GOVERNMENT OF TAMILNADU

Naan Muthalvan - Project-Based Experiential Learning

Thyroid Disease Classification Using Machine Learning

Submitted by

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Under the guidance of

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Guest Lecturer

PG and Research Department of Computer Science

M.V.MUTHIAH GOVERNMENT ARTS COLLEGE FOR WOMEN

(Affiliated To Mother Teresa Women's University, Kodaikanal)

Reaccredited with "A" Grade by NAAC

DINDIGUL-624001.

APRIL - 2023

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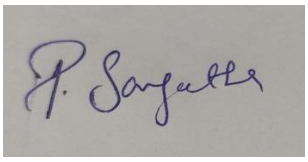
PG & RESEARCH DEPARTMENT OF COMPUTER SCIENCE
BONAFIDE CERTIFICATE

This is to certify that this is a bonafide record of the project entitled, "Thyroid Disease Classification Using Machine Learning" done by Ms.K.AGALYA (20326ER039), Ms.A.AMEERA BANU (20326ER040) , Ms. P. ANUPRIYA (20326ER041) ,Ms.A.ARUL AKILA (20326ER042). This is Submitted in partial fulfillment for the award of the degree of Bachelor of Science in Computer Science in M.V.MUTHIAH GOVERNMENT ARTS COLLEGE FOR WOMEN,DINDIGUL during the period of December 2022 to April 2023.



Project Mentor(s) **Head of the Department**

Submitted for viva-voce Examination held on 11.04.2023

Thyroid Disease Classification Using Machine Learning

TABLE OF CONTENTS

1 INTRODUCTION

1.1 Overview

The Thyroid gland is a vascular gland and one of the most important organs of the human body. This gland secretes two hormones which help in controlling the metabolism of the body. The two types of Thyroid disorders are Hyperthyroidism and Hypothyroidism. When this disorder occurs in the body, they release certain types of hormones into the body which imbalances the body's metabolism. A thyroid-related Blood test is used to detect this disease but it is often blurred and noise will be present Thyroid disease is a common endocrine disorder that affects millions of people worldwide. It is a complex disease that can manifest in many different ways, making diagnosis and treatment challenging for clinicians. Machine learning algorithms have shown promise in aiding the classification of thyroid disease, using data-driven approaches to identify patterns and make accurate predictions. . Machine Learning algorithms, SVM - support vector machine, Random Forest Classifier, XGB Classifier and ANN - Artificial Neural Networks are used to predict the patient's risk of getting thyroid disease. The web app is created to get data from users to predict the type of disease.

1.2 Purpose

Machine learning algorithms can help improve the accuracy and efficiency of thyroid disease diagnosis by analyzing large amounts of data from diverse sources, such as medical records, laboratory tests, and imaging studies. These algorithms can learn from the data and develop models that can accurately classify different types of thyroid diseases based on their features and characteristics.

The use of machine learning algorithms for thyroid disease classification can also help reduce the time and cost involved in diagnosis, leading to faster and more efficient patient care. Additionally, these algorithms can help identify patterns and correlations in the data that may not be apparent to

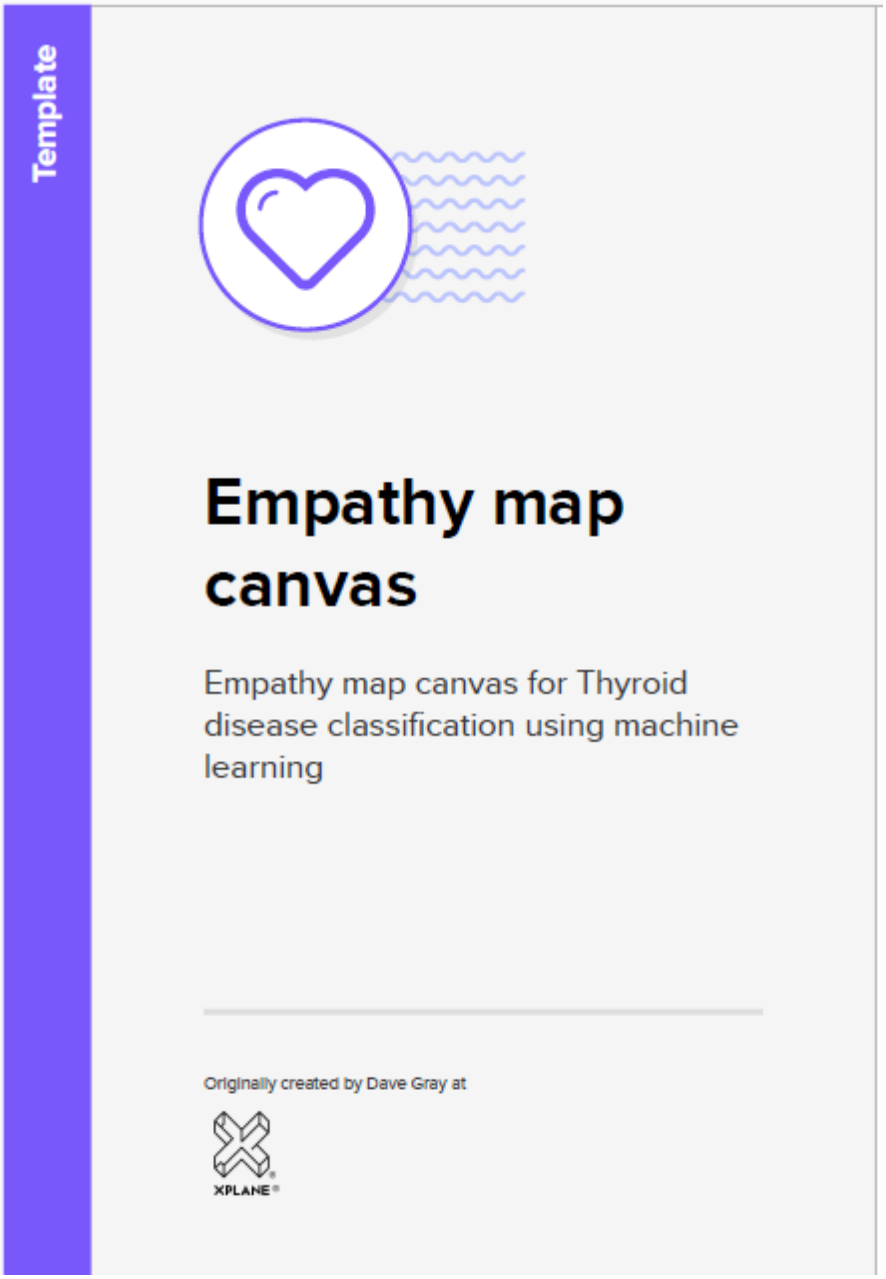
human clinicians, leading to improved understanding of thyroid diseases and better treatment outcomes.

2. Define Problem / Problem Understanding

2.1 Empathy map

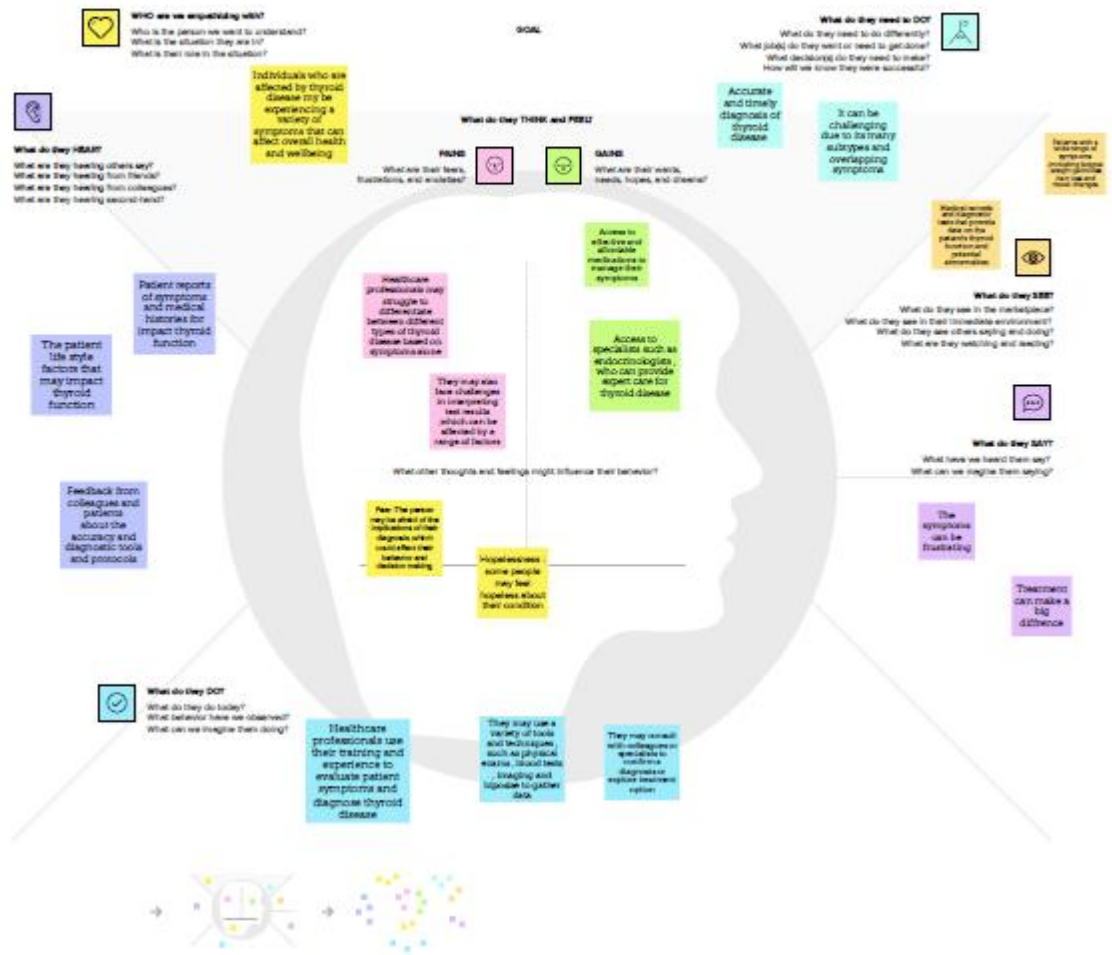
The empathy map is a tool used in design thinking and customer experience design to better understand the needs and experiences of customers or users. It is a simple framework that helps

teams develop empathy for their users by visualizing their thoughts, feelings, and behaviors.



Develop shared understanding and empathy

Summarize the data you have gathered related to the people that are impacted by your work. It will help you generate ideas, prioritize features, or discuss decisions.



2.2 Ideation & Brainstorming Map

Brainstorming is a process of generating creative and innovative ideas through group discussion and collaboration. It is typically used in the early stages of a project or problem-solving process to generate a wide range of ideas without judgment or criticism.

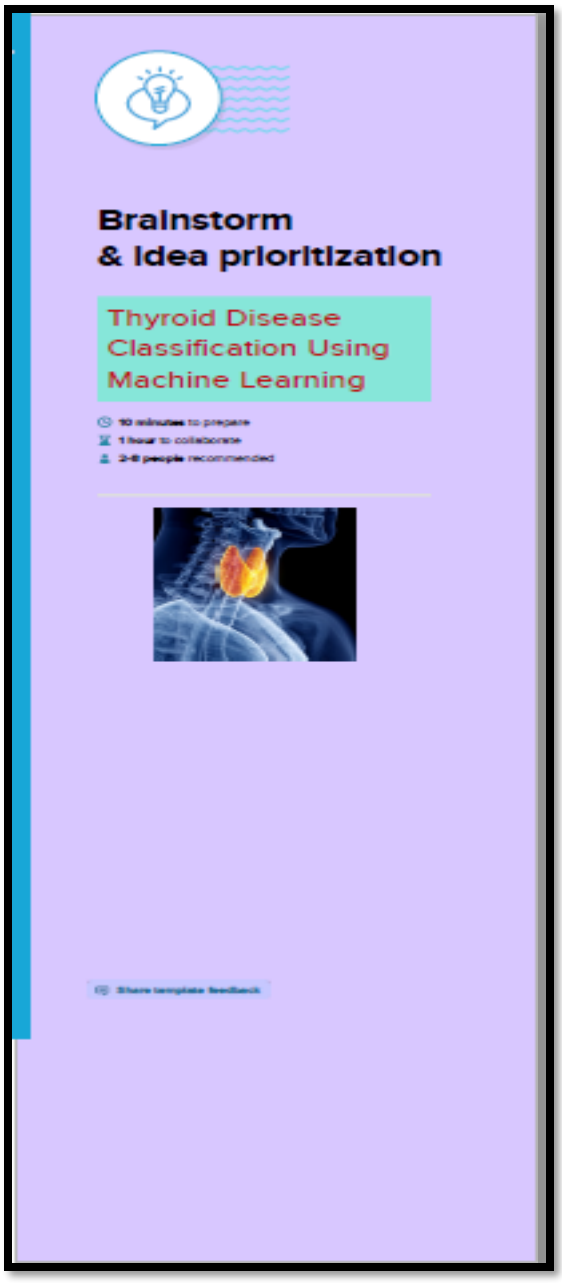
Here are some tips for effective brainstorming:

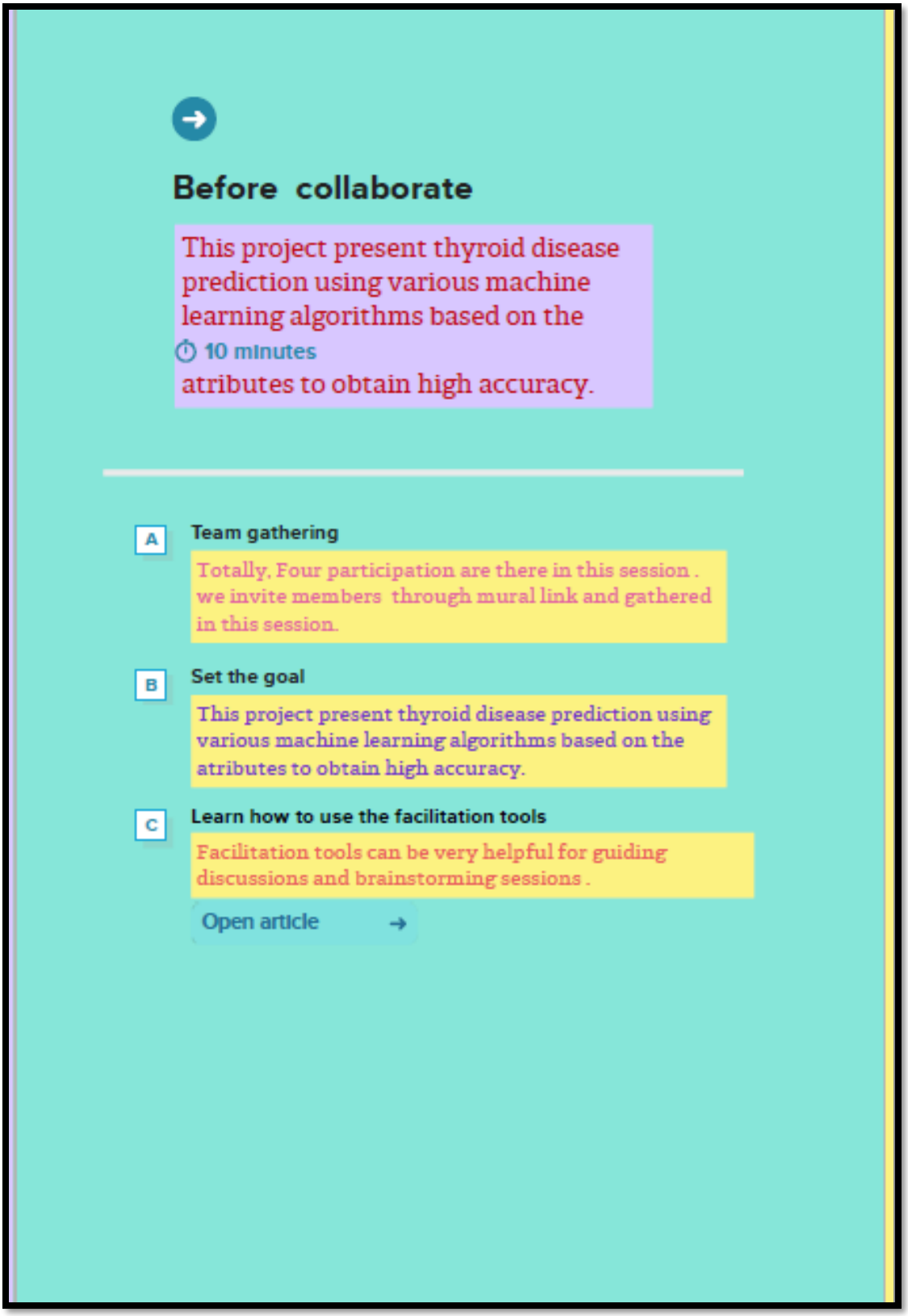
Set clear goals and objectives: Before starting the brainstorming session, it's essential to define the problem or challenge you want to address and set clear goals and objectives for the session.

Encourage participation: Encourage all participants to contribute their ideas and opinions, no matter how unconventional or outlandish they may seem. The goal is to generate as many ideas as possible.

Avoid criticism and judgment: Criticism and judgment can stifle creativity and prevent participants from sharing their ideas. Encourage participants to build on each other's ideas and avoid negative feedback.

Use visual aids: Visual aids such as whiteboards, sticky notes, and mind maps can help participants organize and visualize their ideas and facilitate group discussion.


Brainstorm
& Idea prioritization
Thyroid Disease Classification Using Machine Learning


Before collaborate
This project present thyroid disease prediction using various machine learning algorithms based on the
10 minutes
atributes to obtain high accuracy.
A
Team gathering
Totally, Four participation are there in this session . we invite members through mural link and gathered in this session.
B
Set the goal
This project present thyroid disease prediction using various machine learning algorithms based on the atributes to obtain high accuracy.
C
Learn how to use the facilitation tools
Facilitation tools can be very helpful for guiding discussions and brainstorming sessions .
Open article

1

Problem statement

1.The Thyroid Disease can be easily identify based on symptoms in the patient's history.

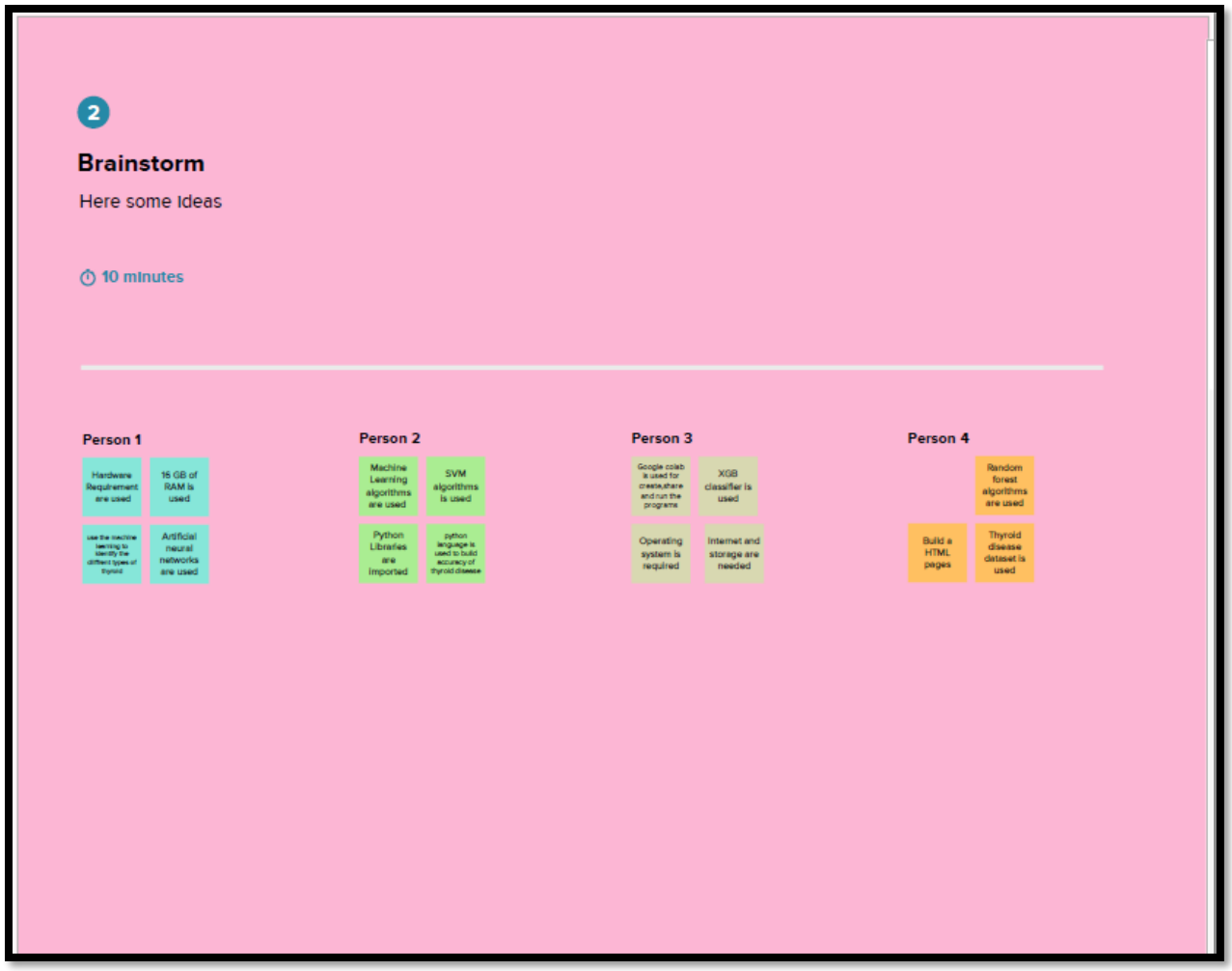
5 minutes

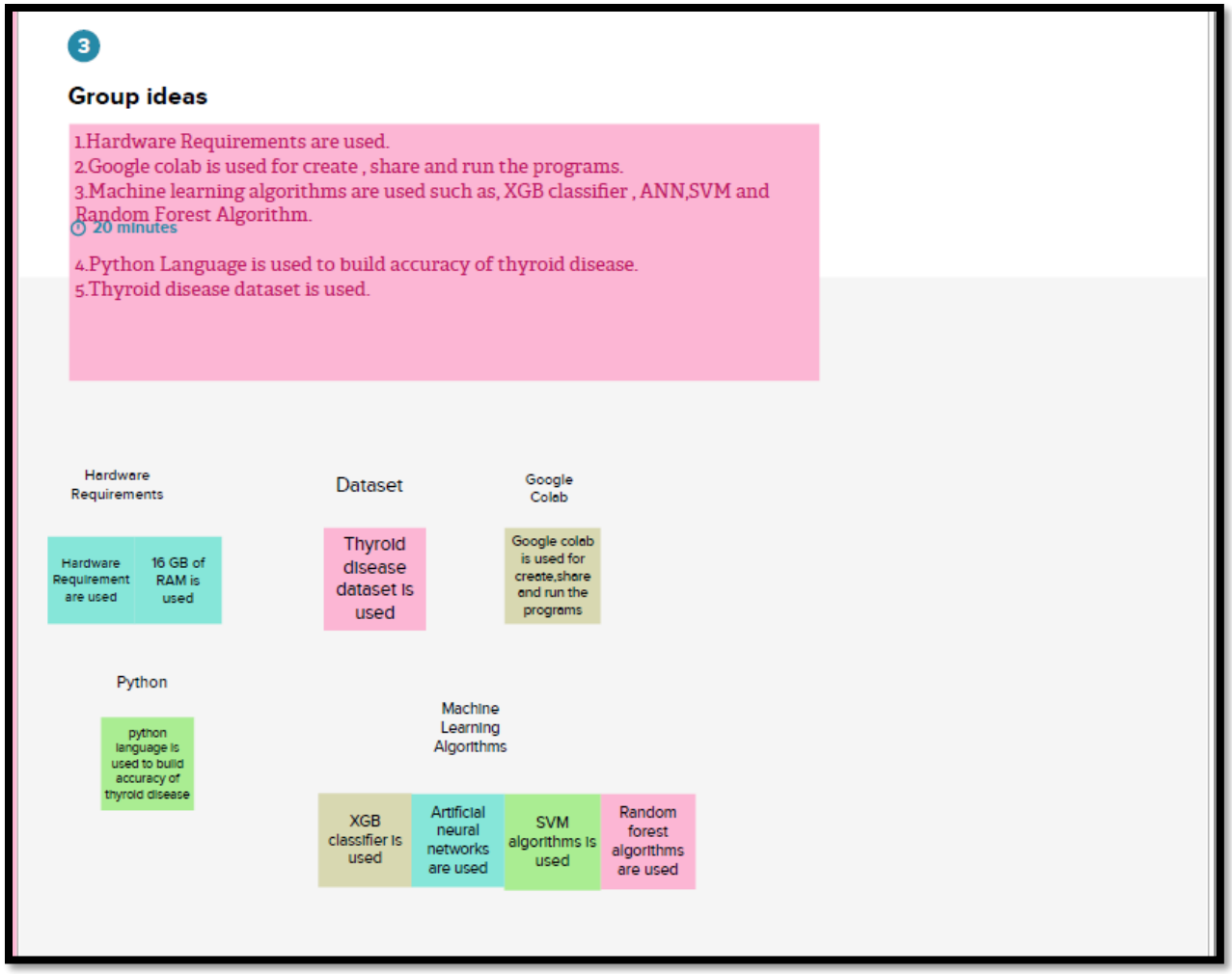
2.Thyroid disease is a medical condition that affects the function of the thyroid gland

3.This project present thyroid disease predction using various machine learning algorithms based on the atributes to obtain high accuracy

4.That dataset create for this project is apply from the kaggle thyroid disease dataset.

5.The important of feature show be estimated to select the option number of features thyroid disease classification.

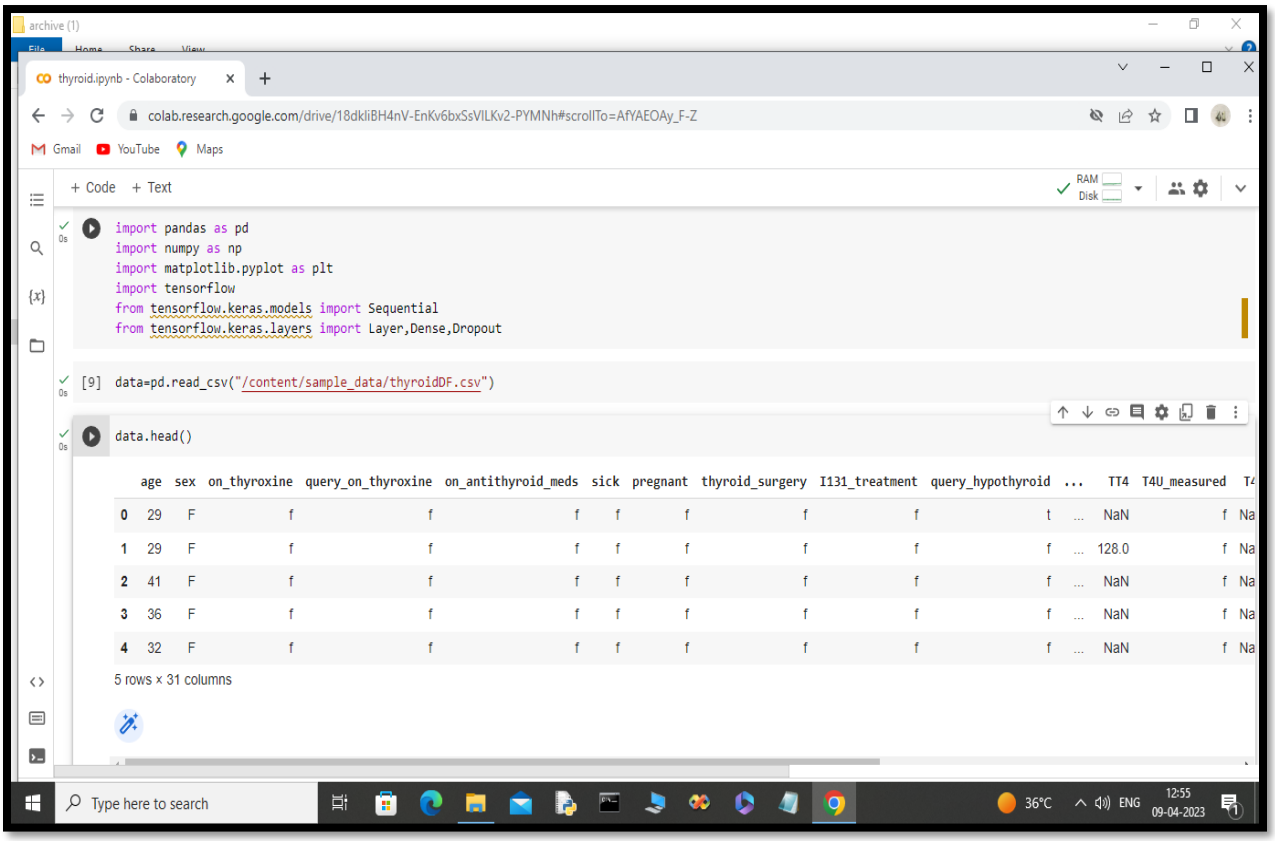

2
Brainstorm
Here some ideas
10 minutes
Person 1
Hardware Requirement are used
16 GB of RAM is used
use the machine learning to identify the different types of thyroid
Artificial neural networks are used
Person 2
Machine Learning algorithms are used
SVM algorithms is used
Python Libraries are imported
python language is used to build accuracy of thyroid disease
Person 3
Google colab is used for create,share and run the programs
XGB classifier is used
Operating system is required
Internet and storage are needed
Person 4
Random forest algorithms are used
Build a HTML pages
Thyroid disease dataset is used

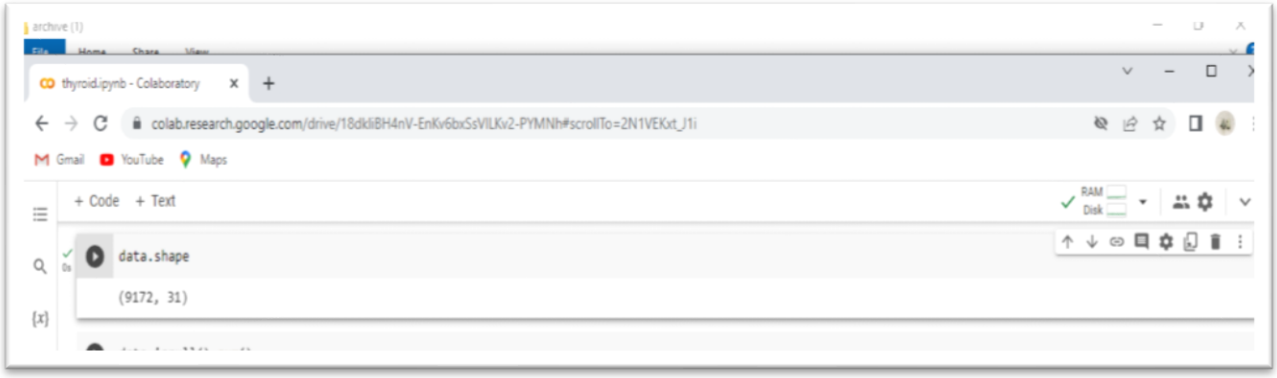

3
Group ideas
1.Hardware Requirements are used.
2.Google colab is used for create , share and run the programs.
3.Machine learning algorithms are used such as, XGB classifier , ANN,SVM and Random Forest Algorithm.
20 minutes
4.Python Language is used to build accuracy of thyroid disease.
5.Thyroid disease dataset is used.
Hardware Requirements
Hardware Requirement are used
16 GB of RAM is used
Dataset
Thyroid disease dataset is used
Google Colab
Google colab is used for create,share and run the programs
Python
python language is used to build accuracy of thyroid disease
Machine Learning Algorithms
XGB classifier is used
Artificial neural networks are used
SVM algorithms is used
Random forest algorithms are used


4
Prioritize
Prioritize the ideas
20 minutes
Feasibility


After collaborate
we can export the mural as pdf to share . It is helpful to getting information.

3 SCREEN LAYOUT

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RAM
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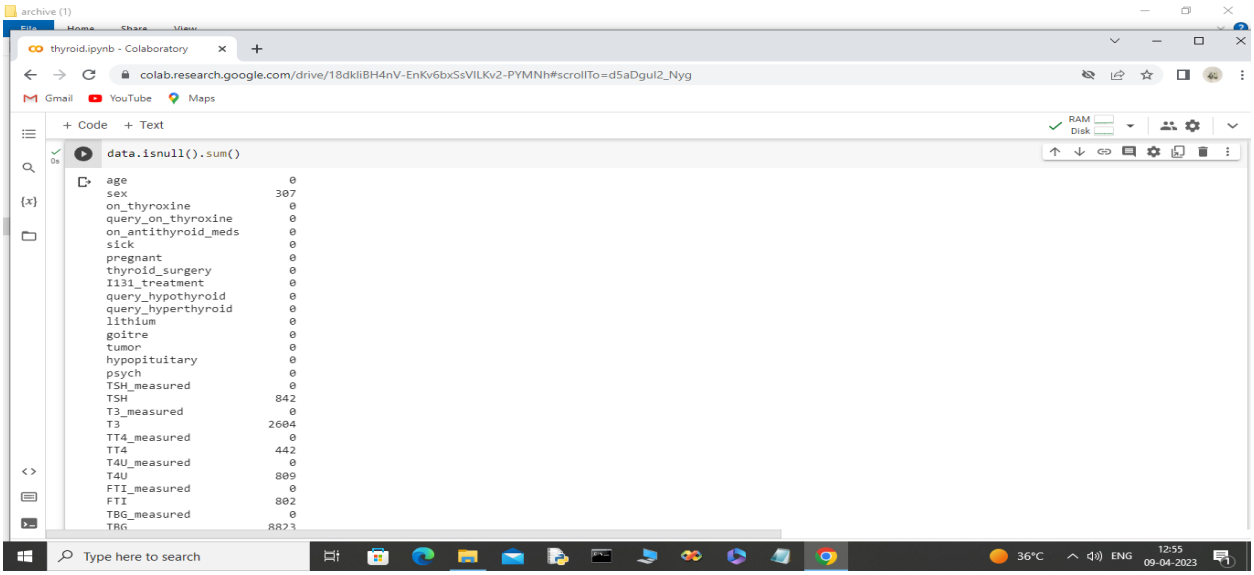
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Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
data.isnull().sum()
age 0
sex 307
on_thyroxine 0
query_on_thyroxine 0
on_antithyroid_meds 0
sick 0
pregnant 0
thyroid_surgery 0
I131_treatment 0
query_hypothyroid 0
query_hyperthyroid 0
lithium 0
goitre 0
tumor 0
hypopituitary 0
psych 0
TSH_measured 0
TSH 842
T3_measured 0
T3 2604
TT4_measured 0
TT4 442
T4U_measured 0
T4U 809
FTI_measured 0
FTI 802
TBG_measured 0
TBG 8823
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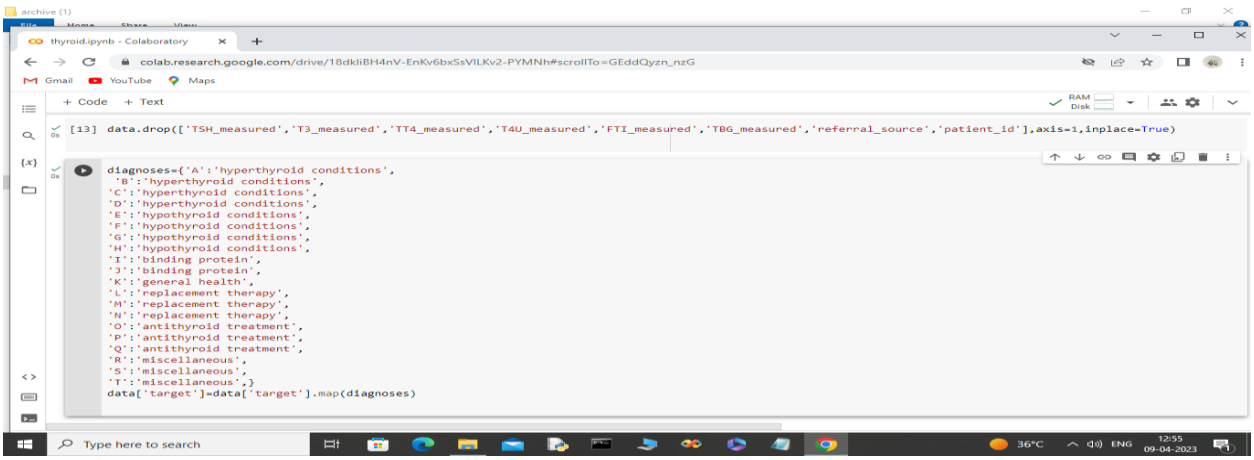
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colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=GEddQyzn_nzG
+ Code + Text
[13] data.drop(['TSH_measured','T3_measured','TT4_measured','T4U_measured','FTI_measured','TBG_measured','referral_source','patient_id'],axis=1,inplace=True)
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)
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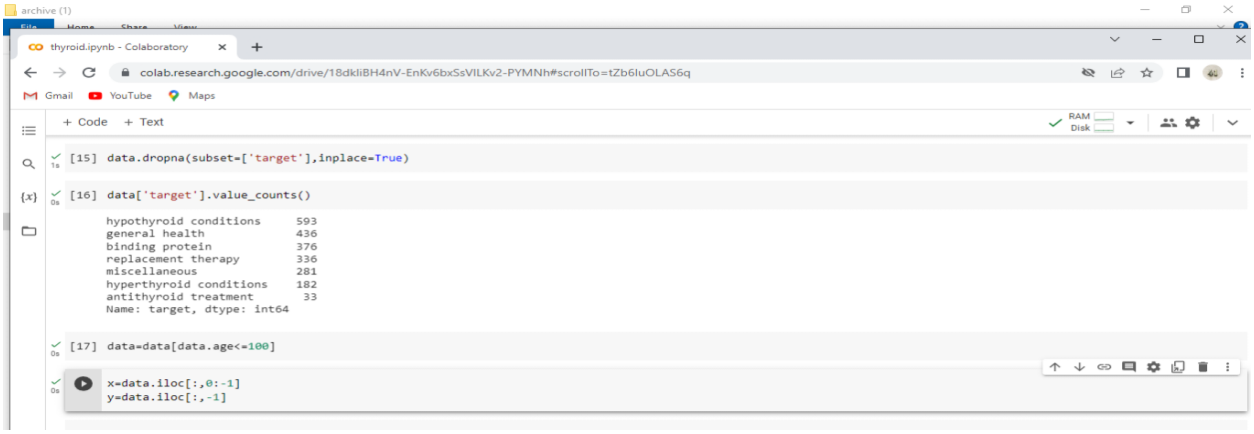
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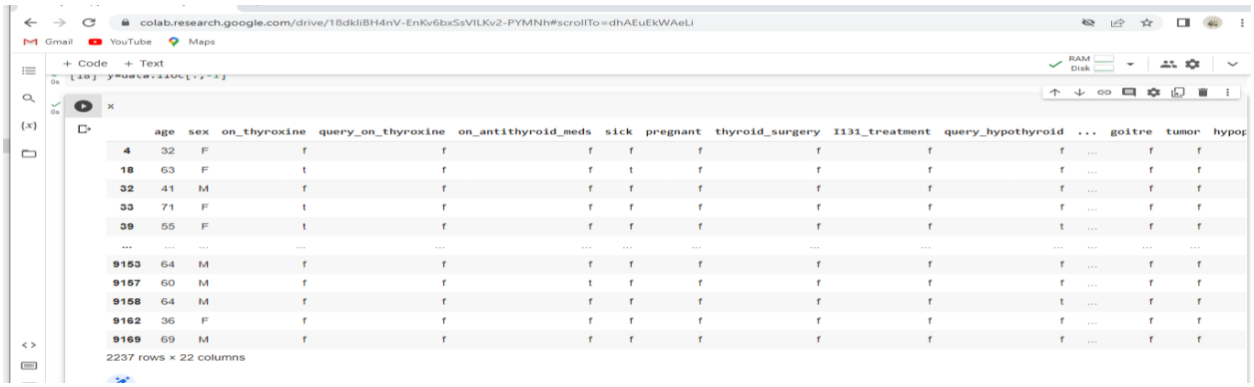
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=tZb6luOLAS6q
+ Code + Text
[15] data.dropna(subset=['target'],inplace=True)
[16] data['target'].value_counts()
hypothyroid conditions 593
general health 436
binding protein 376
replacement therapy 336
miscellaneous 281
hyperthyroid conditions 182
antithyroid treatment 33
Name: target, dtype: int64
[17] data=data[data.age<=100]
x=data.iloc[:,0:-1]
y=data.iloc[:,-1]



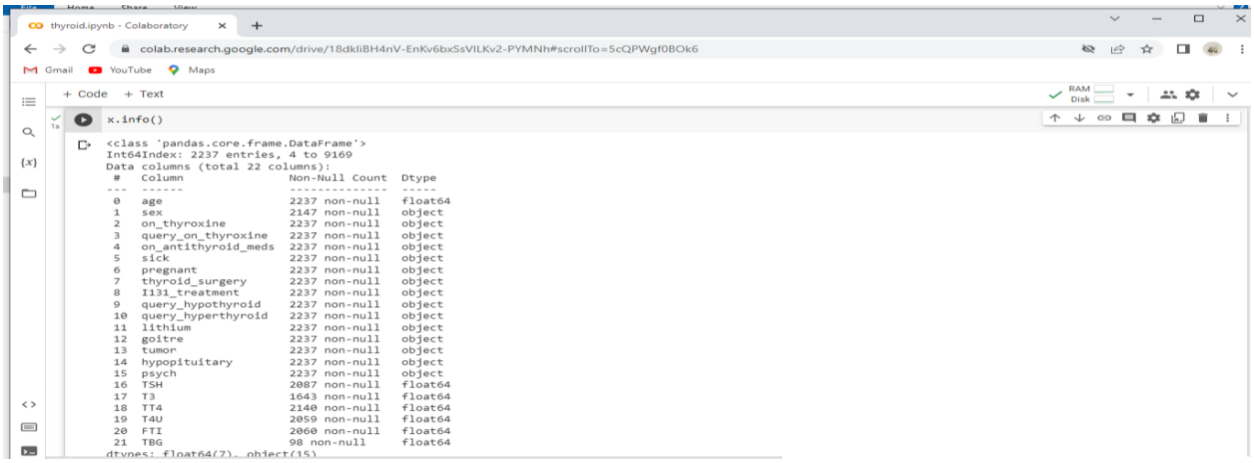
	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumor	hypop
4	32	F	f	f	f	f	f	f	f	f	...	f	f	
18	63	F	t	f	f	t	f	f	f	f	...	f	f	
32	41	M	f	f	f	f	f	f	f	f	...	f	f	
33	71	F	t	f	f	f	f	f	f	f	...	f	f	
39	55	F	t	f	f	f	f	f	f	t	...	f	f	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	
9153	64	M	f	f	f	f	f	f	f	f	...	f	f	
9157	60	M	f	f	t	f	f	f	f	f	...	f	f	
9158	64	M	f	f	f	f	f	f	f	t	...	f	f	
9162	36	F	f	f	f	f	f	f	f	f	...	f	f	
9169	69	M	f	f	f	f	f	f	f	f	...	f	f	

2237 rows × 22 columns

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

F    1611
M     536
Name: sex, dtype: int64
```

```
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')
```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RAM
Disk
x.info()
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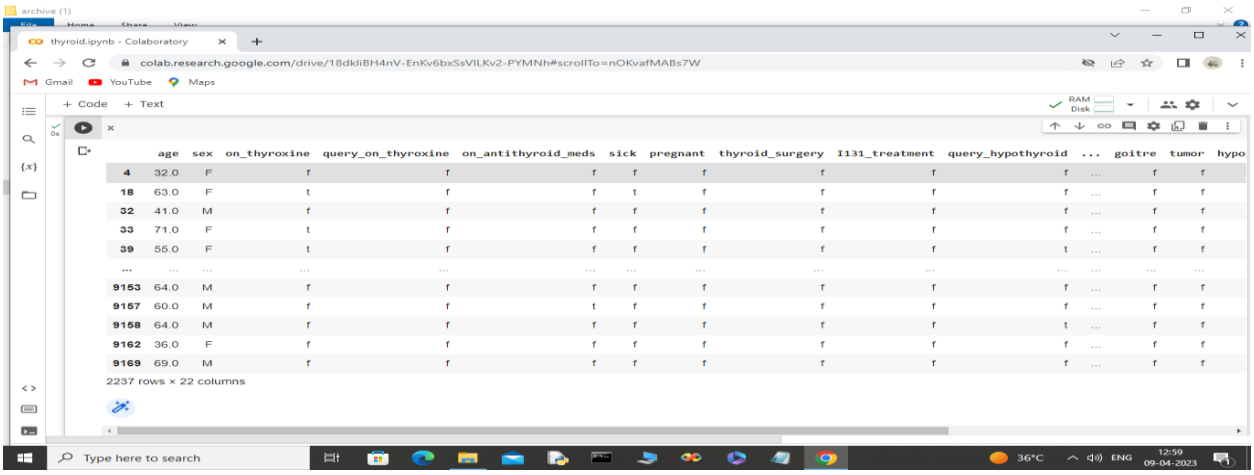
Int64Index: 2237 entries, 4 to 9169
Data columns (total 22 columns):
Column Non-Null Count Dtype
--- ------ -------------- -----
0 age 2237 non-null float64
1 sex 2147 non-null object
2 on_thyroxine 2237 non-null object
3 query_on_thyroxine 2237 non-null object
4 on_antithyroid_meds 2237 non-null object
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
dtypes: float64(7), object(15)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4 32.0 F f f f f f f f f ... f f
18 63.0 F t f f f f f f f ... f f
32 41.0 M f f f f f f f f ... f f
33 71.0 F t f f f f f f f ... f f
39 55.0 F t f f f f f f t ... f f
... ...
9153 64.0 M f f f f f f f f ... f f
9157 60.0 M f f t f f f f f ... f f
9158 64.0 M f f f f f f f t ... f f
9162 36.0 F f f f f f f f f ... f f
9169 69.0 M f f f f f f f f ... f f
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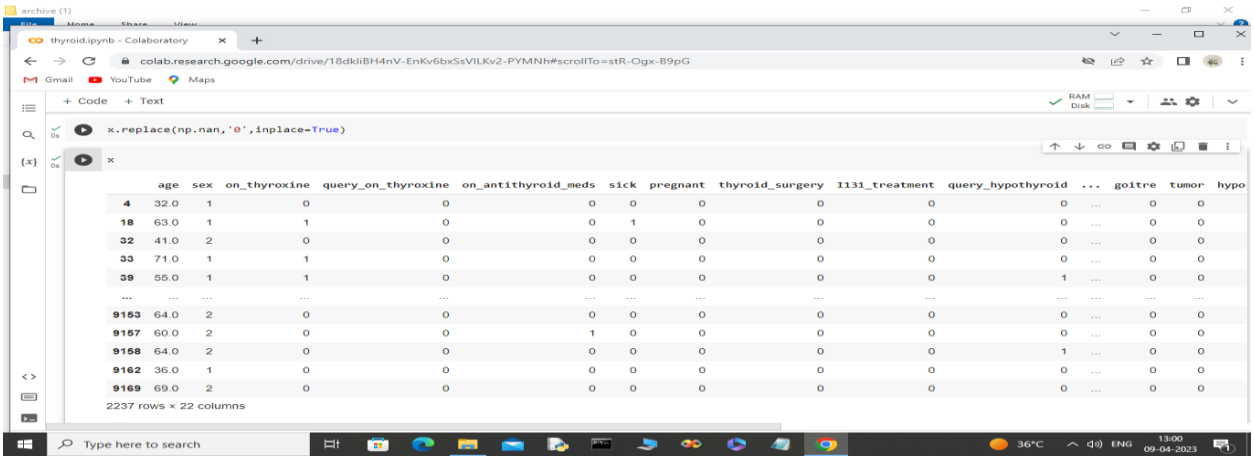
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Gmail
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RAM
Disk
x.replace(np.nan,'0',inplace=True)
x
age sex on_thyroxine query_on_thyroxine on_antithyroid_meds sick pregnant thyroid_surgery I131_treatment query_hypothyroid ... goitre tumor hypo
4 32.0 1 0 0 0 0 0 0 0 0 ... 0 0
18 63.0 1 1 0 0 1 0 0 0 0 ... 0 0
32 41.0 2 0 0 0 0 0 0 0 0 ... 0 0
33 71.0 1 1 0 0 0 0 0 0 0 ... 0 0
39 55.0 1 1 0 0 0 0 0 0 1 ... 0 0
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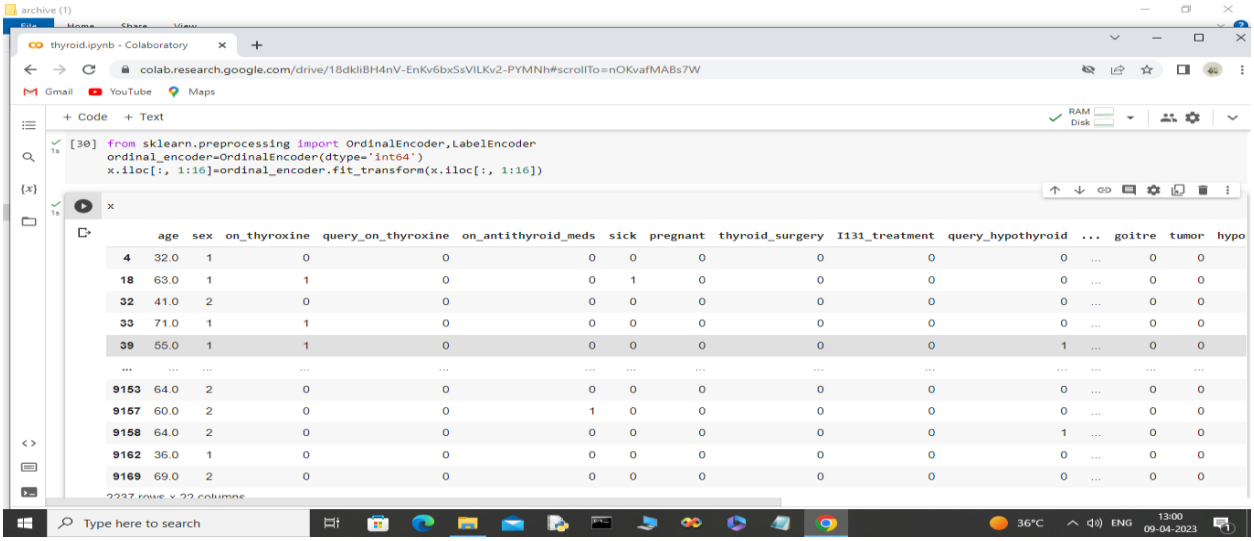
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Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
[30] from sklearn.preprocessing import OrdinalEncoder,LabelEncoder
ordinal_encoder=OrdinalEncoder(dtype='int64')
x.iloc[:, 1:16]=ordinal_encoder.fit_transform(x.iloc[:, 1:16])
x
age sex on_thyroxine query_on_thyroxine on_antithyroid_meds sick pregnant thyroid_surgery I131_treatment query_hypothyroid ... goitre tumor hypo
4 32.0 1 0 0 0 0 0 0 0 0 ... 0 0
18 63.0 1 1 0 0 1 0 0 0 0 ... 0 0
32 41.0 2 0 0 0 0 0 0 0 0 ... 0 0
33 71.0 1 1 0 0 0 0 0 0 0 ... 0 0
39 55.0 1 1 0 0 0 0 0 0 1 ... 0 0
... ...
9153 64.0 2 0 0 0 0 0 0 0 0 ... 0 0
9157 60.0 2 0 0 1 0 0 0 0 0 ... 0 0
9158 64.0 2 0 0 0 0 0 0 0 1 ... 0 0
9162 36.0 1 0 0 0 0 0 0 0 0 ... 0 0
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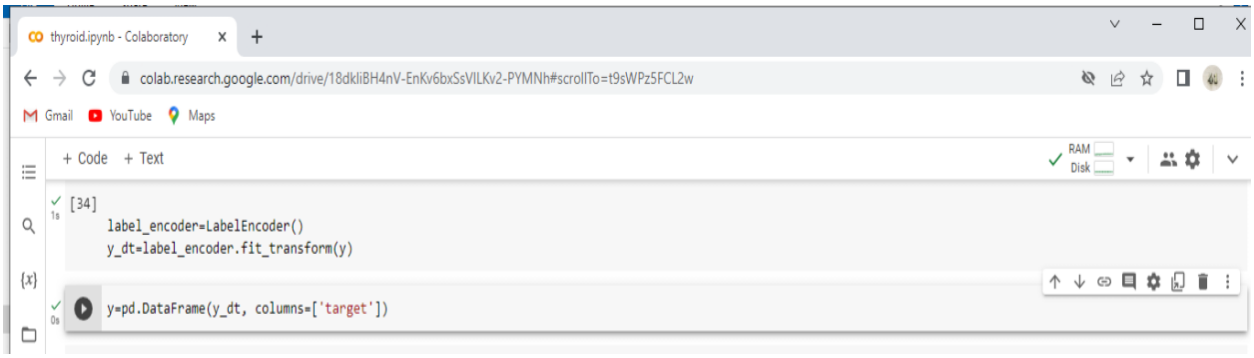
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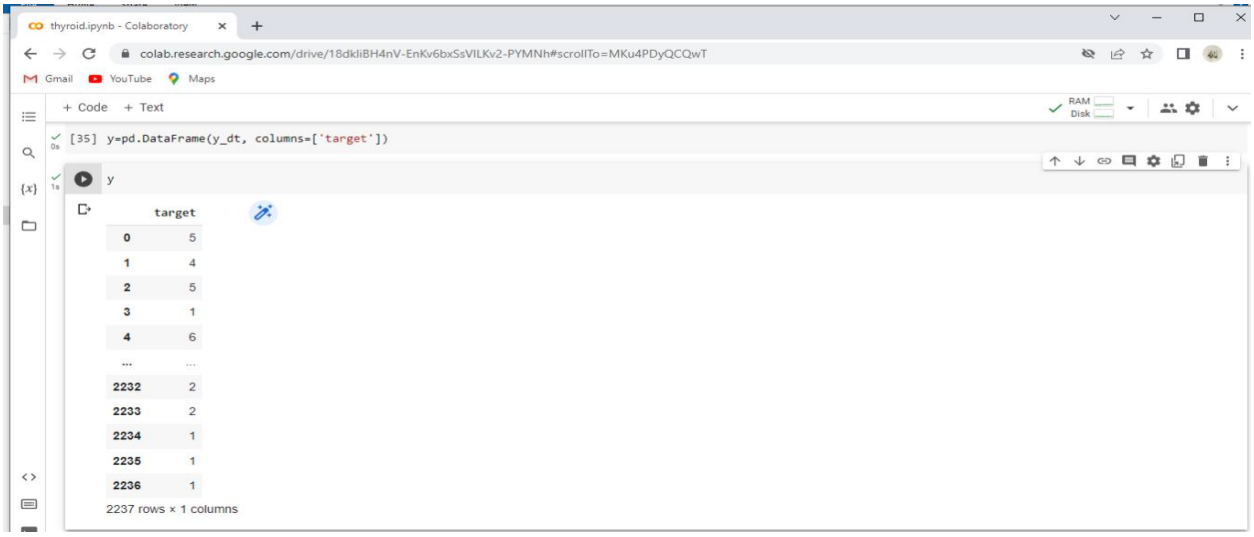
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=t9sWPz5FCL2w
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
[34]
label_encoder=LabelEncoder()
y_dt=label_encoder.fit_transform(y)
y=pd.DataFrame(y_dt, columns=['target'])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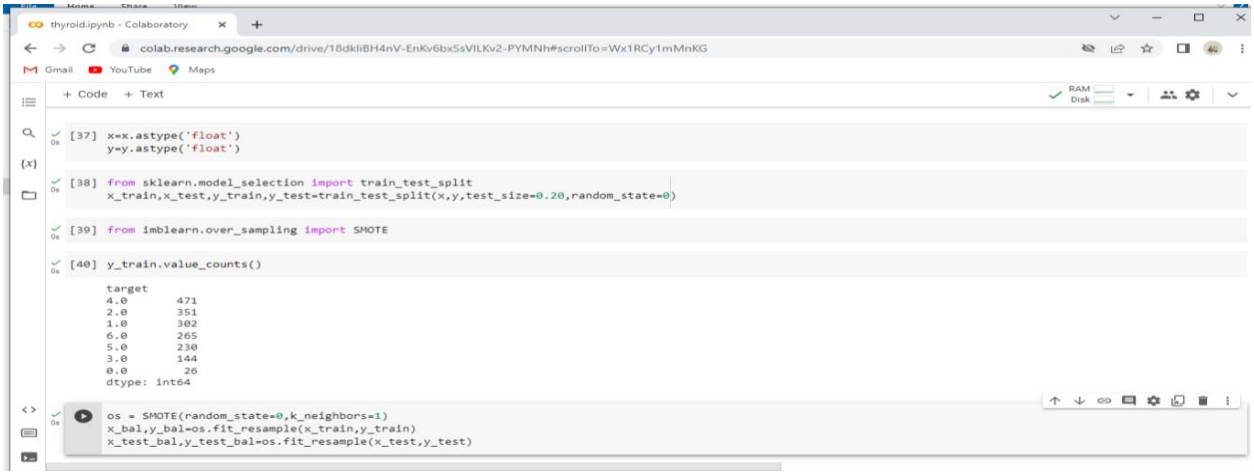
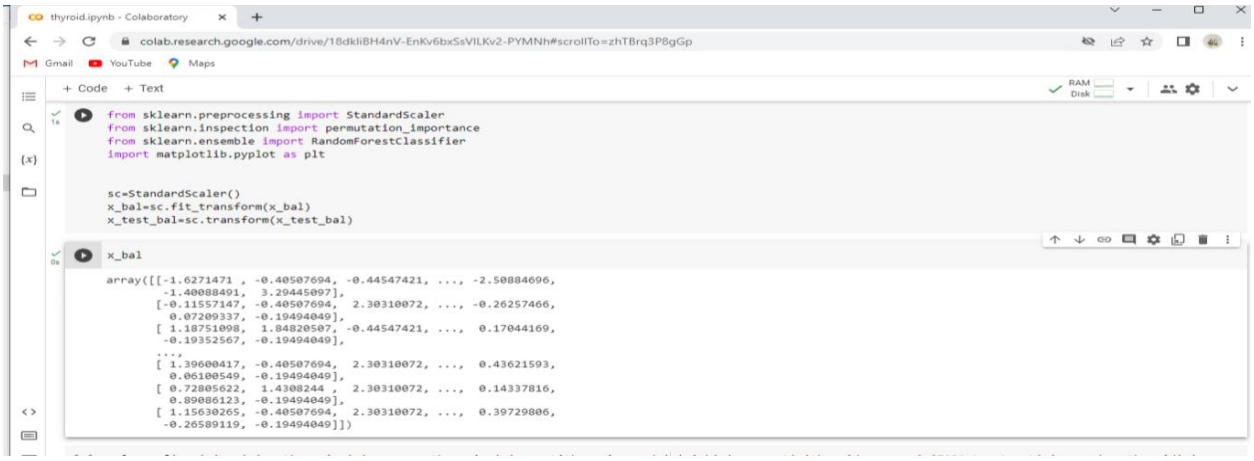
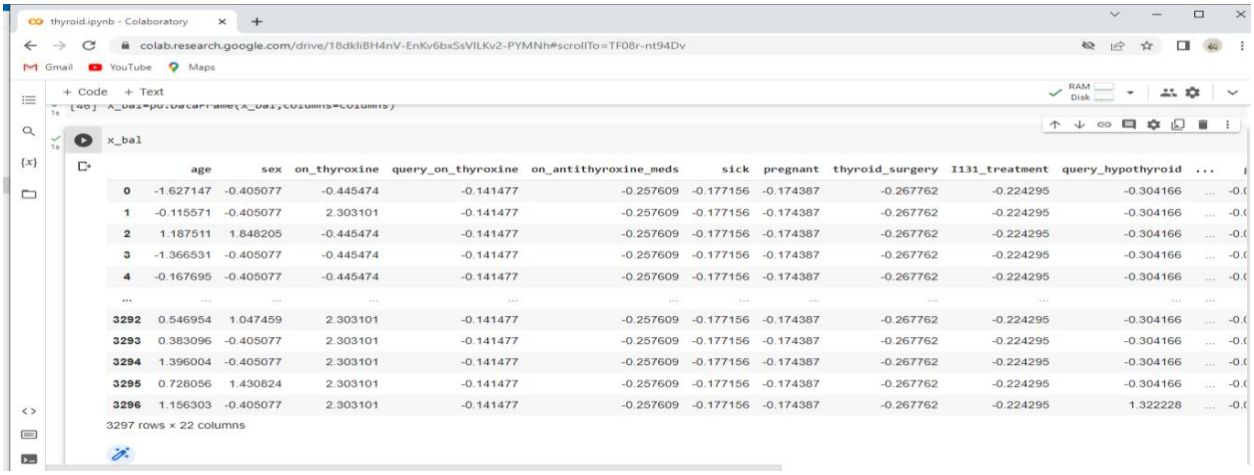
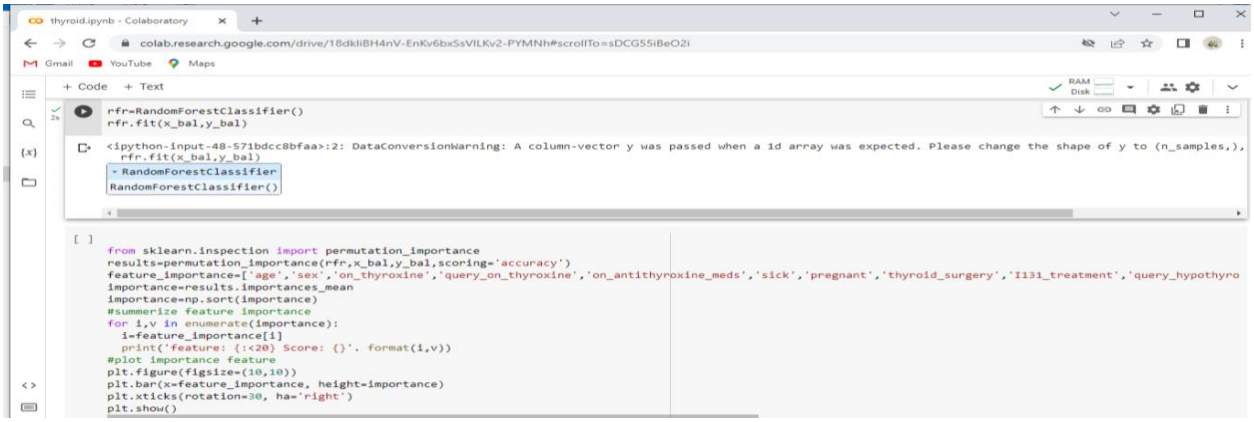
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
[35] y=pd.DataFrame(y_dt, columns=['target'])
y
target
0 5
1 4
2 5
3 1
4 6
... ...
2232 2
2233 2
2234 1
2235 1
2236 1
2237 rows × 1 columns

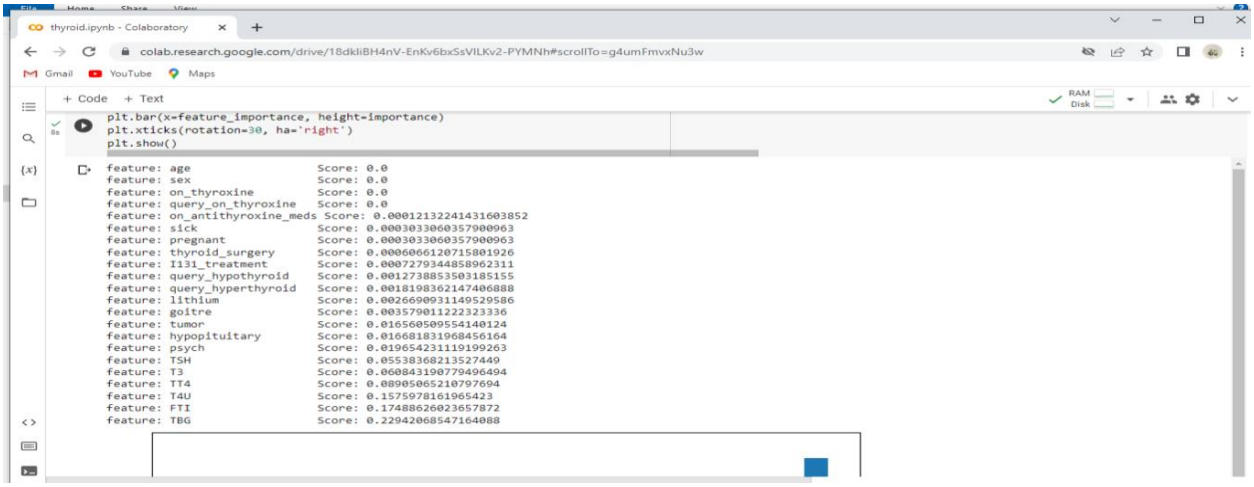

thyroid.ipynb - Colaboratory
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=Wx1RCy1mMnKG
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
[37] x=x.astype('float')
y=y.astype('float')
[38] from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.20,random_state=0)
[39] from imblearn.over_sampling import SMOTE
[40] y_train.value_counts()
target
4.0 471
2.0 351
1.0 302
6.0 265
5.0 230
3.0 144
0.0 26
dtype: int64
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)

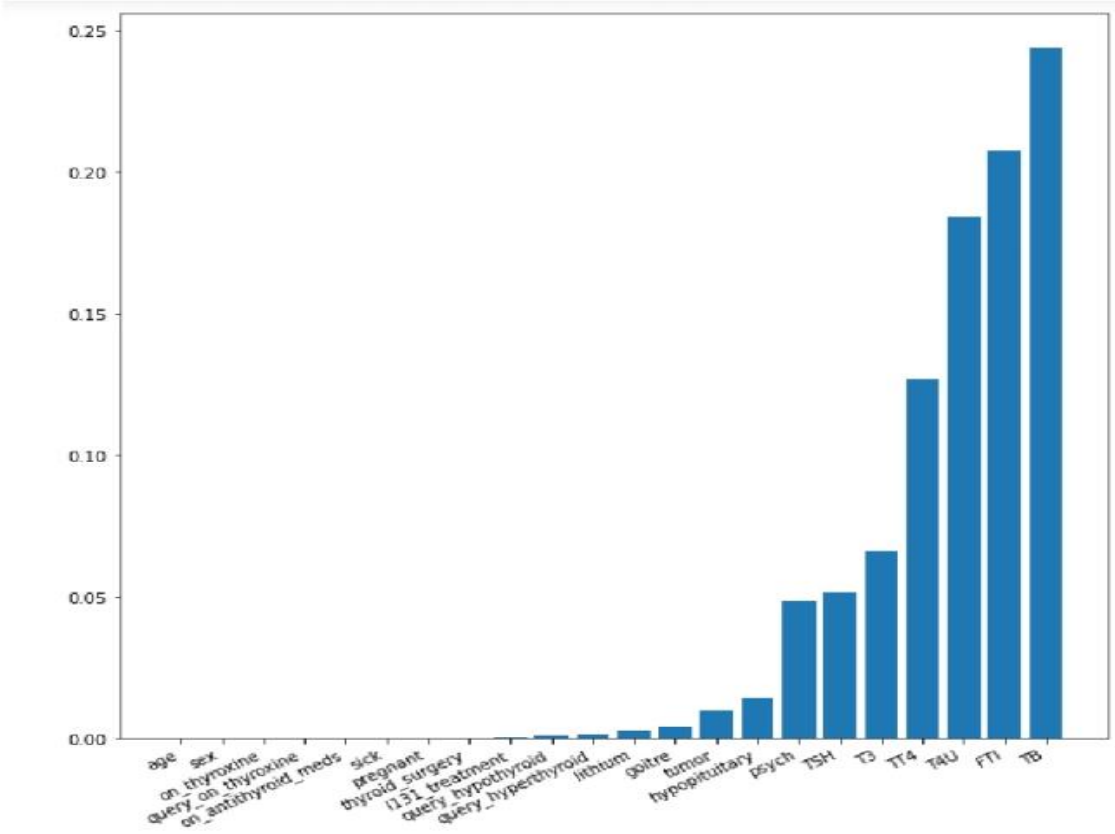

thyroid.ipynb - Colaboratory
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=zhTBrq3P8gGp
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
from sklearn.preprocessing import StandardScaler
from sklearn.inspection import permutation_importance
from sklearn.ensemble import RandomForestClassifier
import matplotlib.pyplot as plt
sc=StandardScaler()
x_bal=sc.fit_transform(x_bal)
x_test_bal=sc.transform(x_test_bal)
x_bal
array([[-1.6271471 , -0.40507694, -0.44547421, ..., -2.50884696,
-1.40088491, 3.29445097],
[-0.11557147, -0.40507694, 2.30310072, ..., -0.26257466,
0.07209337, -0.19494049],
[1.18751098, 1.84820507, -0.44547421, ..., 0.17044169,
-0.19352567, -0.19494049],
...,
[1.39600417, -0.40507694, 2.30310072, ..., 0.43621593,
0.06100549, -0.19494049],
[0.72805622, 1.4308244 , 2.30310072, ..., 0.14337816,
0.89086123, -0.19494049],
[1.15630265, -0.40507694, 2.30310072, ..., 0.39729806,
-0.26589119, -0.19494049]])



	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroxine_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...
0	-1.627147	-0.405077	-0.445474	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
1	-0.115571	-0.405077	2.303101	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
2	1.187511	1.848205	-0.445474	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
3	-1.366531	-0.405077	-0.445474	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
4	-0.167695	-0.405077	-0.445474	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
...	...	...	...	...	...	...	...	...	...	...	...
3292	0.546954	1.047459	2.303101	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
3293	0.383096	-0.405077	2.303101	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
3294	1.396004	-0.405077	2.303101	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
3295	0.728056	1.430824	2.303101	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	-0.304166	...
3296	1.156303	-0.405077	2.303101	-0.141477	-0.257609	-0.177156	-0.174387	-0.267762	-0.224295	1.322228	...


thyroid.ipynb - Colaboratory
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=sDCG55iBeO2i
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
rfr=RandomForestClassifier()
rfr.fit(x_bal,y_bal)
<ipython-input-48-571bdcc8bfaa>:2: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples,),
rfr.fit(x_bal,y_bal)
RandomForestClassifier
RandomForestClassifier()
from sklearn.inspection import permutation_importance
results=permutation_importance(rfr,x_bal,y_bal,scoring='accuracy')
feature_importance=['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroxine_meds','sick','pregnant','thyroid_surgery','I131_treatment','query_hypothyro
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 importance feature
plt.figure(figsize=(10,10))
plt.bar(x=feature_importance, height=importance)
plt.xticks(rotation=30, ha='right')
plt.show()


thyroid.ipynb - Colaboratory
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=g4umFmvxNu3w
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
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_antithyroxine_meds Score: 0.00012132241431603852
feature: sick Score: 0.0003033060357900963
feature: pregnant Score: 0.0003033060357900963
feature: thyroid_surgery Score: 0.0006066120715801926
feature: I131_treatment Score: 0.0007279344858962311
feature: query_hypothyroid Score: 0.0012738853503185155
feature: query_hyperthyroid Score: 0.0018198362147406888
feature: lithium Score: 0.0026690931149529586
feature: goitre Score: 0.003579011222323336
feature: tumor Score: 0.016560509554140124
feature: hypopituitary Score: 0.016681831968456164
feature: psych Score: 0.019654231119199263
feature: TSH Score: 0.055383682135274490
feature: T3 Score: 0.06084319077949649 4
feature: TT4 Score: 0.08905065210797694
feature: T4U Score: 0.1575978161965423
feature: FTI Score: 0.17488626023657872
feature: TBG Score: 0.22942068547164088


0.25
0.20
0.15
0.10
0.05
0.00
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
TSH
T3
TT4
T4U
FTI
TB

```
x.head()
```

	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_meds	sick	pregnant	thyroid_surgery	I131_treatment	query_hypothyroid	...	goitre	tumor	hypopi
4	32.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	
18	63.0	1.0	1.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	...	0.0	0.0	
32	41.0	2.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	
33	71.0	1.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	
39	55.0	1.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	...	0.0	0.0	

5 rows x 22 columns

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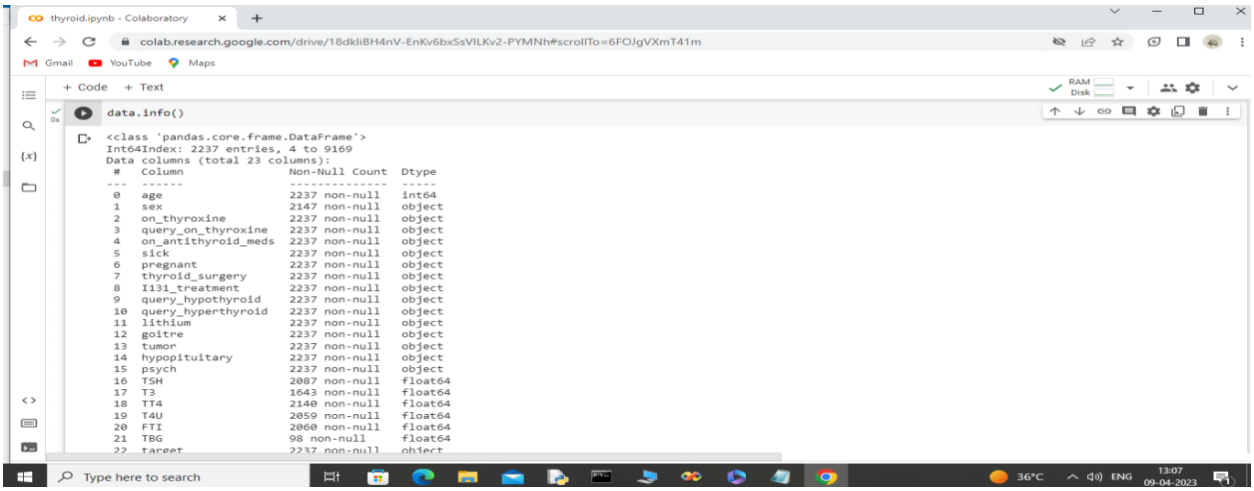
Gmail YouTube Maps

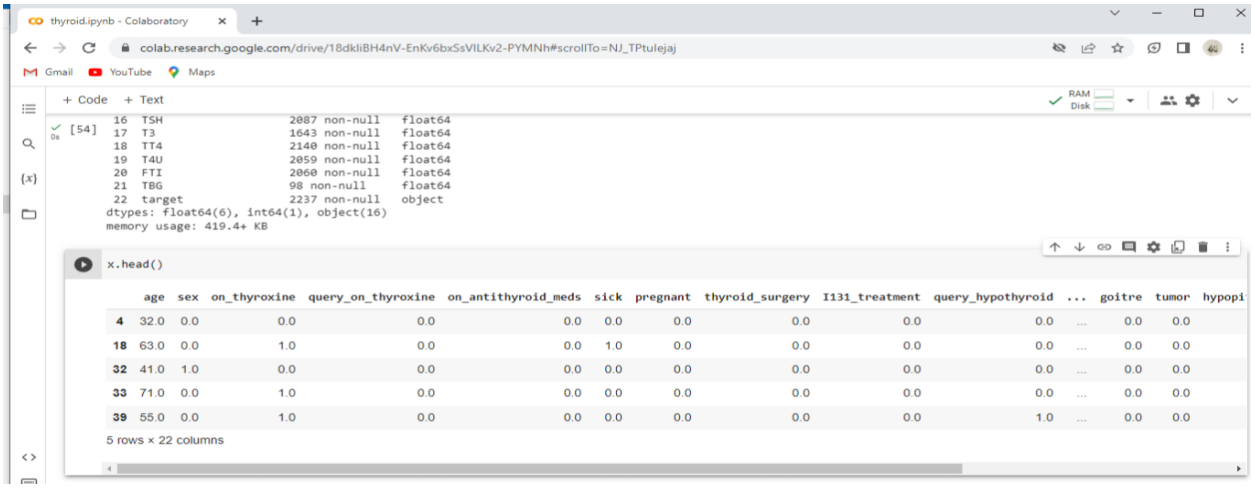
+ Code + Text

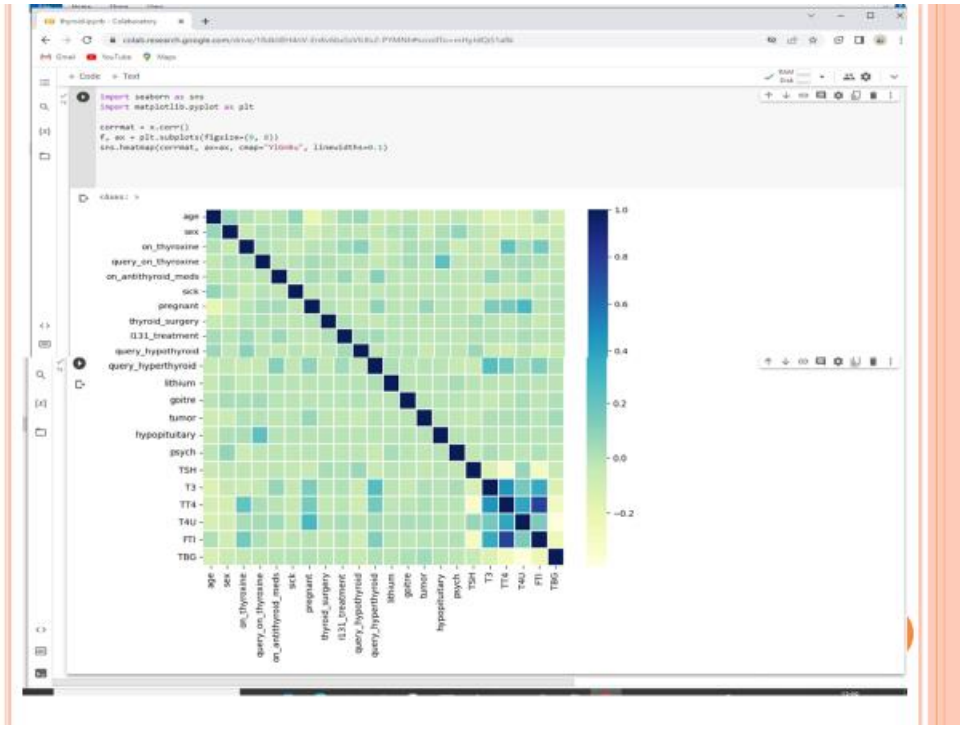
RAM Disk

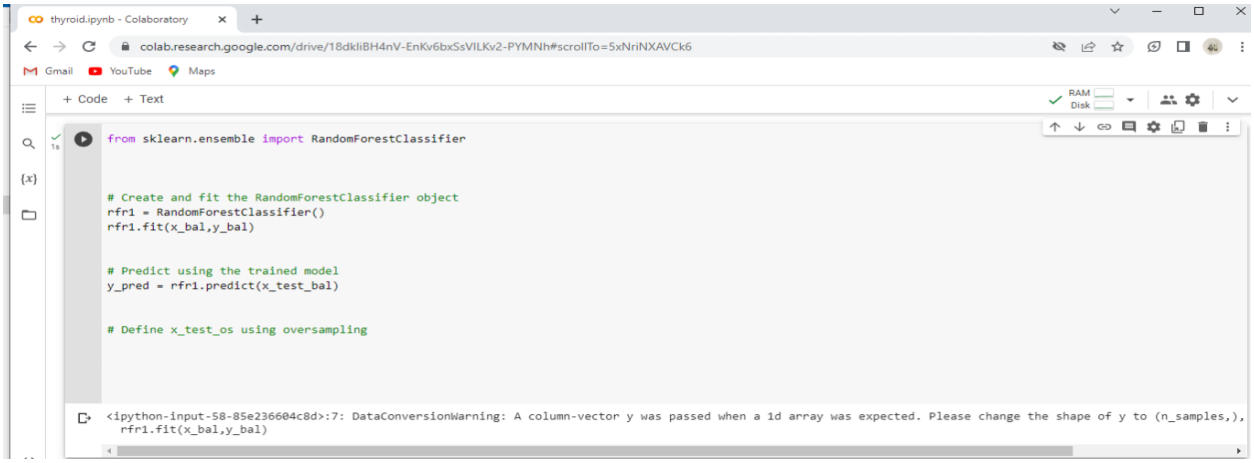
```
[50]
[51] x_bal=x_bal.drop(['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroxine_meds','sick','pregnant','thyroid_surgery','I131_treatment','query_hypothyroid
[52] x_test_bal=x_test_bal.drop(['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroxine_meds','sick','pregnant','thyroid_surgery','I131_treatment','query_h
x_bal.head()
```

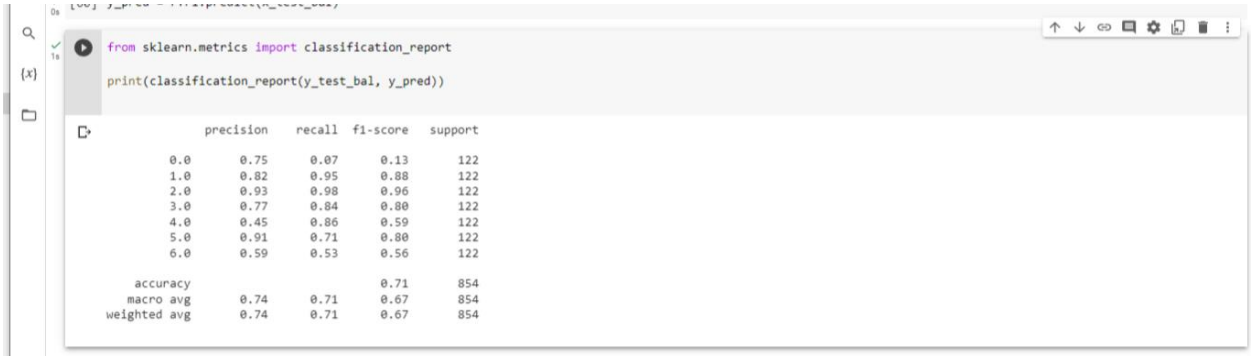
	goitre	tumor	hypopituitary	psych	TSH	T3	TT4	T4U	FTI	TBG
0	-0.073367	-0.185723	-0.037741	-0.144603	-0.315459	-1.035381	-1.704953	-2.508847	-1.400885	3.294451
1	-0.073367	-0.185723	-0.037741	-0.144603	-0.090056	0.154862	-0.197213	-0.262575	0.072093	-0.194940
2	-0.073367	-0.185723	-0.037741	-0.144603	-0.278907	-0.471581	-0.227069	0.170442	-0.193526	-0.194940
3	-0.073367	6.169673	-0.037741	-0.144603	-0.284999	0.969239	0.041637	0.495204	-0.133158	-0.194940
4	-0.073367	-0.185723	-0.037741	-0.144603	-0.306321	4.539969	1.459807	-0.127257	1.496777	-0.194940


thyroid.ipynb - Colaboratory
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=6FOJgVXmT41m
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
data.info()
<class 'pandas.core.frame.DataFrame'>
Int64Index: 2237 entries, 4 to 9169
Data columns (total 23 columns):
Column Non-Null Count Dtype
--- ------ -------------- -----
0 age 2237 non-null int64
1 sex 2147 non-null object
2 on_thyroxine 2237 non-null object
3 query_on_thyroxine 2237 non-null object
4 on_antithyroid_meds 2237 non-null object
5 sick 2237 non-null object
6 pregnant 2237 non-null object
7 thyroid_surgery 2237 non-null object
8 I131_treatment 2237 non-null object
9 query_hypothyroid 2237 non-null object
10 query_hyperthyroid 2237 non-null object
11 lithium 2237 non-null object
12 goitre 2237 non-null object
13 tumor 2237 non-null object
14 hypopituitary 2237 non-null object
15 psych 2237 non-null object
16 TSH 2087 non-null float64
17 T3 1643 non-null float64
18 TT4 2140 non-null float64
19 T4U 2059 non-null float64
20 FTI 2060 non-null float64
21 TBG 98 non-null float64
22 target 2237 non-null object
Type here to search
36°C
ENG
13:07
09-04-2023


thyroid.ipynb - Colaboratory
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=NJ_TPtulejaj
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
[54]
16 TSH 2087 non-null float64
17 T3 1643 non-null float64
18 TT4 2140 non-null float64
19 T4U 2059 non-null float64
20 FTI 2060 non-null float64
21 TBG 98 non-null float64
22 target 2237 non-null object
dtypes: float64(6), int64(1), object(16)
memory usage: 419.4+ KB
x.head()
age sex on_thyroxine query_on_thyroxine on_antithyroid_meds sick pregnant thyroid_surgery I131_treatment query_hypothyroid ... goitre tumor hypopi
4 32.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 ... 0.0 0.0
18 63.0 0.0 1.0 0.0 0.0 1.0 0.0 0.0 0.0 0.0 ... 0.0 0.0
32 41.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 ... 0.0 0.0
33 71.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 ... 0.0 0.0
39 55.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 1.0 ... 0.0 0.0
5 rows × 22 columns


import seaborn as sns
import matplotlib.pyplot as plt
corrmat = x.corr()
f, ax = plt.subplots(figsize=(9, 8))
sns.heatmap(corrmat, ax=ax, cmap="YlGnBu", linewidths=0.1)
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
TSH
T3
TT4
T4U
FTI
TBG
1.0
0.8
0.6
0.4
0.2
0.0
−0.2


thyroid.ipynb - Colaboratory
colab.research.google.com/drive/18dkliBH4nV-EnKv6bxSsVILKv2-PYMNh#scrollTo=5xNriNXAVCk6
Gmail
YouTube
Maps
+ Code
+ Text
RAM
Disk
from sklearn.ensemble import RandomForestClassifier
# Create and fit the RandomForestClassifier object
rfr1 = RandomForestClassifier()
rfr1.fit(x_bal,y_bal)
# Predict using the trained model
y_pred = rfr1.predict(x_test_bal)
# Define x_test_os using oversampling
<ipython-input-58-85e236604c8d>:7: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples,),
rfr1.fit(x_bal,y_bal)



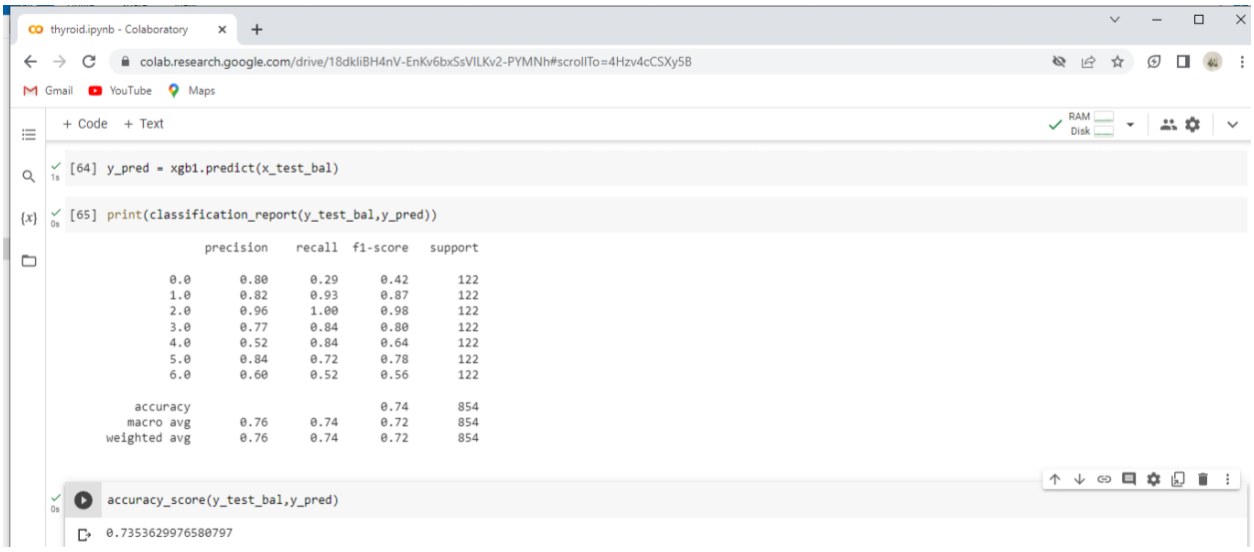
```
from sklearn.metrics import classification_report

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

```
              precision    recall  f1-score   support

         0.0       0.75      0.07      0.13       122
         1.0       0.82      0.95      0.88       122
         2.0       0.93      0.98      0.96       122
         3.0       0.77      0.84      0.80       122
         4.0       0.45      0.86      0.59       122
         5.0       0.91      0.71      0.80       122
         6.0       0.59      0.53      0.56       122

    accuracy                           0.71       854
   macro avg       0.74      0.71      0.67       854
weighted avg       0.74      0.71      0.67       854
```

```
[62] from sklearn.metrics import accuracy_score
     train_score = accuracy_score(y_bal, rfr1.predict(x_bal))
     train_score

     1.0
```

```
from xgboost import XGBClassifier
xgb1 = XGBClassifier()
xgb1.fit(x_bal,y_bal)
```

```
XGBClassifier(base_score=None, booster=None, callbacks=None,
              colsample_bylevel=None, colsample_bynode=None,
              colsample_bytree=None, early_stopping_rounds=None,
              enable_categorical=False, eval_metric=None, feature_types=None,
              gamma=None, gpu_id=None, grow_policy=None, importance_type=None,
              interaction_constraints=None, learning_rate=None, max_bin=None,
              max_cat_threshold=None, max_cat_to_onehot=None,
              max_delta_step=None, max_depth=None, max_leaves=None,
              min_child_weight=None, missing=nan, monotone_constraints=None,
              n_estimators=100, n_jobs=None, num_parallel_tree=None,
              objective='multi:softprob', predictor=None, ...)
```




```
[64] y_pred = xgb1.predict(x_test_bal)
```

```
[65] print(classification_report(y_test_bal,y_pred))
```

	precision	recall	f1-score	support
0.0	0.80	0.29	0.42	122
1.0	0.82	0.93	0.87	122
2.0	0.96	1.00	0.98	122
3.0	0.77	0.84	0.80	122
4.0	0.52	0.84	0.64	122
5.0	0.84	0.72	0.78	122
6.0	0.60	0.52	0.56	122
accuracy			0.74	854
macro avg	0.76	0.74	0.72	854
weighted avg	0.76	0.74	0.72	854

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

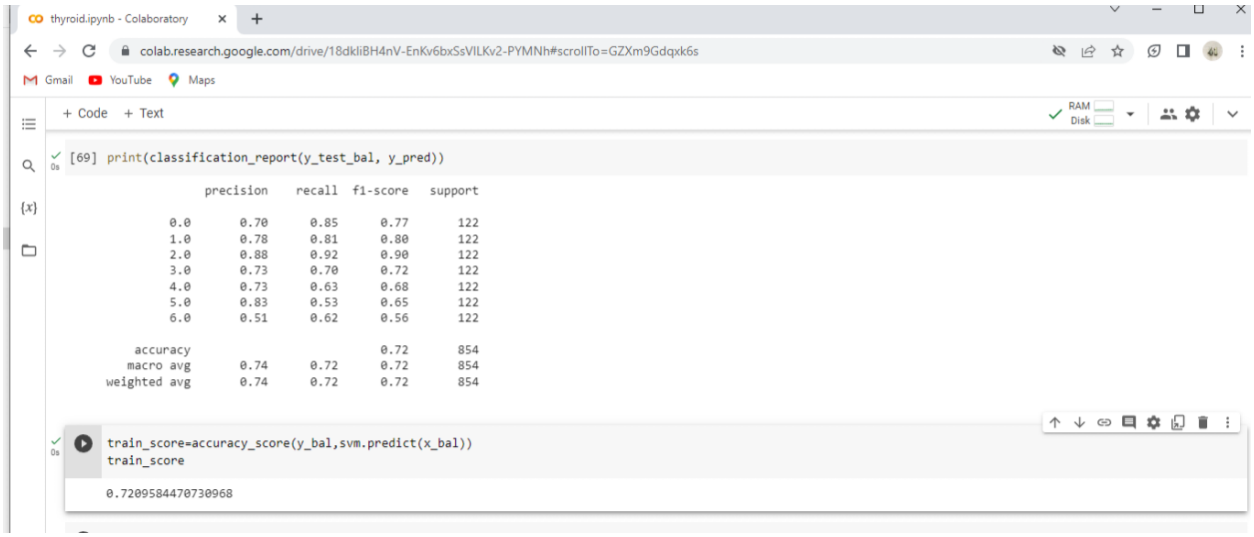
```
0.7353629976580797
```

```
[67] from sklearn.svm import SVC
     from sklearn.metrics import accuracy_score, classification_report

     svm = SVC()
     svm.fit(x_bal, y_bal)
```

```
/usr/local/lib/python3.9/dist-packages/sklearn/utils/validation.py:1143: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please
  y = column_or_1d(y, warn=True)
```

SVC()

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




```
[69] print(classification_report(y_test_bal, y_pred))
```

	precision	recall	f1-score	support
0.0	0.70	0.85	0.77	122
1.0	0.78	0.81	0.80	122
2.0	0.88	0.92	0.90	122
3.0	0.73	0.70	0.72	122
4.0	0.73	0.63	0.68	122
5.0	0.83	0.53	0.65	122
6.0	0.51	0.62	0.56	122
accuracy			0.72	854
macro avg	0.74	0.72	0.72	854
weighted avg	0.74	0.72	0.72	854

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

```
0.7209584470730968
```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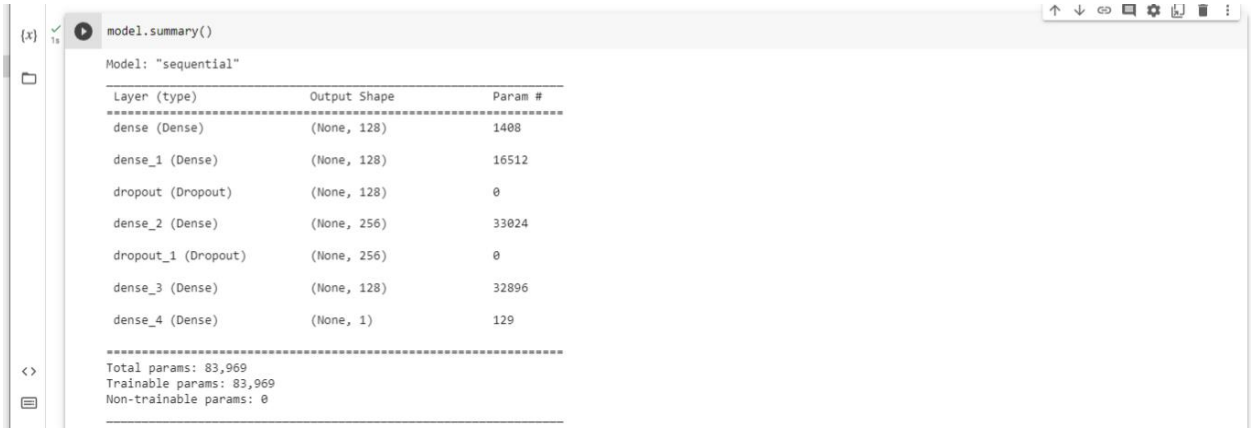
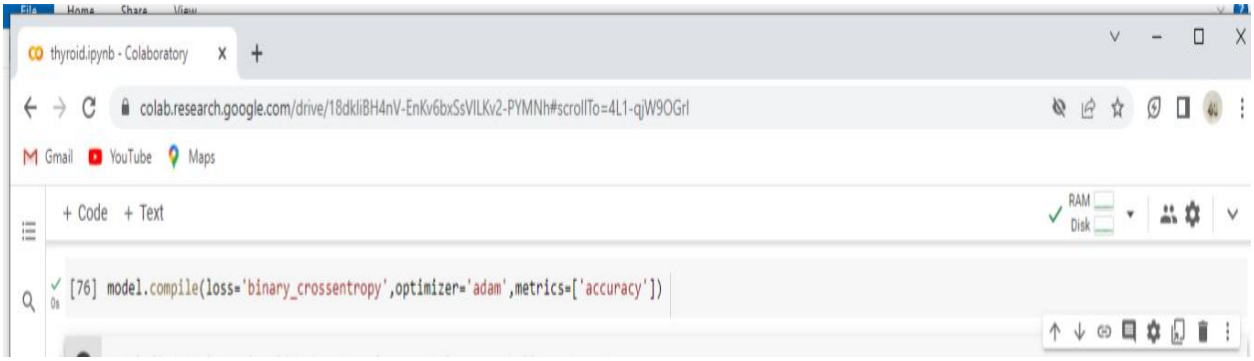
[71] model= Sequential()
[72] model.add(Dense(units=128,activation='relu',input_shape=(10,)))
[73] model.add(Dense(units=128,activation='relu',kernel_initializer='random_uniform'))
model.add(Dropout(0.2))
model.add(Dense(units=256,activation='relu',kernel_initializer='random_uniform'))
model.add(Dropout(0.2))
model.add(Dense(units=128,activation='relu',kernel_initializer='random_uniform'))
model.add(Dense(units=1,activation='sigmoid'))


model.summary()
Model: "sequential"
Layer (type) Output Shape Param #
dense (Dense) (None, 128) 1408
dense_1 (Dense) (None, 128) 16512
dropout (Dropout) (None, 128) 0
dense_2 (Dense) (None, 256) 33024
dropout_1 (Dropout) (None, 256) 0
dense_3 (Dense) (None, 128) 32896
dense_4 (Dense) (None, 1) 129
Total params: 83,969
Trainable params: 83,969
Non-trainable params: 0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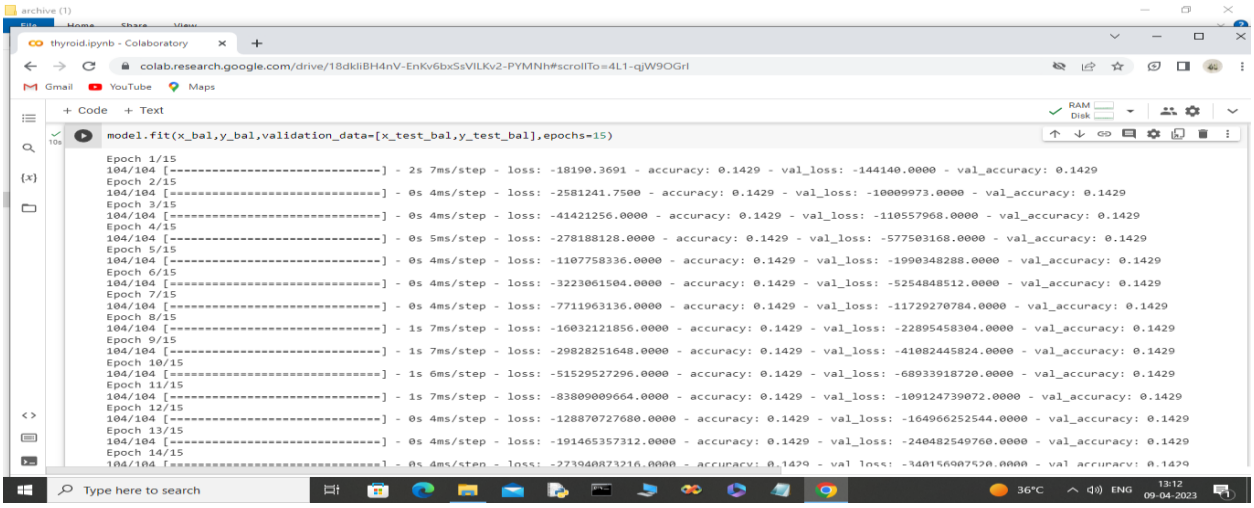
[76] model.compile(loss='binary_crossentropy',optimizer='adam',metrics=['accuracy'])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model.fit(x_bal,y_bal,validation_data=[x_test_bal,y_test_bal],epochs=15)
Epoch 1/15
104/104 [==============================] - 2s 7ms/step - loss: -18190.3691 - accuracy: 0.1429 - val_loss: -144140.0000 - val_accuracy: 0.1429
Epoch 2/15
104/104 [==============================] - 0s 4ms/step - loss: -2581241.7500 - accuracy: 0.1429 - val_loss: -10009973.0000 - val_accuracy: 0.1429
Epoch 3/15
104/104 [==============================] - 0s 4ms/step - loss: -41421256.0000 - accuracy: 0.1429 - val_loss: -110557968.0000 - val_accuracy: 0.1429
Epoch 4/15
104/104 [==============================] - 0s 5ms/step - loss: -278188128.0000 - accuracy: 0.1429 - val_loss: -577503168.0000 - val_accuracy: 0.1429
Epoch 5/15
104/104 [==============================] - 0s 4ms/step - loss: -1107758336.0000 - accuracy: 0.1429 - val_loss: -1990348288.0000 - val_accuracy: 0.1429
Epoch 6/15
104/104 [==============================] - 0s 4ms/step - loss: -3223061504.0000 - accuracy: 0.1429 - val_loss: -5254848512.0000 - val_accuracy: 0.1429
Epoch 7/15
104/104 [==============================] - 0s 4ms/step - loss: -7711963136.0000 - accuracy: 0.1429 - val_loss: -11729270784.0000 - val_accuracy: 0.1429
Epoch 8/15
104/104 [==============================] - 1s 7ms/step - loss: -16032121856.0000 - accuracy: 0.1429 - val_loss: -22895458304.0000 - val_accuracy: 0.1429
Epoch 9/15
104/104 [==============================] - 1s 7ms/step - loss: -29828251648.0000 - accuracy: 0.1429 - val_loss: -41082445824.0000 - val_accuracy: 0.1429
Epoch 10/15
104/104 [==============================] - 1s 6ms/step - loss: -51529527296.0000 - accuracy: 0.1429 - val_loss: -68933918720.0000 - val_accuracy: 0.1429
Epoch 11/15
104/104 [==============================] - 1s 7ms/step - loss: -83809009664.0000 - accuracy: 0.1429 - val_loss: -109124739072.0000 - val_accuracy: 0.1429
Epoch 12/15
104/104 [==============================] - 0s 4ms/step - loss: -128870727680.0000 - accuracy: 0.1429 - val_loss: -164966252544.0000 - val_accuracy: 0.1429
Epoch 13/15
104/104 [==============================] - 0s 4ms/step - loss: -191465357312.0000 - accuracy: 0.1429 - val_loss: -240482549760.0000 - val_accuracy: 0.1429
Epoch 14/15
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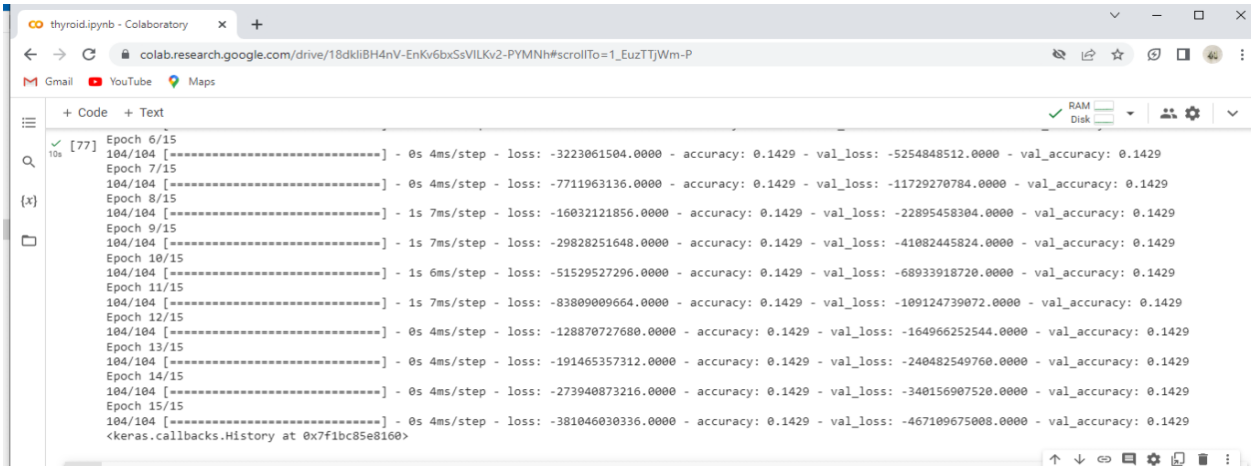
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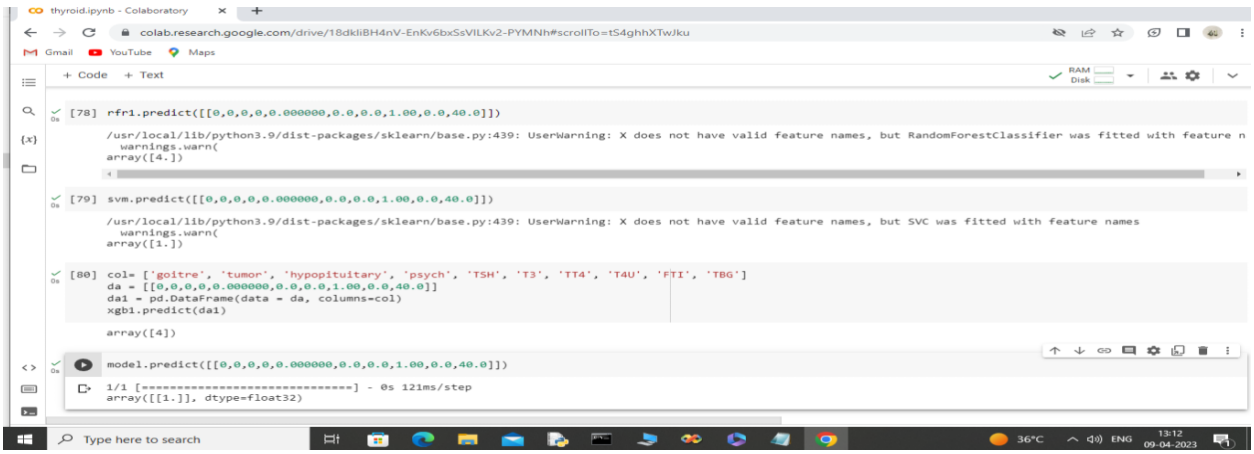
[77]
Epoch 6/15
104/104 [==========] - 0s 4ms/step - loss: -3223061504.0000 - accuracy: 0.1429 - val_loss: -5254848512.0000 - val_accuracy: 0.1429
Epoch 7/15
104/104 [==========] - 0s 4ms/step - loss: -7711963136.0000 - accuracy: 0.1429 - val_loss: -11729270784.0000 - val_accuracy: 0.1429
Epoch 8/15
104/104 [==========] - 1s 7ms/step - loss: -16032121856.0000 - accuracy: 0.1429 - val_loss: -22895458304.0000 - val_accuracy: 0.1429
Epoch 9/15
104/104 [==========] - 1s 7ms/step - loss: -29828251648.0000 - accuracy: 0.1429 - val_loss: -41082445824.0000 - val_accuracy: 0.1429
Epoch 10/15
104/104 [==========] - 1s 6ms/step - loss: -51529527296.0000 - accuracy: 0.1429 - val_loss: -68933918720.0000 - val_accuracy: 0.1429
Epoch 11/15
104/104 [==========] - 1s 7ms/step - loss: -83809009664.0000 - accuracy: 0.1429 - val_loss: -109124739072.0000 - val_accuracy: 0.1429
Epoch 12/15
104/104 [==========] - 0s 4ms/step - loss: -128870727680.0000 - accuracy: 0.1429 - val_loss: -164966252544.0000 - val_accuracy: 0.1429
Epoch 13/15
104/104 [==========] - 0s 4ms/step - loss: -191465357312.0000 - accuracy: 0.1429 - val_loss: -240482549760.0000 - val_accuracy: 0.1429
Epoch 14/15
104/104 [==========] - 0s 4ms/step - loss: -273940873216.0000 - accuracy: 0.1429 - val_loss: -340156907520.0000 - val_accuracy: 0.1429
Epoch 15/15
104/104 [==========] - 0s 4ms/step - loss: -381046030336.0000 - accuracy: 0.1429 - val_loss: -467109675008.0000 - val_accuracy: 0.1429
<keras.callbacks.History at 0x7f1bc85e8160>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[78] rfr1.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but RandomForestClassifier was fitted with feature n
warnings.warn(
array([4.])
[79] svm.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but SVC was fitted with feature names
warnings.warn(
array([1.])
[80] col= ['goitre', 'tumor', 'hypopituitary', 'psych', 'TSH', 'T3', 'TT4', 'T4U', 'FTI', 'TBG']
da = [[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]]
da1 = pd.DataFrame(data = da, columns=col)
xgb1.predict(da1)
array([4])
model.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
1/1 [==========] - 0s 121ms/step
array([[1.]], dtype=float32)
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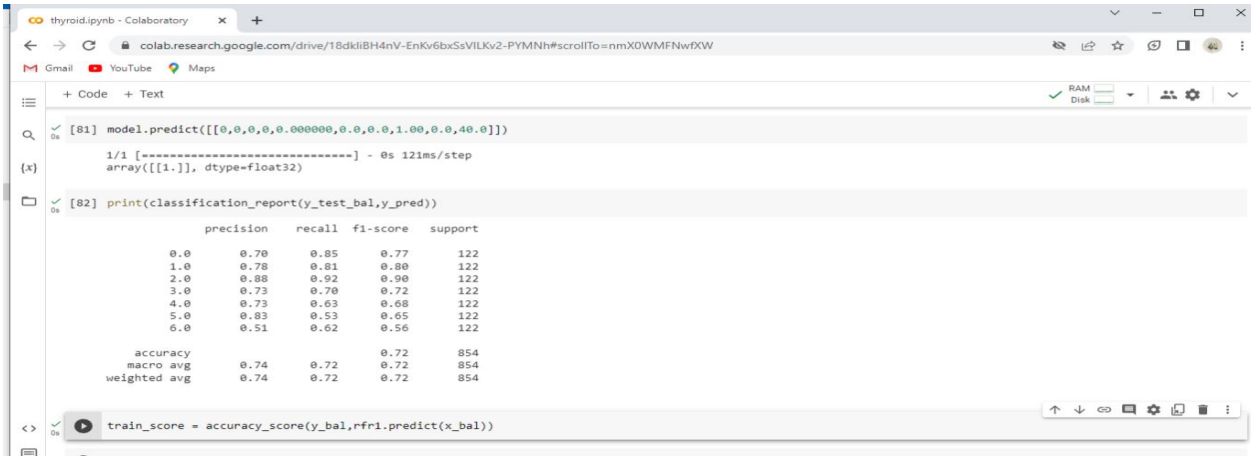
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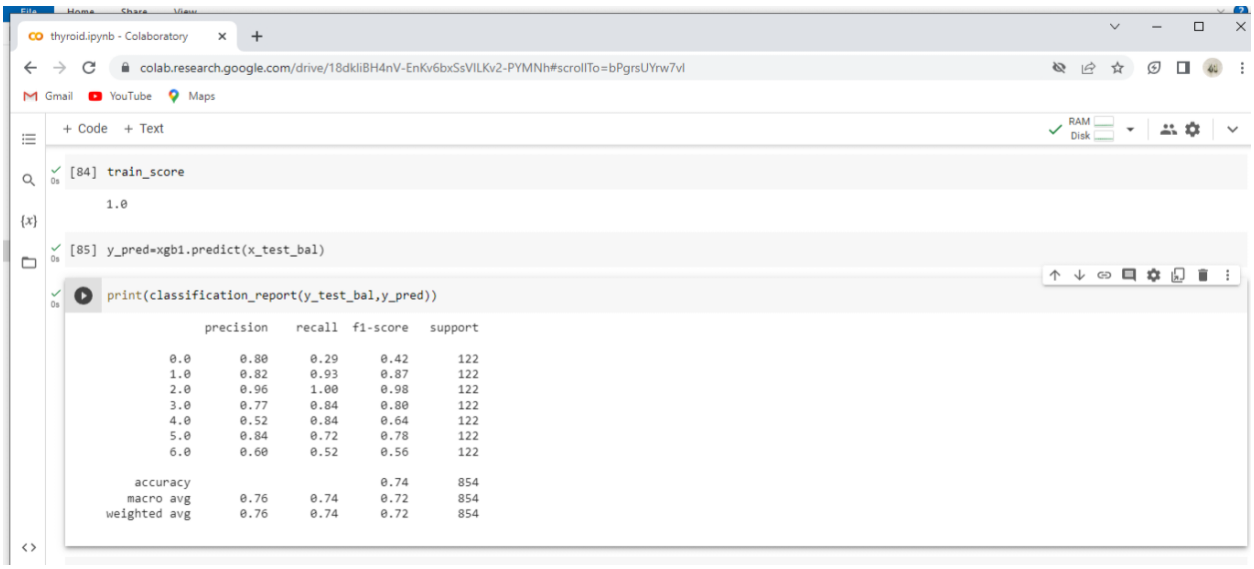
[81] model.predict([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
1/1 [==============================] - 0s 121ms/step
array([[1.]], dtype=float32)
[82] print(classification_report(y_test_bal,y_pred))
precision recall f1-score support
0.0 0.70 0.85 0.77 122
1.0 0.78 0.81 0.80 122
2.0 0.88 0.92 0.90 122
3.0 0.73 0.70 0.72 122
4.0 0.73 0.63 0.68 122
5.0 0.83 0.53 0.65 122
6.0 0.51 0.62 0.56 122
accuracy 0.72 854
macro avg 0.74 0.72 0.72 854
weighted avg 0.74 0.72 0.72 854
train_score = accuracy_score(y_bal,rfr1.predict(x_bal))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RAM
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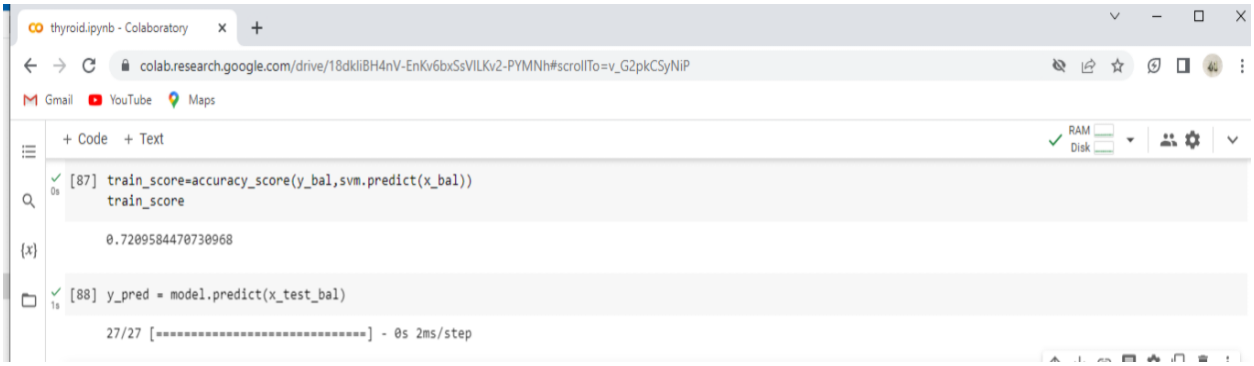
[84] train_score
1.0
[85] y_pred=xgb1.predict(x_test_bal)
print(classification_report(y_test_bal,y_pred))
precision recall f1-score support
0.0 0.80 0.29 0.42 122
1.0 0.82 0.93 0.87 122
2.0 0.96 1.00 0.98 122
3.0 0.77 0.84 0.80 122
4.0 0.52 0.84 0.64 122
5.0 0.84 0.72 0.78 122
6.0 0.60 0.52 0.56 122
accuracy 0.74 854
macro avg 0.76 0.74 0.72 854
weighted avg 0.76 0.74 0.72 854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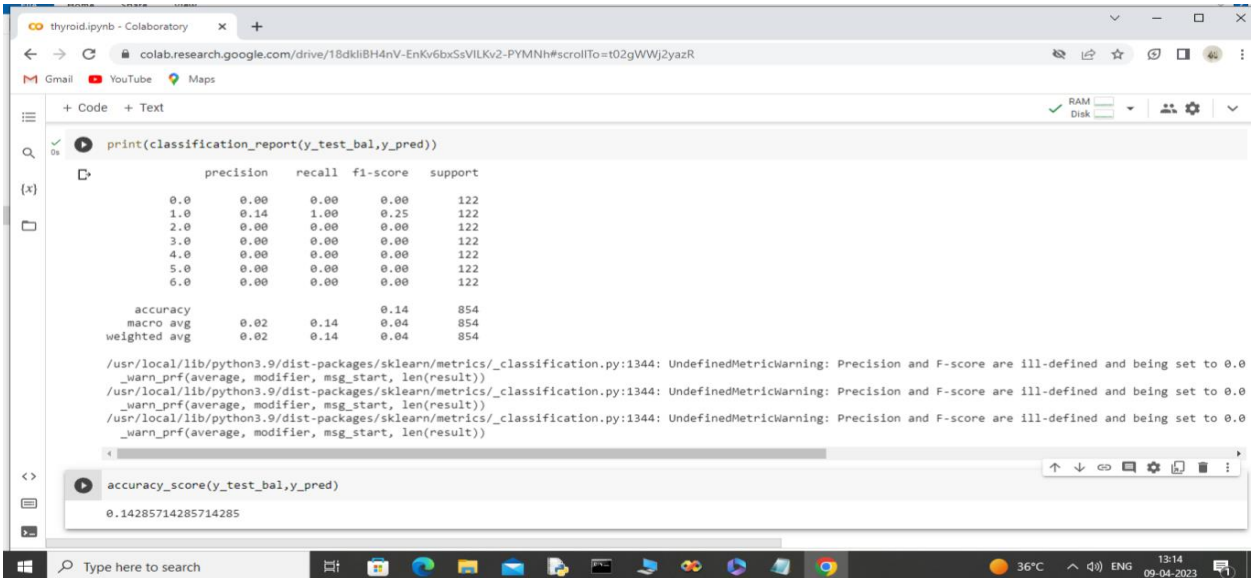
[87] train_score=accuracy_score(y_bal,svm.predict(x_bal))
train_score
0.7209584470730968
[88] y_pred = model.predict(x_test_bal)
27/27 [==============================] - 0s 2ms/step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Gmail
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Maps
+ Code
+ Text
RAM
Disk
print(classification_report(y_test_bal,y_pred))
precision recall f1-score support
0.0 0.00 0.00 0.00 122
1.0 0.14 1.00 0.25 122
2.0 0.00 0.00 0.00 122
3.0 0.00 0.00 0.00 122
4.0 0.00 0.00 0.00 122
5.0 0.00 0.00 0.00 122
6.0 0.00 0.00 0.00 122
accuracy 0.14 854
macro avg 0.02 0.14 0.04 854
weighted avg 0.02 0.14 0.04 854
/usr/local/lib/python3.9/dist-packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0
_warn_prf(average, modifier, msg_start, len(result))
/usr/local/lib/python3.9/dist-packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0
_warn_prf(average, modifier, msg_start, len(result))
/usr/local/lib/python3.9/dist-packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0
_warn_prf(average, modifier, msg_start, len(result))
accuracy_score(y_test_bal,y_pred)
0.14285714285714285
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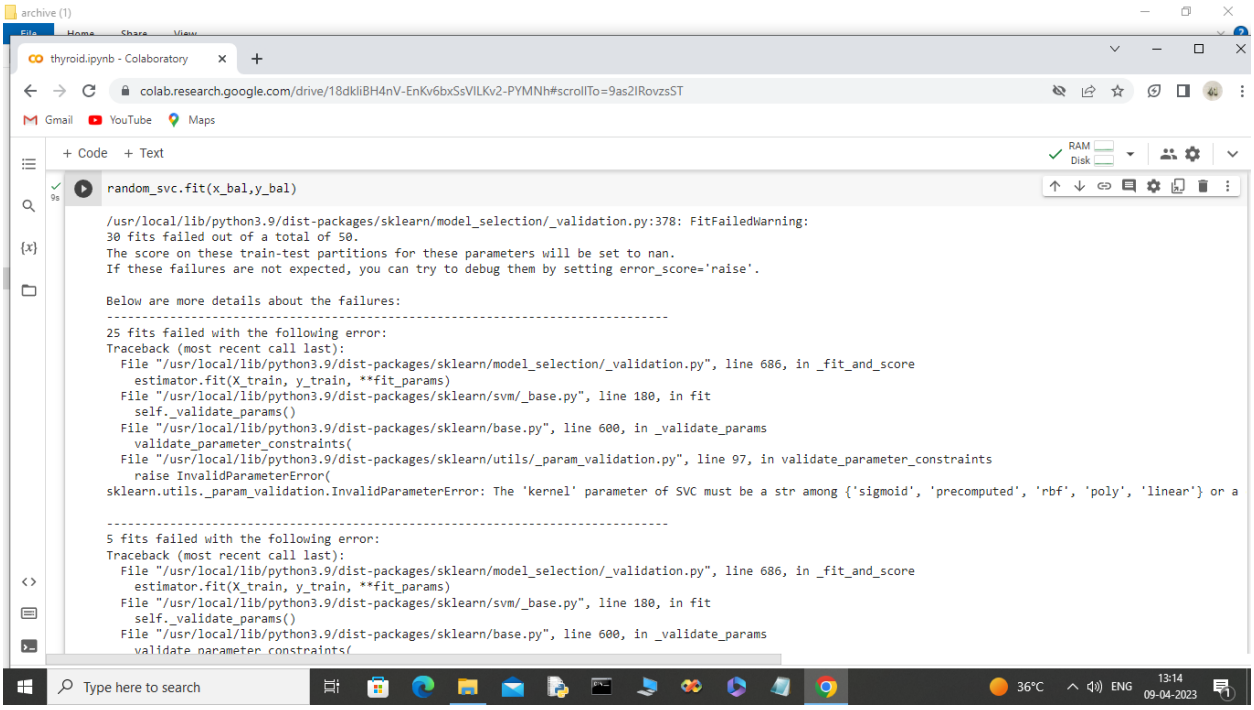
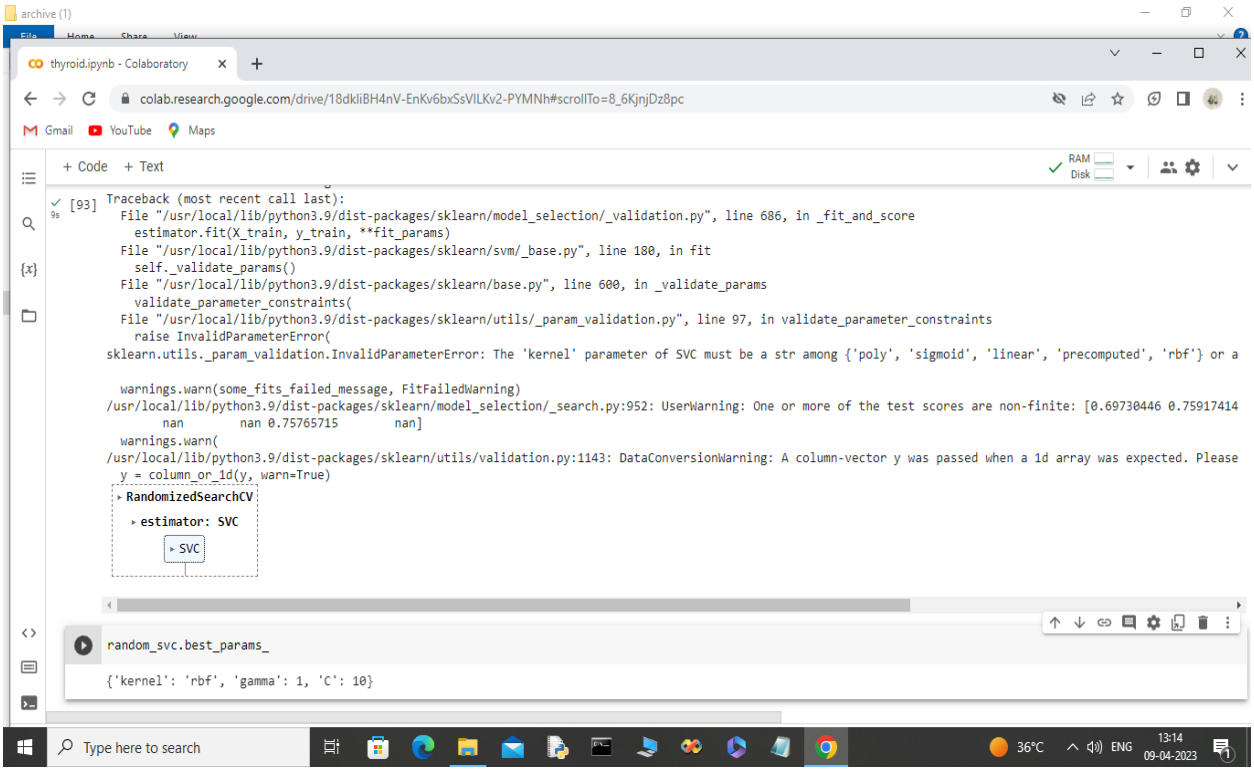
```
[91] params = {

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

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

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[93] Traceback (most recent call last):
File "/usr/local/lib/python3.9/dist-packages/sklearn/model_selection/_validation.py", line 686, in _fit_and_score
estimator.fit(X_train, y_train, **fit_params)
File "/usr/local/lib/python3.9/dist-packages/sklearn/svm/_base.py", line 180, in fit
self._validate_params()
File "/usr/local/lib/python3.9/dist-packages/sklearn/base.py", line 600, in _validate_params
validate_parameter_constraints(
File "/usr/local/lib/python3.9/dist-packages/sklearn/utils/_param_validation.py", line 97, in validate_parameter_constraints
raise InvalidParameterError(
sklearn.utils._param_validation.InvalidParameterError: The 'kernel' parameter of SVC must be a str among {'poly', 'sigmoid', 'linear', 'precomputed', 'rbf'} or a
warnings.warn(some_fits_failed_message, FitFailedWarning)
/usr/local/lib/python3.9/dist-packages/sklearn/model_selection/_search.py:952: UserWarning: One or more of the test scores are non-finite: [0.69730446 0.75917414
nan nan 0.75765715 nan]
warnings.warn(
/usr/local/lib/python3.9/dist-packages/sklearn/utils/validation.py:1143: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please
y = column_or_1d(y, warn=True)
RandomizedSearchCV
estimator: SVC
SVC
random_svc.best_params_
{'kernel': 'rbf', 'gamma': 1, 'C': 10}
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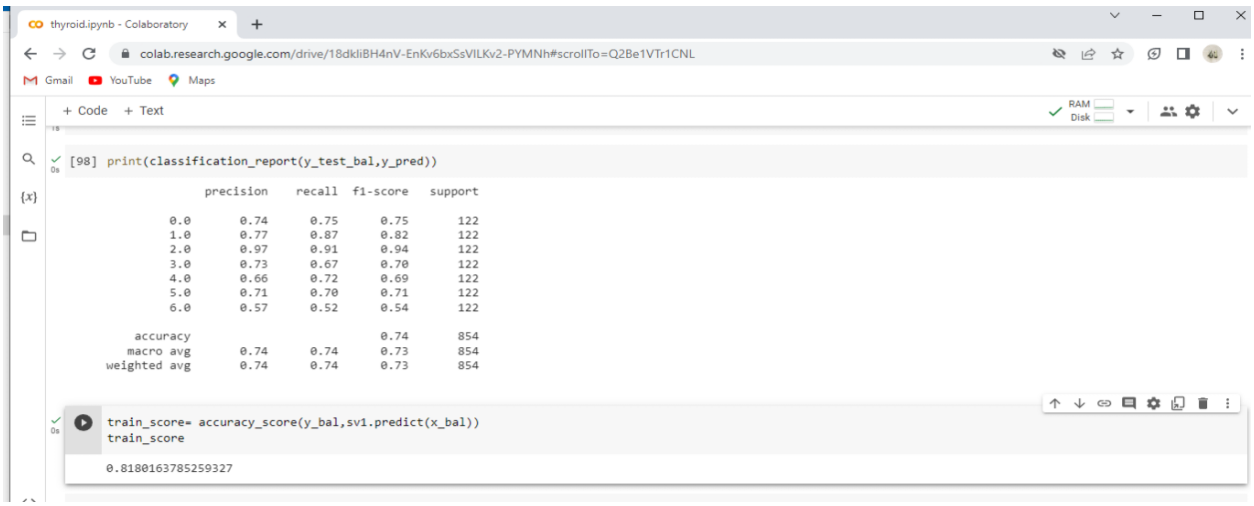
[95] sv1=SVC(kernel= 'rbf', gamma= 0.1, C=100)
[96] sv1.fit(x_bal,y_bal)
/usr/local/lib/python3.9/dist-packages/sklearn/utils/validation.py:1143: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please
y = column_or_1d(y, warn=True)
SVC
SVC(C=100, gamma=0.1)
y_pred= sv1.predict(x_test_bal)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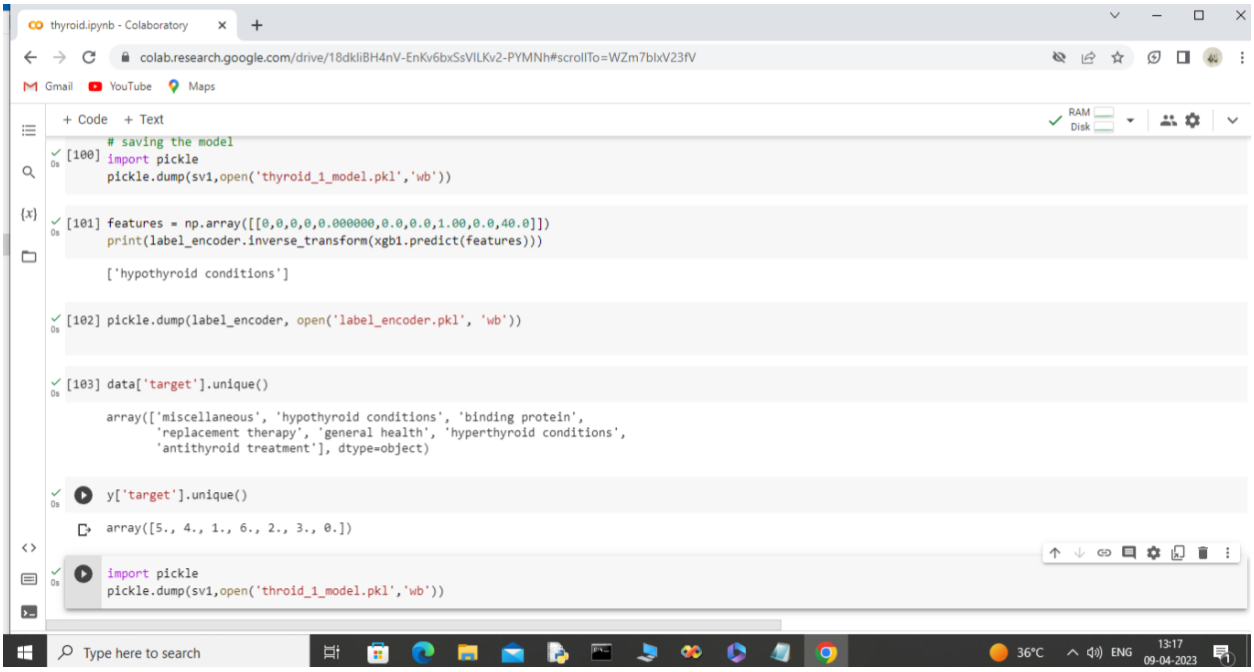
[98] print(classification_report(y_test_bal,y_pred))
precision recall f1-score support
0.0 0.74 0.75 0.75 122
1.0 0.77 0.87 0.82 122
2.0 0.97 0.91 0.94 122
3.0 0.73 0.67 0.70 122
4.0 0.66 0.72 0.69 122
5.0 0.71 0.70 0.71 122
6.0 0.57 0.52 0.54 122
accuracy 0.74 854
macro avg 0.74 0.74 0.73 854
weighted avg 0.74 0.74 0.73 854
train_score= accuracy_score(y_bal,sv1.predict(x_bal))
train_score
0.8180163785259327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[100] # saving the model
import pickle
pickle.dump(sv1,open('thyroid_1_model.pkl','wb'))
[101] features = np.array([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])
print(label_encoder.inverse_transform(xgb1.predict(features)))
['hypothyroid conditions']
[102] pickle.dump(label_encoder, open('label_encoder.pkl', 'wb'))
[103] data['target'].unique()
array(['miscellaneous', 'hypothyroid conditions', 'binding protein',
'replacement therapy', 'general health', 'hyperthyroid conditions',
'antithyroid treatment'], dtype=object)
y['target'].unique()
array([5., 4., 1., 6., 2., 3., 0.])
import pickle
pickle.dump(sv1,open('throid_1_model.pkl','wb'))
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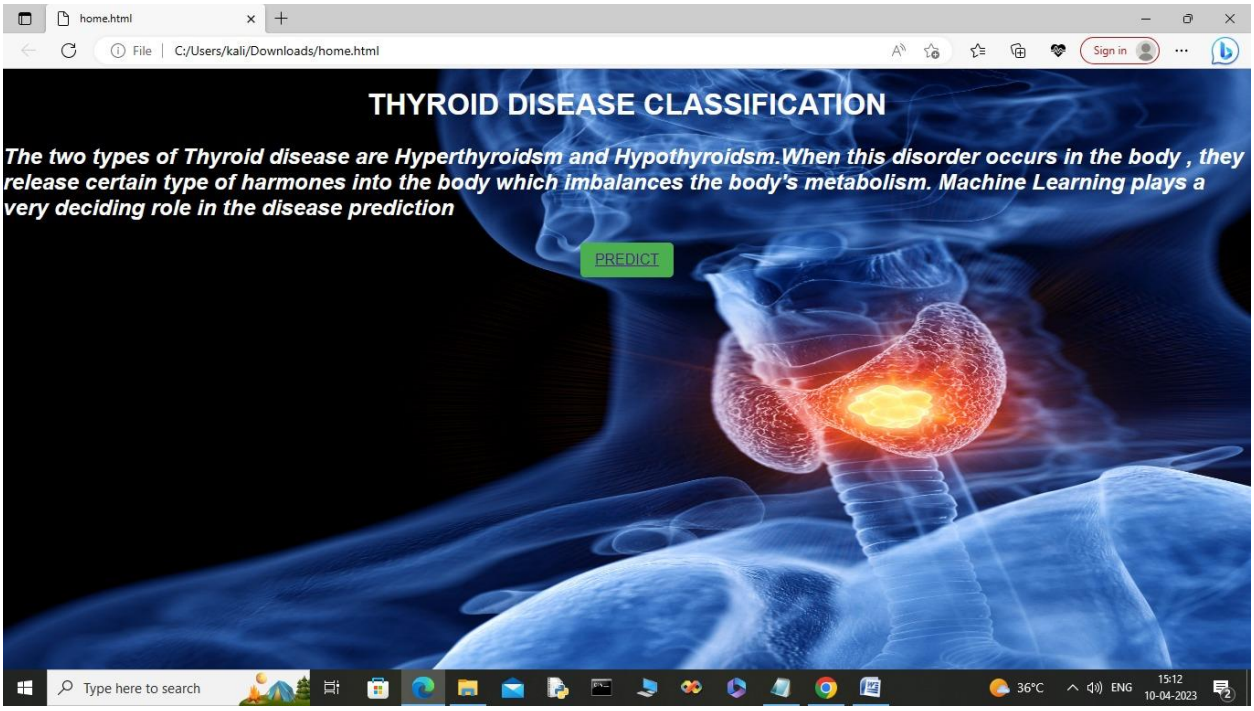
4. RESULT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File | C:/Users/kali/Downloads/home.html
Sign in
THYROID DISEASE CLASSIFICATION
The two types of Thyroid disease are Hyperthyroidsm and Hypothyroidsm.When this disorder occurs in the body , they release certain type of harmones into the body which imbalances the body's metabolism. Machine Learning plays a very deciding role in the disease prediction
PREDICT
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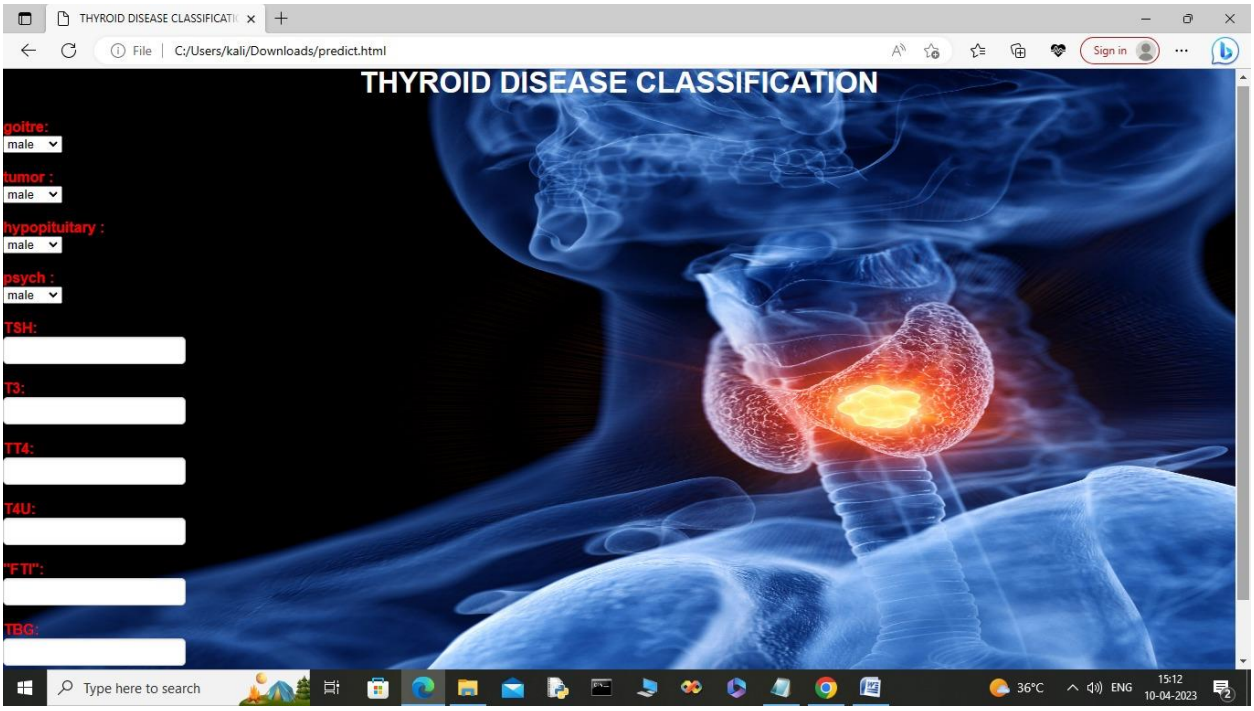
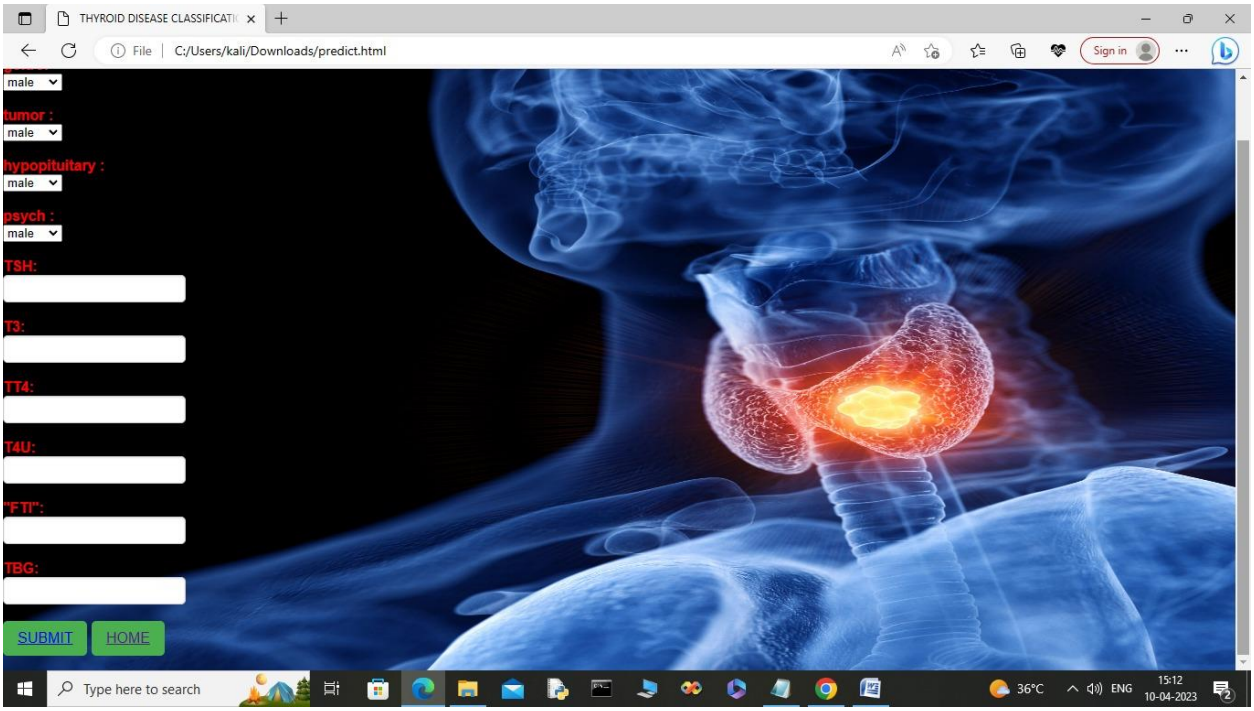
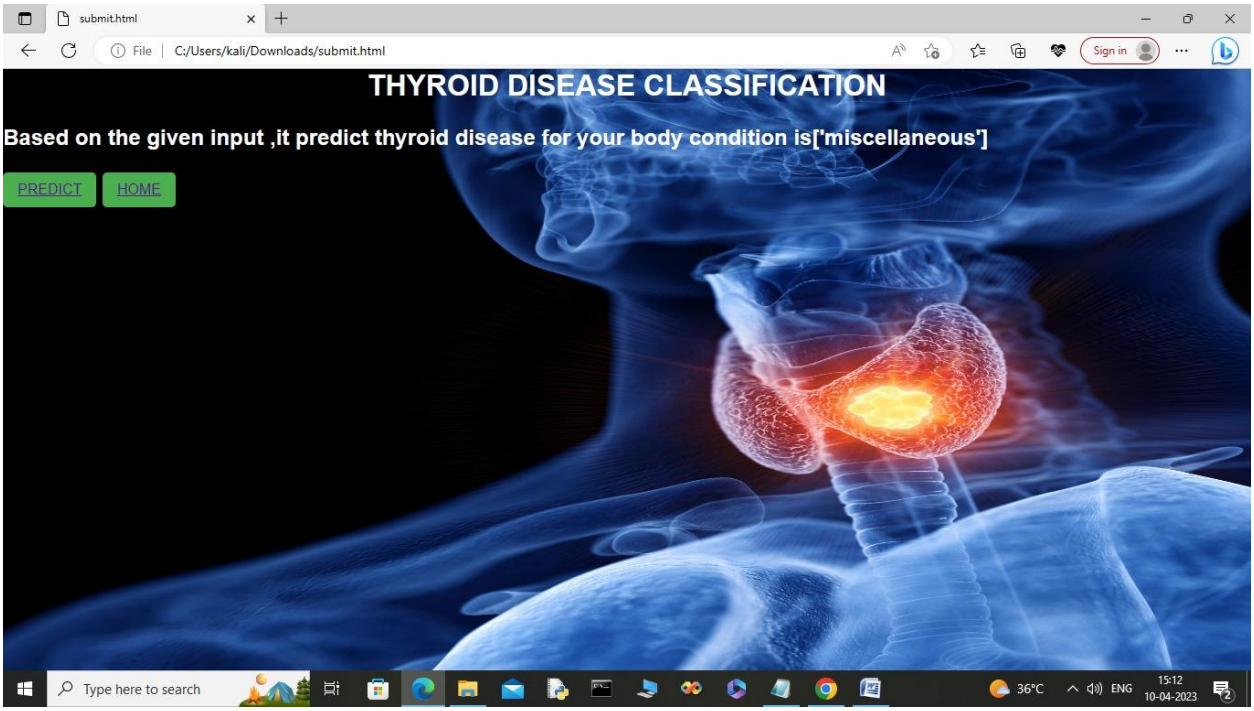
15:12
10-04-2023


THYROID DISEASE CLASSIFICATI
File | C:/Users/kali/Downloads/predict.html
Sign in
THYROID DISEASE CLASSIFICATION
goitre:
male
tumor :
male
hypopituitary :
male
psych :
male
TSH:
T3:
TT4:
T4U:
"FTI":
TBG:
Type here to search
36°C
ENG
15:12
10-04-2023


THYROID DISEASE CLASSIFICATI
File | C:/Users/kali/Downloads/predict.html
Sign in
male
tumor :
male
hypopituitary :
male
psych :
male
TSH:
T3:
TT4:
T4U:
"FTI":
TBG:
SUBMIT
HOME
Type here to search
36°C
ENG
15:12
10-04-2023


submit.html
File | C:/Users/kali/Downloads/submit.html
Sign in
THYROID DISEASE CLASSIFICATION
Based on the given input ,it predict thyroid disease for your body condition is['miscellaneous']
PREDICT
HOME
Type here to search
36°C
ENG
15:12
10-04-2023

5. ADVANTAGES

Accuracy: Machine learning algorithms can accurately classify thyroid diseases based on patterns and relationships found in large datasets, which can improve accuracy compared to traditional diagnostic methods.

Speed: Machine learning algorithms can process large amounts of data much faster than humans, reducing the time required for diagnosis and treatment.

Personalization: Machine learning algorithms can be trained to personalize diagnosis and treatment based on individual patient characteristics, such as age, gender, and medical history.

Consistency: Machine learning algorithms can provide consistent results across different medical professionals and institutions, reducing the risk of misdiagnosis and improving patient outcomes.

Cost-effectiveness: Machine learning can reduce the cost of thyroid disease diagnosis and treatment by reducing the need for expensive and invasive tests and procedures.

6. APPLICATIONS

Automated diagnosis: Machine learning models can be trained on medical images (such as ultrasound or MRI) to automatically diagnose thyroid disease. This could potentially reduce the need for invasive diagnostic procedures, such as biopsies.

Predictive modeling: Machine learning models can be used to predict the likelihood of thyroid disease in patients based on their medical history, lifestyle factors, and genetic data. This could help clinicians identify high-risk patients and provide targeted preventive care.

Treatment optimization: Machine learning models can be used to predict the most effective treatment for individual patients based on their medical history and other factors. This could help optimize treatment outcomes and reduce the risk of adverse effects.

Disease subtype classification: Machine learning models can be used to classify different subtypes of thyroid disease based on clinical and genetic data. This could help clinicians develop more targeted treatment plans for each patient.

Patient stratification: Machine learning models can be used to stratify patients into different risk groups based on their medical history, genetic data, and other factors. This could help clinicians identify patients who may benefit from more intensive monitoring or treatment.

7.CONCLUSION

In conclusion, machine learning algorithms can be effective in classifying thyroid disease based on various features and characteristics. The accuracy of the classification models depends on the quality and quantity of data used for training, the selection of appropriate features, and the choice of suitable algorithms.

Different machine learning algorithms such as Random Forest Classifier, SVM classsifier, XGB classifier and neural networks have been used in the literature to classify thyroid diseases. Ensemble methods

machine learning algorithms have the potential to assist clinicians in the diagnosis and treatment of thyroid diseases by providing accurate and timely predictions.

8.FUTURE SCOPE

Feature engineering: One of the critical aspects of machine learning is feature selection or engineering. Researchers can explore the creation of new features or the extraction of existing features from thyroid disease data. This may include demographic data, medical history, lab results, and imaging data, among others.

Deep learning models: Deep learning models, such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs), can learn high-level representations of the data, leading to more accurate classification. Researchers can explore the use of these models for thyroid disease classification.

Explainable AI: Explainable AI (XAI) aims to make machine learning models more interpretable to humans. Researchers can explore the use of XAI techniques such as LIME, SHAP, and attention mechanisms to provide explanations for the decisions made by the machine learning models for thyroid disease classification.

9. APPENDIX

9.1 Source Code

```
import pandas as pd

import numpy as np

import matplotlib.pyplot as plt

import tensorflow

from tensorflow.keras.models import Sequential

from tensorflow.keras.layers import Layer,Dense,Dropout

data=pd.read_csv("/content/sample_data/thyroidDF.csv")

data.head()

data.shape

data.isnull().sum()

data.drop(['TSH_measured','T3_measured','TT4_measured','T4U_measured','FTI_measured','TBG_measured','referral_source','patient_id'],axis=1,inplace=True)

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)

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

data['target'].value_counts()

data=data[data.age<=100]

x=data.iloc[:,0:-1]

y=data.iloc[:,-1]

x

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

x.fillna(0,inplace=True)

x['sex'].value_counts()

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')



x.info()

from sklearn.preprocessing import OrdinalEncoder,LabelEncoder
```

```
ordinal_encoder=OrdinalEncoder(dtype='int64')

x.iloc[:, 1:16]=ordinal_encoder.fit_transform(x.iloc[:, 1:16])

x

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

x

label_encoder=LabelEncoder()

y_dt=label_encoder.fit_transform(y)

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

y

x=x.astype('float')

y=y.astype('float')

from sklearn.model_selection import train_test_split

x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.20,random_state=0)

from imblearn.over_sampling import SMOTE

y_train.value_counts()

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)

from sklearn.preprocessing import StandardScaler
```

```
from sklearn.inspection import permutation_importance

from sklearn.ensemble import RandomForestClassifier

import matplotlib.pyplot as plt



sc=StandardScaler()

x_bal=sc.fit_transform(x_bal)

x_test_bal=sc.transform(x_test_bal)

x_bal

columns=['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroxine_meds','sick','p
regnant','thyroid_surgery','I131_treatment','query_hypothyroid','query_hyperthyroid','lit
hium','goitre','tumor','hypopituitary','psych','TSH','T3','TT4','T4U','FTI','TBG']

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

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

x_bal

rfr=RandomForestClassifier()

rfr.fit(x_bal,y_bal)



from sklearn.inspection import permutation_importance

results=permutation_importance(rfr,x_bal,y_bal,scoring='accuracy')
```

```
feature_importance=['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroxine_meds','sick','pregnant','thyroid_surgery','I131_treatment','query_hypothyroid','query_hyperthyroid','lithium','goitre','tumor','hypopituitary','psych','TSH','T3','TT4','T4U','FTI','TBG']

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 importance feature

plt.figure(figsize=(10,10))

plt.bar(x=feature_importance, height=importance)

plt.xticks(rotation=30, ha='right')

plt.show()

x.head()

x_bal=x_bal.drop(['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroxine_meds','sick','pregnant','thyroid_surgery','I131_treatment','query_hypothyroid','query_hyperthyroid','lithium'],axis=1)

x_test_bal=x_test_bal.drop(['age','sex','on_thyroxine','query_on_thyroxine','on_antithyroxine_meds','sick','pregnant','thyroid_surgery','I131_treatment','query_hypothyroid','query_hyperthyroid','lithium'],axis=1)
```

```
x_bal.head()

x.head()

import seaborn as sns

import matplotlib.pyplot as plt

corrmat = x.corr()

f, ax = plt.subplots(figsize=(9, 8))

sns.heatmap(corrmat, ax=ax, cmap="YlGnBu", linewidths=0.1)

from sklearn.ensemble import RandomForestClassifier

# Create and fit the RandomForestClassifier object

rfr1 = RandomForestClassifier()

rfr1.fit(x_bal,y_bal)

# Predict using the trained model

y_pred = rfr1.predict(x_test_bal)

rfr1 = RandomForestClassifier()

rfr1.fit(x_bal, y_bal)



y_pred = rfr1.predict(x_test_bal)

from sklearn.metrics import classification_report

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

```
from sklearn.metrics import accuracy_score

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

train_score

from xgboost import XGBClassifier

xgb1 = XGBClassifier()

xgb1.fit(x_bal,y_bal)

y_pred = xgb1.predict(x_test_bal)

print(classification_report(y_test_bal,y_pred))

accuracy_score(y_test_bal,y_pred)

from sklearn.svm import SVC

from sklearn.metrics import accuracy_score, classification_report


svm = SVC()

svm.fit(x_bal, y_bal)

y_pred = svm.predict(x_test_bal)

print(classification_report(y_test_bal, y_pred))

train_score=accuracy_score(y_bal,svm.predict(x_bal))

train_score

model= Sequential()
```

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

model.add(Dense(units=128,activation='relu',kernel_initializer='random_uniform'))

model.add(Dropout(0.2))

model.add(Dense(units=256,activation='relu',kernel_initializer='random_uniform'))

model.add(Dropout(0.2))

model.add(Dense(units=128,activation='relu',kernel_initializer='random_uniform'))

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

model.summary()

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

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

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

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

col= ['goitre', 'tumor', 'hypopituitary', 'psych', 'TSH', 'T3', 'TT4', 'T4U', 'FTI', 'TBG']

da = [[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]]

da1 = pd.DataFrame(data = da, columns=col)

xgb1.predict(da1)

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

print(classification_report(y_test_bal,y_pred))

train_score = accuracy_score(y_bal, xgb1.predict(x_bal))
```

```
train_score

y_pred = svm.predict(x_test_bal)

print(classification_report(y_test_bal,y_pred))

train_score = accuracy_score(y_bal, xgb1.predict(x_bal))

train_score

y_pred = svm.predict(x_test_bal)

print(classification_report(y_test_bal,y_pred))

train_score=accuracy_score(y_bal,svm.predict(x_bal))

train_score

y_pred = model.predict(x_test_bal)

print(classification_report(y_test_bal,y_pred))

accuracy_score(y_test_bal,y_pred)

params = {


    'C': [0.1, 1, 10, 100, 1000],

    'gamma': [1, 0.1, 0.01, 0.001, 0.0001],

      'kernel': ['rbf','sqrt']

}

from sklearn.model_selection import RandomizedSearchCV
```

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

random_svc.best_params_

random_svc.fit(x_bal,y_bal)

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

sv1.fit(x_bal,y_bal)

print(classification_report(y_test_bal,y_pred))

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

train_score

import pickle

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

features = np.array([[0,0,0,0,0.000000,0.0,0.0,1.00,0.0,40.0]])

print(label_encoder.inverse_transform(xgb1.predict(features)))

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

data['target'].unique()

y['target'].unique()

import pickle

pickle.dump(sv1,open('throid_1_model.pkl','wb'))

HOME.HTML

<!DOCTYPE html>

<html>

<head>

** <h1>THYROID DISEASE CLASSIFICATION</h1> **

<link rel ="stylesheet" href="style.css" type="text/css" >

</head>

<body>

<h2> The two types of Thyroid disease are Hyperthyroidsm and Hypothyroidsm.When

this disorder occurs in the body , they release certain type of harmones into the body which

imbalances the body's metabolism. Machine Learning plays a very deciding role in the disease

prediction </h2>

** <button type="predict"> PREDICT</button> **

** **

</body>

</html>

PREDICT.HTML

<html>

<head>

```
    <title>THYROID DISEASE CLASSIFICATION</title>
    <link rel="stylesheet" href="style.css" type="text/css">
</head>
<body>
    <div class="main">
        <div class="Thyroid disease classification">
            <h1>THYROID DISEASE CLASSIFICATION</h1>
            <form id="thyroid" method="post">
                <label for="goitre">goitre:</label>
                <br>
                <select id="goitre" name="goitre">
                    <option value="male">male</option>
                    <option value="female">female</option>
                </select>
                <br><br>
                <label for="tumor">tumor :</label>
                <br>
                <select id="tumor" name="tumor">
                    <option value="male">male</option>
```

```
    <option value="female">female</option>
</select>
<br><br>
<label for="hypopituitary">hypopituitary :</label>
<br>
<select id="hypopituitary" name="hypopituitary">
    <option value="male">male</option>
    <option value="female">female</option>
</select>
<br><br>
<label for="psych">psych :</label>
<br>
<select id="psych" name="psych">
    <option value="male">male</option>
    <option value="female">female</option>
</select>
<br><br>
<label for="TSH">TSH:</label>
<br>
```

```
            <input type="text" name="TSH" id="TSH">
            <br><br>
            <label for="T3">T3:</label>
<br>
            <input type="text" name="T3" id="T3">
            <br><br>
            <label for="TT4">TT4:</label>
<br>
            <input type="text" name="TT4" id="TT4">
            <br><br>
            <label for="T4U">T4U:</label>
<br>
            <input type="text" name="T4U" id="T4U">
            <br><br>
            <label for="FTI">"FTI":</label>
<br>
            <input type="text" name="FTI" id="FTI">
            <br><br>
            <label for="TBG">TBG:</label>
```

```
<br>
                <input type="text" name="TBG" id="TBG">
               <br><br>
               <button type="submit"> <a href="submit.html">SUBMIT</a></button>


               <button type="home"> <a href="home.html">HOME</a></button>
            </form>
         </div>
      </div>
</body>
</html>
```

SUBMIT.HTML

```
<html>
<head>
   <center><b><h1>THYROID  DISEASE CLASSIFICATION</h1></b></center>
<link rel ="stylesheet" href="style.css" type="text/css" >
</head>
<div class="row"  style="margin-bottom: 477px;">
```

```
        <div class="col-md-3"></div>
        <div class="col-md-6">
<h2><p> Based on the given input ,it predict thyroid disease for your body condition
is['miscellaneous']


          <div class="row">
            <div class="col-md-4"></div>
                        <button type="predict"> <a
href="predict.html">PREDICT</a></button>

            <button type="home"> <a href="home.html">HOME</a></button>
            <div class="col-md-4"></div>
          </div>
        </div>
        <div class="col-md-3"></div>
    </div>
```

STYLE.CSS

```
body {
                        margin: 0;
```

```
        padding: 0;
        background: url("Thyroid-Nodule-scaled.jpg");
        background-size: 140% 100%;
        background-repeat: no-repeat;
        background-attachment: fixed;
        font-family: sans-serif;
        color: white;
}
h1 {
        text-align: center;
}
label {
        font-weight: bold;
        margin-right: 10px;
        color: red;
}
input[type="text"] {
        border: 1px solid #ccc;
        padding: 5px;
```

```
        font-size: 16px;
        border-radius: 5px;
        box-shadow: inset 0 1px 2px rgba(0,0,0,0.1);
        width: 200px;
}
button[type="submit"] {
        background-color: #4CAF50;
        color: white;
        padding: 10px 16px;
        font-size: 16px;
        border: none;
        border-radius: 5px;
        cursor: pointer;
}
button[type="predict"] {
        background-color: #4CAF50;
        color: white;
        padding: 10px 16px;
        font-size: 16px;
```

```
        border: none;
        border-radius: 5px;
        cursor: pointer;
}
button[type="home"] {
        background-color: #4CAF50;
        color: white;
        padding: 10px 16px;
        font-size: 16px;
        border: none;
        border-radius: 5px;
        cursor: pointer;
}
```