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AI-Based Intelligent Model to Predict Epidemics Using Machine Learning Technique

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Abstract: The immediate international spread of severe acute respiratory syndrome revealed the potential threat of infectious diseases in a closely integrated and interdependent world. When an outbreak occurs, each country must have a well-coordinated and preventative plan to address the situation. Information and Communication Technologies have provided innovative approaches to dealing with numerous facets of daily living. Although intelligent devices and applications have become a vital part of our everyday lives, smart gadgets have also led to several physical and psychological health problems in modern society. Here, we used an artificial intelligence AI-based system for disease prediction using an Artificial Neural Network (ANN). The ANN improved the regularization of the classification model, hence increasing its accuracy. The unconstrained optimization model reduced the classifier's cost function to obtain the lowest possible cost. To verify the performance of the intelligent system, we compared the outcomes of the suggested scheme with the results of previously proposed models. The proposed intelligent system achieved an accuracy of 0.89, and the miss rate 0.11 was higher than in previously proposed models.

Keywords: Intelligent model; epidemics; artificial intelligence; machine learning techniques

1 Introduction

When the prevalence of an illness surpasses the typical expectancy, it can lead to a global pandemic. Disease spread depends on the disease-causing agent and the size of the previous and current exposures to the agent. Since 2019, the entire world has been dealing with a dangerous pandemic caused by SARS-CoV-2 2019 (COVID-19) [1]. The first instances of COVID-19 were reported in December 2019 in

Wuhan, China. Since then, it has affected over 200 nations and regions worldwide, with 2,000,000 cases and 120 thousand deaths by April 21, 2020. As a result of this growing emergency, organizations and professionals globally have been searching for ways to address the medical complications and psychological impacts of the virus, as well as to halt the spread [2,3].

According to Chinese epidemiological assessments of the present COVID-19 scenario, Europe was one of the pandemic epicentres in May. A significant outbreak of COVID-19 occurred in March 2020, primarily in Italy and Spain. Given that this is a new virus, future projections of virus propagation and acquired herd immunity in the worldwide population are not possible [4]. Furthermore, records from the last similar epidemic, which occurred a century ago, are restricted. Given the well-known impact of severe economic measures on health, policymakers in the most affected nations have been dealing with the complex problem of combining outdated public health measures with economic survival [5]. That the 1918 Spanish flu pandemic produced a second lethal epidemic wave, owing to alterations in the H1N1 viral strain, has sparked a lively debate about whether current activities should account for this possibility with COVID-19. It's difficult to imagine how best to deal with the unknown future of the COVID-19 epidemic [6].

Science and engineering are essential tools in the battle against COVID-19. As AI had already been used to examine other types of particles in motion, this technology was adapted to examine the spread of COVID-19 particles in the air. Many scientists and software engineers have used AI to test novel therapies for COVID-19, with the aid of X-rays and computed tomography (CT) scans.

AI has also contributed to the characterization of patient health status based on physiological indicators. Various sensors that measure biological signals can be used to obtain input values. When examining ways in which AI could be used to combat COVID-19, researchers have considered several technical innovations that could lessen or obscure the effects of viral outbreaks. In the present study, we evaluated the effectiveness of various methods and made recommendations regarding their use. We particularly focused on the use of AI and other new technologies in fighting COVID-19 and other epidemics. When paired with real-time data collection, AI could deliver new insights that could help prevent the spread of COVID-19 infection. For instance, it could be used to predict infection sites, virus spread, and the need for beds and medical personnel during an epidemic.

Machine learning (ML) is a branch of AI that can be used to increase the accuracy of predictions made using inputted historical data, without requiring explicit programming.

2 Literature Review

Many researchers have been working on intelligent AI systems for predicting epidemics. Some of these works are highlighted in this section. Individuals with COVID-19 can be identified by their respiratory patterns, which differ from those associated with a conventional cold or influenza virus. Specifically, COVID-19 infection can cause tachypnea or rapid breathing. COVID-19 can also be verified using a depth camera to collect non-contact respiratory data, which can then be evaluated using AI recognition algorithms.

Another COVID-19 symptom is fever. Infrared thermal cameras can detect real-time transient or constant changes in energy emission, allowing surface temperature assessments. Thermal infrared cameras with AI algorithms can instantly detect and track suspected COVID-19 patients with minimal human monitoring [7].

Kang and Milinovich established a system for forecasting influenza interest by utilizing Internet search queries acquired from influenza inspection services in China [8]. Since the outbreak of COVID-19, scientists have been working to assess the possible impacts of the pandemic and to develop plans to alleviate its impacts on the population. Several solutions have been presented, from ML techniques to better comprehend virus progression and enhance forecasting to traditional modelling approaches built on differential equations. Multiple approaches are useful because different model configurations can address different parts of the issue.

The Ebola virus is the etiological agent of Ebola virus disease (EVD). This hemorrhagic fever occurs in Western and Equatorial Africa, and is a confined, negative-sense, single-stranded RNA virus that belongs to the Ebola virus genus and the Filoviridae family. Zaire, Bundibugyo, Sudan, Côte d'Ivoire (Ta Forest), and Reston comprise the five species of Ebola virus. It is transmitted to humans through direct contact with an infected person's or animal's blood or bodily fluids. Fever, myalgia, aberrant inflammatory reactions, dehydration, electrolyte imbalance, bleeding, and mortality are the most common clinical symptoms of EVD. Several epidemics have occurred in Sub-Saharan Africa since the first outbreak in 1976, claiming thousands of lives. The latest outbreak in West Africa, which occurred from 2014 to 2016, was the most widespread, killing more than 11,000 people and resulting in a case fatality of over 40%. As of August 18, 2020, researchers had identified over 3,470 cases and 2,287 deaths in the Democratic Republic of Congo [9].

AI can be used to detect infrequent symptoms and other red flags for disease, which can alert healthcare administration and patients, allowing for a quicker decision-making process and lower costs. Fast and effective algorithms could enable a solid management and diagnosis scheme for COVID-19. AI could assist in the detection of the causes of COVID-19 via various imaging techniques such as magnetic resonance imaging (MRI) or CT [10]. Patients could collect data using personal digital assistants (PDAs), tablets, and other intelligent devices, and these data could be saved in electronic health records (EHRs). When needed, these data could be rapidly shared.

ML approaches [11], transfer learning [12], deep ensemble learning [13], computational intelligence approaches [14], the fuzzy inference system [15], particle swarm optimization (PSO) [16], supervised ML [17], deep extreme ML [18], soft computing approaches, ECG denoising methods [19], image propagation [20], decision mode algorithms [21], and watermarking schemes [22,23] have all been used to develop disease monitoring and management systems.

3 Proposed Methodology

A pandemic is a worldwide disease epidemic with a high transmission rate. Limiting mass travel can reduce the impact of a pandemic. ML is a type of AI that may help to stop a pandemic by identifying which people should be screened for the disease. Fig. 1 gives a flow chart of a proposed model, and a detailed description is given in Fig. 2.

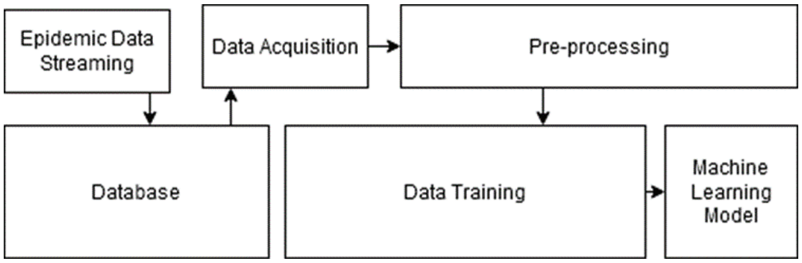

Figure 1: Flow chart of the proposed model

As shown in Fig. 1, patient data is stored in the database and then passed to the data acquisition, preprocessing, and training models. At the end, the data is sent to the ML model.

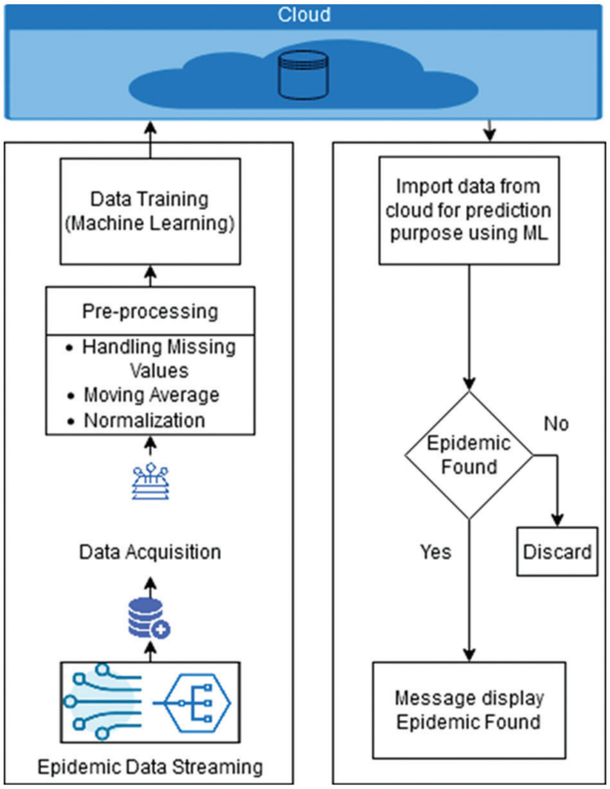

Figure 2: Proposed methodology

As shown in Fig. 2, patient data is transferred to the data acquisition layer, which stores the data acquired from the database in its raw form. The raw data is delivered to the preprocessing layer, where noise is removed via normalization, adjustment of missing values, and moving averages. After this, the data is trained using an Artificial Neural Network (ANN) ML approach.

The input layer, hidden layer, and output layer are utilized in ANN, in which every neuron that exists in the hidden layer has an activation function like f(x) = Sigmoid(x). The sigmoid function for an input can be described as

$$\text{ɓ}_j = {}'\Upsilon_1 + \sum_{i=1}^{m} (\omega_{ij} * r_i) \tag{1}$$

$$\text{ᶃ}_j = \frac{1}{1 + e^{-\text{ɓ}_j}} \qquad where\, j = 1, 2, 3 \ldots n \tag{2}$$

Input from the output layer in Eq. (3)

$$\text{ɓ}_k = {}'\Upsilon_2 + \sum_{j=1}^{n} \left(\upsilon_{jk} * \text{ᶃ}_j \right) \tag{3}$$

The output layer activation function is

$$\text{ᶃ}_k = \frac{1}{1 + e^{-\text{ɓ}_k}} \qquad where\ k = 1, 2, 3 \ldots r \tag{4}$$

Error in back propagation is

$$E = \frac{1}{2}\sum\nolimits_{k} \left(\tau_k - \mathrm{g}_k\right)^2 \tag{5}$$

where τ_k r represents the desired output and out_k represents a calculated output. In Eq. (6), the rate of change in the weight for the output is calculated.

$$\Delta W \ \propto \ -\frac{\partial E}{\partial W}$$

$$\Delta \upsilon_{j,k} = -\,\epsilon \frac{\partial E}{\partial v_{j,k}} \tag{6}$$

Chain rule method as in (6)

$$\Delta \upsilon_{j,k} = -\,\epsilon\ \frac{\partial E}{\partial \mathrm{g}_k} \times \frac{\partial \mathrm{g}_k}{\partial \mathrm{b}_k} \times \frac{\partial \mathrm{b}_k}{\partial v_{j,k}} \tag{7}$$

After substituting Eq. (7), the value of weight changed in Eq. (8)

$$\Delta \upsilon_{j,k} = \ \epsilon(\tau_k - \mathrm{g}_k) \times \mathrm{g}_k(1 - \mathrm{g}_k) \times \left(\mathrm{g}_j\right)$$

$$\Delta \upsilon_{j,k} = \epsilon \xi_k \mathrm{g}_j \tag{8}$$

where

$$\xi_k = (\tau_k - \mathrm{g}_k) \times \mathrm{g}_k(1 - \mathrm{g}_k)$$

$$\Delta \omega_{i,j} \propto -\ \left[\sum\nolimits_k \frac{\partial E}{\partial \mathrm{g}_k} \times \frac{\partial \mathrm{g}_k}{\partial \mathrm{g}_k} \times \frac{\partial \mathrm{g}_k}{\partial \mathrm{g}_j}\right] \times \frac{\partial \mathrm{g}_j}{\partial \mathrm{g}_j} \times \frac{\partial \mathrm{g}_j}{\partial \omega_{i,j}}$$

$$\Delta \omega_{i,j} = -\,\epsilon\ \left[\sum\nolimits_k \frac{\partial E}{\partial \mathrm{g}_k} \times \frac{\partial \mathrm{g}_k}{\partial \mathrm{g}_k} \times \frac{\partial \mathrm{g}_k}{\partial \mathrm{g}_j}\right] \times \frac{\partial \mathrm{g}_j}{\partial \mathrm{g}_j} \times \frac{\partial \mathrm{g}_j}{\partial \omega_{i,j}}$$

$$\Delta \omega_{i,j} = \ \epsilon\ \left[\sum\nolimits_k (\tau_k - \mathrm{g}_k) \times \mathrm{g}_k(1 - \mathrm{g}_k) \times \left(v_{j,k}\right)\right] \times \mathrm{g}_k(1 - \mathrm{g}_k) \times r_i$$

$$\Delta \omega_{i,j} = \ \epsilon\ \left[\sum\nolimits_k (\tau_k - \mathrm{g}_k) \times \mathrm{g}_k(1 - \mathrm{g}_k) \times \left(v_{j,k}\right)\right] \times \mathrm{g}_j\left(1 - \mathrm{g}_j\right) \times r_i$$

$$\Delta \omega_{i,j} = \ \epsilon\ \left[\sum_k \xi_k \left(v_{j,k}\right)\right] \times \mathrm{g}_j\left(1 - \mathrm{g}_j\right) \times r_i$$

$$\Delta \omega_{i,j} = \ \epsilon \xi_j\, r_i \tag{9}$$

where

$$\xi_j = \left[\sum\nolimits_k \xi_k \left(v_{j,k}\right)\right] \times \mathrm{g}_j\left(1 - \mathrm{g}_j\right)$$

Output and hidden layer are shown in Eq. (10)

$$v_{j,k}^{+} = v_{j,k} + \lambda_F \Delta v_{j,k} \tag{10}$$

Updating weight and bias in Eq. (11)

$$\omega_{i,j}^{+} = \omega_{i,j} + \lambda_F \Delta \omega_{i,j} \tag{11}$$

λ_{F} is the learning rate of the proposed model. The convergence of the proposed model hinges upon the careful selection of λ_{F}.

The validation phase checks whether an epidemic has been found. If the answer is no, the operation is discarded; if the answer is yes, a notification will state that an epidemic has been detected. Then, the trained data is saved in the cloud, which can be imported for prediction purposes using the ML technique.

4 Simulation Results

Modern medical imaging techniques are increasingly used to assess complex hierarchical structures in various tissues and organs. Computer-aided diagnostic (CAD) processes incorporate medical image analysis as a critical feature. Recent deep learning methods have made it possible to build an end-to-end model to quantify final classification labels from raw medical image pixels. In medical classification, the ANN-based deep neural system has been used extensively. The ANN is an excellent feature extractor, so it may save time and money in classifying medical images.

We examined an intelligent model for synergizing medical images via the ANN approach. We applied the proposed ANN-based approach to a dataset gathered from the UCI ML data repository. Specifically, we used the ANN approach to synergize data from 50654 medical images. The dataset was divided into training constitutes of 70% (35458 samples) and 30% (15196 samples) for the training and validation purposes. The parameters for performance calculation were defined by the following formulas:

$$Sensitivity = \frac{\sum True\ Positive}{\sum Condition\ Positive} \tag{12}$$

$$Specificity = \frac{\sum True\ Negative}{\sum Condition\ Negative} \tag{13}$$

$$Accuracy = \frac{\sum True\ Positive + \sum True\ Positive}{\sum Total\ Population} \tag{14}$$

$$Miss - Rate = \frac{\sum False\ Negative}{\sum Condition\ Positive} \tag{15}$$

$$Fallout = \frac{\sum False\ Positive}{\sum Condition\ Negative} \tag{16}$$

$$Likelihood\ Positive\ Ratio = \frac{\sum True\ Positive\ Ratio}{\sum False\ Positive\ Ratio} \tag{17}$$

$$Likelihood\ Negative\ Ratio = \frac{\sum True\ Positive\ Ratio}{\sum False\ Positive\ Ratio} \tag{18}$$

$$Positive\ Predictive\ Value = \frac{\sum True\ Positive}{\sum\ Predicted\ Condition\ Positive} \tag{19}$$

$$Negative\ Predictive\ Value = \frac{\sum True\ Negative}{\sum\ Predicted\ Condition\ Negative} \tag{20}$$

As shown in Tab. 1, the proposed system synergizes the medical images during the training period. During training, 35458 samples were divided into 16486 negative and 18972 positive samples. When 15242 true positives were successfully forecast, no epidemic was detected. However, when 1244 records were mistakenly predicted as negatives, an epidemic was detected. Likewise, 18972 samples were obtained, where negative samples indicated an epidemic and positive samples indicated no epidemic. With 17079 samples correctly identified as negative, an epidemic was recognized, and 1893 samples were inaccurately foreseen as positive, indicating no epidemic, despite the presence of an epidemic.

Table 1: Proposed model training using ANN

Proposed Model Training			
Input	Total number of samples (35458)	Result (output)	
	Expected output	Predicted Positive	Predicted Negative
		True Positive (TP)	False Positive (FP)
	16486 Positive	15242	1244
		False Negative (FN)	True Negative (TN)
	18972 Negative	1893	17079

As shown in Tab. 2, the proposed system synergized the medical images examined during the training period. 15196 samples were used for training, divided into 6385 negative and 8811 positive samples. When 6112 true positives were successfully forecast, no epidemic was recognized, but 273 records were mistakenly predicted as negatives, indicating an epidemic. Likewise, 8811 samples were obtained, where a negative value reflected an epidemic and positive values indicated no epidemic. With 7540 samples correctly identified as negative, an epidemic was identified. 1271 samples were inaccurately forecast as positive, indicating that there was no epidemic, despite the presence of an epidemic.

Table 2: Proposed model validation using ANN

Proposed Model Validation			
Input	Samples (15196)	Result (output)	
	Expected output	Predicted Positive	Predicted Negative
		True Positive (TP)	False Positive (FP)
	6385 Positive	6112	273
		False Negative (FN)	True Negative (TN)
	8811 Negative	1271	7540

As shown in Tab. 3 (ANN), during training, the performance of the proposed system in terms of accuracy sensitivity, specificity, miss rate, and precision was 0.911, 0.889, 0.932, 0.089, and 0.924, respectively. During validation, the values for the proposed model were 0.898, 0.922, 0.965, 0.063, and 0.982, respectively. In addition, the fall out, likelihood positive ratio, likelihood negative ratio, and negative predictive values for the proposed system during training were 0.067, 13.26, 0.095, and 0.90, respectively, and those during validation were 0.034, 27.11, 0.065, and 0.855, respectively.

Table 3: Proposed model performance in training and validation (ANN)

ANN	Accuracy	Sensitivity TPR	Specificity TNR	Miss-Rate (%) FNR	Fall-out FPR	L+R	L-R	PPV (Precision)	NPV
Training	0.911	0.889	0.932	0.089	0.067	13.26	0.09	0.924	0.90
Validation	0.898	0.922	0.965	0.063	0.034	27.11	0.05	0.982	0.855

Tab. 4 compares the performance of the proposed model in predicting epidemics to the ANN and other previous approaches [18]. The proposed technique was clearly superior in terms of accuracy and miss rate.

Table 4: Comparing the proposed approach with previous strategies

Technique	Accuracy	Miss-rate
ANN [18]	0.60	0.40
Forest j48 [18]	0.77	0.23
Random Forest [18]	0.79	0.21
Random Tree [18]	0.85	0.15
Bayes Net [18]	0.83	0.17
Naïve Bayes [18]	0.83	0.17
The proposed approach for predicting epidemics	0.89	0.11

5 Conclusion

An epidemic describes the spread of a disease within a country or area, and a pandemic occurs when a disease spreads across several countries or continents. There are two types of outbreaks: common source outbreaks, in which a single agent affects the entire population, and propagated outbreaks, in which a disease spreads from person to person. ML techniques are beneficial for automating classification, clustering, and predictions. In most cases, ML techniques have data sets for training and testing. With the help of training data sets, a system can learn to classify test data sets, and by analyzing this classification, one can make future decisions. The analysis indicates that an AI-based intelligent model with an ANN-based ML approach can be used to predict epidemics, with better results than those obtained using previous approaches in terms of accuracy 0.89 and the miss-rate 0.11.

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