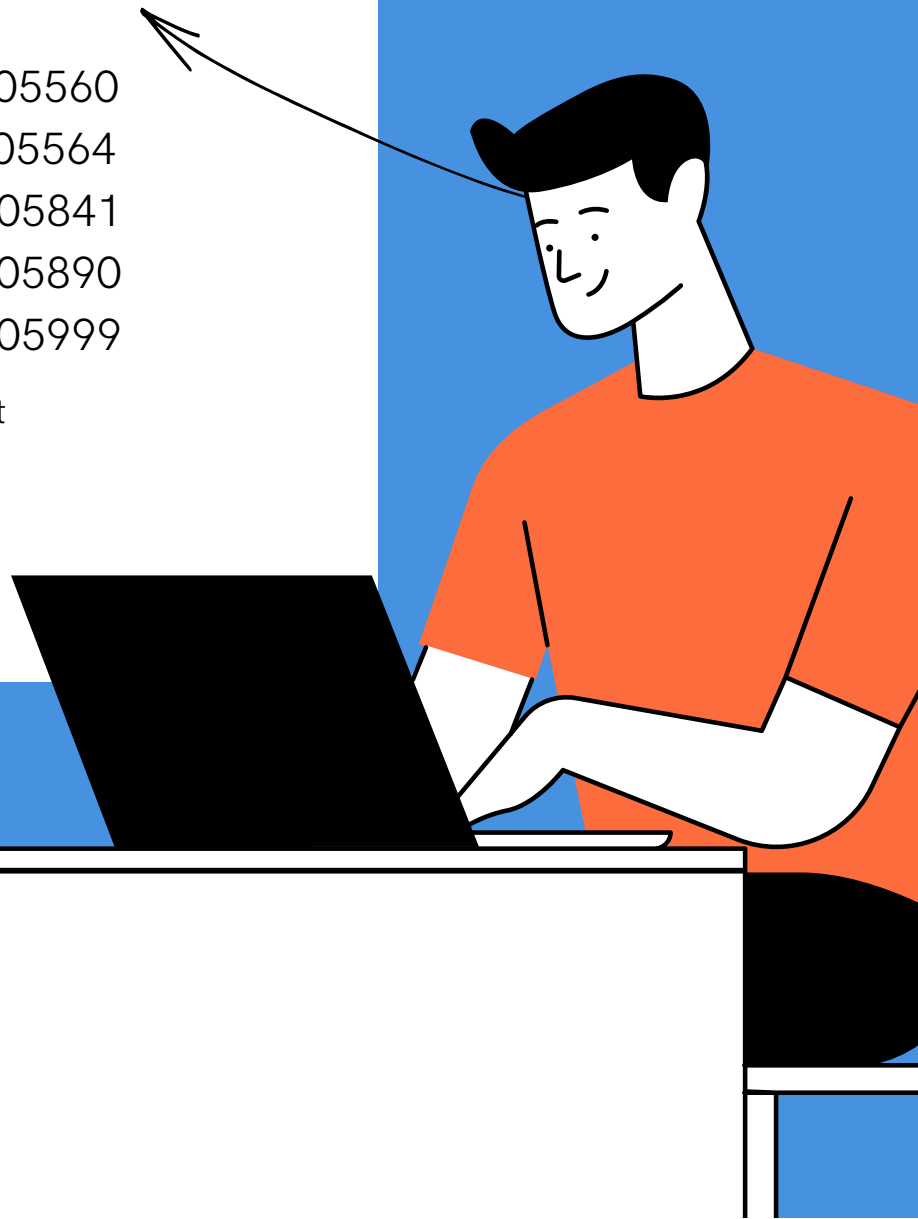




# Disease Prediction Using Machine Learning

Raneen Alshehri	2005560
Ghaid Althobaity	2005564
Noor O. Alamoudi	2005841
Taif A. Basheikh	2005890
Raghad Alqithmi	2005999

Applied machine learning project  
Dr. Enas Abo Fateh  
2023



# CONTENT

1-INTRODUCTION

2-PROBLEM DEFINITION AND OBJECTIVES

3-APPROACH

3.1 DATA SET

3.2 DATA COLLECTION

3.3 MACHINE LEARNING MODEL

3.3.1 RANDOM FOREST CLASSIFIER

4- ANALYSIS AND RESULTS

4.1 QUESTION / HYPOTHESIS

4.2 CODE AND ANALYSIS

4.3 IMPORTING THE DATA

4.4 PREPROCESSING

4.5 SPLITTING THE DATA

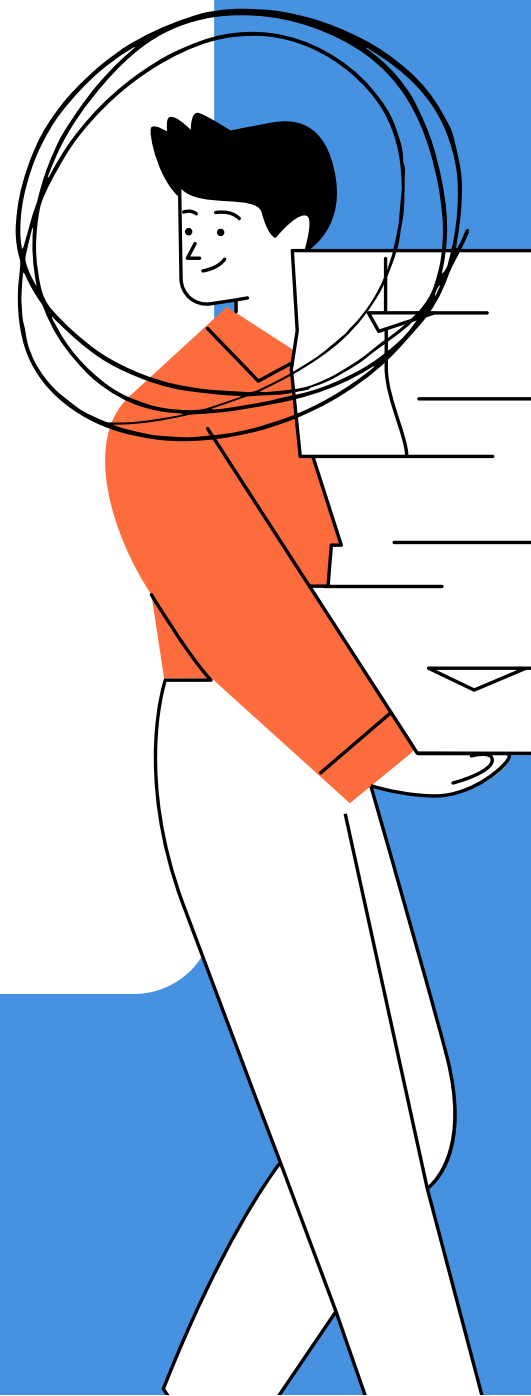
4.6 TRAINING THE MODEL

4.7 PERFORMANCE

5- CONCLUSION

6- REFERENCE

7- APPENDIX



# Introduction

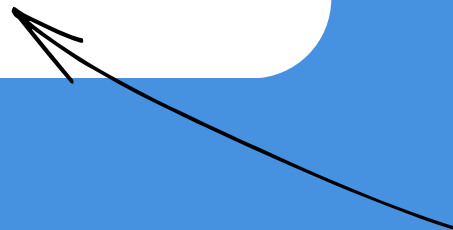
People face various diseases due to the environmental condition and their living habits. So the prediction of disease at earlier stage becomes important task. But the accurate prediction on the basis of symptoms becomes too difficult for doctor. The correct prediction of disease is the most challenging task, and medical science has large amount of data growth per year. Due to increase amount of data growth in medical and healthcare field the accurate analysis on medical data has been benefits from early patient care. So, we proposed Disease Prediction Using Machine Learning





## PROBLEM DEFINITION & OBJECTIVES

The purpose of constructing this project called "Disease Prediction Using Machine Learning" is to predict the accurate disease of the patient using all their general information's and also the symptoms. If this Prediction is completed at the first stages of the disease with the assistance of this project and everyone other necessary, measure disease is cured and generally this prediction system can even be very useful in health industry. The final purpose of this Disease prediction is to supply prediction for the assorted and customarily occurring diseases that when unchecked and sometimes ignored can turn into fatal disease and cause a lot of problem to the patient and moreover as their members of the family. So, with the assistance of algorithms, techniques and methodologies we've done this project which is able to help the people who are within the need.



# APPROACH :

## DATA SET

The dataset we will use in our project is Disease Prediction consists of 2 CSV files. One of them is for training and the other is for testing your model. Each CSV file has 133 columns. 132 of these columns are symptoms that a person experiences and the last column is the prognosis. And making the task of physicians easy is the main purpose of this dataset. Determined by the type of disease using the Random Forest model.

## DATA COLLECTION

We download the Disease Prediction dataset from Kaggle, and this is the website <https://www.kaggle.com/datasets/kaushil268/disease-prediction-using-machine-learning> Because our project is Disease Prediction Using a Machine Learning scenario, we need to choose a dataset containing various diseases. The dataset selected is the best between different data on the same subject because it contains many types of diseases and symptoms.

## MACHINE LEARNING MODEL

We have tried multiple prediction models but using the Random Forest classifier model has shown the best results:

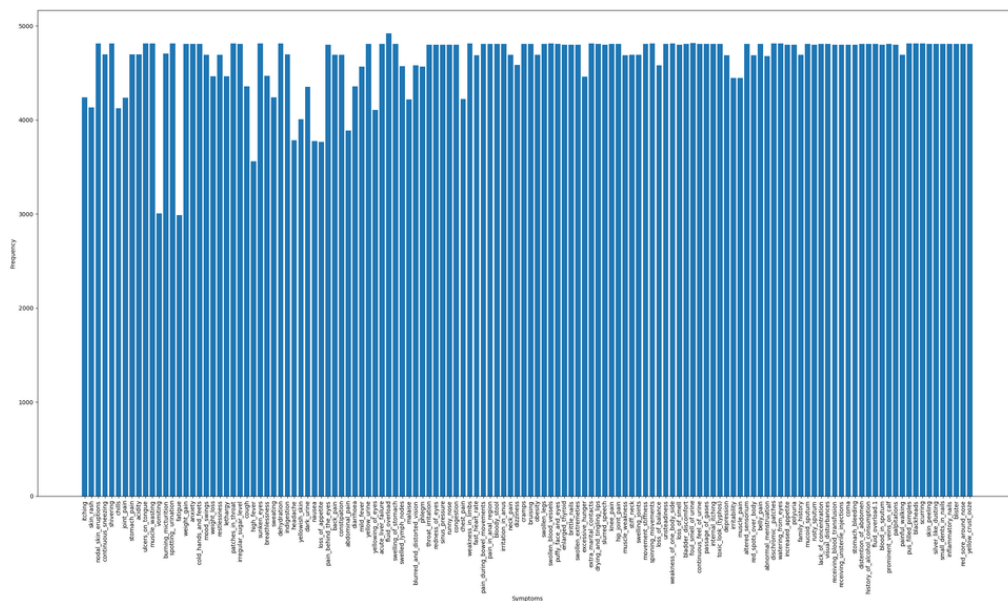
- Random Forest classifier

# Random Forest classifier

The random forest classifier is a supervised learning algorithm that you can use for regression and classification problems. It is among the most popular machine learning algorithms due to its high flexibility and ease of implementation. So, The Random Forest is an ensemble learning method that can give more accurate predictions than most other machine learning algorithms. It is commonly used in decision tree learning. A forest is created using decision trees, each decision tree is a strong classifier on its own. These decision trees are used to create a forest of strong classifiers. This forest of strong classifiers gives a better prediction than decision trees or other machine learning algorithms.



This picture shows the frequency of the symptom, we see that many of the symptoms occurred at about the same times, and the conclusion from this analysis inspired us to write these questions.



Predict whether the symptoms indicate a specific disease or not?

Is the increase in the proportion of symptoms a good indicator for the diagnosis of the disease or not?



# Code and Analysis

We start with initial libraries such as:

- "Panda's library" is used in data analysis and data visualization in Python. It allows you to import data quickly from various sources, take it back to your machine to analyze it, and create compelling graphics.
- "Sklearn and Model\_selection" Sklearn It is a Python library that offers various features for data processing that can be used for classification, clustering, and model selection. Model\_selection is a method for setting a blueprint to analyze data and then using it to measure new data. Selecting a proper model allows you to generate accurate results when making a prediction. "train\_test\_split" is a function in Sklearn model selection for splitting data arrays into two subsets: for training data and for testing data.
- "Sklearn metrics" are import metrics in SciKit Learn API to evaluate your machine learning algorithms.
- And For training the "random forest classifier" we have used sklearn RandomForestClassifier to make a classifier model. We are keeping most of its parameters as default and then pass our training data to fit.

```
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn import metrics
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
from sklearn.ensemble import RandomForestClassifier
import matplotlib.pyplot as plt
```

## Importing the Data

Our data is divided into 2 files, Training and Testing. We used the read\_csv() method provided by pandas to import our CSV files and assign it to our variables - train and test.

### Import Data

```
train = pd.read_csv('Dataset/Training.csv')
test = pd.read_csv('Dataset/Testing.csv')
```



# Preprocessing

Before splitting our data, we have to pre-process it to make sure the data is ready to be trained. Firstly, we check for missing (Nan) values. Using the `isnull()` function. It is visible that all features have 'False' as a result, meaning no missing values.

## Preprocess

```
# check for null values
train.isnull().any()
```

itching	False	yellow_urine	False
skin_rash	False	yellowing_of_eyes	False
nodal_skin_eruptions	False	acute_liver_failure	False
continuous_sneezing	False	fluid_overload	False
shivering	False	swelling_of_stomach	False
chills	False	swelled_lymph_nodes	False
joint_pain	False	malaise	False
stomach_pain	False	blurred_and_distorted_vision	False
acidity	False	phlegm	False
ulcers_on_tongue	False	throat_irritation	False
muscle_wasting	False	redness_of_eyes	False
vomiting	False	sinus_pressure	False
burning_micturition	False	runny_nose	False
spotting_urination	False	congestion	False
fatigue	False	chest_pain	False
weight_gain	False	weakness_in_limbs	False
anxiety	False	fast_heart_rate	False
cold_hands_and_feets	False	pain_during_bowel_movements	False
mood_swings	False	pain_in_anal_region	False
weight_loss	False	bloody_stool	False
restlessness	False	irritation_in_anus	False
lethargy	False	neck_pain	False
patches_in_throat	False	dizziness	False
irregular_sugar_level	False	cramps	False
cough	False	bruising	False
high_fever	False	obesity	False
sunken_eyes	False	swollen_legs	False
breathlessness	False	swollen_blood_vessels	False
sweating	False	puffy_face_and_eyes	False
dehydration	False	enlarged_thyroid	False
indigestion	False	brittle_nails	False
headache	False	swollen_extremeties	False
yellowish_skin	False	excessive_hunger	False
dark_urine	False	extra_marital_contacts	False
nausea	False	drying_and_tingling_lips	False

spinning_movements	False	loss_of_appetite	False
loss_of_balance	False	pain_behind_the_eyes	False
unsteadiness	False	back_pain	False
weakness_of_one_body_side	False	constipation	False
loss_of_smell	False	abdominal_pain	False
bladder_discomfort	False	diarrhoea	False
foul_smell_of_urine	False	mild_fever	False
continuous_feel_of_urine	False	slurred_speech	False
passage_of_gases	False	knee_pain	False
internal_itching	False	hip_joint_pain	False
toxic_look_(typhos)	False	muscle_weakness	False
depression	False	stiff_neck	False
irritability	False	swelling_joints	False
muscle_pain	False	movement_stiffness	False
altered_sensorium	False		
red_spots_over_body	False	silver_like_dusting	False
belly_pain	False	small_dents_in_nails	False
abnormal_menstruation	False	inflammatory_nails	False
dischromic_patches	False	blister	False
watering_from_eyes	False	red_sore_around_nose	False
increased_appetite	False	yellow_crust_ooze	False
polyuria	False	prognosis	False
family_history	False		
mucooid_sputum	False		
rusty_sputum	False		
lack_of_concentration	False		
visual_disturbances	False		
receiving_blood_transfusion	False		
receiving_unsterile_injections	False		
coma	False		
stomach_bleeding	False		
distention_of_abdomen	False		
history_of_alcohol_consumption	False		
fluid_overload.1	False		
blood_in_sputum	False		
prominent_veins_on_calf	False		
palpitations	False		
painful_walking	False		
pus_filled_pimples	False		
blackheads	False		
scurring	False		
skin_peeling	False		

We've also displayed how much the diseases were mentioned in the set to make sure the data is unbiased. Using the `value_counts()` function to count the records of each disease, we observe that each disease has exactly 120 records, meaning the data is balanced and unbiased.

```
# check if balanced
train['prognosis'].value_counts()
```

Fungal infection	120	Allergy	120
Hepatitis C	120	hepatitis A	120
Hepatitis E	120	GERD	120
Alcoholic hepatitis	120	Chronic cholestasis	120
Tuberculosis	120	Drug Reaction	120
Common Cold	120	Peptic ulcer disease	120
Pneumonia	120	AIDS	120
Dimorphic hemmorhoids(piles)	120	Diabetes	120
Heart attack	120	Gastroenteritis	120
Varicose veins	120	Bronchial Asthma	120
Hypothyroidism	120	Hypertension	120
Hyperthyroidism	120	Migraine	120
Hypoglycemia	120	Cervical spondylosis	120
Osteoarthritis	120	Paralysis (brain hemorrhage)	120
Arthritis	120	Jaundice	120
(vertigo) Paroymsal	120	Malaria	120
Acne	120	Chicken pox	120
Urinary tract infection	120	Dengue	120
Psoriasis	120	Typhoid	120
Hepatitis D	120	Impetigo	120
Hepatitis B	120		

## Splitting the data

Now comes the splitting! We divide the training data to diseases and symptoms, A and B alternately. Then we split the data into 80% training and 20% testing datasets for the purpose of training and testing the model to help determine the accuracy of the machine learning algorithm. C will contain the symptoms from the testing csv file, that we will use to compare the actual and predicted value.

### Split data

```
A = train[["prognosis"]] # diseases
B = train.drop(["prognosis"],axis=1) # symptoms
C = test.drop(["prognosis"],axis=1) # symptoms - testing
x_train, x_test, y_train, y_test = train_test_split(B,A,test_size=0.2)
```

## Training the model

We set parameters:

- n\_estimators: The number of trees in the forest = 100
- criterion: The function to measure the quality of a split = entropy (Used for information gain).
- n\_jobs: The number of jobs to run in parallel = 5
- random\_statet: Controls sampling and the randomness of bootstrapping = 42

Fitting the model, using fit(), to the training data is essentially the training part of the modelling process. Reval() is used to reshape the array created. Then, the model classifies the data using predict() by passing the symptoms to predict the diseases.

```
# Training random forest model
mod = RandomForestClassifier(n_estimators = 100,n_jobs = 5, criterion= 'entropy',random_state = 42)
mod = mod.fit(x_train,y_train.values.ravel())
pred = mod.predict(x_test)
```

# Performance

## THE MODEL HAS AN ACCURACY OF 100%

Using `metrics.accuracy_score()` to calculate the accuracy, we get 100%

### Accuracy

```
metrics.accuracy_score(y_test, pred)
```

```
1.0
```

We then used `classification_report()` to check the precision (ration of true positive to the sum of true and false positive), recall (ratio of true positive to the sum of true positive and false negative), f1-score (weighted mean of precision and recall, the closer to 1 the better expected performance) and support (number of occurrences of the class in the dataset).

```
report = classification_report(y_test, pred, output_dict=True)
pd.DataFrame(report).transpose()
```

	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.0	1.0	1.0	27.0
AIDS	1.0	1.0	1.0	13.0
Acne	1.0	1.0	1.0	25.0
Alcoholic hepatitis	1.0	1.0	1.0	20.0
Allergy	1.0	1.0	1.0	28.0
Arthritis	1.0	1.0	1.0	28.0
Bronchial Asthma	1.0	1.0	1.0	21.0
Cervical spondylosis	1.0	1.0	1.0	27.0
Chicken pox	1.0	1.0	1.0	17.0
Chronic cholestasis	1.0	1.0	1.0	28.0
Common Cold	1.0	1.0	1.0	26.0
Dengue	1.0	1.0	1.0	23.0
Diabetes	1.0	1.0	1.0	32.0
Dimorphic hemmorhoids(piles)	1.0	1.0	1.0	23.0
Drug Reaction	1.0	1.0	1.0	28.0
Fungal infection	1.0	1.0	1.0	18.0
GERD	1.0	1.0	1.0	20.0
Gastroenteritis	1.0	1.0	1.0	22.0
Heart attack	1.0	1.0	1.0	21.0
Hepatitis B	1.0	1.0	1.0	26.0
Hepatitis C	1.0	1.0	1.0	14.0
Hepatitis D	1.0	1.0	1.0	20.0
Hepatitis E	1.0	1.0	1.0	24.0
Hypertension	1.0	1.0	1.0	22.0
Hyperthyroidism	1.0	1.0	1.0	26.0
Hypoglycemia	1.0	1.0	1.0	28.0
Hypothyroidism	1.0	1.0	1.0	28.0
Impetigo	1.0	1.0	1.0	30.0
Jaundice	1.0	1.0	1.0	24.0
Malaria	1.0	1.0	1.0	25.0
Migraine	1.0	1.0	1.0	27.0
Osteoarthritis	1.0	1.0	1.0	26.0
Paralysis (brain hemorrhage)	1.0	1.0	1.0	25.0
Peptic ulcer diseae	1.0	1.0	1.0	22.0
Pneumonia	1.0	1.0	1.0	24.0
Psoriasis	1.0	1.0	1.0	27.0
Tuberculosis	1.0	1.0	1.0	22.0
Typhoid	1.0	1.0	1.0	24.0
Urinary tract infection	1.0	1.0	1.0	24.0
Varicose veins	1.0	1.0	1.0	21.0
hepatitis A	1.0	1.0	1.0	28.0
accuracy	1.0	1.0	1.0	1.0
macro avg	1.0	1.0	1.0	984.0
weighted avg	1.0	1.0	1.0	984.0

# Performance



## Confusion Matrix

```
cm = confusion_matrix(y_test, pred)
pd.DataFrame(cm)
```

This is a sample view of the matrix. A full one will be provided in the Appendix.

Now to make sure that our model is not overfitted. We used the model on the testing symptoms and compared the actual values to the predicted ones. We can see that all predictions are correct. Unlike the decision tree classification model shown in the appendix.

```
test = test.join(pd.DataFrame(mod.predict(C), columns=["predicted"]))[["prognosis", "predicted"]]

test['result'] = ''
for i in range(len(test)):
    if test["prognosis"][i] == test["predicted"][i]:
        test['result'].iloc[i] = 'Correct'
    else:
        test['result'].iloc[i] = 'Incorrect'
```

	prognosis	predicted	result
0	Fungal infection	Fungal infection	Correct
1	Allergy	Allergy	Correct
2	GERD	GERD	Correct
3	Chronic cholestasis	Chronic cholestasis	Correct
4	Drug Reaction	Drug Reaction	Correct
5	Peptic ulcer disease	Peptic ulcer disease	Correct
6	AIDS	AIDS	Correct
7	Diabetes	Diabetes	Correct
8	Gastroenteritis	Gastroenteritis	Correct
9	Bronchial Asthma	Bronchial Asthma	Correct
10	Hypertension	Hypertension	Correct
11	Migraine	Migraine	Correct
12	Cervical spondylosis	Cervical spondylosis	Correct
13	Paralysis (brain hemorrhage)	Paralysis (brain hemorrhage)	Correct
14	Jaundice	Jaundice	Correct
15	Malaria	Malaria	Correct
16	Chicken pox	Chicken pox	Correct
17	Dengue	Dengue	Correct

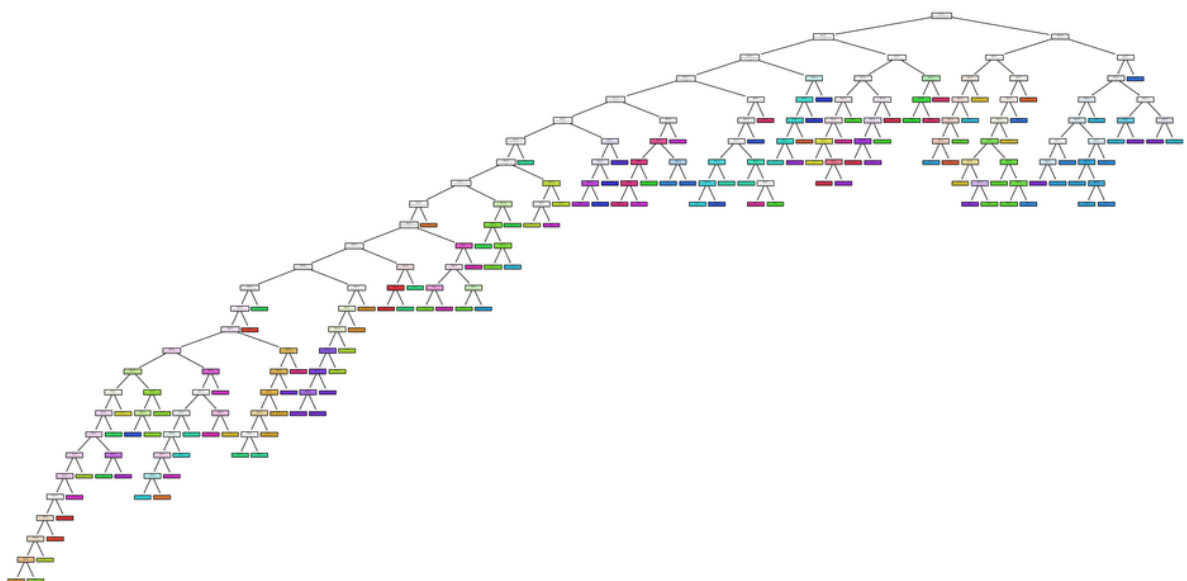


# Performance

18	Typhoid	Typhoid	Correct
19	hepatitis A	hepatitis A	Correct
20	Hepatitis B	Hepatitis B	Correct
21	Hepatitis C	Hepatitis C	Correct
22	Hepatitis D	Hepatitis D	Correct
23	Hepatitis E	Hepatitis E	Correct
24	Alcoholic hepatitis	Alcoholic hepatitis	Correct
25	Tuberculosis	Tuberculosis	Correct
26	Common Cold	Common Cold	Correct
27	Pneumonia	Pneumonia	Correct
28	Dimorphic hemorrhoids(piles)	Dimorphic hemorrhoids(piles)	Correct
29	Heart attack	Heart attack	Correct
30	Varicose veins	Varicose veins	Correct
31	Hypothyroidism	Hypothyroidism	Correct
32	Hyperthyroidism	Hyperthyroidism	Correct
33	Hypoglycemia	Hypoglycemia	Correct
34	Osteoarthritis	Osteoarthritis	Correct
35	Arthritis	Arthritis	Correct
36	(vertigo) Paroysmal Positional Vertigo	(vertigo) Paroysmal Positional Vertigo	Correct
37	Acne	Acne	Correct
38	Urinary tract infection	Urinary tract infection	Correct
39	Psoriasis	Psoriasis	Correct
40	Impetigo	Impetigo	Correct
41	Fungal infection	Fungal infection	Correct

Here is a display of one of the decision trees in the forest. We have randomly chosen the tree at index 8:

```
from sklearn import tree
plt.figure(figsize=(30,15))
tree.plot_tree(mod.estimateds_[8],filled = True)
```



# Conclusion

The main aim of this disease prediction model is to predict the disease based on symptoms. This model takes the symptoms of the user from which he or she suffers as input and generates the final output as a prediction of disease. In conclusion, for disease risk modeling, the accuracy of risk prediction depends on the diverse feature of the Health centers' data.

Findings may help inform future developers of Disease Predictability Software and promote personalized patient care. The model predicts Patient Diseases through the Random Forest algorithm. Model accuracy reaches 100%. Machine learning skills are designed for Disease Prediction successfully.



## Resources

<https://www.kaggle.com/datasets/kaushil268/disease-prediction-using-machine-learning>

`sklearn.ensemble.RandomForestClassifier` — scikit-learn  
1.2.1 documentation

Random Forest Classifier using Scikit-learn -  
GeeksforGeeks

<https://www.ijraset.com/research-paper/disease-prediction-using-ml>

Random Forest Classifier: Overview, How Does it Work,  
Pros & Cons | upGrad blog

Random Forest Classifier in Python Sklearn with Example  
- MLK - Machine Learning Knowledge

Sklearn metrics for Machine Learning in Python - Machine  
Learning HD





# Appendix.

Comparison of actual data and predicted values of decision tree classification model:

## Import Data

```
train = pd.read_csv('Dataset/Training.csv')
test = pd.read_csv('Dataset/Testing.csv')
```

## Split Data

```
A = train[["prognosis"]] #diseases
B = train.drop(["prognosis"],axis=1) #symptoms
C = test.drop(["prognosis"],axis=1) #testing - symptoms
x_train, x_test, y_train, y_test = train_test_split(B,A,test_size=0.2)
```

## Model

```
mod = DecisionTreeClassifier()
mod = mod.fit(x_train,y_train)
pred = mod.predict(x_test)
```

```
test = test.join(pd.DataFrame(mod.predict(C),columns=["predicted"]))[["prognosis","predicted"]]
test['result']= ' '
for i in range(len(test)):
    if test["prognosis"][i] == test["predicted"][i]:
        test['result'].iloc[i] = 'Correct'
    else:
        test['result'].iloc[i] = 'Incorrect'
```

	prognosis	predicted	result
0	Fungal infection	Fungal infection	Correct
1	Allergy	Allergy	Correct
2	GERD	GERD	Correct
3	Chronic cholestasis	Chronic cholestasis	Correct
4	Drug Reaction	Drug Reaction	Correct
5	Peptic ulcer disease	Peptic ulcer disease	Correct
6	AIDS	AIDS	Correct
7	Diabetes	Diabetes	Correct
8	Gastroenteritis	Gastroenteritis	Correct
9	Bronchial Asthma	Bronchial Asthma	Correct
10	Hypertension	Hypertension	Correct
11	Migraine	Migraine	Correct
12	Cervical spondylosis	Cervical spondylosis	Correct
13	Paralysis (brain hemorrhage)	Paralysis (brain hemorrhage)	Correct
14	Jaundice	Jaundice	Correct
15	Malaria	Malaria	Correct
16	Chicken pox	Chicken pox	Correct

# Appendix.

17	Dengue	Dengue	Correct
18	Typhoid	Typhoid	Correct
19	hepatitis A	hepatitis A	Correct
20	Hepatitis B	Hepatitis B	Correct
21	Hepatitis C	Hepatitis C	Correct
22	Hepatitis D	Hepatitis D	Correct
23	Hepatitis E	Hepatitis E	Correct
24	Alcoholic hepatitis	Alcoholic hepatitis	Correct
25	Tuberculosis	Tuberculosis	Correct
26	Common Cold	Common Cold	Correct
27	Pneumonia	Pneumonia	Correct
28	Dimorphic hemmorhoids(piles)	Dimorphic hemmorhoids(piles)	Correct
29	Heart attack	Heart attack	Correct
30	Varicose veins	Varicose veins	Correct
31	Hypothyroidism	Hypothyroidism	Correct
32	Hyperthyroidism	Hyperthyroidism	Correct
33	Hypoglycemia	Hypoglycemia	Correct
34	Osteoarthritis	Osteoarthritis	Correct
35	Arthritis	Arthritis	Correct
36	(vertigo) Paroymsal Positional Vertigo	(vertigo) Paroymsal Positional Vertigo	Correct
37	Acne	Acne	Correct
38	Urinary tract infection	Urinary tract infection	Correct
39	Psoriasis	Psoriasis	Correct
40	Impetigo	Impetigo	Correct
41	Fungal infection	Impetigo	Incorrect

The screenshot shows a Jupyter Notebook with the following code and output:

```

1 # Applied Machine Learning Project
2
3 # Author: Ghaid
4
5
6
7 import pandas as pd
8 from sklearn.model_selection import train_test_split
9 from sklearn import metrics
10 from sklearn.metrics import classification_report
11 from sklearn.metrics import confusion_matrix
12 from sklearn.ensemble import RandomForestClassifier
13 import matplotlib.pyplot as plt
14
15 # Import Data
16 train = pd.read_csv('Dataset/Training.csv') # 4920
17 test = pd.read_csv('Dataset/Testing.csv') # 42
18
19 # check for null values
20 train.isnull().any()
21 # check if balanced
22 train['prognosis'].value_counts()
23
24 # Split data
25 A = train[['prognosis']] # diseases
26 B = train.drop(['prognosis'],axis=1) # symptoms
27 C = test.drop(['prognosis'],axis=1) # symptoms - testing
28 x_train, x_test, y_train, y_test = train_test_split(B,A,test_size=0.2) # 20:80
29
30 # Training random forest model
31 mod = RandomForestClassifier(n_estimators = 100,n_jobs = 5, criterion= 'entropy',random_state = 42)
32 mod = mod.fit(x_train,y_train.values.ravel())
33 pred = mod.predict(x_test)
34
35 metrics.accuracy_score(y_test, pred)
36
37 report = classification_report(y_test, pred, output_dict=True)
38 pd.DataFrame(report).transpose()
39
40 cm = confusion_matrix(y_test, pred)
  
```

The output of the code is displayed in the console:

```

In [5]: train.isnull().any()
Out[5]:
itching                False
skin_rash              False
nodal_skin_eruptions   False
continuous_sneezing    False
shivering              False
inflammatory_nails    False
blister               False
red_sore_around_nose   False
yellow_crust_ooze      False
prognosis              False
Length: 133, dtype: bool

In [6]: train['prognosis'].value_counts()
Out[6]:
Fungal infection      120
Hepatitis C           120
Hepatitis E           120
Alcoholic hepatitis   120
Tuberculosis          120
Common Cold           120
Pneumonia             120
Dimorphic hemmorhoids(piles) 120
Heart attack          120
Varicose veins        120
Hypothyroidism        120
Hyperthyroidism       120
Hypoglycemia          120
Osteoarthritis        120
Arthritis             120
  
```

# Appendix.

```
18 # check for null values
19 train.isnull().any()
20 # check if balanced
21 train['prognosis'].value_counts()
22
23 # Split data
24 A = train[['prognosis']] # diseases
25 B = train.drop(['prognosis'],axis=1) # symptoms
26 C = test.drop(['prognosis'],axis=1) # symptoms - testing
27 x_train, x_test, y_train, y_test = train_test_split(0,A,test_size=0.2) # 20:80
28
29 # Training random forest model
30 mod = RandomForestClassifier(n_estimators = 100,n_jobs = 5, criterion= 'entropy',random_state = 42)
31 mod = mod.fit(x_train,y_train.values.ravel())
32 pred = mod.predict(x_test)
33
34 metrics.accuracy_score(y_test, pred)
35
36 report = classification_report(y_test, pred, output_dict=True)
37 pd.DataFrame(report).transpose()
38
39 cm = confusion_matrix(y_test, pred)
40 pd.DataFrame(cm)
41
42 # Compare actual with predicted value
43 test = test.join(pd.DataFrame(mod.predict(C),columns=["predicted"]))[['prognosis',"predicted"]]
44
45 test['result'] = ''
46 for i in range(len(test)):
47     if test['prognosis'][i] == test['predicted'][i]:
48         test['result'].iloc[i] = 'Correct'
49     else:
50         test['result'].iloc[i] = 'Incorrect'
51
52 from sklearn import tree
53 plt.figure(figsize=(30,15))
54 tree.plot_tree(mod.estimators_[0],filled = True)
55
56 import numpy as np
```

The screenshot shows a Jupyter Notebook interface with two main panels. The top panel displays the output of a classification report, which is a DataFrame containing metrics for 14 different diseases. The bottom panel shows a confusion matrix for the 'prognosis' variable.

	Key	Type	Size	Value
(vertigo) Parosymal Positional Vertigo	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':22}	
accuracy	float	1	1.0	
Acne	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':33}	
AIDS	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':17}	
Alcoholic hepatitis	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':28}	
Allergy	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':24}	
Arthritis	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':33}	
Bronchial Asthma	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':26}	
Cervical spondylosis	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':21}	
Chicken pox	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':22}	
Chronic cholestasis	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':17}	
Common Cold	dict	4	{'precision':1.0, 'recall':1.0, 'f1-score':1.0, 'support':17}	

```

35 metrics.accuracy_score(y_test, pred)
36
37 report = classification_report(y_test, pred, output_dict=True)
38 pd.DataFrame(report).transpose()
39
40 cm = confusion_matrix(y_test, pred)
41 pd.DataFrame(cm)
42
43 # Compare actual with predicted value
44 test = test.join(pd.DataFrame(mod.predict(C), columns=["predicted"]))[["prognosis", "predicted"]]
45
46 test['result'] = ''
47 for i in range(len(test)):

```

Name	Type	Size	Value
A	DataFrame	(4920, 1)	Column names: prognosis
B	DataFrame	(4920, 132)	Column names: itching, skin_rash, mod.
C	DataFrame	(42, 132)	Column names: itching, skin_rash, mod.
cm	Array of int64	(41, 41)	[ [22 0 ... 0 0] [0 17 0 ... 0 0]
mod	ensemble_forest.RandomForestClassifier	100	RandomForestClassifier object of sklearn.ensemble._forest module
pred	Array of object	(984,)	narray object of numpy module
report	dict	44	{(vertigo) Parosymal Positional Ver-
test	DataFrame	(42, 133)	Column names: itching, skin_rash, mod.

cm - NumPy object array

	0	1	2	3	4	5	6
0	22	0	0	0	0	0	0
1	0	17	0	0	0	0	0
2	0	0	33	0	0	0	0
3	0	0	0	28	0	0	0
4	0	0	0	0	24	0	0
5	0	0	0	0	0	33	0
6	0	0	0	0	0	0	26
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0

Index	diagnosis	predicted	result
0	Fungal Infection	Fungal Infection	Correct
1	Allergy	Allergy	Correct
2	GERD	GERD	Correct
3	Chronic cholestasis	Chronic cholestasis	Correct
4	Drug Reaction	Drug Reaction	Correct
5	Peptic ulcer disease	Peptic ulcer disease	Correct
6	AIDS	AIDS	Correct
7	Diabetes	Diabetes	Correct
8	Gastroenteritis	Gastroenteritis	Correct
9	Bronchial Asthma	Bronchial Asthma	Correct
10	Hypertension	Hypertension	Correct
11	Migraine	Migraine	Correct
12	Cervical spondylitis	Cervical spondylitis	Correct
13	Paralysis (brain hemorrhage)	Paralysis (brain hemorrhage)	Correct
14	Jaundice	Jaundice	Correct
15	Malaria	Malaria	Correct
16	Chicken pox	Chicken pox	Correct
17	Dengue	Dengue	Correct
18	Typhoid	Typhoid	Correct
19	Hepatitis A	hepatitis A	Correct
20	Hepatitis B	Hepatitis B	Correct
21	Hepatitis C	Hepatitis C	Correct
22	Hepatitis D	Hepatitis D	Correct

```

In [21]:
...: test = test.join(pd.DataFrame(mod.predict(C), columns=["predicted"]))
...: [[ "prognosis", "predicted" ] ]
...:
...: test['result'] = ''
...: for i in range(len(test)):
...:     if test["prognosis"][i] == test["predicted"][i]:
...:         test['result'].iloc[i] = 'Correct'
...:     else:
...:         test['result'].iloc[i] = 'Incorrect'

In [22]:
...: from sklearn import tree
...: plt.figure(figsize=(30,15))
...: tree.plot_tree(mod.estimators_[0], filled = True)
  
```

# Appendix.

