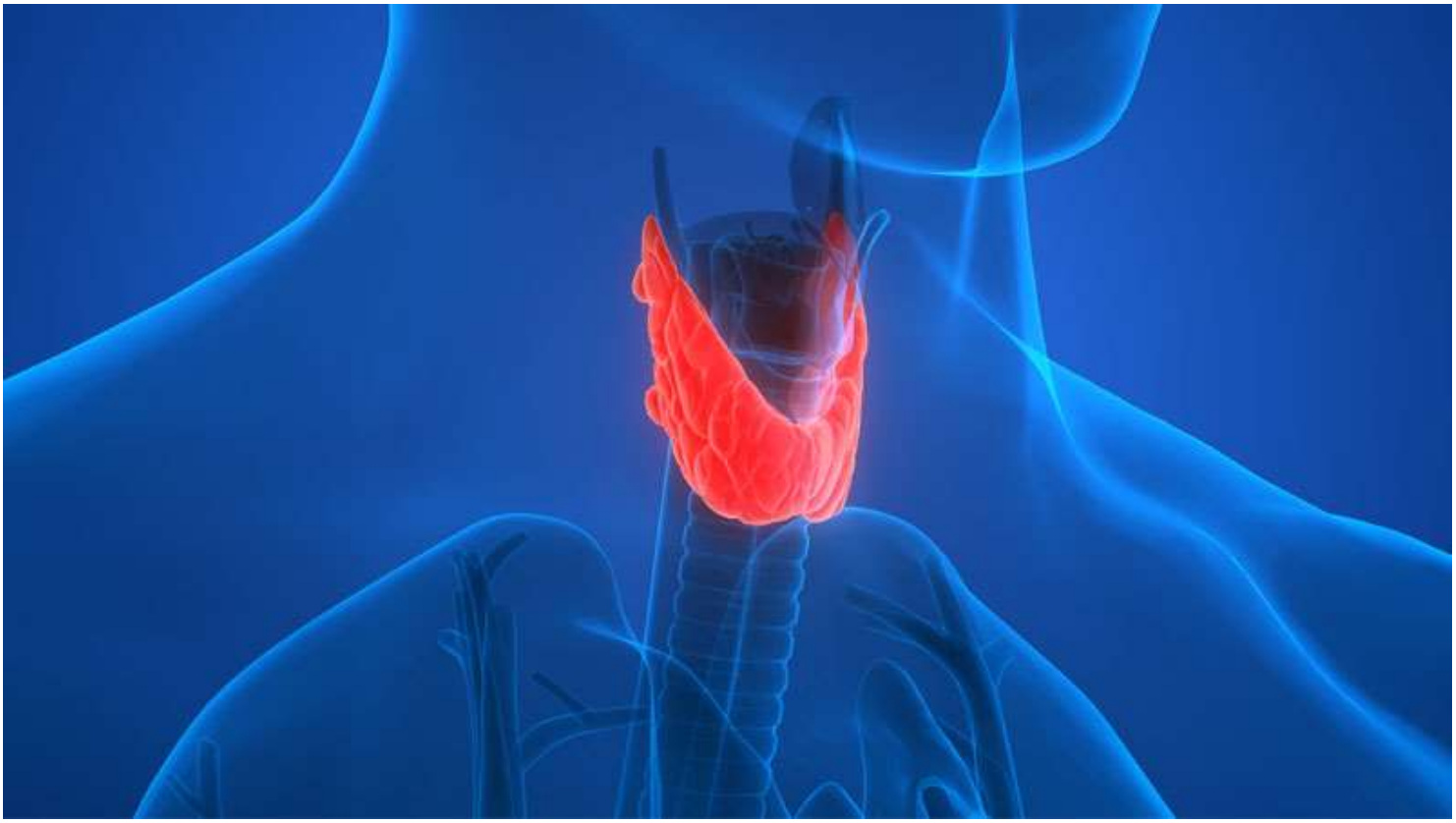

Thyroid Disease Classification Using Machine Learning

DONE BY

Sushmitha .S

Suguna .R

Suvathika .A

Valarmathi .S

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1. INTRODUCTION

1.1 Overview

Thyroid disease is a subset of endocrinology which is one of the most misunderstood and undiagnosed diseases. Thyroid gland diseases are among the most prevalent endocrine disorders in the world, second only to diabetes, according to the World Health Organization. Hyper function hyperthyroidism and hypothyroidism affect about 2% and 1% of individuals, respectively. Men have about a tenth of the prevalence of women. Hyper-and hypothyroidism may be caused by thyroid gland dysfunction, secondary to pituitary gland failure, or tertiary to hypothalamic malfunction. Due to dietary iodine deficiency, goiter or active thyroid nodules may become prevalent in some regions, with a prevalence of up to 15%. The thyroid gland can also be the location of different kinds of tumors and can be a dangerous place where endogenous antibodies wreak havoc (autoantibodies).

Early disease detection, diagnosis, and care, according to doctors, are vital in preventing disease progression and even death. For several different forms of anomalies, early identification and differential diagnosis raises the odds of good treatment. Despite multiple trials, clinical diagnosis is often thought to be a difficult task. The thyroid gland is a butterfly-shaped gland situated at the base of the throat. It comprises two active thyroid hormones, levothyroxine (T4) and

triiodothyronine (T3), which are involved in brain functions such as body temperature control, blood pressure management, and heart rate regulation.

Likewise, thyroid disease is one of the most prevalent diseases worldwide, and it is mostly caused by a deficiency of iodine, but it may also be caused by other factors. The thyroid gland is an endocrine gland that secretes hormones and passes them through the bloodstream. It is situated in the middle of the front of the body. Thyroid gland hormones are responsible for aiding in digestion as well as maintaining the body moist, balanced, and so on. Thyroid gland treatments such as T3 (triiodothyronine), T4 (thyroid hormone), and TSH (thyroid stimulating hormone) are used to assess thyroid activity (thyroid stimulating hormone). Thyroid disorder is classified into two types: hypothyroidism and hyperthyroidism. Data mining is a semi-automated method of looking for correlations in massive datasets.

Machine learning algorithms are one of the best solutions to many problems that are difficult to solve Classification is a data extraction technique (machine learning) used to predict and identify many diseases, such as thyroid disease, which we researched and classified here because machine learning algorithms play a significant role in classifying thyroid disease and because these algorithms are high performing and efficient and aid in classification. Although the application of computer learning and artificial intelligence in medicine dates back to the early days of the field, there has been a new

movement to consider the need for machine learning-driven healthcare solutions. As a result, analysts predict that machine learning will become commonplace in healthcare in the near future.

Hyperthyroidism is a disorder in which the thyroid gland releases so many thyroid hormones. Hyperthyroidism is caused by an increase in thyroid hormone levels. Dry skin, elevated temperature sensitivity, hair thinning, weight loss, increased heart rate, high blood pressure, heavy sweating, neck enlargement, nervousness, menstrual cycles shortening, irregular stomach movements, and hands shaking are some of the signs.

Hypothyroidism is a condition in which the thyroid gland is underactive Hypothyroidism is caused by a decline in thyroid hormone production. Hypo means deficient or less in medical terms. Inflammation and thyroid gland injury are the two primary causes of hypothyroidism. Obesity, low heart rate, increased temperature sensitivity, neck swelling, dry skin, hand numbness, hair issues, heavy menstrual cycles, and intestinal problems are some of the symptoms. If not treated, these symptoms can escalate over time.

Problem Definition

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.

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.

Literature Survey

Thyroid disease is a subset of endocrinology, one of the most misunderstood and underdiagnosed diseases. According to the World Health Organization, thyroid disease is one of the most common endocrine diseases in the world,

coming second only to diabetes. The thyroid gland is an endocrine gland that secretes hormones and passes them through the bloodstream. The thyroid gland, shaped like a butterfly, is situated near the base of the throat. It consists of two active thyroid hormones, T4 and T3, which are involved in brain activities like body temperature regulation, blood pressure control, and heart rate regulation. Thyroid gland hormones are responsible for aiding in digestion and maintaining the body moist, balanced, and so on. Thyroid gland treatments such as T3, T3, and TSH are use to asses thyroid activity. Thyroid disorder is classified into two types; hyperthyroidism and hyperthyroidism. With both types, whether it is Hyperthyroidism or hypothyroidism, if the normal person suffers , either of the two cases, this affects the person and causes health problems.

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.

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.

1. 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

❖ *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
```

❖ *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)
```

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
- Applying Standard Scalar

❖ ***Checking for null values***

✓ For checking the null values,. Data is null () 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
```

✓ Removing the Redundant attributes from the dataset.

```
#Removing Redundant attributes from dataset
data.drop(['TSH_measured','T3_measured'], axis=1, inplace=True)
```

```
data.head()
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	TT4	T4U_measured	T
0	29	F	f	f	f	f	f	f	f	t	...	NaN	f	Na
1	29	F	f	f	f	f	f	f	f	f	...	128.0	f	Na
2	41	F	f	f	f	f	f	f	f	f	...	NaN	f	Na
3	36	F	f	f	f	f	f	f	f	f	...	NaN	f	Na
4	32	F	f	f	f	f	f	f	f	f	...	NaN	f	Na

5 rows × 29 columns

✓ 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	...	TT4	T4U_measured

0 rows × 31 columns

❖ Splitting the data x and y

❖ Splitting the data x and y

```
#splliting 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	...	TT4_measured
4	32	F	f	f	f	f	f	f	f	f	...	f
18	63	F	t	f	f	t	f	f	f	f	...	t
32	41	M	f	f	f	f	f	f	f	f	...	t
33	71	F	t	f	f	f	f	f	f	f	...	t
39	55	F	t	f	f	f	f	f	f	t	...	t
...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64	M	f	f	f	f	f	f	f	f	...	t
9157	60	M	f	f	t	f	f	f	f	f	...	t
9158	64	M	f	f	f	f	f	f	f	t	...	t
9162	36	F	f	f	f	f	f	f	f	f	...	t
9169	69	M	f	f	f	f	f	f	f	f	...	t

2237 rows x 30 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
```

❖ 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 data type 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 30 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   age                  2237 non-null   float64
 1   sex                  2237 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_measured         2237 non-null   object
 17  TSH                  2087 non-null   float64
 18  T3_measured          2237 non-null   object
 19  T3                   1643 non-null   float64
 20  TT4_measured         2237 non-null   object
 21  TT4                  2140 non-null   float64
 22  T4U_measured         2237 non-null   object
 23  T4U                  2059 non-null   float64
 24  FTI_measured         2237 non-null   object
 25  FTI                  2060 non-null   float64
 26  TBG_measured         2237 non-null   object
 27  TBG                  98 non-null     float64
 28  referral_source      2237 non-null   object
 29  target               2237 non-null   object
dtypes: float64(7), object(23)
memory usage: 541.8+ KB
```

❖ ***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	...	TT4_measured	TT4	T4U_measured	T4U	FTI_measured
4	32.0	0	0	0	0	0	0	0	0	0	...	f	NaN	f	NaN	f
18	63.0	0	1	0	0	1	0	0	0	0	...	t	48.0	t	1.02	t
32	41.0	1	0	0	0	0	0	0	0	0	...	t	39.0	t	1.00	t
33	71.0	0	1	0	0	0	0	0	0	0	...	t	126.0	t	1.38	t
39	55.0	0	1	0	0	0	0	0	0	1	...	t	136.0	t	1.48	t
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64.0	1	0	0	0	0	0	0	0	0	...	t	31.0	t	0.55	t
9157	60.0	1	0	0	1	0	0	0	0	0	...	t	28.0	t	0.87	t
9158	64.0	1	0	0	0	0	0	0	0	1	...	t	44.0	t	0.53	t
9162	36.0	0	0	0	0	0	0	0	0	0	...	t	84.0	t	1.26	t
9169	69.0	1	0	0	0	0	0	0	0	0	...	t	113.0	t	1.27	t

2237 rows × 30 columns

- Replacing the nan values with zero() 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	...	TT4_measured	TT4	T4U_measured	T4U	FTI_measured
4	32.0	0	0	0	0	0	0	0	0	0	...	f	0	f	0	f
18	63.0	0	1	0	0	1	0	0	0	0	...	t	48	t	1.02	t
32	41.0	1	0	0	0	0	0	0	0	0	...	t	39	t	1	t
33	71.0	0	1	0	0	0	0	0	0	0	...	t	126	t	1.38	t
39	55.0	0	1	0	0	0	0	0	0	1	...	t	136	t	1.48	t
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64.0	1	0	0	0	0	0	0	0	0	...	t	31	t	0.55	t
9157	60.0	1	0	0	1	0	0	0	0	0	...	t	28	t	0.87	t
9158	64.0	1	0	0	0	0	0	0	0	1	...	t	44	t	0.53	t
9162	36.0	0	0	0	0	0	0	0	0	0	...	t	84	t	1.26	t
9169	69.0	1	0	0	0	0	0	0	0	0	...	t	113	t	1.27	t

2237 rows × 30 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	0
1	1
2	2
3	3
4	4
...	...
2232	2232
2233	2233
2234	2234
2235	2235
2236	2236

2237 rows × 1 columns

❖ *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 from

```
#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	...	TT4_measured	TT4	T4U_measured	T4U	FTI_measured
4	32	F	f	f	f	f	f	f	f	f	...	f	NaN	f	NaN	f
18	63	F	t	f	f	t	f	f	f	f	...	t	48.0	t	1.02	t
32	41	M	f	f	f	f	f	f	f	f	...	t	39.0	t	1.00	t
33	71	F	t	f	f	f	f	f	f	f	...	t	126.0	t	1.38	t
39	55	F	t	f	f	f	f	f	f	t	...	t	136.0	t	1.48	t
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64	M	f	f	f	f	f	f	f	f	...	t	31.0	t	0.55	t
9157	60	M	f	f	t	f	f	f	f	f	...	t	28.0	t	0.87	t
9158	64	M	f	f	f	f	f	f	f	t	...	t	44.0	t	0.53	t
9162	36	F	f	f	f	f	f	f	f	f	...	t	84.0	t	1.26	t
9169	69	M	f	f	f	f	f	f	f	f	...	t	113.0	t	1.27	t

2237 rows × 30 columns

sklearn. As parameters, we are passing, x, y, test_size,

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

```
y_train.value_counts()
```

```
860213067    1
841119034    1
860919070    1
841121055    1
840906018    1
            ..
860730075    1
850320092    1
841204009    1
841018078    1
860205056    1
Name: patient_id, Length: 1789, dtype: int64
```

- ***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)
```

- ***Applying Standard Scaler***
  - 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 data frame(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

❖ ***Performing Feature Importance***

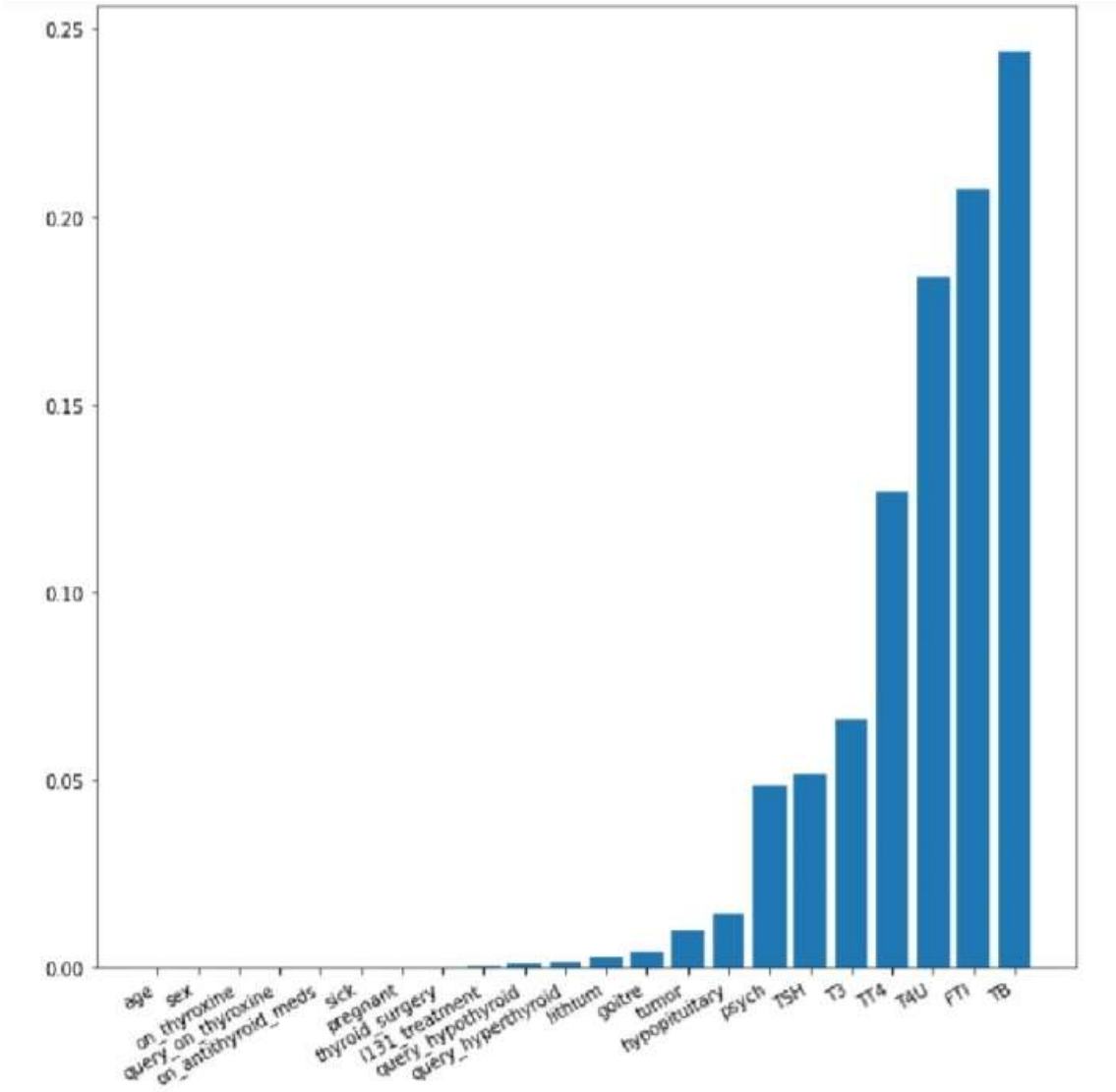
- The idea behind permutation feature importance is simple. The feature importance is calculated by noticing the increase or decrease in error when we permute the values of a feature.
- If permuting the values causes a huge change in the error, it means the feature is important for our model.

```
#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: 0.0002426448286320770 5
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: 0.010009909181073733
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
```



❖ ***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	...	TT4_measured	TT4	T4
0	29	F	f	f	f	f	f	f	f	t	...	f	NaN	
1	29	F	f	f	f	f	f	f	f	f	...	t	128.0	
2	41	F	f	f	f	f	f	f	f	f	...	f	NaN	
3	36	F	f	f	f	f	f	f	f	f	...	f	NaN	
4	32	F	f	f	f	f	f	f	f	f	...	f	NaN	

5 rows × 30 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

Exploratory Data Analysis

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
```

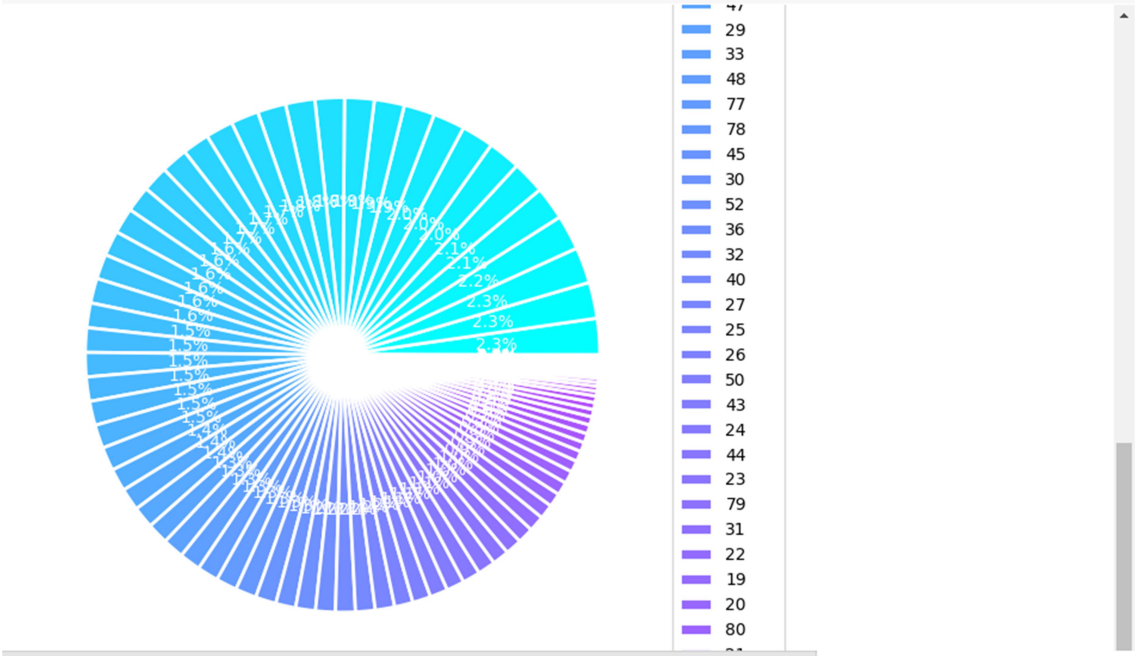
2. *Visual analysis*

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.

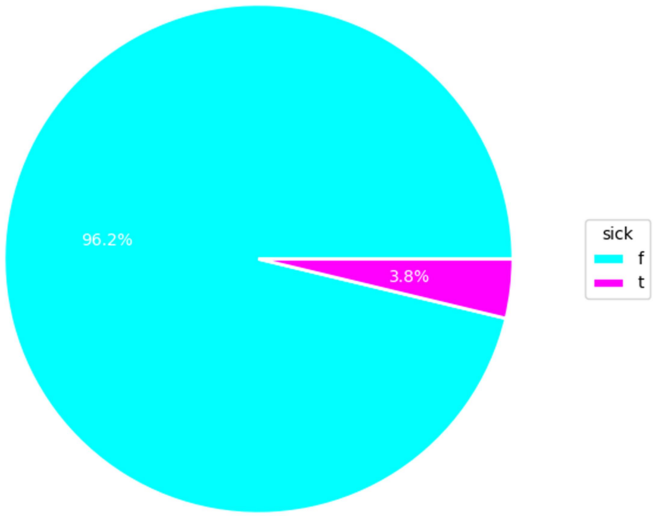
- Visualisation of pie graph

```
def pie_graph(col):
  vc = data[col].value_counts()
  colors = cm.cool(np.linspace(0, 1, len(vc)))
  fig, ax = plt.subplots(figsize = (8,6), subplot_kw = dict(aspect="equal"))
  wedges, texts, autotexts = ax.pie(vc, autopct = '%1.1f%%', textprops=dict(color="w", fontsize = 15),wedgeprops = {'linewidth': 2, 'edgecolor': 'white'}, colors
  ax.legend(wedges, vc.index, title = col, loc = "center left", bbox_to_anchor = (1, 0, 0.5, 1))
```

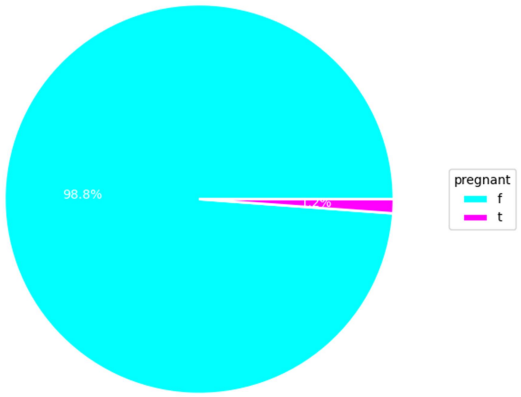
```
pie_graph('age')
```




```
pie_graph('sick')
```



```
pie_graph('pregnant')
```



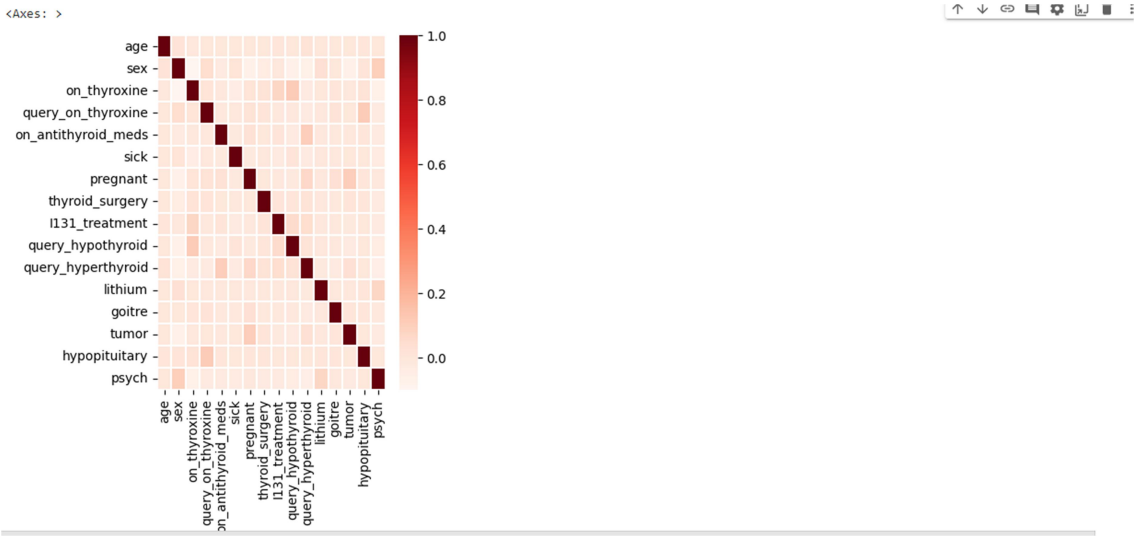
❖ *Checking Correlation*

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.

```
import seaborn as sns
```

```
#checking correlation using heatmap
f, ax = plt.subplots(figsize = (4,5))
sns.heatmap(corrmat, ax = ax, cmap="Reds", linewidths = 0.1)
```



Model Building

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.

❖ ***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
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
```

❖ *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

```
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
```

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.

❖ ***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)
```

```
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
```

❖ ***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.

```
model = Sequential()
```

```
model.add(Dense(units = 128, activation='relu', input_shape=(10,)))
```

```
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'))
```

```
model.add(Dense(units = 1, activation='sigmoid'))
```

```
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
_________________________________________________________________
```

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

```
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
```

❖ ***Testing the model***

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

```
sv.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
```

```
array([1])
```

```
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)
```

```
array([4], dtype=int64)
```

```
model.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
```

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

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

Performance Testing & Hyperparameter Tuning

1.Testing model with multiple evaluation metrices

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.

❖ ***Compare the model***

For comparing the above from models, the compare Model 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
```

```
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
```

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

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

```
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
```

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

```
0.14285714285714285
```

3. *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.

```
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)
```

```
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 thyroid_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(['-', 'S', 'F', 'AK', 'R', 'I', 'M', 'N', 'G', 'K', 'A', 'KJ', 'L',
       'MK', 'Q', 'J', 'C|I', 'O', 'LJ', 'H|K', 'D', 'GK', 'MI', 'P',
       'FK', 'B', 'GI', 'C', 'GKJ', 'OI', 'D|R', 'E'], dtype=object)
```

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

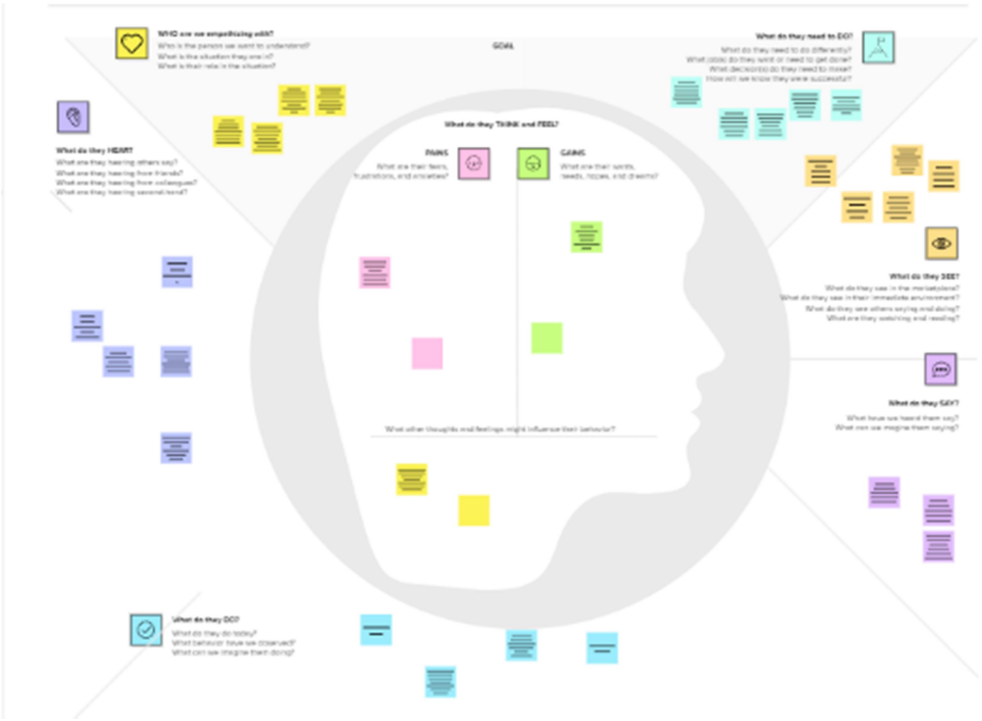
```
array([0, 1, 2])
```

1.2 Purpose

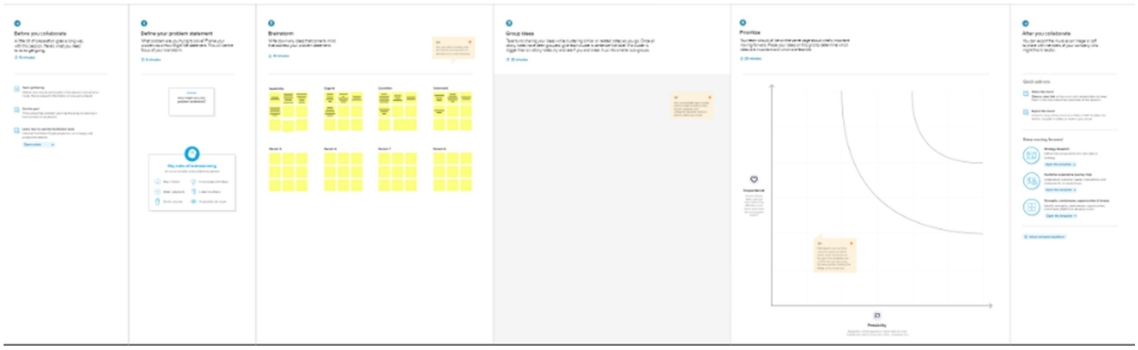
Thyroid diseases makes hormones that control the way the body uses energy. These hormones affect nearly every organ in your body and control many of your body most important functions. The thyroid gland is a vital hormone gland. It plays a major role in the metabolism, growth and development of the human body. It helps to regulate many body functions by constantly releasing a steady amount of thyroid hormones into the bloodstream.

2.PROBLEM DEFINITION & DESIGN THIKING

2.1 Empathy Map



1.2 Ideation & Brainstorming Map



3. RESULT

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(open('thyroid_1_model.pkl','wb'))
```

1. 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

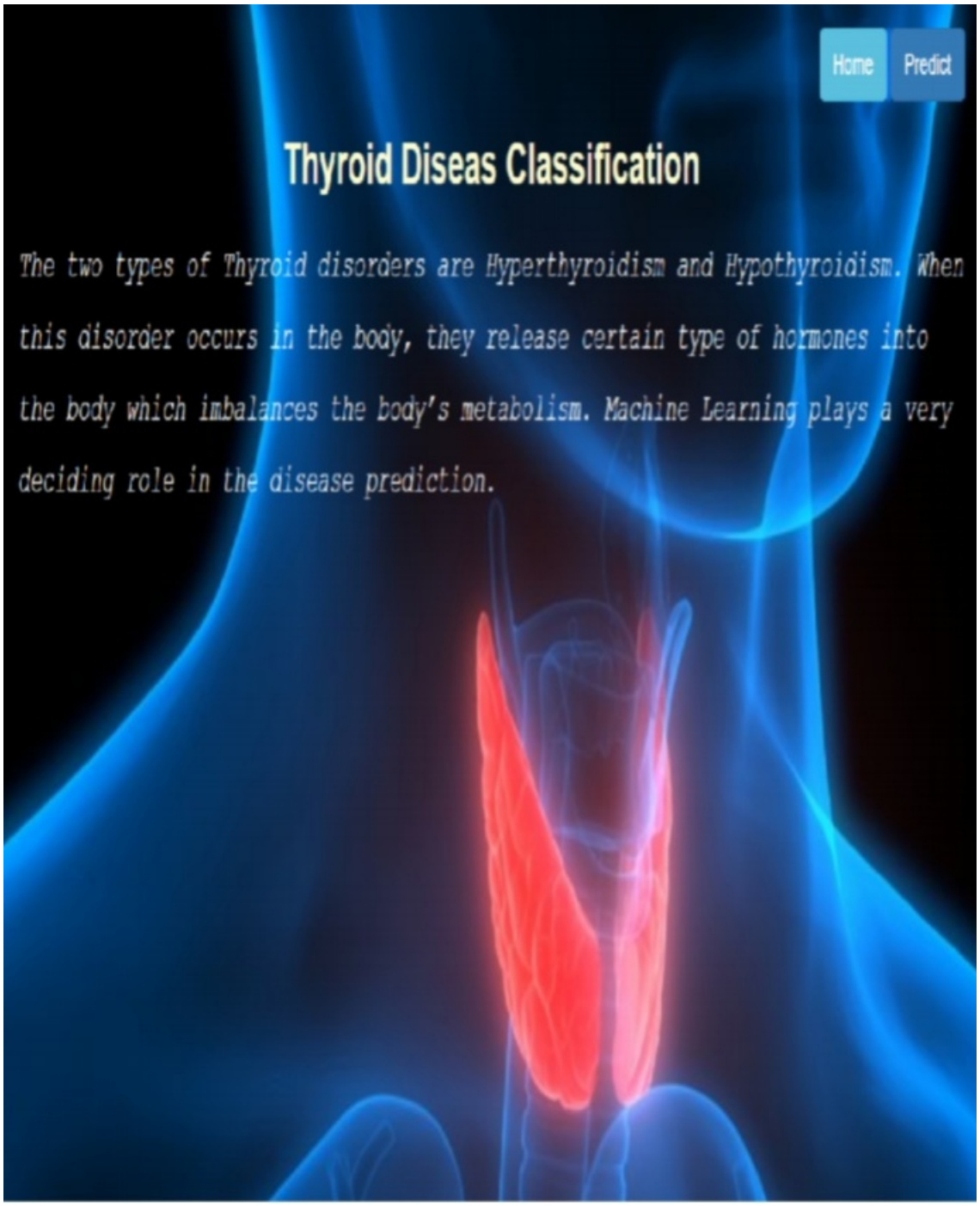
❖ ***Building Html Pages:***

For this project create three HTML files namely

- ✓ Home.html
- ✓ Predict.html
- ✓ Submit.html

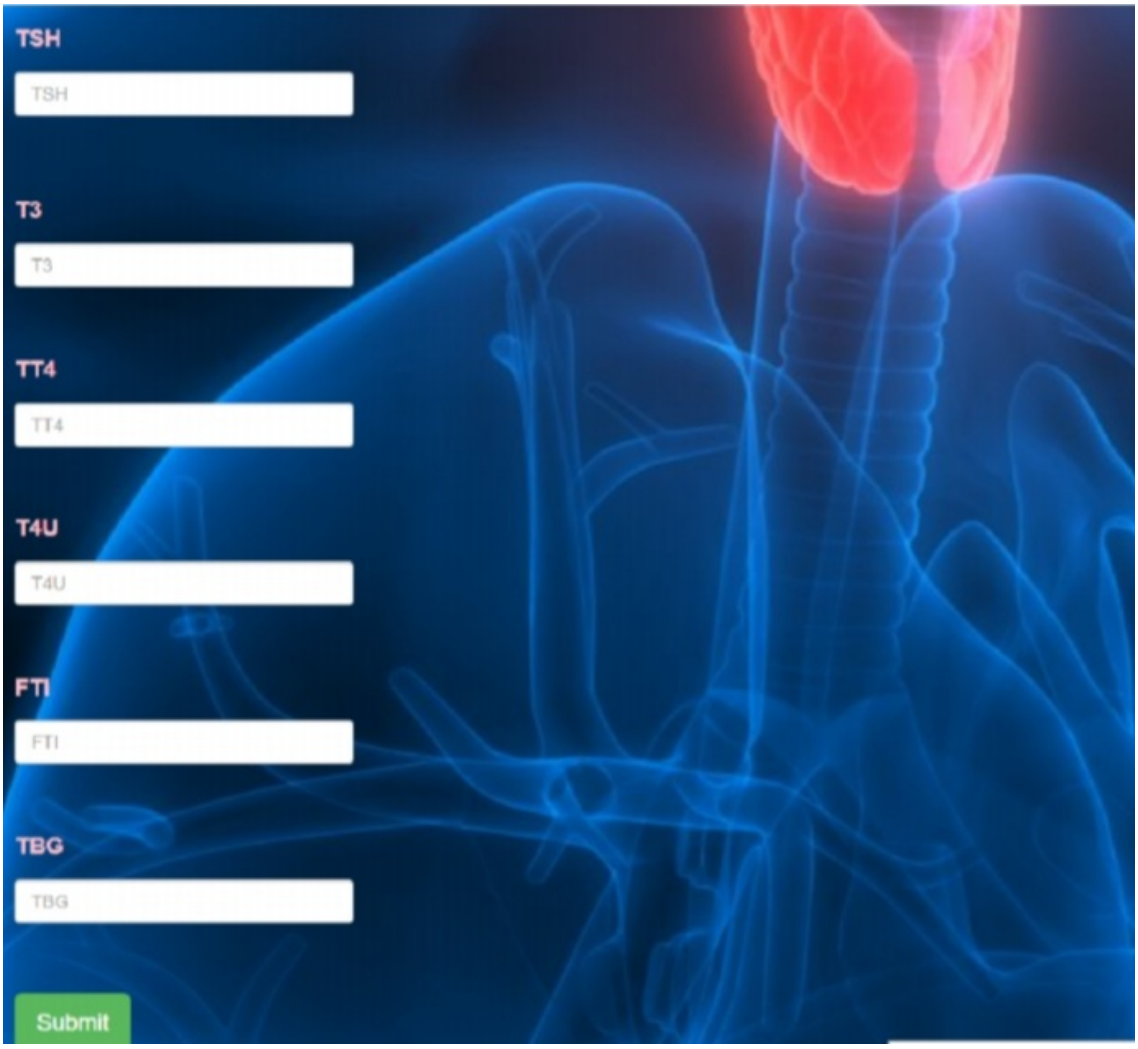
And save them in the templates folder.

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


Home
Predict
Thyroid Diseas Classification
The two types of Thyroid disorders are Hyperthyroidism and Hypothyroidism. When this disorder occurs in the body, they release certain type of hormones into the body which imbalances the body's metabolism. Machine Learning plays a very deciding role in the disease prediction.

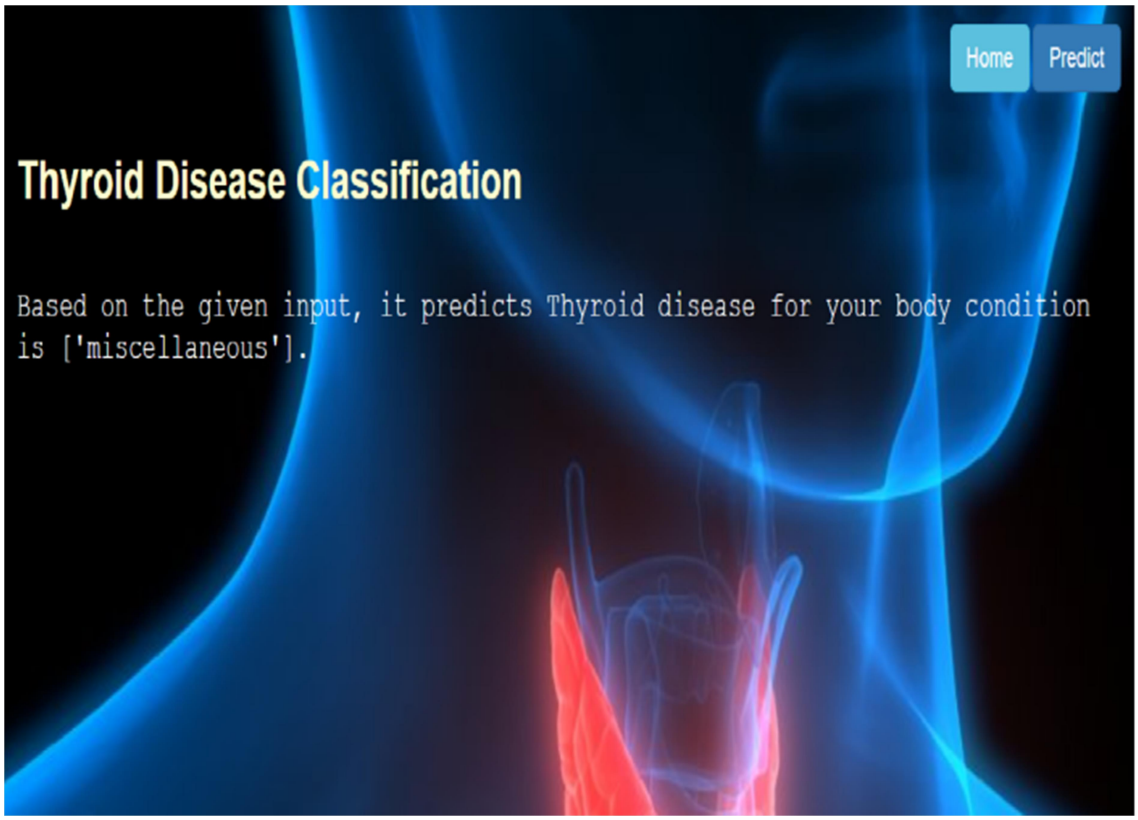
Now when you click on predict button from top right corner you will get redirected to predict.html

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



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'].



❖ ***Build Python code:***

Import the libraries

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

our Load the saved model. Importing the flask module in the project is mandatory. An object of Flask class is 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)
```

❖ ***Run the application***

• Open anaconda prompt from the start menu

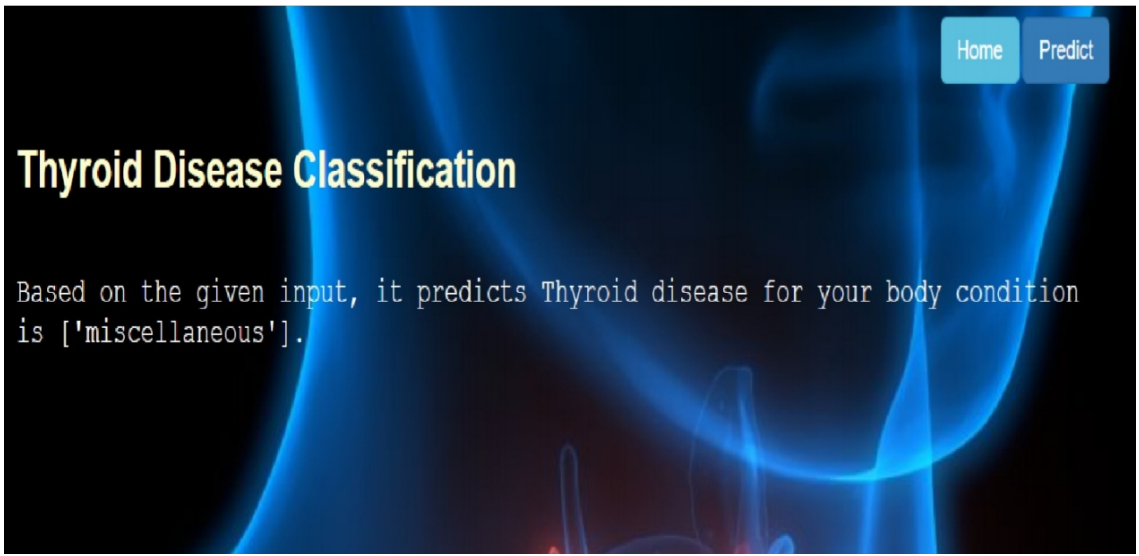
• Navigate to the folder where your python script is.

• Now type “python app.py” command

• Navigate to the local host 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)
```



4. ADVANTAGES & DISADVANTAGES

- ***Advantages***

Thyroid controls how much energy your body uses. It is also involved in digestion how your heart and muscles work, brain development and bone health. When the thyroid gland does not make enough thyroxine, many of the body's functions slow down.

- ***Disadvantages***

When the thyroid makes too much thyroid hormone, your body uses energy too quickly. This is called hyperthyroidisms .Using energy too quickly will do more than make you tired-it can make your heart beat faster, cause you to lose weight without trying and even make you feel nervous.

5. APPLICATIONS

Your thyroid has an important job to do within your body — releasing and controlling thyroid hormones that control metabolism. Metabolism is a process where the food you take into your body is transformed into energy. This energy is used throughout your entire body to keep many of your body's systems working correctly.

6.CONCLUSION

Thyroid disease is one of the diseases that afflict the world's population, and the number of cases of this disease is increasing. Because of medical reports that show serious imbalances in thyroid diseases, our study deals with the

classification of thyroid disease between hyperthyroidism and hypothyroidism. This disease was classified using algorithms. Machine learning showed us good results using several algorithms and was built in the form of two models. In the first model, all the characteristics consisting of 16 inputs and one output were taken, and the result of the accuracy of the random forest algorithm was 1.0, which is the highest accuracy among the other algorithms. In the second embodiment, the following characteristics were omitted based on a previous study. The removed attributes were i. TSH_measured, T3_measured. Here we have included the increased accuracy of some algorithms, as well as the retention of the accuracy of others. It was observed that the accuracy of XGBClassifier algorithm increased the accuracy by 0.70.

7. FUTURE SCOPE

The major difference between the thyroid hormones and tendons disease are clinically relevant. The accurate diagnosis of diseases and providing efficient treatment are the important part of valuable medical services given for the patients in the health-care system. The unique characteristics of these databases are that the challenges for data mining are privacy-sensitive, heterogeneous and voluminous data. These types of data's may have valuable information awaits extraction. The knowledge that has to be found as various encapsulated regularities and patterns that is not in the raw data or pre-processed data. The Feature selection method that may use to identify the most

relevant for classification and it is broadly used to categorize the subset selection method and ranking method.

8. APPENDIX

A. Source code

Read the dataset

```
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)
```

Checking for null values

```
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
```

Removing the Redundant attributes from the dataset.

```
#Removing Redundant attributes from dataset
data.drop(['TSH_measured','T3_measured'], axis=1, inplace=True)
```

```
data.head()
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	TT4	T4U_measured	T
0	29	F	f	f	f	f	f	f	f	t	...	NaN	f	Na
1	29	F	f	f	f	f	f	f	f	f	...	128.0	f	Na
2	41	F	f	f	f	f	f	f	f	f	...	NaN	f	Na
3	36	F	f	f	f	f	f	f	f	f	...	NaN	f	Na
4	32	F	f	f	f	f	f	f	f	f	...	NaN	f	Na

5 rows × 29 columns

```
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
```

```
#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	...	TT4_measured	TT4	T4U_measured	T4U	FTI_measured
4	32	F	f	f	f	f	f	f	f	f	...	f	NaN	f	NaN	f
18	63	F	t	f	f	t	f	f	f	f	...	t	48.0	t	1.02	t
32	41	M	f	f	f	f	f	f	f	f	...	t	39.0	t	1.00	t
33	71	F	t	f	f	f	f	f	f	f	...	t	126.0	t	1.38	t
39	55	F	t	f	f	f	f	f	f	t	...	t	136.0	t	1.48	t
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64	M	f	f	f	f	f	f	f	f	...	t	31.0	t	0.55	t
9157	60	M	f	f	t	f	f	f	f	f	...	t	28.0	t	0.87	t
9158	64	M	f	f	f	f	f	f	f	t	...	t	44.0	t	0.53	t
9162	36	F	f	f	f	f	f	f	f	f	...	t	84.0	t	1.26	t
9169	69	M	f	f	f	f	f	f	f	f	...	t	113.0	t	1.27	t

2237 rows × 30 columns

```
x.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 2237 entries, 4 to 9169
Data columns (total 30 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   age                   2237 non-null   float64
 1   sex                   2237 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_measured          2237 non-null   object
 17  TSH                   2087 non-null   float64
 18  T3_measured           2237 non-null   object
 19  T3                    1643 non-null   float64
 20  TT4_measured          2237 non-null   object
 21  TT4                   2140 non-null   float64
 22  T4U_measured          2237 non-null   object
 23  T4U                   2059 non-null   float64
 24  FTI_measured          2237 non-null   object
 25  FTI                   2060 non-null   float64
 26  TBG_measured          2237 non-null   object
 27  TBG                   98 non-null     float64
 28  referral_source       2237 non-null   object
 29  target                2237 non-null   object
dtypes: float64(7), object(23)
memory usage: 541.8+ KB
```

Handling Categorical 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	...	TT4_measured	TT4	T4U_measured	T4U	FTI_measured
4	32.0	0	0	0	0	0	0	0	0	0	...	f	NaN	f	NaN	f
18	63.0	0	1	0	0	1	0	0	0	0	...	t	48.0	t	1.02	t
32	41.0	1	0	0	0	0	0	0	0	0	...	t	39.0	t	1.00	t
33	71.0	0	1	0	0	0	0	0	0	0	...	t	126.0	t	1.38	t
39	55.0	0	1	0	0	0	0	0	0	1	...	t	136.0	t	1.48	t
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64.0	1	0	0	0	0	0	0	0	0	...	t	31.0	t	0.55	t
9157	60.0	1	0	0	1	0	0	0	0	0	...	t	28.0	t	0.87	t
9158	64.0	1	0	0	0	0	0	0	0	1	...	t	44.0	t	0.53	t
9162	36.0	0	0	0	0	0	0	0	0	0	...	t	84.0	t	1.26	t
9169	69.0	1	0	0	0	0	0	0	0	0	...	t	113.0	t	1.27	t

2237 rows × 30 columns

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

```
y_train.value_counts()
```

```
860213067    1
841119034    1
860919070    1
841121055    1
840906018    1
            ..
860730075    1
850320092    1
841204009    1
841018078    1
860205056    1
Name: patient_id, Length: 1789, dtype: int64
```

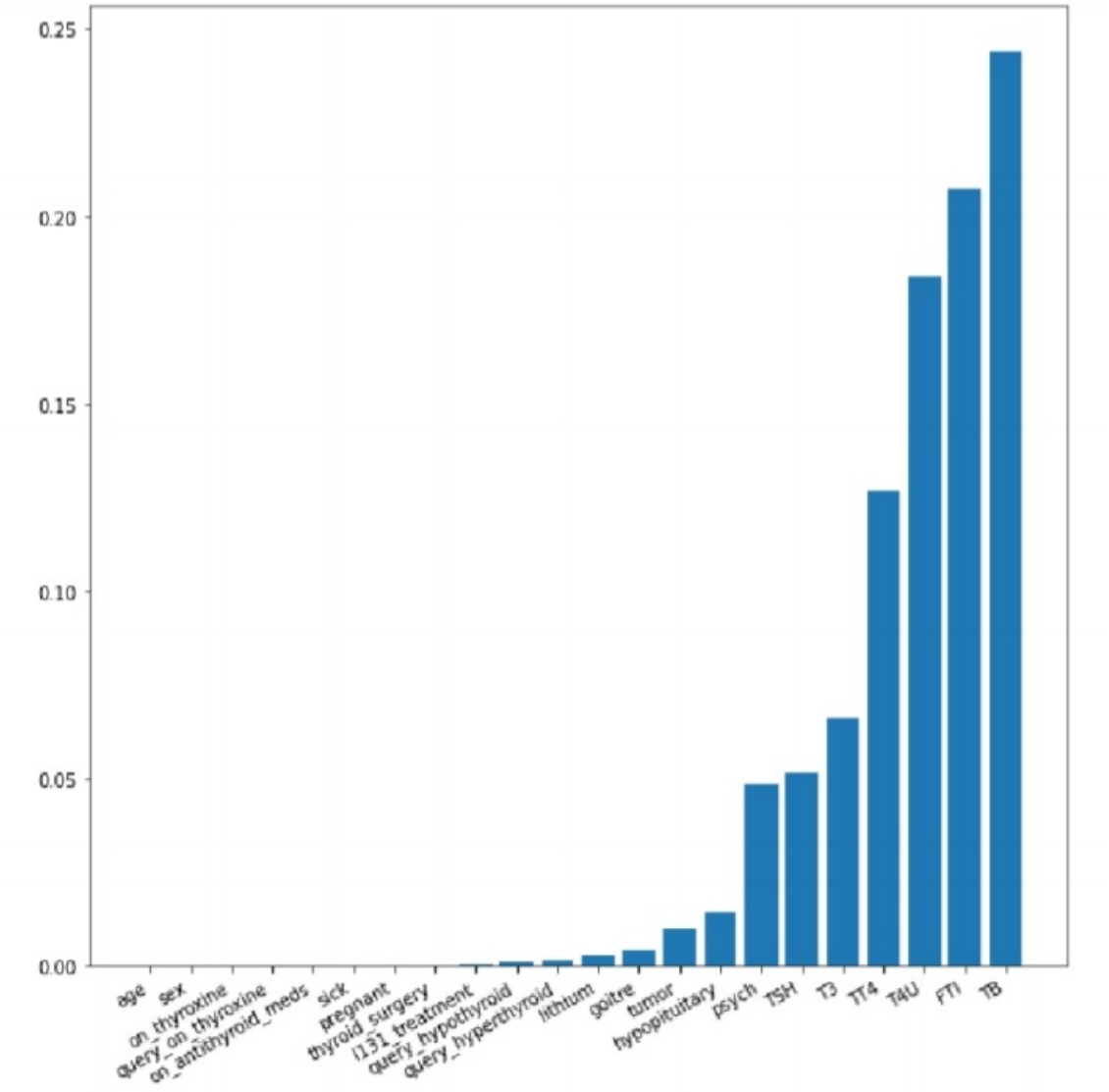
Performing Feature Importance

```
#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: 0.0002426448286320770 5
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: 0.0044282812253565
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
```

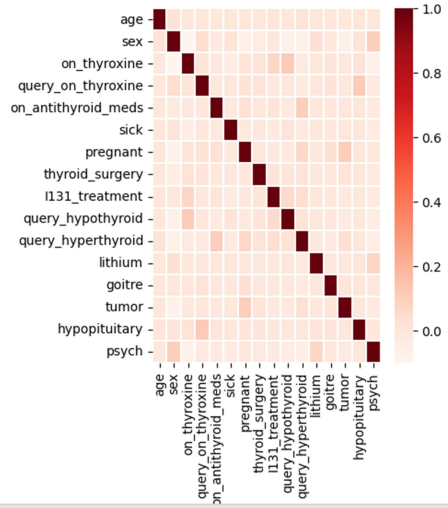


Checking Correlation

```
import seaborn as sns
```

```
#checking correlation using heatmap
f, ax = plt.subplots(figsize = (4,5))
sns.heatmap(corrmat, ax = ax, cmap="Reds", linewidths = 0.1)
```

```
<Axes: >
```




```
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

Random Forest Classifier Model

```
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
```

XGBClassifier Model

```
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
```

SVC Model

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

sv= SVC()
```

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

```
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
```

ANN Model

```
model = Sequential()
```

```
model.add(Dense(units = 128, activation='relu', input_shape=(10,)))
```

```
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'))
```

```
model.add(Dense(units = 1, activation='sigmoid'))
```

```
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
_________________________________________________________________
```

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

```
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
```

Comparing model accuracy before and after applying hyperparameter tuning

```
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)
```

Saving the model as thyroid_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']
```

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

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

```
array(['-', 'S', 'F', 'AK', 'R', 'I', 'M', 'N', 'G', 'K', 'A', 'KJ', 'L',
       'MK', 'Q', 'J', 'C|I', 'O', 'LJ', 'H|K', 'D', 'GK', 'MI', 'P',
       'FK', 'B', 'GI', 'C', 'GKJ', 'OI', 'D|R', 'E'], dtype=object)
```

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

```
array([0, 1, 2])
```

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

Compare the Model

```
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
```

```
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
```

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

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

```
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
```

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

```
0.14285714285714285
```

save the best model

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