

# Thyroid Disease Classification using ML

**Submitted by**

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## **INTRODUCTION**

### **OVERVIEW**

Thyroid diseases, such as hypothyroidism and hyperthyroidism, are common endocrine disorders that affect the function of the thyroid gland. These diseases can have a significant impact on a patient's health and quality of life. Early and accurate diagnosis of thyroid diseases is important for effective treatment.

In recent years, machine learning techniques have been applied to the classification of thyroid diseases. The goal of these studies is to develop models that can accurately diagnose thyroid diseases based on clinical and laboratory data.

### **PURPOSE**

There are several machine learning algorithms that have been used for thyroid disease classification, including decision trees, random forests, k-nearest neighbors (KNN), support vector machines (SVM), artificial neural networks (ANN), and deep learning algorithms such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs).

The input data for these models can include clinical features, such as age, gender, and symptoms, as well as laboratory test results, such as thyroid-stimulating hormone (TSH) levels and levels of thyroxine (T4) and triiodothyronine (T3).

The performance of these models is usually evaluated using metrics such as accuracy, precision, recall, and F1 score. In general, deep learning algorithms have shown better performance than other machine learning algorithms in thyroid disease classification tasks.

## **LITERATURE SURVEY**

### **EXISTING PROBLEM**

The current existing system includes:

**Clinical examination:** This involves a physical examination of the neck to check for any visible signs of thyroid enlargement or nodules.

**Blood tests:** Blood tests are used to measure the levels of hormones produced by the thyroid gland and to check for antibodies that may indicate autoimmune diseases such as Hashimoto's thyroiditis.

**Ultrasound:** An ultrasound scan can provide images of the thyroid gland and help to identify any nodules or other abnormalities.

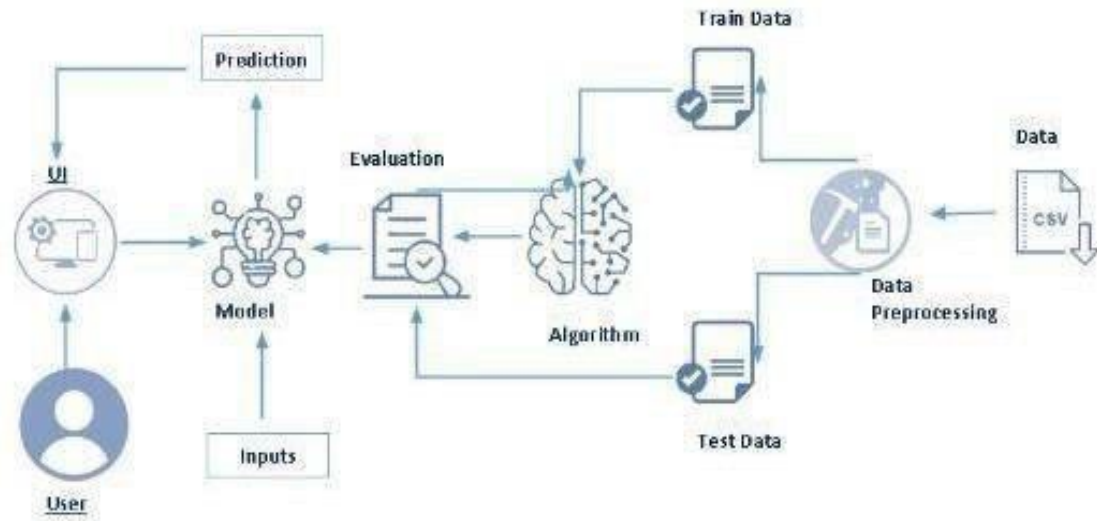
Fine needle aspiration biopsy (FNAB): This is a procedure in which a small sample of tissue is taken from a thyroid nodule using a fine needle, which is then examined under a microscope to check for cancer.

## **PROPOSED SYSTEM**

The proposed system is by using Artificial Intelligence (AI) and Machine Learning (ML) In recent years, there have been several studies exploring the use of AI and ML algorithms for predicting thyroid diseases. These systems are trained on large datasets of patient data and use various features such as demographic information, blood test results, and ultrasound images to make prediction.

## THEORETICAL ANALYSIS

### BLOCK DIAGRAM



## HARDWARE AND SOFTWARE DESIGNING

### Python

Python is an interpreted, object-oriented, high-level programming language with dynamic semantics. It was created by Guido van Rossum, and first released on February 20, 1991. Its high-level built-in data structures, combined with dynamic typing and dynamic binding, make it very attractive for Rapid Application Development, as well as for use as a scripting or glue language to connect existing components together. Python's simple, easy to learn syntax emphasizes readability and therefore reduces the cost of program maintenance. Python supports modules and packages, which encourages program modularity and code reuse. The Python interpreter and the extensive standard library are available in source or binary form without charge for all major platforms, and can be freely distributed.

### Anaconda Navigator

Anaconda Navigator is a free and open-source distribution of the Python and R programming languages for data science and machine learning related applications. It can be installed on Windows, Linux, and macOS. Conda is an open-source, cross platform, package management system. Anaconda comes with

so very nice tools like JupyterLab, Jupyter Notebook, QtConsole, Spyder, Glueviz, Orange, Rstudio, Visual Studio Code. For this project, we will be using Jupyter notebook and Spyder.

## **Jupyter Notebook**

The Jupyter Notebook is an open-source web application that you can use to create and share documents that contain live code, equations, visualizations, and text. Jupyter Notebook is maintained by the people at Project Jupyter. Jupyter Notebooks are a spin-off project from the IPython project, which used to have an IPython Notebook project itself. The name, Jupyter, comes from the core supported programming languages that it supports: Julia, Python, and R. Jupyter ships with the IPython kernel, which allows you to write your programs in Python, but there are currently over 100 other kernels that you can also use

## **Spyder**

Spyder, the Scientific Python Development Environment, is a free integrated development environment (IDE) that is included with Anaconda. It includes editing, interactive testing, debugging, and introspection features. Initially created and developed by Pierre Raybaut in 2009, since 2012 Spyder has been maintained and continuously improved by a team of scientific Python developers and the community. Spyder is extensible with first-party and third party plugins includessupport for interactive tools for data inspection and embeds Python specific code. Spyder is also pre-installed in Anaconda Navigator, which is included in Anaconda.

## **Flask**

Web frame work used for building. It is a web application framework written in python which will be running in local browser with a user interface. In this application, whenever the user interacts with UI and selects emoji, it will suggest the best and top movies of that genre to the use.

### **Hardware Requirements:**

- o Operating system: window 7 and above with 64bit o Processor Type -Intel Core i3-3220
- o RAM: 4Gb and above
- o Hard disk: min 100GB

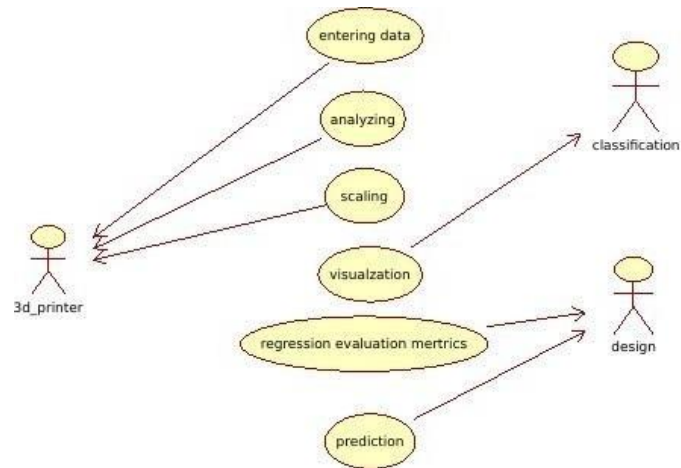
## **1. EXPERIMENTAL INVESTIGATION**

Here we are going to build a machine learning model that predicts whether the given message is a spam or not, based on these parameters a supervised machine learning model is built to predict the best

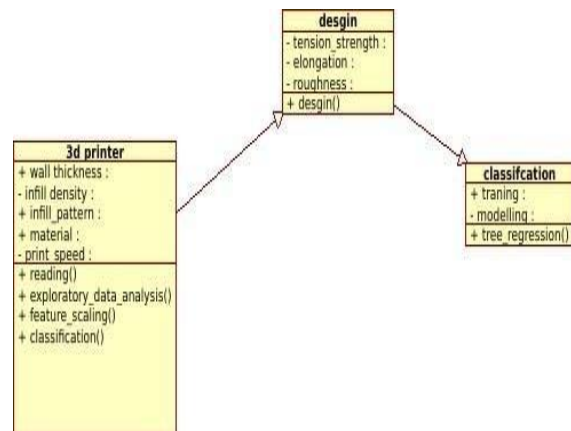
material to be used for building 3D models. A web application is build so that the user can type in the mentioned part a meters and the material which suits the best is showcased on UI.

2.

## FLOWCHART

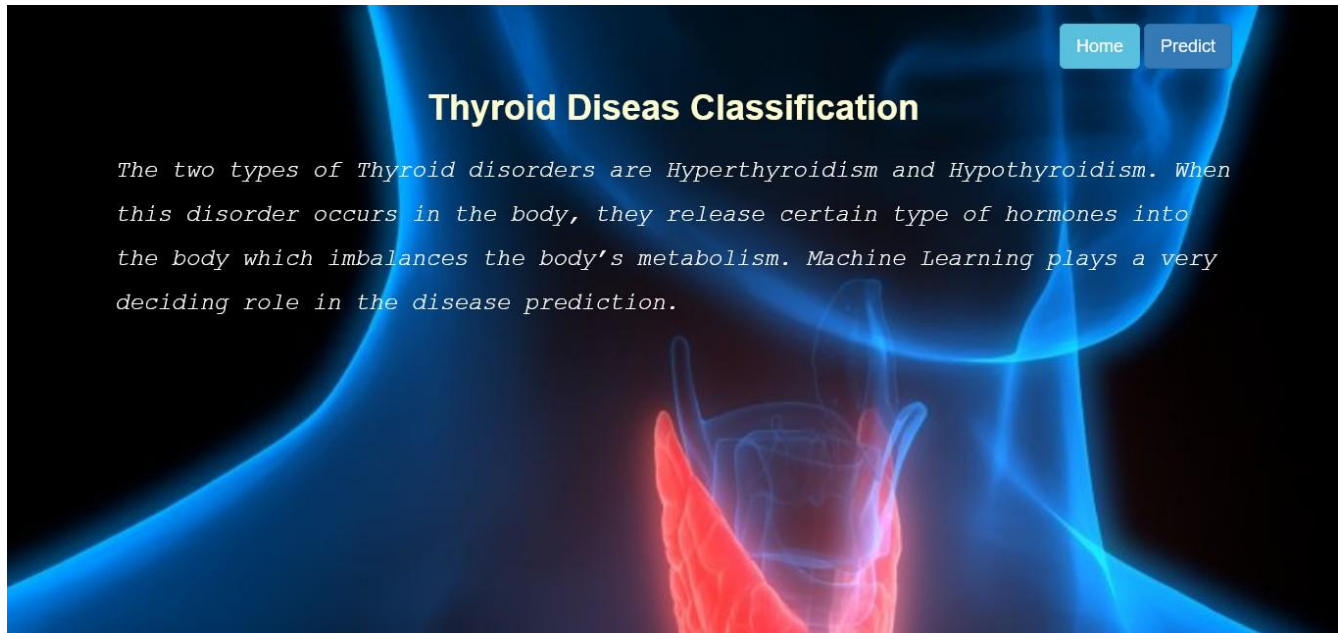


## USE CASE DIAGRAM



3.

## RESULT





[Home](#)[Predict](#)

# Thyroid Disease Classification

goitre

Male

tumor

Male

hypopituitary

Male

psych

Male

TSH

TSH

T3

T3

TT4

TT4

T4U

T4U

FTI

FTI

TBG

TBG

Submit

[Home](#)[Predict](#)

## Thyroid Disease Classification

Based on the given input, it predicts Thyroid disease for your body condition is {{prediction\_text}}.

#### **4.ADVANTAGES & DISADVANTAGES**

##### **ADVANTAGES**

- Easy to use
- Cost efficient
- Time efficient

##### **DISADVANTAGE**

1. Initial costs of printer
2. Post processing
3. Printing time
4. Special skill required for 3D models
5. Manufacturing Job Losses

#### **8. Applications**

3D printing has gone through a number of changes over the years. In the early days, 3D printing was time-consuming and costly, and not very practical for applications outside of industry. However, with the advent of today's more flexible and cost-effective 3D printing methods, there are areas where 3D printing has become a practical tool.

**It is applicable in different sectors such as**

- Engineering And Design
- Consumer products
- Manufacturing
- Education
- Aerospace
- Medical
- Movies / Theatres
- Architectures

#### **9. CONCLUSION**

3D printing technology could revolutionize and re-shape the world. Advance in 3D technology can significantly change and improve the way we manufacture products goods worldwide.

If the last industrial revolution brought us mass production and the advent of economics of scale – the digital 3D printing revolution could bring mass manufacturing back a full of circle – to an era of mass personalization, and return to individual craftsmanship.

## 10. FUTURE SCOPE

Future applications for 3D printing might include creating open-source scientific equipment to create opensource labs

Science-based applications like reconstructing fossils in palaeontology . Replicating ancient and priceless artifacts in archaeology

Reconstructing bones and body parts in forensic pathology. The technology currently being researched for building construction.

## 11. BIBILOGRAPHY

- <http://mashable.com/2014/03/06/3d-printed-blood-vessels/>
- <http://www.3dprinter.net/>

## 12.

## APPENDIX

```
In [1]: import os, types
import pandas as pd
from botocore.client import Config
import ibm_boto3

def __iter__(self): return 0

# @hidden_cell
# The following code accesses a file in your IBM Cloud Object Storage. It includes your credentials.
# You might want to remove those credentials before you share the notebook.
client_3055a99af3464697994102c4e129439e = ibm_boto3.client(service_name='s3',
    ibm_api_key_id='ml1591fkbz019X6Cwp0Vfp3MhCpMELIE6j8My3754',
    ibm_auth_endpoint='https://iam.cloud.ibm.com/oidc/token',
    config=Config(signature_version='oauth'),
    endpoint_url='https://s3.private.us.cloud-object-storage.appdomain.cloud')

body = client_3055a99af3464697994102c4e129439e.get_object(Bucket='thyroid-donotdelete-pr-qkqstuhbfylzjo',Key='data.csv')['Body']
# add missing __iter__ method, so pandas accepts body as file-like object
if not hasattr(body, "__iter__"): body.__iter__ = types.MethodType( __iter__, body )

data = pd.read_csv(body)
data.head()
data.shape
```

Out[1]: (9172, 31)

```
In [13]: 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   float64
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(7), object(16)
memory usage: 419.4+ KB
```

```
In [3]: data.isnull().sum()

Out[3]: 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                 8023
referral_source      0
target              0
patient_id           0
dtype: int64

In [4]: #Removing Redundant attributes from dataset
#The columns listed below were removed because of redundancy.
#They are boolean and state whether or not a value has been recorded for their respective blood tests.
#TSH_measured
#T3_measured
#TT4_measured
#T4U_measured
#FTI_measured
#TBG_measured
data.drop(['TSH_measured', 'T3_measured', 'TT4_measured', 'T4U_measured', 'FTI_measured', 'TBG_measured', 'referral_source', 'patient_id'], axis=1, inplace = True)

In [5]: data.head()

Out[5]:
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG	target
0	29	F	f	f	f	f	f	f	f	f	...	f	f	f	0.3	NaN	NaN	NaN	NaN	NaN	-
1	29	F	f	f	f	f	f	f	f	f	...	f	f	f	1.6	1.9	128.0	NaN	NaN	NaN	-
2	41	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	NaN	NaN	NaN	11.0	-
3	36	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	NaN	NaN	NaN	26.0	-
4	32	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	NaN	NaN	NaN	36.0	S

5 rows x 23 columns

```
In [6]: data['target']

Out[6]:
0      -
1      -
2      -
3      -
4      S
..
9167   -
9168   -
9169   I
9170   -
9171   -
Name: target, Length: 9172, dtype: object

In [7]: #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

In [8]: data

Out[8]:
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG	target
0	29	F	f	f	f	f	f	f	f	f	...	f	f	f	0.3	NaN	NaN	NaN	NaN	NaN	NaN
1	29	F	f	f	f	f	f	f	f	f	...	f	f	f	1.6	1.9	128.0	NaN	NaN	NaN	NaN
2	41	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	NaN	NaN	NaN	11.0	NaN
3	36	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	NaN	NaN	NaN	26.0	NaN
4	32	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	NaN	NaN	NaN	36.0	miscellaneous
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
9167	56	M	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	64.0	0.83	77.0	NaN	NaN
9168	22	M	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	91.0	0.92	99.0	NaN	NaN
9169	69	M	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	113.0	1.27	89.0	NaN	binding protein
9170	47	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	75.0	0.85	88.0	NaN	NaN
9171	31	M	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	66.0	1.02	65.0	NaN	NaN

9172 rows x 23 columns

```
In [9]: data.isnull().sum()

Out[9]: age                0
sex                387
on_thyroxine       0
query_on_thyroxine 0
on_antithyroid_meds 0
sick               0
pregnant          0
thyroid_surgery    0
l131_treatment     0
query_hypothyroid  0
query_hyperthyroid 0
lithium           0
goitre            0
tumor             0
hypopituitary     0
psych            0
TSH              842
T3               2684
TT4              442
T4U              889
FTI              882
TBG              8823
target           6935
dtype: int64

In [10]: data.dropna(subset=['target'], inplace=True)

In [11]: data['target'].value_counts()

Out[11]: hypothyroid conditions    593
general health                    436
binding protein                   376
replacement therapy              336
miscellaneous                     281
hyperthyroid conditions          182
antithyroid treatment            33
Name: target, dtype: int64

In [12]: data.head()

Out[12]:
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	l131_treatment	query_hypothyroid	...	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG	target	
4	32	F	f	f	f	f	f	f	f	f	...	f	f	f	f	NaN	NaN	NaN	NaN	NaN	36.0	miscellaneous
18	63	F	t	f	f	t	f	f	f	f	...	f	f	f	68.000000	NaN	48.0	1.02	47.0	NaN	hypothyroid conditions	
32	41	M	f	f	f	f	f	f	f	f	...	f	f	f	f	0.050000	1.6	39.0	1.00	39.0	NaN	miscellaneous
33	71	F	t	f	f	f	f	f	f	f	...	f	f	f	f	0.050000	NaN	126.0	1.38	91.0	NaN	binding protein
39	55	F	t	f	f	f	f	f	f	f	...	f	f	f	f	9.599999	2.4	136.0	1.48	92.0	NaN	replacement therapy

5 rows x 23 columns

```
In [13]: data.describe()

Out[13]:
```

	age	sex	TSH	T3	TT4	T4U	FTI	TBG
count	2237.000000	2087.000000	1643.000000	2140.000000	2059.000000	2060.000000	98.000000	
mean	52.792579	14.930791	1.961875	116.390495	1.013439	120.363369	47.717347	
std	19.677450	46.204092	1.452238	60.351600	0.280222	70.996728	32.398750	
min	1.000000	0.005000	0.050000	2.000000	0.170000	1.400000	9.299999	
25%	36.000000	0.255000	1.000000	76.000000	0.850000	83.000000	32.000000	
50%	56.000000	2.000000	1.700000	109.000000	0.960000	109.000000	36.000000	
75%	69.000000	8.799999	2.600000	156.000000	1.120000	157.000000	46.750000	
max	95.000000	530.000000	18.000000	600.000000	2.330000	881.000000	200.000000	

```
In [14]: #Checking whether the age above 100
data[data.age>100]

Out[14]:
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	l131_treatment	query_hypothyroid	...	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG	target
0	rows	x	23	columns																	

0 rows x 23 columns

```
In [17]: import numpy as np
#changing age of observation with(age>100) to null
data['age']=np.where((data.age>100), np.nan, data.age)

In [18]: data

Out[18]:
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	l131_treatment	query_hypothyroid	...	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG	target	
4	32.0	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	NaN	NaN	NaN	36.0	miscellaneous	
18	63.0	F	t	f	f	t	f	f	f	f	...	f	f	f	68.000000	NaN	48.0	1.02	47.0	NaN	hypothyroid conditions	
32	41.0	M	f	f	f	f	f	f	f	f	...	f	f	f	f	0.050000	1.6	39.0	1.00	39.0	NaN	miscellaneous
33	71.0	F	t	f	f	f	f	f	f	f	...	f	f	f	f	0.050000	NaN	126.0	1.38	91.0	NaN	binding protein
39	55.0	F	t	f	f	f	f	f	f	f	...	f	f	f	f	9.599999	2.4	136.0	1.48	92.0	NaN	replacement therapy
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
9153	64.0	M	f	f	f	f	f	f	f	f	...	f	f	f	0.810000	NaN	31.0	0.55	56.0	NaN	general health	
9157	60.0	M	f	f	f	t	f	f	f	f	...	f	f	f	0.180000	NaN	26.0	0.87	32.0	NaN	general health	
9158	64.0	M	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	44.0	0.53	83.0	NaN	binding protein	
9162	36.0	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	84.0	1.26	67.0	NaN	binding protein	
9169	69.0	M	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	113.0	1.27	89.0	NaN	binding protein	

2237 rows x 23 columns

#splitting the data values as x and y¶

```
In [19]: #splitting the data values as x and y
x=data.iloc[:,0:-1]
y= data.iloc[:,1]
```

```
In [20]: data.isnull().sum()
```

```
Out[20]: age          0
sex            90
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            150
T3             594
TT4            97
T4U            178
FTI            177
TBG            2139
target         0
dtype: int64
```

```
In [21]: x['sex'].unique()
```

```
Out[21]: array(['F', 'M', nan], dtype=object)
```

```
In [22]: x['sex'].replace(np.nan, 'F', inplace=True)
```

```
In [23]: x['sex'].value_counts()
```

```
Out[23]: F    1701
M      536
Name: sex, dtype: int64
```

```
In [24]: x.isnull().sum()
```

```
Out[24]: age          0
sex            0
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            150
T3             594
TT4            97
T4U            178
FTI            177
TBG            2139
dtype: int64
```

```
In [25]: 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   float64
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(7), object(16)
memory usage: 419.4+ KB
```

```
In [26.: x['age']=xx['age'].astype('float')
x['TSH']=xx['TSH'].astype('float')
x['T3']=xx['T3'].astype('float')
x['TT4']=xx['TT4'].astype('float')
x['T4U']=xx['T4U'].astype('float')
x['FTI']=xx['FTI'].astype('float')
x['TBO']=xx['TBO'].astype('float')
```

converting categorical to numerical values

```
In [27.: #applying ordinal_encoding to 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']])
```

```
In [28.: x.head()
```

```
Out[28]:
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	t13t1_treatment	query_hypothyroid	...	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBO
4	32.0	0	0	0	0	0	0	0	0	0	...	0	0	0	0	0	NaN	NaN	NaN	NaN	36.0
18	63.0	0	1	0	0	0	1	0	0	0	...	0	0	0	0	0	68.000000	NaN	48.0	1.02	47.0
32	41.0	1	0	0	0	0	0	0	0	0	...	0	0	0	0	0	0.050000	1.6	39.0	1.00	39.0
33	71.0	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0	0.050000	NaN	126.0	1.38	91.0
39	55.0	0	1	0	0	0	0	0	0	1	...	0	0	0	0	0	9.599999	2.4	136.0	1.48	92.0

5 rows x 22 columns

```
In [29.: x.replace(np.nan, '0', inplace=True)
x.head()
```

```
Out[29]:
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	t13t1_treatment	query_hypothyroid	...	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBO
4	32.0	0	0	0	0	0	0	0	0	0	...	0	0	0	0	0	0	0	0	0	36.0
18	63.0	0	1	0	0	0	1	0	0	0	...	0	0	0	0	0	68.0	0	48.0	1.02	47.0
32	41.0	1	0	0	0	0	0	0	0	0	...	0	0	0	0	0	0.05	1.6	39.0	1.0	39.0
33	71.0	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0	0.05	0	126.0	1.38	91.0
39	55.0	0	1	0	0	0	0	0	0	1	...	0	0	0	0	0	9.599999	2.4	136.0	1.48	92.0

5 rows x 22 columns

```
In [30.: #applying label_encoding to y values
label_encoder = LabelEncoder()
y_dt= label_encoder.fit_transform(y)
```

```
In [31.: y=pd.DataFrame(y_dt, columns=['target'])
y
```

```
Out[31]:
```

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

2237 rows x 1 columns

```
In [32.: y.value_counts(normalize=True)
```

```
Out[32]: target
4      0.265887
2      0.194984
1      0.168882
6      0.158281
5      0.125615
3      0.081359
0      0.014752
dtype: float64
```

```
In [ ]:
```

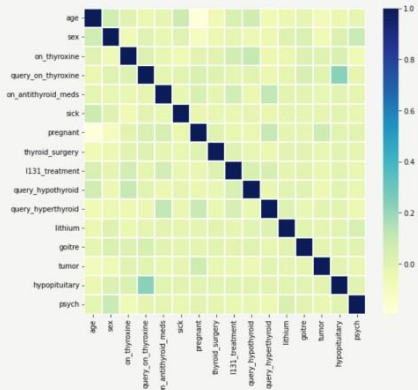


### Checking the Correlation

```
In [35]: import matplotlib.pyplot as plt
#checking correlation using Heatmap
import seaborn as sns
cormat = x.corr()

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

Out[35]: <AxesSubplot>



### splitting the train and test split

```
In [36]: 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)
```

```
In [37]: y_train.value_counts()
```

Out[37]: target  
4 471  
2 351  
1 382  
6 265  
5 230  
3 144  
0 26  
dtype: int64

```
In [38]: pip install imblearn
```

```
Requirement already satisfied: imblearn in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (0.0)
Requirement already satisfied: imbalanced-learn in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from imblearn) (0.9.1)
Requirement already satisfied: numpy>=1.17.3 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from imbalanced-learn->imblearn) (1.20.3)
Requirement already satisfied: scikit-learn>=1.1.0 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from imbalanced-learn->imblearn) (1.1.1)
Requirement already satisfied: scipy>=1.3.2 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from imbalanced-learn->imblearn) (1.7.3)
Requirement already satisfied: threadpoolctl>=2.0.0 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from imbalanced-learn->imblearn) (2.2.0)
Requirement already satisfied: joblib>=1.0.0 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from imbalanced-learn->imblearn) (1.1.0)
Note: you may need to restart the kernel to use updated packages.
```

```
In [39]: from imblearn.over_sampling import SMOTE
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)
```

```
In [40]: from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
x_bal = sc.fit_transform(x_bal)
x_test_bal = sc.transform(x_test_bal)
```

```
In [41]: x_bal
```

Out[41]: array([[ -1.62721585, -0.44068477, -0.4238 , ..., -2.58870684,  
 -1.40088079, 3.29450897],  
 [ -0.11561483, -0.44068477, 2.35960359, ..., -0.26259147,  
 0.0728993 , -0.19494049],  
 [ 1.1874903 , 2.26960776, -0.4238 , ..., 0.17039463,  
 -0.19352104, -0.19494049],  
 ...,  
 [ 1.395987 , -0.44068477, 2.35960359, ..., 0.43615031,  
 0.06181022, -0.19494049],  
 [ 0.72802783, -0.44068477, 2.35960359, ..., 0.143333 ,  
 0.09086631, -0.19494049],  
 [ 1.15628145, -0.44068477, 2.35960359, ..., 0.39723515,  
 -0.26588659, -0.19494049]])

```
In [42]: x_test_bal

Out[42]: array([[ -1.5229667, -0.44860477, -0.4238, ..., 1.06342846,
        [ 0.13246609, -0.19494049],
        [ -0.89747663, -0.44860477, -0.4238, ..., 1.76703086,
        [ -0.38218342, -0.19494049],
        [ -0.94968088, 2.26960776, -0.4238, ..., -0.39789962,
        [ -0.98586329, -0.19494049],
        ...,
        [ 1.39813447, -0.44860477, 2.35960359, ..., 0.81835453,
        [ 0.70094189, -0.19494049],
        [ 1.33846247, -0.44860477, 2.35960359, ..., 0.81987378,
        [ 0.67327619, -0.19494049],
        [ -0.19842352, -0.44860477, -0.4238, ..., 0.24838842,
        [ 0.37618348, -0.19494049]])

In [43]: y_bal.value_counts()

Out[43]: target
0      471
1      471
2      471
3      471
4      471
5      471
6      471
dtype: int64

In [44]: columns=['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroid_meds','sick','pregnant','thyroid_surgery','l131_treatment','query_hypothyroid','query_hyperthyroid','lithium','goitre','tumor','hypopituitary','psych',"

In [45]: x_test_bal= pd.DataFrame(x_test_bal,columns=columns)

In [46]: x_bal= pd.DataFrame(x_bal,columns=columns)

In [47]: x_bal

Out[47]:
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	l131_treatment	query_hypothyroid	...	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TE
0	-1.627215	-0.440605	-0.423800	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.315458	-1.035358	-1.704935	-2.508707	-1.400881	3.2944
1	-0.115614	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.090056	0.155233	-0.197223	-0.262591	0.072098	-0.1949
2	1.187490	2.289608	-0.423800	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.278907	-0.471394	-0.227079	0.170395	-0.193521	-0.1949
3	-1.366594	-0.440605	-0.423800	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	7.283487	-0.024637	-0.107982	-0.284999	0.969848	0.041622	0.495134	-0.133153	-0.1949
4	-0.167738	-0.440605	-0.423800	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.306321	4.541622	1.459767	-0.127283	1.496783	-0.1949
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
3292	0.546923	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.114424	0.343221	-0.148122	-0.146617	0.040168	-0.1949
3293	0.383062	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.309176	-0.856540	0.565143	-0.513902	1.085434	-0.1949
3294	1.395987	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.095452	-0.172405	0.248906	0.436150	0.061010	-0.1949
3295	0.728028	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.311566	0.087864	1.071643	0.143333	0.890866	-0.1949
3296	1.156281	-0.440605	2.359604	-0.105069	-0.158703	-0.141815	-0.137297	-0.239601	-0.162675	-0.230986	...	-0.052319	-0.137297	-0.024637	-0.107982	-0.072439	0.079407	-0.200359	0.397235	-0.265887	-0.1949

3297 rows x 22 columns

```
In [48]: from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, classification_report
rfr = RandomForestClassifier().fit(x_bal,y_bal)
y_pred = rfr.predict(x_test_bal)
accuracy_score(y_test_bal,y_pred)
x_bal.shape,y_bal.shape,x_test_bal.shape,y_test_bal.shape

/tmp/.../ipykernel_18028/2696972469.py:3: 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().
rfr = RandomForestClassifier().fit(x_bal,y_bal)

Out[48]: ((3297, 22), (3297, 1), (854, 22), (854, 1))

In [49]: test_score=accuracy_score(y_test_bal,y_pred)
test_score

Out[49]: 0.9098360655737785

In [50]: train_score = accuracy_score(y_bal,rfr.predict(x_bal))
train_score

Out[50]: 1.0
```

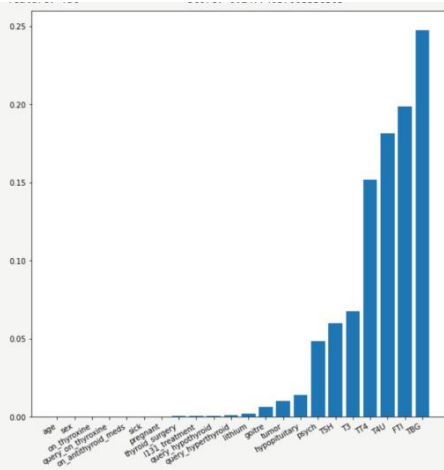
## performing feature importance

```
In [51]: #perform feature importance
from sklearn.inspection import permutation_importance
results = permutation_importance(rfr,x_bal,y_bal, scoring='accuracy')

In [52]: #gets importance
feature_importance=['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroid_meds','sick','pregnant','thyroid_surgery','l131_treatment','query_hypothyroid','query_hyperthyroid','lithium','goitre','tumor','hypopituitary'
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: 0.0
feature: sick Score: 0.0
feature: pregnant Score: 6.066120715801926e-05
feature: thyroid_surgery Score: 0.00036396724294811554
feature: l131_treatment Score: 0.0004852896572641541
feature: query_hypothyroid Score: 0.000066120715801926
feature: query_hyperthyroid Score: 0.0012132241431684962
feature: lithium Score: 0.0018198362147406888
feature: goitre Score: 0.006388765544434336
feature: tumor Score: 0.010130421595389748
feature: hypopituitary Score: 0.013830755232029101
feature: psych Score: 0.04852896572641796
feature: TSH Score: 0.05987261146496816
feature: T3 Score: 0.06781922960266909
feature: TT4 Score: 0.1519563239388462
feature: T4U Score: 0.1816196542311192
feature: FTI Score: 0.19884743706399757
feature: TBG Score: 0.24774037003336363
```



```
In [53]: x_bal.drop(['age', 'sex', 'on_thyroxine', 'query_on_thyroxine', 'on_antithyroid_meds', 'sick', 'pregnant', 'thyroid_surgery', 'I131_treatment', 'query_hypothyroid', 'query_hyperthyroid', 'lithium'], axis=1, inplace=True)
In [54]: x_test_bal.drop(['age', 'sex', 'on_thyroxine', 'query_on_thyroxine', 'on_antithyroid_meds', 'sick', 'pregnant', 'thyroid_surgery', 'I131_treatment', 'query_hypothyroid', 'query_hyperthyroid', 'lithium'], axis=1, inplace=True)
In [55]: 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	-0.282591	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

```
In [56]: x_test_bal.head()
```

	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG
0	-0.052319	-0.137297	-0.024637	-0.107982	-0.312412	0.593872	0.788014	1.063428	0.132466	-0.19494
1	-0.052319	-0.137297	-0.024637	-0.107982	-0.314240	0.781860	0.444674	1.767031	-0.302183	-0.19494
2	-0.052319	-0.137297	-0.024637	-0.107982	1.298911	-0.408731	-1.227244	-0.397900	-0.905863	-0.19494
3	-0.052319	-0.137297	-0.024637	-0.107982	-0.186205	-0.471394	-0.227079	-0.397900	0.132466	-0.19494
4	-0.052319	-0.137297	-0.024637	-0.107982	-0.227125	-0.346068	-0.301718	-0.830886	0.434306	-0.19494

### RandomForest Model-1

```
In [57]: rfr1 = RandomForestClassifier()
rfr1.fit(x_bal, y_bal)
y_pred=rfr1.predict(x_test_bal)

/tmp/vsuser/ipykernel_1020/1228087459.py:2: 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().
rfr1.fit(x_bal, y_bal)

In [58]: print(classification_report(y_test_bal, y_pred))
```

	precision	recall	f1-score	support
0	0.81	0.17	0.28	122
1	0.81	0.93	0.87	122
2	0.93	0.98	0.96	122
3	0.76	0.84	0.80	122
4	0.48	0.87	0.61	122
5	0.87	0.69	0.77	122
6	0.58	0.50	0.54	122
accuracy			0.71	854
macro avg	0.75	0.71	0.69	854
weighted avg	0.75	0.71	0.69	854

```
In [59]: train_score = accuracy_score(y_bal, rfr1.predict(x_bal))
In [60]: train_score
Out[60]: 1.0
```

### SVC Model-3

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

sv = SVC()
```

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

```

/opt/conda/envs/Python-3.9/lib/python3.9/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	0.68	0.93	0.80	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

### Random\_Search for SVC

```
params = {
```

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

```
from sklearn.model_selection import RandomizedSearchCV
random_svc = RandomizedSearchCV(sv, params, scoring='accuracy', cv=5, n_jobs=-1)
```

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

```

/opt/conda/envs/Python-3.9/lib/python3.9/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)
/opt/conda/envs/Python-3.9/lib/python3.9/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)
/opt/conda/envs/Python-3.9/lib/python3.9/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)
/opt/conda/envs/Python-3.9/lib/python3.9/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().
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/opt/conda/envs/Python-3.9/lib/python3.9/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)

```

```

In [78]: random_svc.best_params_
Out[78]: {'kernel': 'rbf', 'gamma': 1, 'C': 1000}
In [78]: sv1=SVC(kernel='rbf', gamma= 0.1,C= 100)
In [79]: sv1.fit(x_bal,y_bal)
/opt/conda/envs/Python-3.9/lib/python3.9/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)
Out[79]: SVC(C=100, gamma=0.1)
In [80]: y_pred= sv1.predict(x_test_bal)
In [81]: 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      0.73      0.73      854
 macro avg      0.73      0.73      0.73      854
 weighted avg      0.73      0.73      0.73      854

In [82]: train_score= accuracy_score(y_bal,sv1.predict(x_bal))
train_score
Out[82]: 0.8125568698817106

In [83]: # saving the model
import pickle
pickle.dump(sv1,open('thyroid_1_model.pkl','wb'))

In [85]: features = np.array([[0,0,0,0,0.000000,0,0,0.0,1.00,0.0,0.40,0]])
print(label_encoder.inverse_transform(sv1.predict(features)))
['binding protein']
/opt/conda/envs/Python-3.9/lib/python3.9/site-packages/sklearn/base.py:450: UserWarning: X does not have valid feature names, but SVC was fitted with feature names
  warnings.warn(

```

```

In [86]: type(features)
Out[86]: numpy.ndarray

In [87]: pickle.dump(label_encoder,open('label_encoder.pkl','wb'))

In [88]: data['target'].unique()
Out[88]: array(['miscellaneous', 'hypothyroid conditions', 'binding protein',
               'replacement therapy', 'general health', 'hyperthyroid conditions',
               'antithyroid treatment'], dtype=object)

In [89]: y['target'].unique()
Out[89]: array([5, 4, 1, 6, 2, 3, 0])

In [90]: !tar -zxvf thyroid_disease_new.tgz thyroid_1_model.pkl
!tar -zxvf thyroid_disease_new.tgz label_encoder.pkl
thyroid_1_model.pkl
label_encoder.pkl

In [91]: ls -l
label_encoder.pkl
thyroid_1_model.pkl
thyroid_disease_new.tgz

In [92]: !pip install watson-machine-learning-client --upgrade
Collecting watson-machine-learning-client
  Downloading watson_machine_learning_client-1.0.391-py3-none-any.whl (538 kB)
    ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 538 kB 24.7 MB/s eta 0:00:01
Requirement already satisfied: ibm-cos-sdk in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (2.11.0)
Requirement already satisfied: urllib3 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (1.26.7)
Requirement already satisfied: boto3 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (1.18.21)
Requirement already satisfied: requests in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (2.26.0)
Requirement already satisfied: tabulate in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (0.8.9)
Requirement already satisfied: pandas in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (1.3.4)
Requirement already satisfied: lomond in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (0.3.3)
Requirement already satisfied: tqdm in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (4.62.3)
Requirement already satisfied: certifi in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from watson-machine-learning-client) (2022.5.18.1)
Requirement already satisfied: jmespath<1.0.0,>=0.7.1 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from boto3->watson-machine-learning-client) (0.10.0)
Requirement already satisfied: s3transfer<0.6.0,>=0.5.0 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from boto3->watson-machine-learning-client) (0.5.0)
Requirement already satisfied: botocore<1.22.0,>=1.21.21 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from boto3->watson-machine-learning-client) (1.21.41)
Requirement already satisfied: python-dateutil<3.0.0,>=2.1 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from botocore->watson-machine-learning-client) (2.8.2)
Requirement already satisfied: six>=1.5 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from python-dateutil<3.0.0,>=2.1->botocore->watson-machine-learning-client) (1.15.0)
Requirement already satisfied: ibm-cos-sdk-s3transfer==2.11.0 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from ibm-cos-sdk->watson-machine-learning-client) (2.11.0)
Requirement already satisfied: ibm-cos-sdk-core==2.11.0 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from ibm-cos-sdk->watson-machine-learning-client) (2.11.0)
Requirement already satisfied: idna<4,>=2.5 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from requests->watson-machine-learning-client) (3.3)
Requirement already satisfied: charset-normalizer<2.0.0 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from requests->watson-machine-learning-client) (2.0.4)
Requirement already satisfied: pytz>=2017.3 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from pandas->watson-machine-learning-client) (2021.3)
Requirement already satisfied: numpy>=1.17.3 in /opt/conda/envs/Python-3.9/lib/python3.9/site-packages (from pandas->watson-machine-learning-client) (1.20.3)
Installing collected packages: watson-machine-learning-client
Successfully installed watson-machine-learning-client-1.0.391

```



```

In [11]: from ibm_watson_machine_learning import APIClient
wml_credentials = {
    "url": "https://us-south.ml.cloud.ibm.com",
    "apikey": "a4hY8b_3PvNDBV0mekwAJuLoP_kIRhj0YcUVYwF8QZv"
}
client = APIClient(wml_credentials)

In [11]: def guid_from_space_name(client, space_name):
space = client.spaces.get_details()
#print(space)
return(next(item for item in space['resources'] if item['entity']['name'] == space_name)['metadata']['id'])

In [12]: space_uid = guid_from_space_name(client, space_name='thyroid_deploy')
print("Space UID = " + space_uid)

Space UID = 77c033bf-40dc-4e25-8afb-5bea7f65de10

In [12]: client.set_default_space(space_uid)

Out[12]: 'SUCCESS'

In [12]: client.software_specifications.list()

```

NAME	ASSET_ID	TYPE
default_py3.6	0062b8c9-8b7d-44a0-a9b9-46c416adcbd9	base
kernel-spark3.2-scala2.12	020d69ce-7ac1-5e68-ac1a-31189867356a	base
pytorch-onnx_1.3-py3.7-edt	069ea134-3346-5748-b513-49120e15d288	base
scikit-learn_0.20-py3.6	09c5a1d8-9c1e-4473-a344-e67b665ff687	base
spark-mllib_3.0-scala_2.12	09f4cf0-98a7-5899-b9ed-1ef348aebdee	base
pytorch-onnx_rt22.1-py3.9	0b848dd4-e681-5599-be41-b5f6fcc6471	base
ai-function_0.1-py3.6	0c0b0f1e-5376-4f4d-92dd-da3b69aa9bda	base
shiny-r3.6	0e6e79df-875e-4f24-8ae9-62dccc2148306	base
tensorflow_2.4-py3.7-horovod	1092590a-3b7d-563d-9062-4eb7064b3722	base
pytorch_1.1-py3.6	10ac12d6-6b30-4cc0-8392-3e922c09e092	base
tensorflow_1.15-py3.6-ddl	111e41b3-de2d-5422-a4d6-bf776828c4b7	base
runtime-22.1-py3.9	12b83a17-24d8-5082-900f-8ab31bf43cb	base
scikit-learn_0.22-py3.6	154010fa-5b3b-4ac1-82af-4d5ee5abbc85	base
default_r3.6	1670a6c3-ab34-40b7-8aa0-a4a3c8296a36	base
pytorch-onnx_1.3-py3.6	1bc6029a-cc97-56da-a8e0-39c3888dbbe7	base
pytorch-onnx_rt22.1-py3.9-edt	1d362186-7ad5-5b59-8b6c-9d0880bdc37f	base
tensorflow_2.1-py3.6	1eb25b84-d6ed-5dde-b6a5-3fbd16656666	base
spark-mllib_3.2	20047f72-0a98-58c7-9ff5-a77b012eb0f5	base
tensorflow_2.4-py3.8-horovod	217c16f6-178f-50bf-82aa-b19f2856a49	base
runtime-22.1-py3.9-cuda	26215705-08c3-5a41-e1b0-da66306ce658	base
do_py3.8	295addb5-9ef9-547e-9bf4-92ae3563e720	base
autoai-ts_3.8-py3.8	2aa0c932-798f-5ae9-abd6-15e0c2402fb5	base
tensorflow_1.15-py3.6	2b73a275-7cbf-420b-a912-aae7f436e0bc	base
pytorch_1.2-py3.6	2c0ef57d-2687-4b7d-acc0-01f94976d0c1	base
spark-mllib_2.3	2e51f700-bca0-4b8d-88dc-5c6791338875	base
pytorch-onnx_1.1-py3.6-edt	32983cea-3f32-4400-8965-dde874a8d67e	base
spark-mllib_3.0-py37	36507ebe-8770-55ba-ab2a-eafe787600e9	base
spark-mllib_2.4	390d21f8-e58b-4fac-9c55-d7ceda621326	base
xgboost_0.82-py3.6	39e31acd-5f30-41d5-ae44-60233c08306e	base
pytorch-onnx_1.2-py3.6-edt	40589d0e-7019-4e28-8daa-fb03b6f4fe12	base
default_r36py38	41c247d3-45f8-5a71-b065-8580229facf0	base
autoai-ts_rt22.1-py3.9	4269d26e-07ba-5d40-8f66-2d4950c71f7	base
autoai-obm_3.0	42b92e18-d9ab-567f-988a-4240ba1ed5f7	base
pmml-3.0_4.3	493bc095-16f1-50c5-bee8-01b0af00e9c7	base
spark-mllib_2.4-r_3.6	49403dff-92e9-4c87-a3d7-a42d0021c095	base

```

In [12]: import sklearn
         sklearn.__version__

Out[123]: '1.1.1'

In [12]: software_spec_uid= client.software_specifications.get_uid_by_name("runtime-22.1-py3.9")
         software_spec_uid

Out[124]: '12b83a17-24d8-5082-908f-8ab31fbfd3cb'

In [13]: model_details = client.repository.store_model(model='thyroid_disease_new.tgz',
         meta_props=(client.repository.ModelMetaNames.NAME:"thyroiddeploy",
                     client.repository.ModelMetaNames.TYPE:"scikit-learn_1.0",
                     client.repository.ModelMetaNames.SOFTWARE_SPEC_UID:software_spec_uid
                     ),
         training_data=x_train,
         training_target=y_train)

In [13]: model_id = client.repository.get_model_id(model_details)
         model_id

Out[133]: '2a67d325-0fcb-471c-9365-70472e8446a4'

In [13]: # Deploy
         deployment = client.deployments.create(
         artifact_uid=model_id,
         meta_props=(client.deployments.ConfigurationMetaNames.NAME:"thyroiddeploy_deploy",
                     client.deployments.ConfigurationMetaNames.ONLINE: {}
                     ))

#####
Synchronous deployment creation for uid: '2a67d325-0fcb-471c-9365-70472e8446a4' started
#####

initializing
Note: online_url is deprecated and will be removed in a future release. Use serving_urls instead.
ready

=====
Successfully finished deployment creation, deployment_uid='93c0fb0f-c7b4-4dbd-a280-8fb0bcee2d8d'
=====

```

