Research Article

An Artificial Intelligent based System for Efficient Swine Flu Prediction using Naive Bayesian Classifier

Pilla Srinivas[1*], Debnath Bhattacharyya[2], Divya Midhun Chakkaravarthy[1]

¹Department of Computer Science and Multimedia, Lincoln University College, Malaysia; ²Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, Guntur, Andhra Pradesh, India.

ABSTRACT

Introduction: Swine Flu cases are rarely observed but are to be found subsequently increasing in many countries and also in India. They can be treated and diagnosed if it is detected at an early stage. However, many times it is difficult to predict as the symptoms are almost similar to other viral fevers. Many researchers used various algorithms and different approaches to predict swine flu.

Aim and Objective: In this paper, we propose Naive Bayesian classifier for an efficient prediction, by comparing the symptoms and applying significant signs and prediction factors to Bayes theorem to predict the patient's condition.

Method: Here in this work, the machine learning algorithm is used on the available data to reduce the time and to predict the disease perfectly. We collected 14 sample records of different swine flu suspected patients from King George Hospital, Visakhapatnam, India, based on the sample reports. We prepare the training SF (Swine Flu) dataset. The ESFP (Efficient Swine Flu Prediction) is first trained by using SF (Swine Flu) dataset with some of the significant symptoms observed in Swine Flu cases.

Conclusion: The first signs and the prediction values are applied to Naive Bayesian Classifier by using the training set, and then the test set is applied to predict the disease prevailing or not..

Key Words: Artificial Intelligent System, Efficient Swine Flu Prediction (ESFP), Naive Bayesian Classifier, Swine Flu

INTRODUCTION

The subclass of Influenza Virus is a virus Influenza A HIN1 causing Swine Flu and was the foremost frequent reason behind human influenza, also called u in the year 2009. H1N1 leaves a few strains that are prevalent in human that creates a slight part of every disease- resembling sickness and a little piece of entire Influenza that are seasonal. Additional strains of the specified virus of other types are also observed in birds and pigs[1].

The Swine Flu is initially generated by viruses related to Influenza that are disease-related to respiration that affect respiratory organs in pigs, leading to careless actions, nasal secretions, decreased hunger and barking cough. The same types of symptoms are observed in people affected by Human u as in pigs affected by Swine Flu [2,3].

In the USA the Swine Influenza U was initially in around 1930 seduced in pigs. A lot of investigations were being done. However, the Swine Flu is first observed in a few places in Mexico and is then coined as H1N1. Later in the USA, the same H1N1 virus is found in people, and drastically that has spread a lot, and more than 10000 persons are severely affected in over forty plus countries. In 2011 the latest one is specified to be H3N2v with Influenza H1N1[5,6].

Machine learning plays a vital role in solving problems for many solutions and also helps to predict future results in today's world. Artificial intelligence makes use of machine learning techniques to solve many problems. It helps to train the algorithms by giving the sample data as input to the algorithms and make it to learn how to make decisions from past experiences or results and execute the tasks smartly [25].

In medical diagnosis system, the main time-consuming task is to identify the disease. Late identification leads to the severity risk some times in diagnosing the condition. Machine learning techniques have played a significant role in the present generation to predict and classify the severity level

Corresponding Author:

Dr. Pilla Srinivas, Department of Computer Science and Multimedia, Lincoln University College, Malaysia.
Email: srinivasp3@gmail.com

in different stages. Machine Learning has predicted many diseases like diabetes, brain tumour and made effective diagnosis plan. One of the most time-consuming conditions nowadays is Swine Flu. By applying the dataset to the machine learning algorithm, we are going to predict the severity levels of H1N1 among the patients[26].

Existing system

Flu viruses are spread mostly from an individual to another individual using any medium either by sneezing or direct coughs from patients suffering from this virus. This can sometimes be affected even by touching the surfaces such as furniture or walls which are touched by the patient by which some people will be hospitalized. If the specified virus is not detected on time and eradication, then diseases like Swine Flu will be spread rapidly. The manual approaches are time taking[7].

Proposed system

The proposed System on Artificial Intelligent System is used for Efficient Swine Flu Detection, which is reliable and competent. This requires a proper training set and test set for training the system. It requires less time to predict the stage of disease by applying the data to the machine learning algorithm.

Efficient Swine Flu Detection using Naive Bayesian Classifier

Many researchers used different machine learning Classifiers to predict Swine Flu[27]. The entire machine learning algorithms has its advantages from a different perspective. Decision trees work better, but it requires a lot of data to get to build the training set. Naïve Bayesian works better even if it doesn't contain all the possibilities, and it also requires less quantity of data. This is the reason why we preferred naïve Bayesian Classifier to predict the severity of Swine Flu based on 14 Swine Flu patients' records. It requires less data as input and produces a fast outcome.

Swine Flu Symptoms

The symptoms such as headache, Joint Pains, Muscle Pains, Chills, running nose, dry cough and fatigue in any Influenzas and they are similar in Swine Flu. However few cases have been reporting that include Diarrhea, fever, vomiting, and neurological issues.

The high risk is observed in an individual with severe complications include elderly age group, kids less than five years of age, children with neurodevelopment anomalies, women who are pregnant and such people who are prone with medical conditions that are abnormal and underlying such as diabetic patients, people who have asthma or cardiac patients and such people who are immune-suppressed, people suffering from obesity in any age group[2,9].

Severe case symptoms

It is stated by WHO, that the medical image in stern case patients is completely variant in Swine Flu compared to disease pattern observed in epidemics. If the people with sick medical history are pretended and expected headed for high risk, numerous critical cases are also found in hale and hearty people with an excellent medical history. Though research is presently going on the influencing factors that amplify the extreme danger of rigorous unhealthiness don't seem to be currently understood, Patients with a severe health condition are found to be okay initially. But around three to five days, generally they begin to get worse after the onset of symptoms. Fast deterioration is being observed with failure in respiration in several patients within twenty-four hours. Immediate respiratory support and intensive care unit support is required with mechanical ventilation in the case of most patients[5].

The Centres for Disease Control (CDC) recommends immediate medical attention if any experience of warning signs of emergency is observed in person attacked with Swine Flu[7]. In adults, they embody problem in respiratory or squatness of breath, pressure and pain within abdomen or chest, Confusion, fast giddiness, severe vomiting persistently and Temperature.

In kids they include difficulty in breathing or speed breathing, skin colour turns blue, not accepting fluids, feeling, lazy and sleepy, non-interacting, behaves irritably that the children usually don't hold, symptoms related to other u that recover but eventually turns to worst cough and high temperature, high temperature with a rash, not eating, having no tear when crying.

Complications

Swine Flu affected patients who are suffering from obesity complications are being observed and are assaulted with prior respiratory disease are mainly infected by pneumonia disease, This happens mostly in adults who may be diagnosed under ventilation in Information and communications technology (ICT) due to acute respiratory organ injury. Infections due to bacteria are more commonly observed in children. Significant complications include different conditions like cardiac problems (myocarditis and pericarditis), myositis, central nervous systems complications, toxic shock syndrome and secondary bacterial pneumonia.

The prominent cause of secondary bacterial pneumonia is due to Staphylococcus aureus, along with Methicillin-Resistant Staphylococcus Aureus (MRSA) with a higher mortality rate. Cardiac complications and Neuromuscular are uncommon, but there's an opportunity of occurrence. Fulminate myocarditis and pulmonary emboli were other complications detected[4].

Naive Bayesian Classifier

It is one of the most used Machine Learning algorithms for predicting and diagnosing diseases [28]. Naive Bayesian is a generative model and works with small data sets where Logistic regression works with large data sets, and it also works faster when compared with K- nearest neighbours. Another main advantage of naïve Bayesian is it not only outputs prediction, but it also generates a degree of certainty, which is very useful in diagnosing.

Naive Bayesian Classifiers belongs to classification algorithms which are based on the Bayes theorem. It is a family of algorithms that share a universal principle, but the pair of features are independent of each other. It is a classification algorithm which is suitable for both binary and multiclass classification. It is a classification technique which supervises and helps to predict the future class labels by assigning instances using the conditional probability.

The Bayes' theorem plays a vital role in dictating the collection of algorithms related to the classification which are categorized as Efficient Naive Bayesian Classifiers. It describes the probability of an event to occur based on the conditions that are related to the game, when applied then the hazards involved in the Bayes theorem have different probability interpretations,

This is tending to be a family of procedures that do not follow the algorithmic approach but follow a common standard principle that is common. Therefore in each mixing of choices that are self-determining in the classification of every alternative[11].

An SF dataset is being collected, and analysis is being done, which is describing the symptoms of Swine Flu based on that go for Initial diagnosis. Proceeding with the symptoms, each tuple is used to classify the prevailing conditions such as "Yes" or "No" for Initial diagnosis.

By applying this SF data set to Naive Bayesian Classifier based upon the instances, it helps to predict the condition of patients by verifying all the possibilities.

As this is the Classifier algorithm, we can classify the data and the requirements based on the symptoms of the Swine Flu patients and applying it to the Bayes theorem gives Efficient results.

Table 1: Representing the SF dataset shows the Symptoms of 14 different patients along with Affected Area, Immunity and Severity of Symptoms.

S. No	Fever Symptoms	Affected Area	Immunity	Severity of Symptoms	Initial Diagnosis
1	Dry cough	Yes	High	No	No
2	Dry cough	Yes	High	No	No

Table 1: *(Continued)*

S. No	Fever Symptoms	Affected Area	Immunity	Severity of Symptoms	Initial Diagnosis
3	Cold	Yes	High	Yes	Yes
4	Body pains	Yes	High	No	No
5	Body pains	No	High	No	No
6	Body pains	Yes	High	Yes	Yes
7	Cold	No	Low	Yes	Yes
8	Dry cough	No	Low	No	No
9	Dry cough	Yes	High	Yes	Yes
10	Body pains	No	Low	Yes	Yes
11	Dry cough	No	Low	Yes	Yes
12	Cold	No	Low	Yes	Yes
13	Cold	No	Low	Yes	Yes
14	Body pains	No	Low	Yes	Yes

The data that is collected from the hospital is categorized into different ways based upon the symptoms faced by the patients. The collected information is trained based upon the various attributes which are not same in all of them. All of those combinations of symptoms are meant for probability and given to the algorithm to predict the stage of Swine Flu (SF).

The data represented is partitioned into two elements, where the first one is SF Feature Matrix, whereas next is SF Response Vector. SF Feature Matrix comprises of tuples of data during where every tuple consists of the significant rate of dependent SF Features.

According to SF dataset referring to Table 1, SF Features are 'Fever symptoms', 'Effected area', 'Immunity' and 'Severity of symptoms'. SF Response Vector comprises the worth of SF class variable, which is either predicted or real expected result for every tuple of SF Feature Matrix related to features. The SF class variable name is the initial diagnoses according to the data considered.

Assumptions

Naive Bayes assumption that is fundamental is where every tuple of SF Feature:

Equal outcome contribution with relation to the SF dataset, this idea is often considered to be in as accomplished area. This is Independent. This is assumed that none of the couples of SF Features is reliant. For instance, the affected area be 'Yes' has not anything to do with the Immunity or Fever symptoms be 'Dry cough' has indeed not any effect on the severity of symptoms. Hence, based on the assumptions, the SF Features are treated to be independent

Next, every SF Feature will be provided equal importance or weight. Hence in an instance where only Effected area is known and Immunity alone won't accurately forecast the result. Not any of attribute is digressive, henceforth understood to be contributory equivalent to the outcome. Assumptions derived by the algorithm Naive Bayes may not be accurate generally inexact real-world scenario. The fact is that independent assumption works well, but it is always incorrect. First, the basic knowledge of Bayes' theorem is required before understanding the Naive Bayes.

Bayes' Theorem

Bayes' Theorem states that based on the probability of an occurring event and likelihood of another occurred event. This is shown mathematically with the equation[1], and here A and B are events considered [12,13]:

$$P(A/B) = \frac{P(B/A)P(A)}{P(B)} \tag{1}$$

Mostly, we tend to try to search out

Probability of an event A; specified that the event B is correct. Event B is additionally termed as evidence.

P (A) be a priority of A, which is the prior probability and is the event Probability earlier than evidence is observed. The proof is attributed worth of an indefinite object, and this can be event B. Hereafter evidence can be visualized the posterior probability of B is considered to be P (A|B) which is the probability of an event.

Then, with deemed to SF dataset, it can apply Bayes' theorem:

$$P(y/X) = \frac{P(X/y)P(y)}{P(X)} \tag{2}$$

Where, X could be dependent SF Feature Vector of the size n and y is class variable, referring to the first tuple

y = No

X = (Dry cough, Yes, High, No)

So in essence, P (X|y) at this point means, that the probability of "No Initial diagnosis" provided that symptoms based conditions can be "dry cough fever symptoms", "Affected area is No", "high immunity" and "no severity of symptoms".

Naive assumption

Now, in this instance, it is required to place a naïve assumption to the Bayes' theorem that can be independent amongst the options regarding SF Features. So at this time, the evidence is split into the separate component[13]. At this instance, if any two events A and B cannot be dependent, therefore it is defined as,

$$P(A, B) = P(A)*P(B).. \tag{3}$$

Henceforth, the result can be denoted, as shown in equation (4).

$$P(y/x_{1,\dots}x_n) = \frac{P(x_1/y)P(x_2/y)\dots\dots P(x_n/y)P(y)}{P(x_1)P(x_2)\dots\dots P(x_n)} \tag{4}$$

This may be expressed as shown in equation (5)

$$P(y/x_{1,\dots}x_n) = \frac{P(y)\prod_{i=1}^{n}P(x_i/y)}{P(x_1)P(x_2)\dots\dots P(x_n)} \tag{5}$$

Next for any given input, being treating the denominator to be constant that term is removed, as shown in equation(6).

$$P(y/x_{1,\dots}x_n) \propto P(y)\prod_{i=1}^{n}P(x_i/y) \tag{6}$$

Now, it is needed to generate a model related to the classifier. So for this, discover the chance of a standard set of inputs for every attainable rate of the class variable y and acquire up the result with a most chance.

The same can be shown mathematically as in equation (7)

$$y = \arg\max_{y} P(y)\prod_{i=1}^{n}P(x_i/y) \tag{7}$$

So, finally, it tends to carry on with the task of calculating P(y) and P (xi | y). P(y) is referred to as class probability, and P (xi | y) is named conditional probability. The naive Bayes classifiers differ principally by the assumptions they create relating to the distribution of P (xi | y).

RESULTS

The results are reflected by a case study on Swine Flu cases observed by patient's history affected by Swine Flu. The main symptoms are listed as follows.

1. **Fever symptoms:**
    The victim is suffering from dry cough, cold, body pains during fever, high body temperature.
2. **Affected area:**
    The victim came from a place where already people around the victim or the people who are residing in the victim's area had been previously suffered by Swine Flu.
3. **Immunity:**
    This is considered if the immunity power or resistance power towards the disease of the victim is high.
4. **The severity of symptoms:**
    The victim is suffering from Breathing Difficulty, Chest pain, Abdomen pain, persistent vomiting, Diarrhea.

All of the above four symptoms are used in prediction of Swine Flu. Now basing on the formulae specified in Section 2, they are applied on Assumptions SF dataset. For this, some pre-computation is done to SF dataset. Then for every xi in x and yj in y calculate the value P (xi | yj) for. The tables below are derived from these calculations and represent the expected probability values.

Table 2: Expected Probability values w.r.to nature of Symptoms.

Symptoms	Nature of the Symptoms	Yes	No	Probability (Yes)	Probability (No)
Fever symptoms	Dry cough	2	3	0.22	0.6
	Cold	4	0	0.44	0
	Body pains	3	2	0.33	0.4
Affected area	Yes	3	3	0.33	0.6
	No	6	2	0.67	0.4
Immunity	High	3	4	0.33	0.8
	Low	6	1	0.67	0.2
Severity of symptoms	Yes	9	0	0.64	0
	No	5	0	0.36	0

So, as shown in the above, P (xi | yj) is calculated for each xi in X and yj in y manually in the tables 2

Table 3: Probability of Initial Diagnosis

Treatment			Probability
Initial diagnosis	Yes	9	0.64
	No	5	0.36

For instance, the probability of Initial diagnosis given that the affected area is No,

i.e P (Effected area = No | Initial diagnosis = Yes) = 6/9.

Also, class probabilities (P(y)) are found that have been evaluated in table 3. For instance, P (Initial diagnosis = Yes) = 9/14. Pre-computations are prepared, and the classifier obtained can be applied. The test is done a new set of SF Features called Treatment.

Treatment = (Body pains, Yes, Low, No)

So, the probability of Initial diagnosis is denoted as

$$P(Yes/treatment) = \frac{P(body\ pains/Yes)P(Effected\ area/Yes)P(immunity/Yes)P(severity\ of\ symptoms/Yes)P(Yes)}{P(treatment)} \quad (8)$$

The probability of no treatment is given usually by:

$$P(No/treatment) = \frac{P(body\ pains/No)P(Effected\ area/No)P(immunity/No)P(severity\ of\ symptoms/No)P(Yes)}{P(treatment)} \quad (9)$$

in equation (10).

$$P(Yes/treatment) \propto \frac{3}{9}.\frac{6}{9}.\frac{9}{14}.\frac{6}{9}.\frac{9}{14} \approx 0.0612 \quad (10)$$

And

$$P(No/treatment) \propto \frac{2}{5}.\frac{2}{5}.\frac{1}{5}.\frac{5}{14}.\frac{5}{14} \approx 0.0040 \quad (11)$$

Now, since

$$P(No/treatment) + P(No/treatment) = 1 \quad (12)$$

However, the numbers will be transformed into probability by accumulating the sum is assumed to be equal to 1 according to normalization.

$$P(Yes/treatment) = \frac{0.0612}{0.0612 + 0.0040} = 0.94 \quad (13)$$

And

$$P(No/treatment) = \frac{0.0040}{0.0612 + 0.0040} = 0.06 \quad (14)$$

Given that

$$P(Yes/treatment) > P(No/treatment)$$

Hence, the prediction is Initial diagnosis would be 'Yes'. The method portrayed applies to the discrete dataset. However, in considering continuous data, Some assumptions are made regarding the distribution of values of every SF Feature. Considering different Naive Bayes classifiers, they usually differ by assumptions considered that they formulate concerning the dissemination of P (xi | y) [14].

The run time complexity of Naïve Bayesian algorithm is O(n K). Where n refers to no. of features and K refers to class labels. It can learn quickly high dimensional features with the limited training dataset.

CONCLUSION

The detection of Swine Flu is done automatically by using the Naïve Bayesian Classifier. The complete system is analyzed and developed. The training and test sets, which are the primary symptoms, are collected from a reputed hospital. The Artificial Intelligent System for efficient Swine Flu Detection is tested and found to be genuine in detection compared to manual predictions. ESFP provides fast outcome with less input of data which leads to quick recognition of the disease and early treatment.

REFERENCES

1. Munjal YP. API Textbook of Medicine (Volume I and II). JP Medical Ltd; 2015 Aug 30.
2. Chrysostomou C, Partaourides H, Seker H. Prediction of Influenza A virus infections in humans using an Artificial Neural Network learning approach. In2017 39th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC) 2017 Jul 11 (pp. 1186-1189). IEEE.
3. Rathod V, Shaikh U, Yadav OP, Rathore A. Swine Influenza Model-Based Optimization using seasonal flu shots (SIMBO-SS). In2015 4th International Conference on Reliability, Infocom Technologies and Optimization (ICRITO)(Trends and Future Directions) 2015 Sep 2 (pp. 1-5). IEEE.
4. Vincent AL, Ma W, Lager KM, Janke BH, Richt JA. Swine influenza viruses: a North American perspective. Advances in virus research. 2008 Jan 1;72:127-54.
5. Gooskens J, Jones M, Claas EC, Meijer A, Kroes AC. Prolonged influenza virus infection during lymphocytopenia and frequent detection of drug-resistant viruses. The Journal of infectious diseases. 2009 May 15;199(10):1435-41.
6. Thompson WW, Shay DK, Weintraub E, Brammer L, Cox N, Anderson LJ, Fukuda K. Mortality associated with influenza and respiratory syncytial virus in the United States. Jama. 2003 Jan 8;289(2):179-86.
7. Meijer A, Lackenby A, Hungnes O, Lina B, van der Werf S, Schweiger B, Opp M, Paget J, van de Kassteele J, Hay A, Zambon M. Oseltamivir-resistant influenza virus A (H1N1), Europe, 2007–08 season. Emerging infectious diseases. 2009 Apr;15(4):552.
8. Berkman BE. Mitigating pandemic influenza: the ethics of implementing a school closure policy. Journal of Public Health Management and Practice. 2008 Jul 1;14(4):372-8.
9. Shinde V, Bridges CB, Uyeki TM, Shu B, Balish A, Xu X, Lindstrom S, Gubareva LV, Deyde V, Garten RJ, Harris M. Triple-reassortant swine influenza A (H1) in humans in the United States, 2005–2009. New England Journal of Medicine. 2009 Jun 18;360(25):2616-25.
10. Centre for disease control and prevention, https://www.cdc.gov/h1n1flu/, accessed on July 22, 2020
11. Martinez-Arroyo M, Sucar LE. Learning an optimal naive bayes classifier. In18th International Conference on Pattern Recognition (ICPR'06) 2006 Aug 20 (Vol. 3, pp. 1236-1239). IEEE.
12. Zhang H, Li D. Naïve Bayes text classifier. In2007 IEEE International Conference on Granular Computing (GRC 2007) 2007 Nov 2 (pp. 708-708). IEEE.
13. Kubat M. An introduction to machine learning. Springer International Publishing AG; 2017.
14. VanderPlas J. Python data science handbook: Essential tools for working with data. " O'Reilly Media, Inc."; 2016 Nov 21.
15. Centers for Disease Control and Prevention (CDC. Outbreak of swine-origin influenza A (H1N1) virus infection-Mexico, March-April 2009. MMWR. Morbidity and mortality weekly report. 2009 May 8;58(17):467.
16. Patient A. Swine influenza A (H1N1) infection in two children—Southern California, March–April 2009. Morbidity and Mortality Weekly Report. 2009 Apr 21;58.
17. World Health Organization. Global alert and response, pandemic (H1N1) 2009, frequently asked questions: what is phase 6.
18. Peiris JM, Poon LL, Guan Y. Emergence of a novel swine-origin influenza A virus (S-OIV) H1N1 virus in humans. Journal of Clinical Virology. 2009 Jul 1;45(3):169-73.
19. Louie JK, Acosta M, Winter K, Jean C, Gavali S, Schechter R, Vugia D, Harriman K, Matyas B, Glaser CA, Samuel MC. Factors associated with death or hospitalization due to pandemic 2009 influenza A (H1N1) infection in California. Jama. 2009 Nov 4;302(17):1896-902.
20. Jain S, Kamimoto L, Bramley AM, Schmitz AM, Benoit SR, Louie J, Sugerman DE, Druckenmiller JK, Ritger KA, Chugh R, Jasuja S. Hospitalized patients with 2009 H1N1 influenza in the United States, April–June 2009. New England journal of medicine. 2009 Nov 12;361(20):1935-44.
21. Chowell G, Bertozzi SM, Colchero MA, Lopez-Gatell H, Alpuche-Aranda C, Hernandez M, Miller MA. Severe respiratory disease was concurrent with the circulation of H1N1 influenza. New England journal of medicine. 2009 Aug 13;361(7):674-9.
22. Rello J, Rodríguez A, Ibañez P, Socias L, Cebrian J, Marques A, Guerrero J, Ruiz-Santana S, Marquez E, Del Nogal-Saez F, Alvarez-Lerma F. Intensive care adult patients with severe respiratory failure caused by Influenza A (H1N1) v in Spain. Critical care. 2009 Oct 1;13(5):R148.
23. Mollura DJ, Asnis DS, Crupi RS, Conetta R, Feigin DS, Bray M, Taubenberger JK, Bluemke DA. Imaging findings in a fatal case of pandemic swine-origin influenza A (H1N1). American Journal of Roentgenology. 2009 Dec;193(6):1500-3.
24. Agarwal PP, Cinti S, Kazerooni EA. Chest radiographic and CT findings in novel swine-origin influenza A (H1N1) virus (S-OIV) infection. American Journal of Roentgenology. 2009 Dec;193(6):1488-93.
25. Rupali M, Amit P. A Review Paper on General Concepts of Artificial Intelligence and Machine Learning. International Advanced Research Journal in Science, Engineering and Technology. 2017;4:79-82.
26. Bhatt D, Vyas D, Kumhar M, Patel A. Swine Flu Prediction Using Machine Learning. information and Communication Technology for Intelligent Systems 2019 (pp. 611-617). Springer, Singapore.
27. Pineda AL, Ye Y, Visweswaran S, Cooper GF, Wagner MM, Tsui FR. Comparison of machine learning classifiers for influenza detection from emergency department free-text reports. Journal of biomedical informatics. 2015 Dec 1;58:60-9.
28. Uddin S, Khan A, Hossain ME, Moni MA. Comparing different supervised machine learning algorithms for disease prediction. BMC Medical Informatics and Decision Making. 2019 Dec;19(1):1-6.