

Classification of influenza H1N1 and COVID-19 patient data using machine learning

Ersin Elbasi, Aymen Zreikat, Shinu Mathew, and Ahmet E. Topcu

College of Engineering and Technology

American University of the Middle East

Egaila, Kuwait

ersin.elbasi@aum.edu.kw, aymen.zreikat@aum.edu.kw, shinu.mathew@aum.edu, ahmet.topcu@aum.edu.kw

Abstract— COVID-19 is a community-acquired infection with symptoms resembling those of influenza and bacterial pneumonia. It has negatively affected the entire world in areas such as the economy, social life, education, and technology. COVID-19 and H1N1 influenza have been compared in recent studies as they are both causative agents of pandemics and have both caused great distress around the world. Since these two diseases have some symptoms and diagnostic features in common, it would be beneficial for health professionals and scientists to analyze and study patient's clinical data for these two diseases. In this work, we propose some machine learning algorithms to classify patient data into the two classes of H1N1 and COVID-19. The study includes 1467 patient data (70% from H1N1 and 30% from COVID-19) with 42 attributes used in classification. Experimental results show that the Bayes network gives 86.57% accuracy, the naive Bayes classifier gives 82.34% accuracy, the multilayer perception algorithm gives 99.31% accuracy, the locally-weighted learning algorithm gives 88.89% accuracy, and random forest gives 83.16% accuracy for the same data set.

Keywords—COVID-19; H1N1; machine learning; multilayer perception; medical data

I. INTRODUCTION

SARS-CoV-2 or COVID-19 disease was declared a global pandemic by the World Health Organization on March 12, 2020. This disease has caused high mortality around the world. Scientists and doctors have analyzed a large variety of laboratory test results and demographic data of patients to clearly define this disease and its symptoms. Due to the unavailability of sufficient data, however, many COVID-19 patients were not identified and this led to delayed treatment protocols [1].

The world has now been facing the COVID-19 pandemic for quite a long time. Similarly, the world witnessed another epidemic, called H1N1 influenza, in 2009. COVID-19 and H1N1 have been compared in recent studies as they are both highly contagious and have created marked chaos in the world. As a result of the fact that some of the symptoms of these two diseases are similar, it is necessary to analyze the symptoms that are unique to each of these diseases to better interpret patient data and thereby provide suitable treatment protocols. This research paper aims to classify the symptoms of COVID-19 and H1N1 from the available patient data using machine

learning (ML) algorithms. The interpretation of such data could help health professionals detect the presence of SARS-CoV-2 and H1N1 diseases in earlier stages of disease progression. López Pineda [2] suggested that analyzing electronic medical records using ML classifiers can yield significant precision in the event that ample clinical reports are available. Technological evolutions have always contributed to the health care sector and ML in particular has played a vital role in the health care industry [3]. Patient data such as age, sex, blood analysis, CT scans, chest X-rays, and other vital signs such as temperature are considered as the input data set for ML algorithms to classify the data into various categories. These derived sets of data are used to train a ML model to make a successful prediction or for decision-making. For instance, patient data sets with successful prediction rates can be used to train a model that can predict a new case based on the symptoms or other clinical lab test results that match with these data sets. These kinds of predictions help doctors to recommend treatments and plan further clinical procedures [3].

ML is a part of data science and it has the capability to solve data-related problems by understanding and analyzing large data sets. For instance, email spam filtering, online recommendation engines, Facebook friend suggestions, stock market predictions, and self-driving cars all benefit from the power of ML algorithms. While solving a problem with ML, the problem will be categorized into suitable groups so that the best ML algorithm can be applied to solve it. These groups are categorized as follows [4]:

- Classification Problems: Data sets that contain fixed output (yes/no or true/false)
- Anomaly Detection Problems: Data sets with anomalies or unusual behaviors compared to the trained pattern
- Regression Problems: Data sets expected to provide answers to questions such as 'how much?' or 'how many?'
- Clustering Problems: Data sets grouped based on how each data set is organized and its behavior
- Reinforcement Problems: Decisions based on previous experiences of learning

Various ML algorithms can perform these separations based on the data and the specific requirements.

In the ML approach, the first requirement is to collect sufficient data for training the model. The collected data then need to be prepared for processing by ML algorithms as some of them are not structured. The next process is to eliminate unnecessary data that are not required for the ML learning process. There are many ML algorithms but not all of them will be used for all problems or analyses. The next phase of ML modeling is to choose the appropriate algorithm that fits each data set or problem. These algorithms require initial variables or attributes and then the ML model needs to be trained using some of these data. Figure 1 shows a sample ML model that processes and analyzes various patient data, which will then be classified, and some of these data will be used to train the model using ML algorithms. The model then predicts whether the patient is affected with COVID-19, H1N1, or neither as the result.

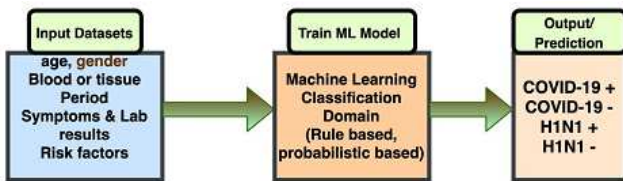


Fig. 1: A sample ML model

The input data sets in the model can be collected through IoT sensors, open-source datasets or internally collected data from hospitals and labs. ML model then perform data analysis to choose the appropriate data and organize these data in different categories of classification, clustering, regression, and prioritizing. Classification algorithms helps ML model to learn and properly recognize those data or objects. After analyzing and arranging these data sets with the help of various ML algorithms, the model should then be able to predict the result as diagnosis result.

This paper is organized as follows. A brief introduction to related works is presented in section 2. Section 3 describes the machine learning algorithms used in proposed work. Experimental results are represented in section 4, and conclusions in section 5.

II. LITERATURE REVIEW

Coronavirus disease 2019 (COVID-19) and the hemagglutinin type 1 and neuraminidase type 1 influenza strain (H1N1, also known as swine flu) have become the most widespread pandemic diseases worldwide. Therefore, the health community and more specifically the World Health Organization are under pressure as these diseases spread throughout the whole world very quickly. In this regard, researchers are trying to find a relationship between patients who suffer from a deficiency in immunity because of H1N1 infection and who have already been infected with COVID-19 disease. Consequently, intensive research work is currently being conducted to study the diagnosis of patients who have been infected with H1N1 and have a low-risk possibility of COVID-19 infection [1-9] due to the similar symptoms of these two diseases, such as headache, fever, mild cough, diarrhea, sore throat, dyspnea, and generalized muscle ache. On the other hand, influenza cases usually have mild to moderate

symptoms compared to COVID-19 cases, where symptoms can be severe [1-4]. In some countries such as Pakistan, there is no clear policy for influenza vaccines [5-9]. Based on medical reports [5-6], 20,000 children are admitted to Pakistani hospitals annually due to flu-based symptoms and children between 5 and 14 years old were likely to become sick due to influenza symptoms. Therefore, to overcome this problem, the Pakistani government should start an intensive vaccination program for both the flu and COVID-19 to avoid the spread of these viruses. In Italy [7], a data set of 1591 COVID-19 patients was studied for patients who had symptoms that required admission to the intensive care unit (ICU) in the Lombardy region of Italy. The authors concluded that the majority of patients who had severe clinical courses and needed to be admitted to the ICU were older men. Similarly, in Iran [8], researchers have studied different cases of SARS-CoV-2 and influenza A co-infection. The results of that study showed that the high occurrence of SARS-CoV-2 and influenza co-infection can lead to an increase in mortality among patients. Another data set of 33 patients living with the human immunodeficiency virus was studied to discover the relationship between human immunodeficiency and COVID-19 deaths. It was found that only three cases out of 33 were reported as ending in death, which means that there was no strong relationship between human immunodeficiency factor and the COVID-19 mortality rate.

Some authors have been interested in the classification of swine flu using gene expression [10-14]. In [10], two optimization algorithms were studied in order to achieve high accuracy by using a gene expression database. The support vector machine (SVM) algorithm and neural network algorithm (NNA) were compared and, based on the given results of this research work, the authors discovered that the NNA provided 81.81% accuracy, outperforming other algorithms. Principal component analysis was used for classification in [11] to analyze different cDNA viral segments of influenza class A. By studying different performance measures, it was shown via the experimental results that the preprocessing speed was reduced from 1.5 hours to 5 minutes. In [12], the M3 lung deep learning system algorithm was suggested, which is based on a multi-task multi-slice principle to separate COVID-19 cases, H1N1 cases, CAP cases, and healthy cases. To show the effectiveness of the suggested model not only in providing statistics but also to help clinicians with diagnoses, the authors conducted experiments with 743 different cases using both slice and patient-level classifications. The main objective of the research in [13] was to enhance the analysis and practical application of statistics on patients in emergency departments in hospitals, and an orthogonal transformation algorithm known as the importance contribution index was suggested. The provided experimental results showed that the accuracy of data prediction was improved by 7.1%. In [14], a multi-channel segmentation algorithm was proposed to effectively monitor health outcomes, especially when changes appear in the data distribution. The proposed algorithm was based on the multivariate hidden Markov model and Fisher's linear discriminant analysis. For example, the experimental data provided by a cohort in the human viral challenge model showed disrupted wake and sleep patterns after exposure to the H1N1 influenza pathogen. Therefore, the experimental results

proved that the suggested algorithm is efficient with respect to periodical shifts of data distribution and would be effective to be used by emergency departments in hospitals.

Other authors [15-17] have studied different algorithms that help provide fast predictions of COVID-19 diagnoses to avoid the spread of the disease by patients. In [15], using a ML algorithm, generic variants of comorbidity patterns were studied with individuals' phenotypes and the random forest classifier. It was shown by the experimental results that ongoing symptoms are more important than history information in the proper prediction of COVID-19. Due to the increased spread of COVID-19 in the world, including Indonesia, the authors of [16] tested a set of data using contrast limited adaptive histogram equalization and convolutional neural network algorithms. The provided experimental and comparative results on data sets showed that the accuracy of COVID-19 prediction was increased. In [17], the authors hypothesized that the procedure for controlling the spread of COVID-19 among people still depends on different factors like patients' symptoms, travelling history, and close contact with infected people. On the other hand, traditional testing methods are based on the nasal test followed by laboratory blood tests for more confirmation. Therefore, these authors emphasized the need to use deep learning to test laboratory data such as series of chest X-ray images for early prediction of disease symptoms. The given numerical results showed that the accuracy was increased to 91.67% for COVID-19 diagnosis.

III. METHODOLOGY

In recent medical studies, very close similarity between the symptoms of H1N1 and COVID-19 has been revealed. For this reason, we compared some ML algorithms to classify patient data (patient demographics, health history, and asymptomatic information) in the two classes of H1N1 and COVID-19 to reveal how effective these symptom similarities are. Our aim in doing so is to determine the similarities between these two diseases separately by different ML methods and to help reveal to what extent the similarities can be used in the future.

In this work, research was conducted on two types of diseases, H1N1 and COVID-19, for a total of 1467 patients. 70% of those patients were diagnosed with H1N1 and the remaining data were from COVID-19 patients. Figure 2 depicts the type of data used in the study. There are different data categories for the patients, including patient age and gender, blood or tissue sample results, the period of the illness, symptoms and lab results, and risk factors. Data from these patients are used in ML algorithms including the Bayesian network (BN), naive Bayes classifier (NBC), multilayer perception (MP), locally weighted learning (LWL), and random forest (RF) algorithms for classification. MP algorithms are artificial neural networks that do not create a feedforward loop between nodes. While 60% of data are used for training, 40% are used for testing.

Models with data trained with different ML methods were tested for both H1N1 and COVID-19 patients and it was investigated which models were more successful. Using different ML algorithms, we aimed to reveal the algorithm that gives the best performance for H1N1 and COVID-19 as a

result of comparing them according to accuracy. To measure the quality of classification results using several different metrics, we wanted to find the values of mean absolute error (MAE), root mean square error (RMSE), relative absolute error (RAE) and to compare these values to find the lowest error rate among the proposed algorithms.

Data Type for Patient	
	age, gender
Blood or tissue	Neutrophil, neutrophil Categorical*, serum levels of white blood cell, serum levels of white blood cell category* lymphocytes, lymphocytes category*, Plateletes, Creactive Protein Levels, Creactive Protein Levels category*, Eosinophils, Red blood cells, Hemoglobin, Procalcitonin
Period	Duration of illness, Days to death
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*
Risk factors	asthma, athero, immuno, diabetes, respiratory, liver disorder, obesity, hypertension, heart disease

Fig. 2. Patient data set (Blood or tissue: * (low, normal, high) Symptoms & Lab: *(Yes, No))

IV. EXPERIMENTAL RESULTS

ML algorithms are developed here to classify patient data including patient demographics, health history, and asymptomatic information. A total of 1467 data are used, 70% of which are from H1N1 cases and 30% from COVID-19 patient data. In this work, we apply the Bayesian network (BN), naive Bayes classifier (NBC), multilayer perception (MP), locally-weighted learning (LWL), and random forest (RF) algorithms. While 60% of data are used for training, 40% are used for testing. Table 1 demonstrates the true positive (TP), false positive (FP), precision, and recall values for each proposed algorithm with H1N1 and COVID-19 data. TP indicates the rate of correctly classified data sets and FP indicates the rate of incorrectly classified data sets. The MP algorithm gives more robust results than the other algorithms, especially for TP and FP. Table 2 shows the F-measure, Matthew's correlation coefficient (MCC), receiver operating characteristic (ROC) curve area, and precision-recall curve (PRC) area for each class. The MCC value should be between -1 and +1. If the MCC value is +1, it means that there is a perfect prediction between classes. Based on Table 2, the MP algorithm's MCC value is 0.983, much higher than those of the other applied algorithms.

TABLE 1: TP RATE, FP RATE, PRECISION, AND RECALL VALUES FOR EACH CLASS

Method	TP Rate	FP Rate	Precision	Recall	Class
BN	0.972	0.423	0.862	0.972	H1N1
	0.577	0.028	0.884	0.577	COVID-19
NBC	0.828	0.190	0.922	0.828	H1N1
	0.810	0.172	0.635	0.810	COVID-19
MP	0.999	0.023	0.992	0.999	H1N1
	0.977	0.001	0.997	0.977	COVID-19
LWL	0.960	0.304	0.896	0.960	H1N1

	0.696	0.040	0.865	0.696	COVID-19
RF	0.977	0.562	0.825	0.977	H1N1
	0.438	0.023	0.874	0.438	COVID-19

TABLE 2: F-MEASURE, MCC, AND ROC AND PRC AREAS FOR EACH CLASS

Method	F-Measure	MCC	ROC Area	PRC Area	Class
BN	0.914	0.640	0.907	0.955	H1N1
	0.698	0.640	0.907	0.820	COVID-19
NBC	0.873	0.596	0.919	0.967	H1N1
	0.712	0.596	0.919	0.849	COVID-19
MP	0.995	0.983	0.991	0.984	H1N1
	0.987	0.983	0.991	0.993	COVID-19
LWL	0.927	0.706	0.959	0.984	H1N1
	0.771	0.706	0.959	0.984	COVID-19
RF	0.894	0.538	0.888	0.953	H1N1
	0.583	0.538	0.888	0.788	COVID-19

The NBC algorithm gives an 82.8% TP rate for Class H1N1 and 81.0% TP rate for Class COVID-19. The RF, BN, and LWL algorithms have the lowest TP rates for Class COVID-19, and MP has the highest TP rate for the COVID-19 class. The F-measure represents the combined accuracy of precision and recall for the given data.

Table 3 shows the accuracy values and build times for each ML algorithm. The BN algorithm yields accuracy of 86.57%, NBC 82.34%, MP 99.31%, LWL 88.89%, and RF 83.16% in the classification of patient data. The LWL and RF build times are much higher than those of the other algorithms. Experimental results show that the MP algorithm is more optimal, robust, and accurate for patient data classification between COVID-19 and H1N1. The NBC algorithm gives the lowest build time for the classification model; however, its accuracy rate is lower than those of the other algorithms [22,23].

TABLE 3: ACCURACY RATES AND BUILD TIME FOR EACH ML ALGORITHM

Method	Accuracy (%)	Build Time (s)
BN	86.57	0.14
NBC	82.34	0.06
MP	99.31	0.24
LWL	88.89	7.72
RF	83.16	6.23

We can measure the quality of classification results using several different metrics. Table 4 shows the mean absolute error (MAE), root mean square error (RMSE), relative absolute error (RAE), and root mean squared error (RMSE) rates. A perfect mean absolute error value is 0. Based on the values in Table 4, the MAE value of the MP algorithm indicates that it has a lower error rate than the other proposed algorithms.

TABLE 4: MAE, RMSE, RAE, AND RMSE ERROR RATES

Method	MAE	RMSE	RAE (%)	RMSE (%)
BN	0.1939	0.3167	49.25	71.41
NBC	0.2203	0.3945	55.96	88.93
MP	0.0116	0.0779	2.95	17.57
LWL	0.1960	0.2946	49.77	66.41
RF	0.2989	0.3568	75.92	80.44

Random forest algorithm extracts 4071 rules. Some of the rules retrieved by machine learning algorithms are given in the below.

- IF {(Gender=M) AND (Diarrhea=YES) AND (Lymphocytes < 2.58) AND (Fever=YES) AND (Risk Factor=AC)} THEN Class: H1N1
- IF {(Gender=M) AND (Diarrhea=YES) AND (Temperature>=38.5) AND (Age >=25.5) AND (Serum Levels= High)} THEN Class: COVID-19
- IF {(Gender=F) AND (Diarrhea=YES) AND (Sore Throat=NO) AND (Coughing=YES) AND (Age <25)} THEN Class: H1N1
- IF {(Gender=F) AND (Temperature >=38.5) AND (Lymphocytes >= 2.58) AND (Sore Throat=YES) AND (Caught= YES) AND (Fever=YES) AND (Risk Factor=AD) AND (Age >=42.5)} THEN Class: COVID-19
- IF {(Gender=F) AND (Lymphocytes=Low) AND (Neutrophil=High) AND (Eosinophils<0.05) AND (Caught= YES) AND (Serum level=High) AND (CT scan report=Negative)} THEN Class: H1N1

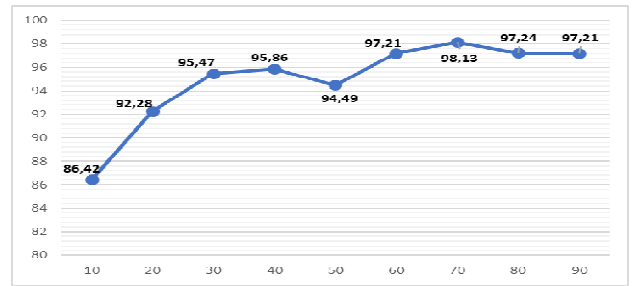


Fig. 3. Accuracy of MP algorithm for training (%10%-90)

Figure 3 demonstrates accuracy of the multilayer perception algorithm for different size of the training data set. When 70% of the data set used for training, accuracy of the algorithm in classification is 98.13%. Figure 4 shows testing modeling time for MP algorithm for allocation of data set for training from 10% to 90% in MP algorithm. If 10% of data allocated for training, testing modeling takes 0.25 seconds.

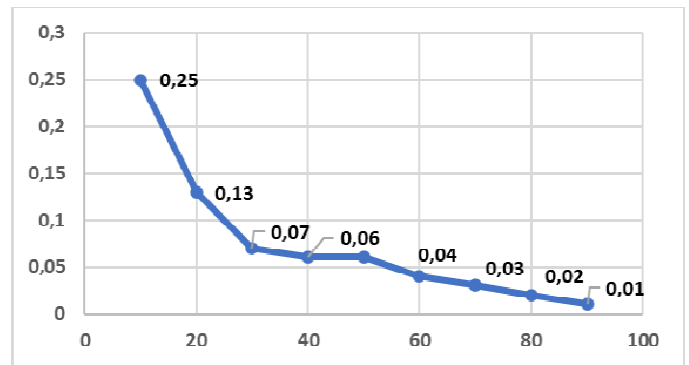


Fig. 4. Testing modeling times for MP algorithm

V. CONCLUSION

As COVID-19 and H1N1 have common symptoms and have become the most widespread pandemic diseases worldwide, it would be beneficial for health professionals and scientists to analyze and study clinical patient data related to

these diseases [24]. Therefore, some ML algorithms to classify patient data into two classes of H1N1 and COVID-19 have been proposed in this research work. A total of 1467 patient data (70% for H1N1 and 30% for COVID-19) with 42 attributes were used in classification. Experimental results showed that the Bayes network (BN) gives 86.57% accuracy, the naive Bayes classifier (NBC) gives 82.34% accuracy, the multilayer perception (MP) algorithm gives 99.31% accuracy, the locally weighted learning (LWL) algorithm gives 88.89% accuracy, and random forest (RF) gives 83.16% accuracy for the same data set. Experimental results show that machine learning algorithms give very promising results in classification of H1N1 and COVID-19 data. In future work, other ML algorithms can be included in the analysis. Other patient information could also be considered in future analysis, such as age, gene information databases, patients in emergency rooms, and hospitalized patients.

REFERENCES

- [1] Q. Xu, H. Samanapally, P. Nathala, V. Salunkhe, S. Furmanek, M. N. Cahill et al., "Outcomes and risk factors for cardiovascular events in hospitalized COVID-19 patients," in *J. Cardiothorac. Vasc. Anesth.*, 27 Mar. 2021, doi:10.1053/j.jvca.2021.03.035.
- [2] A. López Pineda, Y. Ye, S. Visweswaran, G. F. Cooper, M. M. Wagner, and F. R. Tsui, "Comparison of machine learning classifiers for influenza detection from emergency department free-text reports," in *J. Biomed. Inform.*, vol. 58, pp. 60–69, 2015.
- [3] I. Bica, A. M. Alaa, C. Lambert, and M. van der Schaar, "From real-world patient data to individualized treatment effects using machine learning: current and future methods to address underlying challenges," in *Clin. Pharmacol. Ther.*, vol. 109, pp. 87–100, 2021.
- [4] J. Alzubi, A. Nayyar, and A. Kumar, "Machine learning from theory to algorithms: an overview," in *J. Phys. Conf. Ser.*, vol. 1142, 2018.
- [5] Q. Ding, P. Lu, Y. Fan, Y. Xia, and M. Liu, "The clinical characteristics of pneumonia patients coinfecting with 2019 novel coronavirus and influenza virus in Wuhan, China," in *J. Med. Virol.*, vol. 92, pp. 1549–1555, 2020.
- [6] C. Jiang, X. Yao, Y. Zhao, J. Wu, P. Huang, C. Pan et al., "Comparative review of respiratory diseases caused by coronaviruses and influenza A viruses during epidemic season," in *Microb. Infect.*, vol. 22, pp. 236–244, 2020.
- [7] R. Ozaras, R. Cirpin, A. Duran, H. Duman, O. Arslan, Y. Bakcan et al., "Influenza and COVID-19 co-infection: report of 6 cases and review of the Literature," in *J. Med. Virol.*, vol. 92, pp. 2657–2665, 2020.
- [8] V. M. Konala, S. Adapa, V. Gayam, S. Naramala, S. R. Daggubati, C. B. Kammari et al., "Co-infection with Influenza A and COVID-19," in *Eur. J. Case Rep. Internal Med.*, vol. 7, no. 5, pp. 1, 2020.
- [9] N. Nisar, U. B. Aamir, N. Badar, M. R. Mahmood, A. Yaqoob, J. P. Tripathy et al., "Epidemiology of influenza among patients with influenza-like illness and severe acute respiratory illness in Pakistan: a 10-year surveillance study 2008–17," in *J. Med. Virol.*, vol. 92, pp. 3028–3037, 2020.
- [10] M. J. Farrukh, L. C. Ming, S. T. Zaidi, and T. M. Khan, "Barriers and strategies to improve influenza vaccination in Pakistan," in *J. Infect. Public Health.*, vol. 10, no. 6, pp. 881–883, 2017.
- [11] G. Grasselli, A. Zangrillo, A. Zanella, M. Antonelli, L. Cabrini, A. Castelli et al., "Baseline characteristics and outcomes of 1591 patients infected with SARS-CoV-2 admitted to ICUs of the Lombardy region, Italy," in *JAMA*, vol. 323, pp. 1574–1581, 2020.
- [12] S. A. Hashemi, S. Safamanesh, H. Ghasemzadeh-Moghaddam, M. Ghafouri, and A. Azimian, "High prevalence of SARS-CoV-2 and influenza A virus (H1N1) coinfection in dead patients in northeastern Iran," in *J. Med. Virol.*, vol. 93, no. 2 pp. 1008–1012, 2020.
- [13] G. Harter, C. D. Spinner, J. Roeder, M. Bickel, I. Krznaric, S. Grunwald et al., "COVID-19 in people living with human immunodeficiency virus: a case series of 33 patients," in *Infection*, vol. 48, no. 5, 681–686, Oct 2020.
- [14] J. Dhamija, T. Choudhury, P. Kumar, and A. Tatarbe, "Classification of swine flu patients using gene expression: "For a safer future"," in *Proc. Int. Conf. Commun., Computing and Internet of Things*, Chennai, India, 15–17 Feb. 2018, pp. 504–507.
- [15] N. Shaltout, M. Moustafa, A. Rafea, A. Moustafa, and M. El Hefnawi, "Comparing PCA to information gain as a feature selection method for Influenza-A classification," in *Proc. Int. Conf. Intelligent Informatics and Biomedical Sciences*, Okinawa, Japan, 2015, pp. 279–283.
- [16] X. Qian, H. Fu, W. Shi, T. Chen, Y. Fu, F. Shan et al., "MS³Lung-Sys: A deep learning system for multi-class lung pneumonia screening from CT imaging," in *IEEE J. Biomed. Health Inform.*, vol. 24, no. 12, pp. 3539–3550, Dec 2020.
- [17] J. Pei, B. Ling, S. Liao, B. Liu, J. X. Huang, T. Strome et al., "Improving prediction accuracy of influenza-like illnesses in hospital emergency departments," in *Proc. IEEE Int. Conf. Bioinformatics and Biomedicine*, Shanghai, China, 2013, pp. 602–607.
- [18] X. She et al., "Adaptive multi-channel event segmentation and feature extraction for monitoring health outcomes," in *IEEE Trans. Biomedical Engineering*, 18 Nov, 2020, pp. 1–1.
- [19] R. Y. Wang, T. Q. Guo, L. G. Li, J. Y. Jiao, and L. Y. Wang, "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," in *Proc. IEEE 8th Int. Conf. Computer Science and Network Technology*, Dalian, China, pp. 92–96, 2020.
- [20] B. K. Umri, M. Wafa Akhyari, and K. Kusriani, "Detection of COVID-19 in chest X-ray image using CLAHE and convolutional neural network," in *Proc. 2nd Int. Conf. Cybernetics and Intelligent System*, Manado, Indonesia, 2020, pp. 1–5.
- [21] A. Channa, N. Popescu, and N. U. R. Malik, "Robust technique to detect COVID-19 using chest X-ray images," in *Proc. Int. Conf. e-Health and Bioengineering*, Iasi, Romania, pp. 1–6, 2020.
- [22] E. Elbasi, "Reliable abnormal event detection from IoT surveillance systems," in *Proc. 7th Int. Conf. Internet of Things: Systems, Management and Security*, Paris, France, 2020, pp. 1–5.
- [23] E. Elbasi, D. K. Ayanoglu, and A. Zreikat, "Determination of patient's hearing sensitivity using data mining techniques," in *Proc. IEEE 12th Int. Conf. Application of Information and Communication Technologies*, Almaty, Kazakhstan, 2018, pp. 1–6.
- [24] E. Elbasi, S. Mathew, A. Topcu, and W. Abdelbaki, "A survey on machine learning and Internet of Things for COVID-19," in *Proc. World AI IoT Congress*, May 2021.