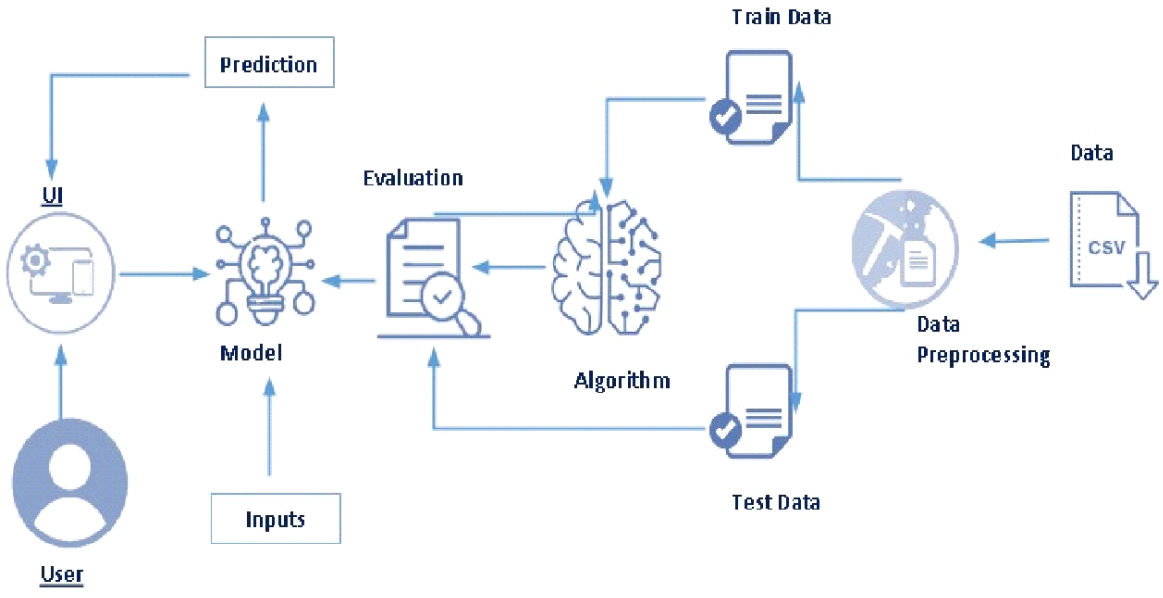
Thyroid disease classification using ML

Project Based Experiential Learning Program

Thyroid Disease Classification Using ML

The Thyroid gland is a vascular gland and one of the most important organs of the human body. This gland secretes two hormones which help in controlling the metabolism of the body. The two types of Thyroid disorders are Hyperthyroidism and Hypothyroidism. When this disorder occurs in the body, they release certain types of hormones into the body which imbalances the body's metabolism. A thyroid-related Blood test is used to detect this disease but it is often blurred and noise will be present. Data cleansing methods were used to make the data primitive enough for the analytics to show the risk of patients getting this disease. Machine Learning plays a very deciding role in disease prediction. Machine Learning algorithms, SVM - support vector machine, Random Forest Classifier, XGB Classifier and ANN - Artificial Neural Networks are used to predict the patient's risk of getting thyroid disease. The web app is created to get data from users to predict the type of disease.

Technical Architecture:



Project Flow:

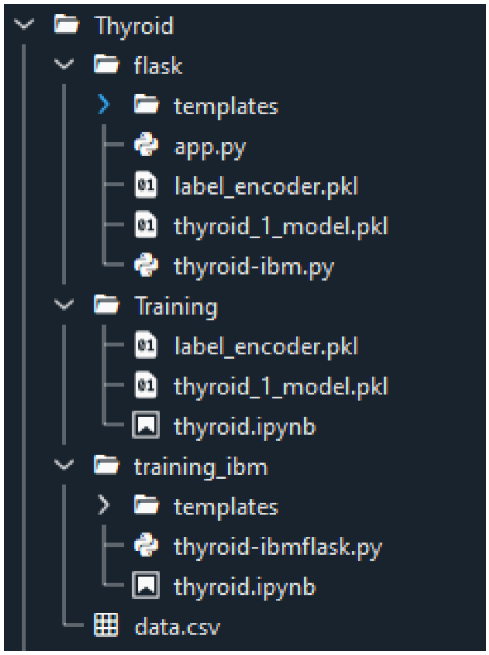
- The user interacts with the UI to enter the input.
- Entered input is analysed by the model which is integrated.
- Once the model analyses the input the prediction is showcased on the UI

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

- Define Problem / Problem Understanding
    - Specify the business problem
    - Business requirements
    - Literature Survey
    - Social or Business Impact.
- Data Collection & Preparation
    - Collect the dataset
    - Data Preparation
- Exploratory Data Analysis
    - Descriptive statistical
    - Visual Analysis
- Model Building
    - Training the model in multiple algorithms
    - Testing the model
- Performance Testing & Hyperparameter Tuning
    - Testing model with multiple evaluation metrics
    - Comparing model accuracy before & after applying hyperparameter tuning
- Model Deployment
    - Save the best model
    - Integrate with Web Framework
- Project Demonstration & Documentation
    - Record explanation Video for project end to end solution
    - Project Documentation-Step by step project development procedure

Project Structure:

Create the Project folder which contains files as shown below



- We are building a flask application which needs HTML pages stored in the templates folder and a python script app.py for scripting.
- thyroid_1_model.pkl is our saved model. Further, we will use this model for flask integration.
- Training folder contains model training files and the training_ibm folder contains IBM deployment files.

Milestone 1: Define Problem / Problem Understanding

Activity 1: Specify the business problem

Refer to Project Description

Activity 2: Business requirements

The business requirements for a machine learning model to predict thyroid disease include the ability to accurately predict thyroid disease based on the scan results, Minimise the number of false positives (wrong thyroid disease confirmations) and false negatives (thyroid is there but got as not thyroid disease). Provide an explanation for the model's decision, to comply with regulations and improve transparency.

Activity 3: Literature Survey (Student Will Write)

The thyroid gland is one of the body's most visible endocrine glands. Its size is determined by the individual's age, gender, and physiological states, such as pregnancy or lactation. It is divided into two lobes (right and left) by an isthmus (a band of tissue). It is imperceptible in everyday life yet can be detected when swallowing. The thyroid hormones T4 and T3 are needed for normal thyroid function. These hormones have a direct effect on the body's metabolic rate. It contributes to the stimulation of glucose, fatty acid, and other molecule consumption. Additionally, it enhances oxygen consumption in the majority of the body's cells by assisting in the processing of uncoupling proteins, which contributes to an improvement in the rate of cellular respiration. Thyroid conditions are difficult to detect in test results, and only trained professionals can do so. However, reading such extensive reports and predicting future results is difficult. Assume a machine learning model can detect the thyroid disease in a patient. The thyroid disease can then be easily identified based on the symptoms in the patient's history. Currently, models are evaluated using accuracy metrics on a validation dataset that is accessible.

Activity 4: Social or Business Impact.

Social Impact:- Untreated/undetected thyroid disease is more dangerous at times it can lead to fatal of the person. So, we can detect it at the earliest then people can get treatment and get cured.

Business Model/Impact:- We can make this application public, offer services as a subscription based or can collaborate with healthcare centres or specialists.

Milestone 2: Data Collection & Preparation

ML depends heavily on data. It is the most crucial aspect that makes algorithm training possible. So this section allows you to download the required dataset.

Activity 1: 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.

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

Activity 1.1: Importing the libraries

Import the necessary libraries as shown in the image.

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import tensorflow
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Layer, Dense, Dropout
```

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.

```
data = pd.read_csv("data.csv")
```

```
data.head()
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	TT4	T4U_measu
0	29	F	f	f	f	f	f	f	f	t	...	NaN	
1	29	F	f	f	f	f	f	f	f	f	...	128.0	
2	41	F	f	f	f	f	f	f	f	f	...	NaN	
3	36	F	f	f	f	f	f	f	f	f	...	NaN	
4	32	F	f	f	f	f	f	f	f	f	...	NaN	

5 rows × 31 columns

```
data.shape
```

```
(9172, 31)
```

Activity 2: 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
- Checking Correlation
- Converting Data Type
- Splitting dataset into training and test set
- Handled Imbalanced Data
- Applying StandardScaler

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.isnull().sum()
```

```
age                        0
sex                      307
on_thyroxine               0
query_on_thyroxine         0
on_antithyroid_meds        0
sick                       0
pregnant                   0
thyroid_surgery            0
I131_treatment             0
query_hypothyroid          0
query_hyperthyroid         0
lithium                    0
goitre                     0
tumor                      0
hypopituitary              0
psych                      0
TSH_measured               0
TSH                      842
T3_measured                0
T3                      2604
TT4_measured               0
TT4                      442
T4U_measured               0
T4U                      809
FTI_measured               0
FTI                      802
TBG_measured               0
TBG                     8823
referral_source            0
target                     0
patient_id                 0
dtype: int64
```

- Removing the Redundant attributes from the dataset.

```
#Removing Redundant attributes from dataset
data.drop(['TSH_measured','T3_measured','TT4_measured','T4U_measured','FTI_measured','TBG_measured','referral_source','patient_id
```

- Re-mapping the 'target' values to the diagnostic Group

```
#re-mapping target values to diagnostic group
diagnoses = {'A': 'hyperthyroid conditions',
             'B': 'hyperthyroid conditions',
             'C': 'hyperthyroid conditions',
             'D': 'hyperthyroid conditions',
             'E': 'hypothyroid conditions',
             'F': 'hypothyroid conditions',
             'G': 'hypothyroid conditions',
             'H': 'hypothyroid conditions',
             'I': 'binding protein',
             'J': 'binding protein',
             'K': 'general health',
             'L': 'replacement therapy',
             'M': 'replacement therapy',
             'N': 'replacement therapy',
             'O': 'antithyroid treatment',
             'P': 'antithyroid treatment',
             'Q': 'antithyroid treatment',
             'R': 'miscellaneous',
             'S': 'miscellaneous',
             'T': 'miscellaneous'}
data['target'] = data['target'].map(diagnoses) #remapping
```

Dropping Null Values

```
data.dropna(subset=['target'],inplace=True)
```

```
data['target'].value_counts()
```

```
hypothyroid conditions     593
general health             436
binding protein            376
replacement therapy        336
miscellaneous              281
hyperthyroid conditions    182
antithyroid treatment       33
Name: target, dtype: int64
```

Checking the 'age' is there any above 100 and we drop the age>100.

```
#Checking whether the age above 100
data[data.age>100]
```

age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	tumor	hypopituitary

0 rows × 23 columns

Activity 2.2: Splitting the data x and y

Splitting the data x and y

```
#splitting the data values as x and y
x=data.iloc[:,0:-1]
y= data.iloc[:,-1]
```

```
x
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumor
4	32.0	F	f	f	f	f	f	f	f	f	...	f	f
18	63.0	F	t	f	f	t	f	f	f	f	...	f	f
32	41.0	M	f	f	f	f	f	f	f	f	...	f	f
33	71.0	F	t	f	f	f	f	f	f	f	...	f	f
39	55.0	F	t	f	f	f	f	f	f	t	...	f	f
...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64.0	M	f	f	f	f	f	f	f	f	...	f	f
9157	60.0	M	f	f	t	f	f	f	f	f	...	f	f
9158	64.0	M	f	f	f	f	f	f	f	t	...	f	f
9162	36.0	F	f	f	f	f	f	f	f	f	...	f	f
9169	69.0	M	f	f	f	f	f	f	f	f	...	f	f

2237 rows × 22 columns

- Making 'F' on wherever we have the 'nan' values on data.

```
x['sex'].unique()
```

```
array(['F', 'M', nan], dtype=object)
```

```
x['sex'].replace(np.nan, 'F', inplace=True)
```

```
x['sex'].value_counts()
```

```
F    1701
M     536
Name: sex, dtype: int64
```

Activity 2.3: Converting the Data Type

Converting the data type from object to float. So that we will get output properly. And Checking info about data.

- Here, we have the object values are 'TSH', 'T3', 'TT4', 'T4U', 'FTI', 'TBG' and convert them to float values.

```
x['age']=x['age'].astype('float')
x['TSH']=x['TSH'].astype('float')
x['T3']=x['T3'].astype('float')
x['TT4']=x['TT4'].astype('float')
x['T4U']=x['T4U'].astype('float')
x['FTI']=x['FTI'].astype('float')
x['TBG']=x['TBG'].astype('float')
```

- Then we can check the datatype information about the dataset by code of x.info()

```
x.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 2237 entries, 4 to 9169
Data columns (total 22 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   age                  2237 non-null   float64
 1   sex                  2237 non-null   int64
 2   on_thyroxine         2237 non-null   int64
 3   query_on_thyroxine   2237 non-null   int64
 4   on_antithyroid_meds  2237 non-null   int64
 5   sick                 2237 non-null   int64
 6   pregnant             2237 non-null   int64
 7   thyroid_surgery      2237 non-null   int64
 8   I131_treatment       2237 non-null   int64
 9   query_hypothyroid    2237 non-null   int64
 10  query_hyperthyroid   2237 non-null   int64
 11  lithium              2237 non-null   int64
 12  goitre               2237 non-null   int64
 13  tumor                2237 non-null   int64
 14  hypopituitary        2237 non-null   int64
 15  psych                2237 non-null   int64
 16  TSH                  2237 non-null   object
 17  T3                   2237 non-null   object
 18  TT4                  2237 non-null   object
 19  T4U                  2237 non-null   object
 20  FTI                  2237 non-null   object
 21  TBG                  2237 non-null   object
dtypes: float64(1), int64(15), object(6)
memory usage: 402.0+ KB
```

Activity 2.4: 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 Ordinal Encoding and Label Encoding.

- In our project, categorical features are x and y values.
- Here, applying Ordinal Encoding on x values.

```
#Encoding the categorical data
#Encoding the independent(output) variable
from sklearn.preprocessing import OrdinalEncoder, LabelEncoder
#categorical data


ordinal_encoder = OrdinalEncoder(dtype = 'int64')
x.iloc[:, 1:16] = ordinal_encoder.fit_transform(x.iloc[:, 1:16])
#ordinal_encoder.fit_transform(x[['sex']])
```

```
x
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumc
4	32.0	0	0	0	0	0	0	0	0	0	...	0	
18	63.0	0	1	0	0	1	0	0	0	0	...	0	
32	41.0	1	0	0	0	0	0	0	0	0	...	0	
33	71.0	0	1	0	0	0	0	0	0	0	...	0	
39	55.0	0	1	0	0	0	0	0	0	1	...	0	
...	...	...	...	...	...	...	...	...	...	...	...	...	
9153	64.0	1	0	0	0	0	0	0	0	0	...	0	
9157	60.0	1	0	0	1	0	0	0	0	0	...	0	
9158	64.0	1	0	0	0	0	0	0	0	1	...	0	
9162	36.0	0	0	0	0	0	0	0	0	0	...	0	
9169	69.0	1	0	0	0	0	0	0	0	0		0	

- Replacing the nan values with zero (0) values.

```
x.replace(np.nan, '0', inplace=True)
```

```
x
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumor
4	32.0	0	0	0	0	0	0	0	0	0	...	0	0
18	63.0	0	1	0	0	1	0	0	0	0	...	0	0
32	41.0	1	0	0	0	0	0	0	0	0	...	0	0
33	71.0	0	1	0	0	0	0	0	0	0	...	0	0
39	55.0	0	1	0	0	0	0	0	0	1	...	0	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64.0	1	0	0	0	0	0	0	0	0	...	0	0
9157	60.0	1	0	0	1	0	0	0	0	0	...	0	0
9158	64.0	1	0	0	0	0	0	0	0	1	...	0	0
9162	36.0	0	0	0	0	0	0	0	0	0	...	0	0
9169	69.0	1	0	0	0	0	0	0	0	0	...	0	0

2237 rows × 22 columns

- Now, applying Label Encoding on y(Independent variable) value.

```
label_encoder = LabelEncoder()
y_dt= label_encoder.fit_transform(y)
```

```
y=pd.DataFrame(y_dt, columns=['target'])
```

```
y
```

	target
0	5
1	4
2	5
3	1
4	6
...	...
2232	2
2233	2
2234	1
2235	1
2236	1

2237 rows × 1 columns

Activity 2.5: 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 the data values as x and y
x=data.iloc[:,0:-1]
y= data.iloc[:,-1]
```

```
x
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumor
4	32.0	F	f	f	f	f	f	f	f	f	...	f	f
18	63.0	F	t	f	f	t	f	f	f	f	...	f	f
32	41.0	M	f	f	f	f	f	f	f	f	...	f	f
33	71.0	F	t	f	f	f	f	f	f	f	...	f	f
39	55.0	F	t	f	f	f	f	f	f	t	...	f	f
...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64.0	M	f	f	f	f	f	f	f	f	...	f	f
9157	60.0	M	f	f	t	f	f	f	f	f	...	f	f
9158	64.0	M	f	f	f	f	f	f	f	t	...	f	f
9162	36.0	F	f	f	f	f	f	f	f	f	...	f	f
9169	69.0	M	f	f	f	f	f	f	f	f	...	f	f

2237 rows × 22 columns


```
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.20,random_state=0)
```

```
from imblearn.over_sampling import SMOTE
y_train.value_counts()
```

```
target
4    471
2    351
1    302
6    265
5    230
3    144
0     26
dtype: int64
```

Activity 2.6: Handling Imbalanced Data

```
os = SMOTE(random_state=0,k_neighbors=1)
x_bal,y_bal=os.fit_resample(x_train,y_train)
x_test_bal,y_test_bal=os.fit_resample(x_test,y_test)
```

Activity 2.7: Applying StandardScaler

- Scaling the features makes the flow of gradient descent smooth and helps algorithms quickly reach the minima of the cost function.
- Without scaling features, the algorithm may be biased toward the feature which has values higher in magnitude. it brings every feature in the same range and the model uses every feature wisely.

```
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
x_bal = sc.fit_transform(x_bal)
x_test_bal= sc.transform(x_test_bal)
```

```
x_bal
```

```
array([[-1.62721505, -0.44060477, -0.4238    , ..., -2.50870684,
        -1.40088079,  3.29445097],
       [-0.11561403, -0.44060477,  2.35960359, ..., -0.26259147,
         0.0720981 , -0.19494049],
       [ 1.1874903 ,  2.26960776, -0.4238    , ...,  0.17039463,
        -0.19352104, -0.19494049],
       ...,
       [ 1.395987  , -0.44060477,  2.35960359, ...,  0.43615031,
         0.06101022, -0.19494049],
       [ 0.72802783, -0.44060477,  2.35960359, ...,  0.143333  ,
         0.89086631, -0.19494049],
       [ 1.15628145, -0.44060477,  2.35960359, ...,  0.39723515,
        -0.26588659, -0.19494049]])
```

- Here, we have the data in array format and we are making it dataframe(table format).

```
columns=['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroid_meds','sick','pregnant','thyroid_surgery','I131_treatmer
```

```
x_test_bal= pd.DataFrame(x_test_bal,columns=columns)
```

```
x_bal= pd.DataFrame(x_bal,columns=columns)
```

```
x_bal
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...
0	-1.627215	-0.440605	-0.423800	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
1	-0.115614	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
2	1.187490	2.269608	-0.423800	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
3	-1.366594	-0.440605	-0.423800	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
4	-0.167738	-0.440605	-0.423800	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
...	...	...	...	...	...	...	...	...	...	...	...
3292	0.546923	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
3293	0.383062	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
3294	1.395987	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
3295	0.728028	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...
3296	1.156281	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...

3297 rows × 22 columns

Activity 2.8: Performing Feature Importance

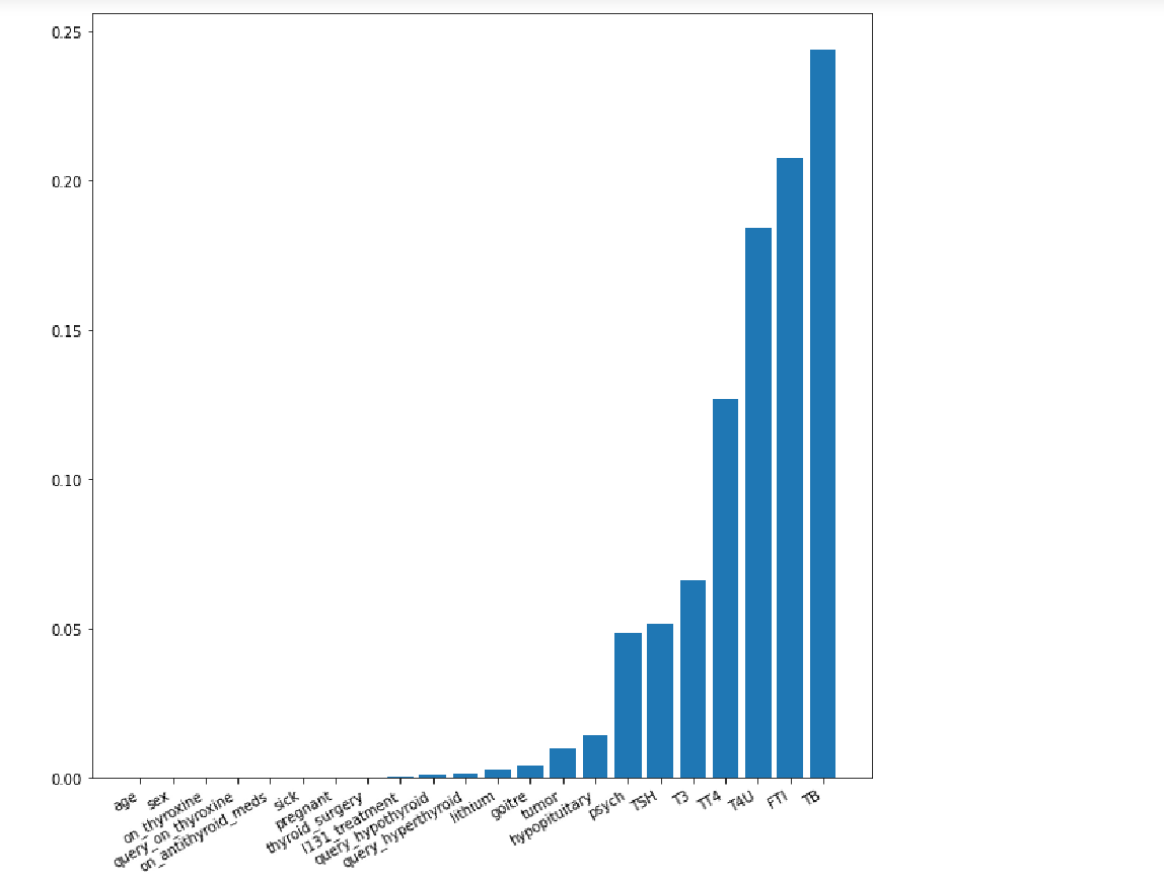
- The idea behind permutation feature importance is simple. The feature importance is calculated by noticing the increase or decrease in error when we permute the values of a feature.
- If permuting the values causes a huge change in the error, it means the feature is important for our model.

```
#perform feature importance
from sklearn.inspection import permutation_importance
results = permutation_importance(rfr,x_bal,y_bal, scoring='accuracy')
```

```
#gets importance
feature_importance=['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroid_meds','sick','pregnant','thyroid_surgery','I1
importance = results.importances_mean
importance = np.sort(importance)
#summerize feature importance
for i,v in enumerate(importance):
    i=feature_importance[i]
    print('feature: {:<20} Score: {}'. format(i,v))
#plot important feature

plt.figure(figsize=(10,10))
plt.bar(x=feature_importance, height = importance)
plt.xticks(rotation=30, ha='right')
plt.show()
```

```
feature: age                 Score: 0.0
feature: sex                 Score: 0.0
feature: on_thyroxine        Score: 0.0
feature: query_on_thyroxine  Score: 0.0
feature: on_antithyroid_meds Score: 6.066120715801926e-05
feature: sick                Score: 0.00024264482863207705
feature: pregnant            Score: 0.0003033060357900963
feature: thyroid_surgery     Score: 0.0003033060357900963
feature: I131_treatment      Score: 0.0006066120715801926
feature: query_hypothyroid   Score: 0.0012132241431604518
feature: query_hyperthyroid  Score: 0.0015165301789505925
feature: lithium             Score: 0.0027904155292689968
feature: goitre              Score: 0.00442826812253565
feature: tumor               Score: 0.010009099181073733
feature: hypopituitary       Score: 0.014376706096451319
feature: psych               Score: 0.0488929329693661
feature: TSH                 Score: 0.05131938125568698
feature: T3                  Score: 0.06618137700940249
feature: TT4                 Score: 0.12684258416742494
feature: T4U                 Score: 0.1841067637245981
feature: FTI                 Score: 0.20752198968759478
feature: TB                  Score: 0.24416135881104034
```



Activity 2.9: Selecting Output Columns

- Before we have this many columns

```
x.head()
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumor	hy
4	32.0	0	0	0	0	0	0	0	0	0	...	0	0	
18	63.0	0	1	0	0	1	0	0	0	0	...	0	0	
32	41.0	1	0	0	0	0	0	0	0	0	...	0	0	
33	71.0	0	1	0	0	0	0	0	0	0	...	0	0	
39	55.0	0	1	0	0	0	0	0	0	1	...	0	0	

5 rows × 22 columns

- After Performing Feature Importance by using 'Permutation Importance' we are dropping some columns which are not important for 'target'.

```
x_bal.drop(['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroid_meds','sick','pregnant','thyroid_surgery','I131_treat
```

```
x_test_bal.drop(['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroid_meds','sick','pregnant','thyroid_surgery','I131_
```

```
x_bal.head()
```

	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG
0	-0.052319	-0.137297	-0.024637	-0.107982	-0.315458	-1.035358	-1.704935	-2.508707	-1.400881	3.294451
1	-0.052319	-0.137297	-0.024637	-0.107982	-0.090056	0.155233	-0.197223	-0.262591	0.072098	-0.194940
2	-0.052319	-0.137297	-0.024637	-0.107982	-0.278907	-0.471394	-0.227079	0.170395	-0.193521	-0.194940
3	-0.052319	7.283487	-0.024637	-0.107982	-0.284999	0.969848	0.041622	0.495134	-0.133153	-0.194940
4	-0.052319	-0.137297	-0.024637	-0.107982	-0.306321	4.541622	1.459767	-0.127283	1.496783	-0.194940

Milestone 3: Exploratory Data Analysis

Activity 1: Descriptive analysis

Descriptive analysis is to study the basic features of data with the statistical process. Here pandas have a worthy function called describe. With this described function we can find mean, std, min, max and percentile values of continuous features.

Checking info about data by using data_info()

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 2237 entries, 4 to 9169
Data columns (total 23 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   age                  2237 non-null   int64
 1   sex                  2147 non-null   object
 2   on_thyroxine         2237 non-null   object
 3   query_on_thyroxine   2237 non-null   object
 4   on_antithyroid_meds  2237 non-null   object
 5   sick                 2237 non-null   object
 6   pregnant             2237 non-null   object
 7   thyroid_surgery      2237 non-null   object
 8   I131_treatment       2237 non-null   object
 9   query_hypothyroid    2237 non-null   object
 10  query_hyperthyroid   2237 non-null   object
 11  lithium              2237 non-null   object
 12  goitre               2237 non-null   object
 13  tumor                2237 non-null   object
 14  hypopituitary        2237 non-null   object
 15  psych                2237 non-null   object
 16  TSH                  2087 non-null   float64
 17  T3                   1643 non-null   float64
 18  TT4                  2140 non-null   float64
 19  T4U                  2059 non-null   float64
 20  FTI                  2060 non-null   float64
 21  TBG                  98 non-null     float64
 22  target               2237 non-null   object
dtypes: float64(6), int64(1), object(16)
memory usage: 419.4+ KB
```

Activity 2: Visual analysis

Visual analysis is the process of using visual representations, such as charts, plots, and graphs, to explore and understand data. It is a way to quickly identify patterns, trends, and outliers in the data, which can help to gain insights and make informed decisions.

Activity 2.1: Checking Correlation.

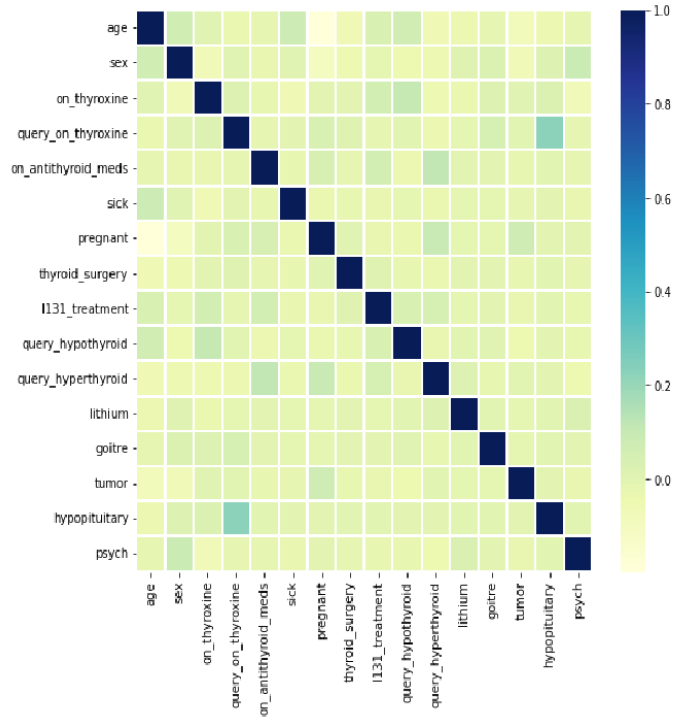
Here, I'm finding the correlation using HeatMap. It visualizes the data in 2-D coloured maps making use of colour variations. It describes the related variables in the form of colours instead of numbers; it will be plotted on both axes.

Here, there is no correlation between columns.

```
#checking correlation using Heatmap
import seaborn as sns
corrmat = x.corr()

f, ax = plt.subplots(figsize =(9, 8))
sns.heatmap(corrmat, ax = ax, cmap ="YlGnBu", linewidths = 0.1)
```

```
<AxesSubplot:>
```



Milestone 4: Model Building

Activity 1: Training the model in multiple algorithms

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.

Activity 1.1: Random Forest Classifier Model

A function named Random Forest Classifier Model is created and train and test data are passed as the parameters. Inside the function, the Random Forest Classifier algorithm is initialized and training data is passed to the model with the .fit() function. Test data is predicted with the .predict() function and saved in a new variable. For evaluating the model, accuracy_score and classification report is done.

```
from sklearn.ensemble import RandomForestClassifier
rfr1 = RandomForestClassifier().fit(x_os,y_os.values.ravel())
y_pred = rfr1.predict(x_test_os)

rfr1 = RandomForestClassifier()
```

```
rfr1.fit(x_os, y_os.values.ravel())
```

```
RandomForestClassifier()
```

```
y_pred = rfr1.predict(x_test_os)
```

```
y_pred = rfr1.predict(x_test_os)
```

```
print(classification_report(y_test_os,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.00      0.00      0.00       122
           1       0.76      0.90      0.83       122
           2       0.91      0.98      0.94       122
           3       0.78      0.83      0.80       122
           4       0.46      0.92      0.62       122
           5       0.75      0.70      0.73       122
           6       0.63      0.48      0.54       122

    accuracy                           0.69       854
   macro avg       0.61      0.69      0.64       854
weighted avg       0.61      0.69      0.64       854
```

```
train_score = accuracy_score(y_os, rfr1.predict(x_os))
train_score
```

```
1.0
```

Activity 1.2: XGBClassifier model

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

```
from xgboost import XGBClassifier
xgb1 = XGBClassifier()
xgb1.fit(x_os,y_os)
```

```
XGBClassifier(base_score=0.5, booster='gbtree', callbacks=None,
              colsample_bylevel=1, colsample_bynode=1, colsample_bytree=1,
              early_stopping_rounds=None, enable_categorical=False,
              eval_metric=None, gamma=0, gpu_id=-1, grow_policy='depthwise',
              importance_type=None, interaction_constraints='',
              learning_rate=0.300000012, max_bin=256, max_cat_to_onehot=4,
              max_delta_step=0, max_depth=6, max_leaves=0, min_child_weight=1,
              missing=nan, monotone_constraints='()', n_estimators=100,
              n_jobs=0, num_parallel_tree=1, objective='multi:softprob',
              predictor='auto', random_state=0, reg_alpha=0, ...)
```

```
y_pred = xgb1.predict(x_test_os)
```

```
print(classification_report(y_test_os,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.70      0.13      0.22       122
           1       0.75      0.93      0.84       122
           2       0.95      0.99      0.97       122
           3       0.76      0.77      0.77       122
           4       0.48      0.85      0.61       122
           5       0.79      0.71      0.75       122
           6       0.62      0.52      0.57       122

    accuracy                           0.70       854
   macro avg       0.72      0.70      0.67       854
weighted avg       0.72      0.70      0.67       854
```

```
accuracy_score(y_test_os,y_pred)
```

```
0.7014051522248244
```

Activity 1.3: SVC model

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

```
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score, classification_report

sv= SVC()
```

```
sv.fit(x_bal,y_bal)
```

```
C:\Users\SmartBridge-PC\anaconda3\lib\site-packages\sklearn\utils\validation.py:1111: DataConversionWarning: A column-vector y
was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example using ravel().
  y = column_or_1d(y, warn=True)
```

▾ SVC

SVC()

```
y_pred = sv.predict(x_test_bal)
```

```
print(classification_report(y_test_bal,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.70      0.85      0.77       122
           1       0.76      0.81      0.79       122
           2       0.88      0.93      0.90       122
           3       0.71      0.65      0.68       122
           4       0.71      0.63      0.67       122
           5       0.76      0.54      0.63       122
           6       0.49      0.57      0.52       122

    accuracy                           0.71       854
   macro avg       0.72      0.71      0.71       854
weighted avg       0.72      0.71      0.71       854
```

```
train_score=accuracy_score(y_bal,sv.predict(x_bal))
train_score
```

```
0.7154989384288747
```

Activity 1.4 ANN Model

Artificial Neural Networks (ANN) are multi-layer fully-connected neural nets. They consist of an input layer, multiple hidden layers, and an output layer. Every node in one layer is connected to every other node in the next layer. We make the network deeper by increasing the number of hidden layers

In [68]:
```
model = Sequential()
```

In [69]:
```
model.add(Dense(units = 128, activation='relu', input_shape=(10,)))
```

In [70]:
```
model.add(Dense(units = 128, activation='relu', kernel_initializer='random_uniform'))
model.add(Dropout(0.2))
model.add(Dense(units = 256, activation='relu', kernel_initializer='random_uniform'))
model.add(Dropout(0.2))
model.add(Dense(units = 128, activation='relu', kernel_initializer='random_uniform'))
```

In [71]:
```
model.add(Dense(units = 1, activation='sigmoid'))
```

In [72]:
```
model.summary()
```

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 dense (Dense)               (None, 128)               1408

 dense_1 (Dense)             (None, 128)               16512

 dropout (Dropout)           (None, 128)               0

 dense_2 (Dense)             (None, 256)               33024

 dropout_1 (Dropout)         (None, 256)               0

 dense_3 (Dense)             (None, 128)               32896

 dense_4 (Dense)             (None, 1)                 129

=================================================================
Total params: 83,969
Trainable params: 83,969
Non-trainable params: 0
_________________________________________________________________
```

In [73]:
```
model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['accuracy'])
```

In [75]:
```
model.fit(x_bal,y_bal, validation_data=[x_test_bal, y_test_bal], epochs=15)
```

```
Epoch 1/15
104/104 [==============================] - 9s 15ms/step - loss: -18416.0605 - accuracy: 0.1429 - val_loss: -142105.5156 - val
_accuracy: 0.1429
Epoch 2/15
104/104 [==============================] - 1s 8ms/step - loss: -2626274.5000 - accuracy: 0.1429 - val_loss: -10219054.0000 -
val_accuracy: 0.1429
Epoch 3/15
104/104 [==============================] - 1s 9ms/step - loss: -42823204.0000 - accuracy: 0.1429 - val_loss: -113329736.0000
- val_accuracy: 0.1429
Epoch 4/15
104/104 [==============================] - 1s 9ms/step - loss: -277232128.0000 - accuracy: 0.1429 - val_loss: -582218880.0000
- val_accuracy: 0.1429
Epoch 5/15
104/104 [==============================] - 1s 8ms/step - loss: -1097882752.0000 - accuracy: 0.1429 - val_loss: -1989677696.00
00 - val_accuracy: 0.1429
Epoch 6/15
104/104 [==============================] - 1s 8ms/step - loss: -3208519680.0000 - accuracy: 0.1429 - val_loss: -5285069824.00
00 - val_accuracy: 0.1429
Epoch 7/15
```

Activity 2: Testing the model

testing the models

```
In [115]: rfr1.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])

C:\Users\Mahidhar reddy\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but
RandomForestClassifier was fitted with feature names
  warnings.warn(

Out[115]: array([4])

In [130]: sv.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])

C:\Users\Mahidhar reddy\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but
SVC was fitted with feature names
  warnings.warn(

Out[130]: array([1])

In [143]: col = ['goitre', 'tumor', 'hypopituitary', 'psych', 'TSH', 'T3', 'TT4', 'T4U', 'FTI', 'TBG']
da = [[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]]
da1 = pd.DataFrame(data = da, columns=col)
xgb1.predict(da1)

Out[143]: array([4], dtype=int64)

In [140]: model.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])

1/1 [==============================] - 0s 238ms/step

Out[140]: array([[1.]], dtype=float32)
```

Milestone 5: Performance Testing & Hyperparameter Tuning

Activity 1: Testing model with multiple evaluation metrics

Multiple evaluation metrics means evaluating the model's performance on a test set using different performance measures. This can provide a more comprehensive understanding of the model's strengths and weaknesses. We are using evaluation metrics for classification tasks including accuracy, precision, recall, support and F1-score.

Activity 1.1: Compare the model

For comparing the above four models, the compareModel function is defined.

```
print(classification_report(y_test_bal,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.87      0.16      0.28       122
           1       0.82      0.94      0.87       122
           2       0.93      0.98      0.96       122
           3       0.77      0.84      0.80       122
           4       0.49      0.89      0.63       122
           5       0.88      0.68      0.77       122
           6       0.59      0.53      0.56       122

    accuracy                           0.72       854
   macro avg       0.76      0.72      0.70       854
weighted avg       0.76      0.72      0.70       854
```

```
train_score = accuracy_score(y_bal,rfr1.predict(x_bal))
```

```
train_score
```

```
1.0
```

```
y_pred=xgb.predict(x_test_bal)
```

```
print(classification_report(y_test_bal,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.80      0.30      0.44       122
           1       0.82      0.94      0.88       122
           2       0.96      1.00      0.98       122
           3       0.77      0.84      0.81       122
           4       0.51      0.81      0.62       122
           5       0.84      0.70      0.76       122
           6       0.59      0.54      0.56       122

    accuracy                           0.73       854
   macro avg       0.76      0.73      0.72       854
weighted avg       0.76      0.73      0.72       854
```

```
train_score = accuracy_score(y_bal, xgb.predict(x_bal))
train_score
```

```
1.0
```

```python
y_pred = sv.predict(x_test_bal)
```

```python
print(classification_report(y_test_bal,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.70      0.85      0.77       122
           1       0.76      0.81      0.79       122
           2       0.88      0.93      0.90       122
           3       0.71      0.65      0.68       122
           4       0.71      0.63      0.67       122
           5       0.76      0.54      0.63       122
           6       0.49      0.57      0.52       122

    accuracy                           0.71       854
   macro avg       0.72      0.71      0.71       854
weighted avg       0.72      0.71      0.71       854
```

```python
train_score=accuracy_score(y_bal,sv.predict(x_bal))
train_score
```

```
0.7154989384288747
```

```python
y_pred = model.predict(x_test_bal)
```

```
27/27 [==============================] - 0s 3ms/step
```

```python
print(classification_report(y_test_bal,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.00      0.00      0.00       122
           1       0.14      1.00      0.25       122
           2       0.00      0.00      0.00       122
           3       0.00      0.00      0.00       122
           4       0.00      0.00      0.00       122
           5       0.00      0.00      0.00       122
           6       0.00      0.00      0.00       122

    accuracy                           0.14       854
   macro avg       0.02      0.14      0.04       854
weighted avg       0.02      0.14      0.04       854
```

```
C:\Users\Mahidhar reddy\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:1318: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\Mahidhar reddy\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:1318: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
C:\Users\Mahidhar reddy\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:1318: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

```python
accuracy_score(y_test_bal,y_pred)
```

```
0.14285714285714285
```

Activity 2:Comparing model accuracy before & after applying hyperparameter tuning

From sklearn, accuracy is used to evaluate the score of the model. On the parameters, we have given xgb1 (model name), x, y, cv (as 3 folds). Our model is performing well. So, we are saving the model by pickle.dump().

Note: To understand cross validation, refer to this link. https://towardsdatascience.com/cross-validation-explained-evaluating-estimator-performance-e51e5430ff85.

```
params = {


         'C': [0.1, 1, 10, 100, 1000],
         'gamma': [1, 0.1, 0.01, 0.001, 0.0001],
             'kernel': ['rbf','sqrt']


}
```

```
random_svc = RandomizedSearchCV(sv,params, scoring='accuracy',cv=5,n_jobs=-1)
```

```
random_svc.fit(x_bal,y_bal)
```

```
random_svc.best_params_
```

```
{'kernel': 'rbf', 'gamma': 1, 'C': 1}
```

```
sv1=SVC(kernel= 'rbf', gamma= 0.1, C= 100)
```

```
sv1.fit(x_bal,y_bal)
```

```
C:\Users\SmartBridge-PC\anaconda3\lib\site-packages\sklearn\utils\validation.py:1111: DataConversionWarning: A column-vector y
was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for example using ravel().
  y = column_or_1d(y, warn=True)
```

```
SVC
SVC(C=100, gamma=0.1)
```

```
y_pred= sv1.predict(x_test_bal)
```

```
print(classification_report(y_test_bal,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.74      0.75      0.75       122
           1       0.77      0.86      0.81       122
           2       0.95      0.91      0.93       122
           3       0.70      0.66      0.68       122
           4       0.66      0.73      0.70       122
           5       0.72      0.72      0.72       122
           6       0.57      0.48      0.52       122

    accuracy                           0.73       854
   macro avg       0.73      0.73      0.73       854
weighted avg       0.73      0.73      0.73       854
```

```
train_score= accuracy_score(y_bal,sv1.predict(x_bal))
train_score
```

```
0.8125568698817106
```

Saving the model as thyroid1_model.pkl

```
# saving the model
import pickle
pickle.dump(sv1,open('thyroid_1_model.pkl','wb'))
```

```
features = np.array([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
print(label_encoder.inverse_transform(xgb1.predict(features)))
```

```
['hypothyroid conditions']
```

Here, we are saving label_encoding also as label_encoder.pkl

```
pickle.dump(label_encoder,open('label_encoder.pkl','wb'))
```

```
data['target'].unique()
```

```
array(['miscellaneous', 'hypothyroid conditions', 'binding protein',
       'replacement therapy', 'general health', 'hyperthyroid conditions',
       'antithyroid treatment'], dtype=object)
```

```
y['target'].unique()
```

```
array([5, 4, 1, 6, 2, 3, 0])
```

Milestone 6: Model Deployment

Activity 1:Save the best model

Saving the best model after comparing its performance using different evaluation metrics means selecting the model with the highest performance and saving its weights and configuration. This can be useful in avoiding the need to retrain the model every time it is needed and also to be able to use it in the future.

```
import pickle
pickle.dump(sv1,open('thyroid_1_model.pkl','wb'))
```

Activity 2: Integrate with Web Framework

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 server side script

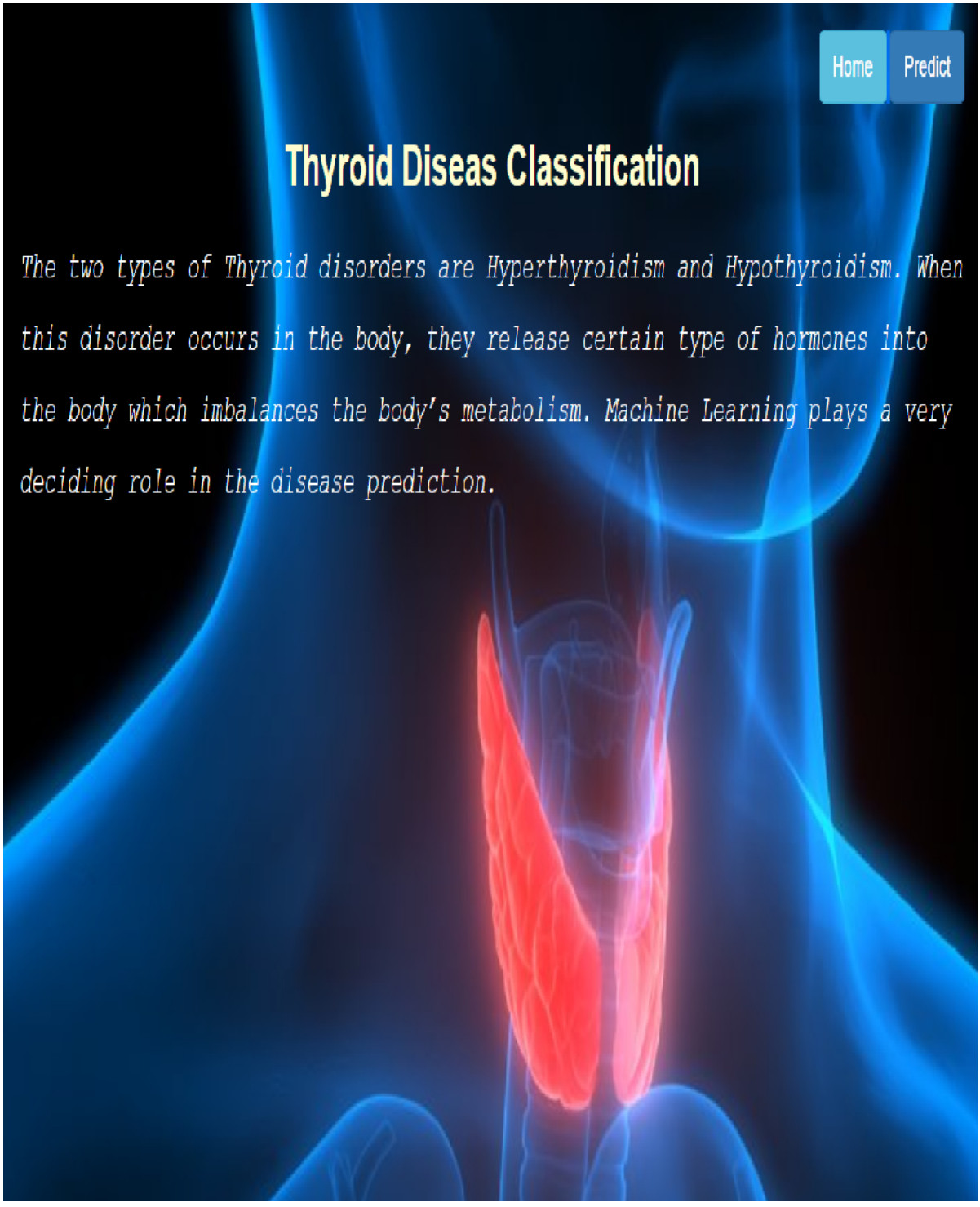
Activity 2.1: Building Html Pages:

For this project create three HTML files namely

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

and save them in the templates folder.

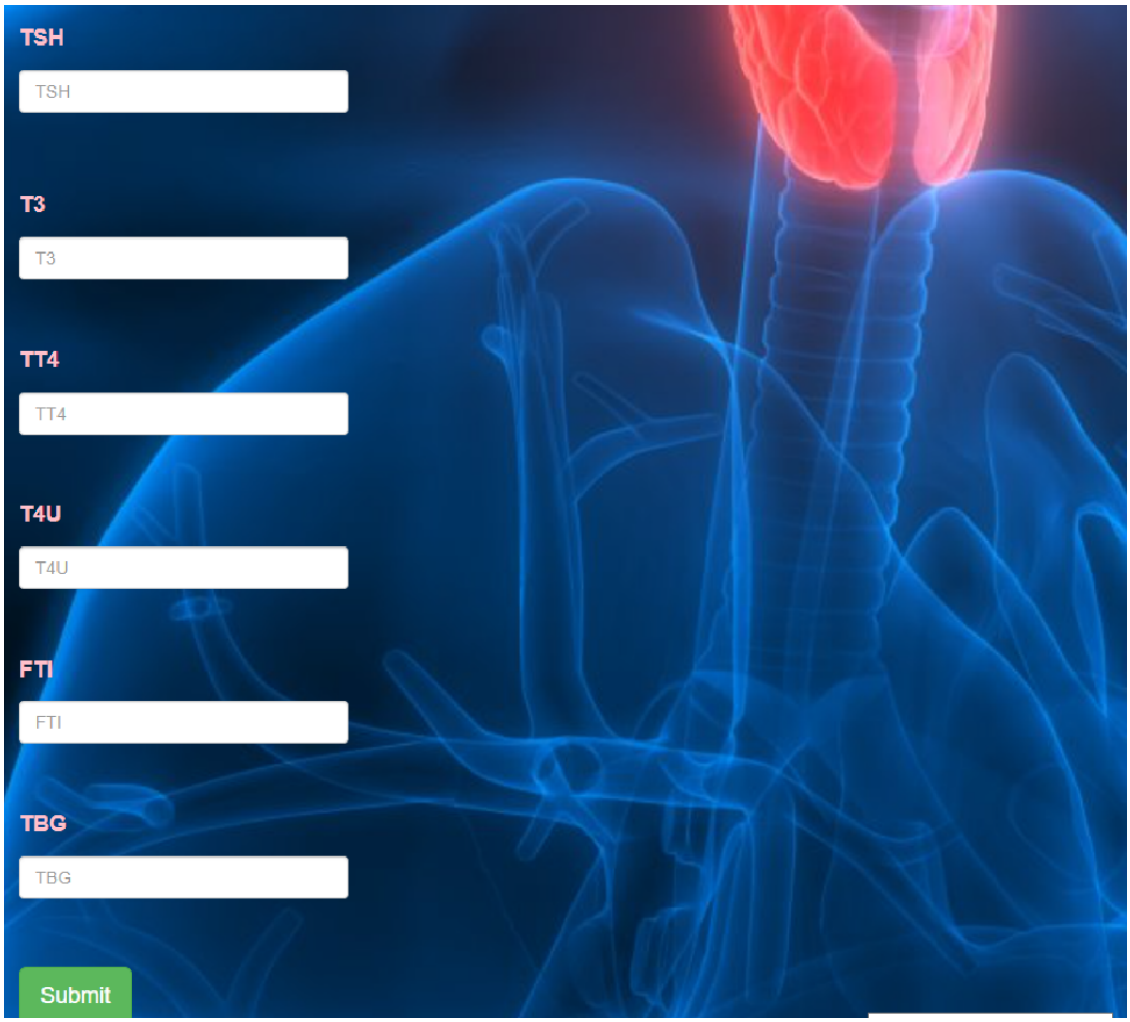
Let’s see how our home.html page looks like:



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

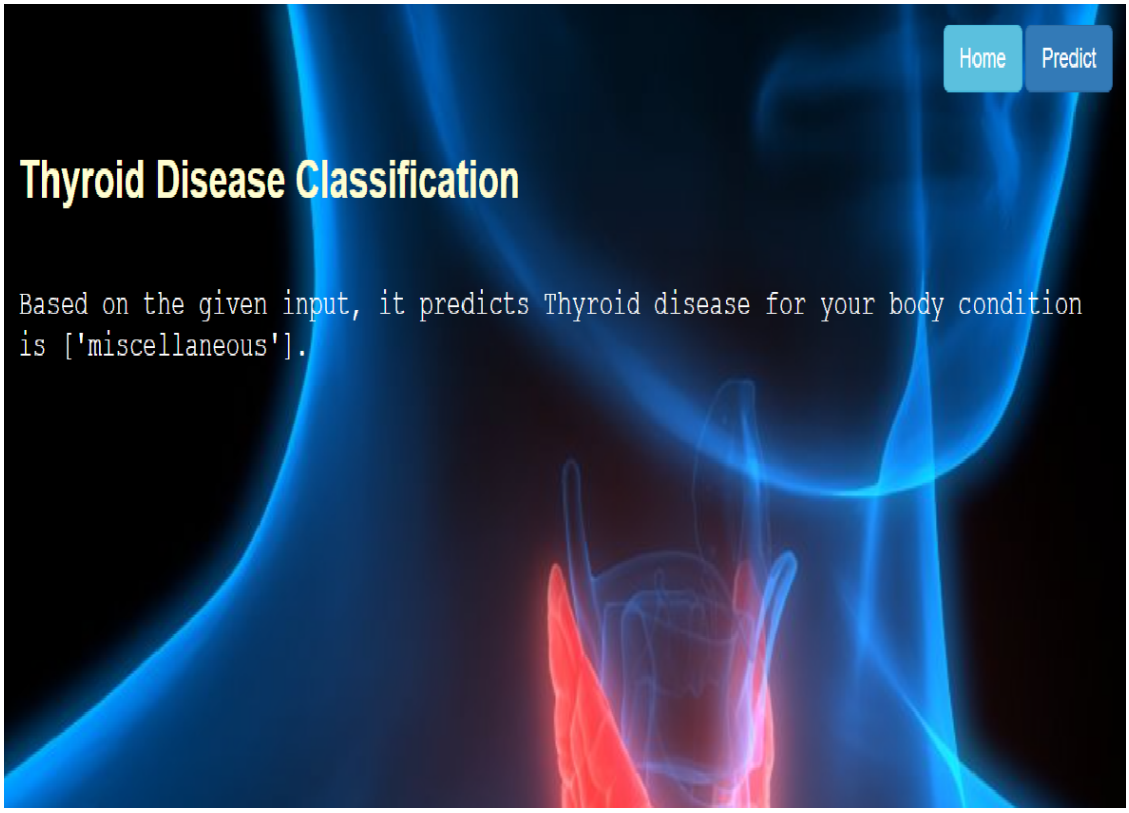
Let's look how our predict.html file looks like:


Home
Predict
Thyroid Disease Classification
goitre
Male
tumor
Male
hypopituitary
Male
psych
Male
TSH
TSH



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

Let's look how our submit.html file looks like: it is ['miscellaneous'].



Activity 2.2: Build Python code:

Import the libraries

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

Load the saved model. Importing the 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(r"C:\Users\SmartBridge-PC\Downloads\Thyroid\thyroid1_model.pkl", 'rb'))
le = pickle.load(open("label_encoder.pkl", 'rb'))


app = Flask(__name__)
```

Render HTML page:

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

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

In the above example, '/' URL is bound with the home.html function. Hence, when the home page of the web server is opened in the 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', 'GET'])
def predict():
    x = [[float(x) for x in request.form.values()]]

    print(x)
    col = ['goitre','tumor','hypopituitary','psych','TSH','T3','TT4','T4U','FTI','TBG']
    x = pd.DataFrame(x, columns=col)


    #print(x.shape)

    print(x)
    pred = model.predict(x)
    pred = le.inverse_transform(pred)
    print(pred[0])
    return render_template('submit.html', prediction_text=str(pred))
```

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 be rendered to the text that we have mentioned in the submit.html page earlier.

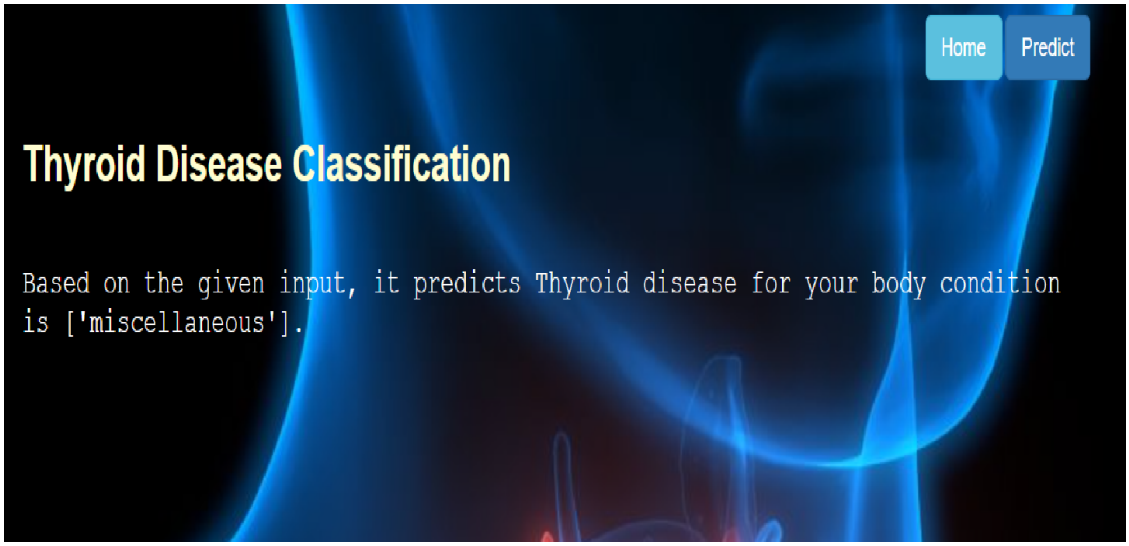
Main Function:

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

Activity 2.3: 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.

```
In [32]: runfile('C:/Users/SmartBridge-PC/
Downloads/Thyroid/app.py', wdir='C:/Users/
SmartBridge-PC/Downloads/Thyroid')
 * Serving Flask app "app" (lazy loading)
 * Environment: production
   WARNING: This is a development server. Do
not use it in a production deployment.
   Use a production WSGI server instead.
 * Debug mode: off
 * Running on http://127.0.0.1:5000/ (Press
CTRL+C to quit)
```



Milestone 7: Project Demonstration & Documentation

Below mentioned deliverables to be submitted along with other deliverables

Activity 1:- Record explanation Video for the project end to end solution

Activity 2:- Project Documentation-Step by step project development procedure

Create document as per the template provided