Thyroid disease Classification using ML

Bachelor of Science
in
Computer Science

Submitted
By

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INTRODUCTION

OVERVIEW

Thyroid diseases,suchas hypothyroid is mandhyper thyroidism, are common end ocrinedisordersthataffect the function of thet hyroidgland. These diseasescan have a significant impacton apatient's healt hand quality of life. Early and accurate diagnosis of thyroid diseases is important for effective treatment.

inrecent years,machine learning techniq ues have been applied to the classification of thyroid diseases.the goal of the sestudiesistodevel opmodels that can accurately diagnose thyroid diseases based on clinicaland 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)andrecurrentneuralnetworks(RNNs).

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

LITERATURESURVEY

EXISTINGPROBLEM

Thecurrentexistingsystemincludes:

Clinical examination: This involves a physical examination of the neck to check for any visible signs ofthyroidenlargementornodules.

Blood tests: Blood tests are used to measure the levels of hormones produced by the thyroid gland and tocheck forantibodiesthatmayindicateautoimmune diseasessuchasHashimoto'sthyroiditis.

Ultrasound: An ultrasound scan can provide images of the thyroid gland and help to identify any nodulesorotherabnormalities.

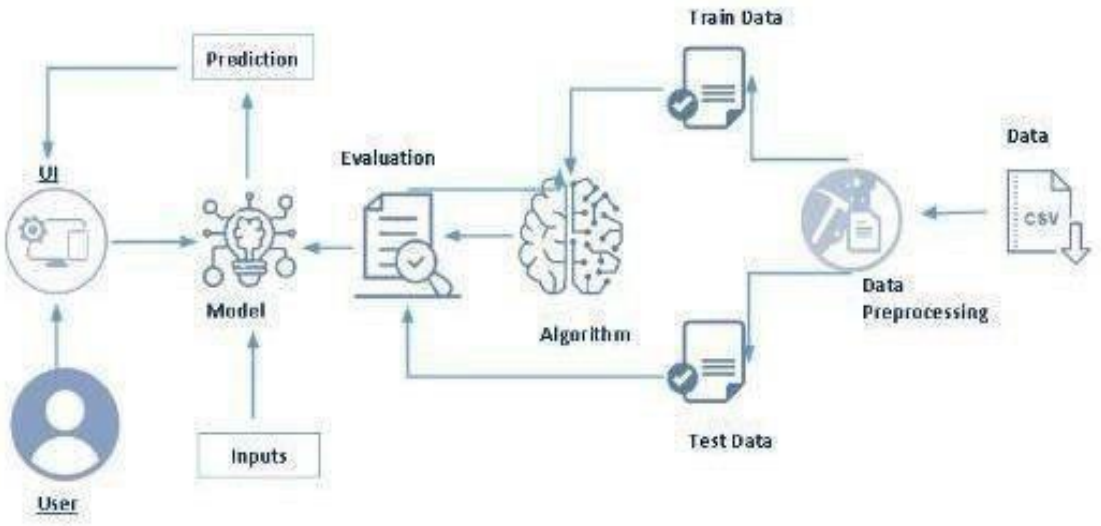
Fine needle aspiration biopsy (FNAB): Thisis a procedure in which a small sample of tissueis takenfrom a thyroid nodule using a fine needle, which is then examined under a microscope to check forcancer.

PROPOSEDSYSTEM

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 algorithmsfor predicting thyroiddiseases. These systems are trained on large datasets of patient data and use various features such asdemographicinformation,bloodtestresults,andultrasoundimagestomakeprediction.

THE ORETICALANALYSIS

BLOCK DIAGRAM



HARDWAREANDSOFTWAREDESIGNING

Python

Pythonisaninterpreted,object-oriented,high-levelprogramminglanguagewithdynamicsemantics. It was created by Guido van Rossum, and first released on February 20, 1991. Itshigh-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 gluelanguagetoconnectexistingcomponentstogether.Python'ssimple,easytolearnsyntaxemphasize s readability and therefore reduces the cost of program maintenance. Python supportsmodules and packages, which encourages program modularity and code reuse. The Pythoninterpreter and the extensive standard library are available in source or binary form withoutchargeforallmajorplatforms,andcanbefreelydistributed.

AnacondaNavigator

AnacondaNavigatorisafreeandopen-sourcedistributionofthePythonandRprogramminglanguagesfor data science and machine learning related applications. It can be installed on Windows, Linux, andmacOS. Conda is an open-source, cross platform,packagemanagement system. Anacondacomeswith

soverynicetoolslikeJupyterLab,JupyterNotebook,QtConsole,Spyder,Glueviz,Orange,Rstudio,VisualStudioCode.Forthisproject,wewillbeusingJupyternotebookandSpyder.

JupyterNotebook

The Jupyter Notebook is an open-source web application that you can use to create and sharedocumentsthatcontainlivecode,equations,visualizations,andtext.JupyterNotebookismaintained by the people at Project Jupyter. Jupyter Notebooks are a spin-off project from theIPythonproject,whichusedtohaveanIPythonNotebookprojectitself.Thename,Jupyter,comesfrom the core supported programming languages that it supports: Julia, Python, and R. Jupyterships with the IPython kernel, which allows you to write your programs in Python, but there arecurrentlyover100otherkernelsthatyoucanalsouse

Spyder

Spyder,theScientificPythonDevelopmentEnvironment,isafreeintegrateddevelopmentenvironment(IDE)thatisincludedwithAnaconda.Itincludesediting,interactivetesting,debugging, and introspection features. Initially created and developed by Pierre Raybaut in 2009,since2012Spyderhasbeenmaintained andcontinuouslyimprovedbya teamofscientificPythondevelopers and the community. Spyderis extensible with first-party and third party pluginsincludessupport for interactive tools for data inspection and embeds Python specific code. SpyderisalsopreinstalledinAnaconda Navigator,whichisincludedinAnaconda.

Flask

Web frame work used for building. It is a web application framework written in python whichwill be running in local browser with a user interface. In this application, whenever the userinteractswithUIandselectsemoji,itwillsuggestthebestandtopmoviesofthatgenretotheuse.

HardwareRequirements:

o Operatingsystem:window7andabovewith64bitoProcessorType-IntelCorei3-3220

o RAM:4Gbandabove

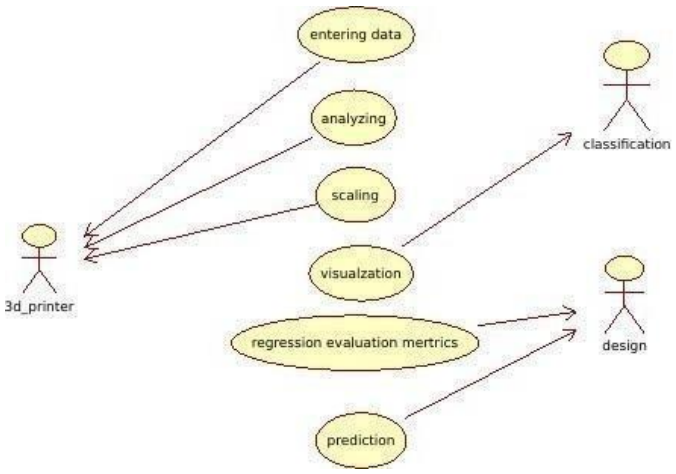
o Harddisk:min100GB

EXPERIMENTALINVESTIGATION

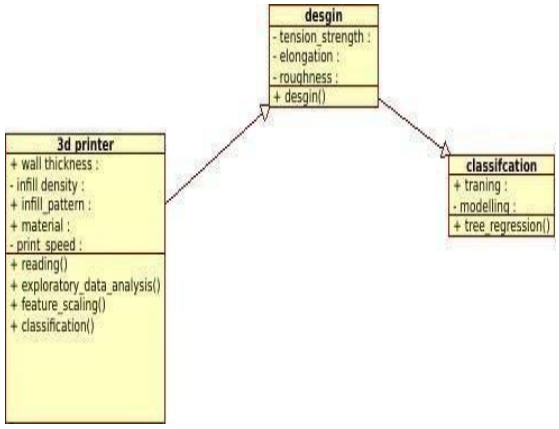
Here we are going to build a machine learning model that predicts whether the given message is aspamornot,based on these parameters a supervised machine learning model is built to predict the best

Material to beused for building 3Dmodels.A web application is build so that the user can type in the mention departameters and the material which suits the best is show case don UI.

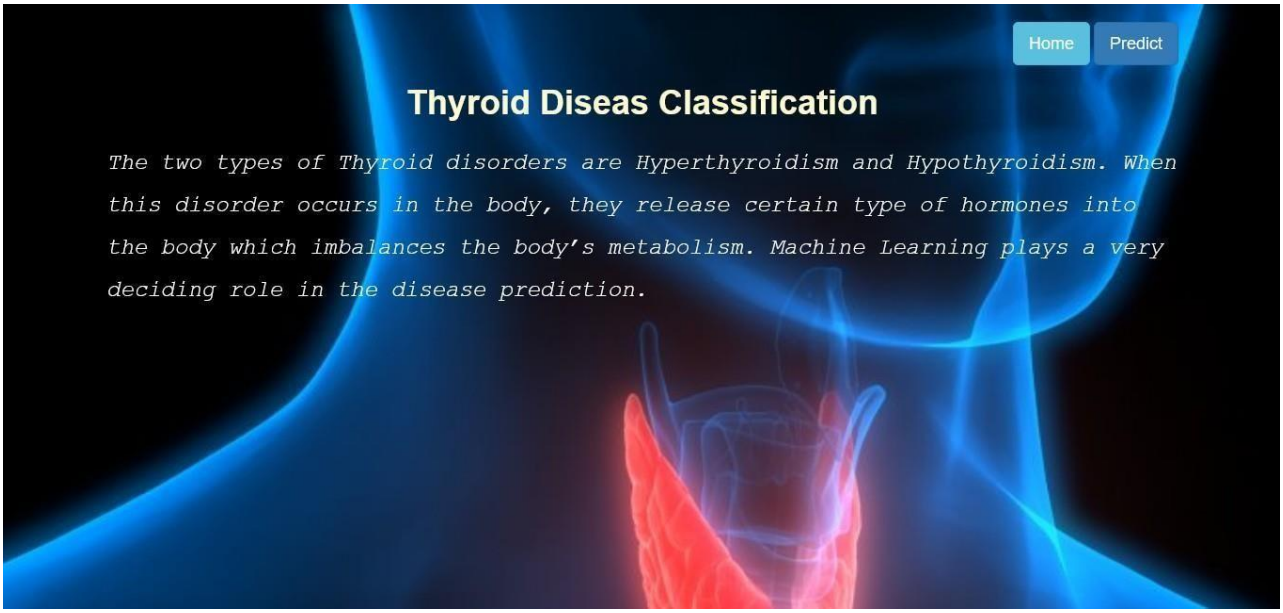
FLOWCHART

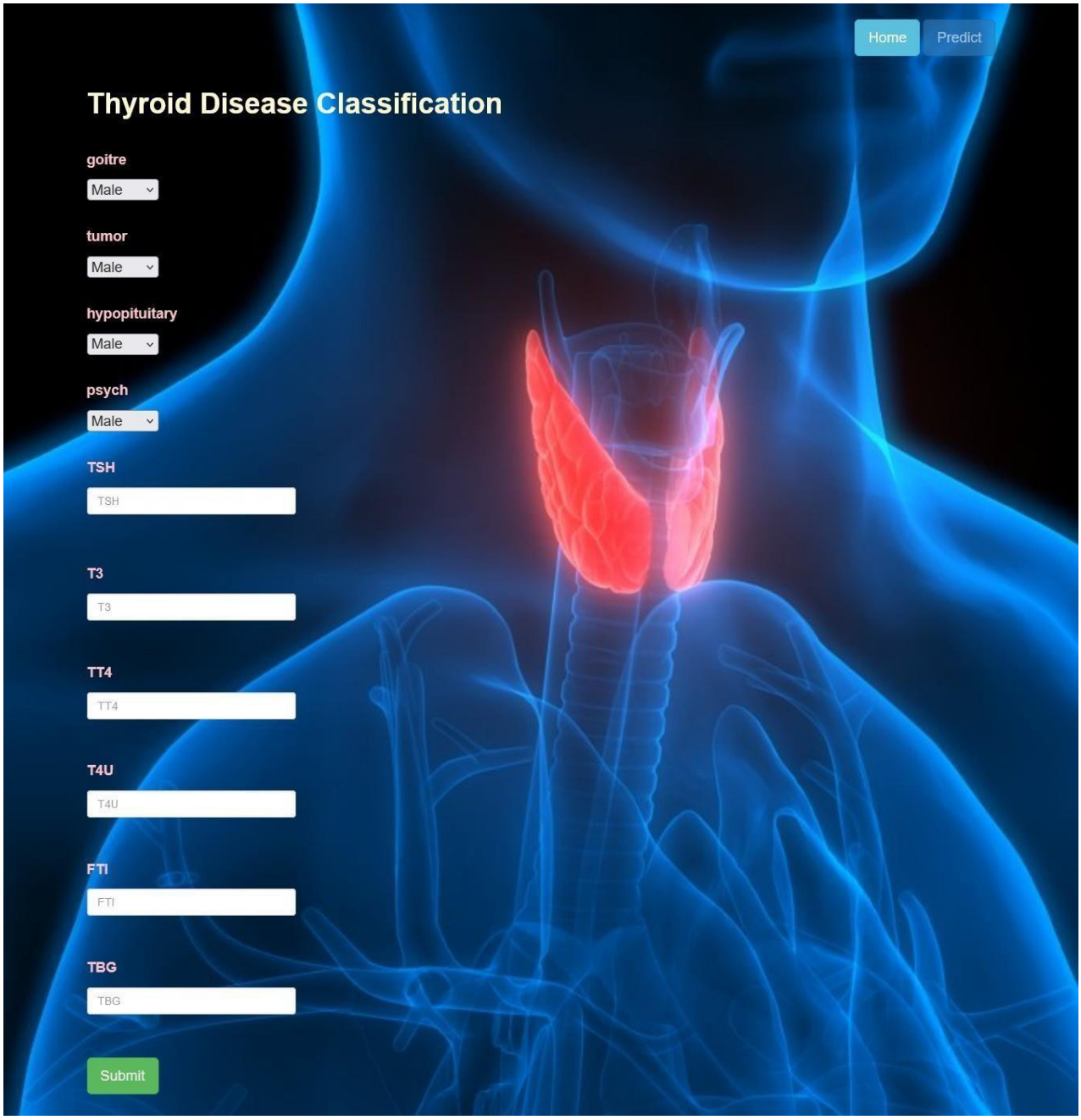


USECASEDIAGRAM



1. RESULT


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


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}}.

2.ADVANTAGES&DISADVANTAGES

ADVANTAGES

- Easytouse
- Costefficient
- Timeefficient

DISADVANTAGE

1. Initialcostsofprinter
2. Postprocessing
3. Printingtime
4. Specialskillrequiredfor3Dmodels
5. ManufacturingJobLosses

8. Applications

3D printing has gone through a number of changes over the years. In the early days, 3D printing wastime-consuming and costly, and not very practical for applications outside of industry. However, with theadventoftoday's moreflexibleandcost-effective3Dprintingmethods,thereareareaswhere3Dprintinghasbecomeapracticaltool.

Itisapplicableindifferentsectorssuchas

- EngineeringAndDesign
- Consumerproducts
- Manufacturing
- Education
- Aerospace
- Medical
- Movies/Theatres
- Architectures

9. CONCLUSION

3D printing technology could revolutionize and re-shape the world. Advance in 3D technology cansignificantlychangeandimprovethe waywe manufacture productsgoods worldwide.
If the last industrial revolution brought us mass production and the advent of economics of scale – thedigital 3D printing revolution could bring mass manufacturing back a full of circle – to an era of masspersonalization,andreturntoindividualcraftsmanship.

10. FUTURESCOPE

Future applications for 3D printing might include creating open-source scientific equipment to createopensourcelabs
Science-basedapplicationslikereconstructingfossilsinpalaeontology.Replicatingancientandpricelessartifacts inarchaeology
Reconstructingbonesandbodypartsinforensicpathology.Thetechnologycurrentlybeingresearchedforbuildi ngconstruction.

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='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 × 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
```

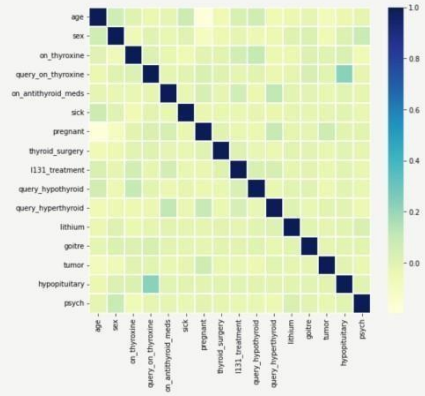
In [ ]:

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
```

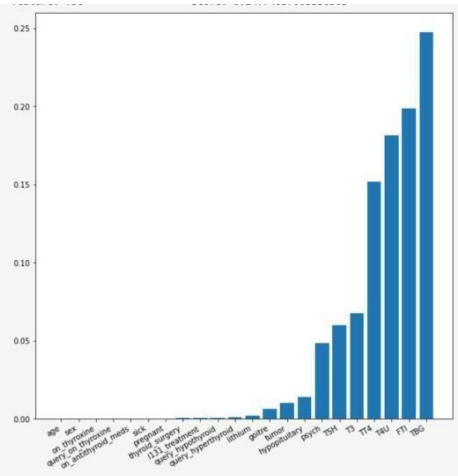
performing feature importance

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: 0.0003639672429481155 4
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: 0.048528965726417 96
feature: TSH                  Score: 0.05987261146496816
feature: T3                   Score: 0.06781922960266909
feature: TT4                  Score: 0.15195632393084 62
feature: T4U                  Score: 0.18161965423111 92
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(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'
------------------------------------------------------------------------------------------------
```