```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt

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

data.head()
```

```
   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]
```

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

```
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)
```

```
data.shape
```

```
(9172, 31)
```

```
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
```

```
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
referral_source            0
target                     0
patient_id                 0
dtype: int64
```

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

```
data.head()
```

```
   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]
```

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

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

```
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
```

```
      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]
```

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

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

```
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
```

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

```
0
```

```
data.head()
```

```
    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]
```

```
data.describe()
```

```
               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
```

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

```
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]
```

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

```
data
```

```
       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]
```

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

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

```
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
```

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

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

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

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

```
F    1701
M     536
Name: sex, dtype: int64
```

```
x.isnull().sum()
```

```
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
```

```
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
```

```
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')

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])
```

```
x.head()
```

```
     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]
```

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

```
     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]
```

```
label_encoder = LabelEncoder()
y_dt = label_encoder.fit_transform(y)
```

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

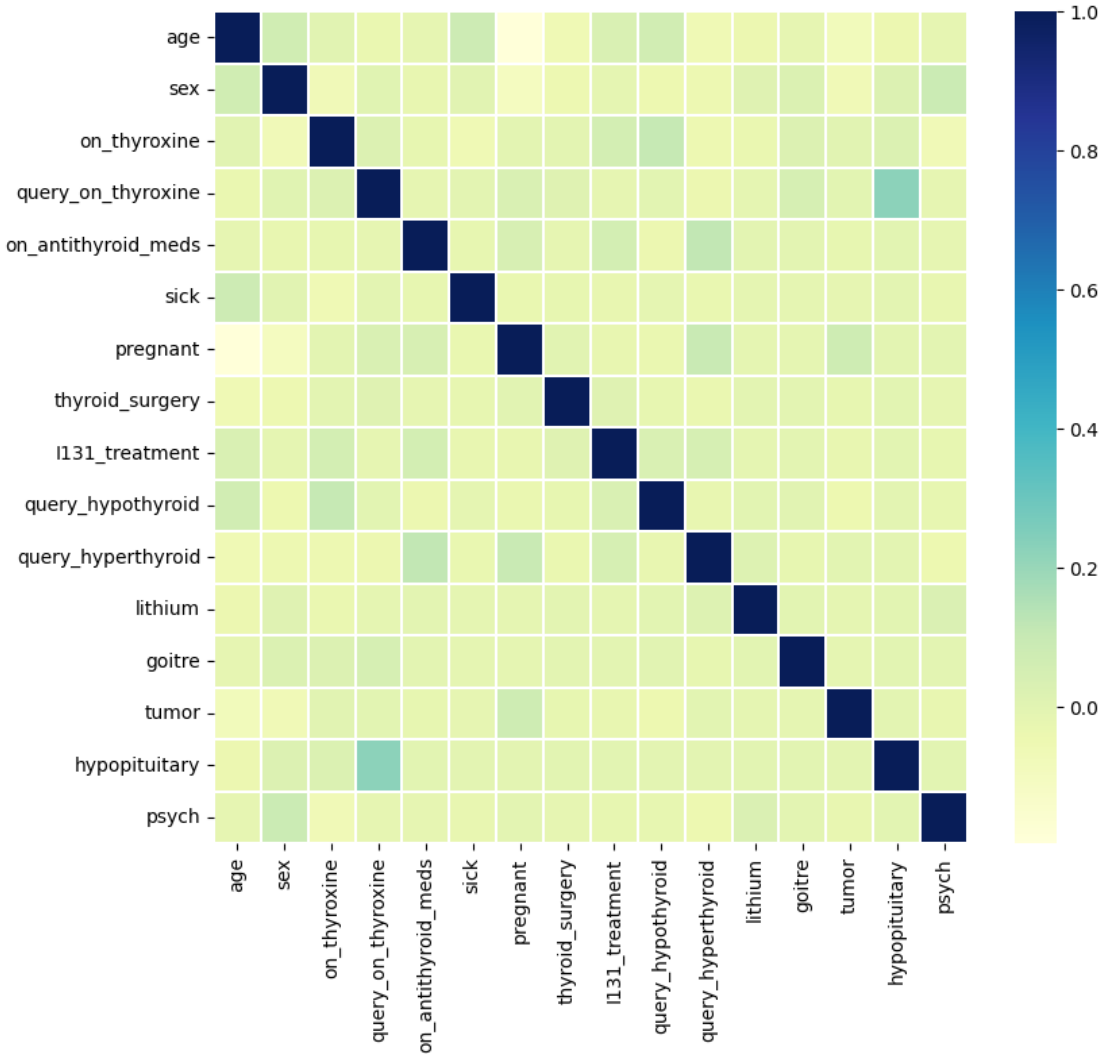
```
      target
0          5
1          4
2          5
3          1
4          6
...      ...
2232       2
2233       2
2234       1
2235       1
2236       1

[2237 rows x 1 columns]
```

```
y.value_counts(normalize=True)
```

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

```
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()

<Axes: >
```




```
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)

y_train.value_counts()
```

```
target
4          471
2          351
1          302
6          265
5          230
3          144
0           26
dtype: int64
```

```
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)
```

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

```
x_bal
```

```
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]])
```

```
x_test_bal
```

```
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]])
```

```
y_bal.value_counts()
```

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

```
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']

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

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

x_bal
```

```
           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
```

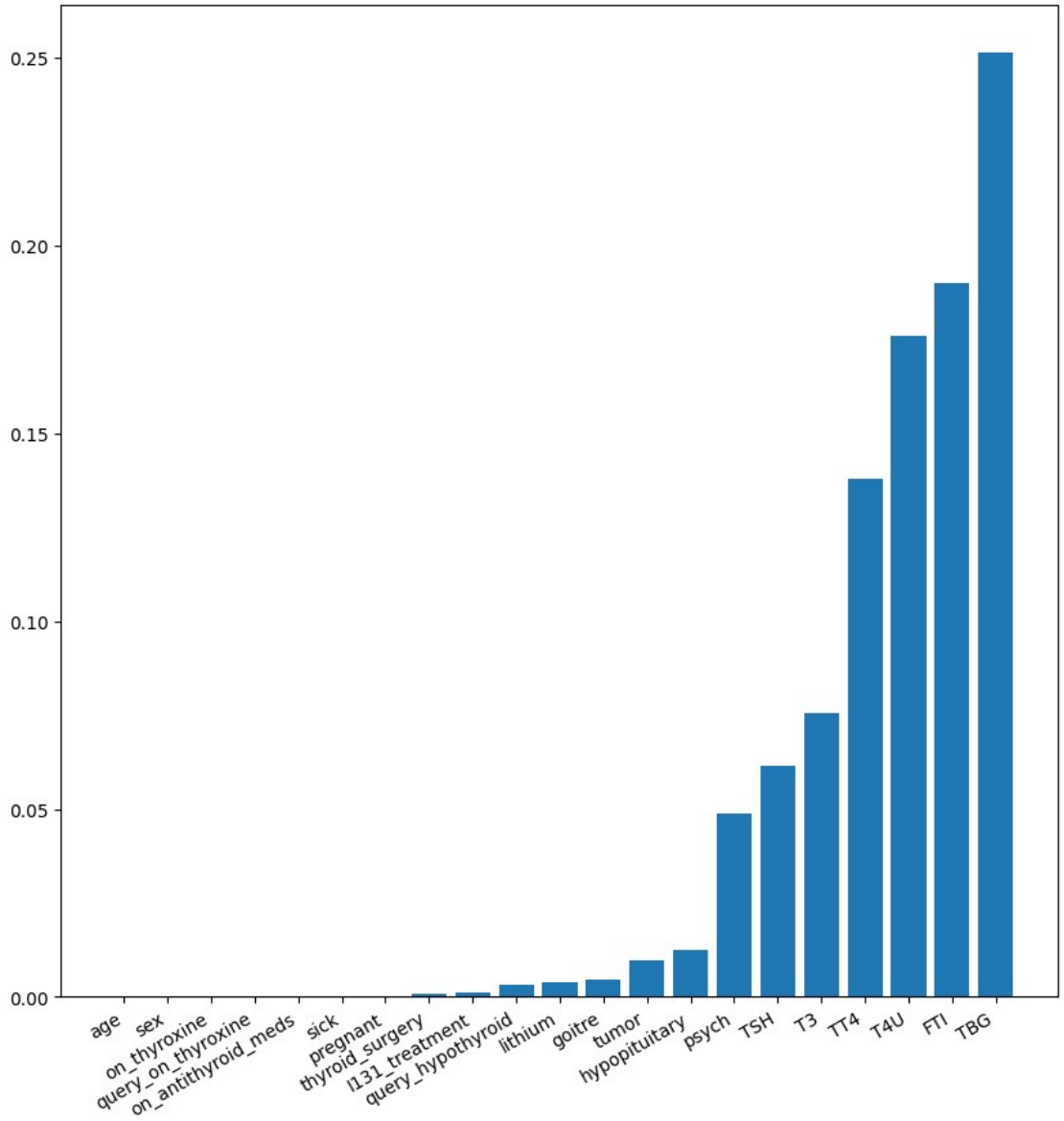
```
      hypopituitary     psych       TSH        T3       TT4       T4U
\
0         -0.024637 -0.107982 -0.315458 -1.035358 -1.704935 -2.508707

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]
```

```
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)

((3297, 22), (3297, 1), (854, 22), (854, 1))

test_score = accuracy_score(y_test_bal, y_pred)
test_score

0.905152224824356

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

1.0

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_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
```




```
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)

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)

x_bal.head()
```

```
     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
```

```
x_test_bal.head()
```

```
     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
```

RandomForest

```
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)
```

```
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
```

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

```
train_score
```

```
1.0
```

XGBClassifier

```
from xgboost import XGBClassifier
xgb = XGBClassifier()
xgb.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, ...)
```

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

```
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
```

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

```
1.0
```

SVC Model

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

```
sv = SVC()
```

```
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)
```

```
SVC()
```

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

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

```
              precision    recall  f1-score   support

           0       0.70      0.85      0.77       122
           1       0.76      0.81      0.79       122
           2       0.88      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
```

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

```
0.7154989384288747
```

```
rfr_gs = RandomForestClassifier(criterion="entropy", max_depth = 16,
n_estimators = 200)
```

```
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)
```

```
RandomForestClassifier(criterion='entropy', max_depth=16,
n_estimators=200)
```

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

```
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
```

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

```
1.0
```

```
xgb1 = XGBClassifier(booster="gbtree", gamma=0, learning_rate=0.1,
n_estimators=500)
```

```
xgb1.fit(x_bal, y_bal)
```

```
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, ...)
```

```
y_pred = xgb1.predict(x_test_bal)
```

```
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
```

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

```
1.0
```

```
sv1 = SVC(C=1000, gamma=1, kernel='rbf')
```

```
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)
```

```
SVC(C=1000, gamma=1)
```

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

```
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
```

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

```
0.9517743403093721
```

```
import pickle
pickle.dump(xgb1, 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)))
```

```
['hypothyroid conditions']
```

```
type(features)
```

```
numpy.ndarray
```

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

```
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])
```