Thyroid Disease Classification Using ML

Project report submitted to
"Madurai Kamaraj University"
in partial fulfillment of the requirements
for the award of the Degree of

Bachelor of Science
in
Computer Science

Submitted

By

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INDEX

1. INTRODUCTION

1.1 OVERVIEW

Thyroid diseases, such as hypothyroidism and hyperthyroidism, are common endocrine disorders that affect thefunction 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 ofthese studies is to develop models that can accurately diagnose thyroid diseases based on clinical and laboratory data.

1.2 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.

2. LITERATURE SURVEY

2.1 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.

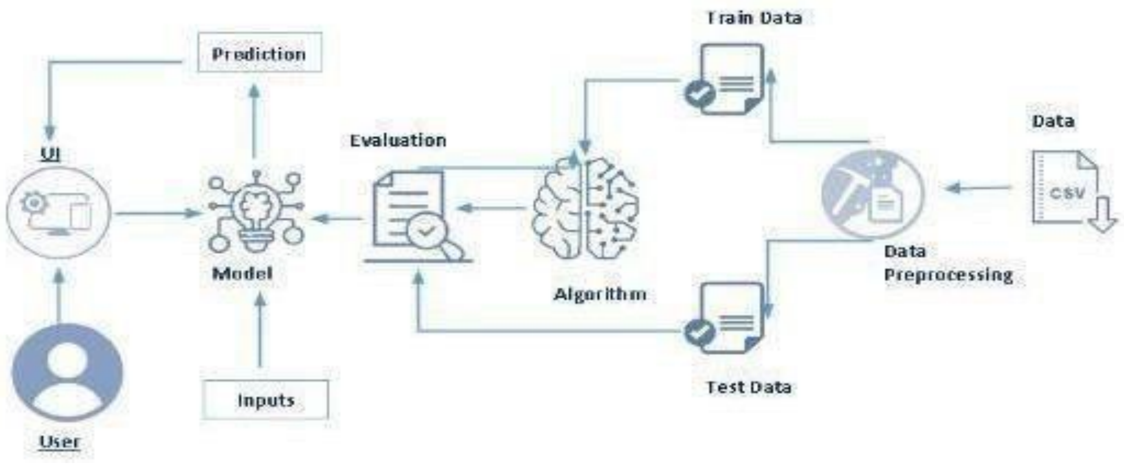
Fine needle aspiration biopsy (FNAB): This is a procedure in which a small sample of tissue is taken From a thyroid nodule using a fine needle, which is then examined under a microscope to check for cancer.

2.2 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.

3. THEORITICAL ANALYSIS

3.1 BLOCK DIAGRAM



3.2 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 itvery 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 supportsmodules 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 languagesfor 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 includes support for interactive tools for data inspection and embeds Python specific code. Spyderis 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.

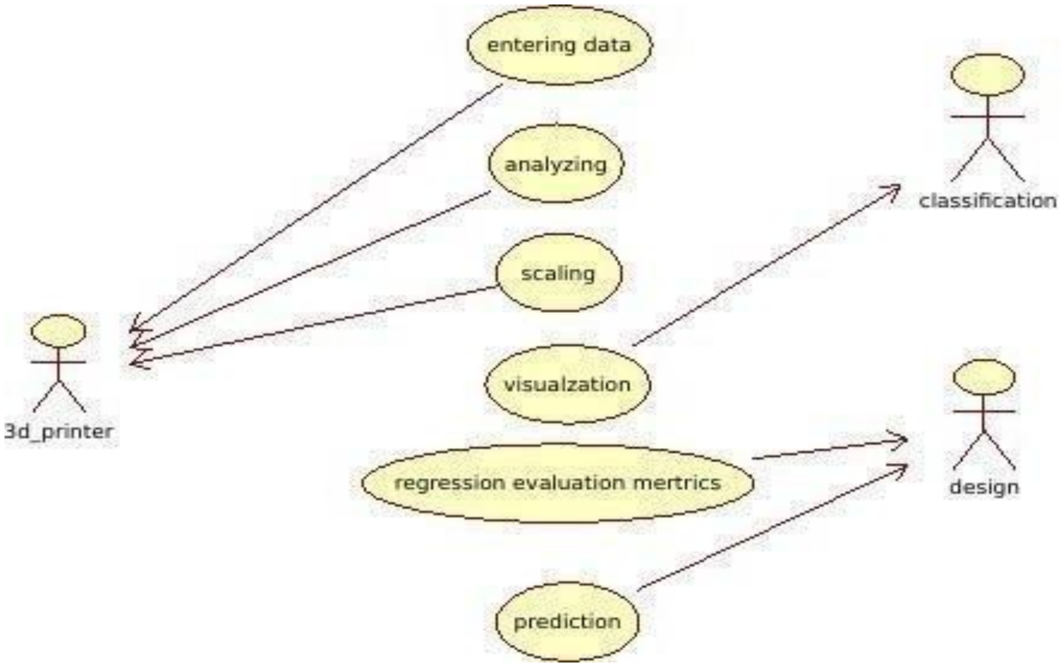
Hardware Requirements:

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

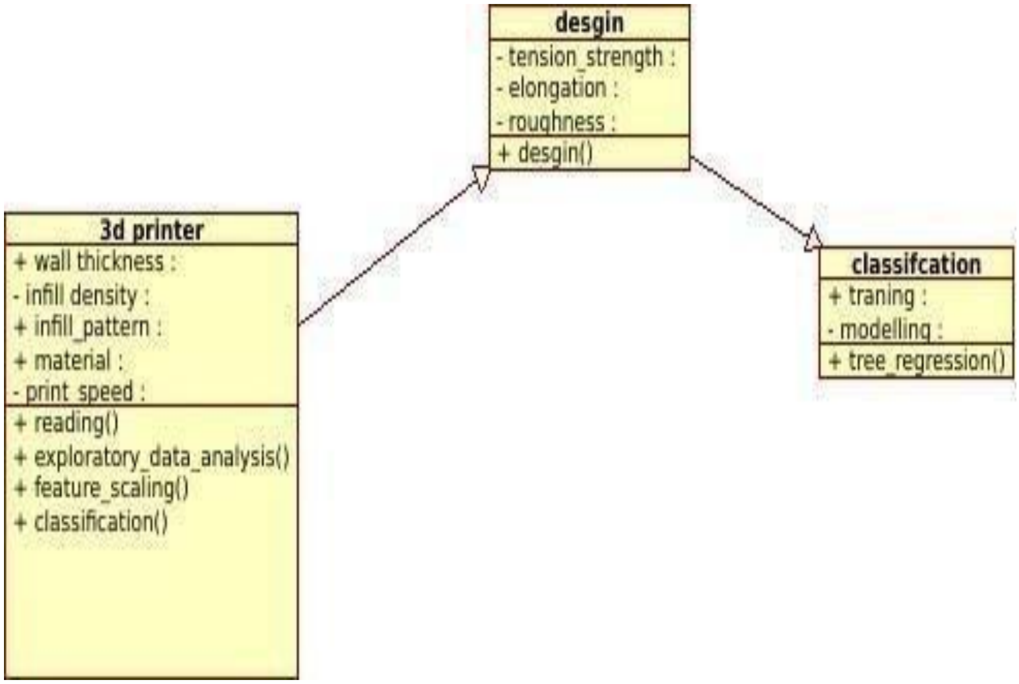
4. EXPERIMENTALINVESTIGATION

Here we are going to build a machine learning model that predicts whether the given message is as pam or not, based on these parameters a supervised machine learning model is built to predict the best Material to be used for building 3Dmodels.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 show case don UI.

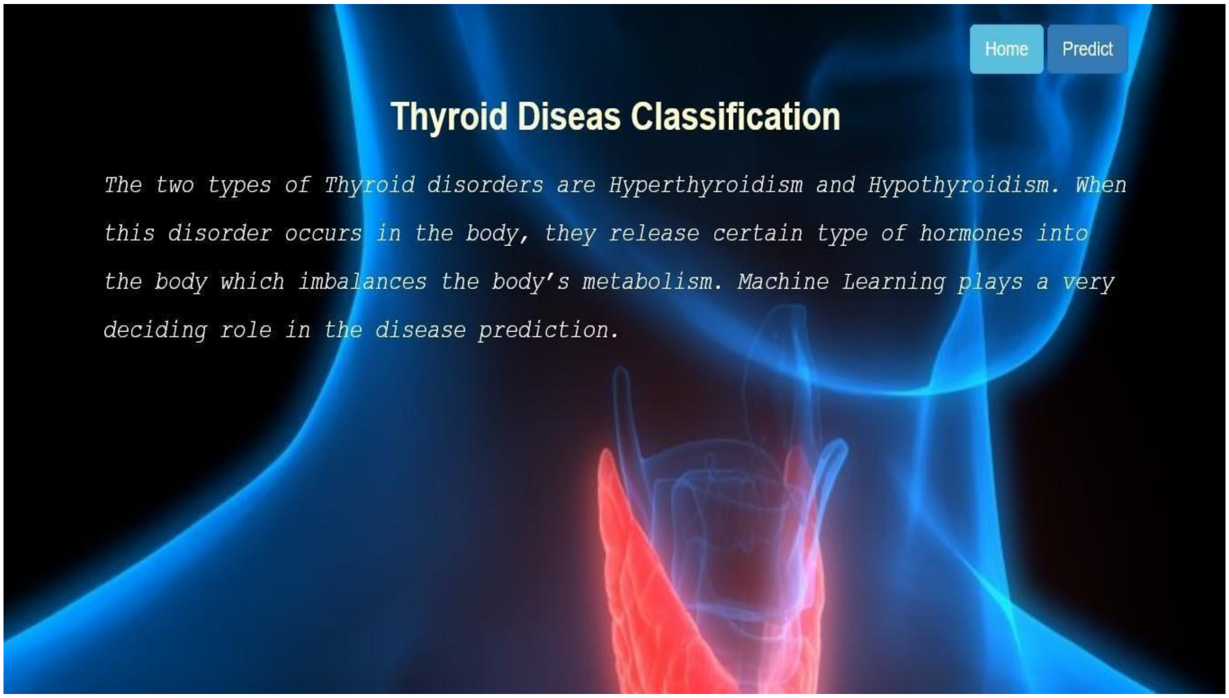
5. FLOWCHART



USECASEDIAGRAM

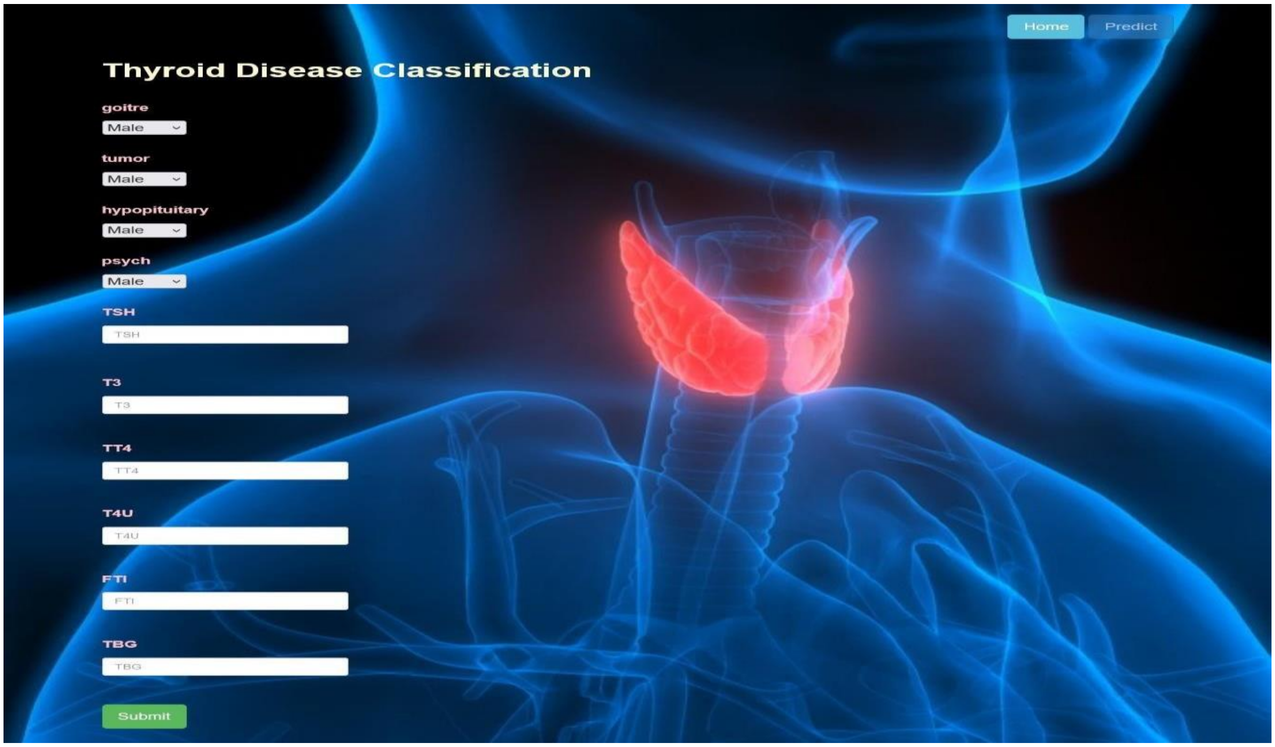


6. RESULT



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.



Thyroid Disease Classification

goitre
Male

tumor
Male

hypopituitary
Male

psych
Male

TSH
TSH

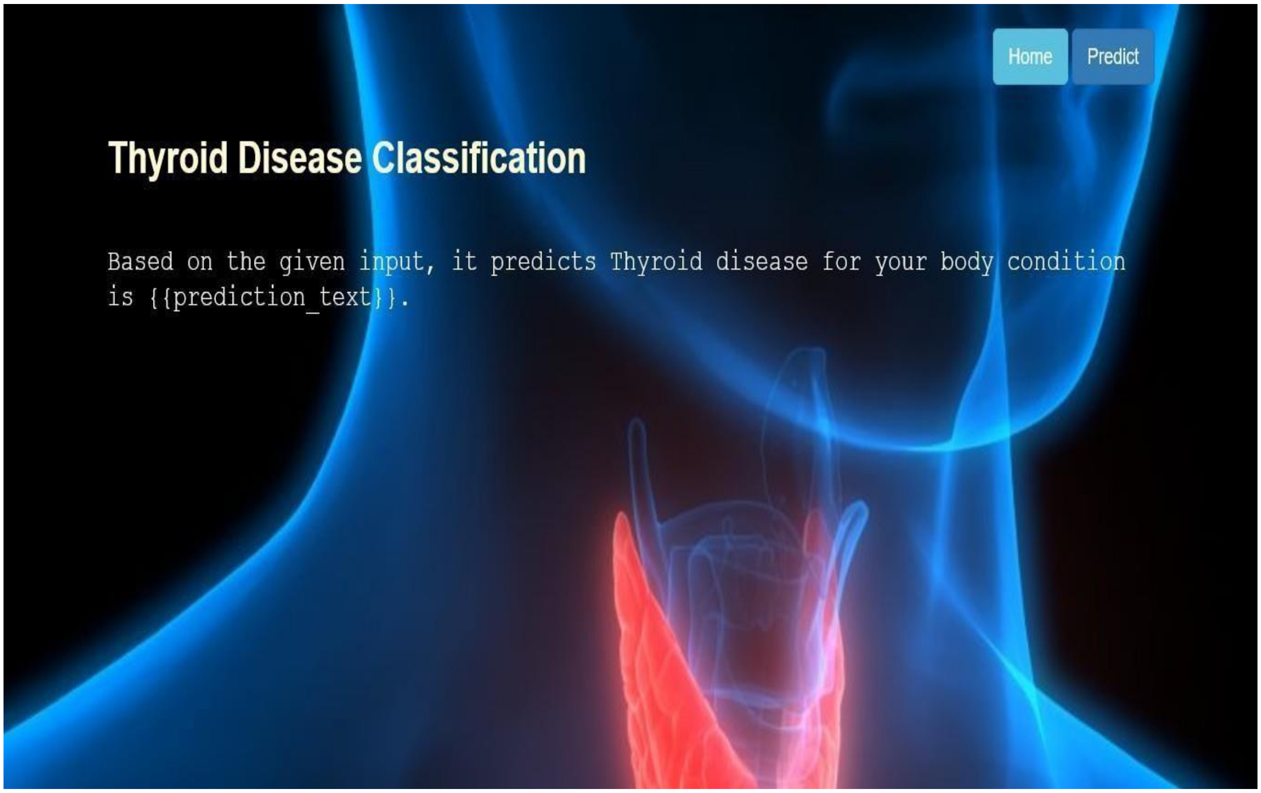
T3
T3

TT4
TT4

T4U
T4U

FTI
FTI

TBG
TBG



Thyroid Disease Classification

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

7. ADVANTAGES & DISADVANTAGES

ADVANTAGES

- Easy to use
- Cost efficient
- Time efficient

DISADVANTAGE

- Initial costs of printer
- Postprocessing
- Printing time
- Special skill required for 3Dmodels
- 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 moreflexibleandcost-effective3D printing methods, there are areas where3D 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.

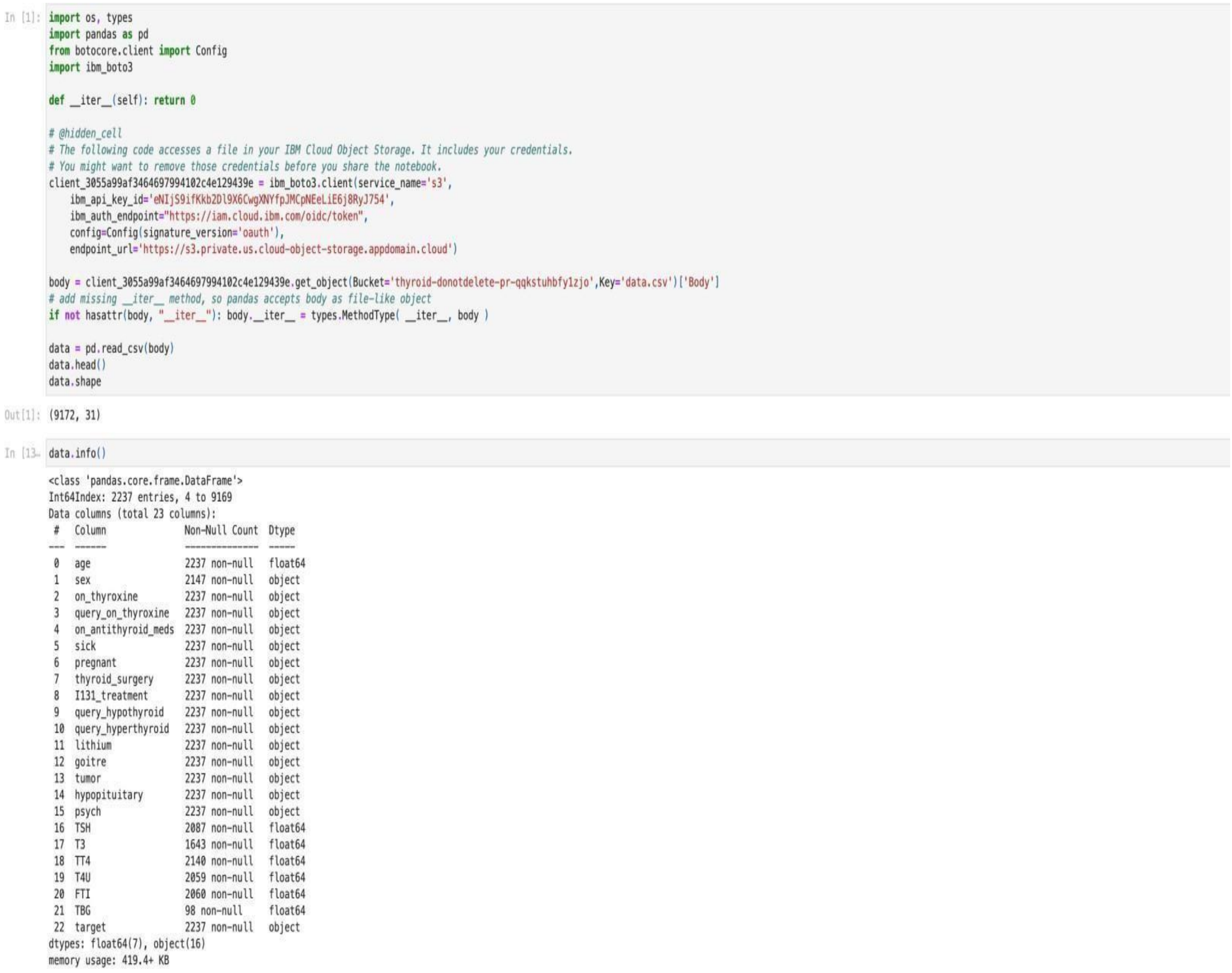
10. FUTURESCOPE

Future applications for 3D printing might include creating open-source scientific equipment to create open-source labs Science- based applications like reconstructing fossils in paleontology. Replicating ancient and priceless sartifacts in archaeology Reconstructing bones and body parts in forensic pathology. The technology currently being researched for building construction.

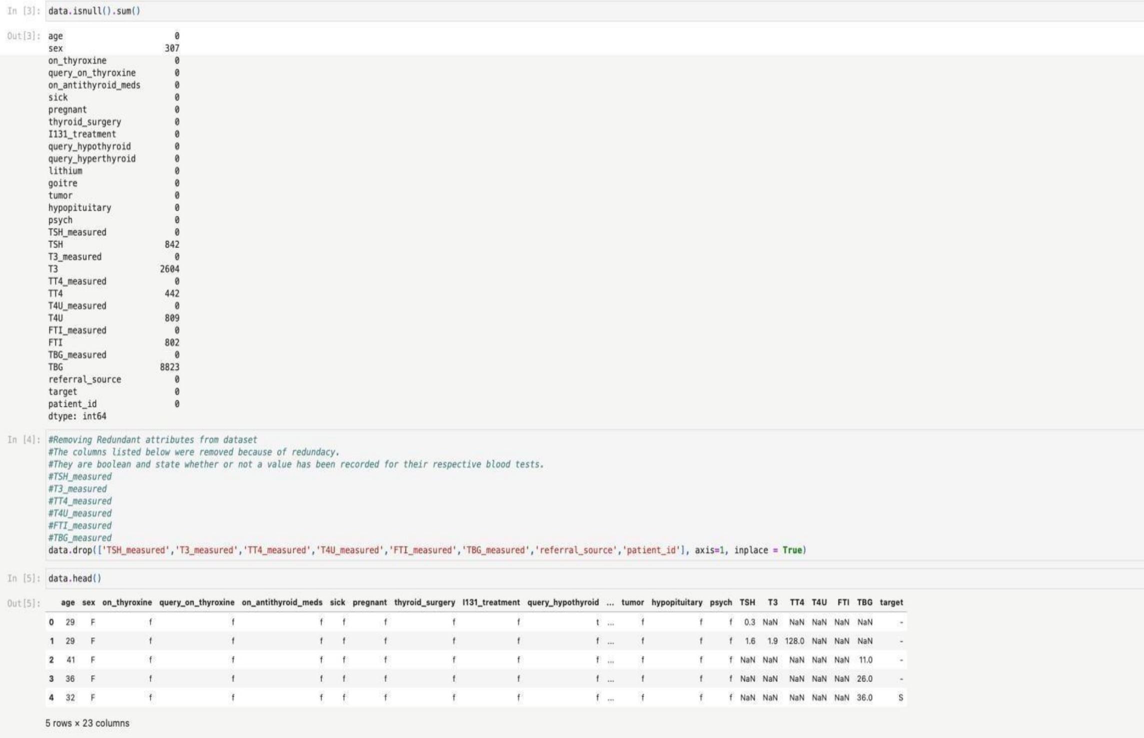
BIBILOGRAPHY

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

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='eNIjS9ifKkb2Dl9X6CwgXNYfpJMCpNEeLiE6j8RyJ754',
            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-qqkstuhbfy1zjo',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                  8823
        referral_source         0
        target                  0
        patient_id              0
        dtype: int64
```

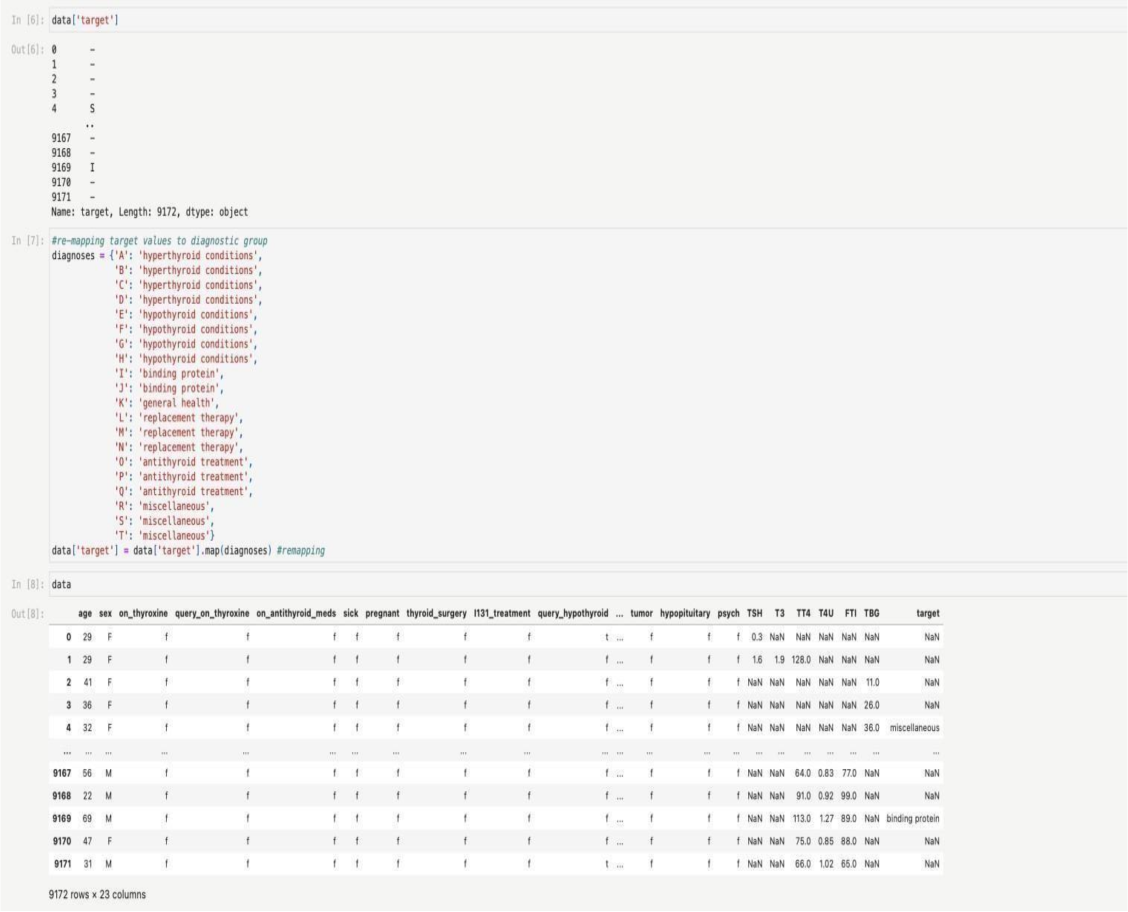
```
In [4]: #Removing Redundant attributes from dataset
        #The columns listed below were removed because of redundacy.
        #They are boolean and state whether or not a value has been recorded for their respective blood tests.
        #TSH_measured
        #T3_measured
        #TT4_measured
        #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	t	...	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 × 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
```

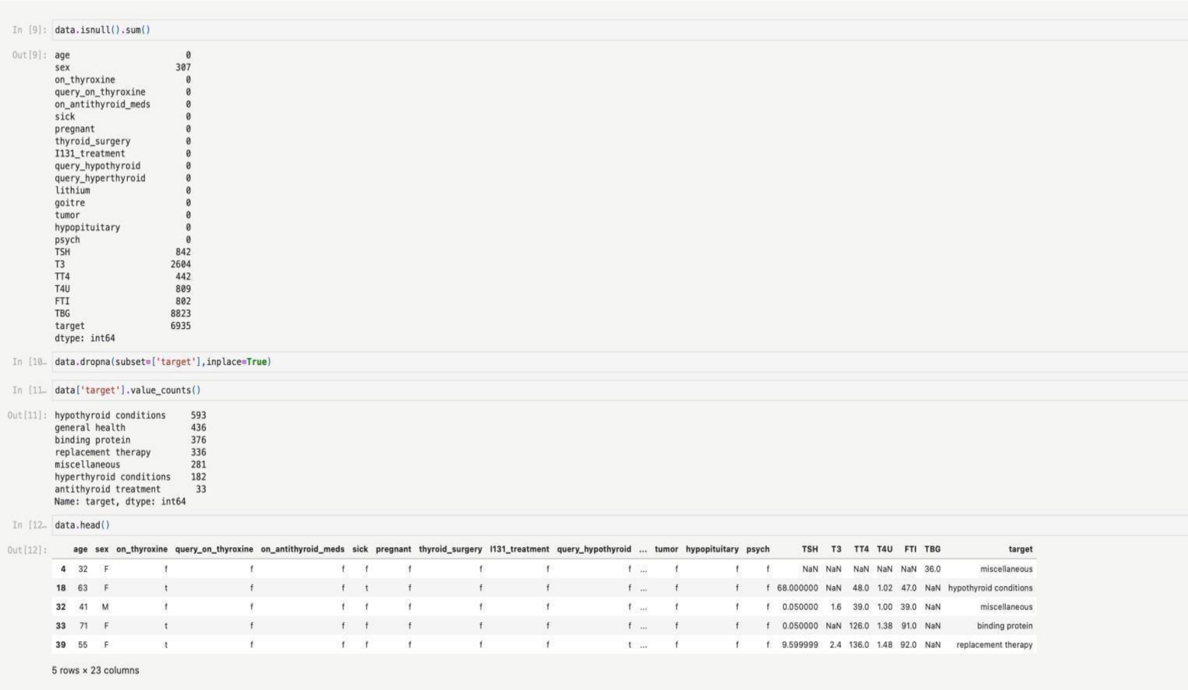
```
In [7]: #re-mapping target values to diagnostic group
        diagnoses = {'A': 'hyperthyroid conditions',
                     'B': 'hyperthyroid conditions',
                     'C': 'hyperthyroid conditions',
                     'D': 'hyperthyroid conditions',
                     'E': 'hypothyroid 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	t	...	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	t	...	f	f	f	NaN	NaN	66.0	1.02	65.0	NaN	NaN

9172 rows × 23 columns



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

Out[9]:
```
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                   842
T3                   2604
TT4                   442
T4U                   809
FTI                   802
TBG                  8823
target               6935
dtype: int64
```

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

In [11…
```
data['target'].value_counts()
```

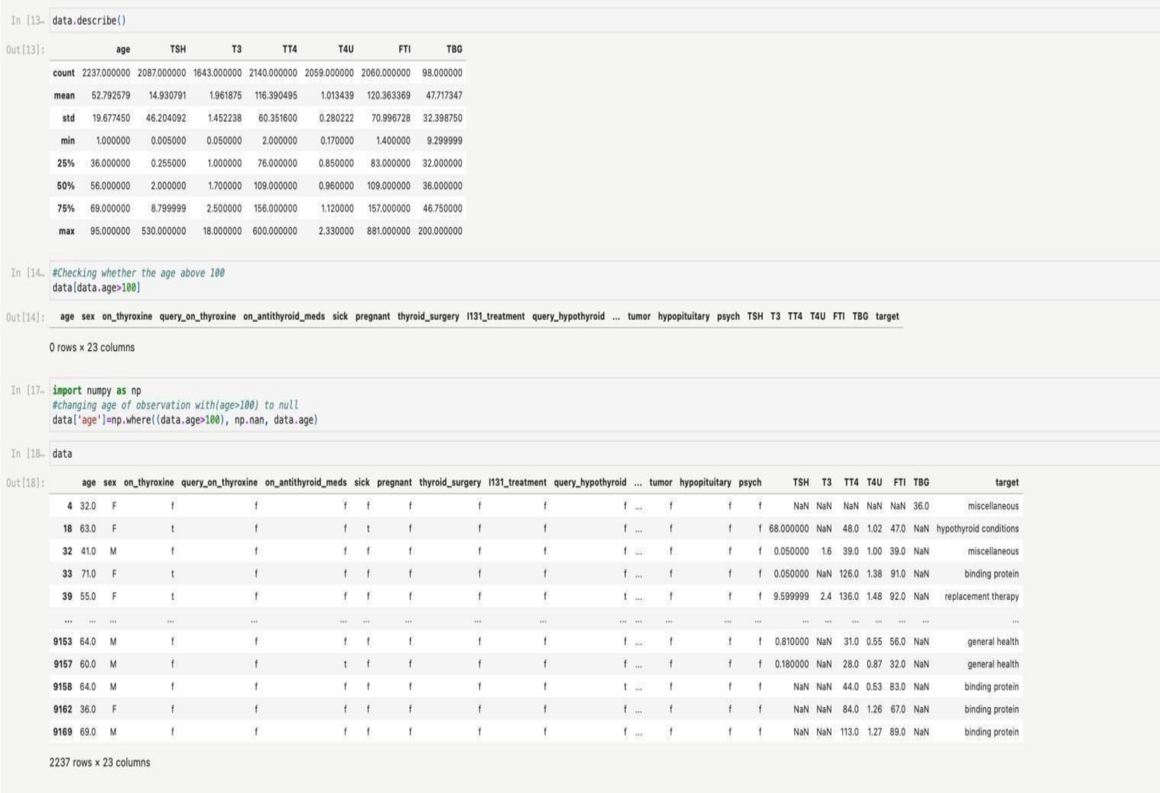
Out[11]:
```
hypothyroid conditions    593
general health            436
binding protein           376
replacement therapy       336
miscellaneous             281
hyperthyroid conditions   182
antithyroid treatment      33
Name: target, dtype: int64
```

In [12…
```
data.head()
```

Out[12]:

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_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	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	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	0.050000	NaN	126.0	1.38	91.0	NaN	binding protein
39	55	F	t	f	f	f	f	f	f	t	...	f	f	f	9.599999	2.4	136.0	1.48	92.0	NaN	replacement therapy

5 rows × 23 columns



In [13…
```
data.describe()
```

Out[13]:

	age	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	2.500000	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	I131_treatment	query_hypothyroid	...	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG	target

0 rows × 23 columns

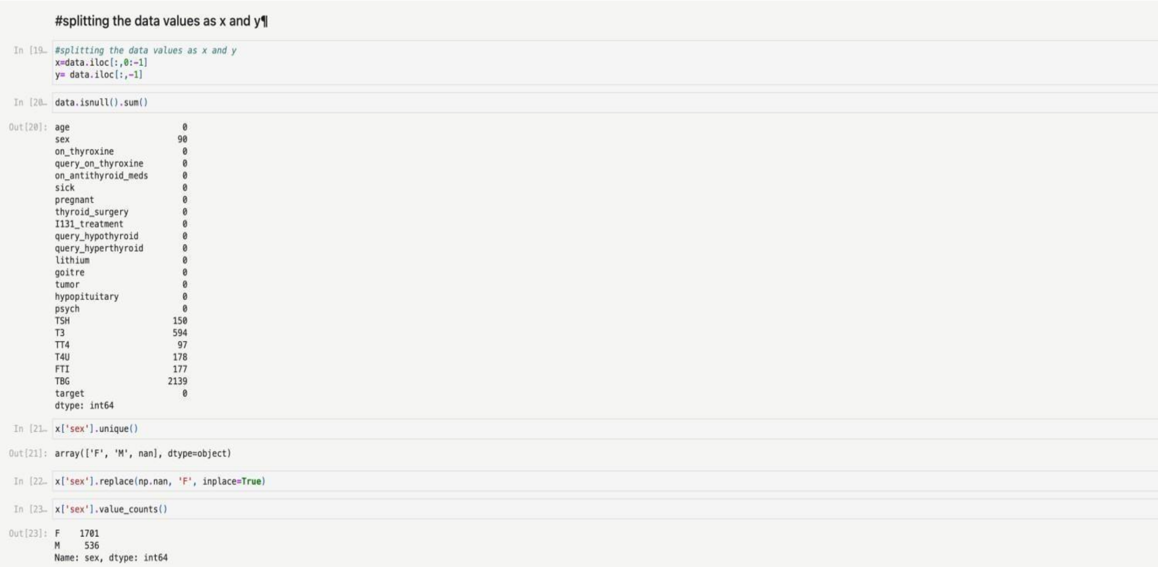
In [17…
```
import numpy as np
#changing age of observation with(age>100) to null
data['age']=np.where((data.age>100), np.nan, data.age)
```

In [18…
```
data
```

Out[18]:

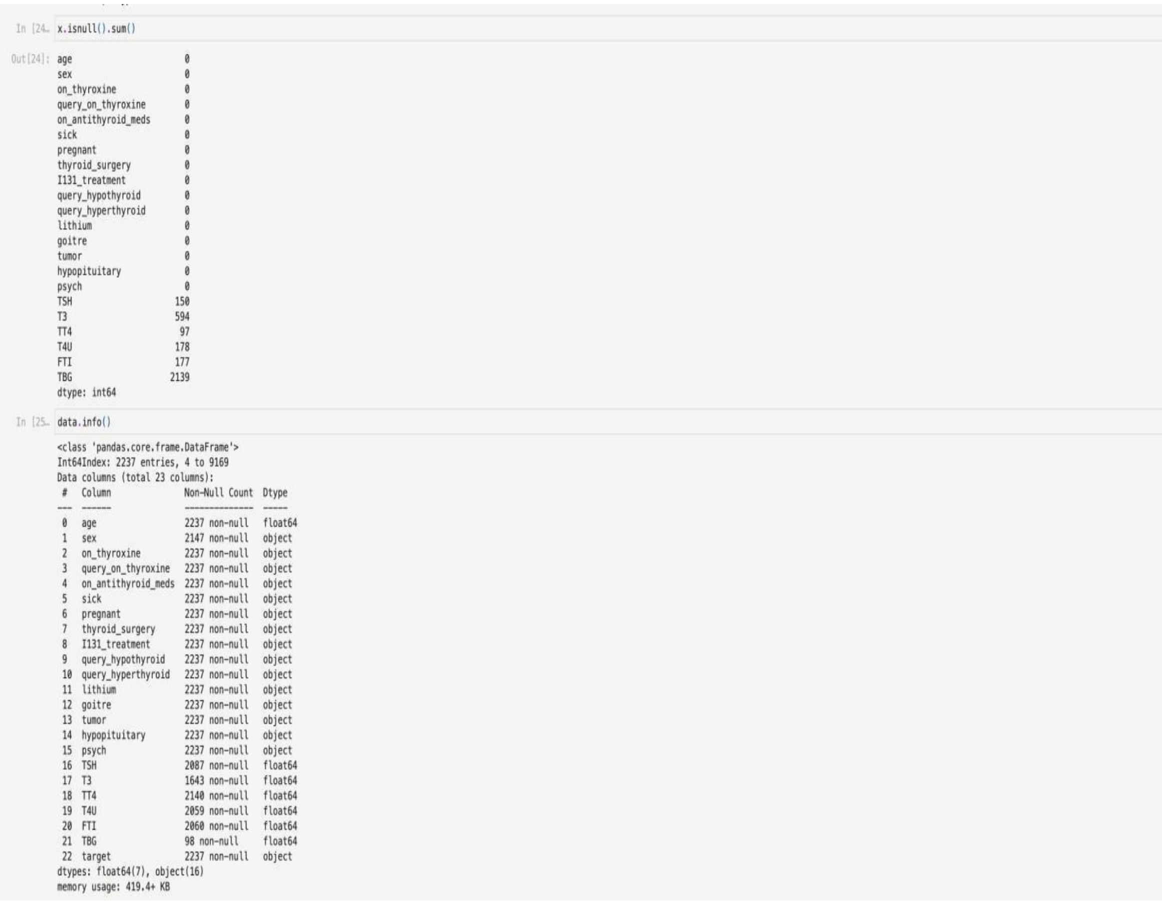
	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG	target
4	32.0	F	f	f	f	f	f	f	f	f	...	f	f	f	NaN	NaN	NaN	NaN	NaN	36.0	miscellaneous
18	63.0	F	t	f	f	t	f	f	f	f	...	f	f	f	68.000000	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	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	0.050000	NaN	126.0	1.38	91.0	NaN	binding protein
39	55.0	F	t	f	f	f	f	f	f	t	...	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	t	f	f	f	f	f	...	f	f	f	0.180000	NaN	28.0	0.87	32.0	NaN	general health
9158	64.0	M	f	f	f	f	f	f	f	t	...	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 × 23 columns

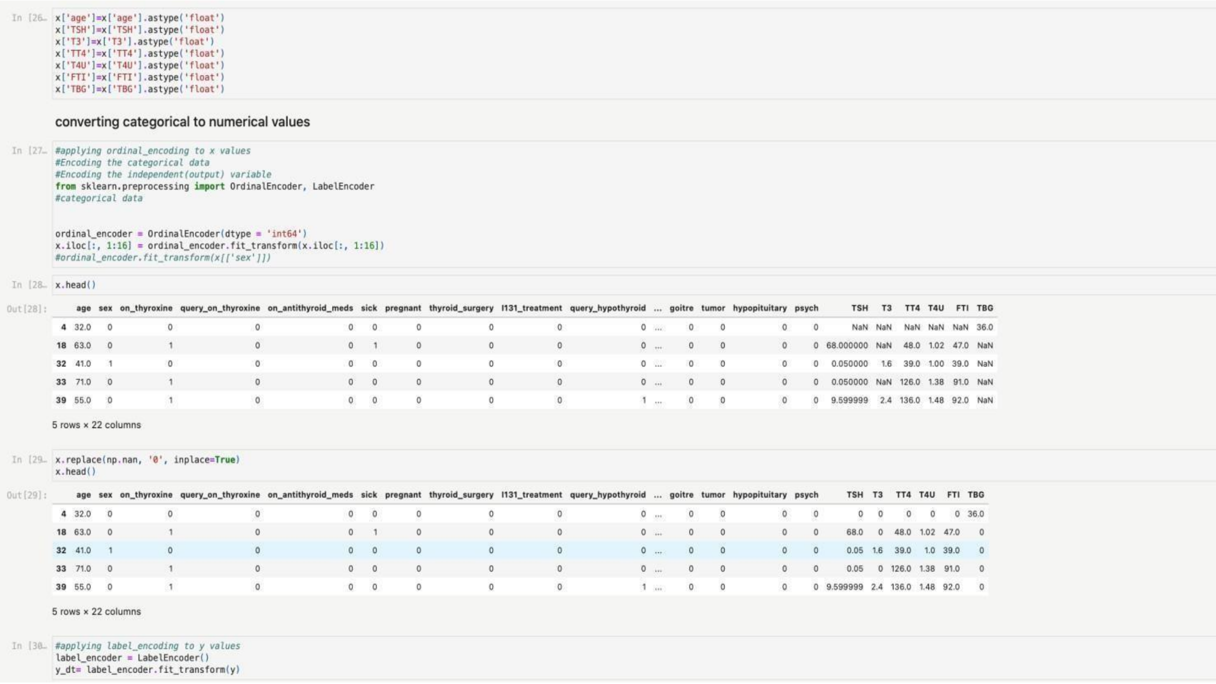


#splitting the data values as x and y¶

```
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']=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')
```

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	I131_treatment	query_hypothyroid	...	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG
4	32.0	0	0	0	0	0	0	0	0	0	...	0	0	0	0	NaN	NaN	NaN	NaN	NaN	36.0
18	63.0	0	1	0	0	1	0	0	0	0	...	0	0	0	0	68.000000	NaN	48.0	1.02	47.0	NaN
32	41.0	1	0	0	0	0	0	0	0	0	...	0	0	0	0	0.050000	1.6	39.0	1.00	39.0	NaN
33	71.0	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0.050000	NaN	126.0	1.38	91.0	NaN
39	55.0	0	1	0	0	0	0	0	0	1	...	0	0	0	0	9.599999	2.4	136.0	1.48	92.0	NaN

5 rows × 22 columns

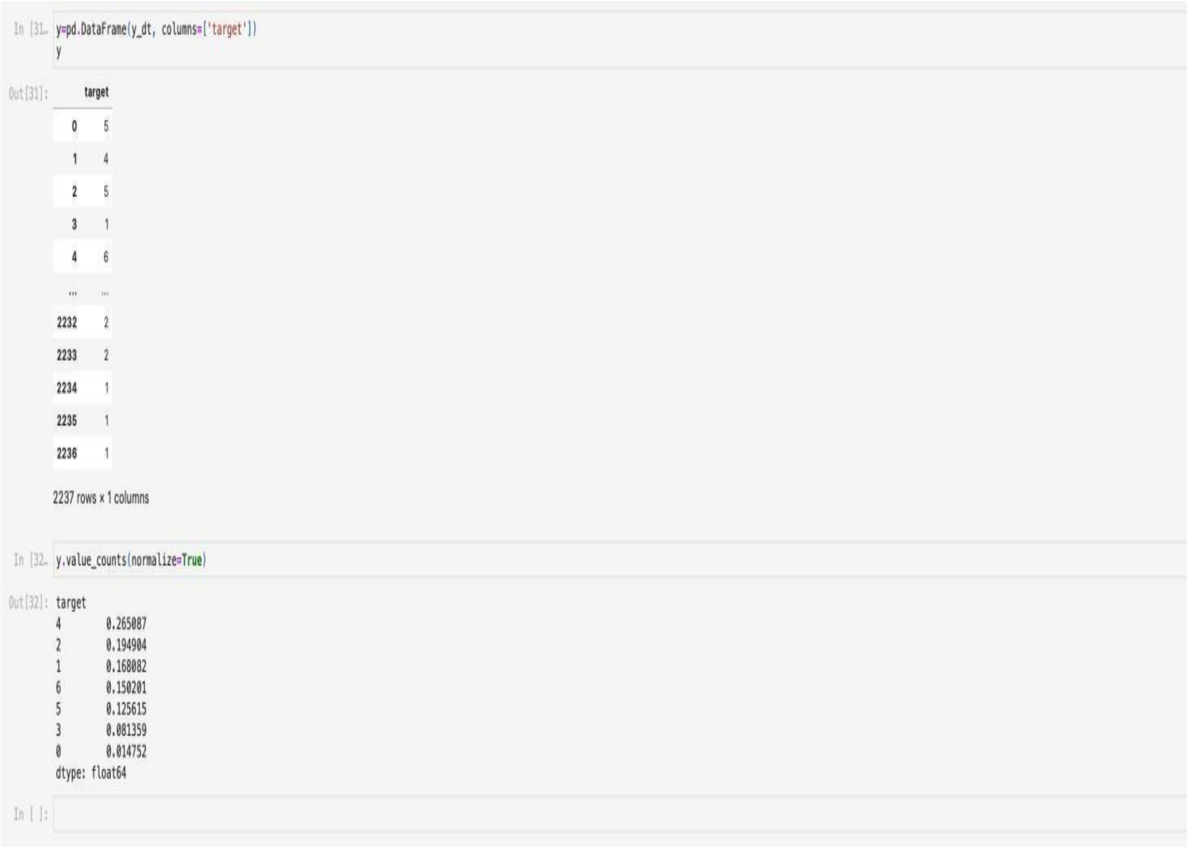
In [29…
```
x.replace(np.nan, '0', inplace=True)
x.head()
```

Out[29]:

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG
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	1	0	0	0	0	...	0	0	0	0	68.0	0	48.0	1.02	47.0	0
32	41.0	1	0	0	0	0	0	0	0	0	...	0	0	0	0	0.05	1.6	39.0	1.0	39.0	0
33	71.0	0	1	0	0	0	0	0	0	0	...	0	0	0	0	0.05	0	126.0	1.38	91.0	0
39	55.0	0	1	0	0	0	0	0	0	1	...	0	0	0	0	9.599999	2.4	136.0	1.48	92.0	0

5 rows × 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]:

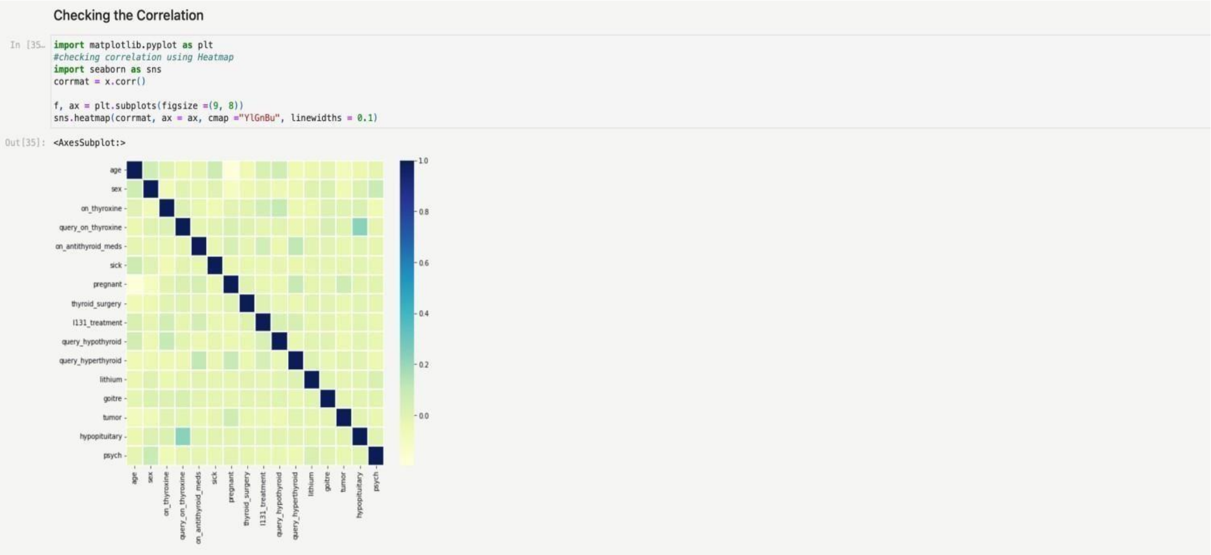
	target
0	5
1	4
2	5
3	1
4	6
...	...
2232	2
2233	2
2234	1
2235	1
2236	1

2237 rows x 1 columns

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

Out[32]:
```
target
4         0.265087
2         0.194904
1         0.168082
6         0.150201
5         0.125615
3         0.081359
0         0.014752
dtype: float64
```

In [ ]:



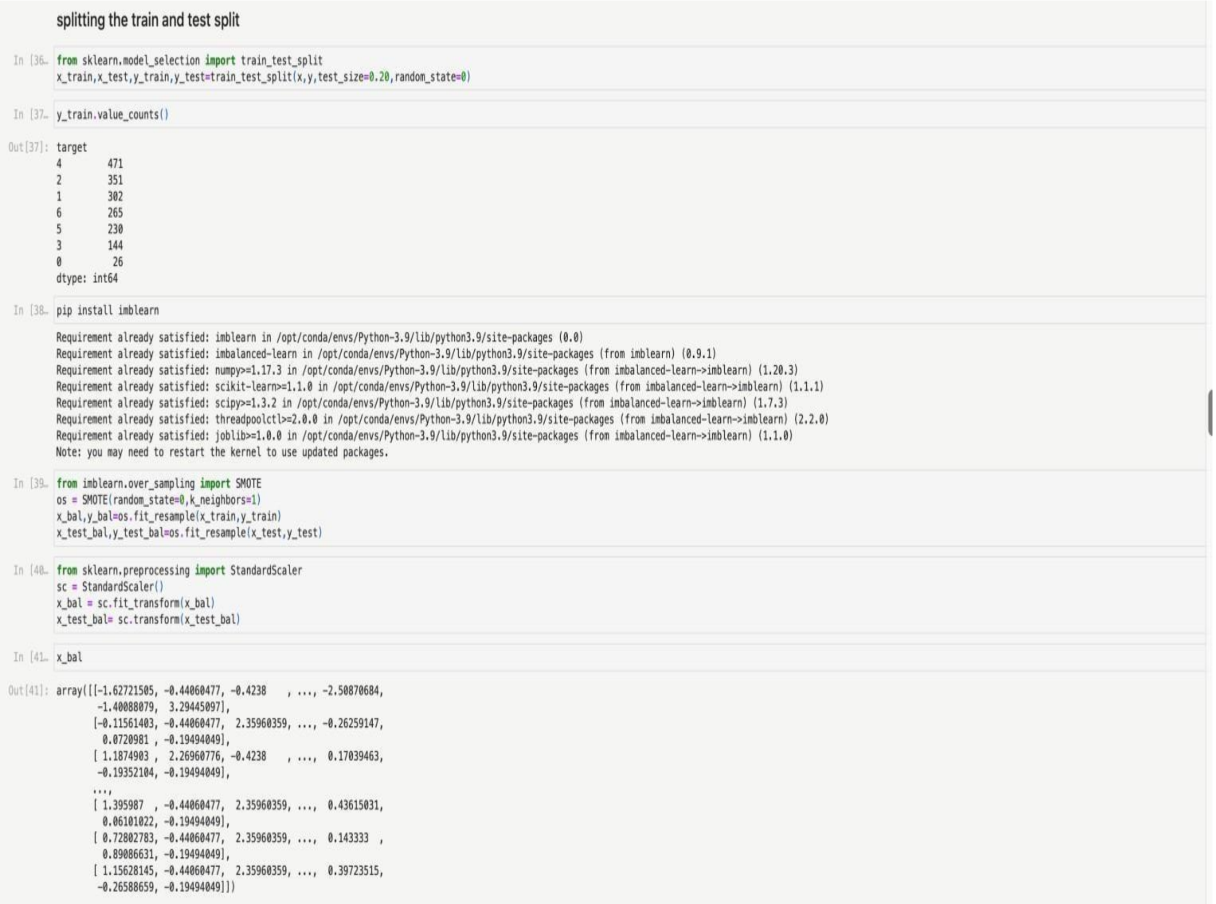
Checking the Correlation

In [35…

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

f, ax = plt.subplots(figsize =(9, 8))
sns.heatmap(corrmat, 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         302
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…

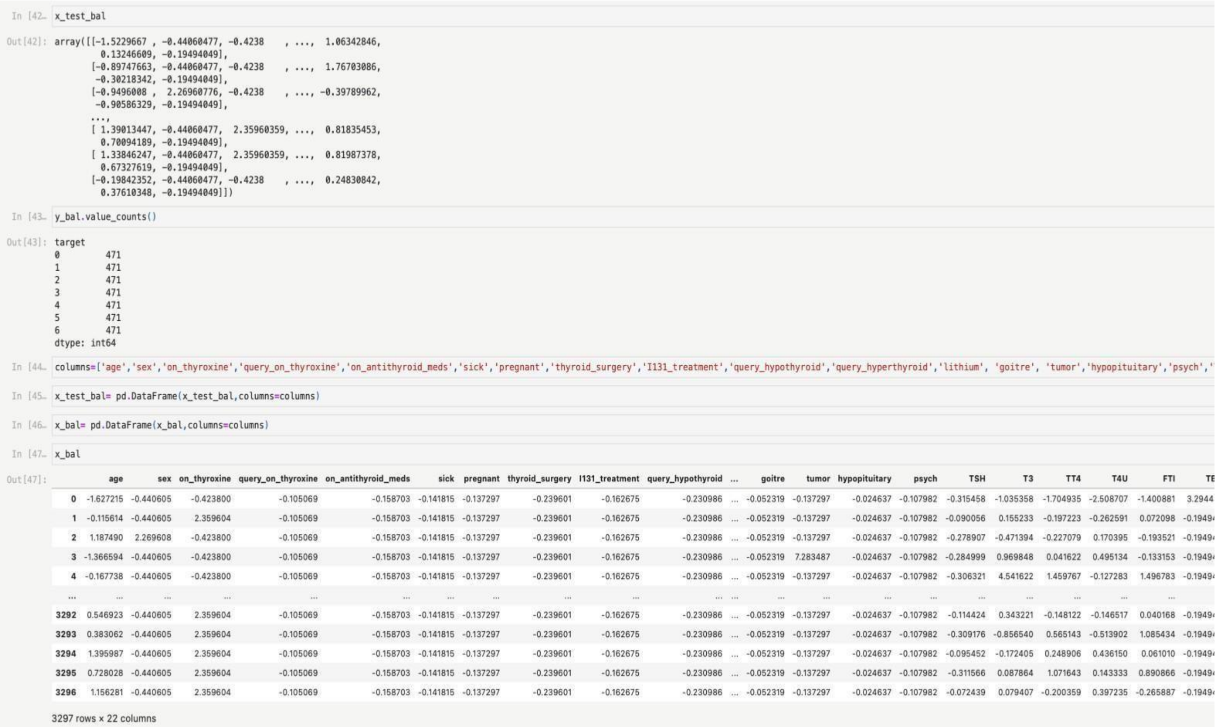
```
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
x_bal = sc.fit_transform(x_bal)
x_test_bal= sc.transform(x_test_bal)
```

In [41…

```
x_bal
```

Out[41]:

```
array([[-1.62721505, -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]])
```

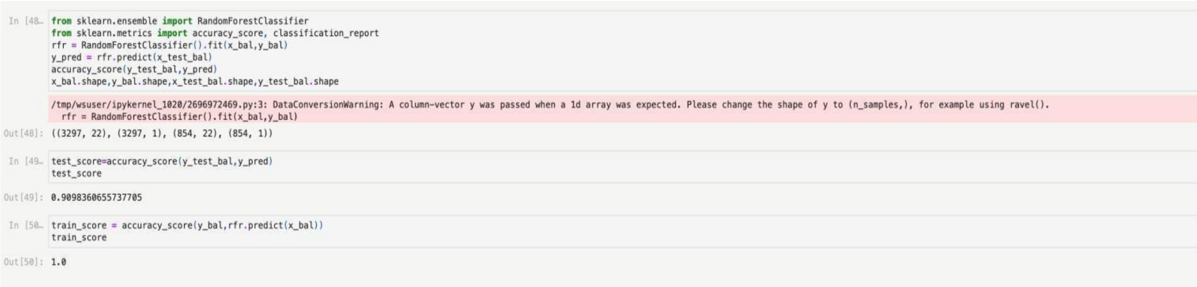


```
In [42… x_test_bal

Out[42]: array([[-1.5229667 , -0.44060477, -0.4238    , ...,  1.06342846,
           0.13246609, -0.19494049],
         [-0.89747663, -0.44060477, -0.4238    , ...,  1.76703086,
          -0.30218342, -0.19494049],
         [-0.9496008 ,  2.26960776, -0.4238    , ..., -0.39789962,
          -0.90586329, -0.19494049],
         ...,
         [ 1.39013447, -0.44060477,  2.35960359, ...,  0.81835453,
           0.70094189, -0.19494049],
         [ 1.33846247, -0.44060477,  2.35960359, ...,  0.81987378,
           0.67327619, -0.19494049],
         [-0.19842352, -0.44060477, -0.4238    , ...,  0.24830842,
           0.37610348, -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','I131_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
```

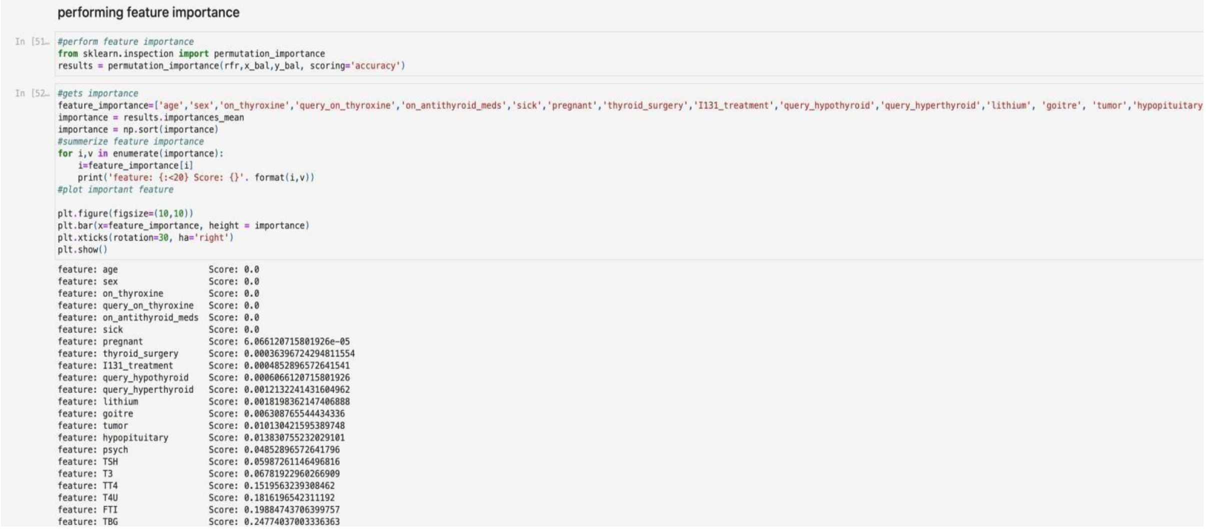
Out[47]:

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TB
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	2.269608	-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	-0.146517	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 × 22 columns

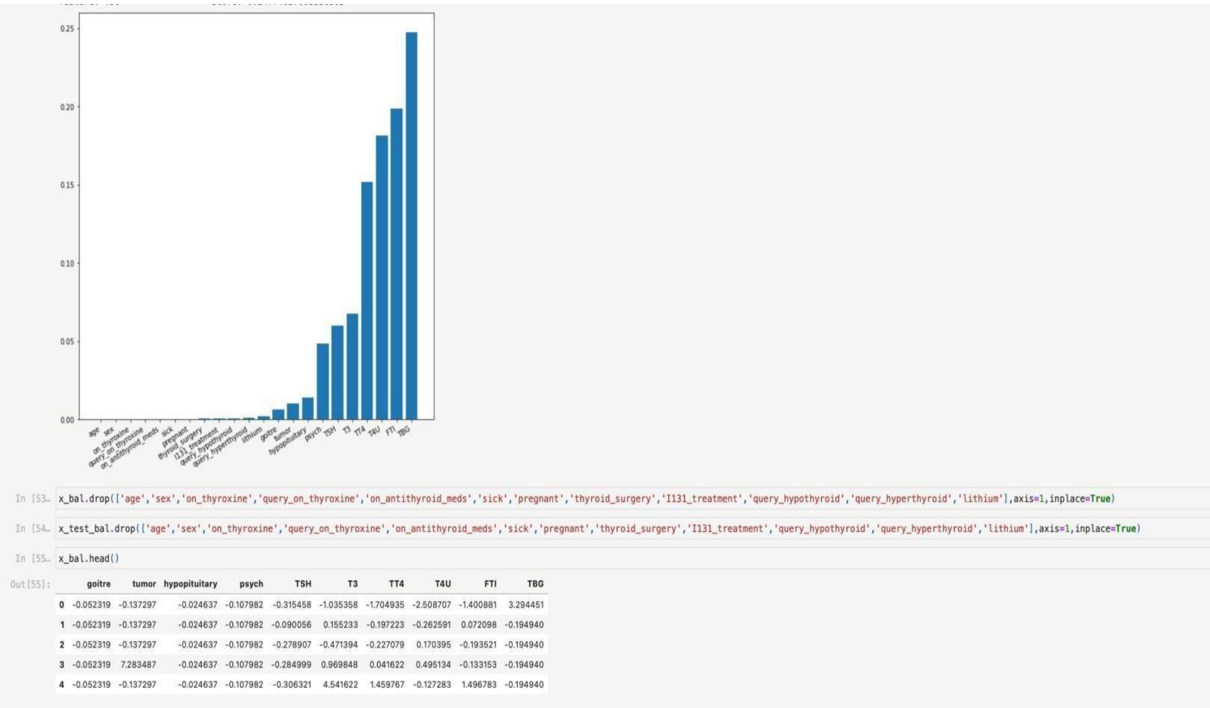


```
In [48… from sklearn.ensemble import RandomForestClassifier
       from sklearn.metrics import accuracy_score, classification_report
       rfr = RandomForestClassifier().fit(x_bal,y_bal)
       y_pred = rfr.predict(x_test_bal)
       accuracy_score(y_test_bal,y_pred)
       x_bal.shape,y_bal.shape,x_test_bal.shape,y_test_bal.shape

       /tmp/wsuser/ipykernel_1020/2696972469.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]: 0.9098360655737705

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','I131_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: I131_treatment      Score: 0.0004852896572641541
       feature: query_hypothyroid   Score: 0.0006066120715801926
       feature: query_hyperthyroid  Score: 0.0012132241431604962
       feature: lithium             Score: 0.0018198362147406888
       feature: goitre              Score: 0.006308765544434336
       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: 0.1519563239308462
       feature: T4U                 Score: 0.1816196542311192
       feature: FTI                 Score: 0.19884743706399757
       feature: TBG                 Score: 0.24774037003336363
```



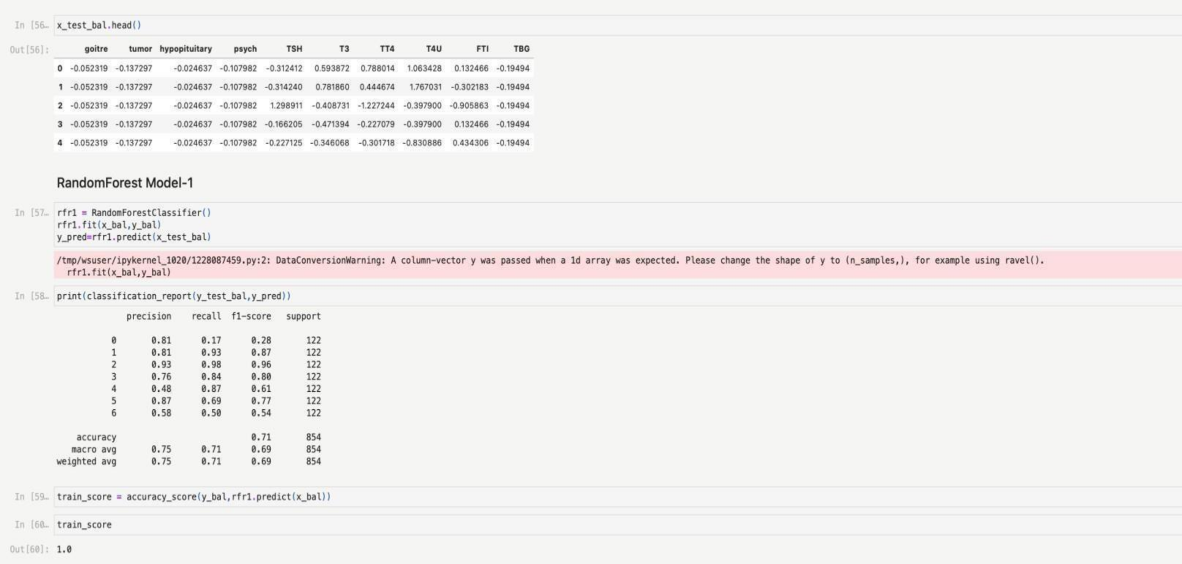
```
In [53… x_bal.drop(['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroid_meds','sick','pregnant','thyroid_surgery','I131_treatment','query_hypothyroid','query_hyperthyroid','lithium'],axis=1,inplace=True)
```

```
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()
```

Out[55]:

	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



```
In [56… x_test_bal.head()
```

Out[56]:

	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	-0.166205	-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/wsuser/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)
```

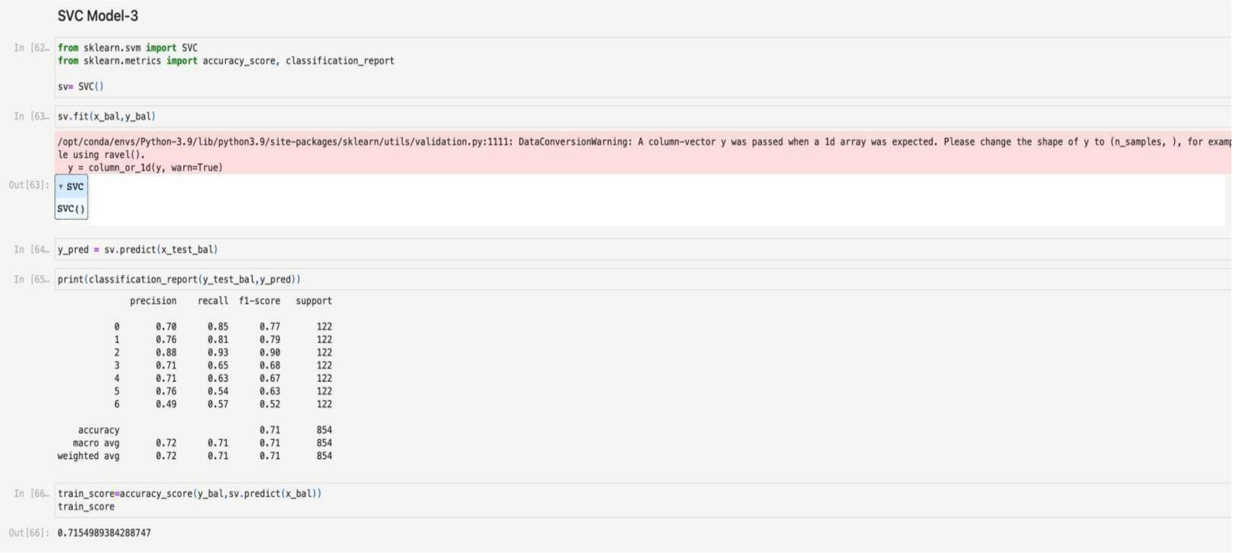
```
In [58… print(classification_report(y_test_bal,y_pred))
```

```
              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))
```

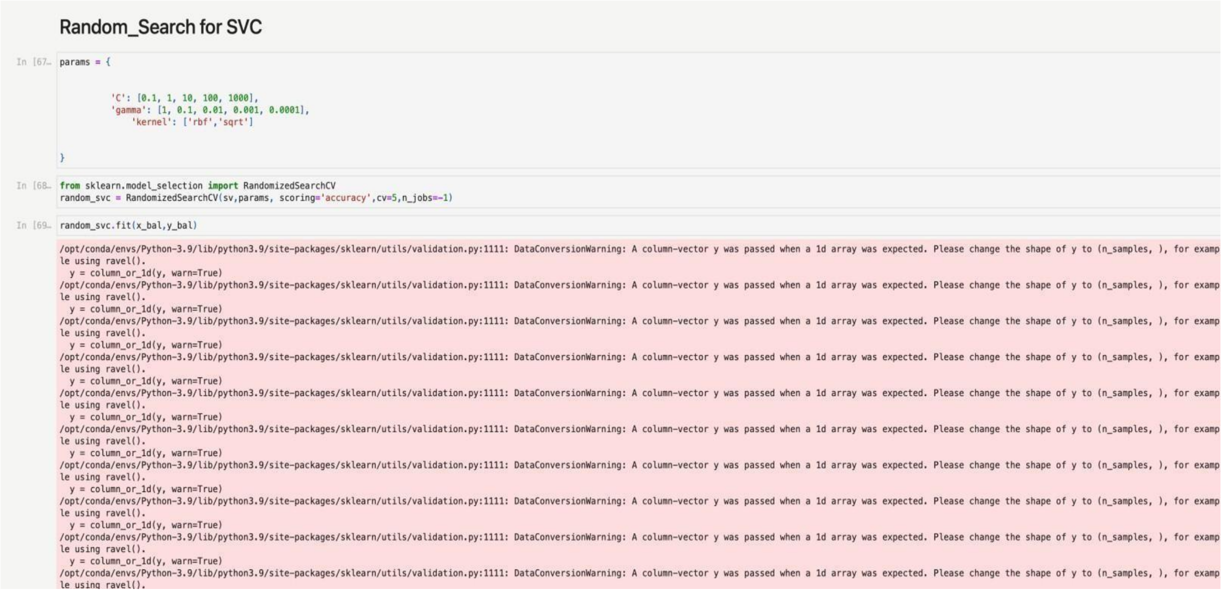
```
In [60… train_score
```

```
Out[60]: 1.0
```



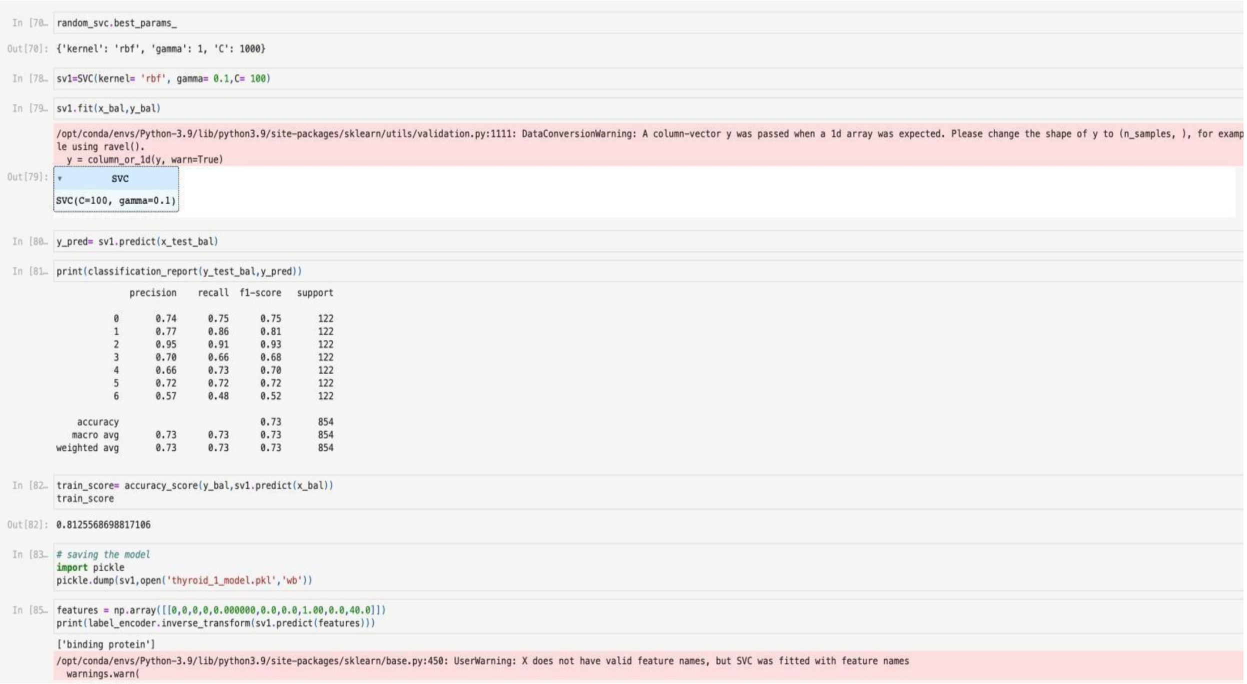
SVC Model-3

```
In [62… from sklearn.svm import SVC
        from sklearn.metrics import accuracy_score, classification_report

        sv= SVC()

In [63… 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 examp
        le using ravel().
          y = column_or_1d(y, warn=True)

Out[63]: ▾ SVC
         SVC()

In [64… y_pred = sv.predict(x_test_bal)

In [65… 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

In [66… train_score=accuracy_score(y_bal,sv.predict(x_bal))
        train_score

Out[66]: 0.7154989384288747
```

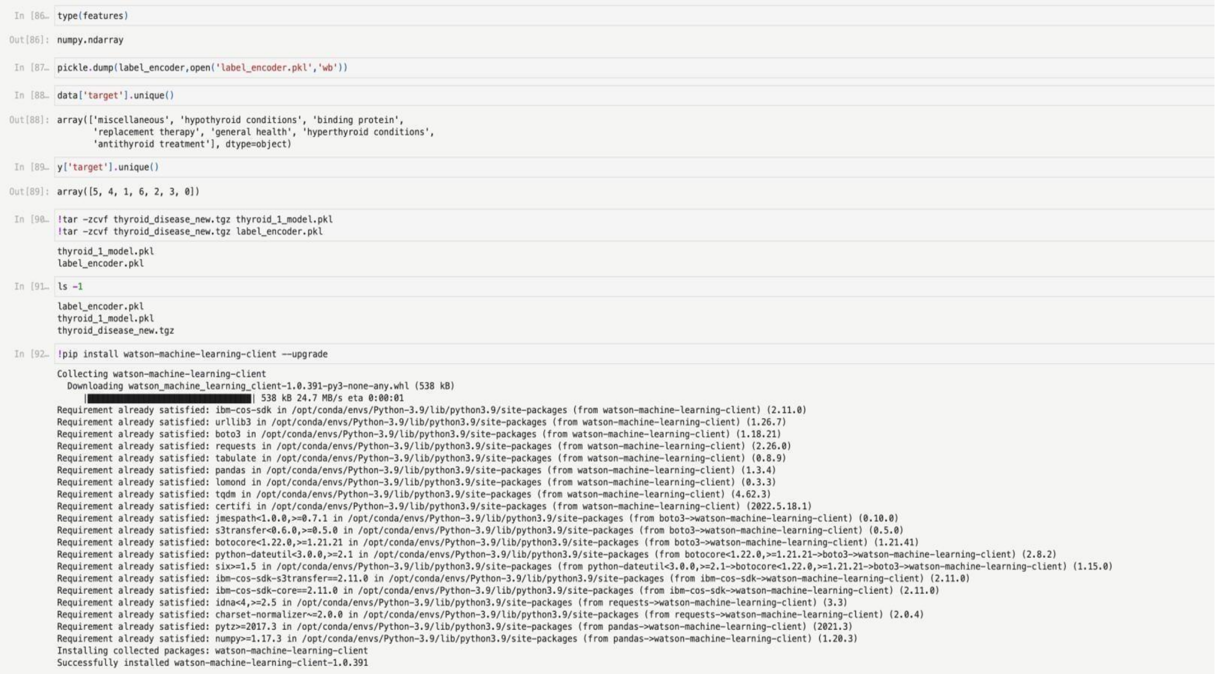


Random_Search for SVC

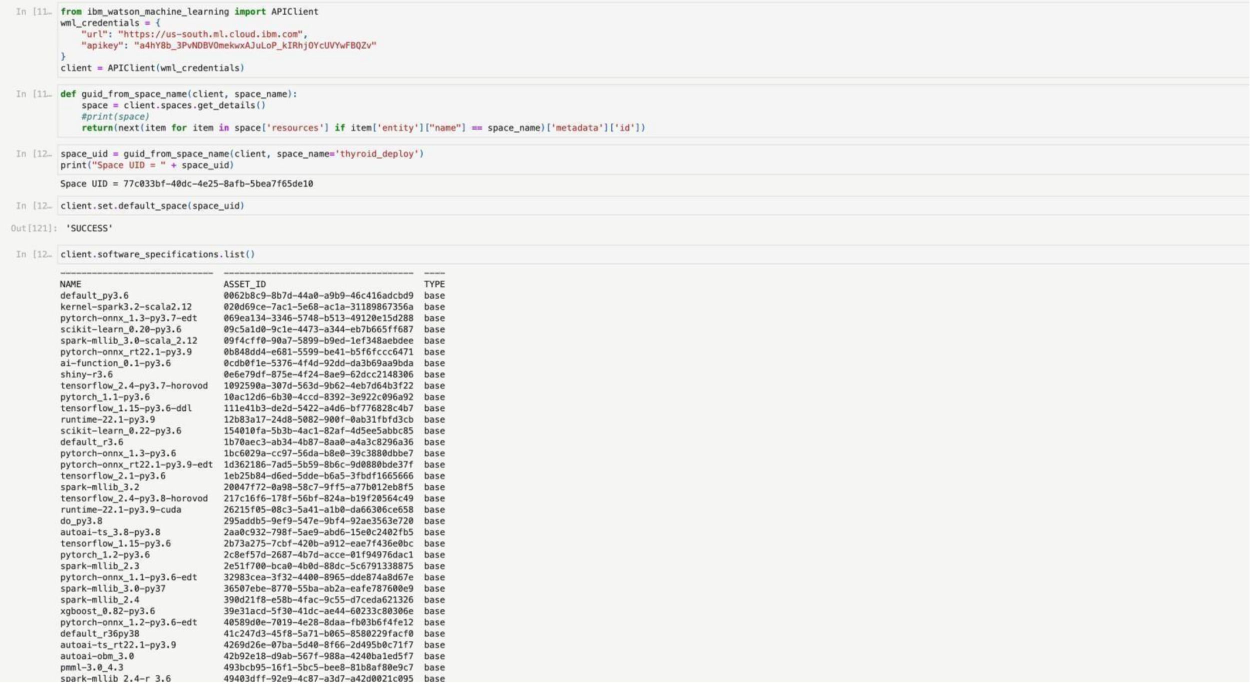
```
In [67… params = {


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


        }

In [68… from sklearn.model_selection import RandomizedSearchCV
        random_svc = RandomizedSearchCV(sv,params, scoring='accuracy',cv=5,n_jobs=-1)

In [69… 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 examp
        le 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 examp
        le 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 examp
        le 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 examp
        le 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 examp
        le 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 examp
        le 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 examp
        le 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 examp
        le 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 examp
        le 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 examp
        le using ravel().
```



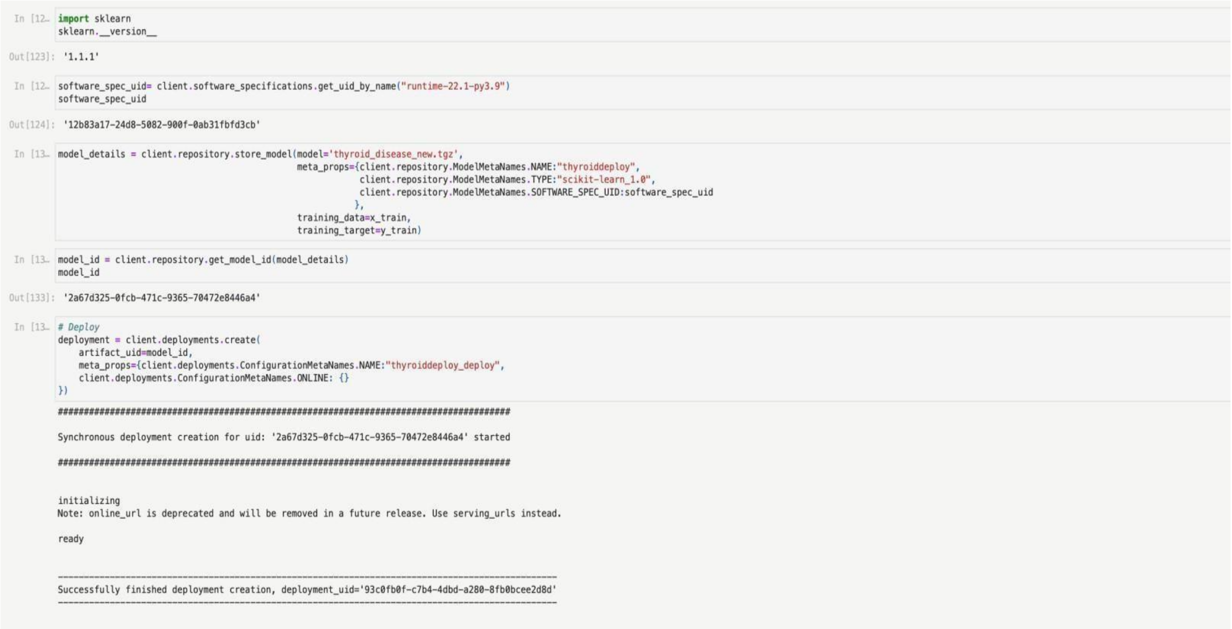
```
In [70… random_svc.best_params_

Out[70]: {'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 examp
         le using ravel().
           y = column_or_1d(y, warn=True)
Out[79]: ▾         SVC
         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       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([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
         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 -zcvf thyroid_disease_new.tgz thyroid_1_model.pkl
         !tar -zcvf thyroid_disease_new.tgz label_encoder.pkl

         thyroid_1_model.pkl
         label_encoder.pkl

In [91… ls -1

         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<1.22.0,>=1.21.21->boto3->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<1.22.0,>=1.21.21->boto3->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_3PvNDBVOmekwxAJuLoP_kIRhjOYcUVYwFBQZv"
        }
        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[121]: '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        09c5a1d0-9c1e-4473-a344-eb7b665ff687  base
        spark-mllib_3.0-scala_2.12     09f4cff0-90a7-5899-b9ed-1ef348aebdee  base
        pytorch-onnx_rt22.1-py3.9      0b848dd4-e681-5599-be41-b5f6fccc6471  base
        ai-function_0.1-py3.6          0cdb0f1e-5376-4f4d-92dd-da3b69aa9bda  base
        shiny-r3.6                     0e6e79df-875e-4f24-8ae9-62dcc2148306  base
        tensorflow_2.4-py3.7-horovod   1092590a-307d-563d-9b62-4eb7d64b3f22  base
        pytorch_1.1-py3.6              10ac12d6-6b30-4ccd-8392-3e922c096a92  base
        tensorflow_1.15-py3.6-ddl      111e41b3-de2d-5422-a4d6-bf776828c4b7  base
        runtime-22.1-py3.9             12b83a17-24d8-5082-900f-0ab31fbfd3cb  base
        scikit-learn_0.22-py3.6        154010fa-5b3b-4ac1-82af-4d5ee5abbc85  base
        default_r3.6                   1b70aec3-ab34-4b87-8aa0-a4a3c8296a36  base
        pytorch-onnx_1.3-py3.6         1bc6029a-cc97-56da-b8e0-39c3880dbbe7  base
        pytorch-onnx_rt22.1-py3.9-edt  1d362186-7ad5-5b59-8b6c-9d0880bde37f  base
        tensorflow_2.1-py3.6           1eb25b84-d6ed-5dde-b6a5-3fbdf1665666  base
        spark-mllib_3.2                20047f72-0a98-58c7-9ff5-a77b012eb8f5  base
        tensorflow_2.4-py3.8-horovod   217c16f6-178f-56bf-824a-b19f20564c49  base
        runtime-22.1-py3.9-cuda        26215f05-08c3-5a41-a1b0-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-eae7f436e0bc  base
        pytorch_1.2-py3.6              2c8ef57d-2687-4b7d-acce-01f94976dac1  base
        spark-mllib_2.3                2e51f700-bca0-4b0d-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-5f30-41dc-ae44-60233c80306e  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-5d40-8f66-2d495b0c71f7  base
        autoai-obm_3.0                 42b92e18-d9ab-567f-988a-4240ba1ed5f7  base
        pmml-3.0_4.3                   493bcb95-16f1-5bc5-bee8-81b8af80e9c7  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]: '12b83a17-24d8-5082-900f-0ab31fbfd3cb'

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'
        ------------------------------------------------------------------------------------------------
```