
      home.html
      home.html.bak
      predict.html
      predict.html.bak
      submit.html
      submit.html.bak
    app.py
    model.pkl
  training
  training_ibm
External Libraries
Scratches and Consoles
```

- We are building a flask application that needs HTML pages stored in the templates folder and a python script app.py for scripting.
- Drug Classification.ipynb is the python file where the ML algorithm is applied to the dataset for testing and training. Finally, the model is saved for future use.
- Model.pkl is our saved model. Further, we will use this model for flask integration.
- The data folder contains the CSV file dataset for training our model.
- The training folder contains model training files and the training_ibm folder contains IBM deployment files.

Download Dataset

Download the dataset

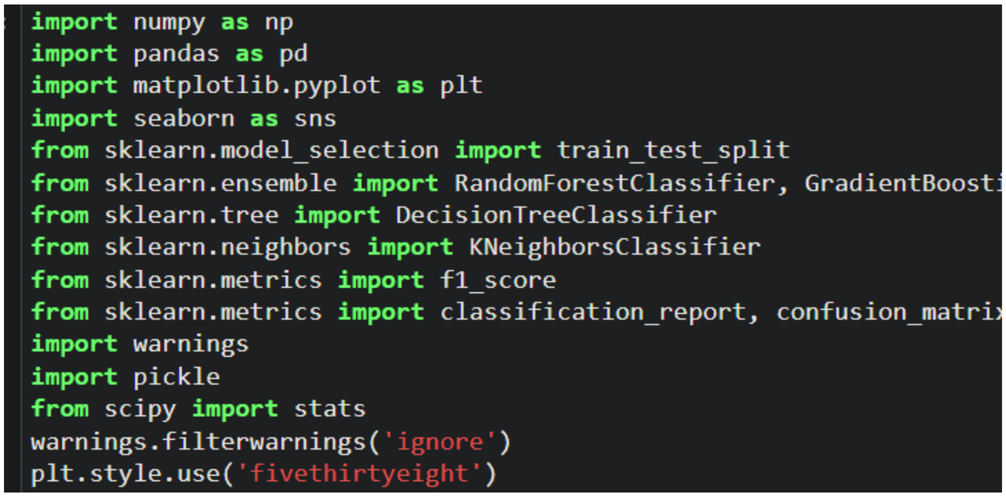
There are many popular open sources for collecting the data. Eg: kaggle.com, UCI repository, etc.

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.

DATASET LINK:::
https://www.kaggle.com/datasets/prathamtripathi/drug-classification

Importing The Libraries

Import the necessary libraries as shown in the image. (optional) Here we have used visualization style as fivethirtyeight.

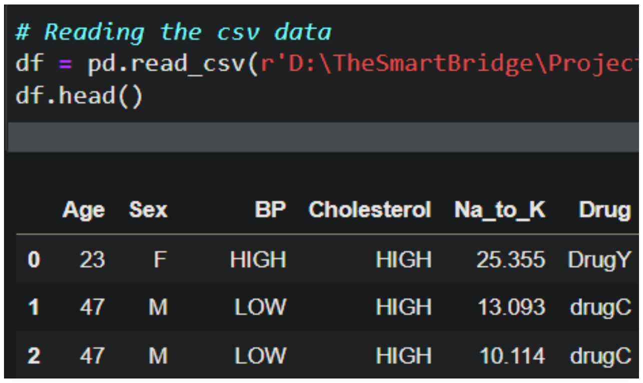


```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier, GradientBoosti
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import f1_score
from sklearn.metrics import classification_report, confusion_matrix
import warnings
import pickle
from scipy import stats
warnings.filterwarnings('ignore')
plt.style.use('fivethirtyeight')
```

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 csv file.



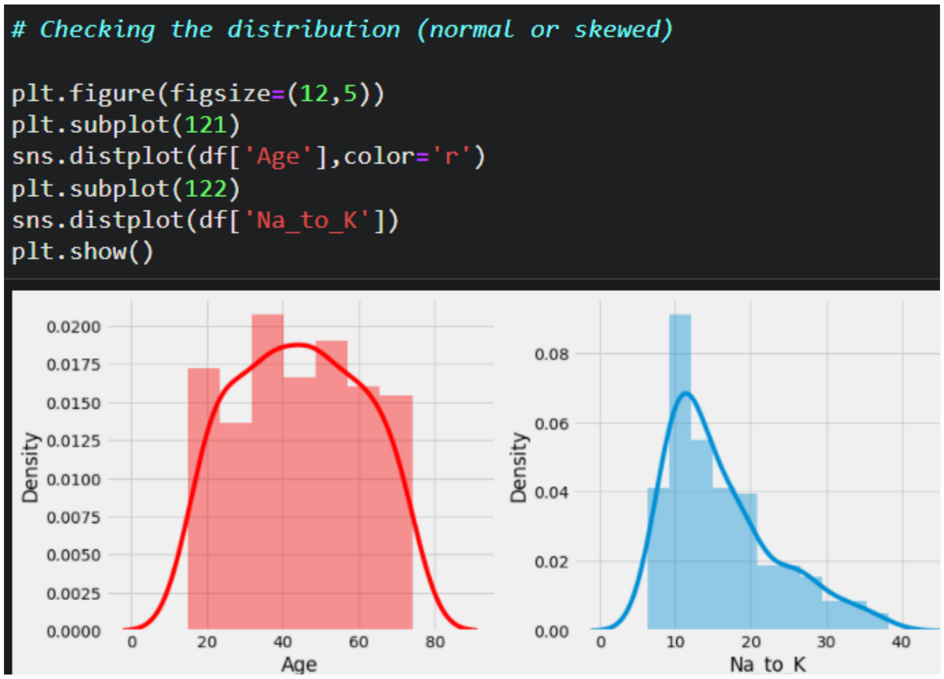
```
# Reading the csv data
df = pd.read_csv(r'D:\TheSmartBridge\Projec
df.head()
```

	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

Univariate Analysis

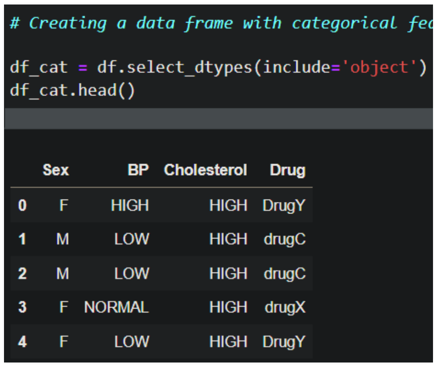
In simple words, univariate analysis is understanding the data with single feature. Here we have displayed two different graphs such as distplot and countplot.

- Seaborn package provides a wonderful function distplot. With the help of distplot, we can find the distribution of the feature. To make multiple graphs in a single plot, we use subplot.



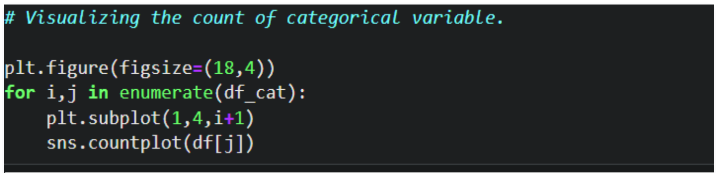
```
# Checking the distribution (normal or skewed)

plt.figure(figsize=(12,5))
plt.subplot(121)
sns.distplot(df['Age'],color='r')
plt.subplot(122)
sns.distplot(df['Na_to_K'])
plt.show()
```

- In our dataset we have some categorical features. With the countplot function, we are going to count the unique category in those features. We have created a dummy data frame with categorical features. With for loop and subplot we have plotted this below graph.
- From the plot we came to know, Most of the patients are using drugY and drugX. And most of the patients have high BP and high Cholesterol.

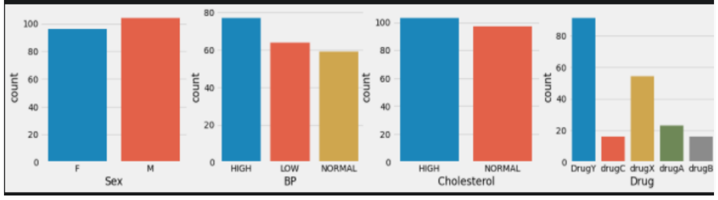


```
# Creating a data frame with categorical fea

df_cat = df.select_dtypes(include='object')
df_cat.head()
```

	Sex	BP	Cholesterol	Drug
0	F	HIGH	HIGH	DrugY
1	M	LOW	HIGH	drugC
2	M	LOW	HIGH	drugC
3	F	NORMAL	HIGH	drugX
4	F	LOW	HIGH	DrugY



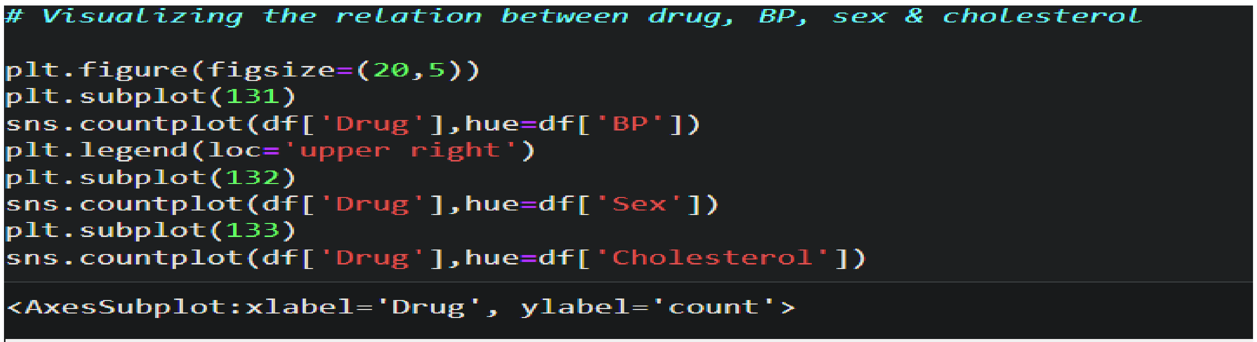
```
# Visualizing the count of categorical variable.

plt.figure(figsize=(18,4))
for i,j in enumerate(df_cat):
    plt.subplot(1,4,i+1)
    sns.countplot(df[j])
```



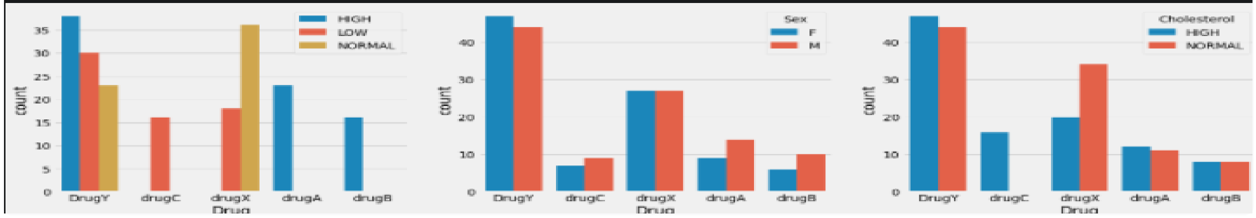
Bivariate Analysis

To find the relation between two features we use bivariate analysis. Here we are visualizing the relationship between drug & BP, drug & sex and drug & cholesterol.

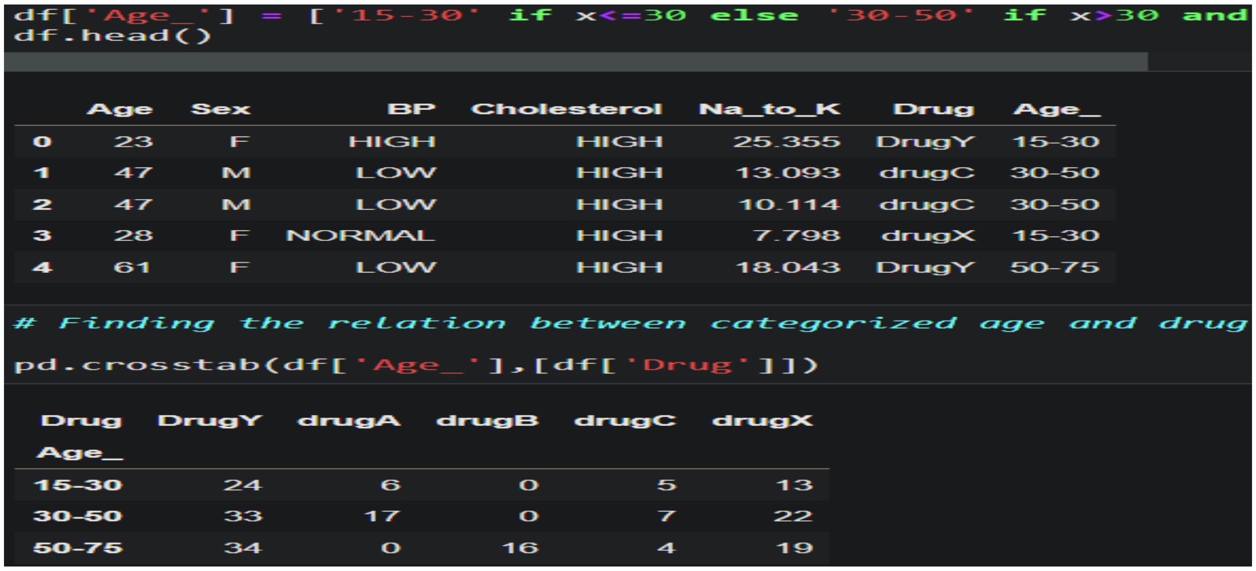
- Countplot is used here. As a 1st parameter we are passing x value and as a 2nd parameter we are passing hue value.
- From the below plot you can understand that drugA and drugB is not preferred to low and normal BP patients. DrugC is preferred only to low BP patients.
- By third graph we can understand, drugC is not preferred to normal cholesterol patients.



```
# Visualizing the relation between drug, BP, sex & cholesterol

plt.figure(figsize=(20,5))
plt.subplot(131)
sns.countplot(df['Drug'],hue=df['BP'])
plt.legend(loc='upper right')
plt.subplot(132)
sns.countplot(df['Drug'],hue=df['Sex'])
plt.subplot(133)
sns.countplot(df['Drug'],hue=df['Cholesterol'])

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



- With the help of age feature we are creating an age interval and finding the relation between drug feature and age interval feature. Function crosstab is used to find the relationship. From the below image we get a clear understanding, DrugB is preferred only for patients above age 50 years. And drugA is not preferred for patients above age 50 years.



```
df['Age_'] = ['15-30' if x<=30 else '30-50' if x>30 and
df.head()
```

```
   Age Sex      BP  Cholesterol  Na_to_K   Drug   Age_
0   23   F    HIGH         HIGH   25.355  DrugY  15-30
1   47   M     LOW         HIGH   13.093  drugC  30-50
2   47   M     LOW         HIGH   10.114  drugC  30-50
3   28   F  NORMAL         HIGH    7.798  drugX  15-30
4   61   F     LOW         HIGH   18.043  DrugY  50-75
```

```
# Finding the relation between categorized age and drug
pd.crosstab(df['Age_'],[df['Drug']])
```

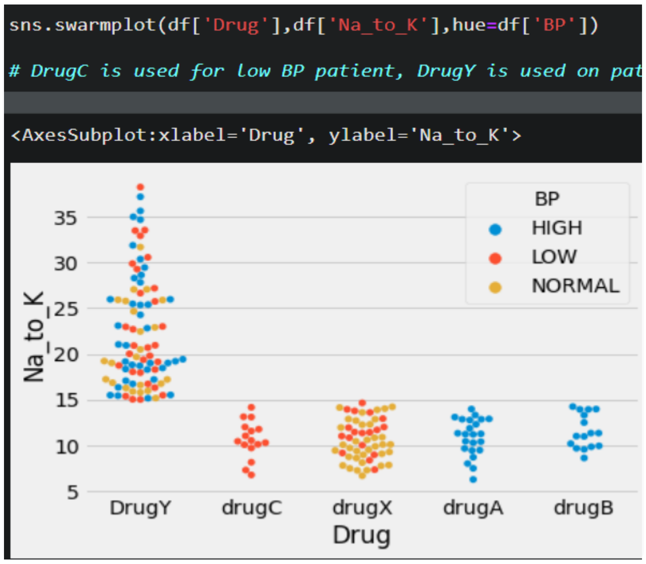
```
Drug   DrugY  drugA  drugB  drugC  drugX
Age_
15-30     24      6      0      5     13
30-50     33     17      0      7     22
50-75     34      0     16      4     19
```

Multivariate Analysis

In simple words, multivariate analysis is to find the relation between multiple features.

Here we have used swarmplot from seaborn package.

- From the below image, we came to a conclusion that DrugY is used by most of patients who has different BP levels. But It is preferred only for patients having Na_to_K > 15 (Na_to_K – Sodium to potassium ratio on blood).

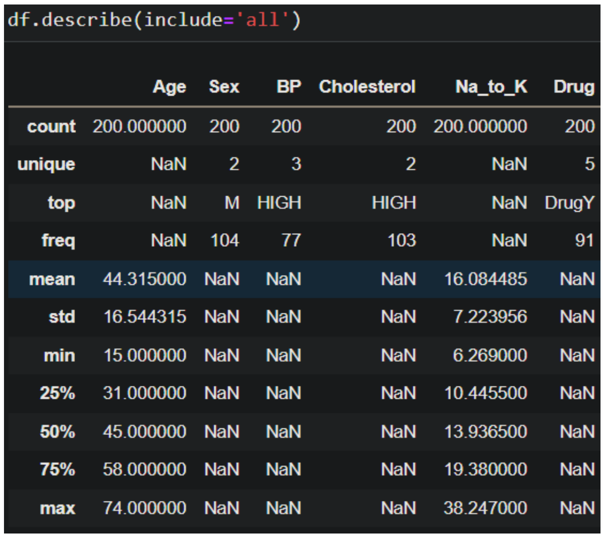


```
sns.swarmplot(df['Drug'],df['Na_to_K'],hue=df['BP'])

# DrugC is used for Low BP patient, DrugY is used on pat
```

```
<AxesSubplot:xlabel='Drug', ylabel='Na_to_K'>
```

Descriptive Analysis

Descriptive analysis is to study the basic features of data with the statistical process. Here pandas has a worthy function called describe. With this describe function we can understand the unique, top and frequent values of categorical features. And we can find mean, std, min, max and percentile values of continuous features.



```
df.describe(include='all')
```

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
count	200.000000	200	200	200	200.000000	200
unique	NaN	2	3	2	NaN	5
top	NaN	M	HIGH	HIGH	NaN	DrugY
freq	NaN	104	77	103	NaN	91
mean	44.315000	NaN	NaN	NaN	16.084485	NaN
std	16.544315	NaN	NaN	NaN	7.223956	NaN
min	15.000000	NaN	NaN	NaN	6.269000	NaN
25%	31.000000	NaN	NaN	NaN	10.445500	NaN
50%	45.000000	NaN	NaN	NaN	13.936500	NaN
75%	58.000000	NaN	NaN	NaN	19.380000	NaN
max	74.000000	NaN	NaN	NaN	38.247000	NaN

Data Pre-Processing

As we have understood how the data is lets pre-process the collected data.

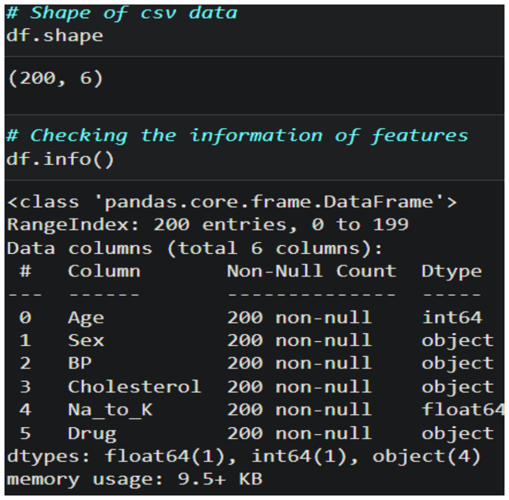
The download data set is not suitable for training the machine learning model as it might have so much of randomness so we need to clean the dataset properly in order to fetch good results. This activity includes the following steps.

- Handling missing values
- Handling categorical data
- Handling outliers
- Scaling Techniques
- 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.

Checking For Null Values

- Let's find the shape of our dataset first, To find the shape of our data, df.shape method is used. To find the data type, df.info() function is used.



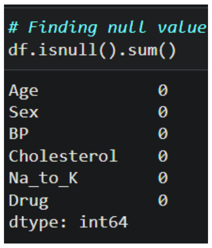
```
# Shape of csv data
df.shape
```

```
(200, 6)
```

```
# Checking the information of features
df.info()
```

```
<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
```

- For checking the null values, df.isnull() function is used. To sum those null values we use .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 of missing values step.



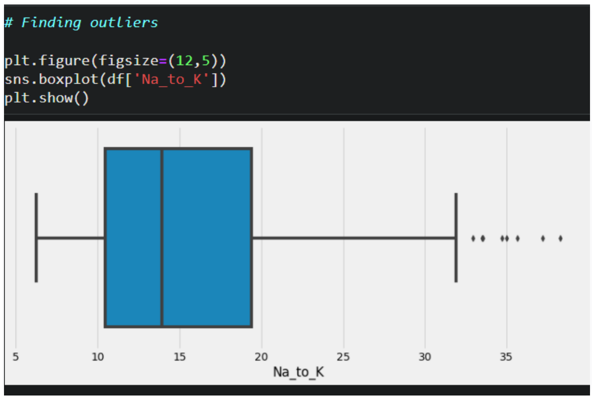
```
# Finding null value
df.isnull().sum()

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

Let’s look for any outliers in the dataset

Handling Outliers

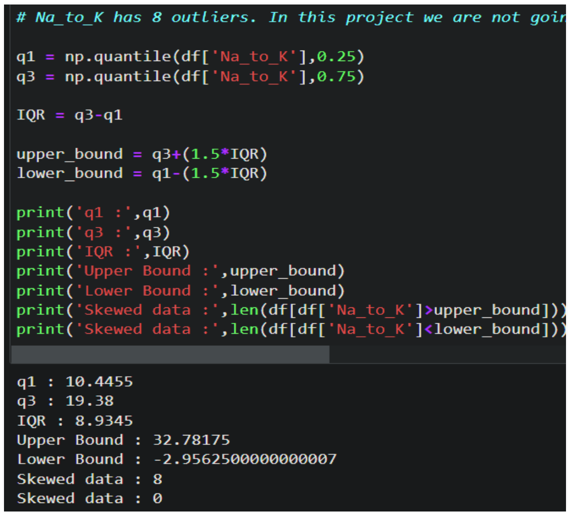
With the help of boxplot, outliers are visualized. And here we are going to find upper bound and lower bound of Na_to_K feature with some mathematical formula.

- From the below diagram, we could visualize that Na_to_K feature has outliers. Boxplot from seaborn library is used here.



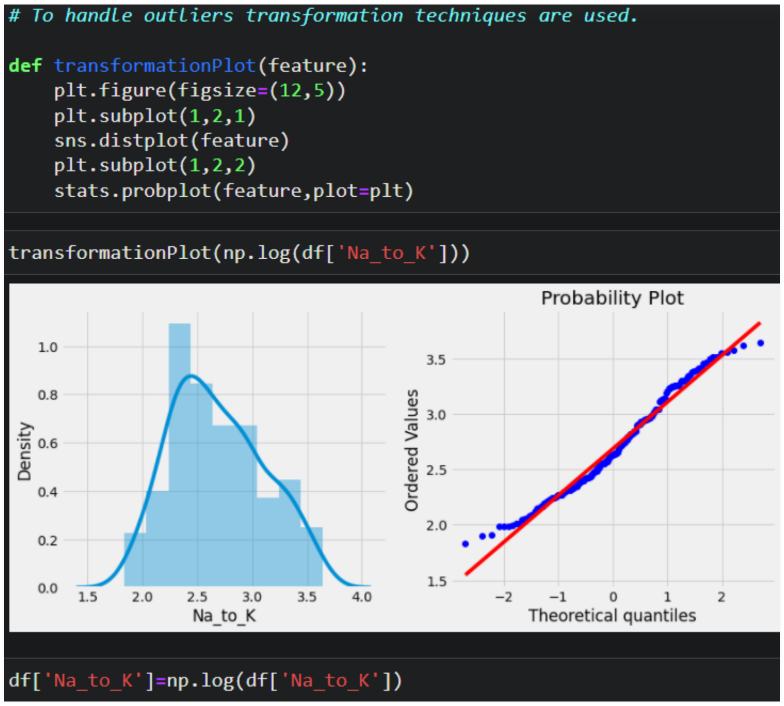
```
# Finding outliers

plt.figure(figsize=(12,5))
sns.boxplot(df['Na_to_K'])
plt.show()
```

- To find upper bound we have to multiply IQR (Interquartile range) with 1.5 and add it with 3rd quantile. To find lower bound instead of adding, subtract it with 1st quantile. Take image attached below as your reference.


```
# Na_to_K has 8 outliers. In this project we are not goir

q1 = np.quantile(df['Na_to_K'],0.25)
q3 = np.quantile(df['Na_to_K'],0.75)

IQR = q3-q1

upper_bound = q3+(1.5*IQR)
lower_bound = q1-(1.5*IQR)

print('q1 :',q1)
print('q3 :',q3)
print('IQR :',IQR)
print('Upper Bound :',upper_bound)
print('Lower Bound :',lower_bound)
print('Skewed data :',len(df[df['Na_to_K']>upper_bound]))
print('Skewed data :',len(df[df['Na_to_K']<lower_bound]))
```

```
q1 : 10.4455
q3 : 19.38
IQR : 8.9345
Upper Bound : 32.78175
Lower Bound : -2.9562500000000007
Skewed data : 8
Skewed data : 0
```

- To handle the outliers transformation technique is used. Here log transformation is used. We have created a function to visualize the distribution and probability plot of Na_to_K feature.


```
# To handle outliers transformation techniques are used.

def transformationPlot(feature):
    plt.figure(figsize=(12,5))
    plt.subplot(1,2,1)
    sns.distplot(feature)
    plt.subplot(1,2,2)
    stats.probplot(feature,plot=plt)
```

```
transformationPlot(np.log(df['Na_to_K']))
```

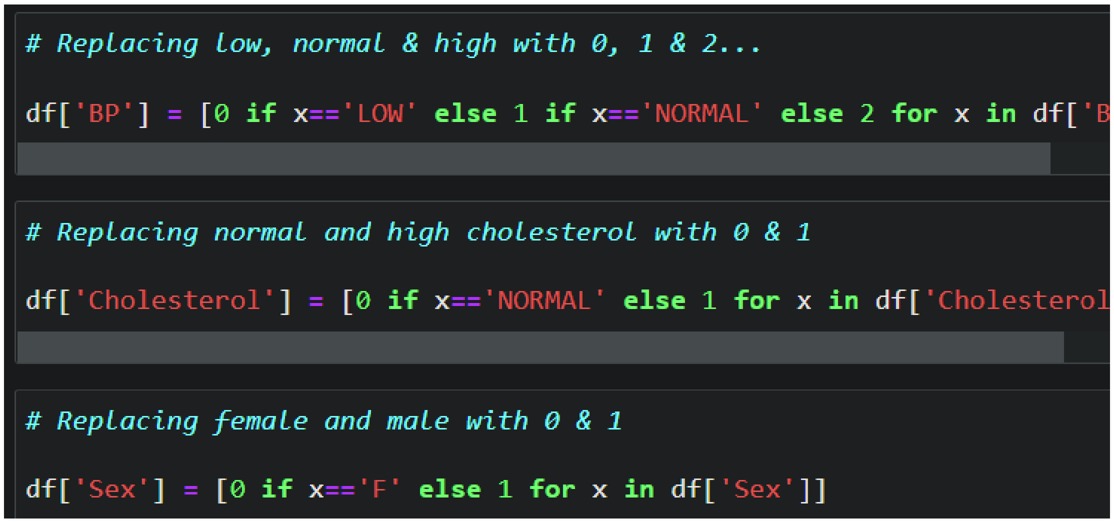
```
df['Na_to_K']=np.log(df['Na_to_K'])
```

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 manual encoding with the help of list comprehension.

- In our project, categorical features are BP, Cholesterol and sex. With list comprehension encoding is done.



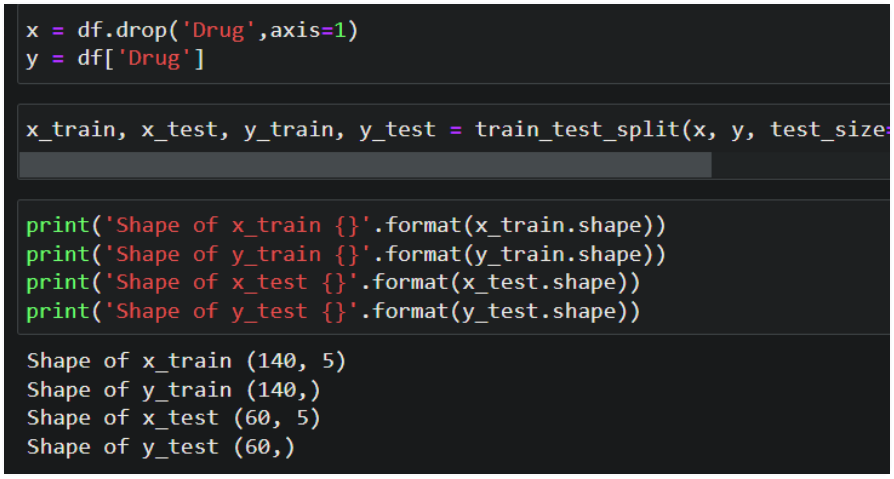
```
# Replacing low, normal & high with 0, 1 & 2...

df['BP'] = [0 if x=='LOW' else 1 if x=='NORMAL' else 2 for x in df['B

# Replacing normal and high cholesterol with 0 & 1

df['Cholesterol'] = [0 if x=='NORMAL' else 1 for x in df['Cholesterol

# Replacing female and male with 0 & 1

df['Sex'] = [0 if x=='F' else 1 for x in df['Sex']]
```

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, df is passed with dropping the target variable. And on y target variable is passed. For splitting training and testing data we are using train_test_split() function from sklearn. As parameters, we are passing x, y, test_size, random_state.



```
x = df.drop('Drug',axis=1)
y = df['Drug']
```

```
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size
```

```
print('Shape of x_train {}'.format(x_train.shape))
print('Shape of y_train {}'.format(y_train.shape))
print('Shape of x_test {}'.format(x_test.shape))
print('Shape of y_test {}'.format(y_test.shape))
```

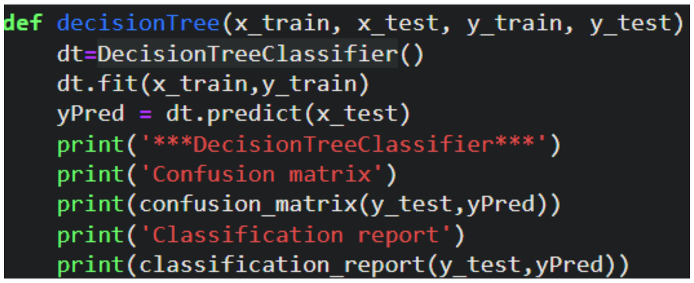
```
Shape of x_train (140, 5)
Shape of y_train (140,)
Shape of x_test (60, 5)
Shape of y_test (60,)
```

Model Building

Now our data is cleaned and it's time to build the model. We can train our data on different algorithms. For this project we are applying four classification algorithms. The best model is saved based on its performance.

Decision Tree Model

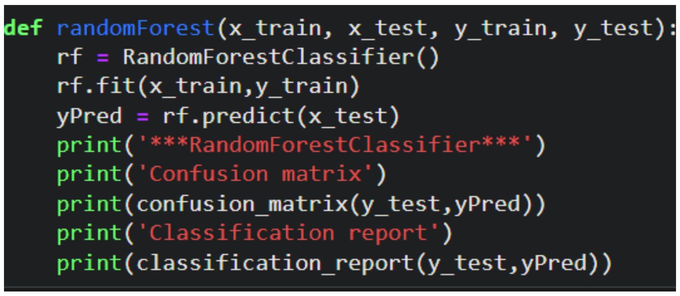
A function named decisionTree is created and train and test data are passed as the parameters. Inside the function, DecisionTreeClassifier algorithm is initialized and training data is passed to the model with .fit() function. Test data is predicted with .predict() function and saved in new variable. For evaluating the model, confusion matrix and classification report is done.



```
def decisionTree(x_train, x_test, y_train, y_test)
    dt=DecisionTreeClassifier()
    dt.fit(x_train,y_train)
    yPred = dt.predict(x_test)
    print('***DecisionTreeClassifier***')
    print('Confusion matrix')
    print(confusion_matrix(y_test,yPred))
    print('Classification report')
    print(classification_report(y_test,yPred))
```

Random Forest Model

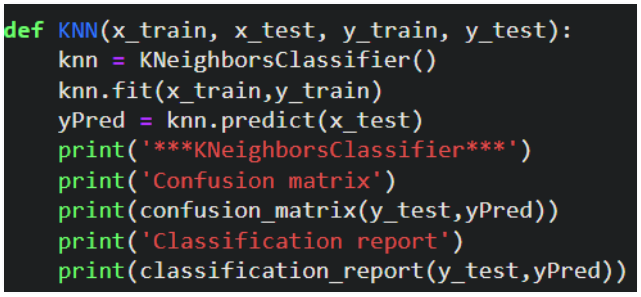
A function named randomForest is created and train and test data are passed as the parameters. Inside the function, RandomForestClassifier algorithm is initialized and training data is passed to the model with .fit() function. Test data is predicted with .predict() function and saved in new variable. For evaluating the model, confusion matrix and classification report is done.



```
def randomForest(x_train, x_test, y_train, y_test):
    rf = RandomForestClassifier()
    rf.fit(x_train,y_train)
    yPred = rf.predict(x_test)
    print('***RandomForestClassifier***')
    print('Confusion matrix')
    print(confusion_matrix(y_test,yPred))
    print('Classification report')
    print(classification_report(y_test,yPred))
```

KNN Model

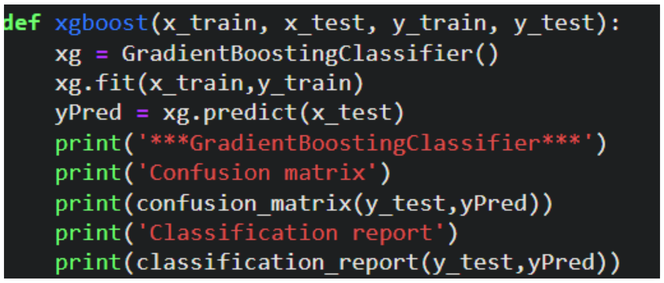
A function named KNN is created and train and test data are passed as the parameters. Inside the function, KNeighborsClassifier algorithm is initialized and training data is passed to the model with .fit() function. Test data is predicted with .predict() function and saved in new variable. For evaluating the model, confusion matrix and classification report is done.



```
def KNN(x_train, x_test, y_train, y_test):
    knn = KNeighborsClassifier()
    knn.fit(x_train,y_train)
    yPred = knn.predict(x_test)
    print('***KNeighborsClassifier***')
    print('Confusion matrix')
    print(confusion_matrix(y_test,yPred))
    print('Classification report')
    print(classification_report(y_test,yPred))
```

Xgboost Model

A function named xgboost is created and train and test data are passed as the parameters. Inside the function, GradientBoostingClassifier algorithm is initialized and training data is passed to the model with .fit() function. Test data is predicted with .predict() function and saved in new variable. For evaluating the model, confusion matrix and classification report is done.

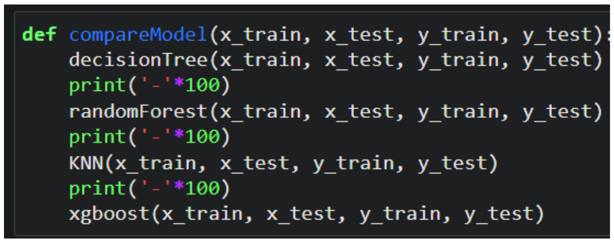


```
def xgboost(x_train, x_test, y_train, y_test):
    xg = GradientBoostingClassifier()
    xg.fit(x_train,y_train)
    yPred = xg.predict(x_test)
    print('***GradientBoostingClassifier***')
    print('Confusion matrix')
    print(confusion_matrix(y_test,yPred))
    print('Classification report')
    print(classification_report(y_test,yPred))
```

Now let's see the performance of all the models and save the best model

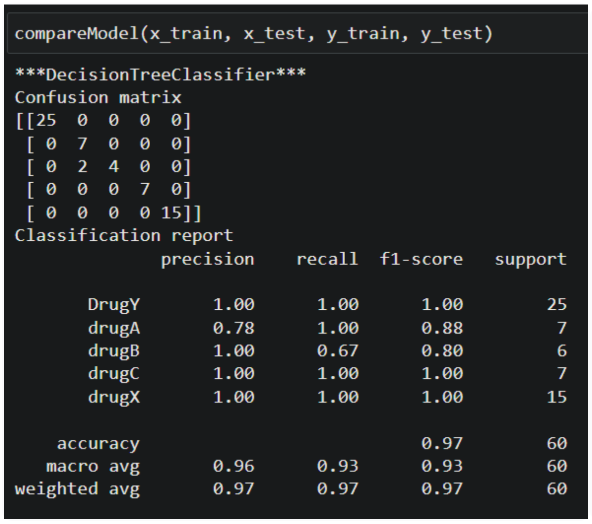
Compare The Model

For comparing the above four models compareModel function is defined.

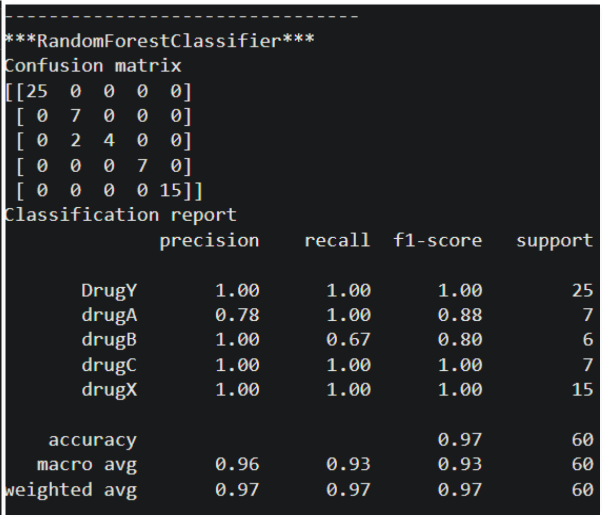


```
def compareModel(x_train, x_test, y_train, y_test):
    decisionTree(x_train, x_test, y_train, y_test)
    print('-'*100)
    randomForest(x_train, x_test, y_train, y_test)
    print('-'*100)
    KNN(x_train, x_test, y_train, y_test)
    print('-'*100)
    xgboost(x_train, x_test, y_train, y_test)
```

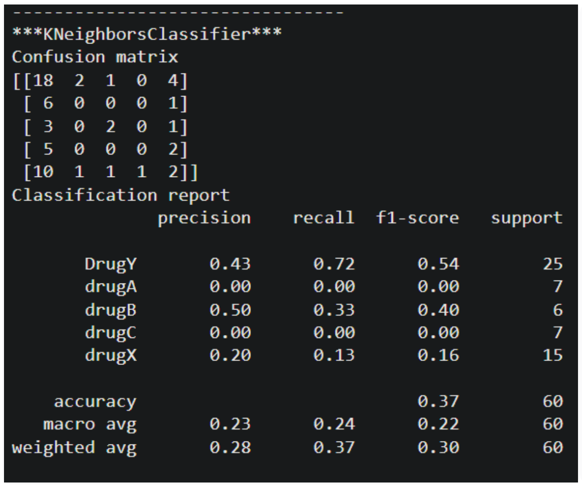
After calling the function, the results of models are displayed as output. From the four model random forest and decision tree is performing well. From the below image, We can see the accuracy of the model. Both models have 97% accuracy. Even confusion matrix also have same results. Training time of decision tree is faster than random forest. In such case we have to select decision tree model (time saving & cost wise profitable). But, here random forest is selected and evaluated with cross validation. Additionally, we can tune the model with hyper parameter tuning techniques.



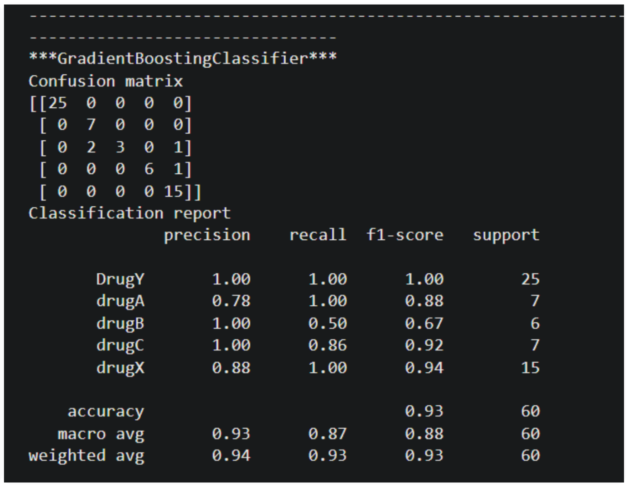
```
compareModel(x_train, x_test, y_train, y_test)

***DecisionTreeClassifier***
Confusion matrix
[[25  0  0  0  0]
 [ 0  7  0  0  0]
 [ 0  2  4  0  0]
 [ 0  0  0  7  0]
 [ 0  0  0  0 15]]
Classification report
              precision    recall  f1-score   support

       DrugY       1.00      1.00      1.00        25
       drugA       0.78      1.00      0.88         7
       drugB       1.00      0.67      0.80         6
       drugC       1.00      1.00      1.00         7
       drugX       1.00      1.00      1.00        15

    accuracy                           0.97        60
   macro avg       0.96      0.93      0.93        60
weighted avg       0.97      0.97      0.97        60
```



```
--------------------------------
***RandomForestClassifier***
Confusion matrix
[[25  0  0  0  0]
 [ 0  7  0  0  0]
 [ 0  2  4  0  0]
 [ 0  0  0  7  0]
 [ 0  0  0  0 15]]
Classification report
              precision    recall  f1-score   support

       DrugY       1.00      1.00      1.00        25
       drugA       0.78      1.00      0.88         7
       drugB       1.00      0.67      0.80         6
       drugC       1.00      1.00      1.00         7
       drugX       1.00      1.00      1.00        15

    accuracy                           0.97        60
   macro avg       0.96      0.93      0.93        60
weighted avg       0.97      0.97      0.97        60
```



```
--------------------------------
***KNeighborsClassifier***
Confusion matrix
[[18  2  1  0  4]
 [ 6  0  0  0  1]
 [ 3  0  2  0  1]
 [ 5  0  0  0  2]
 [10  1  1  1  2]]
Classification report
              precision    recall  f1-score   support

       DrugY       0.43      0.72      0.54        25
       drugA       0.00      0.00      0.00         7
       drugB       0.50      0.33      0.40         6
       drugC       0.00      0.00      0.00         7
       drugX       0.20      0.13      0.16        15

    accuracy                           0.37        60
   macro avg       0.23      0.24      0.22        60
weighted avg       0.28      0.37      0.30        60
```

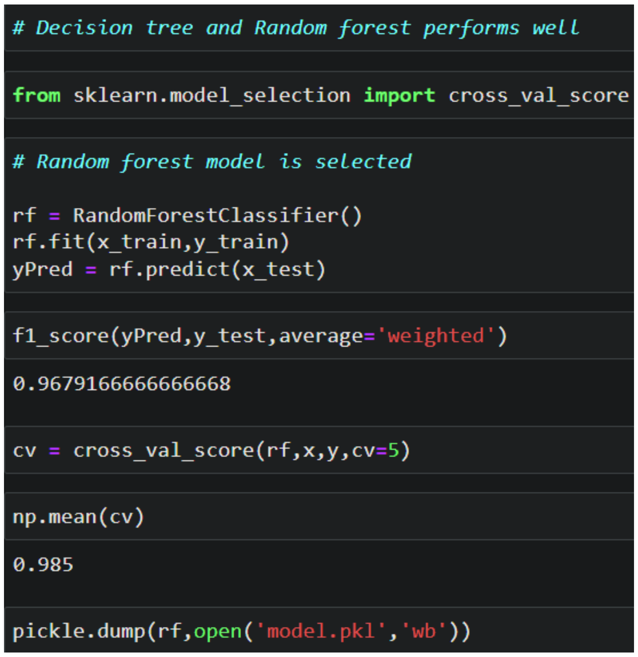


```
-------------------------------------------------------------
--------------------------------
***GradientBoostingClassifier***
Confusion matrix
[[25  0  0  0  0]
 [ 0  7  0  0  0]
 [ 0  2  3  0  1]
 [ 0  0  0  6  1]
 [ 0  0  0  0 15]]
Classification report
              precision    recall  f1-score   support

       DrugY       1.00      1.00      1.00        25
       drugA       0.78      1.00      0.88         7
       drugB       1.00      0.50      0.67         6
       drugC       1.00      0.86      0.92         7
       drugX       0.88      1.00      0.94        15

    accuracy                           0.93        60
   macro avg       0.93      0.87      0.88        60
weighted avg       0.94      0.93      0.93        60
```

Evaluating Performance Of The Model And Saving The Model

From sklearn, cross_val_score is used to evaluate the score of the model. On the parameters, we have given rf (model name), x, y, cv (as 5 folds). Our model is performing well. So, we are saving the model by pickle.dump().

Note: To understand cross validation, refer this link.



```
# Decision tree and Random forest performs well

from sklearn.model_selection import cross_val_score

# Random forest model is selected

rf = RandomForestClassifier()
rf.fit(x_train,y_train)
yPred = rf.predict(x_test)

f1_score(yPred,y_test,average='weighted')

0.9679166666666668

cv = cross_val_score(rf,x,y,cv=5)

np.mean(cv)

0.985

pickle.dump(rf,open('model.pkl','wb'))
```

Application Building

In this section, we will be building a web application that is integrated to the model we built. A UI is provided for the uses where he has to enter the values for predictions. The enter values are given to the saved model and prediction is showcased on the UI.

This section has the following tasks

- Building HTML Pages
- Building serverside script

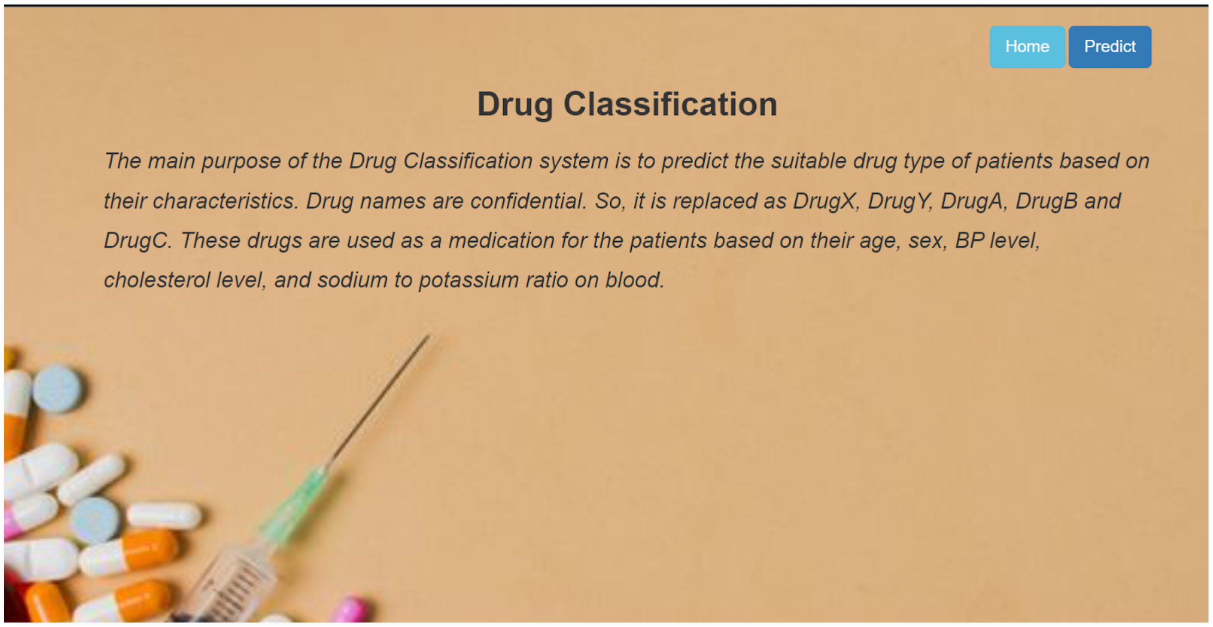
Building Html Pages

For this project create three HTML files namely

- home.html
- predict.html
- submit.html

and save them in templates folder.

Let's see how our home.html page looks like:

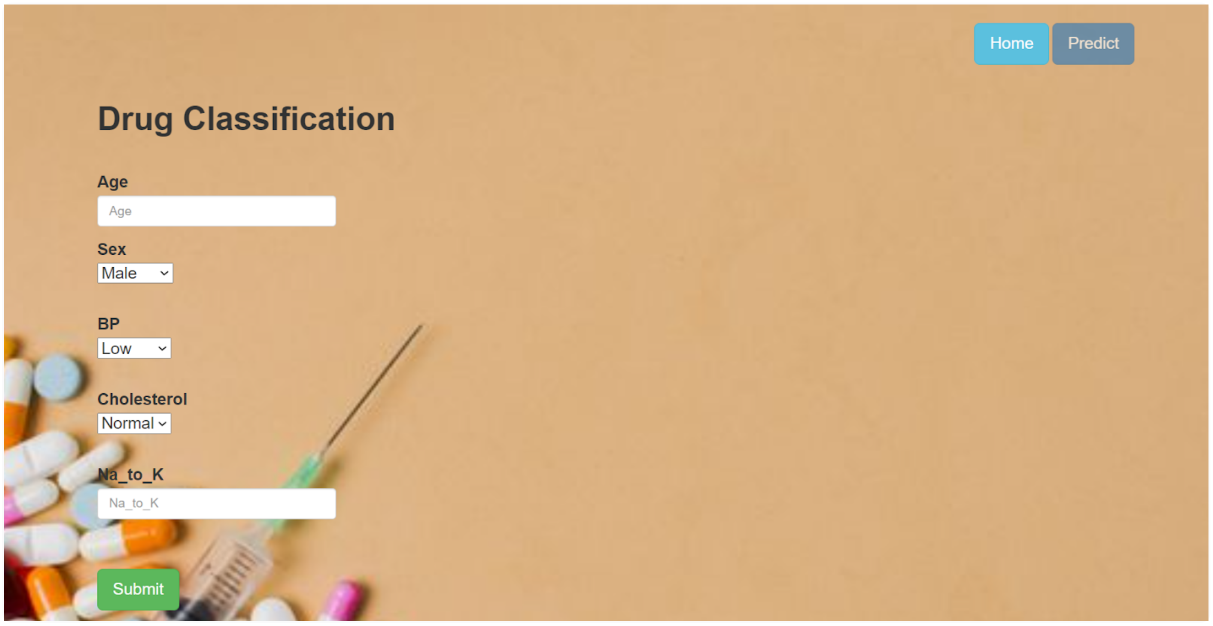


Drug Classification

The main purpose of the Drug Classification system is to predict the suitable drug type of patients based on their characteristics. Drug names are confidential. So, it is replaced as DrugX, DrugY, DrugA, DrugB and DrugC. These drugs are used as a medication for the patients based on their age, sex, BP level, cholesterol level, and sodium to potassium ratio on blood.

Now when you click on predict button from top right corner you will get redirected to predict.html

Lets look how our predict.html file looks like:

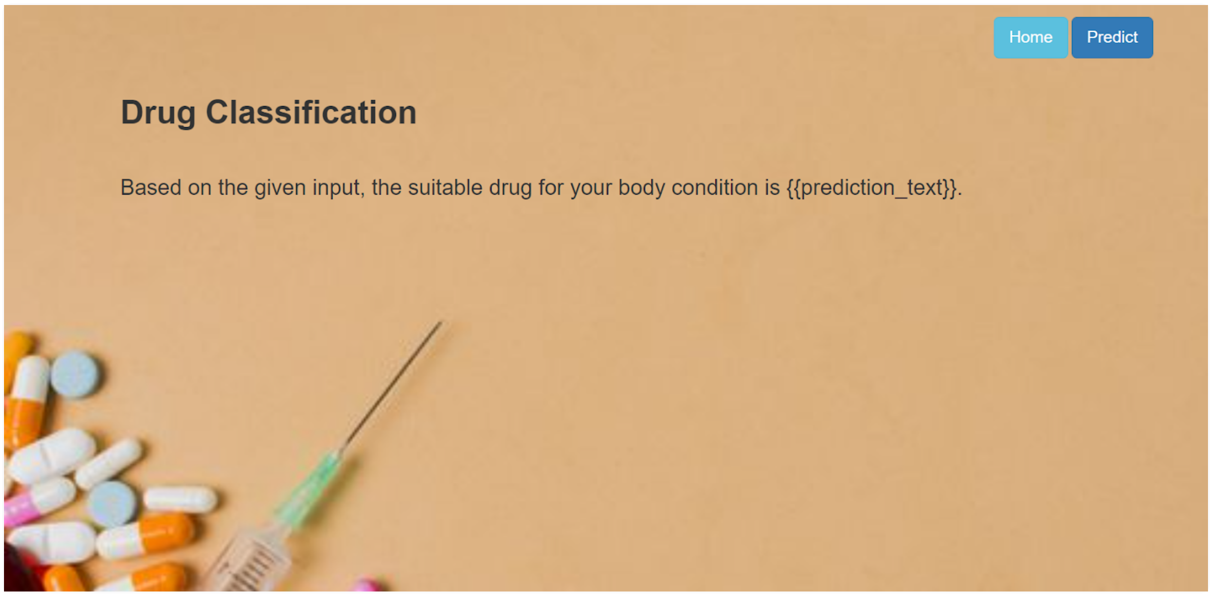


Drug Classification

Age	Age
Sex	Male
BP	Low
Cholesterol	Normal
Na_to_K	Na_to_K

Now when you click on submit button from left bottom corner you will get redirected to submit.html

Lets look how our submit.html file looks like:

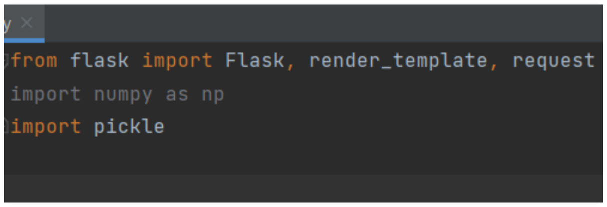


Drug Classification

Based on the given input, the suitable drug for your body condition is {{prediction_text}}.

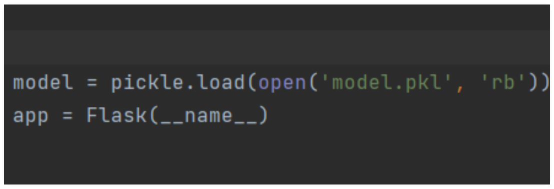
Build Python Code

Import the libraries



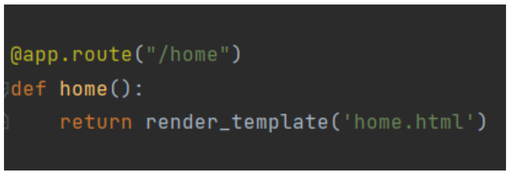
```
from flask import Flask, render_template, request
import numpy as np
import pickle
```

Load the saved model. Importing flask module in the project is mandatory. An object of Flask class is our WSGI application. Flask constructor takes the name of the current module (__name__) as argument.



```
model = pickle.load(open('model.pkl', 'rb'))
app = Flask(__name__)
```

Render HTML page:

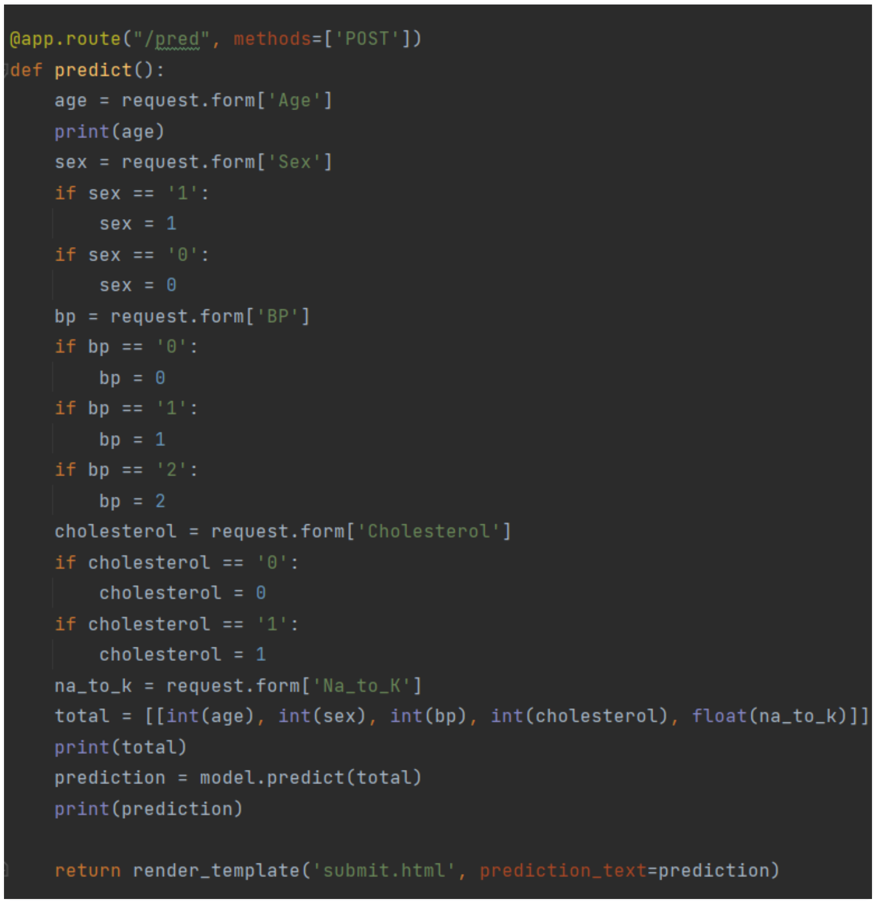


```
@app.route("/home")
def home():
    return render_template('home.html')
```

Here we will be using declared constructor to route to the HTML page which we have created earlier.

In the above example, '/' URL is bound with home.html function. Hence, when the home page of the web server is opened in browser, the html page will be rendered. Whenever you enter the values from the html page the values can be retrieved using POST Method.

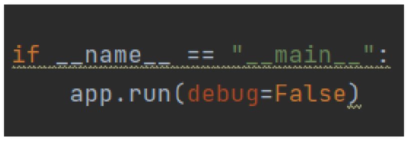
Retrieves the value from UI:



```
@app.route("/pred", methods=['POST'])
def predict():
    age = request.form['Age']
    print(age)
    sex = request.form['Sex']
    if sex == '1':
        sex = 1
    if sex == '0':
        sex = 0
    bp = request.form['BP']
    if bp == '0':
        bp = 0
    if bp == '1':
        bp = 1
    if bp == '2':
        bp = 2
    cholesterol = request.form['Cholesterol']
    if cholesterol == '0':
        cholesterol = 0
    if cholesterol == '1':
        cholesterol = 1
    na_to_k = request.form['Na_to_K']
    total = [[int(age), int(sex), int(bp), int(cholesterol), float(na_to_k)]]
    print(total)
    prediction = model.predict(total)
    print(prediction)

    return render_template('submit.html', prediction_text=prediction)
```

Here we are routing our app to predict() function. This function retrieves all the values from the HTML page using Post request. That is stored in an array. This array is passed to the model.predict() function. This function returns the prediction. And this prediction value will rendered to the text that we have mentioned in the submit.html page earlier.

Main Function:

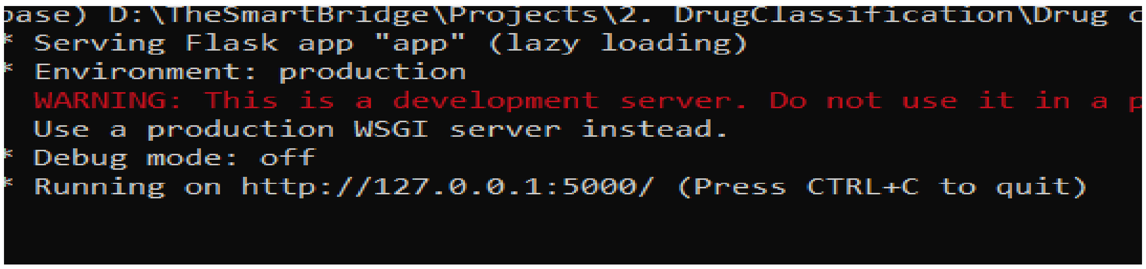


```
if __name__ == "__main__":
    app.run(debug=False)
```

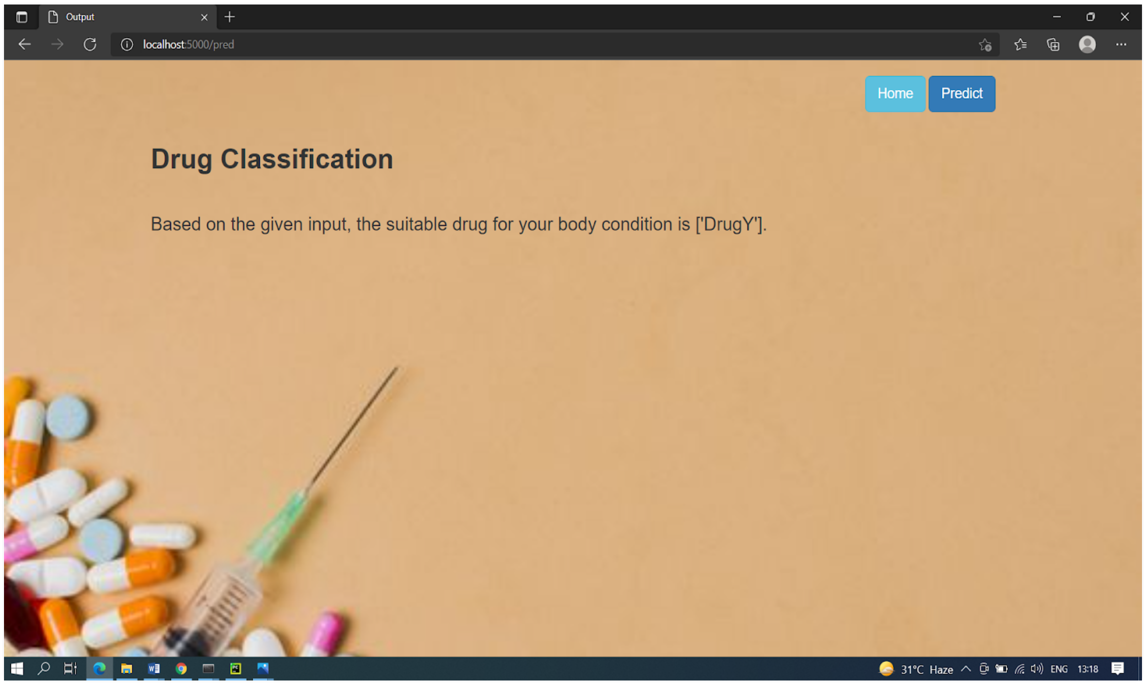
Run The Application

Run the application

- Open anaconda prompt from the start menu
- Navigate to the folder where your python script is.
- Now type “python app.py” command
- Navigate to the localhost where you can view your web page.
- Click on the predict button from the top right corner, enter the inputs, click on the submit button, and see the result/prediction on the web.



```
base) D:\TheSmartBridge\Projects\2. DrugClassification\Drug c
* Serving Flask app "app" (lazy loading)
* Environment: production
  WARNING: This is a development server. Do not use it in a p
  Use a production WSGI server instead.
* Debug mode: off
* Running on http://127.0.0.1:5000/ (Press CTRL+C to quit)
```



Drug Classification

Based on the given input, the suitable drug for your body condition is ['DrugY'].