

# Symptom, Disease, Physician: Who to Visit When You Are Not Feeling Well?

Abstract: Guidance to patient on visiting to the appropriate department is a crucial task during the patient workflow, which means that patient could receive medical intervention well on time if it is accurate enough. This project use the classification algorithm, including **logistic regressor, random forest, K neighbours classifier, Support Vector Classifier, Gradient Boosting Classifier, and Gaussian Naive Bayes Classifier**, to establish a model on guiding patient on visiting the corresponding department based on their main common symptom.

The data preprocessing is referred from

<https://www.kaggle.com/code/ebrahimelgazar/disease-recommendation-system>

## 0. Import packages & data (Set up environment when applicable)

```
In [1]: # import basic packages
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import scipy.stats as st
# !pip install pandasql
import pandasql as ps

# import sqlite3 as lite # maybe this is for google colab
import os
import time
```

```
In [63]: # import machine-learning based general packages
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.naive_bayes import GaussianNB

# This is for confusion matrix
from sklearn import metrics, model_selection
```

```
In [2]: # set up the environment (for google colab only)

# the data source
```

```

# the corresponding file is available at
# https://www.kaggle.com/datasets/ebrahimelgazar/doctor-specialist-recommendation-s

# If you use google colab, PLEASE put the corresponding csv dataset into the root d
# The file will be deleted everytime in google colab!!! And you might use additiona

# If you use jupyter lab, make sure that you set the directory to the place where t

# os.getcwd()
# os.chdir('your directory goes here')
# os.listdir()
disease_description = pd.read_csv('Disease_Description.csv')

doctor_specialist = pd.read_csv('Doctor_Specialist.csv')

doctor_versus_disease = pd.read_csv('Doctor_Versus_Disease.csv', encoding='windows-
                                header = None, usecols=[0,1], names=['Disease',
# 'utf-8' codec can't decode byte 0xa0 in position 490: invalid start byte
# this table has no title...

original_dataset = pd.read_csv('Original_Dataset.csv')

symptom_weights = pd.read_csv('Symptom_Weights.csv', header = None, usecols = [0, 1
# this table also has no title...

```

```

In [3]: # show all columns
pd.set_option('display.max_columns', None)

```

# 1. EDA

## 1.1 Explore Each Table

Disease description (Disease, Description)

```

In [4]: # for jupyter notebook, please use pandasql
# for google colab, please set up a connection before using sqlite3.

# first try...
query = '''
    select * from
    disease_description
    limit 5;
''' # disease_description.head()
ps.sqldf(query)

```

Out[4]:

	Disease	Description
0	Drug Reaction	An adverse drug reaction (ADR) is an injury ca...
1	Malaria	An infectious disease caused by protozoan para...
2	Allergy	An allergy is an immune system response to a f...
3	Hypothyroidism	Hypothyroidism, also called underactive thynoi...
4	Psoriasis	Psoriasis is a common skin disorder that forms...

In [5]: `print(disease_description.info())`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 41 entries, 0 to 40
Data columns (total 2 columns):
#   Column          Non-Null Count  Dtype
---  -
0   Disease         41 non-null    object
1   Description      41 non-null    object
dtypes: object(2)
memory usage: 784.0+ bytes
None
```

Doctor Specialist (Doctor Specialist)

In [6]:

```
query = '''
select * from
doctor_specialist
limit 5
''' # doctor_specialist.head()
ps.sqldf(query)
```

Out[6]:

	Doctor Specialist
0	Dermatologist
1	Allergist
2	Gastroenterologist
3	Hepatologist
4	Osteopathic

In [7]:

```
print(doctor_specialist.info())
print(doctor_specialist.shape)
```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 19 entries, 0 to 18
Data columns (total 1 columns):
#   Column                Non-Null Count  Dtype
---  ---
0   Doctor Specialist      19 non-null    object
dtypes: object(1)
memory usage: 280.0+ bytes
None
(19, 1)

```

Doctor versus Disease (~~Drug Reaction, Allergist~~)(Disease, Doctor\_Specialist)

```

In [8]: query = '''
        select *
        from
        doctor_versus_disease
        limit 5
        ''' # doctor_versus_disease.head()
ps.sqldf(query)

# This table has no title, the corresponding title must be Disease, Doctor Speciali

```

```

Out[8]:

```

	Disease	Doctor_Specialist
0	Drug Reaction	Allergist
1	Allergy	Allergist
2	Hypertension	Cardiologist
3	Heart attack	Cardiologist
4	Psoriasis	Dermatologist

```

In [9]: doctor_versus_disease.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 41 entries, 0 to 40
Data columns (total 2 columns):
#   Column                Non-Null Count  Dtype
---  ---
0   Disease                41 non-null    object
1   Doctor_Specialist      41 non-null    object
dtypes: object(2)
memory usage: 784.0+ bytes

original_dataset (Symptom_1 to Symptom 17)

```

```

In [10]: query = '''
        select * from
        original_dataset
        limit 5
        ''' # original_dataset.head()
ps.sqldf(query)

```

```
# unstructured column-based data, for saving storage
# may be used for train and test
```

```
Out[10]:
```

	Disease	Symptom_1	Symptom_2	Symptom_3	Symptom_4	Symptom_5
0	Fungal infection	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	None
1	Fungal infection	skin_rash	nodal_skin_eruptions	dischromic _patches	None	None
2	Fungal infection	itching	nodal_skin_eruptions	dischromic _patches	None	None
3	Fungal infection	itching	skin_rash	dischromic _patches	None	None
4	Fungal infection	itching	skin_rash	nodal_skin_eruptions	None	None

```
In [11]: original_dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4920 entries, 0 to 4919
Data columns (total 18 columns):
#   Column          Non-Null Count  Dtype
---  -
0   Disease         4920 non-null   object
1   Symptom_1       4920 non-null   object
2   Symptom_2       4920 non-null   object
3   Symptom_3       4920 non-null   object
4   Symptom_4       4572 non-null   object
5   Symptom_5       3714 non-null   object
6   Symptom_6       2934 non-null   object
7   Symptom_7       2268 non-null   object
8   Symptom_8       1944 non-null   object
9   Symptom_9       1692 non-null   object
10  Symptom_10      1512 non-null   object
11  Symptom_11      1194 non-null   object
12  Symptom_12      744 non-null    object
13  Symptom_13      504 non-null    object
14  Symptom_14      306 non-null    object
15  Symptom_15      240 non-null    object
16  Symptom_16      192 non-null    object
17  Symptom_17      72 non-null     object
dtypes: object(18)
memory usage: 692.0+ KB

symptom_weights (abdominal_pain, 1)(Symptom, weight)
```

```
In [12]: query = '''
          select * from
          symptom_weights
          limit 5
          ''' # symptom_weights.head()
```

```
ps.sqldf(query)
```

```
# no title, the title should be Symptom and weight, respectively
```

Out[12]:

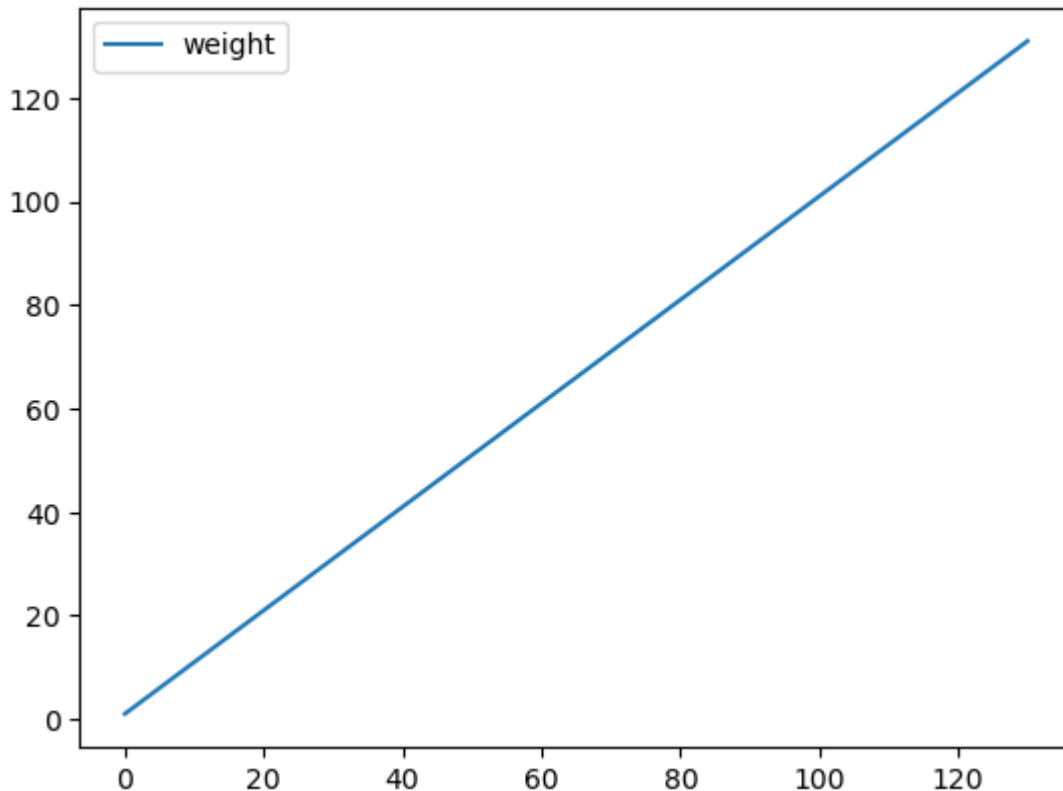
	Symptom	weight
0	abdominal_pain	1
1	abnormal_menstruation	2
2	acidity	3
3	acute_liver_failure	4
4	altered_sensorium	5

In [13]: `symptom_weights.info()`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 131 entries, 0 to 130
Data columns (total 2 columns):
#   Column   Non-Null Count  Dtype
---  -
0   Symptom  131 non-null    object
1   weight   131 non-null    int64
dtypes: int64(1), object(1)
memory usage: 2.2+ KB
```

In [14]: `sns.lineplot(symptom_weights)`  
*# as we see, the second column (weight) might be id-liked data*

Out[14]: <Axes: >



Stage summary: The data generally seems to be clean, with the `original_dataset` contains column-based training and testing dataset. However, the `doctor_versus_disease` and the `symptom_weights` lack of title row, indicating that we should add the title before query.

Therefore, this project rewined to the beginning of the data to modify the reading method of the latter two tables.

Disease description (Disease, Description)

Doctor Specialist (Doctor Specialist)

Doctor versus Disease (Disease, Doctor\_Specialist)

original\_dataset (Symptom\_1 to Symptom 17)

symptom\_weights (Symptom, weight)

## Analysis by SQL

1. Browse all the given disease with itching as symptom

```
In [15]: query = '''
          select distinct Disease
          from
          original_dataset
          where
          Symptom_1 = 'itching' or
          Symptom_2 = 'itching' or
          Symptom_3 = 'itching' or
          Symptom_4 = 'itching' or
          Symptom_5 = 'itching' or
          Symptom_6 = 'itching' or
          Symptom_7 = 'itching' or
          Symptom_8 = 'itching' or
          Symptom_9 = 'itching' or
          Symptom_10 = 'itching' or
          Symptom_11 = 'itching' or
          Symptom_12 = 'itching' or
          Symptom_13 = 'itching' or
          Symptom_14 = 'itching' or
          Symptom_15 = 'itching' or
          Symptom_16 = 'itching' or
          Symptom_17 = 'itching'
          '''
          ps.sqlldf(query)
```

Out[15]:

	Disease
0	Fungal infection
1	Chronic cholestasis
2	Drug Reaction
3	Jaundice
4	Chicken pox
5	Hepatitis B

2. Count how many patient suffering from corresponding syndrome in original dataset

```
In [16]: query = '''
    with col1 as
    (
    select Symptom_1 as Symptom, count(Symptom_1) as counts
    from original_dataset
    group by
    Symptom_1
    )
    ,

    col2 as

    (
    select Symptom_2, count(Symptom_2) as counts
    from original_dataset
    group by
    Symptom_2
    )
    ,

    col3 as

    (
    select Symptom_3, count(Symptom_3) as counts
    from original_dataset
    group by
    Symptom_3
    )
    ,

    col4 as

    (
    select Symptom_4, count(Symptom_4) as counts
    from original_dataset
    group by
    Symptom_4
    )
    ,
```



```
col5 as

(
select Symptom_5, count(Symptom_5) as counts
from original_dataset
group by
Symptom_5
)
,

col6 as

(
select Symptom_6, count(Symptom_6) as counts
from original_dataset
group by
Symptom_6
)
,

col7 as

(
select Symptom_7, count(Symptom_7) as counts
from original_dataset
group by
Symptom_7
)
,

col8 as

(
select Symptom_8, count(Symptom_8) as counts
from original_dataset
group by
Symptom_8
)
,

col9 as

(
select Symptom_9, count(Symptom_9) as counts
from original_dataset
group by
Symptom_9
)
,

col10 as

(
select Symptom_10, count(Symptom_10) as counts
from original_dataset
```

```
group by
Symptom_10
)
,

col11 as

(
select Symptom_11, count(Symptom_11) as counts
from original_dataset
group by
Symptom_11
)
,

col12 as

(
select Symptom_12, count(Symptom_12) as counts
from original_dataset
group by
Symptom_12
)
,

col13 as

(
select Symptom_13, count(Symptom_13) as counts
from original_dataset
group by
Symptom_13
)
,

col14 as

(
select Symptom_14, count(Symptom_14) as counts
from original_dataset
group by
Symptom_14
)
,

col15 as

(
select Symptom_15, count(Symptom_15) as counts
from original_dataset
group by
Symptom_15
)
,

col16 as
```

```

(
select Symptom_16, count(Symptom_16) as counts
from original_dataset
group by
Symptom_16
)
,

col17 as

(
select Symptom_17, count(Symptom_17) as counts
from original_dataset
group by
Symptom_17
)    -- DO EXECUTE the code once before adding a similar sub query !!!

-- 1. THIS SUBQUERY IS TO COUNT THE SYMPTOM FOR EACH COLUMN, PLEASE ENSURE THAT

select Symptom, sum(counts) as counts_all from -- 3. THIS IS ACTUALLY THE LAST

(select * from col1 union all
select * from col2 union all
select * from col3 union all
select * from col4 union all
select * from col5 union all
select * from col6 union all
select * from col7 union all
select * from col8 union all
select * from col9 union all
select * from col10 union all
select * from col11 union all
select * from col12 union all
select * from col13 union all
select * from col14 union all
select * from col15 union all
select * from col16 union all
select * from col17)

-- 2. THIS IS TO UNION ALL THE DISEASE~COUNT PAIR INTO TWO COLUMN BEFORE AGGREG
-- DO NOTE THAT WE MUST NOT DE DUPLICATE THE RECORD, ELSE SOME RECORD MAY GET LO

group by Symptom
order by counts_all desc

...

ps.sqldf(query)

```

*# p.s.: I have tried multiple times to approach each task before duplicating the si  
# the code seems to be complicated though...*

*# do try to execute the code after add each column instead of doing it once for all*

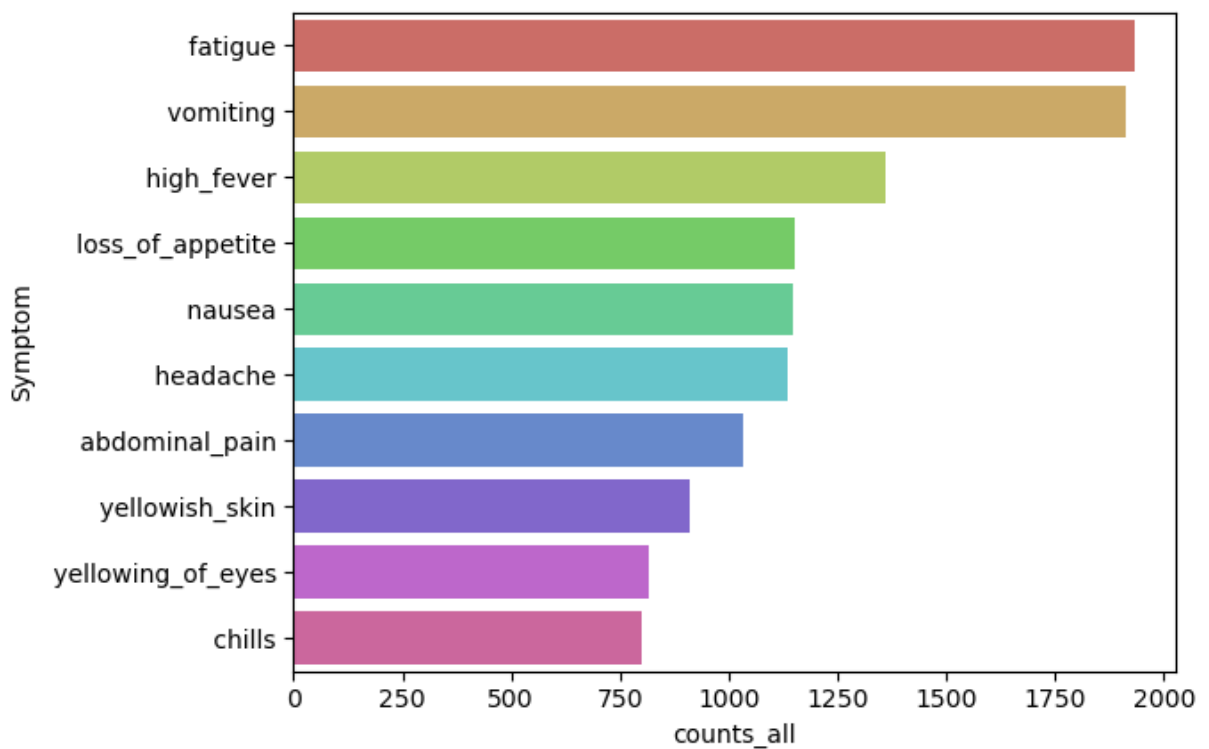
Out[16]:

	Symptom	counts_all
0	fatigue	1932
1	vomiting	1914
2	high_fever	1362
3	loss_of_appetite	1152
4	nausea	1146
...	...	...
127	dischromic_patches	108
128	dehydration	108
129	blackheads	108
130	foul_smell_of_urine	102
131	None	0

132 rows × 2 columns

```
In [17]: # visualize top 10 frequent symptoms
res = ps.sqldf(query)
sns.barplot(res.iloc[: 10, :], y = 'Symptom', x = 'counts_all', palette = 'hls')
```

Out[17]: <Axes: xlabel='counts\_all', ylabel='Symptom'>



It seems that most patient were suffering from fatigue, vomiting, high fever, apppetite lose, and nausea

*This also implies the disadvantage of sql towards column-based dataset...tedius and duplicative subquereies, repetative union of aggregation, which prone to be errornous*

3. If the patient is suffering from itching, which specialist will they probably visit?

```
In [18]: query = '''
-- 1. select the possible disease with fatigue
with diseases as
(
select distinct Disease
from
original_dataset
where
Symptom_1 = 'itching' or
Symptom_2 = 'itching' or
Symptom_3 = 'itching' or
Symptom_4 = 'itching' or
Symptom_5 = 'itching' or
Symptom_6 = 'itching' or
Symptom_7 = 'itching' or
Symptom_8 = 'itching' or
Symptom_9 = 'itching' or
Symptom_10 = 'itching' or
Symptom_11 = 'itching' or
Symptom_12 = 'itching' or
Symptom_13 = 'itching' or
Symptom_14 = 'itching' or
Symptom_15 = 'itching' or
Symptom_16 = 'itching' or
Symptom_17 = 'itching'
)
select distinct Doctor_Specialist
from original_dataset
full join
doctor_versus_disease
on
original_dataset.Disease = doctor_versus_disease.Disease

where
original_dataset.Disease in
(
select Disease from diseases
)

'''
ps.sqldf(query)
```

Out[18]: **Doctor\_Specialist**

0	Dermatologist
1	Hepatologist
2	Allergist
3	Gastroenterologist
4	hepatologist

The patient suffering from itching would possibly go to the Dermatologist, Hepatologist, Allergist, Gastroenterologist, or hepatologist.

## 2. Data preprocessing

This is a **Column-based** dataset. Therefore, we shall convert them to list before undergoing further analysis.

This is also why querying is so tedious through SQL.

```
In [19]: # set a new column, 'Symptoms', in the end
original_dataset['Symptoms'] = 0
original_dataset.head()
```

```
Out[19]:
```

	Disease	Symptom_1	Symptom_2	Symptom_3	Symptom_4	Symptom_5
0	Fungal infection	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	NaN
1	Fungal infection	skin_rash	nodal_skin_eruptions	dischromic _patches	NaN	NaN
2	Fungal infection	itching	nodal_skin_eruptions	dischromic _patches	NaN	NaN
3	Fungal infection	itching	skin_rash	dischromic _patches	NaN	NaN
4	Fungal infection	itching	skin_rash	nodal_skin_eruptions	NaN	NaN

```
In [20]: # the new column, Symptoms shall store the list-based symptoms corresponding to dif

for i in range(original_dataset.shape[0]): # by N of row
    value = original_dataset.iloc[i].tolist() # transfer entire row into list
    original_dataset["Symptoms"][i] = value[1:18] # exclude title & last 0, only in
```

C:\Users\Raymo\AppData\Local\Temp\ipykernel\_8708\2226175210.py:5: SettingWithCopyWarning:  
 A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: [https://pandas.pydata.org/pandas-docs/stable/user\\_guide/indexing.html#returning-a-view-versus-a-copy](https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy)

```
original_dataset["Symptoms"][i] = value[1:18] # exclude title & last 0, only include 17 symptoms in between
```

**Warning!! once we add a column storing lists, pandasql would not work!!!**

In [21]: `original_dataset.head()` *# the last column consists of all the 17 symptoms*

Out[21]:

	Disease	Symptom_1	Symptom_2	Symptom_3	Symptom_4	Symptom_5
0	Fungal infection	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	NaN
1	Fungal infection	skin_rash	nodal_skin_eruptions	dischromic _patches	NaN	NaN
2	Fungal infection	itching	nodal_skin_eruptions	dischromic _patches	NaN	NaN
3	Fungal infection	itching	skin_rash	dischromic _patches	NaN	NaN
4	Fungal infection	itching	skin_rash	nodal_skin_eruptions	NaN	NaN

In [22]: `column_values = original_dataset[['Symptom_1', 'Symptom_2', 'Symptom_3', 'Symptom_4', 'Symptom_5', 'Symptom_6', 'Symptom_7', 'Symptom_8', 'Symptom_9', 'Symptom_10', 'Symptom_11', 'Symptom_12', 'Symptom_13', 'Symptom_14', 'Symptom_15', 'Symptom_16', 'Symptom_17']].values.ravel() # change data the`

In [23]: `# count the total number of symptoms  
symps = pd.unique(column_values).tolist()  
# print(len(symps)) # 132, has a nan  
symps = [i for i in symps if str(i) != "nan"] # remove 'nan'  
print(len(symps))`

131

`ravel data -> unique value -> tolist -> remove nan`

There are 131 symptoms here, identical to sql analysis that has been previously conducted

In [24]: `new_data = symptoms = pd.DataFrame(columns = symps ,index = original_dataset.index)  
# this is done to set unique symptoms as column instead, while the row index is cor  
# and create two copies`

```
In [25]: new_data.head()
```

```
Out[25]:
```

	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	continuous_sneezing	shivering	ch
0	NaN	NaN	NaN	NaN	NaN	NaN	N
1	NaN	NaN	NaN	NaN	NaN	NaN	N
2	NaN	NaN	NaN	NaN	NaN	NaN	N
3	NaN	NaN	NaN	NaN	NaN	NaN	N
4	NaN	NaN	NaN	NaN	NaN	NaN	N

```
In [26]: new_data.tail()
```

```
Out[26]:
```

	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	continuous_sneezing	shivering
4915	NaN	NaN	NaN	NaN	NaN	NaN
4916	NaN	NaN	NaN	NaN	NaN	NaN
4917	NaN	NaN	NaN	NaN	NaN	NaN
4918	NaN	NaN	NaN	NaN	NaN	NaN
4919	NaN	NaN	NaN	NaN	NaN	NaN

```
In [27]: symptoms["Symptoms"] = original_dataset["Symptoms"]
```

The copy of `symptoms` is to store and fill the corresponding symptom into the column.  
By one-hot way

```
In [28]: symptoms.head()
```



Out[28]:

	itching	skin_rash	nodal_skin_eruptions	dischromic_patches	continuous_sneezing	shivering	ch
0	NaN	NaN	NaN	NaN	NaN	NaN	N
1	NaN	NaN	NaN	NaN	NaN	NaN	N
2	NaN	NaN	NaN	NaN	NaN	NaN	N
3	NaN	NaN	NaN	NaN	NaN	NaN	N
4	NaN	NaN	NaN	NaN	NaN	NaN	N

```
In [29]: for i in symps:
          symptoms[i] = symptoms.apply(lambda x:1 if i in x.Symptoms else 0, axis=1) # f
```

```
In [30]: symptoms.head()
```

Out[30]:

	itching	skin_rash	nodal_skin_eruptions	dischromic_patches	continuous_sneezing	shivering	ch
0	1	1	1	1	0	0	
1	0	1	1	1	0	0	
2	1	0	1	1	0	0	
3	1	1	0	1	0	0	
4	1	1	1	0	0	0	

```
In [31]: symptoms["Disease"] = original_dataset["Disease"] # add a Disease column into sympt
          symptoms = symptoms.drop("Symptoms",axis=1) # drop the original list-stored columns
          symptoms.head()
```

Out[31]:

	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	continuous_sneezing	shivering	ch
0	1	1	1	1	0	0	
1	0	1	1	1	0	0	
2	1	0	1	1	0	0	
3	1	1	0	1	0	0	
4	1	1	1	0	0	0	

In [43]: *# this query is to concatenate the corresponding physician into the one-hot-encoded*

```
query = '''
    select * from
    symptoms
    full join
    doctor_versus_disease
    on
    symptoms.Disease = doctor_versus_disease.Disease
'''

analyze_data = ps.sqlldf(query)
```

In [44]: analyze\_data.head()

Out[44]:

	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	continuous_sneezing	shivering	ch
0	1	1	1	1	0	0	
1	0	1	1	1	0	0	
2	1	0	1	1	0	0	
3	1	1	0	1	0	0	
4	1	1	1	0	0	0	

In [48]: analyze\_data['Doctor\_Specialist'].info() *# every cell in Doctor\_Specialist are unnu*

```

<class 'pandas.core.series.Series'>
RangeIndex: 4920 entries, 0 to 4919
Series name: Doctor_Specialist
Non-Null Count  Dtype
-----
4920 non-null   object
dtypes: object(1)
memory usage: 38.6+ KB

```

```
In [46]: analyze_data.describe()
```

```
Out[46]:
```

	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	continuous_sneezing
<b>count</b>	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000
<b>mean</b>	0.137805	0.159756	0.021951	0.021951	0.045122
<b>std</b>	0.344730	0.366417	0.146539	0.146539	0.207593
<b>min</b>	0.000000	0.000000	0.000000	0.000000	0.000000
<b>25%</b>	0.000000	0.000000	0.000000	0.000000	0.000000
<b>50%</b>	0.000000	0.000000	0.000000	0.000000	0.000000
<b>75%</b>	0.000000	0.000000	0.000000	0.000000	0.000000
<b>max</b>	1.000000	1.000000	1.000000	1.000000	1.000000

```
In [51]: guidance = analyze_data.drop('Disease', axis = 1)
```

```
In [52]: guidance.head()
```

```
Out[52]:
```

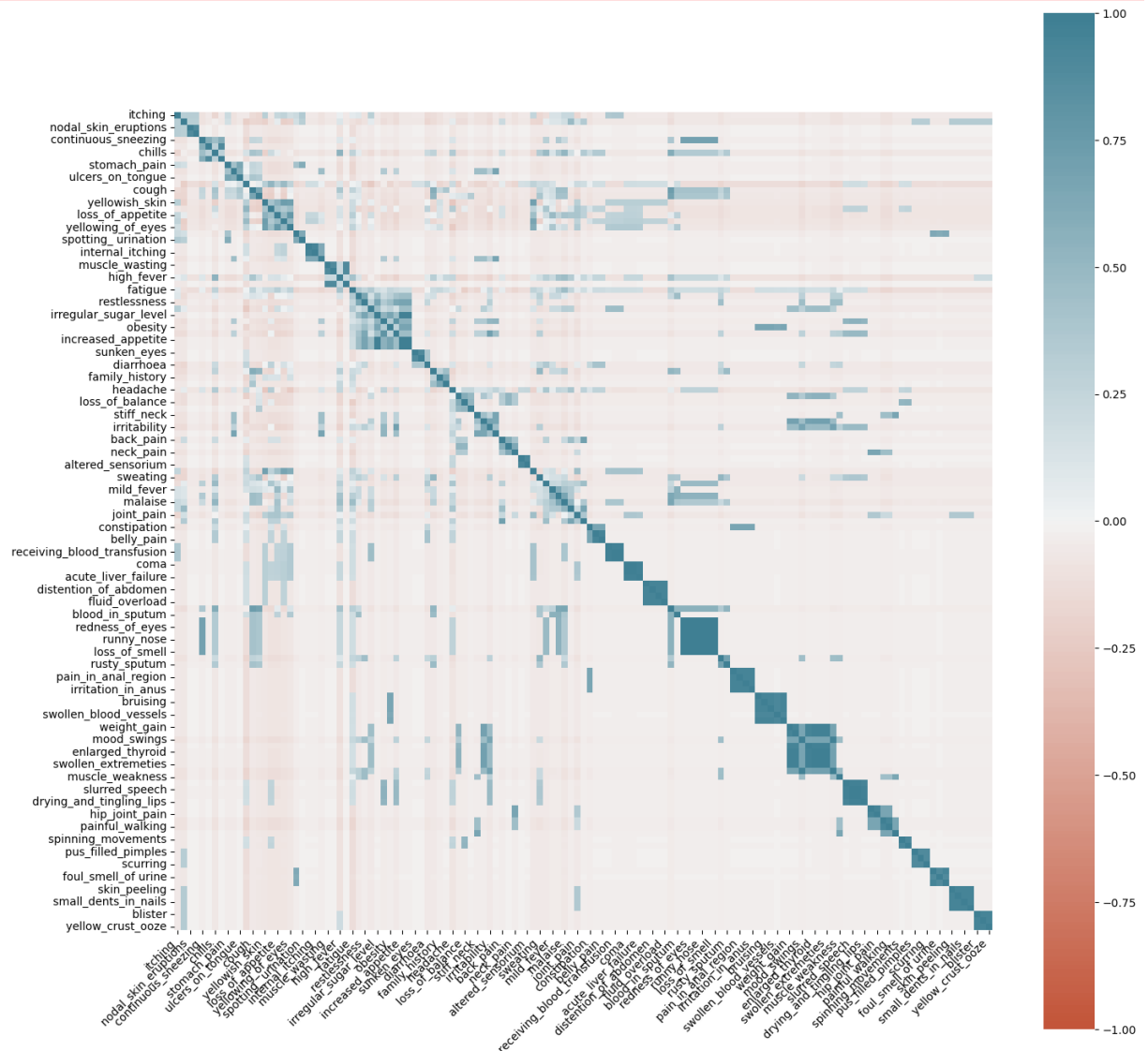
	itching	skin_rash	nodal_skin_eruptions	dischromic _patches	continuous_sneezing	shivering	ch
<b>0</b>	1	1	1	1	0	0	
<b>1</b>	0	1	1	1	0	0	
<b>2</b>	1	0	1	1	0	0	
<b>3</b>	1	1	0	1	0	0	
<b>4</b>	1	1	1	0	0	0	

```
In [62]: # see correlations between symptoms
plt.figure(figsize = (16.5, 16.5))
corr = guidance.corr()
ax = sns.heatmap(
    corr,
    vmin=-1, vmax=1, center=0,
    cmap=sns.diverging_palette(20, 220, n=200),
    square=True, annot = False
)
ax.set_xticklabels(
```

```
ax.get_xticklabels(),
rotation=45,
horizontalalignment='right')
plt.show()
```

C:\Users\Raymo\AppData\Local\Temp\ipykernel\_8708\1612129419.py: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.

```
corr = guidance.corr()
```



Some Symptoms are closely correlated, medically

## Model 1 Train the model for inpatient guidance

### 3. Model Training & Testing

The `guidance` dataset stores the symptoms corresponding to the physician that cope with such a disease

```
In [54]: # Train-test split
x = guidance.drop('Doctor_Specialist', axis = 1)
y = guidance.Doctor_Specialist
```

```
In [64]: x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.1, random_sta
```

```
In [65]: # Logistic Regression
classifier_logistic = LogisticRegression()

# K Nearest Neighbors
classifier_KNN = KNeighborsClassifier()

# Random Forest
classifier_RF = RandomForestClassifier()

# Support Vector Classification
classifier_SVC = SVC(probability=True)

# GB classifier
classifier_GB = GradientBoostingClassifier()

# Gaussian Naive Bayes
classifier_NB = GaussianNB()
```

We shall use Logistic Regression, Random Forest Classifier, KNeighborsClassifier, SVC, GradientBoostingClassifier, and

Workflow:

```
fit model -> predict result by training dataset -> cross validation ->
get cross validation result -> plot confusion matrix
```

Logistic Regression

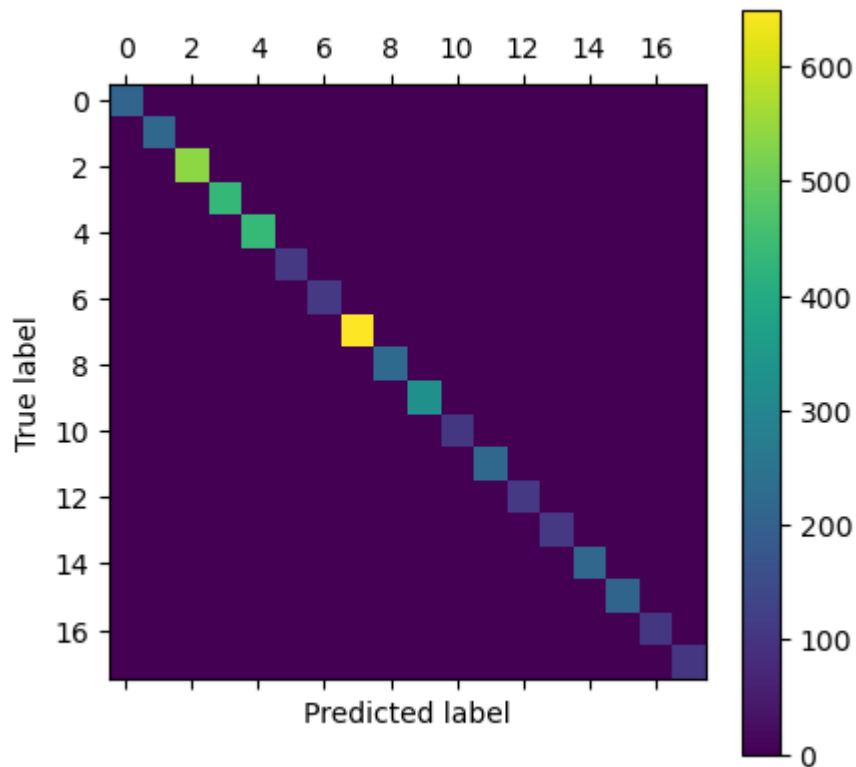
```
In [71]: classifier_logistic.fit(x_train, y_train)
y_predict = classifier_logistic.predict(x_train) # predict the result

scores = model_selection.cross_val_score(classifier_logistic, x_train, y_train, cv
print(f'For Logistic Regression, the accuracy is {round(scores.mean() * 100, 1)} +

# Confusion Matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_train, y_predict))
```

For Logistic Regression, the accuracy is 100.0 +/- 0.0%



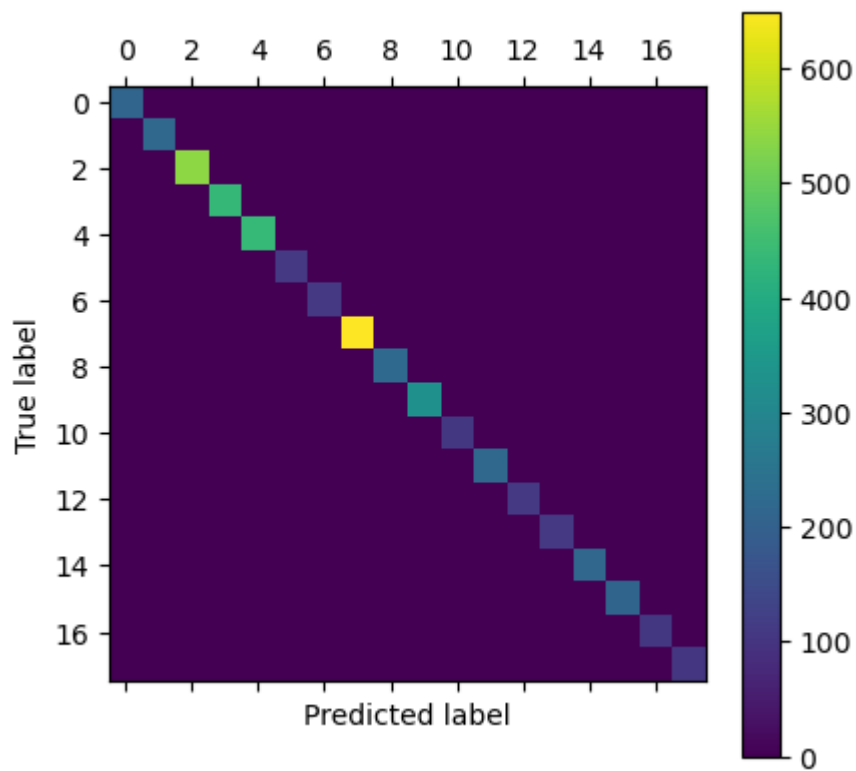
	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	211
Cardiologist	1.00	1.00	1.00	219
Dermatologist	1.00	1.00	1.00	539
Endocrinologist	1.00	1.00	1.00	434
Gastroenterologist	1.00	1.00	1.00	436
Gastroenterologist	1.00	1.00	1.00	109
Gynecologist	1.00	1.00	1.00	108
Hepatologist	1.00	1.00	1.00	650
Internal Medicine	1.00	1.00	1.00	222
Neurologist	1.00	1.00	1.00	327
Osteopathic	1.00	1.00	1.00	106
Otolaryngologist	1.00	1.00	1.00	217
Pediatrician	1.00	1.00	1.00	108
Phlebologist	1.00	1.00	1.00	108
Pulmonologist	1.00	1.00	1.00	215
Rheumatologists	1.00	1.00	1.00	210
Tuberculosis	1.00	1.00	1.00	106
hepatologist	1.00	1.00	1.00	103
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

A logistic regressor could overkill this task...**Shall we continue to use a more complexed model?**

In principle, maybe we can just use a logistic regressor if its test result is also very ideal. But for **Etudie**, we also use other classifier instead

RandomForestClassifier

For Random Forest, the accuracy is 100.0 +/- 0.0%



	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	211
Cardiologist	1.00	1.00	1.00	219
Dermatologist	1.00	1.00	1.00	539
Endocrinologist	1.00	1.00	1.00	434
Gastroenterologist	1.00	1.00	1.00	436
Gastroenterologist	1.00	1.00	1.00	109
Gynecologist	1.00	1.00	1.00	108
Hepatologist	1.00	1.00	1.00	650
Internal Medicine	1.00	1.00	1.00	222
Neurologist	1.00	1.00	1.00	327
Osteopathic	1.00	1.00	1.00	106
Otolaryngologist	1.00	1.00	1.00	217
Pediatrician	1.00	1.00	1.00	108
Phlebologist	1.00	1.00	1.00	108
Pulmonologist	1.00	1.00	1.00	215
Rheumatologists	1.00	1.00	1.00	210
Tuberculosis	1.00	1.00	1.00	106
hepatologist	1.00	1.00	1.00	103
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

### KNeighborsClassifier

```
In [77]: classifier_KNN.fit(x_train, y_train)
y_predict = classifier_KNN.predict(x_train)

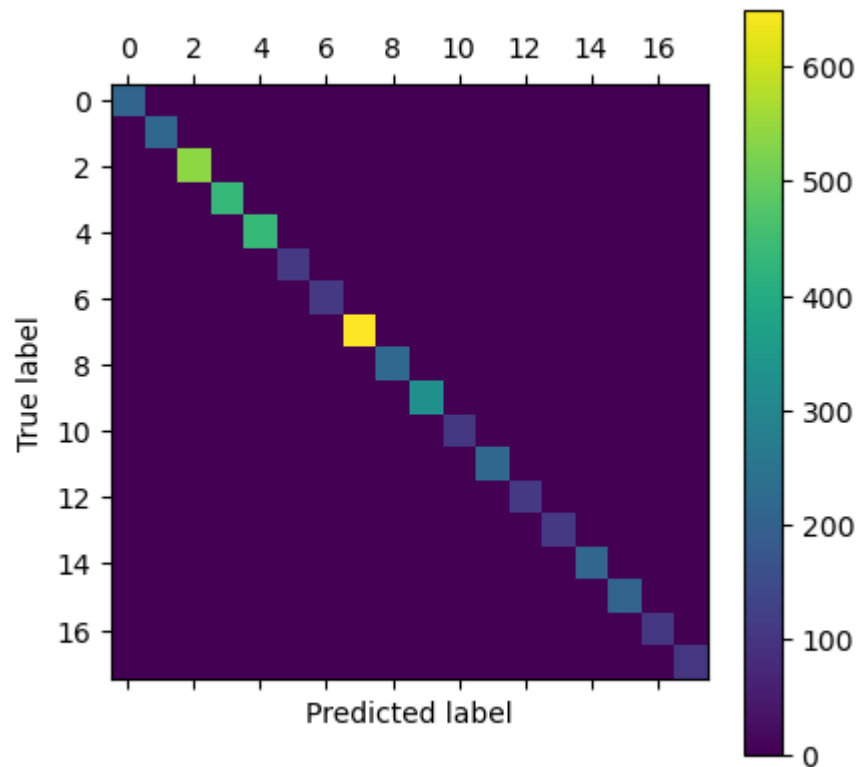
scores = model_selection.cross_val_score(classifier_KNN, x_train, y_train, cv = 10)
print(f'For K-Neighbours Classifier, the accuracy is {round(scores.mean() * 100 ,2)}%')

# Confusion Matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_train, y_predict))
```

For K-Neighbours Classifier, the accuracy is 100.0 +/- 0.0





	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	211
Cardiologist	1.00	1.00	1.00	219
Dermatologist	1.00	1.00	1.00	539
Endocrinologist	1.00	1.00	1.00	434
Gastroenterologist	1.00	1.00	1.00	436
Gastroenterologist	1.00	1.00	1.00	109
Gynecologist	1.00	1.00	1.00	108
Hepatologist	1.00	1.00	1.00	650
Internal Medicine	1.00	1.00	1.00	222
Neurologist	1.00	1.00	1.00	327
Osteopathic	1.00	1.00	1.00	106
Otolaryngologist	1.00	1.00	1.00	217
Pediatrician	1.00	1.00	1.00	108
Phlebologist	1.00	1.00	1.00	108
Pulmonologist	1.00	1.00	1.00	215
Rheumatologists	1.00	1.00	1.00	210
Tuberculosis	1.00	1.00	1.00	106
hepatologist	1.00	1.00	1.00	103
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

SVC

```
In [81]: classifier_SVC.fit(x_train, y_train)
y_predict = classifier_SVC.predict(x_train)

# cross validation
```

```

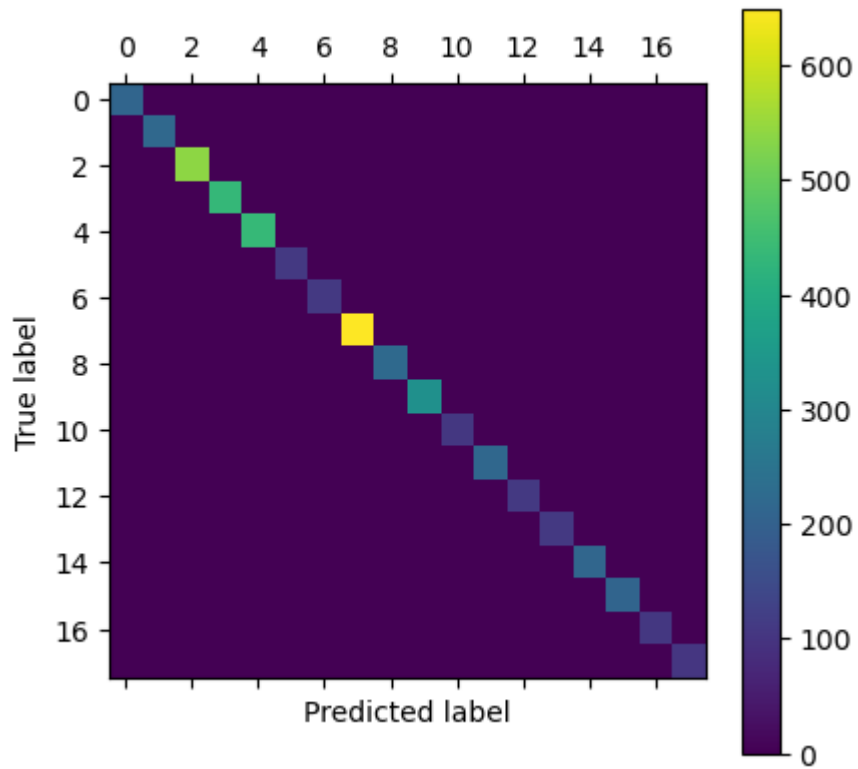
scores = model_selection.cross_val_score(classifier_SVC, x_train, y_train, cv = 10)
print(f'For SVC, the classification accuracy is {round(scores.mean() * 100, 2)} +/-

# confusion matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_train, y_predict))

```

For SVC, the classification accuracy is 100.0 +/- 0.0



	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	211
Cardiologist	1.00	1.00	1.00	219
Dermatologist	1.00	1.00	1.00	539
Endocrinologist	1.00	1.00	1.00	434
Gastroenterologist	1.00	1.00	1.00	436
Gastroenterologist	1.00	1.00	1.00	109
Gynecologist	1.00	1.00	1.00	108
Hepatologist	1.00	1.00	1.00	650
Internal Medicine	1.00	1.00	1.00	222
Neurologist	1.00	1.00	1.00	327
Osteopathic	1.00	1.00	1.00	106
Otolaryngologist	1.00	1.00	1.00	217
Pediatrician	1.00	1.00	1.00	108
Phlebologist	1.00	1.00	1.00	108
Pulmonologist	1.00	1.00	1.00	215
Rheumatologists	1.00	1.00	1.00	210
Tuberculosis	1.00	1.00	1.00	106
hepatologist	1.00	1.00	1.00	103
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

*The model is a bit slow*

GradientBoostingClassifier

```
In [84]: classifier_GB.fit(x_train, y_train)
y_predict = classifier_GB.predict(x_train)

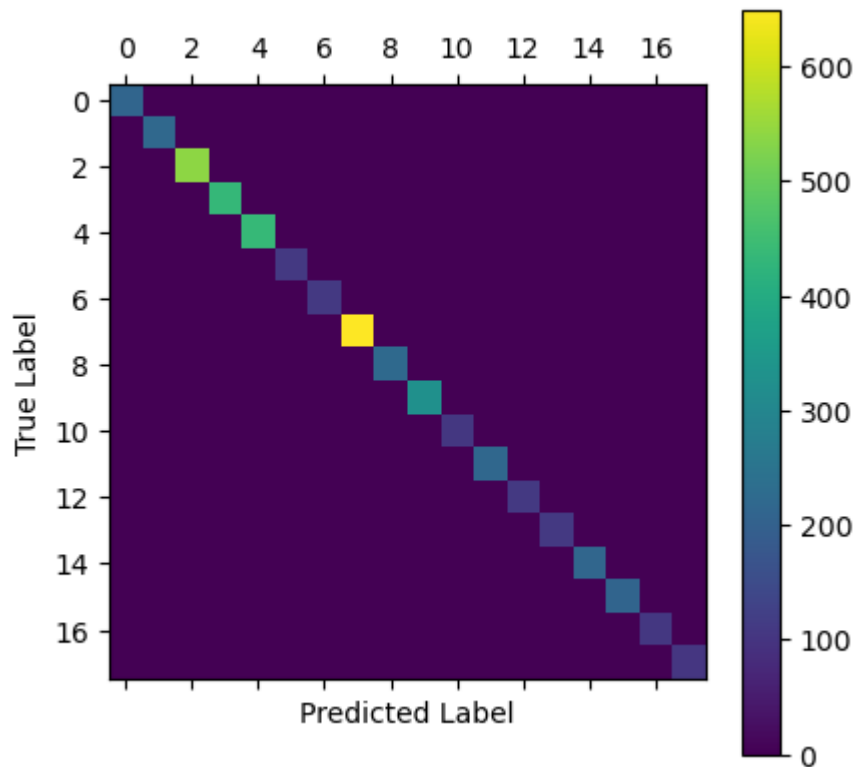
# cross validation
scores = model_selection.cross_val_score(classifier_GB, x_train, y_train, cv = 10)

print(f'For Gradient Boosting Classifier, the accuracy is {round(scores.mean() * 100, 2)}%
      +/- {round(scores.std() * 1.96 / (10 ** 0.5), 2)}%')
```

For Gradient Boosting Classifier, the accuracy is 100.0 +/- 0.0%

```
In [107... # plotting confusing matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()

print(metrics.classification_report(y_train, y_predict))
```



	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	211
Cardiologist	1.00	1.00	1.00	219
Dermatologist	1.00	1.00	1.00	539
Endocrinologist	1.00	1.00	1.00	434
Gastroenterologist	1.00	1.00	1.00	436
Gastroenterologist	1.00	1.00	1.00	109
Gynecologist	1.00	1.00	1.00	108
Hepatologist	1.00	1.00	1.00	650
Internal Medicine	1.00	1.00	1.00	222
Neurologist	1.00	1.00	1.00	327
Osteopathic	1.00	1.00	1.00	106
Otolaryngologist	1.00	1.00	1.00	217
Pediatrician	1.00	1.00	1.00	108
Phlebologist	1.00	1.00	1.00	108
Pulmonologist	1.00	1.00	1.00	215
Rheumatologists	1.00	1.00	1.00	210
Tuberculosis	1.00	1.00	1.00	106
hepatologist	1.00	1.00	1.00	103
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

*This model is much slower...*

GaussianNB

```
In [87]: classifier_NB.fit(x_train, y_train)
y_predict = classifier_NB.predict(x_train)
```



	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	211
Cardiologist	1.00	1.00	1.00	219
Dermatologist	1.00	1.00	1.00	539
Endocrinologist	1.00	1.00	1.00	434
Gastroenterologist	1.00	1.00	1.00	436
Gastroenterologist	1.00	1.00	1.00	109
Gynecologist	1.00	1.00	1.00	108
Hepatologist	1.00	1.00	1.00	650
Internal Medicine	1.00	1.00	1.00	222
Neurologist	1.00	1.00	1.00	327
Osteopathic	1.00	1.00	1.00	106
Otolaryngologist	1.00	1.00	1.00	217
Pediatrician	1.00	1.00	1.00	108
Phlebologist	1.00	1.00	1.00	108
Pulmonologist	1.00	1.00	1.00	215
Rheumatologists	1.00	1.00	1.00	210
Tuberculosis	1.00	1.00	1.00	106
hepatologist	1.00	1.00	1.00	103
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

All of the models above, including logistic regression, are overfitted. Let's see what they perform in test model.

## 4. Model Evaluation

**Precision**(PPV, positive predictive value):  $tp / (tp + fp)$ ; High Precision means low fp

**Recall**(sensitivity, hit rate, true positive rate):  $tp / (tp + fn)$

**Accuracy**:  $(tp + tn) / (tp + tn + fp + fn)$

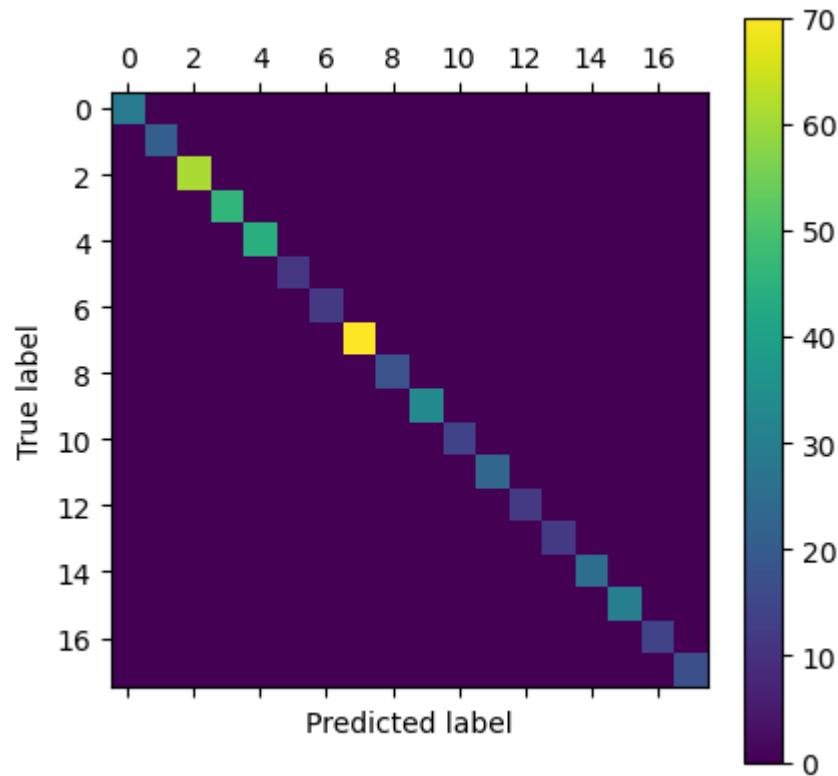
**f1-Score**:  $(2 * P * R) / (P + R)$

### 1. Logistic Regression

```
In [97]: y_final_predict = classifier_logistic.predict(x_test)

cm = metrics.confusion_matrix(y_test, y_final_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_test, y_final_predict))
```



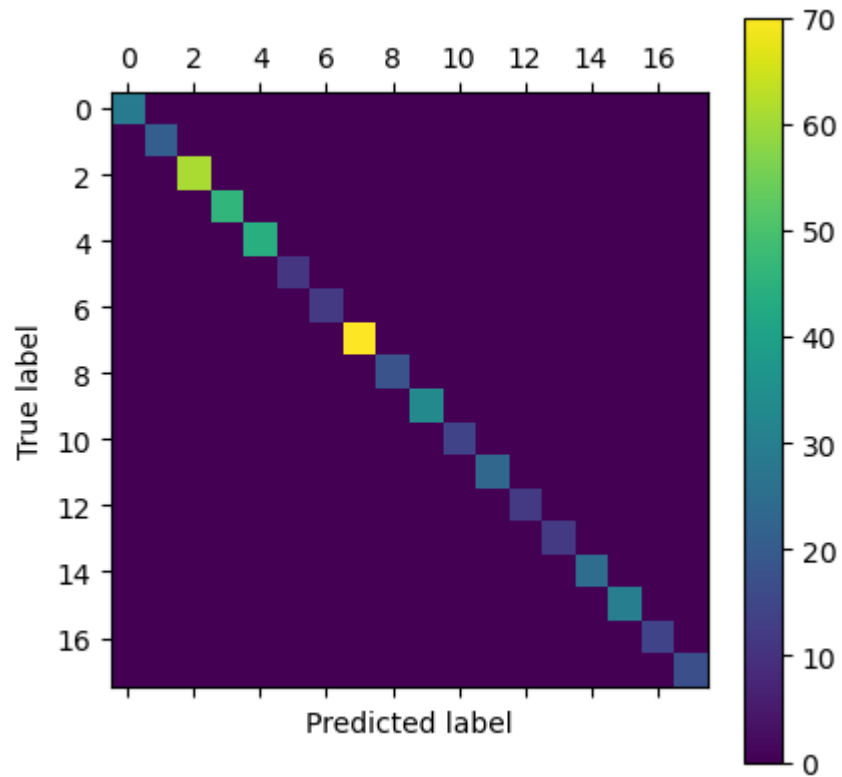
	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	29
Cardiologist	1.00	1.00	1.00	21
Dermatologist	1.00	1.00	1.00	61
Endocrinologist	1.00	1.00	1.00	46
Gastroenterologist	1.00	1.00	1.00	44
Gastroenterologist	1.00	1.00	1.00	11
Gynecologist	1.00	1.00	1.00	12
Hepatologist	1.00	1.00	1.00	70
Internal Medicine	1.00	1.00	1.00	18
Neurologist	1.00	1.00	1.00	33
Osteopathic	1.00	1.00	1.00	14
Otolaryngologist	1.00	1.00	1.00	23
Pediatrician	1.00	1.00	1.00	12
Phlebologist	1.00	1.00	1.00	12
Pulmonologist	1.00	1.00	1.00	25
Rheumatologists	1.00	1.00	1.00	30
Tuberculosis	1.00	1.00	1.00	14
hepatologist	1.00	1.00	1.00	17
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

**If we only use patient symptom data for guidance to the corresponding department, a logistic regression might be enough...**

## 2. RandomForestClassifier

```
In [100... # Confusion Matrix
cm = metrics.confusion_matrix(y_test, classifier_RF.predict(x_test))
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_test, classifier_RF.predict(x_test)))
```



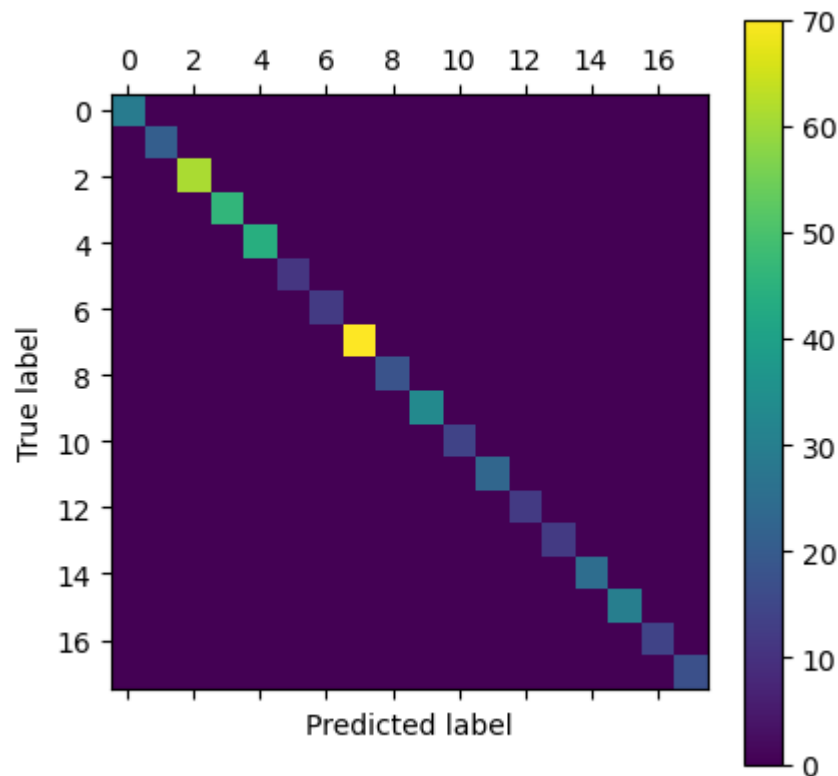


	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	29
Cardiologist	1.00	1.00	1.00	21
Dermatologist	1.00	1.00	1.00	61
Endocrinologist	1.00	1.00	1.00	46
Gastroenterologist	1.00	1.00	1.00	44
Gastroenterologist	1.00	1.00	1.00	11
Gynecologist	1.00	1.00	1.00	12
Hepatologist	1.00	1.00	1.00	70
Internal Medcine	1.00	1.00	1.00	18
Neurologist	1.00	1.00	1.00	33
Osteopathic	1.00	1.00	1.00	14
Otolaryngologist	1.00	1.00	1.00	23
Pediatrician	1.00	1.00	1.00	12
Phlebologist	1.00	1.00	1.00	12
Pulmonologist	1.00	1.00	1.00	25
Rheumatologists	1.00	1.00	1.00	30
Tuberculosis	1.00	1.00	1.00	14
hepatologist	1.00	1.00	1.00	17
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

### 3. KNeighborsClassifier

```
In [102... # Confusion Matrix
cm = metrics.confusion_matrix(y_test, classifier_KNN.predict(x_test))
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_test, classifier_KNN.predict(x_test)))
```



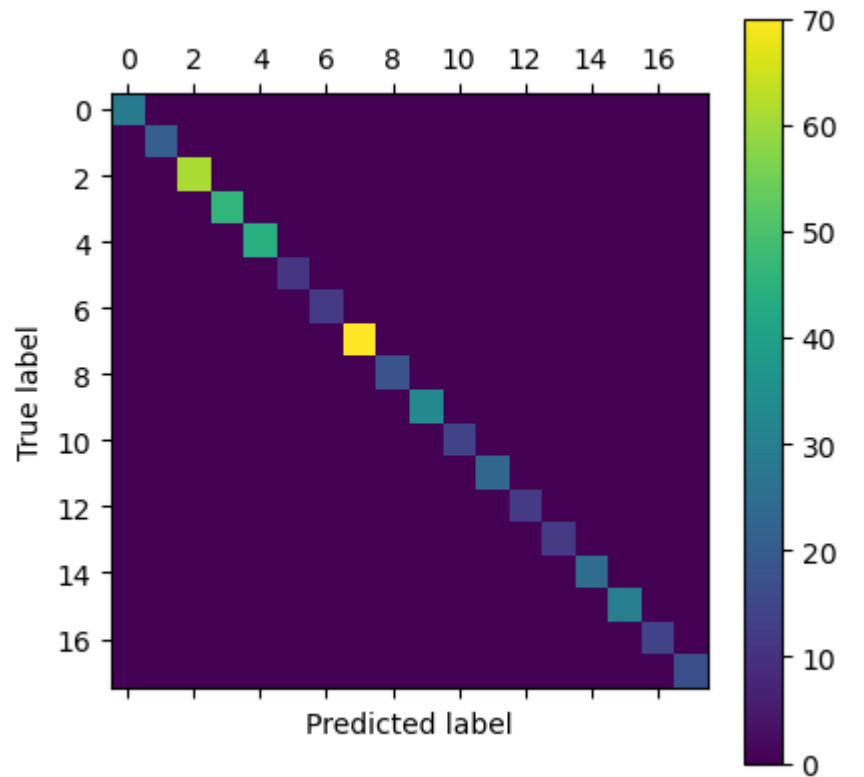
	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	29
Cardiologist	1.00	1.00	1.00	21
Dermatologist	1.00	1.00	1.00	61
Endocrinologist	1.00	1.00	1.00	46
Gastroenterologist	1.00	1.00	1.00	44
Gastroenterologist	1.00	1.00	1.00	11
Gynecologist	1.00	1.00	1.00	12
Hepatologist	1.00	1.00	1.00	70
Internal Medicine	1.00	1.00	1.00	18
Neurologist	1.00	1.00	1.00	33
Osteopathic	1.00	1.00	1.00	14
Otolaryngologist	1.00	1.00	1.00	23
Pediatrician	1.00	1.00	1.00	12
Phlebologist	1.00	1.00	1.00	12
Pulmonologist	1.00	1.00	1.00	25
Rheumatologists	1.00	1.00	1.00	30
Tuberculosis	1.00	1.00	1.00	14
hepatologist	1.00	1.00	1.00	17
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

#### 4. SVC

```
In [106... # confusion matrix
cm = metrics.confusion_matrix(y_test, classifier_SVC.predict(x_test))
plt.matshow(cm)
```

```
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_test, classifier_SVC.predict(x_test)))
```



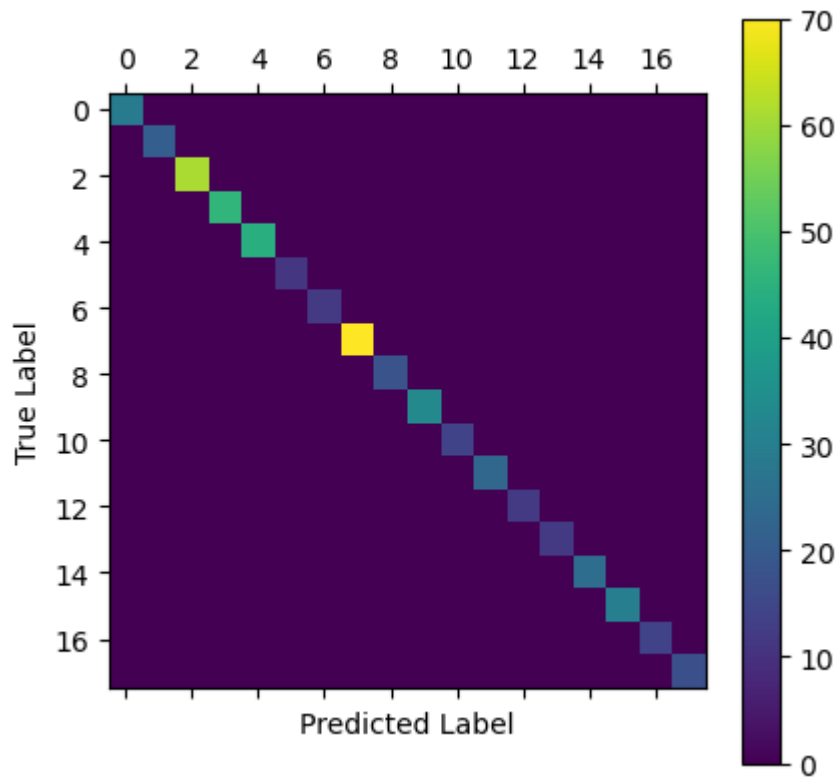
	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	29
Cardiologist	1.00	1.00	1.00	21
Dermatologist	1.00	1.00	1.00	61
Endocrinologist	1.00	1.00	1.00	46
Gastroenterologist	1.00	1.00	1.00	44
Gastroenterologist	1.00	1.00	1.00	11
Gynecologist	1.00	1.00	1.00	12
Hepatologist	1.00	1.00	1.00	70
Internal Medicine	1.00	1.00	1.00	18
Neurologist	1.00	1.00	1.00	33
Osteopathic	1.00	1.00	1.00	14
Otolaryngologist	1.00	1.00	1.00	23
Pediatrician	1.00	1.00	1.00	12
Phlebologist	1.00	1.00	1.00	12
Pulmonologist	1.00	1.00	1.00	25
Rheumatologists	1.00	1.00	1.00	30
Tuberculosis	1.00	1.00	1.00	14
hepatologist	1.00	1.00	1.00	17
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

*The model is a bit slow*

## 5. GradientBoostingClassifier

```
In [111... # plotting confusing matrix
cm = metrics.confusion_matrix(y_test, classifier_GB.predict(x_test))
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()

print(metrics.classification_report(y_test, classifier_GB.predict(x_test)))
```

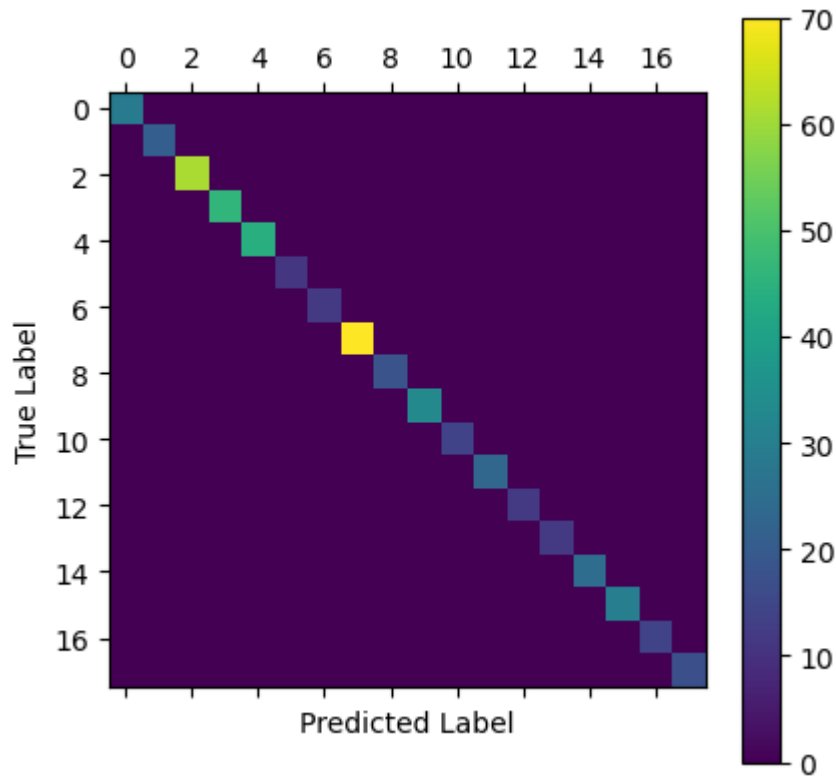


	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	29
Cardiologist	1.00	1.00	1.00	21
Dermatologist	1.00	1.00	1.00	61
Endocrinologist	1.00	1.00	1.00	46
Gastroenterologist	1.00	1.00	1.00	44
Gastroenterologist	1.00	1.00	1.00	11
Gynecologist	1.00	1.00	1.00	12
Hepatologist	1.00	1.00	1.00	70
Internal Medicine	1.00	1.00	1.00	18
Neurologist	1.00	1.00	1.00	33
Osteopathic	1.00	1.00	1.00	14
Otolaryngologist	1.00	1.00	1.00	23
Pediatrician	1.00	1.00	1.00	12
Phlebologist	1.00	1.00	1.00	12
Pulmonologist	1.00	1.00	1.00	25
Rheumatologists	1.00	1.00	1.00	30
Tuberculosis	1.00	1.00	1.00	14
hepatologist	1.00	1.00	1.00	17
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

*This model is much slower...*

GaussianNB

```
In [112... # confusion matrix
cm = metrics.confusion_matrix(y_test, classifier_NB.predict(x_test))
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()
print(metrics.classification_report(y_test, classifier_NB.predict(x_test)))
```



	precision	recall	f1-score	support
Allergist	1.00	1.00	1.00	29
Cardiologist	1.00	1.00	1.00	21
Dermatologist	1.00	1.00	1.00	61
Endocrinologist	1.00	1.00	1.00	46
Gastroenterologist	1.00	1.00	1.00	44
Gastroenterologist	1.00	1.00	1.00	11
Gynecologist	1.00	1.00	1.00	12
Hepatologist	1.00	1.00	1.00	70
Internal Medicine	1.00	1.00	1.00	18
Neurologist	1.00	1.00	1.00	33
Osteopathic	1.00	1.00	1.00	14
Otolaryngologist	1.00	1.00	1.00	23
Pediatrician	1.00	1.00	1.00	12
Phlebologist	1.00	1.00	1.00	12
Pulmonologist	1.00	1.00	1.00	25
Rheumatologists	1.00	1.00	1.00	30
Tuberculosis	1.00	1.00	1.00	14
hepatologist	1.00	1.00	1.00	17
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

All of the models above, including logistic regression, are overfitted, even in testing data.

Therefore, if we have to figure out which one is the best, maybe the only answer would be the **logistic regression** model

## Feature Importance

```
In [119... importances = classifier_RF.feature_importances_  
  
indices = np.argsort(importances)[::-1]  
  
# Print the feature ranking  
print("Feature importance ranking by RF:")  
for ind in range(x.shape[1]):  
    print ("{0} : {1}".format(x.columns[indices[ind]],round(importances[indices[ind]]
```

Feature importance ranking by RF:

skin\_rash : 0.0585  
nausea : 0.0365  
yellowing\_of\_eyes : 0.0358  
vomiting : 0.0301  
yellowish\_skin : 0.0282  
headache : 0.0247  
abdominal\_pain : 0.0239  
breathlessness : 0.0228  
swelling\_joints : 0.0225  
fatigue : 0.0205  
chills : 0.0204  
chest\_pain : 0.0195  
loss\_of\_appetite : 0.0188  
cough : 0.0187  
painful\_walking : 0.0185  
high\_fever : 0.0169  
irritability : 0.0169  
excessive\_hunger : 0.0168  
muscle\_pain : 0.0168  
stomach\_pain : 0.0151  
sweating : 0.0139  
burning\_micturition : 0.0137  
loss\_of\_balance : 0.0121  
weight\_loss : 0.011  
bladder\_discomfort : 0.0108  
malaise : 0.0106  
itching : 0.0105  
spotting\_urination : 0.0105  
abnormal\_menstruation : 0.0104  
constipation : 0.01  
lethargy : 0.0096  
back\_pain : 0.0094  
dark\_urine : 0.009  
lack\_of\_concentration : 0.009  
restlessness : 0.009  
continuous\_feel\_of\_urine : 0.0079  
weakness\_of\_one\_body\_side : 0.0078  
patches\_in\_throat : 0.0075  
altered\_sensorium : 0.0074  
neck\_pain : 0.0073  
extra\_marital\_contacts : 0.0072  
continuous\_sneezing : 0.0072  
diarrhoea : 0.0072  
watering\_from\_eyes : 0.0071  
unsteadiness : 0.0069  
pain\_in\_anal\_region : 0.0068  
receiving\_blood\_transfusion : 0.0067  
mood\_swings : 0.0067  
bloody\_stool : 0.0066  
muscle\_wasting : 0.0065  
spinning\_movements : 0.0062  
prominent\_veins\_on\_calf : 0.0062  
pain\_behind\_the\_eyes : 0.0059  
shivering : 0.0058  
yellow\_urine : 0.0057



swelled\_lymph\_nodes : 0.0057  
indigestion : 0.0056  
obesity : 0.0056  
pain\_during\_bowel\_movements : 0.0054  
blurred\_and\_distorted\_vision : 0.0054  
blood\_in\_sputum : 0.0053  
acidity : 0.0053  
dizziness : 0.0053  
joint\_pain : 0.0053  
history\_of\_alcohol\_consumption : 0.0052  
belly\_pain : 0.0052  
cramps : 0.0051  
internal\_itching : 0.0051  
bruising : 0.005  
toxic\_look\_(typhos) : 0.0049  
irritation\_in\_anus : 0.0049  
receiving\_unsterile\_injections : 0.0048  
sunken\_eyes : 0.0047  
sinus\_pressure : 0.0045  
distention\_of\_abdomen : 0.0044  
phlegm : 0.0043  
swollen\_legs : 0.0043  
runny\_nose : 0.004  
fluid\_overload : 0.0039  
mild\_fever : 0.0039  
congestion : 0.0039  
weakness\_in\_limbs : 0.0037  
stiff\_neck : 0.0037  
visual\_disturbances : 0.0036  
dehydration : 0.0036  
family\_history : 0.0035  
redness\_of\_eyes : 0.0035  
passage\_of\_gases : 0.0033  
mucoid\_sputum : 0.0033  
swelling\_of\_stomach : 0.0033  
foul\_smell\_of\_urine : 0.0032  
depression : 0.0031  
slurred\_speech : 0.0029  
swollen\_blood\_vessels : 0.0028  
ulcers\_on\_tongue : 0.0028  
red\_spots\_over\_body : 0.0028  
hip\_joint\_pain : 0.0027  
loss\_of\_smell : 0.0023  
dischromic\_patches : 0.0022  
rusty\_sputum : 0.0022  
fast\_heart\_rate : 0.0021  
nodal\_skin\_eruptions : 0.002  
brittle\_nails : 0.0018  
movement\_stiffness : 0.0018  
polyuria : 0.0018  
drying\_and\_tingling\_lips : 0.0017  
muscle\_weakness : 0.0017  
palpitations : 0.0016  
knee\_pain : 0.0015  
increased\_appetite : 0.0014  
silver\_like\_dusting : 0.0013

```
yellow_crust_ooze : 0.0013
throat_irritation : 0.0013
irregular_sugar_level : 0.0012
weight_gain : 0.0011
anxiety : 0.0011
swollen_extremeties : 0.0011
small_dents_in_nails : 0.0011
red_sore_around_nose : 0.001
scurring : 0.001
enlarged_thyroid : 0.001
cold_hands_and_feets : 0.0009
blister : 0.0009
pus_filled_pimples : 0.0008
blackheads : 0.0008
acute_liver_failure : 0.0007
inflammatory_nails : 0.0007
stomach_bleeding : 0.0006
puffy_face_and_eyes : 0.0006
coma : 0.0006
skin_peeling : 0.0006
```

## 5. Insights & Conclusion

1. It seems that logistic regression is enough to guide the patient to the corresponding physician. **However, the usability of this model is still needed to be furtherly verified.**
2. Common symptoms, like fatigue, vomiting, headache, abdominal pain generally more decisive on which department we should go.

## Model 2 Train the model for Disease Diagnosis

### 3. Model Training & Testing

The `symptoms` dataset stores the symptoms corresponding to disease

In [135... `symptoms.head()`

Out[135]:

	itching	skin_rash	nodal_skin_eruptions	dischromic_patches	continuous_sneezing	shivering	ch
0	1	1	1	1	0	0	
1	0	1	1	1	0	0	
2	1	0	1	1	0	0	
3	1	1	0	1	0	0	
4	1	1	1	0	0	0	

```
In [138... # Train-test split
x = symptoms.drop('Disease', axis = 1)
y = symptoms.Disease
```

```
In [139... x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.1, random_sta
```

```
In [140... # Logistic Regression
classifier_logistic = LogisticRegression()

# K Nearest Neighbors
classifier_KNN = KNeighborsClassifier()

# Random Forest
classifier_RF = RandomForestClassifier()

# Support Vector Classification
classifier_SVC = SVC(probability=True)

# GB classifier
classifier_GB = GradientBoostingClassifier()

# Gaussian Naive Bayes
classifier_NB = GaussianNB()
```

We shall use Logistic Regression, Random Forest Classifier, KNeighborsClassifier, SVC, GradientBoostingClassifier, and

Workflow:

```
fit model -> predict result by training dataset -> cross validation ->
get cross validation result -> plot confusion matrix
```

Logistic Regression

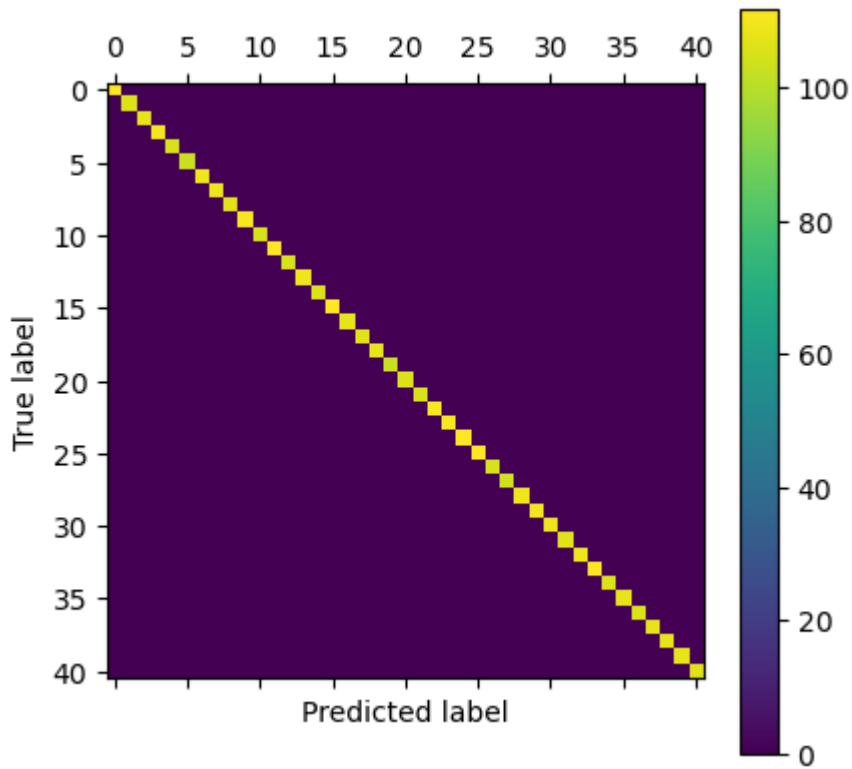
```
In [141... classifier_logistic.fit(x_train, y_train)
y_predict = classifier_logistic.predict(x_train) # predict the result
```

```
scores = model_selection.cross_val_score(classifier_logistic, x_train, y_train, cv
print(f'For Logistic Regression, the accuracy is {round(scores.mean() * 100, 1)} +

# Confusion Matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_train, y_predict))
```

For Logistic Regression, the accuracy is 100.0 +/- 0.0%



	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	112
AIDS	1.00	1.00	1.00	106
Acne	1.00	1.00	1.00	108
Alcoholic hepatitis	1.00	1.00	1.00	110
Allergy	1.00	1.00	1.00	105
Arthritis	1.00	1.00	1.00	103
Bronchial Asthma	1.00	1.00	1.00	109
Cervical spondylosis	1.00	1.00	1.00	109
Chicken pox	1.00	1.00	1.00	107
Chronic cholestasis	1.00	1.00	1.00	111
Common Cold	1.00	1.00	1.00	105
Dengue	1.00	1.00	1.00	112
Diabetes	1.00	1.00	1.00	105
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	109
Drug Reaction	1.00	1.00	1.00	106
Fungal infection	1.00	1.00	1.00	112
GERD	1.00	1.00	1.00	108
Gastroenteritis	1.00	1.00	1.00	107
Heart attack	1.00	1.00	1.00	108
Hepatitis B	1.00	1.00	1.00	103
Hepatitis C	1.00	1.00	1.00	106
Hepatitis D	1.00	1.00	1.00	105
Hepatitis E	1.00	1.00	1.00	111
Hypertension	1.00	1.00	1.00	111
Hyperthyroidism	1.00	1.00	1.00	112
Hypoglycemia	1.00	1.00	1.00	112
Hypothyroidism	1.00	1.00	1.00	105
Impetigo	1.00	1.00	1.00	104
Jaundice	1.00	1.00	1.00	109
Malaria	1.00	1.00	1.00	110
Migraine	1.00	1.00	1.00	109
Osteoarthritis	1.00	1.00	1.00	107
Paralysis (brain hemorrhage)	1.00	1.00	1.00	109
Peptic ulcer diseae	1.00	1.00	1.00	112
Pneumonia	1.00	1.00	1.00	106
Psoriasis	1.00	1.00	1.00	108
Tuberculosis	1.00	1.00	1.00	106
Typhoid	1.00	1.00	1.00	108
Urinary tract infection	1.00	1.00	1.00	108
Varicose veins	1.00	1.00	1.00	108
hepatitis A	1.00	1.00	1.00	107
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

A logistic regressor could overkill this task...**Shall we continue to use a more complexed model?**

In principle, maybe we can just use a logistic regressor if its test result is also very ideal. But for **Etudie**, we also use other classifier instead

The following training and cross validation may for etudie purpose only

RandomForestClassifier

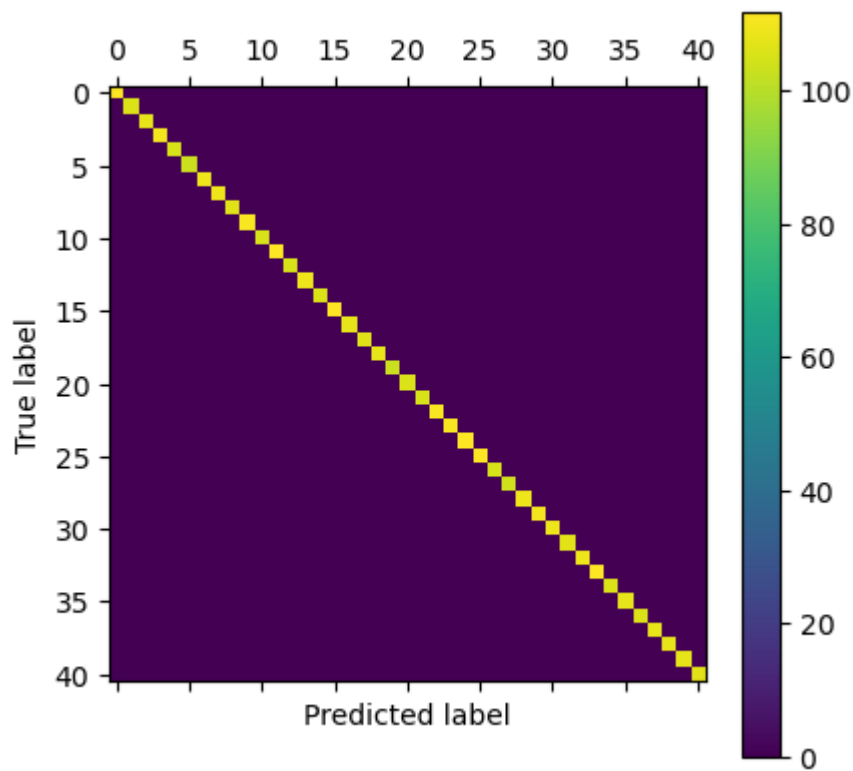
```
In [142... classifier_RF.fit(x_train, y_train)
y_predict = classifier_RF.predict(x_train) # predict the result

scores = model_selection.cross_val_score(classifier_RF, x_train, y_train, cv = 10)
print(f'For Random Forest, the accuracy is {round(scores.mean() * 100, 1)} +/- {ro

# Confusion Matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_train, y_predict))
```

For Random Forest, the accuracy is 100.0 +/- 0.0%



	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	112
AIDS	1.00	1.00	1.00	106
Acne	1.00	1.00	1.00	108
Alcoholic hepatitis	1.00	1.00	1.00	110
Allergy	1.00	1.00	1.00	105
Arthritis	1.00	1.00	1.00	103
Bronchial Asthma	1.00	1.00	1.00	109
Cervical spondylosis	1.00	1.00	1.00	109
Chicken pox	1.00	1.00	1.00	107
Chronic cholestasis	1.00	1.00	1.00	111
Common Cold	1.00	1.00	1.00	105
Dengue	1.00	1.00	1.00	112
Diabetes	1.00	1.00	1.00	105
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	109
Drug Reaction	1.00	1.00	1.00	106
Fungal infection	1.00	1.00	1.00	112
GERD	1.00	1.00	1.00	108
Gastroenteritis	1.00	1.00	1.00	107
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Hepatitis C	1.00	1.00	1.00	106
Hepatitis D	1.00	1.00	1.00	105
Hepatitis E	1.00	1.00	1.00	111
Hypertension	1.00	1.00	1.00	111
Hyperthyroidism	1.00	1.00	1.00	112
Hypoglycemia	1.00	1.00	1.00	112
Hypothyroidism	1.00	1.00	1.00	105
Impetigo	1.00	1.00	1.00	104
Jaundice	1.00	1.00	1.00	109
Malaria	1.00	1.00	1.00	110
Migraine	1.00	1.00	1.00	109
Osteoarthritis	1.00	1.00	1.00	107
Paralysis (brain hemorrhage)	1.00	1.00	1.00	109
Peptic ulcer diseae	1.00	1.00	1.00	112
Pneumonia	1.00	1.00	1.00	106
Psoriasis	1.00	1.00	1.00	108
Tuberculosis	1.00	1.00	1.00	106
Typhoid	1.00	1.00	1.00	108
Urinary tract infection	1.00	1.00	1.00	108
Varicose veins	1.00	1.00	1.00	108
hepatitis A	1.00	1.00	1.00	107
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

### KNeighborsClassifier

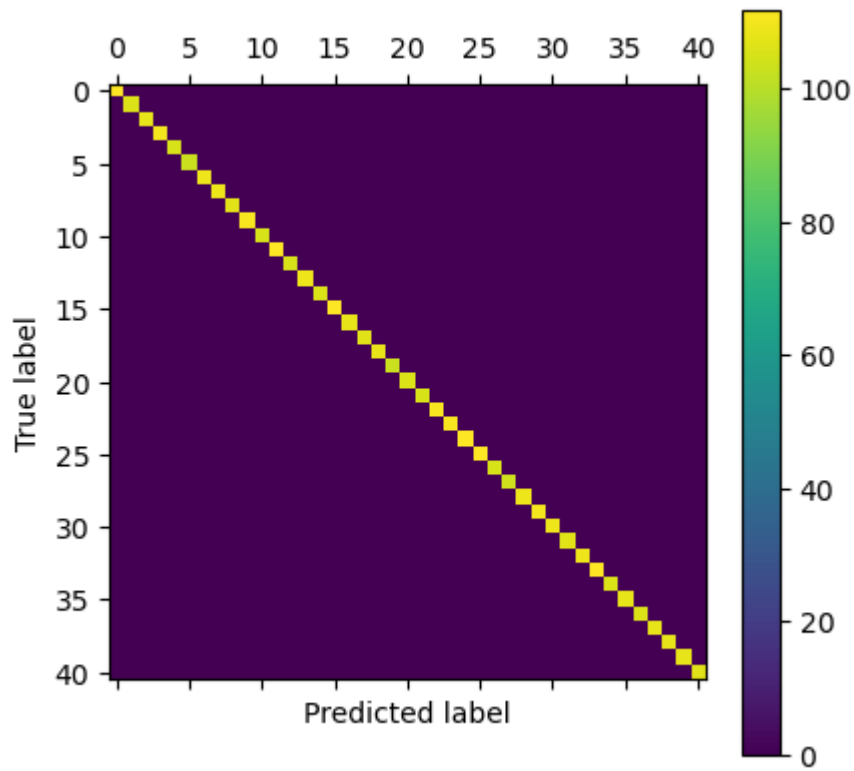
```
In [143... classifier_KNN.fit(x_train, y_train)
y_predict = classifier_KNN.predict(x_train)

scores = model_selection.cross_val_score(classifier_KNN, x_train, y_train, cv = 10)
print(f'For K-Neighbours Classifier, the accuracy is {round(scores.mean() * 100 ,2
```

```
# Confusion Matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_train, y_predict))
```

For K-Neighbours Classifier, the accuracy is 100.0 +/- 0.0





	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	112
AIDS	1.00	1.00	1.00	106
Acne	1.00	1.00	1.00	108
Alcoholic hepatitis	1.00	1.00	1.00	110
Allergy	1.00	1.00	1.00	105
Arthritis	1.00	1.00	1.00	103
Bronchial Asthma	1.00	1.00	1.00	109
Cervical spondylosis	1.00	1.00	1.00	109
Chicken pox	1.00	1.00	1.00	107
Chronic cholestasis	1.00	1.00	1.00	111
Common Cold	1.00	1.00	1.00	105
Dengue	1.00	1.00	1.00	112
Diabetes	1.00	1.00	1.00	105
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	109
Drug Reaction	1.00	1.00	1.00	106
Fungal infection	1.00	1.00	1.00	112
GERD	1.00	1.00	1.00	108
Gastroenteritis	1.00	1.00	1.00	107
Heart attack	1.00	1.00	1.00	108
Hepatitis B	1.00	1.00	1.00	103
Hepatitis C	1.00	1.00	1.00	106
Hepatitis D	1.00	1.00	1.00	105
Hepatitis E	1.00	1.00	1.00	111
Hypertension	1.00	1.00	1.00	111
Hyperthyroidism	1.00	1.00	1.00	112
Hypoglycemia	1.00	1.00	1.00	112
Hypothyroidism	1.00	1.00	1.00	105
Impetigo	1.00	1.00	1.00	104
Jaundice	1.00	1.00	1.00	109
Malaria	1.00	1.00	1.00	110
Migraine	1.00	1.00	1.00	109
Osteoarthritis	1.00	1.00	1.00	107
Paralysis (brain hemorrhage)	1.00	1.00	1.00	109
Peptic ulcer diseae	1.00	1.00	1.00	112
Pneumonia	1.00	1.00	1.00	106
Psoriasis	1.00	1.00	1.00	108
Tuberculosis	1.00	1.00	1.00	106
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Urinary tract infection	1.00	1.00	1.00	108
Varicose veins	1.00	1.00	1.00	108
hepatitis A	1.00	1.00	1.00	107
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

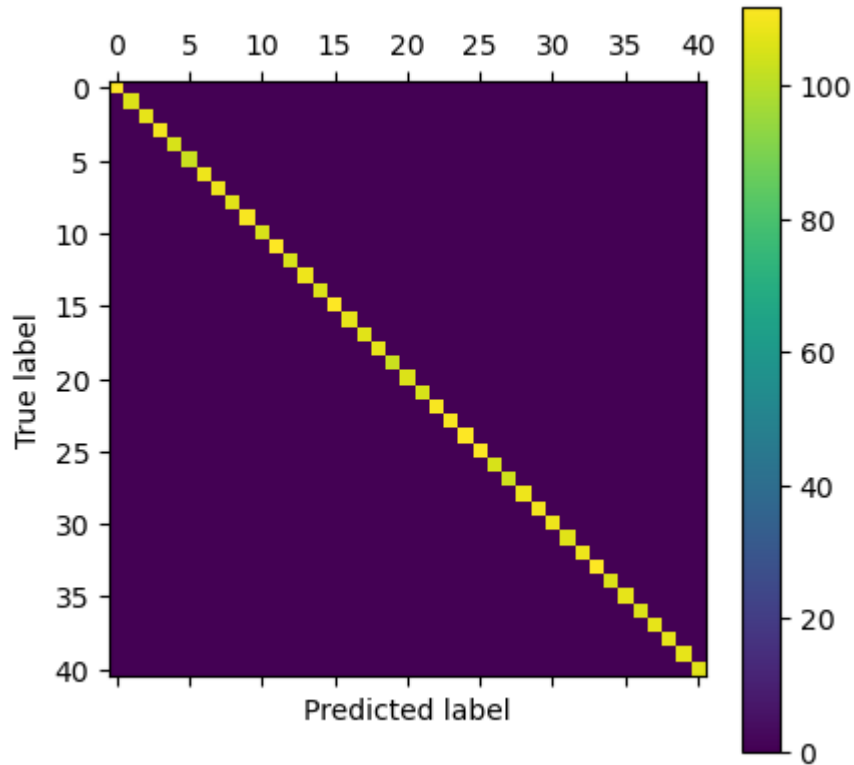
SVC

```
In [144... classifier_SVC.fit(x_train, y_train)
y_predict = classifier_SVC.predict(x_train)

# cross validation
scores = model_selection.cross_val_score(classifier_SVC, x_train, y_train, cv = 10)
```

```
print(f'For SVC, the classification accuracy is {round(scores.mean() * 100, 2)} +/-  
  
# confusion matrix  
cm = metrics.confusion_matrix(y_train, y_predict)  
plt.matshow(cm)  
plt.colorbar()  
plt.ylabel('True label')  
plt.xlabel('Predicted label')  
plt.show()  
  
print(metrics.classification_report(y_train, y_predict))
```

For SVC, the classification accuracy is 100.0 +/- 0.0



	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	112
AIDS	1.00	1.00	1.00	106
Acne	1.00	1.00	1.00	108
Alcoholic hepatitis	1.00	1.00	1.00	110
Allergy	1.00	1.00	1.00	105
Arthritis	1.00	1.00	1.00	103
Bronchial Asthma	1.00	1.00	1.00	109
Cervical spondylosis	1.00	1.00	1.00	109
Chicken pox	1.00	1.00	1.00	107
Chronic cholestasis	1.00	1.00	1.00	111
Common Cold	1.00	1.00	1.00	105
Dengue	1.00	1.00	1.00	112
Diabetes	1.00	1.00	1.00	105
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	109
Drug Reaction	1.00	1.00	1.00	106
Fungal infection	1.00	1.00	1.00	112
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Hepatitis B	1.00	1.00	1.00	103
Hepatitis C	1.00	1.00	1.00	106
Hepatitis D	1.00	1.00	1.00	105
Hepatitis E	1.00	1.00	1.00	111
Hypertension	1.00	1.00	1.00	111
Hyperthyroidism	1.00	1.00	1.00	112
Hypoglycemia	1.00	1.00	1.00	112
Hypothyroidism	1.00	1.00	1.00	105
Impetigo	1.00	1.00	1.00	104
Jaundice	1.00	1.00	1.00	109
Malaria	1.00	1.00	1.00	110
Migraine	1.00	1.00	1.00	109
Osteoarthritis	1.00	1.00	1.00	107
Paralysis (brain hemorrhage)	1.00	1.00	1.00	109
Peptic ulcer diseae	1.00	1.00	1.00	112
Pneumonia	1.00	1.00	1.00	106
Psoriasis	1.00	1.00	1.00	108
Tuberculosis	1.00	1.00	1.00	106
Typhoid	1.00	1.00	1.00	108
Urinary tract infection	1.00	1.00	1.00	108
Varicose veins	1.00	1.00	1.00	108
hepatitis A	1.00	1.00	1.00	107
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

*The model is a bit slow*

GradientBoostingClassifier

```
In [145... classifier_GB.fit(x_train, y_train)
y_predict = classifier_GB.predict(x_train)
```

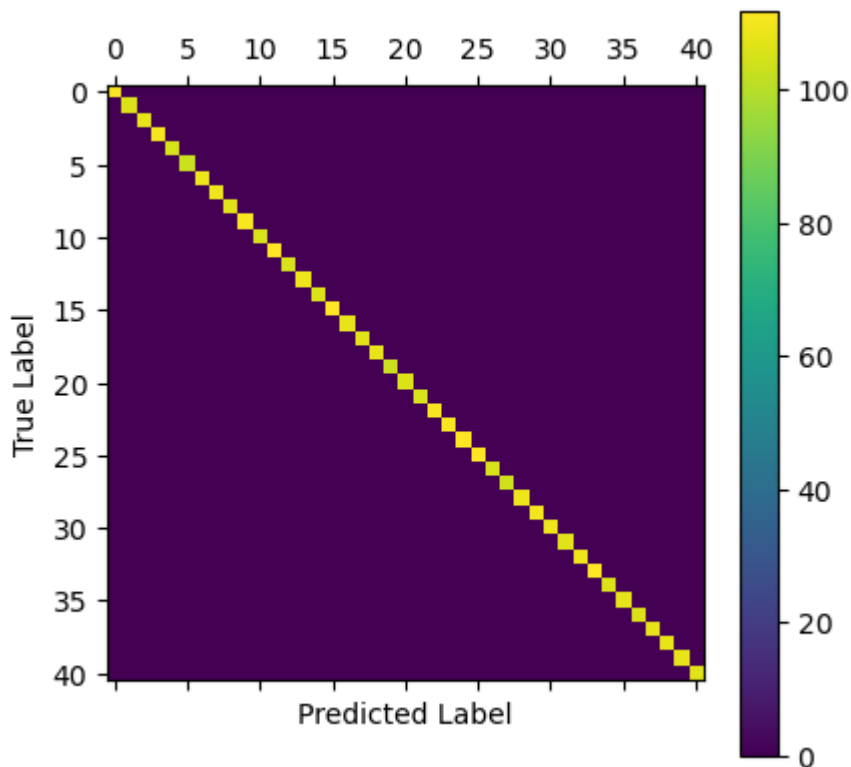
```
# cross validation
scores = model_selection.cross_val_score(classifier_GB, x_train, y_train, cv = 10)

print(f'For Gradient Boosting Classifier, the accuracy is {round(scores.mean() * 100, 2)}%  
+/- {round(scores.std() * 1.96 / (10 ** 0.5), 2)}%')
```

For Gradient Boosting Classifier, the accuracy is 100.0 +/- 0.0%

```
In [146... # plotting confusing matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()

print(metrics.classification_report(y_train, y_predict))
```



	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	112
AIDS	1.00	1.00	1.00	106
Acne	1.00	1.00	1.00	108
Alcoholic hepatitis	1.00	1.00	1.00	110
Allergy	1.00	1.00	1.00	105
Arthritis	1.00	1.00	1.00	103
Bronchial Asthma	1.00	1.00	1.00	109
Cervical spondylosis	1.00	1.00	1.00	109
Chicken pox	1.00	1.00	1.00	107
Chronic cholestasis	1.00	1.00	1.00	111
Common Cold	1.00	1.00	1.00	105
Dengue	1.00	1.00	1.00	112
Diabetes	1.00	1.00	1.00	105
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	109
Drug Reaction	1.00	1.00	1.00	106
Fungal infection	1.00	1.00	1.00	112
GERD	1.00	1.00	1.00	108
Gastroenteritis	1.00	1.00	1.00	107
Heart attack	1.00	1.00	1.00	108
Hepatitis B	1.00	1.00	1.00	103
Hepatitis C	1.00	1.00	1.00	106
Hepatitis D	1.00	1.00	1.00	105
Hepatitis E	1.00	1.00	1.00	111
Hypertension	1.00	1.00	1.00	111
Hyperthyroidism	1.00	1.00	1.00	112
Hypoglycemia	1.00	1.00	1.00	112
Hypothyroidism	1.00	1.00	1.00	105
Impetigo	1.00	1.00	1.00	104
Jaundice	1.00	1.00	1.00	109
Malaria	1.00	1.00	1.00	110
Migraine	1.00	1.00	1.00	109
Osteoarthritis	1.00	1.00	1.00	107
Paralysis (brain hemorrhage)	1.00	1.00	1.00	109
Peptic ulcer diseae	1.00	1.00	1.00	112
Pneumonia	1.00	1.00	1.00	106
Psoriasis	1.00	1.00	1.00	108
Tuberculosis	1.00	1.00	1.00	106
Typhoid	1.00	1.00	1.00	108
Urinary tract infection	1.00	1.00	1.00	108
Varicose veins	1.00	1.00	1.00	108
hepatitis A	1.00	1.00	1.00	107
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

*This model is much slower...*

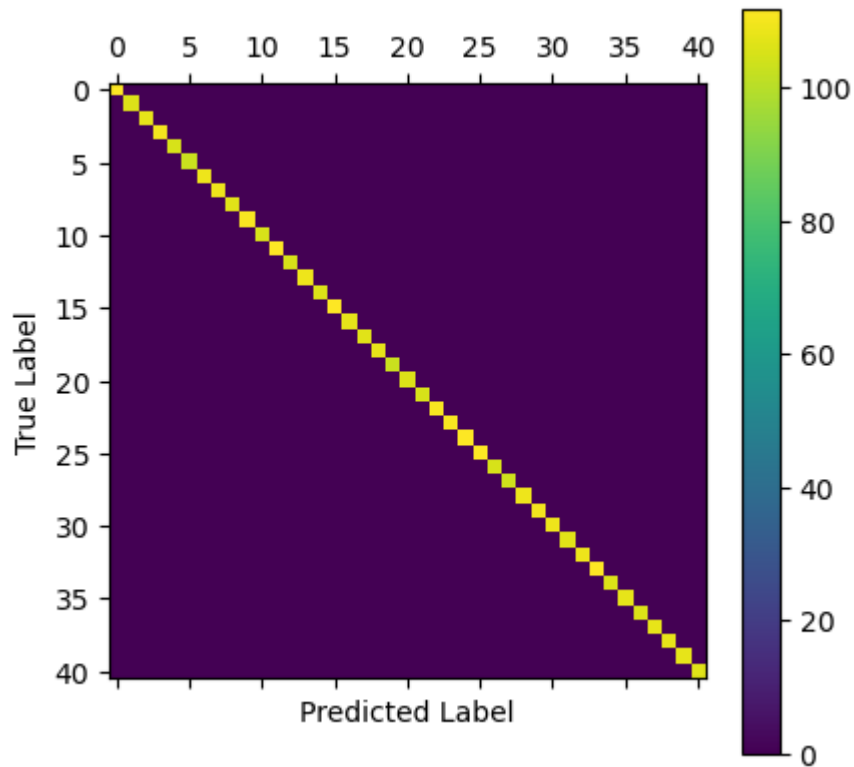
GaussianNB

```
In [147... classifier_NB.fit(x_train, y_train)
y_predict = classifier_NB.predict(x_train)
```

```
# Cross Validation
scores = model_selection.cross_val_score(classifier_NB, x_train, y_train, cv = 10)
print(f'Fore Gaussian Naive Bayes Model, the accuracy is {round(scores.mean() * 10
```

Fore Gaussian Naive Bayes Model, the accuracy is 100.0 +/- 0.0

```
In [148... # confusion matrix
cm = metrics.confusion_matrix(y_train, y_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()
print(metrics.classification_report(y_train, y_predict))
```



	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	112
AIDS	1.00	1.00	1.00	106
Acne	1.00	1.00	1.00	108
Alcoholic hepatitis	1.00	1.00	1.00	110
Allergy	1.00	1.00	1.00	105
Arthritis	1.00	1.00	1.00	103
Bronchial Asthma	1.00	1.00	1.00	109
Cervical spondylosis	1.00	1.00	1.00	109
Chicken pox	1.00	1.00	1.00	107
Chronic cholestasis	1.00	1.00	1.00	111
Common Cold	1.00	1.00	1.00	105
Dengue	1.00	1.00	1.00	112
Diabetes	1.00	1.00	1.00	105
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	109
Drug Reaction	1.00	1.00	1.00	106
Fungal infection	1.00	1.00	1.00	112
GERD	1.00	1.00	1.00	108
Gastroenteritis	1.00	1.00	1.00	107
Heart attack	1.00	1.00	1.00	108
Hepatitis B	1.00	1.00	1.00	103
Hepatitis C	1.00	1.00	1.00	106
Hepatitis D	1.00	1.00	1.00	105
Hepatitis E	1.00	1.00	1.00	111
Hypertension	1.00	1.00	1.00	111
Hyperthyroidism	1.00	1.00	1.00	112
Hypoglycemia	1.00	1.00	1.00	112
Hypothyroidism	1.00	1.00	1.00	105
Impetigo	1.00	1.00	1.00	104
Jaundice	1.00	1.00	1.00	109
Malaria	1.00	1.00	1.00	110
Migraine	1.00	1.00	1.00	109
Osteoarthritis	1.00	1.00	1.00	107
Paralysis (brain hemorrhage)	1.00	1.00	1.00	109
Peptic ulcer diseae	1.00	1.00	1.00	112
Pneumonia	1.00	1.00	1.00	106
Psoriasis	1.00	1.00	1.00	108
Tuberculosis	1.00	1.00	1.00	106
Typhoid	1.00	1.00	1.00	108
Urinary tract infection	1.00	1.00	1.00	108
Varicose veins	1.00	1.00	1.00	108
hepatitis A	1.00	1.00	1.00	107
accuracy			1.00	4428
macro avg	1.00	1.00	1.00	4428
weighted avg	1.00	1.00	1.00	4428

All of the models above, including logistic regression, are overfitted. Let's see what they perform in test model.

## 4. Model Evaluation

**Precision**(PPV, positive predictive value):  $\frac{tp}{(tp + fp)}$ ; High Precision means low fp

**Recall**(sensitivity, hit rate, true positive rate):  $tp / (tp + fn)$

**Accuracy**:  $(tp + tn) / (tp + tn + fp + fn)$

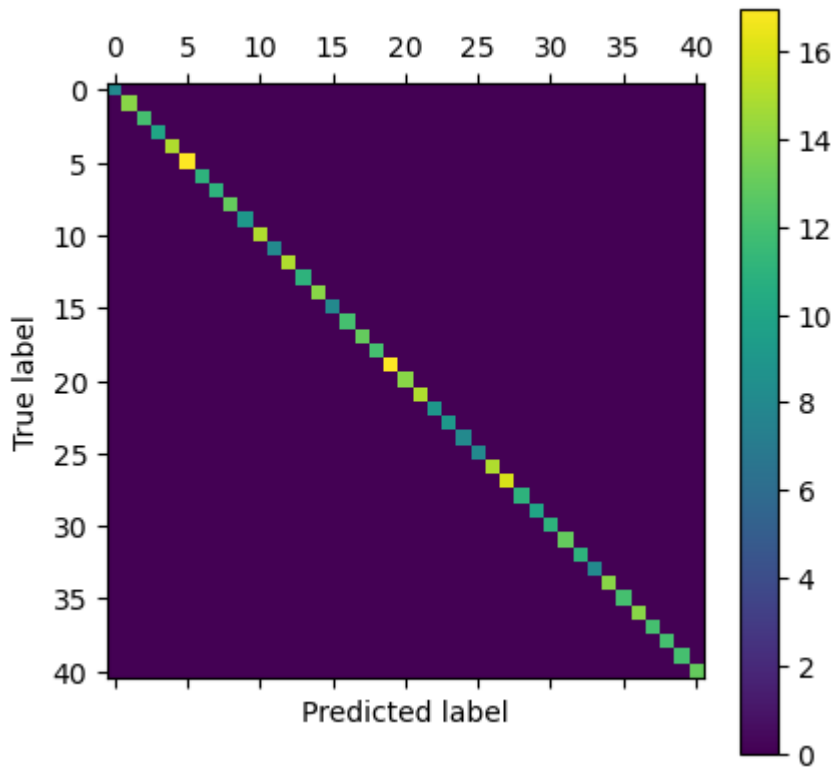
**f1-Score**:  $(2 * P * R) / (P + R)$

## 1. Logistic Regression

```
In [149... y_final_predict = classifier_logistic.predict(x_test)

cm = metrics.confusion_matrix(y_test, y_final_predict)
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_test, y_final_predict))
```





	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	8
AIDS	1.00	1.00	1.00	14
Acne	1.00	1.00	1.00	12
Alcoholic hepatitis	1.00	1.00	1.00	10
Allergy	1.00	1.00	1.00	15
Arthritis	1.00	1.00	1.00	17
Bronchial Asthma	1.00	1.00	1.00	11
Cervical spondylosis	1.00	1.00	1.00	11
Chicken pox	1.00	1.00	1.00	13
Chronic cholestasis	1.00	1.00	1.00	9
Common Cold	1.00	1.00	1.00	15
Dengue	1.00	1.00	1.00	8
Diabetes	1.00	1.00	1.00	15
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	11
Drug Reaction	1.00	1.00	1.00	14
Fungal infection	1.00	1.00	1.00	8
GERD	1.00	1.00	1.00	12
Gastroenteritis	1.00	1.00	1.00	13
Heart attack	1.00	1.00	1.00	12
Hepatitis B	1.00	1.00	1.00	17
Hepatitis C	1.00	1.00	1.00	14
Hepatitis D	1.00	1.00	1.00	15
Hepatitis E	1.00	1.00	1.00	9
Hypertension	1.00	1.00	1.00	9
Hyperthyroidism	1.00	1.00	1.00	8
Hypoglycemia	1.00	1.00	1.00	8
Hypothyroidism	1.00	1.00	1.00	15
Impetigo	1.00	1.00	1.00	16
Jaundice	1.00	1.00	1.00	11
Malaria	1.00	1.00	1.00	10
Migraine	1.00	1.00	1.00	11
Osteoarthritis	1.00	1.00	1.00	13
Paralysis (brain hemorrhage)	1.00	1.00	1.00	11
Peptic ulcer diseae	1.00	1.00	1.00	8
Pneumonia	1.00	1.00	1.00	14
Psoriasis	1.00	1.00	1.00	12
Tuberculosis	1.00	1.00	1.00	14
Typhoid	1.00	1.00	1.00	12
Urinary tract infection	1.00	1.00	1.00	12
Varicose veins	1.00	1.00	1.00	12
hepatitis A	1.00	1.00	1.00	13
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

**If we only use patient symptom data for diagnosis, a logistic regression might be enough...**

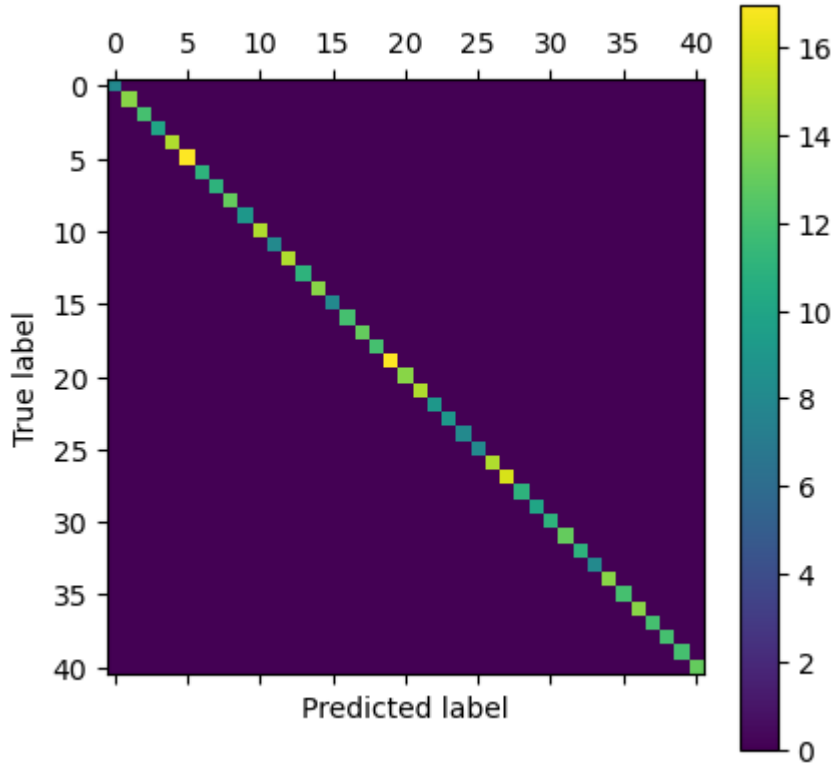
**However, it might be a bit unrealistic because the disease diagnosis task is a relative complexed one**

**This dataset seems to be a bit ideal.**

## 2. RandomForestClassifier

```
In [150... # Confusion Matrix
cm = metrics.confusion_matrix(y_test, classifier_RF.predict(x_test))
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_test, classifier_RF.predict(x_test)))
```



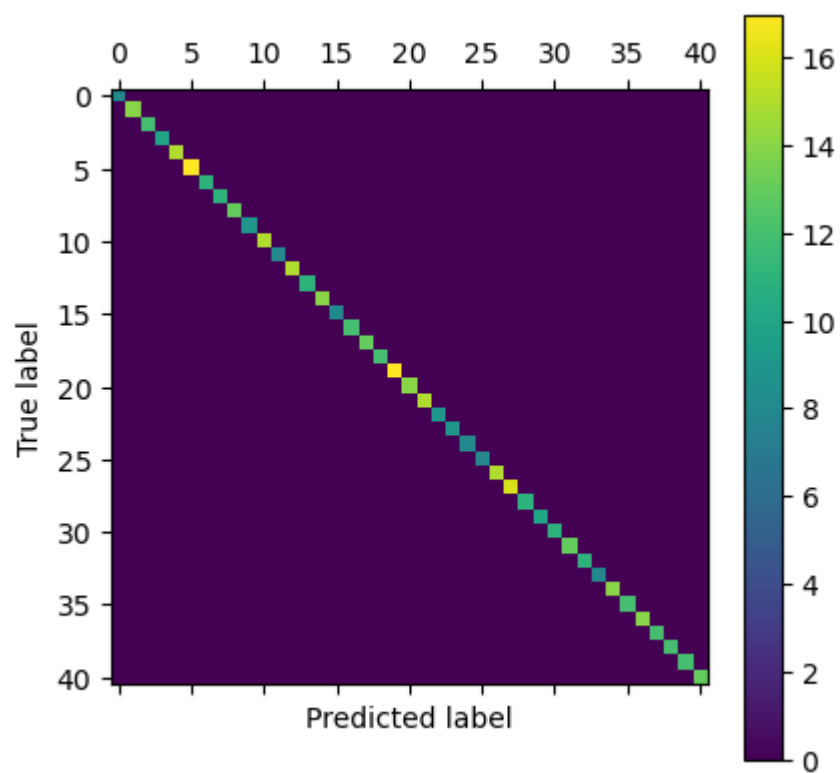
	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	8
AIDS	1.00	1.00	1.00	14
Acne	1.00	1.00	1.00	12
Alcoholic hepatitis	1.00	1.00	1.00	10
Allergy	1.00	1.00	1.00	15
Arthritis	1.00	1.00	1.00	17
Bronchial Asthma	1.00	1.00	1.00	11
Cervical spondylosis	1.00	1.00	1.00	11
Chicken pox	1.00	1.00	1.00	13
Chronic cholestasis	1.00	1.00	1.00	9
Common Cold	1.00	1.00	1.00	15
Dengue	1.00	1.00	1.00	8
Diabetes	1.00	1.00	1.00	15
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	11
Drug Reaction	1.00	1.00	1.00	14
Fungal infection	1.00	1.00	1.00	8
GERD	1.00	1.00	1.00	12
Gastroenteritis	1.00	1.00	1.00	13
Heart attack	1.00	1.00	1.00	12
Hepatitis B	1.00	1.00	1.00	17
Hepatitis C	1.00	1.00	1.00	14
Hepatitis D	1.00	1.00	1.00	15
Hepatitis E	1.00	1.00	1.00	9
Hypertension	1.00	1.00	1.00	9
Hyperthyroidism	1.00	1.00	1.00	8
Hypoglycemia	1.00	1.00	1.00	8
Hypothyroidism	1.00	1.00	1.00	15
Impetigo	1.00	1.00	1.00	16
Jaundice	1.00	1.00	1.00	11
Malaria	1.00	1.00	1.00	10
Migraine	1.00	1.00	1.00	11
Osteoarthritis	1.00	1.00	1.00	13
Paralysis (brain hemorrhage)	1.00	1.00	1.00	11
Peptic ulcer diseae	1.00	1.00	1.00	8
Pneumonia	1.00	1.00	1.00	14
Psoriasis	1.00	1.00	1.00	12
Tuberculosis	1.00	1.00	1.00	14
Typhoid	1.00	1.00	1.00	12
Urinary tract infection	1.00	1.00	1.00	12
Varicose veins	1.00	1.00	1.00	12
hepatitis A	1.00	1.00	1.00	13
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

### 3. KNeighborsClassifier

```
In [151... # Confusion Matrix
cm = metrics.confusion_matrix(y_test, classifier_KNN.predict(x_test))
plt.matshow(cm)
plt.colorbar()
```

```
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_test, classifier_KNN.predict(x_test)))
```



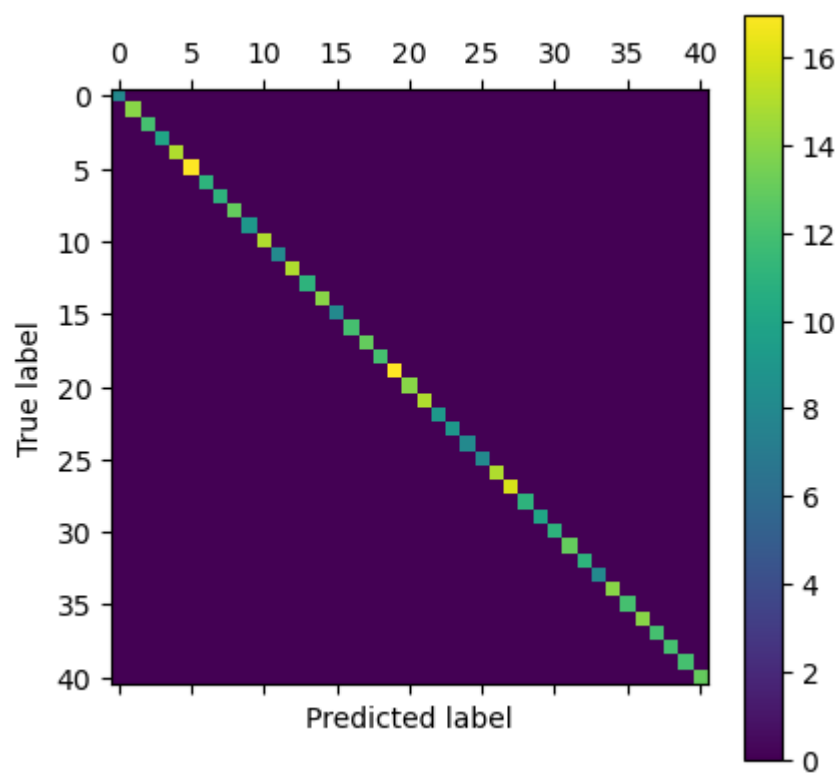
	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	8
AIDS	1.00	1.00	1.00	14
Acne	1.00	1.00	1.00	12
Alcoholic hepatitis	1.00	1.00	1.00	10
Allergy	1.00	1.00	1.00	15
Arthritis	1.00	1.00	1.00	17
Bronchial Asthma	1.00	1.00	1.00	11
Cervical spondylosis	1.00	1.00	1.00	11
Chicken pox	1.00	1.00	1.00	13
Chronic cholestasis	1.00	1.00	1.00	9
Common Cold	1.00	1.00	1.00	15
Dengue	1.00	1.00	1.00	8
Diabetes	1.00	1.00	1.00	15
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	11
Drug Reaction	1.00	1.00	1.00	14
Fungal infection	1.00	1.00	1.00	8
GERD	1.00	1.00	1.00	12
Gastroenteritis	1.00	1.00	1.00	13
Heart attack	1.00	1.00	1.00	12
Hepatitis B	1.00	1.00	1.00	17
Hepatitis C	1.00	1.00	1.00	14
Hepatitis D	1.00	1.00	1.00	15
Hepatitis E	1.00	1.00	1.00	9
Hypertension	1.00	1.00	1.00	9
Hyperthyroidism	1.00	1.00	1.00	8
Hypoglycemia	1.00	1.00	1.00	8
Hypothyroidism	1.00	1.00	1.00	15
Impetigo	1.00	1.00	1.00	16
Jaundice	1.00	1.00	1.00	11
Malaria	1.00	1.00	1.00	10
Migraine	1.00	1.00	1.00	11
Osteoarthritis	1.00	1.00	1.00	13
Paralysis (brain hemorrhage)	1.00	1.00	1.00	11
Peptic ulcer diseae	1.00	1.00	1.00	8
Pneumonia	1.00	1.00	1.00	14
Psoriasis	1.00	1.00	1.00	12
Tuberculosis	1.00	1.00	1.00	14
Typhoid	1.00	1.00	1.00	12
Urinary tract infection	1.00	1.00	1.00	12
Varicose veins	1.00	1.00	1.00	12
hepatitis A	1.00	1.00	1.00	13
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

#### 4. SVC

```
In [152... # confusion matrix
cm = metrics.confusion_matrix(y_test, classifier_SVC.predict(x_test))
plt.matshow(cm)
plt.colorbar()
```

```
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()

print(metrics.classification_report(y_test, classifier_SVC.predict(x_test)))
```



	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	8
AIDS	1.00	1.00	1.00	14
Acne	1.00	1.00	1.00	12
Alcoholic hepatitis	1.00	1.00	1.00	10
Allergy	1.00	1.00	1.00	15
Arthritis	1.00	1.00	1.00	17
Bronchial Asthma	1.00	1.00	1.00	11
Cervical spondylosis	1.00	1.00	1.00	11
Chicken pox	1.00	1.00	1.00	13
Chronic cholestasis	1.00	1.00	1.00	9
Common Cold	1.00	1.00	1.00	15
Dengue	1.00	1.00	1.00	8
Diabetes	1.00	1.00	1.00	15
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	11
Drug Reaction	1.00	1.00	1.00	14
Fungal infection	1.00	1.00	1.00	8
GERD	1.00	1.00	1.00	12
Gastroenteritis	1.00	1.00	1.00	13
Heart attack	1.00	1.00	1.00	12
Hepatitis B	1.00	1.00	1.00	17
Hepatitis C	1.00	1.00	1.00	14
Hepatitis D	1.00	1.00	1.00	15
Hepatitis E	1.00	1.00	1.00	9
Hypertension	1.00	1.00	1.00	9
Hyperthyroidism	1.00	1.00	1.00	8
Hypoglycemia	1.00	1.00	1.00	8
Hypothyroidism	1.00	1.00	1.00	15
Impetigo	1.00	1.00	1.00	16
Jaundice	1.00	1.00	1.00	11
Malaria	1.00	1.00	1.00	10
Migraine	1.00	1.00	1.00	11
Osteoarthritis	1.00	1.00	1.00	13
Paralysis (brain hemorrhage)	1.00	1.00	1.00	11
Peptic ulcer diseae	1.00	1.00	1.00	8
Pneumonia	1.00	1.00	1.00	14
Psoriasis	1.00	1.00	1.00	12
Tuberculosis	1.00	1.00	1.00	14
Typhoid	1.00	1.00	1.00	12
Urinary tract infection	1.00	1.00	1.00	12
Varicose veins	1.00	1.00	1.00	12
hepatitis A	1.00	1.00	1.00	13
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

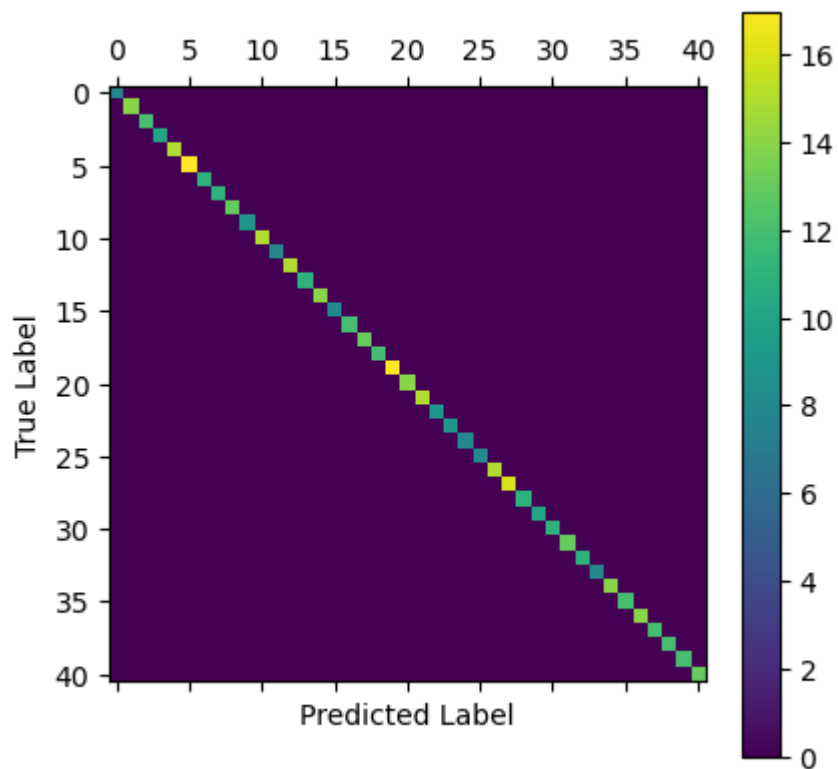
*The model is a bit slow*

## 5. GradientBoostingClassifier

```
In [153... # plotting confusing matrix
cm = metrics.confusion_matrix(y_test, classifier_GB.predict(x_test))
```

```
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()

print(metrics.classification_report(y_test, classifier_GB.predict(x_test)))
```





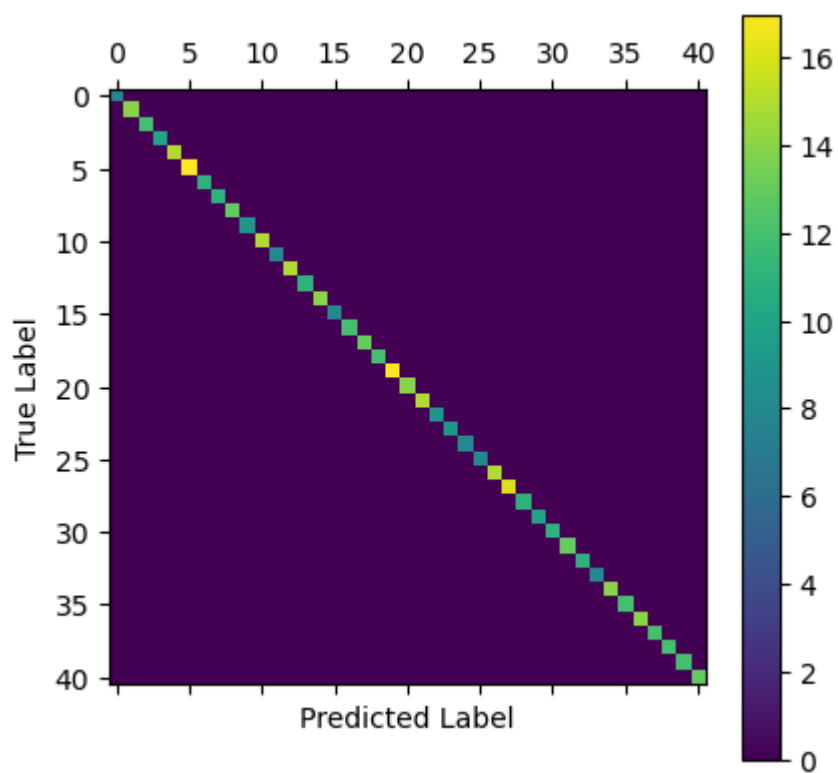
	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	8
AIDS	1.00	1.00	1.00	14
Acne	1.00	1.00	1.00	12
Alcoholic hepatitis	1.00	1.00	1.00	10
Allergy	1.00	1.00	1.00	15
Arthritis	1.00	1.00	1.00	17
Bronchial Asthma	1.00	1.00	1.00	11
Cervical spondylosis	1.00	1.00	1.00	11
Chicken pox	1.00	1.00	1.00	13
Chronic cholestasis	1.00	1.00	1.00	9
Common Cold	1.00	1.00	1.00	15
Dengue	1.00	1.00	1.00	8
Diabetes	1.00	1.00	1.00	15
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	11
Drug Reaction	1.00	1.00	1.00	14
Fungal infection	1.00	1.00	1.00	8
GERD	1.00	1.00	1.00	12
Gastroenteritis	1.00	1.00	1.00	13
Heart attack	1.00	1.00	1.00	12
Hepatitis B	1.00	1.00	1.00	17
Hepatitis C	1.00	1.00	1.00	14
Hepatitis D	1.00	1.00	1.00	15
Hepatitis E	1.00	1.00	1.00	9
Hypertension	1.00	1.00	1.00	9
Hyperthyroidism	1.00	1.00	1.00	8
Hypoglycemia	1.00	1.00	1.00	8
Hypothyroidism	1.00	1.00	1.00	15
Impetigo	1.00	1.00	1.00	16
Jaundice	1.00	1.00	1.00	11
Malaria	1.00	1.00	1.00	10
Migraine	1.00	1.00	1.00	11
Osteoarthritis	1.00	1.00	1.00	13
Paralysis (brain hemorrhage)	1.00	1.00	1.00	11
Peptic ulcer diseae	1.00	1.00	1.00	8
Pneumonia	1.00	1.00	1.00	14
Psoriasis	1.00	1.00	1.00	12
Tuberculosis	1.00	1.00	1.00	14
Typhoid	1.00	1.00	1.00	12
Urinary tract infection	1.00	1.00	1.00	12
Varicose veins	1.00	1.00	1.00	12
hepatitis A	1.00	1.00	1.00	13
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

*This model is much slower...*

GaussianNB

```
In [154... # confusion matrix
cm = metrics.confusion_matrix(y_test, classifier_NB.predict(x_test))
```

```
plt.matshow(cm)
plt.colorbar()
plt.ylabel('True Label')
plt.xlabel('Predicted Label')
plt.show()
print(metrics.classification_report(y_test, classifier_NB.predict(x_test)))
```



	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	8
AIDS	1.00	1.00	1.00	14
Acne	1.00	1.00	1.00	12
Alcoholic hepatitis	1.00	1.00	1.00	10
Allergy	1.00	1.00	1.00	15
Arthritis	1.00	1.00	1.00	17
Bronchial Asthma	1.00	1.00	1.00	11
Cervical spondylosis	1.00	1.00	1.00	11
Chicken pox	1.00	1.00	1.00	13
Chronic cholestasis	1.00	1.00	1.00	9
Common Cold	1.00	1.00	1.00	15
Dengue	1.00	1.00	1.00	8
Diabetes	1.00	1.00	1.00	15
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	11
Drug Reaction	1.00	1.00	1.00	14
Fungal infection	1.00	1.00	1.00	8
GERD	1.00	1.00	1.00	12
Gastroenteritis	1.00	1.00	1.00	13
Heart attack	1.00	1.00	1.00	12
Hepatitis B	1.00	1.00	1.00	17
Hepatitis C	1.00	1.00	1.00	14
Hepatitis D	1.00	1.00	1.00	15
Hepatitis E	1.00	1.00	1.00	9
Hypertension	1.00	1.00	1.00	9
Hyperthyroidism	1.00	1.00	1.00	8
Hypoglycemia	1.00	1.00	1.00	8
Hypothyroidism	1.00	1.00	1.00	15
Impetigo	1.00	1.00	1.00	16
Jaundice	1.00	1.00	1.00	11
Malaria	1.00	1.00	1.00	10
Migraine	1.00	1.00	1.00	11
Osteoarthritis	1.00	1.00	1.00	13
Paralysis (brain hemorrhage)	1.00	1.00	1.00	11
Peptic ulcer diseae	1.00	1.00	1.00	8
Pneumonia	1.00	1.00	1.00	14
Psoriasis	1.00	1.00	1.00	12
Tuberculosis	1.00	1.00	1.00	14
Typhoid	1.00	1.00	1.00	12
Urinary tract infection	1.00	1.00	1.00	12
Varicose veins	1.00	1.00	1.00	12
hepatitis A	1.00	1.00	1.00	13
accuracy			1.00	492
macro avg	1.00	1.00	1.00	492
weighted avg	1.00	1.00	1.00	492

All of the models above, including logistic regression, are overfitted, even in testing data.

Therefore, if we have to figure out which one is the best, maybe the only answer would be the **logistic regression** model

## Feature Importance

```
In [155... importances = classifier_RF.feature_importances_  
  
indices = np.argsort(importances)[::-1]  
  
# Print the feature ranking  
print("Feature importance ranking by RF:")  
for ind in range(x.shape[1]):  
    print ("{0} : {1}".format(x.columns[indices[ind]],round(importances[indices[ind]]
```

Feature importance ranking by RF:

muscle\_pain : 0.0195  
chest\_pain : 0.0164  
itching : 0.0151  
yellowing\_of\_eyes : 0.0151  
altered\_sensorium : 0.0149  
diarrhoea : 0.0144  
dark\_urine : 0.0144  
lack\_of\_concentration : 0.014  
family\_history : 0.0135  
weight\_loss : 0.0131  
mild\_fever : 0.0129  
vomiting : 0.0128  
mucoid\_sputum : 0.0126  
unsteadiness : 0.0125  
joint\_pain : 0.0123  
red\_spots\_over\_body : 0.012  
nausea : 0.012  
fatigue : 0.0119  
chills : 0.0117  
loss\_of\_balance : 0.0117  
internal\_itching : 0.0117  
loss\_of\_appetite : 0.0114  
abdominal\_pain : 0.0114  
high\_fever : 0.0114  
bladder\_discomfort : 0.0114  
muscle\_weakness : 0.0113  
headache : 0.0112  
sweating : 0.0111  
stomach\_pain : 0.0109  
coma : 0.0108  
irritability : 0.0107  
dischromic\_patches : 0.0105  
pain\_behind\_the\_eyes : 0.0105  
rusty\_sputum : 0.0104  
spotting\_urination : 0.0103  
breathlessness : 0.0103  
back\_pain : 0.0102  
nodal\_skin\_eruptions : 0.0096  
patches\_in\_throat : 0.0092  
blackheads : 0.0091  
fluid\_overload : 0.0091  
stomach\_bleeding : 0.009  
increased\_appetite : 0.0088  
fast\_heart\_rate : 0.0088  
continuous\_feel\_of\_urine : 0.0086  
silver\_like\_dusting : 0.0086  
receiving\_unsterile\_injections : 0.0085  
yellowish\_skin : 0.0085  
palpitations : 0.0084  
malaise : 0.0082  
pus\_filled\_pimples : 0.0081  
passage\_of\_gases : 0.008  
blood\_in\_sputum : 0.0079  
hip\_joint\_pain : 0.0079  
blister : 0.0078

yellow\_crust\_ooze : 0.0077  
sunken\_eyes : 0.0077  
swelling\_joints : 0.0076  
neck\_pain : 0.0076  
continuous\_sneezing : 0.0074  
swelling\_of\_stomach : 0.0073  
cough : 0.0073  
weakness\_of\_one\_body\_side : 0.0073  
swelled\_lymph\_nodes : 0.0072  
dehydration : 0.0072  
phlegm : 0.0071  
belly\_pain : 0.0071  
polyuria : 0.0069  
receiving\_blood\_transfusion : 0.0069  
movement\_stiffness : 0.0068  
prominent\_veins\_on\_calf : 0.0068  
slurred\_speech : 0.0067  
pain\_in\_anal\_region : 0.0067  
extra\_marital\_contacts : 0.0067  
red\_sore\_around\_nose : 0.0067  
toxic\_look\_(typhos) : 0.0065  
burning\_micturition : 0.0065  
abnormal\_menstruation : 0.0065  
inflammatory\_nails : 0.0064  
ulcers\_on\_tongue : 0.0063  
shivering : 0.0062  
spinning\_movements : 0.0061  
depression : 0.0061  
acidity : 0.0059  
pain\_during\_bowel\_movements : 0.0059  
excessive\_hunger : 0.0059  
constipation : 0.0057  
scurring : 0.0056  
watering\_from\_eyes : 0.0056  
cramps : 0.0055  
dizziness : 0.0055  
brittle\_nails : 0.0054  
indigestion : 0.0054  
skin\_rash : 0.0053  
stiff\_neck : 0.0051  
acute\_liver\_failure : 0.005  
knee\_pain : 0.005  
distention\_of\_abdomen : 0.0047  
painful\_walking : 0.0047  
irritation\_in\_anus : 0.0047  
bloody\_stool : 0.0046  
muscle\_wasting : 0.0046  
loss\_of\_smell : 0.0045  
restlessness : 0.0044  
throat\_irritation : 0.0043  
enlarged\_thyroid : 0.0043  
visual\_disturbances : 0.0043  
skin\_peeling : 0.0043  
blurred\_and\_distorted\_vision : 0.0042  
small\_dents\_in\_nails : 0.0041  
lethargy : 0.004

swollen\_extremeties : 0.004  
weakness\_in\_limbs : 0.0038  
history\_of\_alcohol\_consumption : 0.0038  
congestion : 0.0038  
obesity : 0.0037  
runny\_nose : 0.0034  
swollen\_legs : 0.0034  
bruising : 0.0034  
mood\_swings : 0.0031  
anxiety : 0.0031  
yellow\_urine : 0.0027  
redness\_of\_eyes : 0.0025  
weight\_gain : 0.0024  
drying\_and\_tingling\_lips : 0.0024  
irregular\_sugar\_level : 0.0024  
swollen\_blood\_vessels : 0.0021  
sinus\_pressure : 0.002  
foul\_smell\_of\_urine : 0.0017  
cold\_hands\_and\_feets : 0.0014  
puffy\_face\_and\_eyes : 0.0009

## 5. Insights & Conclusion

1. It seems that logistic regression is enough to diagnose some common disease.

**However, the usability of this model is still needed to be furtherly verified due to the possible overly-ideal.**

2. muscle pain, chest pain, itching, yellowing of eyes, and altered sensorium are 5 symptoms with high specificity.