

# Machine Learning Approaches for the Diagnosis of H1N1 and COVID-19

Ahmet E. Topcu<sup>1</sup>, Aymen I. Zreikat<sup>1</sup>, Ersin Elbasi<sup>1\*</sup>

Submitted: 18/09/2023

Revised: 17/11/2023

Accepted: 29/11/2023

**Abstract:** COVID-19 and H1N1 are infections with similar symptoms that are often confused. These dis-eases cause adverse effects for individuals in the fields of economy, education, health, and technology. This study was planned to distinguish these two diseases by identifying the similarities between COVID-19 and H1N1 influenza. They are both pandemics that have caused significant distress worldwide. In this study, clinical data obtained from individuals diagnosed with H1N1 or COVID-19 were obtained for the analysis and an array of various machine learning algorithms were utilized for the categorization of that data. The results obtained from 23 different machine learning algorithms were compared and evaluated, indicating that our model success-fully classified the two diseases. The multilayer perceptron neural network algorithm displayed 95.87% accuracy. While sequential minimal optimization had 90.7% accuracy, the decision table algorithm had 90.91% accuracy. Using these three different algorithms, we achieved accuracy above 90% for the prediction of the studied diseases.

**Keywords:** algorithms, classification, COVID-19, H1N1, machine learning, pandemic

## 1. Introduction

The World Health Organization (WHO) has described influenza as a common seasonal disease that affects people with some common symptoms such as muscle pain, fever, and headache [1]. It might also cause some symptoms in the upper respiratory tract such as sneezing and coughing. In addition to the mentioned symptoms for standard influenza, COVID-19, caused by a novel strain of coronavirus, may involve other symptoms such as a lack of smell and taste. In general, however, there are some common symptoms for influenza and COVID-19. Consequently, it may be difficult to distinguish whether an illness is influenza or COVID-19, especially as the effects may depend on an individual's specific immunity to such viruses. Therefore, in all circumstances, to avoid such viruses, people should consider certain general preventive measures such as wearing masks, washing their hands, maintaining physical distance, and keeping rooms properly ventilated. These types of diseases have severe effects for older adults suffering from chronic diseases such as cancer, chronic respiratory system illnesses, and cardiovascular diseases.

These diseases also have negative effects for children and pregnant women. In short, both of these diseases should be considered as a threat to all people in the world of all ages and it is vital to control them by maintaining the necessary

preventive measures and administering vaccines periodically to avoid any harmful consequences of the diseases for human health.

Based on the destructive effects of COVID-19 around the world, the WHO declared COVID-19 a pandemic in March 2020. H1N1 flu, on the other hand, is popularly known as swine flu. As per the Mayo Clinic's recent reports [2], the H1N1 strain of the influenza virus is considered to be the leading cause of seasonal flu cases. This particular virus is a mixture of viruses from pigs, birds, and human beings. "Swine flu" caused severe symptoms in the human respiratory system and the WHO proclaimed it to be a pandemic in 2009, subsequently declaring the end of the pandemic in 2010. The flu vaccine can now largely protect people from the harmful consequences of H1N1 for the human respiratory system during seasonal cases of influenza.

In brief, machine learning (ML), deep learning (DL), and artificial intelligence (AI) are three related concepts, but they are not identical to each other as some people might think. AI refers to the possibility that computers might act like human beings. On the other hand, ML is a subgroup of AI approaches where machines access large sets of data and learn how to extract some patterns from them with some important features. DL, in turn, is a subgroup of ML where additional ML algorithms train deep neural networks to achieve more accurate results.

In ML, a classification concept is used whereby sets of data are classified into different classes using different ML algorithms. These classifications can be binary or multi-class. In binary classification, the outcome can be either "true" or "false." For example, imagine that we need to

<sup>1</sup> College of Engineering and Technology, American University of the Middle East, Kuwait

ORCID: 0000-0003-1929-5358

<sup>2</sup> College of Engineering and Technology, American University of the Middle East, Kuwait

ORCID: 0000-0003-4900-497X

<sup>3</sup> College of Engineering and Technology, American University of the Middle East, Kuwait

ORCID: 0000-0002-8603-1435

\* Corresponding Author Email: ersin.elbasi@aum.edu.kw

classify patients according to a specific disease, such as COVID-19. The classifier will train the given inputs regarding the patients to decide whether a particular patient has COVID-19 or not. In multi-class classification, multiple classes are considered, but each sample of data is assigned to only one target or one class.

ML represents an important branch of data science, offering the ability to resolve data-related challenges with the understanding and analysis of larger datasets. A few of the valuable applications of ML approaches include the sorting and filtering of email spam messages, “friend” suggestions on social media platforms, tools for making stock market predictions, and internet-based recommendation engines. When resolving such problems with the use of ML algorithms, problems are divided into smaller groups as appropriate, allowing for the selection of the most suitable ML algorithm for the needs at hand. Examples of these subcategorizations of ML applications are as follows [3]:

- Classification problems: These are problems involving datasets with fixed outputs like yes/no and true/false
- Anomaly detection problems: These are problems involving datasets that contain anomalies or reveal abnormal behavior in contrast to expected trained patterns
- Regression problems: These are problems involving datasets compiled with the expectation of answering questions related to quantities
- Clustering problems: These are problems involving datasets that are considered according to their organization and behaviors
- Reinforcement problems: These are problems involving decisions that should be made according to prior learning experiences

An array of different ML algorithms are able to provide successful categorizations according to the provided data and specified requirements. In these approaches, the initial step is the collection of an adequate volume of data for the training of the model. These data then undergo preparation for being processed by the selected ML algorithm because not all selected data will be appropriately structured. Processes applied at this point can eliminate irrelevant data that will not be necessary in the course of the ML algorithm’s learning process. Furthermore, many different ML algorithms have been introduced to date, and they are not all equally suitable for all potential problems or analyses. Therefore, in the next step of establishing ML models, it is necessary to choose the best algorithm for the particular dataset or situation being considered. All such algorithms need to be provided with initial attributes or variables, and models will subsequently need to undergo training with the application of some of the selected data.

Datasets to be used as input in such models may be obtained from other open-source datasets, from IoT sensors, or from internal collection by employees in hospitals or medical laboratories. With these health-related data, the ML model can undertake the process of data analysis in order to select the most suitable data and sort them into specific classification categories with processes of clustering, regression, and prioritization. Employing classification algorithms allows the ML model to learn and identify the relevant data to an adequate level. Upon the analysis and arrangement of the selected datasets with support from the chosen ML algorithms, models can then be expected to offer a predicted diagnosis as a final result.

The remainder of this work is divided into four further sections. A review of the literature is offered in Section 2, while Section 3 explains the specific ML algorithms used in this research. Subsequently, the experimental results are described in detail in Section 4 and the conclusions of the study are outlined in Section 5.

## 2. Literature Review

The coronavirus family of viruses causes, among other diseases, COVID-19, which was identified in Wuhan, China, in December 2019. From that point onward, the virus spread quickly around the world. It causes illness in humans ranging from minor symptoms to severe symptoms that may cause death based on underlying medical conditions and the immunity levels of exposed people. Consequently, researchers have become interested in studying this disease from different perspectives to help the medical community find appropriate medications or vaccines to save the lives of those who have been infected or have a risk of becoming infected by this virus as well as stopping the spread and mutation of the virus. H1N1 and COVID-19 have both previously been classified with the use of ML algorithms [4]. For example, to accurately diagnose patients infected with COVID-19, Pathak et al. [5] confirmed that radiological examinations such as chest computed tomography (CT) can be efficient in the early detection of the disease.

A deep bidirectional model has been suggested with the multi criteria adaptive differential evolution (MADE) algorithm. Based on the analyzed dataset with the provided comparative results for different performance parameters such as accuracy, area under the curve (AUC), F-measure, and sensitivity, authors have claimed that such a model can be used for COVID-19 classification. For example, Wang et al. [6] utilized ML algorithms to analyze datasets related to the severity of COVID-19 infection by studying the co-association between COVID-19 and comorbid diseases. Using the random forest classifier technique and based on given performance parameters, these authors claimed that the prediction accuracy for COVID-19 symptoms increased to about 92%. Utilizing the concepts of ML, data mining, and the internet of things (IoT), Nalavade [7] collected

information about patients from the health authorities in India. Through the training of the obtained dataset based on 5000 patients, early prediction of symptoms could be achieved. If a patient's symptoms are observed daily from day 1 to day 4, fast prediction of the disease can be achieved.

A comprehensive literature review including studies and available datasets regarding the history and origin of COVID-19 was presented by Vidushee and Rakhi [8]. Due to the extensive distribution of COVID-19 worldwide, in a book chapter, Jain et al. [9] provided information about the fast prediction of diseases in early stages using different technologies. For example, it is possible that AI algorithms may help in the fast discovery of treatment for diseases. On the other hand, deep learning neural networks may also help in COVID-19 diagnosis. Robotics technology is also utilized in some countries where the virus has spread very fast in order to eliminate humans' direct contact with the virus. According to the recommendations offered by Jain et al., real-time data regarding COVID-19 information and updates can be found on the Kaggle and GitHub websites.

Because the guidelines used in the diagnosis and treatment of COVID-19 are usually in textual form, a new system called H1N1Diagnose was proposed with two stages [10]. In the first stage, a machine-accessible format of the guidelines called GLIF is used, and in the second stage, an execution engine is proposed to process the guidelines. This system was found to be beneficial for practitioners and the health industry to analyze patients' data and provide an appropriate diagnosis in a timely manner. In a study by Elembaby et al. [11], a gene regulatory network (GRN) was created based on the genetic characteristics of cells infected by H1N1 disease. The authors of that work proposed two methodologies. The first methodology considered only synthetic data in evaluating different algorithms such as Pearson's correlation, mutual information (MI), MRNET, ARCENE, CLR, and GENIE3. The second methodology entailed an examination of ANOVA tests of all algorithms to identify the most critical gene causing H1N1 infection. A survey of Lie group machine learning was presented by Lu and Li [12], who demonstrated Lie group machine learning within three classes: supervised, unsupervised, and semi-supervised. The main objective of that survey was to provide researchers with more information about Lie group machine learning techniques and applications to help them conduct research in this area. Arslan and Aygün [13], on the other hand, undertook a comparative evaluation of various ML algorithms including AdaBoost and random forest, support vector machine (SVMs), the k-nearest neighbor algorithm, artificial neural networks, and the naive Bayes approach.

Algorithms evaluated in a previous work were considered with a dataset of information from 10,000 patients suffering from the main symptoms of COVID-19, including shortness of breath, cough, sore throat, and headache. As per the provided analysis and results, it was shown that the artificial

neural network algorithm outperformed other algorithms in terms of accuracy in detecting the disease, with accuracy reaching 87%. In comparison, the other algorithms only gave 84% accuracy. Via medical images, including chest X-rays and CT results, a general uncertainty awareness framework was introduced using four different neural network algorithms [14]. These authors further applied the extracted features from X-ray and CT images to the VGG16, ResNet50, DenseNet121, and InceptionResNetV2 algorithms and, based on that, COVID-19 cases were detected. Based on the analysis and comparative results, it was concluded that neural network models always give better results concerning accuracy. This study also showed that uncertainty estimates are higher for CT images compared to X-ray images.

A review of ML algorithms was also undertaken [15] in consideration of the difficulties researchers face in processing COVID-19 data, such as the effects of datasets, utilizing better ML algorithms for analysis, and focusing on research specific to COVID-19 diagnoses and issues. As China was the origin of COVID-19, that country delivered vital information to the rest of the world for detecting, preventing, and treating the virus. Based on data published by the Xinjiang Health Commission, researchers have made efforts to analyze the data and confirm COVID-19-positive cases. Such results were expected to be helpful for the health industry to overcome the pandemic in the Xinjiang region of China. Data from 60 infected and 480 healthy individuals were investigated in another study using ML classifiers based on artificial intelligence [16]. Different algorithms were applied for the classifier, such as decision tree, logistic regression (LR), SVM, and k-nearest neighbor algorithms. As dry cough samples were collected for the analysis, this research was considered to be novel because it facilitated a better investigation of the diagnosis of the disease. Utilizing ML algorithms and techniques, other researchers investigated the relationship between blood test results and confirmed COVID-19 cases using a dataset obtained from a Brazilian hospital [17]. The results showed that the best accuracy was achieved by using the SVM algorithm in contrast to others. These authors concluded no strong relationship between normal blood tests and COVID-19 detection.

Other scholars have devoted attention to the classification of H1N1 with the application of gene expression techniques [18-22]. For example, in one such study, two different optimization algorithms were considered together with a gene expression database with the aim of achieving high levels of accuracy [18]. Specifically, the SVM and neural network algorithms were compared in that study and it was reported that neural networks yielded accuracy of 81.81%, surpassing the performance of the other considered algorithms. In another study, principal component analysis was applied in classification processes with the aim of

analyzing various cDNA viral segments from influenza A [19]. By considering a variety of performance measures, these authors found that the preprocessing time could be decreased from 1.5 hours to 5 minutes with their suggested approach. In another relevant work [20], the M3 lung deep learning system was proposed as a helpful algorithm using a multi-task, multi-slice approach for distinguishing among cases of H1N1, COVID-19, community-acquired pneumonia, and healthy individuals. With the aim of confirming the model's success in the provision of both statistical information and assistance for clinicians in the diagnostic process, experiments were undertaken with 743 unique cases while applying both slice-level and patient-level classification. In other re-cent research [21], the primary goal was enhancing the analytical process and the real-life application of statistics for patients admitted to hospital emergency departments. To reach that goal, an orthogonal transformation algorithm was proposed, which the authors referred to as the critical contribution index. The findings of this study revealed an improvement in predictive accuracy of 7.1%. In another relevant study [22], the authors introduced a multi-channel segmentation algorithm for use in effectively monitoring patients' health outcomes and particularly in cases where fluctuations are observed in data distributions. The new algorithm was inspired by both Fisher's linear discriminant analysis and the multivariate hidden Markov model. In the evaluation of experimental data obtained from a cohort used with the human viral challenge model, disrupted waking and sleeping patterns following contact with the H1N1 influenza pathogen were identified. Thus, the results of the experiments suggested that the new algorithm was efficient in the evaluation of periodic changes in data distributions and that it could be effectively applied in hospital emergency departments.

Other researchers [23-25] explored different algorithms with the aim of ensuring the timely prediction of a diagnosis of COVID-19 and thus limiting the spread of the disease from those patients to other individuals. For example, with the application of ML, the role of genetic variations in patterns of comorbidity was considered, utilizing patients' phenotypes together with the random forest classifier. The findings of those experiments suggested that the current presence of symptoms may be more important than the patient's history in efforts to make accurate predictions of COVID-19. In response to the global spread of the pandemic, other scholars examined a dataset with the application of convolutional neural network algorithms and contrast limited adaptive histogram equalization [24]. Those authors demonstrated increased accuracy in predicting COVID-19 with the selected datasets. In another relevant study [25], it was suggested that the protocol for limiting the spread of COVID-19 remains dependent on various factors including the symptoms, travel histories, and direct or extended contact with individuals who have already contracted the disease. However, typical testing methods

utilize nasal swab specimens with subsequent laboratory blood tests for further confirmation. Researchers have accordingly stressed the importance of applying deep learning methods while processing laboratory findings such as chest X-ray results to achieve earlier disease prediction. With this experimental approach, the level of diagnostic accuracy rose to 91.67% [24].

### 3. Methodology

The ML solution suggested here is essential for classifying data and providing an effective solution for distinguishing between COVID-19 and H1N1 influenza. The main idea is to find the most suitable algorithms to categorize the diseases based on patient data, including 41 different parameters. The correct categorization of the factors results in the building of an accurate model. We used different algorithms to compare them in this re-search, and we then obtained results using the one that gave the best comparative out-come. We considered 41 different types of patient data as parameters in the analysis, which is important for comparing COVID-19 and H1N1.

With the aim of facilitating the specific diagnoses of COVID-19 and H1N1, this work was carried out using data obtained from 1467 individuals, 30% having a diagnosis of COVID-19 while 70% had been officially diagnosed with H1N1. Figure 1 illustrates the data types selected for analysis. An assortment of categories of patient data were analyzed, with variables including age and gender, results of blood or tissue sample testing, duration of the illness, reported symptoms, laboratory test results, and underlying risk factors. These data were evaluated with ML algorithms for classification, including the naive Bayes classifier (NBC), Bayesian network (BN), multilayer perceptron (MP), locally weighted learning (LWL), and random forest (RF) algorithms. MP algorithms utilize artificial neural networks, which will not generate feedforward loops between the nodes. In all cases, training data constituted 60% of the total data while 40% of the data were applied for testing.

Symptoms & Lab	CT scan results (Inconclusive, negative, positive), Xray results (negative, positive), smoking results*, Number affected lobes, Asymptomatic*, Diarrhea*, Fever*, Coughing*, Shortness of breath*, Sore throat*, Temperature, Hematocrit, Urea, Fatigue*, Cancer*		
Blood or tissue	Neutrophil, neutrophil Categorical*, serum levels of white blood cell, serum levels of white blood cell category* lymphocytes, lymphocytes category*, Platelets, Creative Protein Levels, Creative Protein Levels category*, Eosinophils, Red blood cells, Hemoglobin, Procalcitonin		
Period	Duration of illness, Days to death	Human	Age, gender
Risk factors	asthma, athero, immuno, diabetes, respiratory, liver disorder, obesity, hypertension, heart disease		

**Fig. 1.** Patient dataset (Blood or tissue: \*low, normal, high; Symptoms & Lab: \*yes, no).

In this study, 23 different machine learning algorithms were compared and evaluated to find better algorithms by successfully classifying the two diseases. The multilayer perceptron neural network algorithm displayed sequential minimal optimization had 90.7% accuracy. The decision

table algorithm also had 90.91% accuracy. These three different algorithms have better accuracy results compared with other machine learning algorithms for the prediction of the studied H1N1 and COVID-19. In the following sections, these algorithms which have higher accuracy results are explained:

### 3.1. Multilayer Perceptron Algorithm

The multilayer perceptron (MP) algorithm represents a wider category of ANNs capable of learning about how linear and nonlinear data are connected. These algorithms comprise various layers, which include input, hidden, and output layers, and they will produce output with the use of feedforward neural networks. Hidden layers of a randomly selected number perform the computational processes between input and output layers. MP algorithms, similarly to feedforward networks, operate on the basis of data flowing from input layers to output layers. In these cases, the neurons present within the MP algorithms undergo training with the application of backpropagation learning algorithms.

---

#### Algorithm 1: Multilayer perceptron algorithm

---

```

CHOOSE the initial weight vector
    Initialize minimization approach
REPEAT
    FOR all ((~x, ~d) ∈ D
        Apply ~x to the network
        Calculate network output
        Calculate ∂e(~x)
    END FOR
    Calculate ∂E(D)
    Add all weights using training forms
    Perform one update step of the minimization approach
UNTIL error converged

```

---

### 3.2. Simple Logistic Regression

Simple logistic regression is analogous to linear regression and exploits other variables to estimate a binary variable. It determines the numerical relationship between two such variables. The predicted variable must be binary, and the data must meet the other itemized assumptions. This is a commonly used algorithm for ML and it builds a block for neural networks. Simple logistic regression is used when two distinct values are pre-sent, namely a nominal variable that is the dependent parameter and a measurement variable that is the independent value.

---

#### Algorithm 2: Simple logistic regression algorithm

---

```

FUNCTION grad (Predictor parameter, target parameter,
weights)
    Calculate gradient descent
    Parameter=weight + rate x gradient descent
RETURN parameter
Normalize dataset
REPEAT
    Weight = grad (parameter list)
    Update weights
UNTIL convergence
m=product of the predictor variables
Update weights
Prediction limit= sigmoid function (m)
PREDICT target class

```

---

### 3.3. Decision Tree

Decision trees (DTs) are commonly employed for the creation of training models through the estimation of classes or values of targeted variables after straightforward decision rules shaped according to previous data have been learned. DTs are particularly helpful in solving problems that involve regression or classification processes. With this type of algorithm, the root is located at the top and subsequently splits into a number of nodes. All conditions for these trees will be checked, and then the process advances to the next node that happens to be related to the decision being considered. DTs possess decision nodes and leaf nodes, with decisions being finalized at the nodes. Leaf nodes serve as outputs of the decisions that are being made and they do not split into any further branches.

---

#### Algorithm 3: Decision tree algorithm

---

```

INPUT: Data warehouse K, Attributes vector B, Class list
C
Build root node X
IF data vector for each record in K belongs to Class C
    THEN return X
FIND optimal new split
FOR each output j of tree
    Kj vector for an optimal outcome
    IF Kj is empty
        THEN add leaf node into the tree

```

---

```

ELSE
    Add the node returned by the function render
tree
ENDFOR
OUTPUT: A decision tree for classification

```

Figure 2 presents the step of the model using ML to process and analyze assorted types of patient data. After that, the data are subjected to classification, and parts of the dataset will be selected for the training of the model(s) with ML algorithms. As a subsequent step, the model will use this information to make a prediction regarding whether patients have H1N1 influenza, COVID-19, or neither.

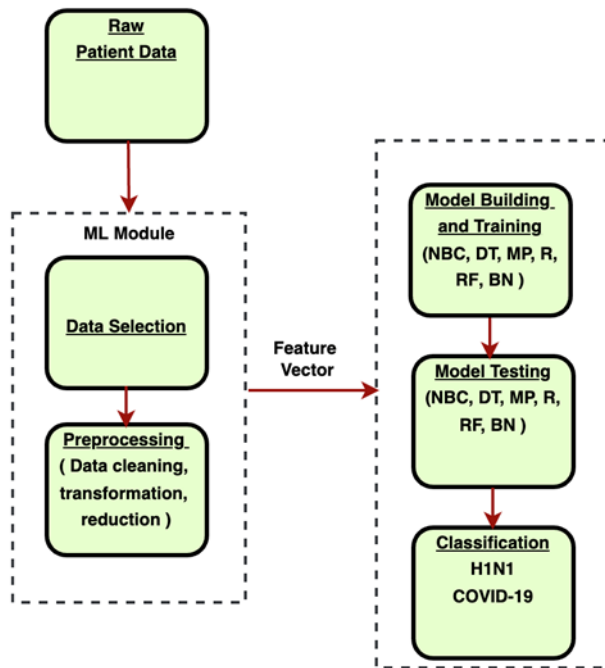


Fig. 2. Model for H1N1 and COVID-19 prediction.

## 4. Results

### 4.1. Data Classification and Rates

Classification of diseases as H1N1 or COVID-19 is the desired outcome of this study. In the literature, there are several classification algorithms proposed for medical data analysis. In this work, we used 1481 rows of patient data with 41 attributes. The attribute list included patient information (age, sex, region, etc.), symptoms (fever, coughing, sore throat, temperature, etc.), risk factors (diabetes, asthma, liver disease, etc.), and lab values (CT scans, serum levels, X-ray reports, procalcitonin, etc.). The first phase of classification in this work was data preprocessing. Data were then converted to a structured format for classification and several ML algorithms were applied to classify data into the categories of H1N1 and COVID-19. The Bayes network (BN), naive Bayes classifier (NBC), logistic (L), multilayer perceptron (MP), stochastic

gradient descent (SGD), simple logistic (SL), sequential minimal optimization (SMO), IBK, KSTAR, locally weighted learning (LWL), AdaBoost (AB), regression (R), multiclass (MC), randomizable filtered classifier (RFC), decision table, PART, Hoeffding tree (HT), J48, random forest (RF), random tree (RT), and REP algorithms were considered. The true positive (TP) and false positive (FP) rates for COVID-19 and H1N1 are displayed in Table 1 together with additional statistical information including recall, precision, F-measure values, areas of receiver operating characteristic (ROC) curves, the Matthews correlation coefficient (MCC), and precision-recall (PRC) area values. TP and FP rates are seen to be higher for the H1N1 class than the COVID-19 class for all methods except IBK classification [28].

The TP rate represents the correct identification of data, such as classifying data as COVID-19 that do in fact represent COVID-19. The FP rate represents the incorrect classification of data, such as classifying data as COVID-19 that actually represent H1N1.

$$TP \text{ rate} = \frac{TP}{TP+FN} \quad (1)$$

$$FP \text{ rate} = \frac{FP}{FP+TN} \quad (2)$$

Precision is another metric for imbalanced classification. Precision rates signify the numbers of correct positive predictions. In contrast, recall rates signify the numbers of correct positive predictions from among the total number of all positive predictions that were made. The F-measure is a combination of precision and recall measurement rates. The minimum possible value of the F-measure is 0 and the maximum value is 1, which is the perfect ratio. The MCC is used in two-class classification problems with true positive, false positive, true negative, and false negative data. It is very effective, even for two datasets with a large difference in size.

$$Precision \text{ rate} = \frac{TP}{TP+FP} \quad (3)$$

$$Recall \text{ rate} = \frac{TP}{TP+FN} \quad (4)$$

$$F - \text{measure rate} = \frac{2 \times Precision \times Recall}{Precision+Recall} \quad (5)$$

$$MCC \text{ rate} = \frac{TP \times TN - FP \times FN}{\sqrt{(TF+FP)(TP+FN)(TN+FP)(TN+FN)}} \quad (6)$$

## 4.2. Accuracy and Performance

Table 2 presents the accuracy, build time, and test time for each ML algorithm. Accuracy is one of the most commonly used measurement metrics in ML classification and clustering algorithms. It represents the total number of correctly classified data divided by the total number of instances. The MP algorithm is a type of neural network algorithm and it gives 95.87% accuracy. In addition to the MP approach, the SL and decision table algorithms give more than 90% accuracy. NBC has 0.01, SMO has 0.82, and

R has built time of 2.03 for creating a model for classification. LWL has 2.29 testing time, RF has 1.95, MP has 0.05, and L has 0.01. Accuracy is the most important measure in selecting an algorithm, but build time and test time are also important measurements according to the application..

**Table 1.** TP rate, FP rate, precision, recall, F-measure, MCC, ROC area, and PRC area values for ML algorithms.

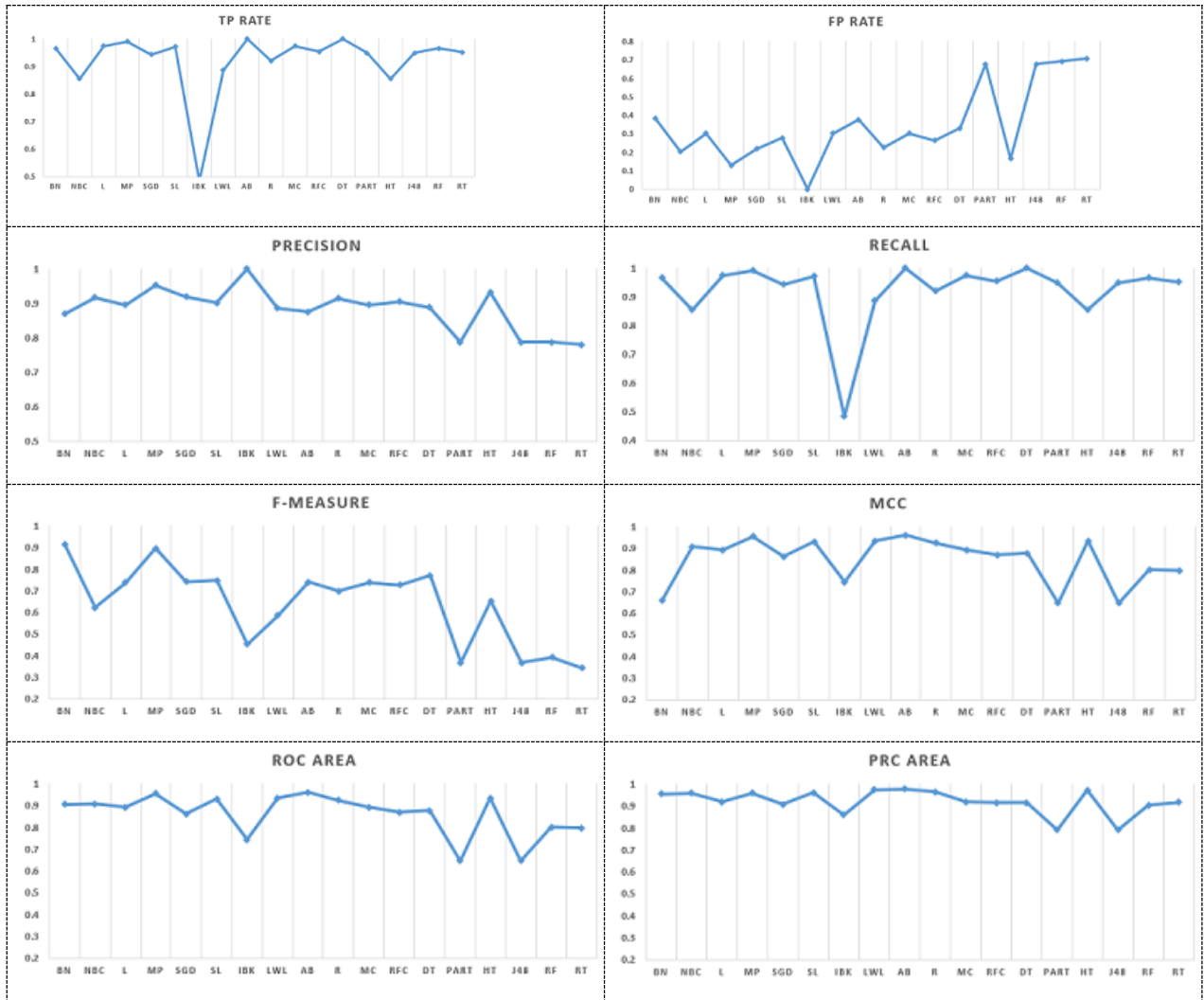
Method	TP Rate	FP Rate	Precision	Recall	F-Measure	MCC	ROC Area	PRC Area	Class
BN	0.966	0.383	0.869	0.966	0.915	0.657	0.905	0.954	H
	0.617	0.034	0.872	0.617	0.722	0.657	0.905	0.822	C
NBC	0.855	0.203	0.917	0.855	0.885	0.621	0.907	0.958	H
	0.797	0.145	0.675	0.797	0.731	0.621	0.907	0.852	C
L	0.974	0.301	0.895	0.974	0.933	0.737	0.891	0.919	H
	0.699	0.026	0.912	0.699	0.791	0.737	0.891	0.870	C
MP	0.991	0.128	0.953	0.991	0.972	0.895	0.955	0.959	H
	0.872	0.009	0.975	0.872	0.921	0.895	0.955	0.955	C
SGD	0.943	0.218	0.919	0.943	0.931	0.741	0.862	0.908	H
	0.782	0.057	0.839	0.782	0.809	0.741	0.862	0.716	C
SL	0.972	0.278	0.902	0.972	0.936	0.748	0.930	0.961	H
	0.722	0.028	0.906	0.722	0.803	0.748	0.930	0.898	C
SMO	0.980	0.286	0.901	0.980	0.939	0.760	0.847	0.897	H
	0.714	0.020	0.931	0.714	0.809	0.760	0.847	0.744	C
IBK	0.484	0.000	1.000	0.484	0.653	0.453	0.744	0.859	H
	1.000	0.516	0.424	1.000	0.595	0.453	0.744	0.428	C
KSTAR	0.946	0.414	0.858	0.946	0.900	0.594	0.747	0.856	H
	0.586	0.054	0.804	0.586	0.678	0.594	0.747	0.612	C
LWL	0.886	0.301	0.886	0.886	0.886	0.585	0.934	0.973	H
	0.699	0.114	0.699	0.699	0.699	0.585	0.934	0.874	C
AB	1.000	0.376	0.875	1.000	0.934	0.739	0.960	0.978	H
	0.624	0.000	1.000	0.624	0.769	0.739	0.960	0.893	C
R	0.920	0.226	0.915	0.920	0.918	0.698	0.924	0.964	H
	0.774	0.080	0.786	0.774	0.780	0.698	0.924	0.828	C
MC	0.974	0.301	0.895	0.974	0.933	0.737	0.891	0.919	H
	0.699	0.026	0.912	0.699	0.791	0.737	0.891	0.870	C
RFC	0.954	0.263	0.905	0.954	0.929	0.727	0.870	0.915	H

	0.737	0.046	0.860	0.737	0.794	0.727	0.870	0.733	C
DTable	1.000	0.331	0.889	1.000	0.941	0.771	0.876	0.914	H
	0.669	0.000	1.000	0.669	0.802	0.771	0.876	0.820	C
PART	0.949	0.677	0.787	0.949	0.860	0.366	0.647	0.791	H
	0.323	0.051	0.705	0.323	0.443	0.366	0.647	0.438	C
HT	0.855	0.165	0.932	0.855	0.892	0.652	0.933	0.971	H
	0.835	0.145	0.685	0.835	0.753	0.652	0.933	0.886	C
J48	0.949	0.677	0.787	0.949	0.860	0.366	0.647	0.791	H
	0.323	0.051	0.705	0.323	0.443	0.366	0.647	0.438	C
RF	0.966	0.692	0.787	0.966	0.867	0.392	0.800	0.904	H
	0.308	0.034	0.774	0.308	0.441	0.392	0.800	0.630	C
RT	0.952	0.707	0.780	0.952	0.858	0.342	0.796	0.917	H
	0.293	0.048	0.696	0.293	0.413	0.342	0.796	0.576	C
REP	0.932	0.624	0.798	0.932	0.859	0.382	0.767	0.869	H
	0.376	0.068	0.676	0.376	0.483	0.382	0.767	0.563	C

**Table 3.** TP rate, FP rate, precision, recall, F-measure, MCC, ROC area, and PRC area values for MP algorithm with different training set sizes.

Training Set	TP Rate	FP Rate	Precision	Recall	F-Measure	MCC	ROC Area	PRC Area	Class
10%	0.954	0.461	0.852	0.954	0.900	0.569	0.829	0.890	H
	0.539	0.046	0.807	0.539	0.646	0.569	0.829	0.752	C
20%	0.960	0.255	0.912	0.960	0.935	0.744	0.914	0.931	H
	0.745	0.040	0.873	0.745	0.804	0.744	0.914	0.772	C
30%	0.989	0.212	0.926	0.989	0.957	0.832	0.945	0.949	H
	0.788	0.011	0.965	0.788	0.867	0.832	0.945	0.937	C
40%	0.989	0.192	0.930	0.989	0.959	0.845	0.936	0.929	H
	0.808	0.011	0.966	0.808	0.880	0.845	0.936	0.936	C
50%	0.983	0.219	0.918	0.983	0.949	0.813	0.897	0.897	H
	0.781	0.017	0.948	0.781	0.856	0.813	0.897	0.900	C
60%	0.981	0.160	0.941	0.981	0.961	0.853	0.949	0.953	H
	0.840	0.019	0.944	0.840	0.889	0.853	0.949	0.940	C
70%	0.997	0.129	0.952	0.997	0.974	0.904	0.975	0.982	H
	0.871	0.003	0.991	0.871	0.927	0.904	0.975	0.969	C
80%	0.995	0.127	0.955	0.995	0.975	0.904	0.932	0.935	H
	0.873	0.005	0.986	0.873	0.926	0.904	0.932	0.940	C
90%	0.990	0.136	0.944	0.990	0.967	0.886	0.956	0.972	H
	0.864	0.010	0.974	0.864	0.916	0.866	0.956	0.954	C





**Fig. 3.** Rates for the H1N1 class for each classification algorithm.

**Table 2.** Accuracy, build time, and test time for classification algorithms

Training Set	Accuracy	Build Time	Test Time
BN	86.98	0.08	0
NBC	83.88	0.01	0.06
L	89.88	-	0.01
MP	95.87	113.54	0.05
SGD	89.88	0.58	0.02
SL	90.29	0.06	0.02
SMO	90.7	0.82	0.04
IBK	62.6	-	0.41
KSTAR	84.71	0	1.36
LWL	83.47	0	2.29
AB	89.67	0.01	0
R	88.02	2.03	0.05
MC	89.88	0.52	0
RFC	89.46	0.18	0.2

DTable	90.91	0.85	0
PART	77.69	0.86	0
HT	84.92	0.18	0.01
J48	77.69	0.33	0.01
RF	78.51	20.89	1.95
RT	77.07	0.46	0.03
REP	77.89	0.34	0.01

Table 3 shows the rates for different training sets with neural network algorithms. For example, if we use 10% of the data for training, the TP rate is 0.954 for the H1N1 class and 0.539 for COVID-19. It is seen that using 80% training data gives the best results for a neural network. When we use 80% of the data for training in the MP algorithm, the TP rate is 0.995 and the FP rate is 0.873.

### 4.3. Multilayer Perceptron

Table 4 demonstrates the accuracy, build time, and test time for training sets ranging in size from 10% to 90% for a neural network algorithm. If we use 10% of the data for training, accuracy is 84.39%; for other set sizes, accuracy is more than 90%. The best accuracy is 96.25% if we use 80% of the data for training. Build time for the MP algorithm is more than 110 seconds for all training sets. Testing a network takes less time than building a network, requiring 0.01 seconds if we use 90% of the data for training [4, 28].

**Table 4.** Accuracy, build time, and test time for neural network algorithm.

Training Set	Accuracy	Build Time	Test Time
10%	84.39	111.34	0.22
20%	90.29	112.12	0.07
30%	93.48	111.85	0.07
40%	93.86	110.9	0.05
50%	92.5	117.26	0.05
60%	94.21	113.54	0.03
70%	96.14	114.02	0.03
80%	96.25	112.88	0.04
90%	95.24	112.82	0.01

Figure 3 shows the TP rate, FP rate, precision, recall, F-measure, MCC, ROC area, and PRC area values for all ML classification algorithms for the H1N1 class. The IBK algorithm has lower performance than the others based on all considered measurements.

### 4.4. Measurement Techniques

Table 5 shows the measurement metrics for the ML algorithms. For example, for the Bayes network algorithm, the kappa statistics value is 0.6407, the mean absolute value is 0.192, and the root mean squared error value is 0.3151.

The MP algorithm gives better results than the other algorithms, as seen in Table 5. The mean absolute error value with the MP algorithm is 0.0487, which is the lowest error value obtained among all ML classification algorithms. We can formulate the error metrics as follows [29-32]:

$$k = \frac{p_0 - p_e}{1 - p_e} \quad (7)$$

Here,  $p_0$  represents actual and  $p_e$  represents expected values.

$$MAE = \sum_{i=1}^n |p_0 - p_e| \quad (8)$$

$$RMSE = \sqrt{\sum_{i=1}^n (p_0 - p_e)^2} \quad (9)$$

**Table 5.** Kappa statistics, mean absolute error, root mean squared error, relative absolute error, and root relative squared error for machine learning algorithms.

Metho d	Kapp a	MAE	RMS E	RAE	RRSE
BN	0.6407	0.192	0.3151	48.59	70.57
		0		%	%
NBC	0.6171	0.213	0.3843	53.84	86.07
		1		%	%
L	0.7262	0.142	0.2867	35.97	64.21
		1		%	%
MP	0.8928	0.048	0.1903	12.31	42.62
		7		%	%
SGD	0.7405	0.101	0.3182	25.62	71.26
		2		%	%
LWL	0.5853	0.221	0.3234	56.01	72.42
		2		%	%
R	0.6979	0.183	0.2997	46.49	67.13
		7		%	%
HT	0.6456	0.203	0.3753	51.45	84.05
		3		%	%
J48	0.3270	0.349	0.4219	88.54	94.48
		8		%	%

RF	0.3370	0.332	0.3958	84.09	88.66
		2		%	%

Machine learning algorithms formulate the problem and some algorithms create rules, such as the decision tree, random forest, and Hoeffding tree algorithms. In this work, thousands of rules were produced and some examples are as follows:

- IF {(age > 42) AND (Gender=F) AND (Fever=Yes) AND (Sore Throat=No) AND (Fatigue=No)} THEN Class=H1N1
- IF {(age > 42) AND (Gender=M) AND (Risk Factor=AD) AND (Fever=No) AND (Coughing=Yes) AND (Fatigue=No)} THEN Class=H1N1
- IF {(age <= 42) AND (Gender=F) AND (Risk Factor=A) AND (Fever=Yes) AND (Sore Throat=No) AND (Shortness of Breath=No)} THEN Class=H1N1
- IF {(age > 23) AND (Gender=M) AND (Neutrophil>11) AND (Serum level of White Blood Cell > 9.2) AND (lymphocytes Categorical=low) AND (C-Reactive Protein Levels>12.5) AND (CT Scan Result=Positive) AND (Temperature > 38)} THEN Class=COVID19
- IF {(Neutrophil Categorical=High) AND (Serum Level >= 14.95) AND (Lymphocytes Categorical=Normal) AND (Risk Factor=L) AND (Ground Glass Opacity=Yes) AND (Shortness of Breath=Yes)} THEN Class=H1N1

## 5. Conclusion

This work was designed with the aim of applying new ML algorithms to facilitate more accurate differentiation of COVID-19 and H1N1 influenza. A total of 41 different parameters were utilized in the analysis to obtain more accurate results. While analyzing the different algorithms, precision and accuracy performance measures were considered. The results obtained from 23 different ML algorithms were compared and evaluated. The demonstrated experimental results and analysis showed that, regarding precision, the IBK algorithm gave the worst performance compared to the other algorithms. Accuracy is also a significant measure of analysis; in this regard, accuracy, build time, and test time were studied for training set sizes for different algorithms. The MP neural network algorithm displayed 95.87% accuracy, while sequential minimal optimization and the decision table algorithm had 90.7% and 90.91% accuracy, respectively. Using these three different algorithms, we achieved accuracy above 90% for the prediction of the studied diseases. The results demonstrated that our model successfully classified H1N1 influenza and COVID-19.

### Author contributions

**Ahmet E. Topcu:** Conceptualization, Methodology,

Software, Data collection **Aymen I. Zreikat:** Data curation, Writing-Original draft preparation, and Validation. **Ersin Elbasi:** Software and Experiments.

### Conflicts of interest

The authors declare no conflicts of interest.

### References

- [1] World Health Organization (WHO). Available online: <https://www.who.int/> (accessed on 26 March 2022).
- [2] Mayo Clinic. H1N1 flu (swine flu). Available online <https://www.mayoclinic.org/diseases-conditions/swine-flu/symptoms-causes/syc-20378103> (accessed on 26 March 2022).
- [3] J. Alzubi, A. Nayyar, and A. Kumar, "Machine learning from theory to algorithms: an overview", *J. Phys. Conf. Ser.*, 1142, 2018.
- [4] E. Elbasi, A. Zreikat, S. Mathew and A. E. Topcu, "Classification of influenza H1N1 and COVID-19 patient data using machine learning", *44th International Conference on Telecommunications and Signal Processing (TSP)*, Brno, Czech Republic, 26-28 July 2021.
- [5] Y. Pathak, P. K. Shukla and K. V. Arya, "Deep bidirectional classification model for COVID-19 disease infected patients", *IEEE/ACM Trans. Comput. Biol. Bioinform.*, 18, 1234-1241, 2021.
- [6] R. Y. Wang et al., "Predictions of COVID-19 infection severity based on co-associations between the SNPs of co-morbid diseases and COVID-19 through machine learning of genetic data", *IEEE 8th International Conference on Computer Science and Network Technology (ICCSNT)*, Dalian, China, 20-22 November 2020.
- [7] J. E. Nalavade, "Digital screening tool to detect Covid-19 infected people", *International Conference on Computer Communication and Informatics (ICCCI)*, Coimbatore, India, 27-29 January 2021.
- [8] N. Vidushee and P. Rakhi, "Tracing the origins of COVID-19. In Use of AI, Robotics, and Modern Tools to Fight Covid-19" Jain, A., Sharma, A., Wang, J., Ram, M., Eds.; River Publishers: Gistrup, Denmark, 2021, pp. 17-28.
- [9] A. Jain et al., "Use of AI, robotics, and modern tools to fight Covid-19", *In Use of AI, Robotics, and Modern Tools to Fight Covid-19*; Jain, A., Sharma, A., Wang, J., Ram, M., Eds.; River Publishers: Gistrup, Denmark, 2021.
- [10] S. Koç, G. Yilmaz and Y. Kabak, "The clinical guidelines usage towards the diagnosis and treatment of H1N1", *5th International Symposium on Health*

*Informatics and Bioinformatics*, Ankara, Turkey, 20-22 April 2010.

- [11] S.M. Elembaby et al., “Gene regulatory network for H1N1 gene expression data”, *32nd National Radio Science Conference (NRSC)*, Giza, Egypt, 24-26 March 2015.
- [12] M. Lu and F. Li, “Survey on Lie group machine learning”, *Big Data Min. Anal.* 2020, 3, 235-258.
- [13] H. Arslan and B. Aygün, “Performance analysis of machine learning algorithms in detection of COVID-19 from common symptoms”, *29th Signal Processing and Communications Applications Conference (SIU)*, Istanbul, Turkey, 9-11 June 2021.
- [14] A. Shamsi et al., “An uncertainty-aware transfer learning-based framework for COVID-19 diagnosis”, *IEEE Trans. Neural Network. Learn. Syst.* 2021, 32, 1408-1417.
- [15] S. Tiwari, P. Chanak and S. K. Singh, “A review of the machine learning algorithms for Covid-19 case analysis”, *IEEE Trans. Artificial Intelligent* 2022.
- [16] A. Anupam, N.J. Mohan, S. Sahoo and S. Chakraborty, “Preliminary diagnosis of COVID-19 based on cough sounds using machine learning algorithms”, *5th International Conference on Intelligent Computing and Control Systems (ICICCS)*, Madurai, India, 6-8 May 2021.
- [17] M. Almansoor and N. M. Hewahi, “Exploring the relation between blood tests and Covid-19 using machine learning”, *International Conference on Data Analytics for Business and Industry: Way Towards a Sustainable Economy (ICDABI)*, Sakheer, Bahrain, 26-27 October 2020.
- [18] M. J. Farrukh, L. C. Ming, S. T. Zaidi and T. M. Khan, “Barriers and strategies to improve influenza vaccination in Pakistan”, *Journal Infect. Public Health* 2017, 10, 881-883.
- [19] G. Grasselli et al., COVID-19 Lombardy ICU Network. Baseline characteristics and outcomes of 1591 patients infected with SARS-CoV-2 admitted to ICUs of the Lombardy region, Italy. *JAMA* 2020, 323, 1574-1581.
- [20] S. A. Hashemi et al., “High prevalence of SARS-CoV-2 and influenza A virus (H1N1) coinfection in dead patients in northeastern Iran”, *Journal Medical Virol.* 2020, 93, 1008-1012.
- [21] G. Härter et al., “COVID-19 in people living with human immunodeficiency virus: a case series of 33 patients”, *Infection* 2020, 48, 681-686.
- [22] J. Dhamija, T. Choudhury, P. Kumar and A. Tetarbe, “Classification of swine flu patients using gene expression: For a safer future.” *In Proceedings of the International Conference on Communication, Computing and Internet of Things*, Chennai, India, 15-17 February 2018.
- [23] N. Shaltout et. al., “Comparing PCA to information gain as a feature selection method for Influenza-A classification”, *In Proceedings of the International Conference on Intelligent Informatics and Biomedical Sciences*, Okinawa, Japan, 28-30 November 2015.
- [24] X. Qian et al., “M3 Lung-Sys: A deep learning system for multi-class lung pneumonia screening from CT imaging” *IEEE Journal Biomedical Health Information*, 2020, 24, 3539-3550.
- [25] J. Pei, et al. “Improving prediction accuracy of influenza-like illnesses in hospital emergency departments”, *In Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine*, Shanghai, China, 18-21 December 2013.
- [26] E. Elbasi, “Reliable abnormal event detection from IoT surveillance systems”, *In Proceedings of the 7th International Conference on the Internet of Things: Systems, Management and Security*, Paris, France, 14-16 December 2020.
- [27] E. Elbasi, D. K. Ayanoglu and A. I. Zreikat, “Determination of patient’s hearing sensitivity using data mining techniques”, *In Proceedings of the IEEE 12th International Conference on Application of Information and Communication Technologies*, Almaty, Kazakhstan, 17-19 October 2018.
- [28] E. Elbasi, S. Mathew, A. Topcu and W. Abdelbaki, “A survey on machine learning and Internet of Things for COVID-19”, *In Proceedings of the World AI IoT Congress*, Seattle, USA, 10-13 May 2021.
- [29] E. Elbasi et al., “Crop Prediction Model Using Machine Learning Algorithms”, *Applied Sciences*, 2023, 13, 9288.
- [30] A. E. Topcu et al., “Social Media Zero-Day Attack Detection Using TensorFlow”, *Electronics* 2023, 12, 3554.
- [31] A. E. Topcu et al., “Text Analysis of Smart Cities: A Big Data-based Model”, *International Journal of Intelligent Systems and Applications in Engineering*, vol 11, issue 4, 724-733, 2023.
- [32] B. Yildiz, “Reinforcement learning using fully connected, attention, and transformer models in knapsack problem solving”, *Concurrency and Computation: Practice and Experience*, vol. 34, issue 9, 2022.