ARIGNAR ANNA GOVERNMENT ARTS COLLEGE VILLUPURAM

THYROID DISEASE CLASSIFICATION

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INTRODUCTION

OVERVIEW

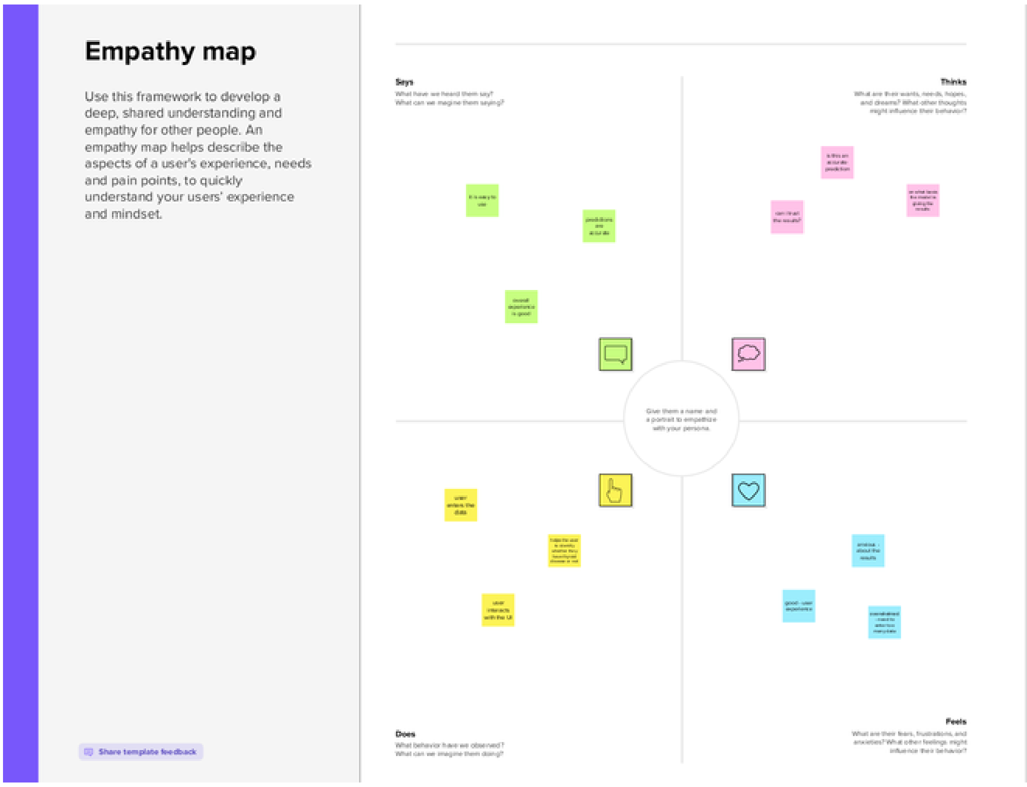
Thyroid disease classification project is used to predict the type of thyroid disease the user has based on their input value. Machine learning algorithms plays a very important role in disease prediction. The web app is used to collect the data from the user and the model will predict the disease type. The result is shown on the user interface of the web app.

PURPOSE

Purpose of this project is to predict the type of thyroid disease. Machine algorithm is trained by a huge amount of data set. Based on that data the model will predict the type of thyroid disease. The main purpose of this project is to classify the thyroid disease. This project is also focused on solving the problem in health system by analyzing huge amounts of data set and predict the type of disease.

PROBLEM DEFINITION & DESIGN THINKING

EMPATHY MAP



Empathy map

Use this framework to develop a deep, shared understanding and empathy for other people. An empathy map helps describe the aspects of a user's experience, needs and pain points, to quickly understand your users' experience and mindset.

Share template feedback

Says
What have we heard them say?
What can we imagine them saying?

Thinks
What are their wants, needs, hopes, and dreams? What other thoughts might influence their behavior?

it is easy to use

predictions are accurate

overall experience is good

is this an accurate prediction

can i trust the results?

on what basis the model is giving the results

Give them a name and a portrait to empathize with your persona.

user enters the data

helps the user to identify whether they have thyroid disease or not

user interacts with the UI

anxious - about the results

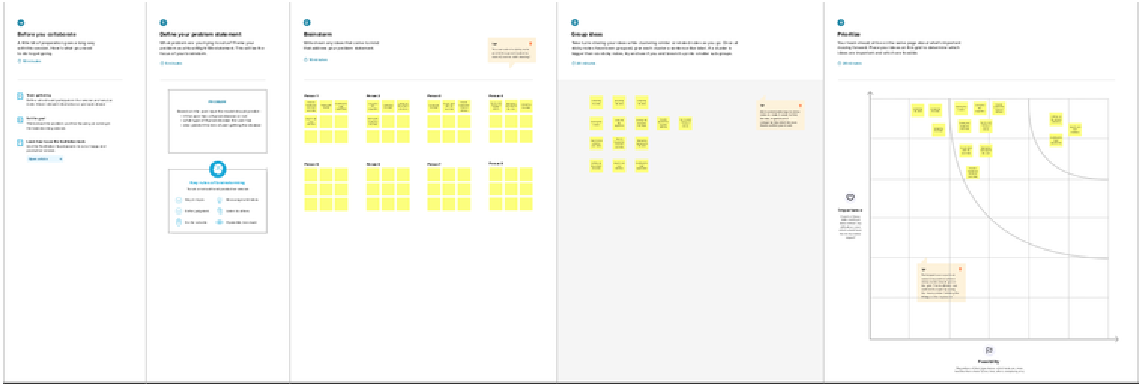
good - user experience

overwhelmed - need to enter too many data

Does
What behavior have we observed?
What can we imagine them doing?

Feels
What are their fears, frustrations, and anxieties? What other feelings might influence their behavior?

IDEATION & BRAINSTORMING MAP



Before you collaborate

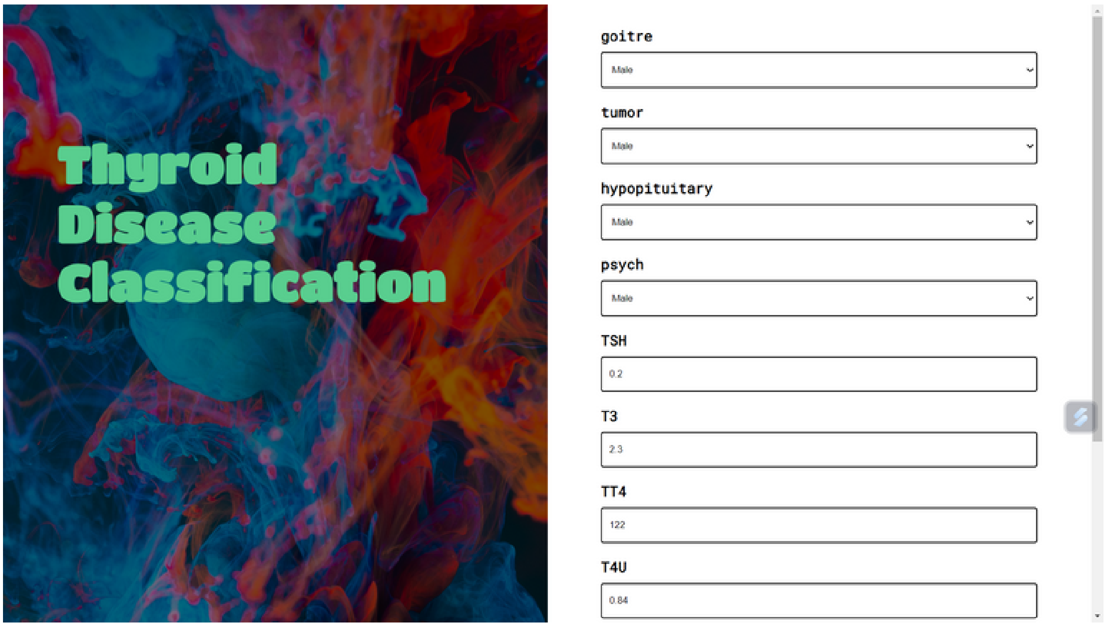
Define your problem statement

Brainstorm

Group ideas

Prioritize

RESULT



Thyroid Disease Classification

goitre: Male

tumor: Male

hypopituitary: Male

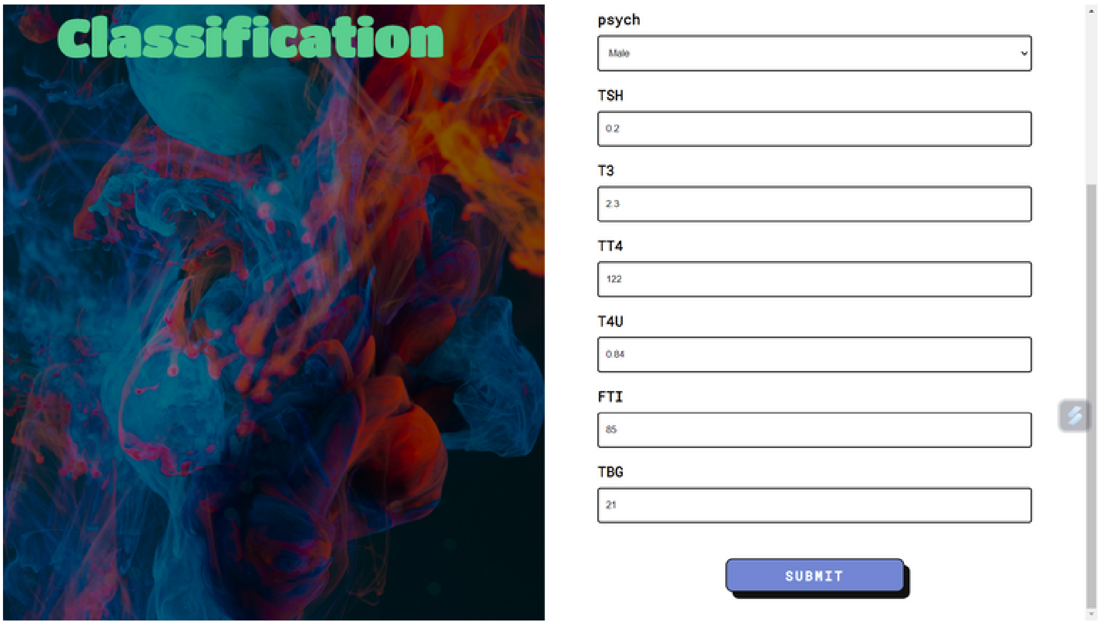
psych: Male

TSH: 0.2

T3: 2.3

TT4: 122

T4U: 0.84



Classification

psych: Male

TSH: 0.2

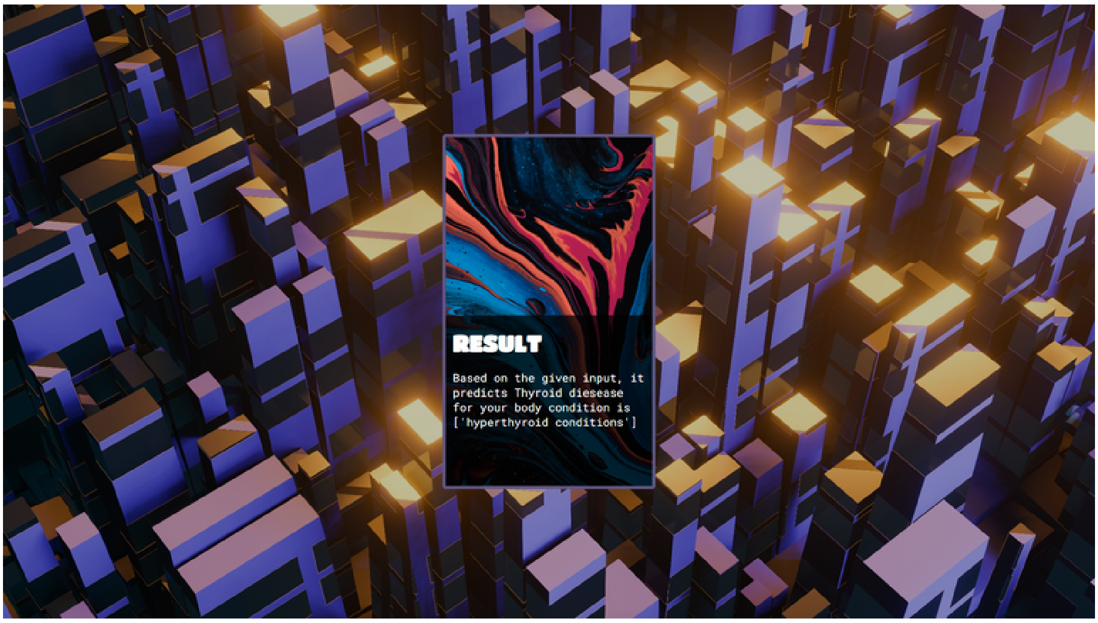
T3: 2.3

TT4: 122

T4U: 0.84

FTI: 85

TBG: 21



RESULT

Based on the given input, it predicts Thyroid dieseae for your body condition is ['hyperthyroid conditions']

ADVANTAGES

- Reliable prediction
- if the model predicts the disease in the early stage then the disease can get cured
- it helps to solve problems in the health care

DISADVANTAGES

- Predictions are not 100% accurate
- False positives
- False negatives

APPLICATIONS

- DISEASE PREDICTION
- HEALTH CARE
- MORE ACCURATE HEALTH RECORDS
- VISUALIZATION OF MEDICAL DATA
- IMPROVED DIAGNOSIS

CONCLUSION

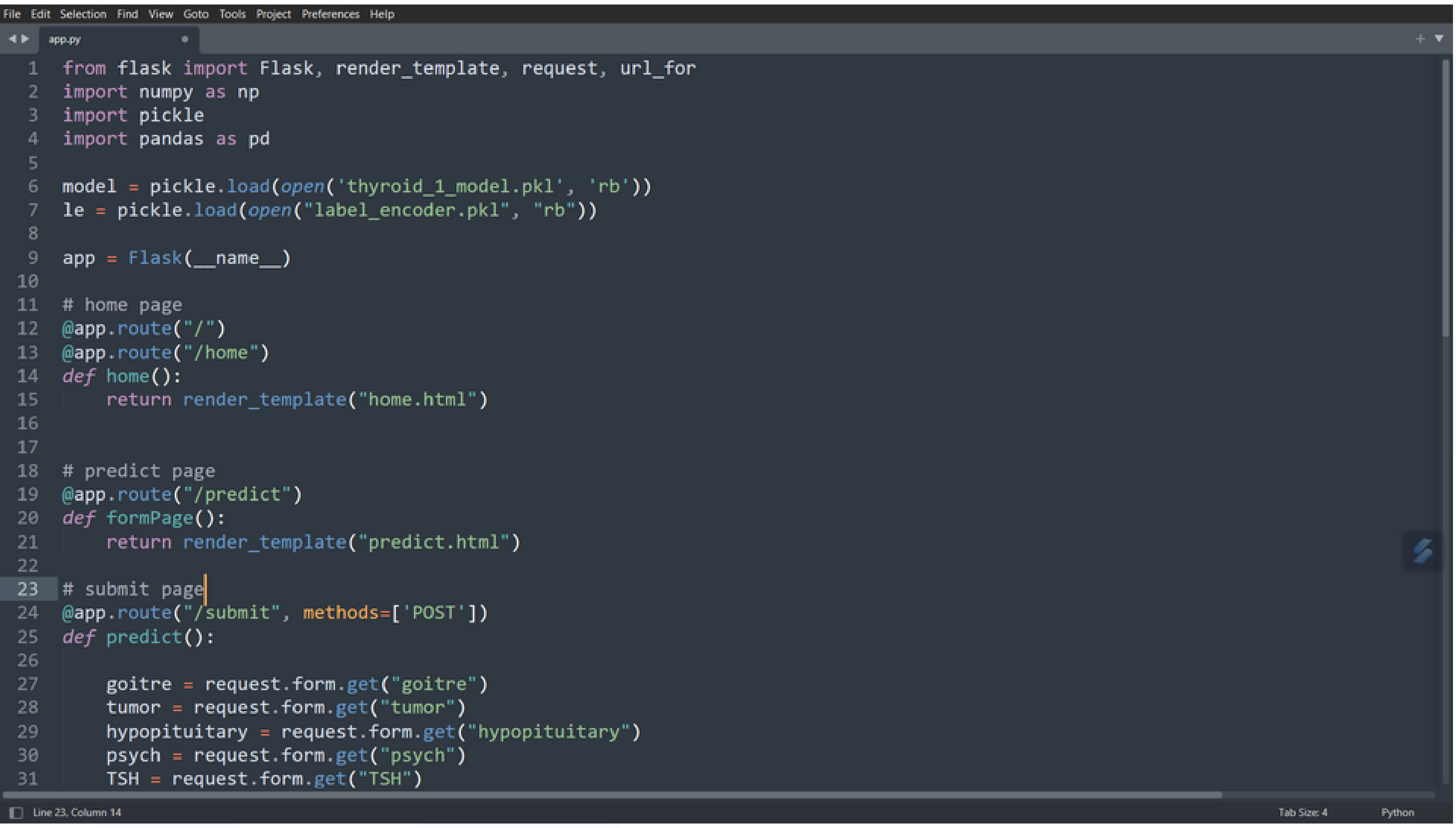
In this project we try to find the type of thyroid disease of a user based on their data. Machine learning algorithms are used for the prediction of the disease. Machine learning models are trained to improve the accuracy of the result and to minimize the false positives and false negatives errors. We built a flask application for the user to input the data. Machine learning model is integrated within the flask application and process the data entered by the user and predicts the type of thyroid disease.

FUTURE SCOPE

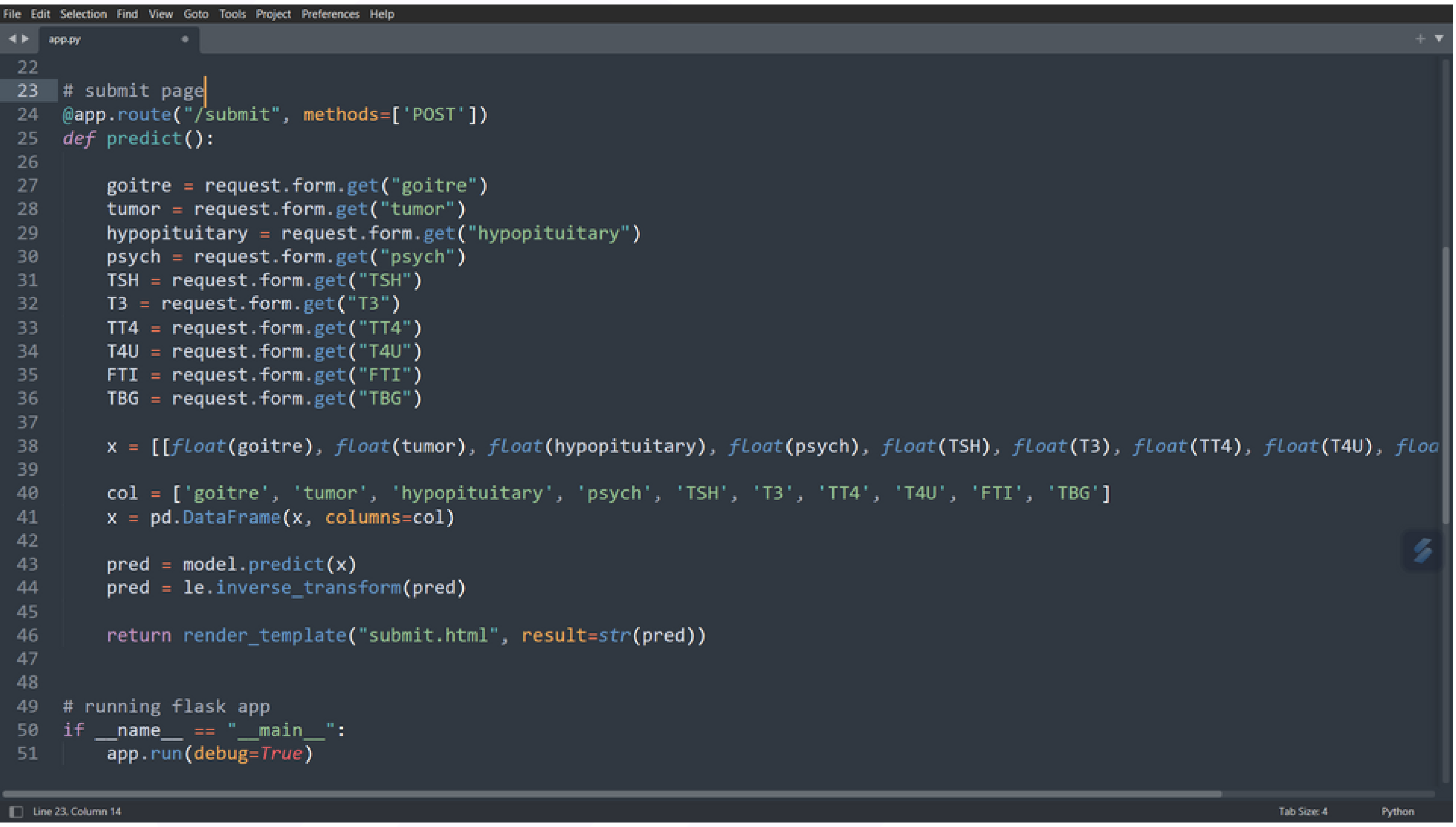
In Future we would like to increase the prediction of the machine learning algorithm to 100% accuracy. Train the model with even huge amount of dataset. Then try to minimize the errors for false positives and false negatives

APPENDIX

SOURCE CODE


File Edit Selection Find View Goto Tools Project Preferences Help
app.py
Line 23, Column 14
Tab Size: 4
Python

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

model = pickle.load(open('thyroid_1_model.pkl', 'rb'))
le = pickle.load(open("label_encoder.pkl", "rb"))

app = Flask(__name__)

# home page
@app.route("/")
@app.route("/home")
def home():
    return render_template("home.html")


# predict page
@app.route("/predict")
def formPage():
    return render_template("predict.html")

# submit page
@app.route("/submit", methods=['POST'])
def predict():

    goitre = request.form.get("goitre")
    tumor = request.form.get("tumor")
    hypopituitary = request.form.get("hypopituitary")
    psych = request.form.get("psych")
    TSH = request.form.get("TSH")
```


File Edit Selection Find View Goto Tools Project Preferences Help
app.py
Line 23, Column 14
Tab Size: 4
Python

```python

# submit page
@app.route("/submit", methods=['POST'])
def predict():

    goitre = request.form.get("goitre")
    tumor = request.form.get("tumor")
    hypopituitary = request.form.get("hypopituitary")
    psych = request.form.get("psych")
    TSH = request.form.get("TSH")
    T3 = request.form.get("T3")
    TT4 = request.form.get("TT4")
    T4U = request.form.get("T4U")
    FTI = request.form.get("FTI")
    TBG = request.form.get("TBG")

    x = [[float(goitre), float(tumor), float(hypopituitary), float(psych), float(TSH), float(T3), float(TT4), float(T4U), floa

    col = ['goitre', 'tumor', 'hypopituitary', 'psych', 'TSH', 'T3', 'TT4', 'T4U', 'FTI', 'TBG']
    x = pd.DataFrame(x, columns=col)

    pred = model.predict(x)
    pred = le.inverse_transform(pred)

    return render_template("submit.html", result=str(pred))


# running flask app
if __name__ == "__main__":
    app.run(debug=True)
```

SOURCE CODE

[1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
```

[2]:
```
data = pd.read_csv("/content/data.csv")
```

[3]:
```
data.head()
```

[3]:
```
   age sex on_thyroxine query_on_thyroxine on_antithyroid_meds sick pregnant  \
0   29   F            f                  f                   f    f        f
1   29   F            f                  f                   f    f        f
2   41   F            f                  f                   f    f        f
3   36   F            f                  f                   f    f        f
4   32   F            f                  f                   f    f        f

  thyroid_surgery I131_treatment query_hypothyroid  …    TT4 T4U_measured  \
0               f              f                 t  …    NaN            f
1               f              f                 f  …  128.0            f
2               f              f                 f  …    NaN            f
3               f              f                 f  …    NaN            f
4               f              f                 f  …    NaN            f

  T4U FTI_measured FTI TBG_measured   TBG  referral_source target  patient_id
0 NaN            f NaN            f   NaN            other      -   840801013
1 NaN            f NaN            f   NaN            other      -   840801014
2 NaN            f NaN            t  11.0            other      -   840801042
3 NaN            f NaN            t  26.0            other      -   840803046
4 NaN            f NaN            t  36.0            other      S   840803047

[5 rows x 31 columns]
```

[4]:
```
data['target'].unique()
```

[4]:
```
array(['-', 'S', 'F', 'AK', 'R', 'I', 'M', 'N', 'G', 'K', 'A', 'KJ', 'L',
       'MK', 'Q', 'J', 'C|I', 'O', 'LJ', 'H|K', 'D', 'GK', 'MI', 'P',
       'FK', 'B', 'GI', 'C', 'GKJ', 'OI', 'D|R', 'E'], dtype=object)
```

[5]:
```
data.shape
```

[5]:
```
(9172, 31)
```

[6]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 9172 entries, 0 to 9171
Data columns (total 31 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   age                  9172 non-null   int64
 1   sex                  8865 non-null   object
 2   on_thyroxine         9172 non-null   object
 3   query_on_thyroxine   9172 non-null   object
 4   on_antithyroid_meds  9172 non-null   object
 5   sick                 9172 non-null   object
 6   pregnant             9172 non-null   object
 7   thyroid_surgery      9172 non-null   object
 8   I131_treatment       9172 non-null   object
 9   query_hypothyroid    9172 non-null   object
 10  query_hyperthyroid   9172 non-null   object
 11  lithium              9172 non-null   object
 12  goitre               9172 non-null   object
 13  tumor                9172 non-null   object
 14  hypopituitary        9172 non-null   object
 15  psych                9172 non-null   object
 16  TSH_measured         9172 non-null   object
 17  TSH                  8330 non-null   float64
 18  T3_measured          9172 non-null   object
 19  T3                   6568 non-null   float64
 20  TT4_measured         9172 non-null   object
 21  TT4                  8730 non-null   float64
 22  T4U_measured         9172 non-null   object
 23  T4U                  8363 non-null   float64
 24  FTI_measured         9172 non-null   object
 25  FTI                  8370 non-null   float64
 26  TBG_measured         9172 non-null   object
 27  TBG                  349 non-null    float64
 28  referral_source      9172 non-null   object
 29  target               9172 non-null   object
 30  patient_id           9172 non-null   int64
dtypes: float64(6), int64(2), object(23)
memory usage: 2.2+ MB
```

[7]:
```
data.isnull().sum()
```

[7]:
```
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
```

[8]:
```
data.drop(['TSH_measured', 'T3_measured', 'TT4_measured', 'T4U_measured',␣
 ↪'FTI_measured', 'TBG_measured', 'referral_source', 'patient_id'], axis=1,␣
 ↪inplace = True)
```

[9]:
```
data.head()
```

[9]:
```
   age sex on_thyroxine query_on_thyroxine on_antithyroid_meds sick pregnant  \
0   29   F            f                  f                   f    f        f
1   29   F            f                  f                   f    f        f
2   41   F            f                  f                   f    f        f
3   36   F            f                  f                   f    f        f
4   32   F            f                  f                   f    f        f

  thyroid_surgery I131_treatment query_hypothyroid  … tumor hypopituitary  \
0               f              f                 t  …     f             f
1               f              f                 f  …     f             f
2               f              f                 f  …     f             f
3               f              f                 f  …     f             f
4               f              f                 f  …     f             f

  psych  TSH   T3    TT4  T4U  FTI   TBG  target
0     f  0.3  NaN    NaN  NaN  NaN   NaN       -
1     f  1.6  1.9  128.0  NaN  NaN   NaN       -
2     f  NaN  NaN    NaN  NaN  NaN  11.0       -
3     f  NaN  NaN    NaN  NaN  NaN  26.0       -
4     f  NaN  NaN    NaN  NaN  NaN  36.0       S

[5 rows x 23 columns]
```

[10]:

```
data['target']
```

[10]:

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

[11]:

```
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)
```

[12]:
```
data
```

[12]:
```
      age sex on_thyroxine query_on_thyroxine on_antithyroid_meds sick  \
0      29   F            f                  f                   f    f
1      29   F            f                  f                   f    f
2      41   F            f                  f                   f    f
3      36   F            f                  f                   f    f
4      32   F            f                  f                   f    f
…   …  ..          …                …                 …  …
9167   56   M            f                  f                   f    f
9168   22   M            f                  f                   f    f
9169   69   M            f                  f                   f    f
9170   47   F            f                  f                   f    f
9171   31   M            f                  f                   f    f

     pregnant thyroid_surgery I131_treatment query_hypothyroid  … tumor  \
0           f               f              f                 t  …     f
1           f               f              f                 f  …     f
2           f               f              f                 f  …     f
3           f               f              f                 f  …     f
4           f               f              f                 f  …     f
…       …             …            …              …  …   …
9167        f               f              f                 f  …     f
9168        f               f              f                 f  …     f
9169        f               f              f                 f  …     f
9170        f               f              f                 f  …     f
9171        f               f              f                 t  …     f

     hypopituitary psych  TSH   T3    TT4   T4U   FTI   TBG           target
0                f     f  0.3  NaN    NaN   NaN   NaN   NaN              NaN
1                f     f  1.6  1.9  128.0   NaN   NaN   NaN              NaN
2                f     f  NaN  NaN    NaN   NaN   NaN  11.0              NaN
3                f     f  NaN  NaN    NaN   NaN   NaN  26.0              NaN
4                f     f  NaN  NaN    NaN   NaN   NaN  36.0    miscellaneous
…            …   …  …  …    …   …   …   …              …
9167             f     f  NaN  NaN   64.0  0.83  77.0   NaN              NaN
9168             f     f  NaN  NaN   91.0  0.92  99.0   NaN              NaN
9169             f     f  NaN  NaN  113.0  1.27  89.0   NaN  binding protein
9170             f     f  NaN  NaN   75.0  0.85  88.0   NaN              NaN
9171             f     f  NaN  NaN   66.0  1.02  65.0   NaN              NaN
```

```
[9172 rows x 23 columns]
```

[13]:

```
data.isnull().sum()
```

[13]:

```
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
```

[14]:

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

[15]:

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

[15]:

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

[16]:

```
data['target'].isnull().sum()
```

[16]:

```
0
```

[17]:

```
data.head()
```

[17]:
```
     age sex on_thyroxine query_on_thyroxine on_antithyroid_meds sick pregnant  \
4     32   F            f                  f                   f    f        f
18    63   F            t                  f                   f    t        f
32    41   M            f                  f                   f    f        f
33    71   F            t                  f                   f    f        f
39    55   F            t                  f                   f    f        f

   thyroid_surgery I131_treatment query_hypothyroid  … tumor hypopituitary  \
4                f              f                 f  …     f             f
18               f              f                 f  …     f             f
32               f              f                 f  …     f             f
33               f              f                 f  …     f             f
39               f              f                 t  …     f             f

   psych        TSH  T3    TT4   T4U   FTI   TBG                  target
4      f        NaN  NaN    NaN   NaN   NaN  36.0           miscellaneous
18     f  68.000000  NaN   48.0  1.02  47.0   NaN  hypothyroid conditions
32     f   0.050000  1.6   39.0  1.00  39.0   NaN           miscellaneous
33     f   0.050000  NaN  126.0  1.38  91.0   NaN         binding protein
39     f   9.599999  2.4  136.0  1.48  92.0   NaN     replacement therapy

[5 rows x 23 columns]
```

[18]:
```
data.describe()
```

[18]:
```
               age          TSH           T3          TT4          T4U  \
count  2237.000000  2087.000000  1643.000000  2140.000000  2059.000000
mean     52.792579    14.930791     1.961875   116.390495     1.013439
std      19.677450    46.204092     1.452238    60.351600     0.280222
min       1.000000     0.005000     0.050000     2.000000     0.170000
25%      36.000000     0.255000     1.000000    76.000000     0.850000
50%      56.000000     2.000000     1.700000   109.000000     0.960000
75%      69.000000     8.799999     2.500000   156.000000     1.120000
max      95.000000   530.000000    18.000000   600.000000     2.330000

               FTI         TBG
count  2060.000000   98.000000
mean    120.363369   47.717347
std      70.996728   32.398750
min       1.400000    9.299999
25%      83.000000   32.000000
50%     109.000000   36.000000
75%     157.000000   46.750000
max     881.000000  200.000000
```

[19]:
```
data[data.age > 100]
```

[19]:
```
Empty DataFrame
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, TSH, T3, TT4,
T4U, FTI, TBG, target]
Index: []

[0 rows x 23 columns]
```

[20]:
```
data['age']=np.where((data.age > 100), np.nan, data.age)
```

[21]:
```
data
```

[21]:
```
       age sex on_thyroxine query_on_thyroxine on_antithyroid_meds sick  \
4     32.0   F            f                  f                   f    f   
18    63.0   F            t                  f                   f    t   
32    41.0   M            f                  f                   f    f   
33    71.0   F            t                  f                   f    f   
39    55.0   F            t                  f                   f    f   
…      …  . .          …                 …                  …  …   
9153  64.0   M            f                  f                   f    f   
9157  60.0   M            f                  f                   t    f   
9158  64.0   M            f                  f                   f    f   
9162  36.0   F            f                  f                   f    f   
9169  69.0   M            f                  f                   f    f   

     pregnant thyroid_surgery I131_treatment query_hypothyroid  … tumor  \
4           f               f              f                 f  …     f   
18          f               f              f                 f  …     f   
32          f               f              f                 f  …     f   
33          f               f              f                 f  …     f   
39          f               f              f                 t  …     f   
…        …             …            …               …  …   …   
9153        f               f              f                 f  …     f   
9157        f               f              f                 f  …     f   
9158        f               f              f                 t  …     f   
9162        f               f              f                 f  …     f   
9169        f               f              f                 f  …     f   

     hypopituitary psych        TSH   T3    TT4   T4U   FTI   TBG  \
4                f     f        NaN  NaN    NaN   NaN   NaN  36.0   
18               f     f  68.000000  NaN   48.0  1.02  47.0   NaN   
32               f     f   0.050000  1.6   39.0  1.00  39.0   NaN   
33               f     f   0.050000  NaN  126.0  1.38  91.0   NaN   
39               f     f   9.599999  2.4  136.0  1.48  92.0   NaN   
…             …   …        …  …    …  …   …   …   
9153             f     f   0.810000  NaN   31.0  0.55  56.0   NaN   
```

```
9157             f     f    0.180000  NaN   28.0  0.87  32.0   NaN
9158             f     f         NaN  NaN   44.0  0.53  83.0   NaN
9162             f     f         NaN  NaN   84.0  1.26  67.0   NaN
9169             f     f         NaN  NaN  113.0  1.27  89.0   NaN

                      target
4              miscellaneous
18    hypothyroid conditions
32             miscellaneous
33           binding protein
39       replacement therapy
…                      …
9153          general health
9157          general health
9158         binding protein
9162         binding protein
9169         binding protein

[2237 rows x 23 columns]
```

[22]:

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

[23]:

```
data.isnull().sum()
```

[23]:

```
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
```

[24]:
```
x['sex'].unique()
```

[24]:
```
array(['F', 'M', nan], dtype=object)
```

[25]:
```
x['sex'].replace(np.nan, 'F', inplace=True)
```

[26]:
```
x['sex'].value_counts()
```

[26]:
```
F    1701
M     536
Name: sex, dtype: int64
```

[27]:
```
x.isnull().sum()
```

[27]:
```
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
```

[28]:
```
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
```

[29]:

```python
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')
```

[30]:

```python
from sklearn.preprocessing import OrdinalEncoder, LabelEncoder

ordinal_encoder = OrdinalEncoder(dtype = 'int64')
x.iloc[:, 1:16] = ordinal_encoder.fit_transform(x.iloc[:, 1:16])
```

```
<ipython-input-30-6681d58b2586>:4: DeprecationWarning: In a future version,
`df.iloc[:, i] = newvals` will attempt to set the values inplace instead of
always setting a new array. To retain the old behavior, use either
`df[df.columns[i]] = newvals` or, if columns are non-unique, `df.isetitem(i,
newvals)`
  x.iloc[:, 1:16] = ordinal_encoder.fit_transform(x.iloc[:, 1:16])
```

```
[31]: x.head()
```

```
[31]:      age  sex  on_thyroxine  query_on_thyroxine  on_antithyroid_meds  sick  \
      4   32.0    0             0                   0                    0     0
      18  63.0    0             1                   0                    0     1
      32  41.0    1             0                   0                    0     0
      33  71.0    0             1                   0                    0     0
      39  55.0    0             1                   0                    0     0

          pregnant  thyroid_surgery  I131_treatment  query_hypothyroid  ...  goitre  \
      4          0                0               0                  0  ...       0
      18         0                0               0                  0  ...       0
      32         0                0               0                  0  ...       0
      33         0                0               0                  0  ...       0
      39         0                0               0                  1  ...       0

          tumor  hypopituitary  psych        TSH   T3    TT4   T4U   FTI   TBG
      4       0              0      0        NaN  NaN    NaN   NaN   NaN  36.0
      18      0              0      0  68.000000  NaN   48.0  1.02  47.0   NaN
      32      0              0      0   0.050000  1.6   39.0  1.00  39.0   NaN
      33      0              0      0   0.050000  NaN  126.0  1.38  91.0   NaN
      39      0              0      0   9.599999  2.4  136.0  1.48  92.0   NaN

      [5 rows x 22 columns]
```

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

```
[32]:      age  sex  on_thyroxine  query_on_thyroxine  on_antithyroid_meds  sick  \
      4   32.0    0             0                   0                    0     0
      18  63.0    0             1                   0                    0     1
      32  41.0    1             0                   0                    0     0
      33  71.0    0             1                   0                    0     0
      39  55.0    0             1                   0                    0     0

          pregnant  thyroid_surgery  I131_treatment  query_hypothyroid  ...  goitre  \
      4          0                0               0                  0  ...       0
      18         0                0               0                  0  ...       0
      32         0                0               0                  0  ...       0
      33         0                0               0                  0  ...       0
      39         0                0               0                  1  ...       0

          tumor  hypopituitary  psych       TSH   T3    TT4   T4U   FTI   TBG
      4       0              0      0         0    0      0     0     0  36.0
      18      0              0      0      68.0    0   48.0  1.02  47.0     0
      32      0              0      0      0.05  1.6   39.0   1.0  39.0     0
      33      0              0      0      0.05    0  126.0  1.38  91.0     0
```

```
39      0              0      0  9.599999  2.4  136.0  1.48  92.0     0

[5 rows x 22 columns]
```

[33]:
```
label_encoder = LabelEncoder()
y_dt = label_encoder.fit_transform(y)
```

[34]:
```
y = pd.DataFrame(y_dt, columns=['target'])
y
```

[34]:
```
      target
0          5
1          4
2          5
3          1
4          6
…        …
2232       2
2233       2
2234       1
2235       1
2236       1

[2237 rows x 1 columns]
```

[35]:
```
y.value_counts(normalize=True)
```

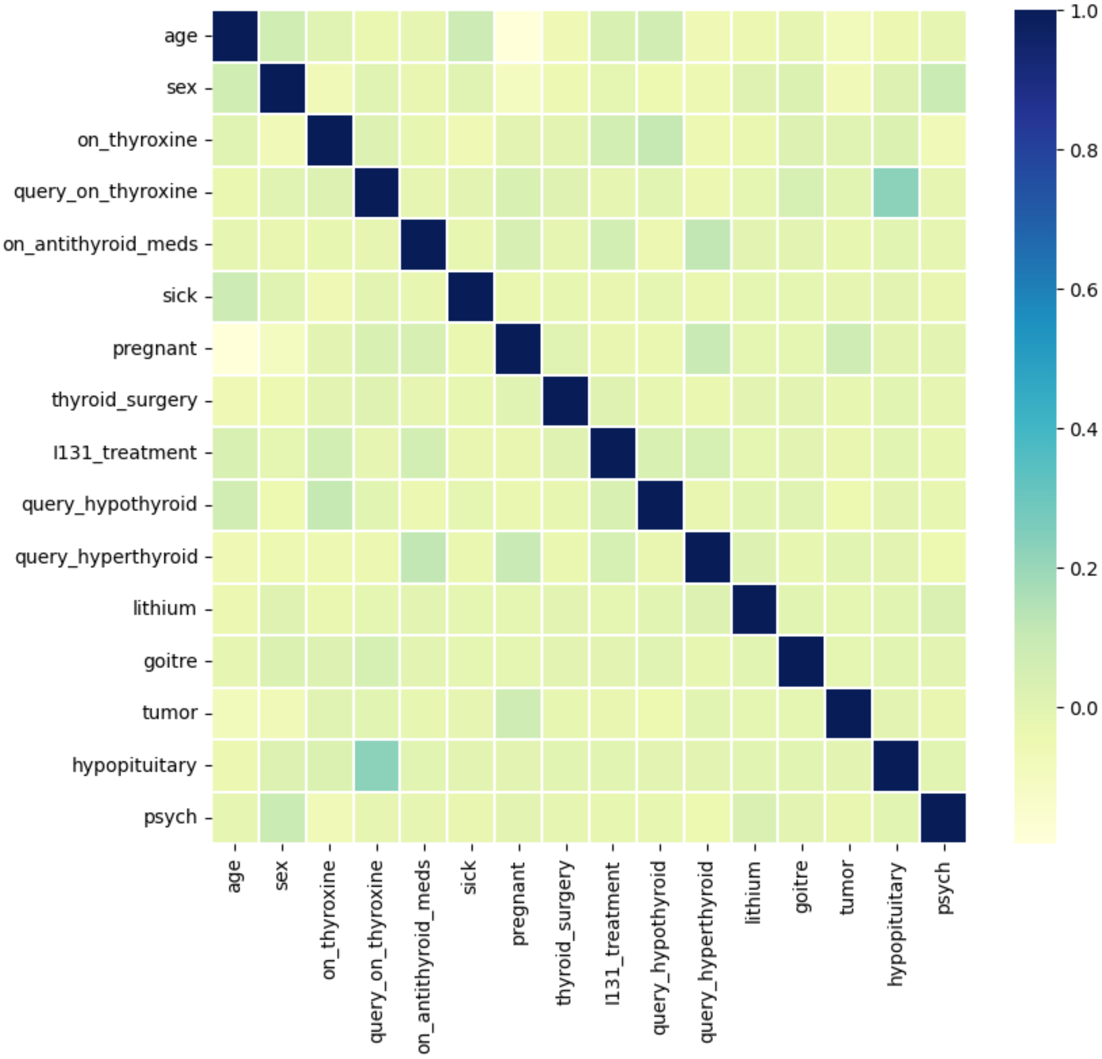
[35]:
```
target
4         0.265087
2         0.194904
1         0.168082
6         0.150201
5         0.125615
3         0.081359
0         0.014752
dtype: float64
```

[36]:
```
import seaborn as sns
corrmat = x.corr()

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

```
<ipython-input-36-64415348dfec>:2: FutureWarning: The default value of
numeric_only in DataFrame.corr is deprecated. In a future version, it will
default to False. Select only valid columns or specify the value of numeric_only
to silence this warning.
```

```
corrmat = x.corr()
```

[36]:
```
<Axes: >
```



[37]:
```
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)
```

[38]:
```
y_train.value_counts()
```

[38]:
```
target
4         471
2         351
1         302
```

```
6        265
5        230
3        144
0         26
dtype: int64
```

[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)
```

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

[41]:
```
x_bal
```

[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]])
```

[42]:
```
x_test_bal
```

[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]])
```

[43]:
```
y_bal.value_counts()
```

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

[44]:
```
columns = ['age', 'sex', 'on_thyroxine', 'query_on_thyroxine',␣
 ↪'on_antithyroid_meds', 'sick', 'pregnant', 'thyroid_surgery',␣
 ↪'I131_treatment', 'query_hypothyroid', 'query_hypothyroid', 'lithium',␣
 ↪'goitre', 'tumor', 'hypopituitary', 'psych', 'TSH', 'T3', 'TT4', 'T4U',␣
 ↪'FTI', 'TBG']
```

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

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

[47]:
```
x_bal
```

[47]:
```
           age       sex  on_thyroxine  query_on_thyroxine  \
0    -1.627215 -0.440605     -0.423800           -0.105069
1    -0.115614 -0.440605      2.359604           -0.105069
2     1.187490  2.269608     -0.423800           -0.105069
3    -1.366594 -0.440605     -0.423800           -0.105069
4    -0.167738 -0.440605     -0.423800           -0.105069
…         …       …           …                 …
3292  0.546923 -0.440605      2.359604           -0.105069
3293  0.383062 -0.440605      2.359604           -0.105069
3294  1.395987 -0.440605      2.359604           -0.105069
3295  0.728028 -0.440605      2.359604           -0.105069
3296  1.156281 -0.440605      2.359604           -0.105069

      on_antithyroid_meds      sick  pregnant  thyroid_surgery  \
0               -0.158703 -0.141815 -0.137297        -0.239601
1               -0.158703 -0.141815 -0.137297        -0.239601
2               -0.158703 -0.141815 -0.137297        -0.239601
3               -0.158703 -0.141815 -0.137297        -0.239601
4               -0.158703 -0.141815 -0.137297        -0.239601
…                   …       …       …              …
3292            -0.158703 -0.141815 -0.137297        -0.239601
3293            -0.158703 -0.141815 -0.137297        -0.239601
3294            -0.158703 -0.141815 -0.137297        -0.239601
```

```
3295            -0.158703 -0.141815 -0.137297        -0.239601
3296            -0.158703 -0.141815 -0.137297        -0.239601

      I131_treatment  query_hypothyroid  …    goitre     tumor  \
0          -0.162675          -0.230986  … -0.052319 -0.137297
1          -0.162675          -0.230986  … -0.052319 -0.137297
2          -0.162675          -0.230986  … -0.052319 -0.137297
3          -0.162675          -0.230986  … -0.052319  7.283487
4          -0.162675          -0.230986  … -0.052319 -0.137297
…              …                …  …       …       …
3292       -0.162675          -0.230986  … -0.052319 -0.137297
3293       -0.162675          -0.230986  … -0.052319 -0.137297
3294       -0.162675          -0.230986  … -0.052319 -0.137297
3295       -0.162675          -0.230986  … -0.052319 -0.137297
3296       -0.162675          -0.230986  … -0.052319 -0.137297

      hypopituitary     psych       TSH        T3       TT4       T4U  \
0         -0.024637 -0.107982 -0.315458 -1.035358 -1.704935 -2.508707
1         -0.024637 -0.107982 -0.090056  0.155233 -0.197223 -0.262591
2         -0.024637 -0.107982 -0.278907 -0.471394 -0.227079  0.170395
3         -0.024637 -0.107982 -0.284999  0.969848  0.041622  0.495134
4         -0.024637 -0.107982 -0.306321  4.541622  1.459767 -0.127283
…             …       …       …       …       …       …
3292      -0.024637 -0.107982 -0.114424  0.343221 -0.148122 -0.146517
3293      -0.024637 -0.107982 -0.309176 -0.856540  0.565143 -0.513902
3294      -0.024637 -0.107982 -0.095452 -0.172405  0.248906  0.436150
3295      -0.024637 -0.107982 -0.311566  0.087864  1.071643  0.143333
3296      -0.024637 -0.107982 -0.072439  0.079407 -0.200359  0.397235

           FTI       TBG
0    -1.400881  3.294451
1     0.072098 -0.194940
2    -0.193521 -0.194940
3    -0.133153 -0.194940
4     1.496783 -0.194940
…        …       …
3292  0.040168 -0.194940
3293  1.085434 -0.194940
3294  0.061010 -0.194940
3295  0.890866 -0.194940
3296 -0.265887 -0.194940

[3297 rows x 22 columns]
```

[48]:
```python
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
```

```
<ipython-input-48-0d8934587252>: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)
```

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

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

```
[49]: 0.905152224824356
```

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

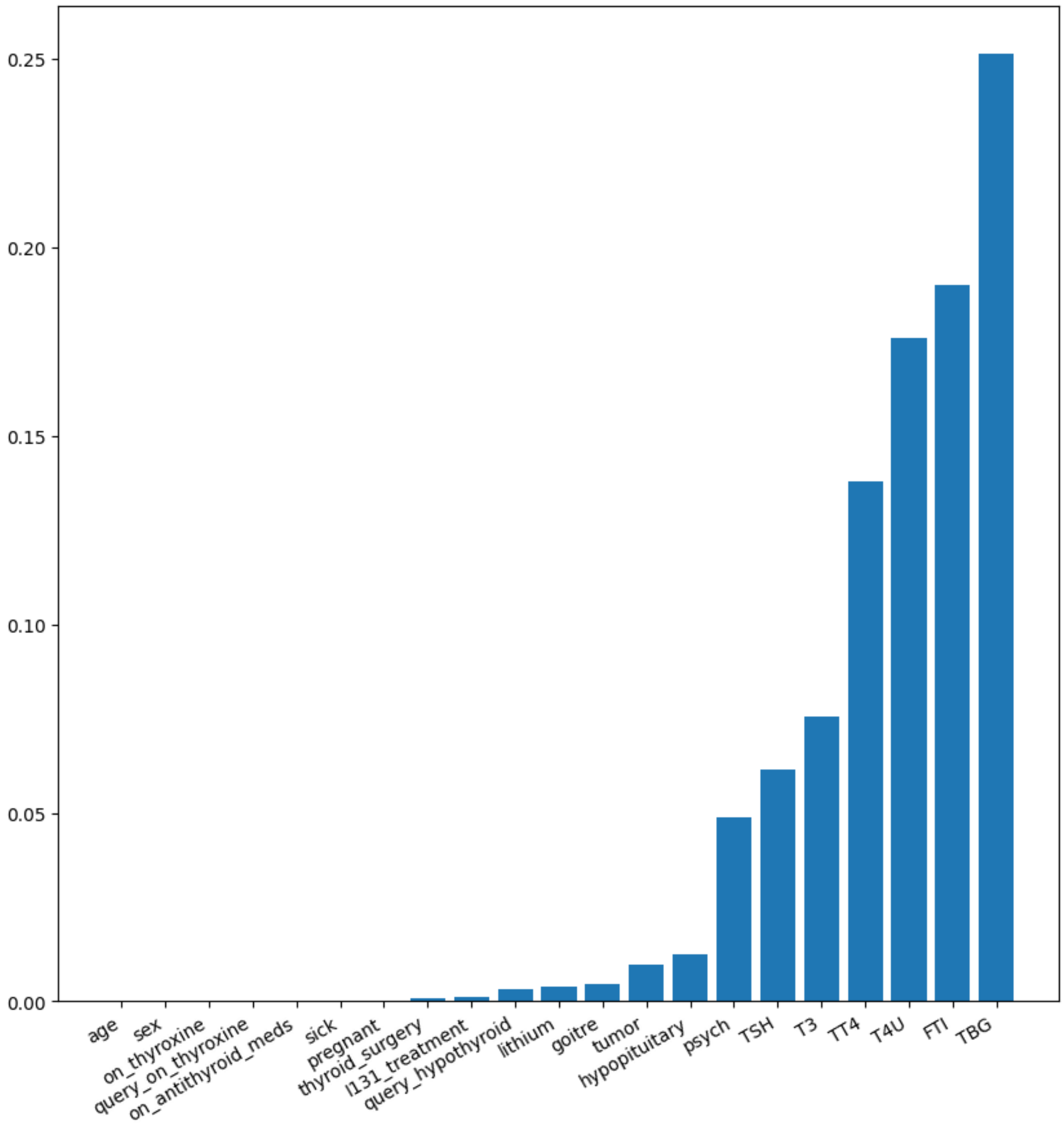
```
[50]: 1.0
```

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

```
[52]: feature_importance = ['age', 'sex', 'on_thyroxine', 'query_on_thyroxine',␣
        ↪'on_antithyroid_meds', 'sick', 'pregnant', 'thyroid_surgery',␣
        ↪'I131_treatment', 'query_hypothyroid', 'query_hypothyroid', 'lithium',␣
        ↪'goitre', 'tumor', 'hypopituitary', 'psych', 'TSH', 'T3', 'TT4', 'T4U',␣
        ↪'FTI', 'TBG']
      importance = results.importances_mean
      importance = np.sort(importance)

      for i, v in enumerate(importance):
        i = feature_importance[i]
        print('feature: {:<20} Score: {}'.format(i, v))

      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: 0.00024264482863207705
feature: pregnant             Score: 0.0003033060357900963
```

```
feature: thyroid_surgery      Score: 0.0008492569002122918
feature: I131_treatment       Score: 0.0012132241431604962
feature: query_hypothyroid    Score: 0.0015165301789505925
feature: query_hypothyroid    Score: 0.0032757051865332175
feature: lithium              Score: 0.003760994843797394
feature: goitre               Score: 0.00461025174400973
feature: tumor                Score: 0.009766454352441657
feature: hypopituitary        Score: 0.012617531088868672
feature: psych                Score: 0.048892932969366074
feature: TSH                  Score: 0.06138914164391873
feature: T3                   Score: 0.07540188049742189
feature: TT4                  Score: 0.13794358507734306
feature: T4U                  Score: 0.17585683955110704
feature: FTI                  Score: 0.18999090081892628
feature: TBG                  Score: 0.251319381255687
```



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

[54]:
```
x_test_bal.drop(["age", "sex", "on_thyroxine", "query_on_thyroxine", "on_antithyroid_meds", "sick", "pregnant", "thyroid_surgery", "I131_treatment", "query_hypothyroid", "query_hypothyroid", "lithium"], axis= 1, inplace=True)
```

[55]:
```
x_bal.head()
```

[55]:

```
     goitre    tumor  hypopituitary     psych       TSH        T3       TT4  \
0 -0.052319 -0.137297      -0.024637 -0.107982 -0.315458 -1.035358 -1.704935
1 -0.052319 -0.137297      -0.024637 -0.107982 -0.090056  0.155233 -0.197223
2 -0.052319 -0.137297      -0.024637 -0.107982 -0.278907 -0.471394 -0.227079
3 -0.052319  7.283487      -0.024637 -0.107982 -0.284999  0.969848  0.041622
4 -0.052319 -0.137297      -0.024637 -0.107982 -0.306321  4.541622  1.459767

        T4U       FTI       TBG
0 -2.508707 -1.400881  3.294451
1 -0.262591  0.072098 -0.194940
2  0.170395 -0.193521 -0.194940
3  0.495134 -0.133153 -0.194940
4 -0.127283  1.496783 -0.194940
```

[56]:

```
x_test_bal.head()
```

[56]:

```
     goitre    tumor  hypopituitary     psych       TSH        T3       TT4  \
0 -0.052319 -0.137297      -0.024637 -0.107982 -0.312412  0.593872  0.788014
1 -0.052319 -0.137297      -0.024637 -0.107982 -0.314240  0.781860  0.444674
2 -0.052319 -0.137297      -0.024637 -0.107982  1.298911 -0.408731 -1.227244
3 -0.052319 -0.137297      -0.024637 -0.107982 -0.166205 -0.471394 -0.227079
4 -0.052319 -0.137297      -0.024637 -0.107982 -0.227125 -0.346068 -0.301718

        T4U       FTI      TBG
0  1.063428  0.132466 -0.19494
1  1.767031 -0.302183 -0.19494
2 -0.397900 -0.905863 -0.19494
3 -0.397900  0.132466 -0.19494
4 -0.830886  0.434306 -0.19494
```

1 RandomForest

[57]:

```
rfr1 = RandomForestClassifier()
rfr1.fit(x_bal, y_bal)
y_pred = rfr1.predict(x_test_bal)
```

```
<ipython-input-57-24f1fecb0a9c>: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)
```

[58]:

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

```
              precision    recall  f1-score   support

           0       0.83      0.16      0.26       122
           1       0.81      0.95      0.88       122
           2       0.92      0.98      0.95       122
           3       0.76      0.84      0.80       122
           4       0.48      0.89      0.63       122
           5       0.89      0.67      0.77       122
           6       0.58      0.51      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
```

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

[60]:
```
train_score
```

[60]:
```
1.0
```

2 XGBClassifier

[61]:
```
from xgboost import XGBClassifier
xgb = XGBClassifier()
xgb.fit(x_bal, y_bal)
```

[61]:
```
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, …)
```

[62]:
```
y_pred = xgb.predict(x_test_bal)
```

[63]:
```
print(classification_report(y_test_bal, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.80      0.30      0.44       122
           1       0.82      0.94      0.88       122
           2       0.96      1.00      0.98       122
           3       0.77      0.84      0.81       122
           4       0.51      0.81      0.62       122
           5       0.84      0.70      0.76       122
           6       0.59      0.54      0.56       122

    accuracy                           0.73       854
   macro avg       0.76      0.73      0.72       854
weighted avg       0.76      0.73      0.72       854
```

[64]:

```python
train_score = accuracy_score(y_bal, xgb.predict(x_bal))
train_score
```

[64]:

```
1.0
```

3 SVC Model

[65]:

```python
# model 3
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score, classification_report

sv = SVC()
```

[66]:

```python
sv.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 change the shape of y to (n_samples, ), for example using
ravel().
  y = column_or_1d(y, warn=True)
```

[66]:

```
SVC()
```

[67]:

```python
y_pred = sv.predict(x_test_bal)
```

[68]:

```python
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
```

[69]:
```
train_score = accuracy_score(y_bal, sv.predict(x_bal))
train_score
```

[69]:
```
0.7154989384288747
```

[70]:
```
rfr_gs = RandomForestClassifier(criterion="entropy", max_depth = 16,␣
  ↪n_estimators = 200)
```

[71]:
```
rfr_gs.fit(x_bal, y_bal)
```

```
<ipython-input-71-9d9e92e85fd9>:1: 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_gs.fit(x_bal, y_bal)
```

[71]:
```
RandomForestClassifier(criterion='entropy', max_depth=16, n_estimators=200)
```

[72]:
```
y_pred = rfr_gs.predict(x_test_bal)
```

[73]:
```
print(classification_report(y_test_bal, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.64      0.06      0.11       122
           1       0.82      0.95      0.88       122
           2       0.93      0.99      0.96       122
           3       0.76      0.84      0.80       122
           4       0.45      0.87      0.59       122
           5       0.90      0.68      0.78       122
           6       0.57      0.52      0.54       122

    accuracy                           0.70       854
   macro avg       0.72      0.70      0.66       854
weighted avg       0.72      0.70      0.66       854
```

[74]:
```
train_score = accuracy_score(y_bal, rfr_gs.predict(x_bal))
train_score
```

[74]:
```
1.0
```

[75]:
```
xgb1 = XGBClassifier(booster="gbtree", gamma=0, learning_rate=0.1,␣
  ↪n_estimators=500)
```

[76]:
```
xgb1.fit(x_bal, y_bal)
```

```
[76]: XGBClassifier(base_score=None, booster='gbtree', 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=0, gpu_id=None, grow_policy=None, importance_type=None,
                    interaction_constraints=None, learning_rate=0.1, 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=500, n_jobs=None, num_parallel_tree=None,
                    objective='multi:softprob', predictor=None, …)
```

```
[77]: y_pred = xgb1.predict(x_test_bal)
```

```
[78]: print(classification_report(y_test_bal, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.83      0.32      0.46       122
           1       0.83      0.93      0.88       122
           2       0.96      1.00      0.98       122
           3       0.77      0.84      0.80       122
           4       0.51      0.80      0.62       122
           5       0.83      0.70      0.76       122
           6       0.56      0.52      0.54       122

    accuracy                           0.73       854
   macro avg       0.75      0.73      0.72       854
weighted avg       0.75      0.73      0.72       854
```

```
[79]: train_score = accuracy_score(y_bal, xgb1.predict(x_bal))
      train_score
```

```
[79]: 1.0
```

```
[80]: sv1 = SVC(C=1000, gamma=1, kernel='rbf')
```

```
[81]: 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 change the shape of y to (n_samples, ), for example using
ravel().
  y = column_or_1d(y, warn=True)
```

```
[81]: SVC(C=1000, gamma=1)
```

[82]:

```
y_pred = sv1.predict(x_test_bal)
```

[83]:

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

```
              precision    recall  f1-score   support

           0       0.78      0.43      0.56       122
           1       0.65      0.90      0.75       122
           2       0.92      0.90      0.91       122
           3       0.68      0.63      0.65       122
           4       0.58      0.80      0.67       122
           5       0.82      0.67      0.74       122
           6       0.47      0.44      0.46       122

    accuracy                           0.68       854
   macro avg       0.70      0.68      0.68       854
weighted avg       0.70      0.68      0.68       854
```

[84]:

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

[84]:

```
0.9517743403093721
```

[85]:

```
import pickle
pickle.dump(xgb1, open("thyroid_1_model.pkl", "wb"))
```

[86]:

```
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']
```

[87]:

```
type(features)
```

[87]:

```
numpy.ndarray
```

[88]:

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

[89]:

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

[89]:

```
array(['miscellaneous', 'hypothyroid conditions', 'binding protein',
       'replacement therapy', 'general health', 'hyperthyroid conditions',
       'antithyroid treatment'], dtype=object)
```

[90]:

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

[90]:

```
array([5, 4, 1, 6, 2, 3, 0])
```