Multiple Disease Prediction

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Abstract- **Data mining techniques are used for a variety of applications. In the healthcare industry, data mining plays an important role in predicting diseases based on the patient symptoms. For detecting a disease number of tests should be required from the patient to know what are the symptoms that they have. This paper analyzes data mining techniques which can be used for predicting different types of diseases by using three types of different models which are decision tree, random forest and naive bayes in order to choose the best model for this problem.**

Keywords : **Data mining, symptoms, predicting disease, decision tree, random forest, naive bayes.**

I. INTRODUCTION

There are more than tens of thousands of diseases that affect humans that have been discovered in the world. But most of the diseases tend to be cured for two reasons which is because it shows symptoms and second is because there is availability in medicine or treatment. Some diseases show symptoms on the human body physically or mentally.

Early detection of preventive diseases can play a crucial role in timely intervention and management. It also assists in efficient distribution of resources in the healthcare sector. We endeavour to develop a system that facilitates early detection of multiple critical diseases based on their symptoms by using data analysis. The dataset that is being used states many types of disease with their symptoms.

II. OBJECTIVE

- To clean the dataset.
- To make a model with different types of algorithms that can predict multiple diseases.
- To choose the best algorithm based on their performance.
- To build a model that accurately detects any kind of disease in an individual.

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III. GOAL

Our main goal in this project is being able to detect some of the disease in an individual by using our disease detector. This detector helps to find the disease in an individual and alerts them so that they can control or cure their disease from becoming worse. Moreover, we are focused on the younger generation's health. This detector also shows the symptoms of any disease in our body. This detector would help to identify if that person is affected by serious illness, it helps to find it in an early stage and we can start to treat it before it becomes worse.

Besides that , we can also lower the rate of disease in the country as quick actions can be taken in order to eliminate multiple diseases and we can increase the

healthy population rate in the country and get the best standing among other countries for the best health quality . Data science and Artificial Intelligence plays an important role in the making of this detector. The technology and knowledge helps to create this useful and technological detector.

IV. QUESTION

How can we help the current generation to overcome various diseases in early stages and how to determine if an individual is under any illness based on columns of data that show the symptoms for various diseases?

V. SUCCESS AND MEASUREMENT

This project will build a model to analyze the data according to the related attributes or characteristics of a disease's symptoms to diagnose or detect whether the person has a disease or not. The model considered being successful when it is able to diagnose the disease and the success of this project will be measured by the performance of the model which is the accuracy of the model. This project is a success when the model performs good enough and has less errors.

Measurable result:

- Model able to diagnose the disease
- Model built able to diagnose with great accuracy

VI. DATA SOURCE

The dataset contains 4921 rows including the header which has 4920 instances and 18 attributes or columns which consists of the diseases' symptoms and the diagnosed diseases. The first column in the dataset is labeled 'Disease' while the others labeled 'Symptom_x' in which the x is in increasing order from 1 to 17. Each row is a diagnosed disease based on the symptoms. The purpose of the data is to record the symptoms of each disease diagnosed.

Column entries (attributes):
Disease - The diagnosed disease
Symptom_(1-17) - Diseases' symptom

VII. DATA MANAGEMENT PLAN

Multiple disease prediction project is a project that can predict the disease that has in the human body that gives a sign like a symptom of the disease. This project involves the data analysis on how to predict using data mining techniques. Data mining techniques are used for a variety of applications. In the healthcare industry, data mining plays an important role in predicting diseases. Data mining is the process of selecting, discovering and modeling huge amounts of data. This process has become an increasingly insidious activity in all areas of medical science research.

0. Project Name

Multiple Disease Prediction

1. Description of the data

1.1 Type of study

The study of this data is about the multiple type of disease with their symptoms which are collected from the kaggle website dataset

1.2 Type of data

The type of the data that is being recorded is qualitative that deals with characteristics of the symptoms of the disease which only can be observed but not to be measured. The data type for the dataset is object.

1.3 Format and scale of the data

The data format for this dataset is more to string which is the symptom and the type of disease. Most of the data scale is nominal scales or could be simply called as labels for the symptoms for the disease.

2. Data collection/generation

Data collection is one of the important processes of gathering and measuring the information. The method that is being used for the collection of the data should be one of the major concerns because the data that is being collected must be precisely perfect for the future use.

2.1 Methodology for data collection / generation

This is the primary data collection which is qualitative data that is being recorded based on the observation and research.

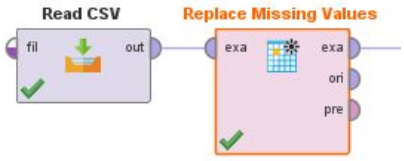
3. Data management, documentation and curation

The dataset provides the column containing symptoms of the disease and the type of the disease. This dataset can be obtained via kaggle website. This website allows you to make any documentation and get the details for the symptom, precaution, disease type and the weights. This data is placed in the kaggle for the long-term storage and preservation with no limit to the retention period.

The plan after this process is about getting the best cleaned data by the process of cleaning, restructuring and enriching the raw data available into a more usable format. It is easier to call it a data wrangling process. This will help in the process of decision making, and thus get better insights in less time. Data wrangling, like most data analytics processes, is an iterative one – the practitioner will need to carry out these steps repeatedly in order to produce the results desired.

VIII. DATA WRANGLING

Dataset that we obtained from kaggle is already cleaned and there is no need to do data wrangling. The data is already in appropriate and tidy form that is easy to analyze and manipulate. However the dataset contains null values which there might be a little cleaning to do with the data like switching the null values with something that holds value like ‘none’ instead of ‘?’. We are using RapidMiner Studio to do the data wrangling. We use the operator ‘Read CSV’ to read the csv file of the disease dataset. Then, we use the operator ‘Replace Missing Values’ to replace all the null values or ‘?’ in the dataset to ‘none’. Below is the operator used.



Below is the result of the data wrangling:

Row No.	Disease	Symptom_1	Symptom_2	Symptom_3	Symptom_4	Symptom_5	Symptom_6	Symptom_7	Sympto
1	Fungal infecti...	itching	skin_rash	nodal_skin_e...	dischromic _...	?	?	?	?
2	Fungal infecti...	skin_rash	nodal_skin_e...	dischromic _...	?	?	?	?	?
3	Fungal infecti...	itching	nodal_skin_e...	dischromic _...	?	?	?	?	?
4	Fungal infecti...	itching	skin_rash	dischromic _...	?	?	?	?	?
5	Fungal infecti...	itching	skin_rash	nodal_skin_e...	?	?	?	?	?
6	Fungal infecti...	skin_rash	nodal_skin_e...	dischromic _...	?	?	?	?	?
7	Fungal infecti...	itching	nodal_skin_e...	dischromic _...	?	?	?	?	?
8	Fungal infecti...	itching	skin_rash	dischromic _...	?	?	?	?	?
9	Fungal infecti...	itching	skin_rash	nodal_skin_e...	?	?	?	?	?
10	Fungal infecti...	itching	skin_rash	nodal_skin_e...	dischromic _...	?	?	?	?
11	Allergy	continuous_s...	shivering	chills	watering_fro...	?	?	?	?
12	Allergy	shivering	chills	watering_fro...	?	?	?	?	?
13	Allergy	continuous_s...	chills	watering_fro...	?	?	?	?	?
14	Allergy	continuous_s...	shivering	watering_fro...	?	?	?	?	?
15	Allergy	continuous_s...	shivering	chills	?	?	?	?	?
16	Allergy	shivering	chills	watering_fro...	?	?	?	?	?

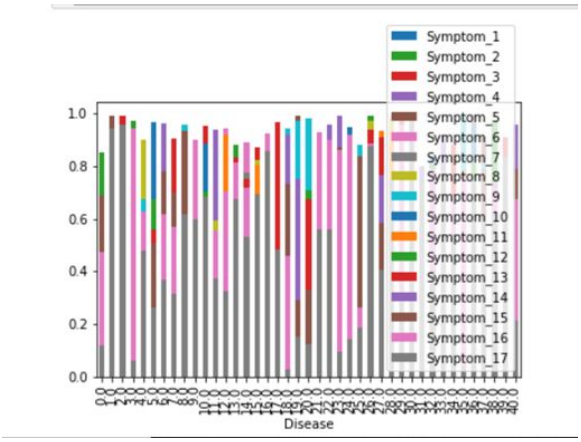
Figure 1.1: Before replacing missing values.

Row No.	Disease	Symptom_1	Symptom_2	Symptom_3	Symptom_4	Symptom_5	Symptom_6	Symptom_7	Symptom_8	Sympto
1	Fungal infecti...	itching	skin_rash	nodal_skin_e...	dischromic _...	none	none	none	none	none
2	Fungal infecti...	skin_rash	nodal_skin_e...	dischromic _...	none	none	none	none	none	none
3	Fungal infecti...	itching	nodal_skin_e...	dischromic _...	none	none	none	none	none	none
4	Fungal infecti...	itching	skin_rash	dischromic _...	none	none	none	none	none	none
5	Fungal infecti...	itching	skin_rash	nodal_skin_e...	none	none	none	none	none	none
6	Fungal infecti...	skin_rash	nodal_skin_e...	dischromic _...	none	none	none	none	none	none
7	Fungal infecti...	itching	nodal_skin_e...	dischromic _...	none	none	none	none	none	none
8	Fungal infecti...	itching	skin_rash	dischromic _...	none	none	none	none	none	none
9	Fungal infecti...	itching	skin_rash	nodal_skin_e...	none	none	none	none	none	none
10	Fungal infecti...	itching	skin_rash	nodal_skin_e...	dischromic _...	none	none	none	none	none
11	Allergy	continuous_s...	shivering	chills	watering_fro...	none	none	none	none	none
12	Allergy	shivering	chills	watering_fro...	none	none	none	none	none	none
13	Allergy	continuous_s...	chills	watering_fro...	none	none	none	none	none	none
14	Allergy	continuous_s...	shivering	watering_fro...	none	none	none	none	none	none
15	Allergy	continuous_s...	shivering	chills	none	none	none	none	none	none
16	Allergy	shivering	chills	watering_fro...	none	none	none	none	none	none

Figure 1.2: After replacing missing values.

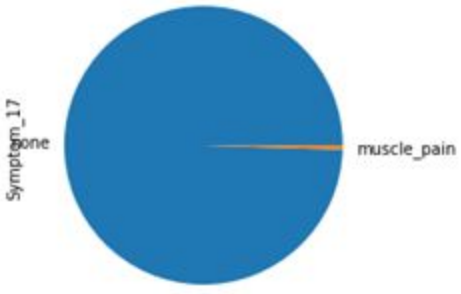
IX. EXPLORATORY DATA ANALYSIS (EDA)

After cleaning and transforming the data into an appropriate form by replacing the missing values, we decided to view and observe the data for what we can or might find in the data if there is a pattern or important information in it. Again we are using RapidMiner Studio to visualize the data that has been cleaned. For the visualization, we are using scatter plots to visualize the data into a graph. Below is the result of the visualization.



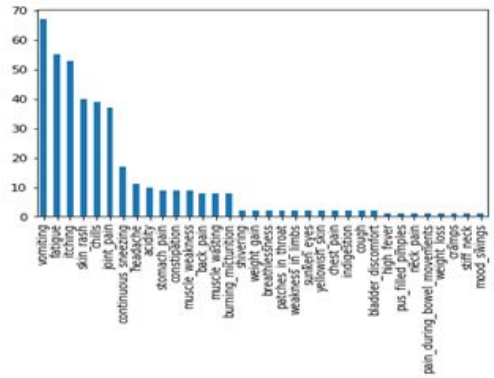
This figure above shows a Stacked Bar Chart. In the stacked bar plot, the bars at each index are literally "stacked" on top of one another. It shows the visual representation of the total symptoms each disease has, and the breakdown of each symptom. Many of the diseases share several symptoms. Based on this stacked bar chart, majority of the people experience Symptom 16 and Symptom 17 which means they experience no symptoms according to the pie chart shown below.

```
df['Symptom_17'].value_counts().plot(kind='pie')
plt.show()
```



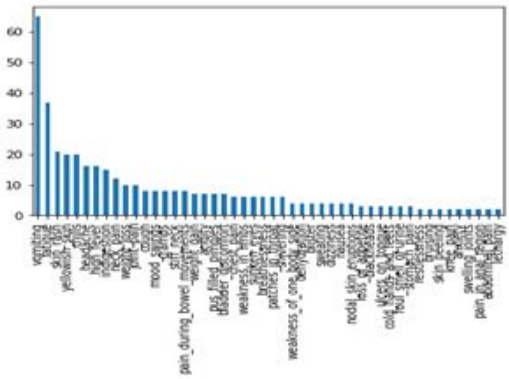
The figure above shows that majority had no symptom 17 and very few people had muscle pain as their 17th symptom

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

df = pd.read_csv(r"C:\Users\User\Downloads\disease_dataset.csv")

df['Symptom_1'].value_counts().plot(kind='bar')
plt.show()
```



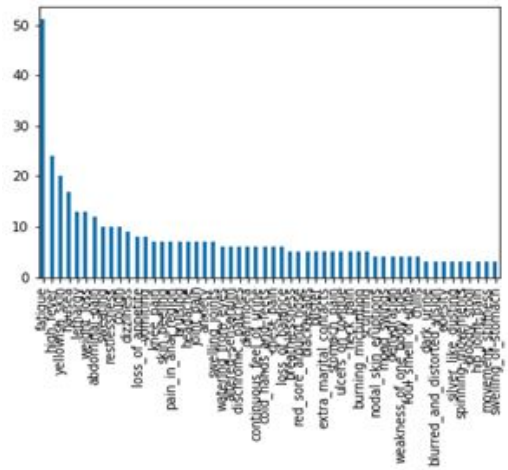
The figure above shows that the majority of the people have been vomiting as their symptom for Symptom 1 followed by fatigue, itching ,skin rash and so on. Symptoms such as shivering, indigestion and mood swings are less experienced by the people.

```
df['Symptom_2'].value_counts().plot(kind='bar')
plt.show()
```



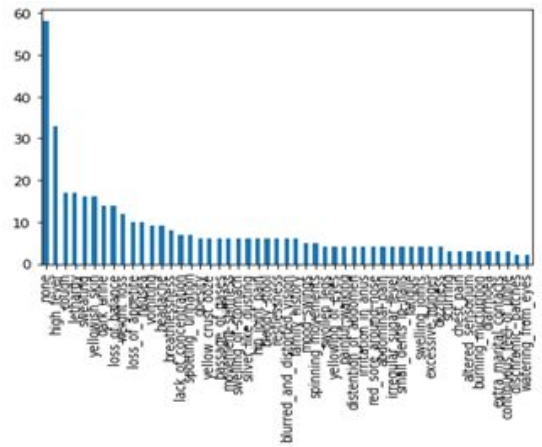
The figure above shows that the majority of the people have been vomiting for Symptom 2 followed by fatigue,skin rash,yellowish skin and so on. They also experienced very less symptoms such as swelling joints and abdominal pain.

```
df['Symptom_3'].value_counts().plot(kind='bar')
plt.show()
```



The figure above shows that more than 50 people have fatigue as Symptom 3. They also experience high_fever ,yellowish skin and so on. Very few people have symptoms such as swelling of stomach and dark urine.

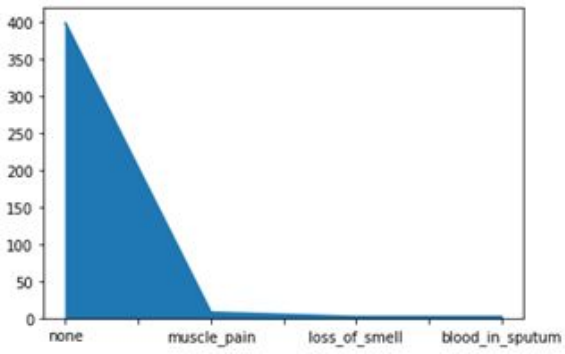
```
df['Symptom_4'].value_counts().plot(kind='bar')
plt.show()
```



The figure above shows that less than 35 people had high fever as their symptom 4 and less than 20 people had

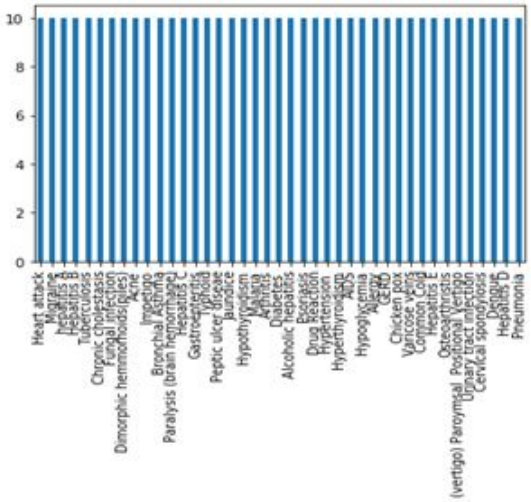
other symptoms. Very few people experience symptoms such as dischromic _patches and watering from their eyes.

```
df['Symptom_16'].value_counts().plot(kind='area')
plt.show()
```



The figure above shows that very few people had blood in sputum, loss of smell and muscle pain as their 16th symptom. Majority people didn't have symptoms.

```
df['Disease'].value_counts().plot(kind='bar')
plt.show()
```



The figure above shows the list of diseases the people may experience based on the symptoms mentioned previously. All the diseases were had by almost 10 people.

X. DATA MODELLING AND VALIDATION

The flow is shown below:

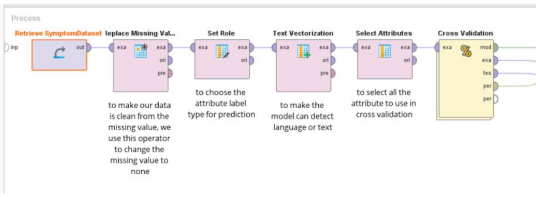


Figure above is the flow for the three algorithms that we used naive bayes, decision tree and random forest.

XI. CLASSIFICATION TECHNIQUES

Naive Bayes

Naive Bayes is a classification algorithm for binary (two-class) and multi-class classification problems. The technique is easiest to understand when described using binary or categorical input values.

Rather than attempting to calculate the values of each attribute value P(d1, d2, d3|h), they are assumed to be conditionally independent given the target value and calculated as P(d1|h) * P(d2|H) and so on.

Decision Tree

A Decision Tree is a simple representation for classifying examples. It is a Supervised Machine Learning where the data is continuously split according to a certain parameter.

Random Forest

Random Forest is an ensemble learning technique which implements a large number of decision trees based on different samples and different feature combinations. These trees are trained on bootstrapped subsets of the Example Set provided at the Input Port. Each node of a tree represents a splitting rule for one specific Attribute. Only a subset of Attributes, specified with the subset ratio criterion, is considered for the splitting rule selection.

Random forests can handle large numbers of variables in a dataset. Also, during the forest building process they generate an internal unbiased estimate of the generalization error. In addition, they can estimate missing data well. A major drawback of random forests is the lack of reproducibility, as the process of building the forest is random. Further, interpreting the final model and subsequent results is difficult since it contains many independent decision trees.

VALIDATION PROCESS

Cross Validation

Cross-validation is a statistical method used to estimate the skill of machine learning models. It is also a resampling procedure used to evaluate machine learning models on a limited data sample. It is commonly used in applied machine learning to compare and select a model for a given predictive modeling problem because it is easy to understand, easy to implement, and results in skill estimates that generally have a lower bias than other methods.

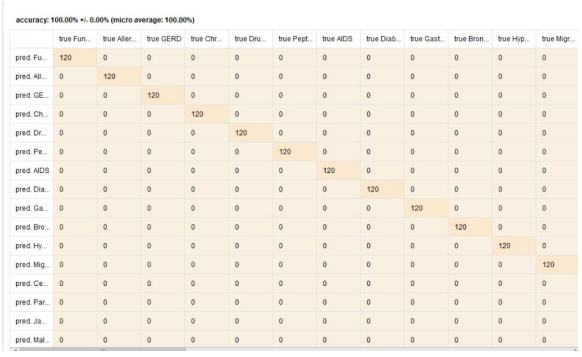
XII. PERFORMANCE MEASURE/RESULTS

We used three performance measures to evaluate the three models that we built so that we can compare which one had the best performance in detecting diseases.

Accuracy

Relative number of correctly classified examples or in other words the percentage of correct predictions made. The higher the value the better the accuracy.

In the model we used the Performance (Classification) operator. Performance (Classification) operator is used with classification tasks only. On the other hand, the Performance operator automatically determines the learning task type and calculates the most common criteria for that type.



accuracy: 100.00% +/- 0.00% (micro average: 100.00%)

	true Fun...	true Aller...	true GERD	true Chr...	true Dru...	true Pept...	true AIDS	true Diab...	true Gast...	true Bron...	true Hyp...	true Migr...
pred. Fu...	120	0	0	0	0	0	0	0	0	0	0	0
pred. All...	0	120	0	0	0	0	0	0	0	0	0	0
pred. GE...	0	0	120	0	0	0	0	0	0	0	0	0
pred. Ch...	0	0	0	120	0	0	0	0	0	0	0	0
pred. Dr...	0	0	0	0	120	0	0	0	0	0	0	0
pred. Pe...	0	0	0	0	0	120	0	0	0	0	0	0
pred. AIDS	0	0	0	0	0	0	120	0	0	0	0	0
pred. Dia...	0	0	0	0	0	0	0	120	0	0	0	0
pred. Ga...	0	0	0	0	0	0	0	0	120	0	0	0
pred. Bro...	0	0	0	0	0	0	0	0	0	120	0	0
pred. Hy...	0	0	0	0	0	0	0	0	0	0	120	0
pred. Mig...	0	0	0	0	0	0	0	0	0	0	0	120
pred. Ce...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Par...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Ja...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Mal...	0	0	0	0	0	0	0	0	0	0	0	0

Figure above shows the accuracy for Naive Bayes model.

accuracy: 92.76% +/- 0.89% (micro average: 92.76%)

	true Fun...	true Aller...	true GERD	true Chr...	true Dru...	true Pept...	true AIDS	true Diab...	true Gast...	true Bron...	true Hyp...	true Migr...
pred. Fu...	120	0	0	0	17	0	0	0	0	0	0	0
pred. All...	0	110	0	0	0	0	4	0	4	0	0	0
pred. GE...	0	0	114	0	0	0	0	0	0	0	0	0
pred. Ch...	0	0	0	119	0	0	0	0	0	0	0	0
pred. Dr...	0	0	0	0	86	5	0	0	0	0	0	0
pred. Pe...	0	0	0	0	0	114	0	0	0	0	0	0
pred. AIDS	0	4	0	0	0	0	108	0	2	0	0	0
pred. Dia...	0	0	0	0	0	0	0	120	0	0	0	0
pred. Ga...	0	1	0	0	0	0	2	0	101	0	0	0
pred. Bro...	0	0	4	0	0	0	0	0	0	110	0	0
pred. Hy...	0	0	0	0	12	0	0	0	0	0	120	0
pred. Mig...	0	0	0	0	0	0	0	0	0	0	0	120
pred. Ce...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Par...	0	3	0	0	0	0	5	0	7	0	0	0
pred. Ja...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Mal...	0	0	0	0	0	0	0	0	0	0	0	0

Figure above shows the accuracy for the Decision Tree model.

accuracy: 98.76% +/- 0.56% (micro average: 98.76%)

	true Fun...	true Aller...	true GERD	true Chr...	true Dru...	true Pept...	true AIDS	true Diab...	true Gast...	true Bron...	true Hyp...	true Migr...
pred. Fu...	120	0	0	0	0	0	0	0	0	0	0	0
pred. All...	0	120	0	0	0	0	0	0	0	0	0	0
pred. GE...	0	0	116	0	0	0	0	0	0	0	0	0
pred. Ch...	0	0	0	113	0	0	0	0	0	0	0	0
pred. Dr...	0	0	0	0	117	0	0	0	0	0	0	0
pred. Pe...	0	0	0	0	0	120	0	0	0	0	0	0
pred. AIDS	0	0	0	0	0	0	118	0	0	0	0	0
pred. Dia...	0	0	0	0	0	0	0	120	0	0	0	0
pred. Ga...	0	0	0	0	0	0	2	0	114	0	0	0
pred. Bro...	0	0	0	0	0	0	0	0	0	120	0	0
pred. Hy...	0	0	0	0	0	0	0	0	0	0	120	0
pred. Mig...	0	0	4	0	0	0	0	0	0	0	0	120
pred. Ce...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Par...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Ja...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Mal...	0	0	0	0	0	0	0	0	0	0	0	0

Figure above shows the accuracy for the Random Forest model.

Classification Error

Relative number of misclassified examples or in other words percentage of incorrect predictions. The below formula is used to calculate classification error rate

Error rate (ERR) is calculated as the number of all incorrect predictions divided by the total number of the dataset. The best error rate is 0.0, whereas the worst is 1.0. The below formula is used to calculate classification error rate:

$$\mathrm{ERR} = \frac{\mathrm{FP} + \mathrm{FN}}{\mathrm{TP} + \mathrm{TN} + \mathrm{FN} + \mathrm{FP}} = \frac{\mathrm{FP} + \mathrm{FN}}{\mathrm{P} + \mathrm{N}}$$

classification_error: 0.00% +/- 0.00% (micro average: 0.00%)

	true Fun...	true Aller...	true GERD	true Chr...	true Dru...	true Pept...	true AIDS	true Diab...	true Gast...	true Bron...	true Hyp...	true Migr...
pred. Fu...	120	0	0	0	0	0	0	0	0	0	0	0
pred. All...	0	120	0	0	0	0	0	0	0	0	0	0
pred. GE...	0	0	120	0	0	0	0	0	0	0	0	0
pred. Ch...	0	0	0	120	0	0	0	0	0	0	0	0
pred. Dr...	0	0	0	0	120	0	0	0	0	0	0	0
pred. Pe...	0	0	0	0	0	120	0	0	0	0	0	0
pred. AIDS	0	0	0	0	0	0	120	0	0	0	0	0
pred. Dia...	0	0	0	0	0	0	0	120	0	0	0	0
pred. Ga...	0	0	0	0	0	0	0	0	120	0	0	0
pred. Bro...	0	0	0	0	0	0	0	0	0	120	0	0
pred. Hy...	0	0	0	0	0	0	0	0	0	0	120	0
pred. Mig...	0	0	0	0	0	0	0	0	0	0	0	120
pred. Ce...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Par...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Ja...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Mal...	0	0	0	0	0	0	0	0	0	0	0	0

Figure above shows the Classification Error for Naive Bayes model.

classification_error: 7.24% +/- 0.89% (micro average: 7.24%)

	true Fun...	true Aller...	true GERD	true Chr...	true Dru...	true Pept...	true AIDS	true Diab...	true Gast...	true Bron...	true Hyp...	true Migr...
pred. Fu...	120	0	0	0	17	0	0	0	0	0	0	0
pred. All...	0	110	0	0	0	0	4	0	4	0	0	0
pred. GE...	0	0	114	0	0	0	0	0	0	0	0	0
pred. Ch...	0	0	0	119	0	0	0	0	0	0	0	0
pred. Dr...	0	0	0	0	86	5	0	0	0	0	0	0
pred. Pe...	0	0	0	0	0	114	0	0	0	0	0	0
pred. AIDS	0	4	0	0	0	0	108	0	2	0	0	0
pred. Dia...	0	0	0	0	0	0	0	120	0	0	0	0
pred. Ga...	0	1	0	0	0	0	2	0	101	0	0	0
pred. Bro...	0	0	4	0	0	0	0	0	0	110	0	0
pred. Hy...	0	0	0	0	12	0	0	0	0	0	120	0
pred. Mig...	0	0	0	0	0	0	0	0	0	0	0	120
pred. Ce...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Par...	0	3	0	0	0	0	5	0	7	0	0	0
pred. Ja...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Mal...	0	0	0	0	0	0	0	0	0	0	0	0

Figure above shows the Classification Error for Decision Tree model.

classification_error: 1.24% +/- 0.56% (micro average: 1.24%)

	true Fun...	true Aller...	true GERD	true Chr...	true Dru...	true Pept...	true AIDS	true Diab...	true Gast...	true Bron...	true Hyp...	true Migr...
pred. Fu...	120	0	0	0	0	0	0	0	0	0	0	0
pred. All...	0	120	0	0	0	0	0	0	0	0	0	0
pred. GE...	0	0	116	0	0	0	0	0	0	0	0	0
pred. Ch...	0	0	0	113	0	0	0	0	0	0	0	0
pred. Dr...	0	0	0	0	117	0	0	0	0	0	0	0
pred. Pe...	0	0	0	0	0	120	0	0	0	0	0	0
pred. AIDS	0	0	0	0	0	0	118	0	0	0	0	0
pred. Dia...	0	0	0	0	0	0	0	120	0	0	0	0
pred. Ga...	0	0	0	0	0	0	2	0	114	0	0	0
pred. Bro...	0	0	0	0	0	0	0	0	0	120	0	0
pred. Hy...	0	0	0	0	0	0	0	0	0	0	120	0
pred. Mig...	0	0	4	0	0	0	0	0	0	0	0	120
pred. Ce...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Par...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Ja...	0	0	0	0	0	0	0	0	0	0	0	0
pred. Mal...	0	0	0	0	0	0	0	0	0	0	0	0

Figure above shows the Classification Error for Random Forest model.

Logistic Loss

The loss function for linear regression is squared loss. The loss function for logistic regression is Log Loss, which is defined as follows:

$$\text{Log Loss} = \sum_{(x,y)\in D} -y\log(y') - (1-y)\log(1-y')$$

where:

- $(x,y)\in D$ is the data set containing many labeled examples, which are (x,y) pairs.
- y is the label in a labeled example. Since this is logistic regression, every value of y must either be 0 or 1.
- y' is the predicted value (somewhere between 0 and 1), given the set of features in x.

Figure above shows the Logistic Loss for Naive Bayes model.

Figure above shows the Logistic Loss for Decision Tree model.

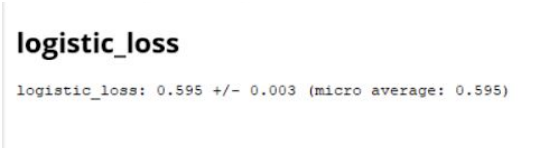


Figure above shows the Logistic Loss for Random Forest model.

XIII. FUTURE IMPLEMENTATION

In the future, we will be looking forward to integrating our multiple disease detection system to detect more diseases and in the end will be able to detect every disease that has been found and will be updated from time to time when new diseases are being found.

XIV. CONCLUSION

In conclusion, this project is hoped to help every individual and healthcare industry to easily diagnose several diseases that are discoverable by their symptoms. This algorithm will be updated and the dataset will also be updated frequently with new diseases and their respective symptoms so that the system will accurately predict the disease of the newly entered symptoms

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XV. REFERENCE

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