

Article title: Cmbatting COVID-19: Artificial Intelligence Technologies & Challenges

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COMBATTING COVID-19: ARTIFICIAL INTELLIGENCE TECHNOLOGIES & CHALLENGES

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Abstract-- AI works proficiently to emulate human intellect. It may also play an important role in understanding and recommending the creation of a COVID-19 vaccine. This outcome-driven technology is utilized for effective screening, assessing, forecasting, and tracking of present and potential future patients. Traditional network designs are unable to cope calmly with the impact of COVID-19 due to massive network data traffic and resource optimization requirements. As indicated by the growing amount of restorative clinical data, artificial intelligence (AI) has the potential to successfully boost the upper limit of the medical and health network. We discuss the primary uses of artificial intelligence technology in the process of suppressing the coronavirus from three main perspectives: prediction, symptom detection, and development, based on an extensive literature study. Furthermore, the advancement of next-generation network (NGN) technologies based on machine learning (ML) has given limitless opportunities for the formation of novel medical approaches. We have also discussed the challenges related to AI technologies in combatting COVID-19. The devastating epidemic of the Novel Coronavirus (Covid-19) has highlighted the importance of accurate prediction mathematical models. We have also discussed different mathematical models, their predictive capabilities, drawbacks, and practical validity.

Index Terms—COVID-19, SVM, Neural Networks, NLP, Mathematical modeling, Gaussian models, Epidemic prevention and control

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1. INTRODUCTION

The COVID-19 epidemic, which was caused by the SARS-CoV-2 virus, has triggered a global catastrophe, putting people's lives and property at risk all over the world. Since the COVID-19 epidemic in December of this year, the total number of confirmed cases has risen to over a million. Currently, there are 51 million people in the country. Even though there are more than 35 million people have been cured of the virus, [1, and 2].

It's worth noting that the number of verified cases continues to rise steadily every year. All information on COVID19 patients should be recorded in time that contains; two weeks, activity trajectories, persons nearby, body temperature fluctuations, and clinical treatment records were all examined. Since network technologies are used to execute the current medical system (prevention, monitoring, and treatment), one issue worth mentioning is that as the number of verified patients grows, tremendous network data traffic and resource requirements have placed severe stress on the network system. Improving the performance of the networks to properly respond to COVID-19 and another global pandemic has become a key issue for all the researchers. The burden of traffic and resource requests brought on by network big data is the present network community's key challenge due to the constant and rapid expansion of medical data. Artificial intelligence (AI) is commonly employed in medical treatment. It not only improves epidemic prevention and diagnosis accuracy but also helps to improve medical research and production efficiency. More crucially, AI big data technology may be used to sample viruses on a global scale and speed the research of virus activity modeling on a national scale, allowing massive outbreaks of identical epidemics to be efficiently predicted and responded to.

In the case of medical image diagnosis, for example, AI's artificial neural network (ANN) technology can reliably detect the image and diagnose COVID19. It reduces the pressure on the network by avoiding the creation of duplicate medical data to some extent. This paper explores the most recent developments in AI in response to the COVID-19 outbreak to further achieve the effective use of AI in the medical network system.

2. COVID-19 AND AI TECHNOLOGIES

In a contemporary medical network system, AI's job should be to completely train the data created in medical trials, including monitoring and diagnosis, case analysis, and therapy recovery and particularly in the fight against COVID-19.

AI has played a critical role in computer tomography (CT), positron emission tomography (PET), and optical and digital microscopy imaging. The use of artificial intelligence (AI) in radiology is a crucial part of the diagnosis and treatment of COVID-19, with deep neural networks (DNN) being the most often utilized AI technology. A deep neural network (DNN) is just a neural network with extra layers. When a biological neural network or an ANN has additional layers, they are all referred to be DNNs. Image recognition is a key feature of the DNN model.

Medical researchers can use the DNN model from the World Health Organization to train the COVID-19 data set (WHO). The ability of AI to accurately recognize lung scanning pictures can demonstrate that it can reach ideal outcomes in epidemic diagnosis, which is difficult for clinicians to do using human resources. The following will describe common AI learning approaches to understand the function of AI in reacting to COVID-19-like diseases. Because of the necessity of detecting and treating COVID-19 patients, the aforementioned AI learning technologies have begun to be tested in the medical network system. Some researchers have developed high-performance medical network architectures from the perspectives of prompt energy efficiency, regional traffic, and spectrum efficiency to assist in monitoring, diagnosing, and treating patients with COVID19 using network technologies driven by AI and ML (5G, Beyond Fifth Generation (B5G), and even 6G), with the help of network technologies driven by AI and ML (5G, Beyond Fifth Generation (B5G), and even 6G.

The authors of [1] recognized two key faults in existing DL algorithms. To begin, model training

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needed a significant number of COVID-19 data sets,

which were sometimes challenging to collect and maintain. Another problem was that DL algorithms were often created and utilized by academics, making them difficult to recognize by healthcare professionals or even the general public. Furthermore, several researchers have merged AI technology with other medicinal approaches. Crowd monitoring is a good technique to stop COVID-19 from spreading. Currently, several nations have taken the necessary steps to keep track of the audience. Installing programmers on mobile phones to track personal activity is a widespread method.

Marotta et al., [2] used a hybrid distributed application to monitor the population at a specific location at a certain time on campus. The program can detect and locate employees using Wi-Fi signals, and it will send a warning if there is a reported instance in the immediate vicinity. Authors in [3, 4] primarily discussed COVID-19's clinical characteristics and preventative approaches, as well as diagnostic and treatment techniques based on DL. The usage of AI technology in all of the aforementioned contributions is severely limited. Hossain et al. [5] proposed that 5G networks use DL to intelligently distribute wireless resources. A deep tree model and a long short-term memory (LSTM) network were developed by the author as a framework for anticipating future traffic congestion. The outcome shows that the framework may ensure a reduced packet loss rate and greater throughput rate.

Li et al. [6] presented a device edge and edge computing paradigm for DNN collaborative reasoning. The framework may divide the calculation between the device and the edge in real-time, reducing the time it takes to calculate the DNN's right size. In addition, the writers took into account the possibility of network oscillations during deployment. To address the problematic challenge of COVID19 data collecting, Jiang et al. [7] suggested a comprehensive CT image processing approach based on a conditional generation confrontation network. This approach may efficiently create high-quality COVID-19 CT images for medical usage, according to the results. Researchers are encouraged by the findings to attempt deploying COVID-19 treatment locations on edge servers to increase COVID-19 treatment efficiency and minimize mortality. It is required to automate the processing of COVID-19 abnormal pictures to lessen the difficulties of manually segmenting the pathological characteristics of CT images.

Paluru et al. [8] suggested a convolutional neural

network based on distorted deep embedding to segregate aberrant features in COVID-19 CT images as a result of this. The lightweight network efficiently reduced the network model's training parameters and enhanced picture diagnostic efficiency, according to the findings. Table 2 summarizes the essential literature on the COVID-19 outbreak response and provides a technical comparison.

3. AI IN DEALING WITH COVID-19

Certain broad AI algorithms are suited for current medical systems at the moment. A collection of approaches that can benefit the global medical and health systems in fighting COVID-19-like outbreaks can be outlined through these tactics. These AI techniques are updated regularly based on enough COVID-19related data. The overall procedure of using AI to battle COVID-19-like diseases is depicted in Fig. 1. Providing data input for the AI system is the first step which usually contains medical information such as medical record reports, medical records, and medical images.

Through sophisticated processing, this data should be translated into a format that medical devices can understand. Data is structured and different large data sets are produced through aggregation, classification, operations throughout and other the data transformation process. This stage is mostly carried out with the help of ML. Researchers can intervene in this process to obtain the most organized and representative data information while minimizing the impact of poor data quality. As previously stated, supervised learning, unsupervised learning, DL, and RL are the most common AI methodologies. DRL algorithm, which is commonly consisting of multi-layer algorithms, can deal with big-scale data sets much beyond human comprehension capacity as a representative ML approach.

Due to its potential to produce somewhat accurate prediction techniques and to finely identify differences in gene sequences of different viruses, AI technology can be attempted and extensively deployed to battle COVID-19-like outbreaks. Numerous more AI technologies have proven effective in clinical applications, in addition to the general AI technologies discussed in the preceding section for identifying and treating pandemic outbreaks.

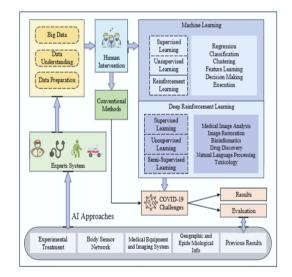


Fig.1. A typical process of AI technologies against COVID-19

(A) Support Vector Machine (SVM):

SVM is a supervised learning linear classifier that classifies sample data [43]. SVM has been used to differentiate imaging indicators of mental and neurological illnesses, to analyze and determine the malignant growth of tumors, and to integrate with other measuring equipment to forecast Alzheimer's disease early, among other uses in medicine.

(B) Neural Network:

ANN and biological neural networks are examples of neural networks. Through intricate fundamental neuron connections, a neural network achieves the goal of information processing. It is commonly employed in medical fields such as stroke diagnosis, malignant tumor analysis, and Parkinson's disease analysis, among others.

Research Content	Method Classification
Prediction	Neural Networks [21, 22, 23]
Symptom Recognition	Neural Networks [24, 25]
Development	Neural Networks [26, 27]

Table.1. Method classification of Neural Networks in the process of inhibiting COVID-19

The first significant relevant neural network applications were associated with the use of artificial neural networks (ANN) with one hidden layer and a finite number of neurons. According to the universal approximation theorem [37], ANN may learn any nonlinear function by estimating the weights of these neurons; however, this may necessitate a huge number of neurons. Deeper neural networks (many hidden layers) may give a more efficient option for modeling complicated multivariate functions, such as the number of people infected with COVID-19. Since each hidden layer of an ANN has its weights and behaves independently, ANN cannot capture sequential information of time series, such as the total number of infected individuals. However, this is readily accomplished using recurrent neural networks (RNN), in which the current state of the hidden layers h at each time step *t* is calculated by integrating the current input *x* with the past state of the hidden layers.

$$Ht = \sigma f = (w_{hh} h_{t-1} + w_{xh} X_t) \tag{1}$$

In this equation, σ is the activation function, w is the recurrent neuron weights, and w is the input neuron weights. The ultimate state of the hidden layers is calculated after the network has progressively processed all of the time series inputs. The prediction of the RNN is given by; where w is the weights of the output neurons.

(C) Natural Language Processing (NLP):

The primary goal of NLP is to achieve effective natural language communication in computer systems. The medical data encountered in current medical therapy is redundant and complicated, and some important data must be removed from it. Typical applications include deciphering the etiology of brain aneurysm disorders and evaluating chest X-ray diagnostic results, among others.

The significance of AI in COVID-19-like epidemics are primarily discussed in three areas: high-risk population surveillance, epidemic breakout and control, and illness treatment and diagnosis. ANN has addressed the complex challenges of current computers in the medical industry as a hot subject of AI research. ANN appears to be specifically created for the COVID-19 pandemic, particularly in the realm of picture identification and analysis.

The schematic fig.2. depicts the function of ANN in controlling COVID-19-like outbreaks. The schematic diagram is composed of five levels. The input layer receives medical data from the database, and the two are intimately related via a high-speed channel. The database may transport a huge number of data packets to the input layer by using a large number of microprocessors and high-performance database processing software. According to the system experience, the selection layer based on the ANN intelligent selector uses the best image technology. If the imaging technique is authorized by medical specialists, the third imaging layer will capture the necessary medical pictures. Imaging methods that are commonly utilized include the aforementioned CT, PET, optical and electron microscope imaging, and so on. The optimization layer is mostly utilized for picture correction and enhancement, which directly influences the doctor's intuitive judgment. This layer frequently uses DL technology and ResNet to extract visual attributes to differentiate different types of epidemics. The diagnosis results are mostly saved and outputted by the final output layer. The input layer's database information may also be immediately communicated to the optimization layer and the output layer, improving diagnostic efficiency by directly comparing to the original data. At the same time, the diagnosis information from each layer may be given back to the input layer to improve the illness information in the database, making further disease diagnosis and treatment easier, [9].

The performance of AI technology is often evaluated in the field of AI. Similarly, when deploying AI technology to tackle COVID19-like outbreaks, assessment indications should be supplied. The assessment indices of AI-based medical technologies in the diagnosis and treatment of COVID-19-like outbreaks primarily involve accuracy, sensitivity, and specificity. The accuracy rate is primarily concerned with the four possible manifestations of the observation object, which are true positive (COVID-19 patients are diagnosed as positive), false positive (non-COVID-19 patients are diagnosed as positive), true negative (non-COVID-19 patients are diagnosed as negative), and false negative (non-COVID-19 patients are diagnosed as negative) (COVID-19 patients are diagnosed as negative). The ratio of the sum of true positive and true negative to the sum of the four is the final accuracy rate. The number of right findings that may finally be identified is referred to as sensitivity. The sensitivity of this AI system is defined as the ratio of true positives plus true positives plus false negatives. Specificity is defined as the estimated repeatability or expected right number, which may be used to calculate the fraction of "healthy" persons among all actually negative people. The ratio of true negatives to the sum of true negatives and false positives is used to compute the final specificity.

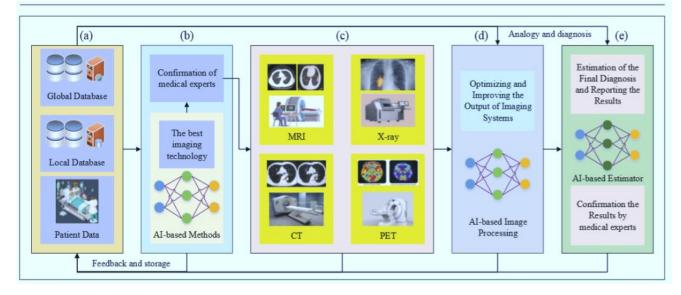


Fig.2. ANN diagnosis of COVID-19- flow chart: a) input layer; b) selection Layer; c) imaging layer; d) optimization layer; e) output layer

4. MATHEMATICAL MODELS AND COVID-19

The mathematical modeling of epidemics has a long and storied history, dating back to 1927 with the Kermack-McKendrick model, [39]. The population is separated into susceptible, infectious, and recovered (removed) sub-populations in this groundbreaking work. Then, specific ordinary differential equations defining the temporal evolution of the functions representing these populations are developed.

In the mathematical epidemiology community, there is an underlying idea that these parameters may, in theory, be calculated from epidemiological data on the number of infected and ill persons. However, the study of the six ODEs demonstrates that this is not possible (on the other hand, it is likely to determine those combinations of the nine model parameters that specify a fourth-order ODE characterizing the time evolution of the number of deaths [38]). It was predicted to be contaminated. These factors necessitate the pursuit of a direct approach to modeling the cumulative number N(t) of persons reported to be infected by a viral epidemic at time t. In this paper, we show that the function N(t) obeys the ordinary differential equation.

Below is a Riccati equation (2) with the timedependent function (t) and the constant parameter N is specified.

$$\frac{dN(t)}{dt} = \sigma(t) \left(N(t) - \frac{N(t)^2}{N_f} \right)$$
(2)

The function (*t*) is determined by the basic properties of the specific virus and the cumulative effect of the many different actions implemented by the given country to limit the spread of viral illness. The reliance of (*t*) on time reflects several time-dependent elements, notably the fact that the effect of the different government measures depends on *t*. The situation of (t) = constant might be thought of as an 'ideal' case. Interestingly, this simple formula is adequate for capturing the evolution *N*(*t*) of typical viral epidemics.

Gaussian Model

The Gaussian model fits a bell-shaped Gaussian function to current data of accumulated fatalities or diagnosed illnesses to project the numbers to future dates. Although the Gaussian Model looks to be very simplistic and unsophisticated, it has a wide range of applications. To begin, GM looks to be a subset of Continuum models, as stated by [28]. To anticipate the emergence of the coronavirus in Italy, a model was created utilizing the Gaussian error function and Monte Carlo simulation [29]. Based on the distribution seen in a seasonal influenza study [30], the total number of diagnosed cases and fatalities in China were fitted using a Gaussian error function with four parameters (see Fig.3).

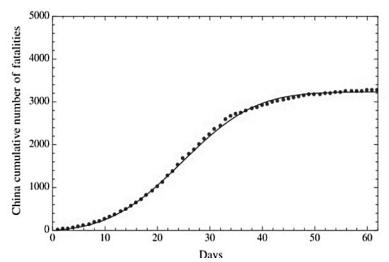


Fig.3. Gaussian Error Function fitted to the cumulative number of deaths caused by COVID-19 in China (red dots) from January 22, 2022

Equation (3) represents the Gaussian function that was employed, where *erf* shows the error function.

$$a + b \operatorname{erf}(cx + d) \tag{3}$$

$$erf(z) = \frac{2}{\sqrt{\pi}} \int_0^z e^{-t^2 dt}$$
 (4)

Another model, comparable to IHME COVID-19, was created to forecast viral transmission in Germany, [41] and Europe, [42]. It varies from the previous work [40] in that it suggests using measured doubling times to estimate the overall duration of the first wave and the point of time with peak fatalities. According to the findings of this article, higher-order coefficients tend to suit noise better than the signal itself. To suit logarithmic daily deaths, a second-order polynomial (GM) is utilized. Daily fatalities as a function of time are indicated by d(t), while total deaths are denoted by *D*. (*t*). And c₀, c₁, and c₂ are coefficients of the polynomial function of degree 2. The Gaussian model employed may be characterized using the equations shown below:

$$d(t) = d_{max} exp\left\{\frac{(t - t_{d,max})^2}{\omega_d^2}\right\}$$
(5)

$$d_m(t) = \frac{dD_m(t)}{dt} \tag{6}$$

$$\ln(dm(t)) = \ln(d_{max} - (t - t_{d,max}/\omega^2 d)^2) = c_0 + c_1 t + c_2 t^2$$
(7)

$$c_0 = \ln d_{max} - \left(t_{d,max}^2 / \omega_d^2 \right), c_1 = 2t_{d,max} / \omega_d^2, \ c_2 = 1 / \omega_d^2$$
(8)

The Flex (i.e., the day when the number of daily positive cases begins to decline) is expected to occur in Italy between March 23rd and March 27th. However, it was spotted on April 3, 2020. Furthermore, the day with the greatest decline in the number of daily positive cases (a fall of more than 100) was expected to be between April 17th and April 27th. This significant decline was noted on the 5th and 6th of April, 2020. The IHME COVID-19 health services use forecasting team created a similar model, [10]. This model predicts the effect of Covid-19 on hospital beds and ventilator demand in the United States. This study's findings were critical in creating lockdown methods and supporting the use of Non-Pharmaceutical Interventions.

A holistic agent model can be used to confirm the applicability of such a paradigm [33]. It has also been found that the breadth of GM is between 10 and 15 days, and the peak in mortality occurs at 20 deaths per million. The major drawback of mathematical models utilizing sigmoidal functions is their propensity to overthe data, (ii) great sensitivity to beginning fit circumstances, and (iii) the huge number of parameters required. However, sigmoidal functions have been recognized for automatically accounting for epidemic curves' exponential development phase and subsequent flattening phase. Most exponential models rely on doubling times, which necessitates considerable data pre-processing. It is vital to emphasize that GM can correctly fit and model data generated by the agentbased method as long as the degree of social distance remains constant. Gaussian models are so simple to execute that no extensive knowledge of statistics or epidemiology is necessary.

NON-PHARMACEUTICAL INTERVENTIONS

Non-Pharmaceutical Interventions (NPI) are actions that individuals and communities may do (apart from immunization and the use of pharmaceutical medications) to help reduce the spread of illnesses such as influenza and Covid-19. These approaches are also known as community mitigation techniques. NPIs are roughly categorized into four classes. (a) Communication for behavioral impact, (b) Personal protective measures (for example, hand hygiene and face masks), (c) Environmental measures (for example, changing humidity and increasing ventilation), (d) Social Distancing measures, and (d) travel-related measures. Confirmatory evidence of efficacy and overall effectiveness in an influenza pandemic has been found in studies[35][36]. The flattening of the curve is critical because a more steady increase in the number of cases may overload healthcare services (see Fig. 4). The logic behind "flattening the curve" is that adequate social intervention methods would stagger the increase in the number of new instances over time. This would minimize the number of active cases during the epidemic's height and relieve pressure on public infrastructure. As a result, more people will have access to restricted medical services.

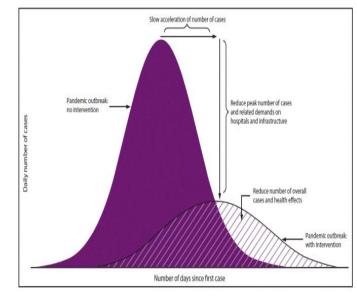


Fig.4. "Flatten the Curve"

Recent research [31] that examined data from the epidemic's early exponential development era revealed the effectiveness of social distance and intervention strategies.

A Bayesian inference method based on Markov chain Monte Carlo sampling is used in a class of compartmental SIR models in this paper. The spreading rate, recovery rate, and reporting delay (D) are all important elements in this model (Equation 9). In this case, **Ro** is the fundamental reproduction number.

$$R_{O=\lambda/\mu} \tag{9}$$

The UK government stated its preparations for a total lockdown on May 8, 2020. In this regard, research[30] was conducted on the consequences of lockdown if it had been imposed one week sooner or one week later. A two-layered Gaussian process in which the upper layer employs a compartmental SEIR model as a prior mean function with country and policy-specific characteristics, while the lower layer parameters are common across all nations. According to the findings of this study, implementing the lockdown one week sooner would have saved 13,827 lives. If it had been enacted one week later, 22,405 more people would have died. Also, if the UK government's current plans to reopen the prison are implemented, daily fatalities would be capped at 200. However, if the lockdown is maintained, the daily death toll will fall below 100 in August, saving an additional 6,215 lives. Integrating epidemic models with health-care and economic models can give a comprehensive framework for anticipating the societal consequences of various policy initiatives.

• Continuum models

State-Space models have been utilized to provide a statistical foundation for our mechanistic knowledge of disease transmission by linking reported incidence illness dynamics with underlying population disease burden and susceptibility. Continuum models can describe the rough dynamics of the disease in the population. Continuum models can project the severity of epidemics as a function of age distributions or the evolution of disease transmission under Non-Pharmaceutical Interventions. The classical SIR model divides the population into 3 groups: susceptible individuals (S), infected individuals (I), and recovered individuals(R). Successive models SIRD, and SEIRD also include e dead individuals (D) and exposed but asymptomatic individuals (E).

The odds of population movement from one compartment to the other are represented by Equations 10 and 11. The symbols and (1/) represent the average value of the chance of disease transmission and the average period during which an infected individual can spread the disease before fully healing, respectively.

$$\frac{dP_t(S)}{dt} = -\rho_{S \to 1} \sum_{N(S)} p_t(S, I), \quad \frac{P_t(I)}{dt} = -\rho_{I \to R} P_t(I), \qquad \frac{P_t(R)}{dt} = -\rho_{I \to R} P_t(I)$$
(10)

$$\frac{dS}{dt} = -\alpha SI, \qquad \frac{dI}{dt} = \alpha SI - \beta I, \qquad \frac{dR}{dt} = \beta I \tag{11}$$

$$\frac{dS}{dt} = -\alpha SI + \gamma R, \qquad \frac{dI}{dt} = \alpha SI - \beta I, \qquad \frac{dR}{dt} = \beta I - \gamma R \tag{12}$$

A fascinating study [42] was conducted that included three forms of the traditional SIR model: a timedependent SIR model, a discrete-time dependent SIR model, and a SIR model that took undiagnosed sick people into account. The following difference equations can be used to construct a discrete-time time-dependent model:

$$S(t+1) - S(t) = \frac{-\beta(t)S(t)X(t)}{n}$$
(13)

$$X(t+1) - X(t) = \frac{-\beta(t)S(t)X(t)}{n} - \gamma(t)X(t)$$
 (14)

$$R(t+1) - R(t) = \gamma(t)X(t)$$
(15)

According to WHO [44], only 87.9 percent of Covid-19 patients suffer fever, and only 67.7 percent develop a

The difficulties that mathematical modelers confront are outlined as follows:

dry cough. In other studies [45, 46] on the result, it is critical to include undiagnosed infected individuals while creating mathematical models. virus's properties have reached similar findings. As The SIR model is intended to account for undiscovered infected individuals, with w1 representing the likelihood of detectable cases and w2 representing the chance of undetectable cases. The entire set of notations used in Equations 5-16 may be found in *Table 2*.

$$\omega_1 + \omega_2 = 1 \tag{16}$$

$$X_{1} (t+1) - X_{1} (t) = \beta_{1} X_{1}(t)_{\omega 1} + \beta_{2} X_{2}(t)_{\omega 1} - \gamma_{1} X_{1}(t) (17)$$

$$X_{12} (t+1) - X_2 (t) = \beta_1 X_1 (t)_{\omega 2} + \beta_2 X_2 (t)_{\omega 2} - \gamma_2 X_2 (t)$$
(18)

$$R(t+1) - R(t) = \gamma_1 X_1(t) + \gamma_2 X_2(t)$$
(19)

(a) Pathogen evolution: Covid-19, like other flu viruses, has experienced mutations, which disturb the model design and dynamically modify parameters.

(b) Statistical uncertainties: The impact of an epidemic in a specific location is determined by unknown factors such as the general population's

underlying immunity. Such variables are subject to significant temporal and geographical fluctuations. Statistical strategies for extracting factors that define the disease's features and transmission patterns from incomplete and noisy surveillance data are still being developed.

(c) Contact Patterns: Laws like "mass action" are predicated on the premise that contagious encounters between people are completely random. However, if individual interactions are not random, it will result in localized saturation of infection, undermining these rules. Such mixing would result in complicated epidemics that would be impossible to anticipate using existing modeling tools.

(d) One model fits all: The adage "one model fits all" does not apply when developing a mathematical model in epidemiology. The nature of the problem aids in determining the best model. The crucial component is not to specify which model is correct but to determine the model that meets the requirements and solves the problem.

Notation	Description	
β	Transmission rate of disease	
$\boldsymbol{\beta}(\boldsymbol{t})$	Transmission rate of disease as a function of time	
B ₁	The disease transmission rate of detectable cases	
B ₂	The disease transmission rate of detectable cases	
γ	Recovery rate	
$\gamma_{(t)}$	Recovery rate as a function of time	
Y (1)	The recovery rate of detectable cases	
γ2	The recovery rate of undetectable cases	
n	Total population	
R ₀	Basic reproduction number	
$R_0(t)$	Basic reproduction number as a function of time	
R(t)	Number of recovered persons at time t	
ω_1	The probability that an infected person is detectable	
ω2	The probability that an infected person is	
undetectabl	e	
X(t)	Number of an infected person at time t	

Table 2. List of Notations Used

5. CHALLENGES IN DEPLOYING AI FOR COVID-19

The most typical constraint in creating cough-based AI diagnoses is the limited amount and low quality of the audio data used to train the system. COUGHVID, COVID-19 Sounds, Verify, and the Indian Institute of Science's Coswara have used crowdsourcing to obtain big datasets, [11, 12, 13]. Although such non-validated data is important for training baseline AI models, it falls short of the construction of reliable and reproducible screening systems since participating users may not represent a representative sample of the population at large. Furthermore, incentives for user engagement other than benevolence are frequently missing, and marketing necessitates major expenditure for extensive data collecting. High data quality is also required, and care must be made to reduce background noise and

prevent audio signal clipping. AI model makers must additionally examine the influence of audio compression and microphone quality across diverse smartphone devices on algorithm performance.

It is important to note that even if some COVID-19 individuals are asymptomatic, they can spread the virus. Although a polymerase chain test can confirm the infection, COVID-19 individuals with pneumonia symptoms may present a pattern on chest X-ray or CT imaging that is only modestly typical for doctors. It is difficult to locate persons who are infected with COVID-19 yet have no symptoms. The accuracy of a single AI diagnostic is still being questioned. To address clinical demands, AI algorithms that integrate chest imaging with clinical symptoms, exposure history, and laboratory testing are necessary for the diagnosis of COVID-19, [17, 18].

Data privacy is another crucial and related concern.

Regulations such as the European General Data Protection Regulation (GDPR) risk multi-million dollar fines for inconsistent permission or data leakage, particularly when it comes to sensitive biometricidentifying data, such as voice samples combined with PCR test results. On certain occasions, various groups have acquired vast amounts of data only to discover later that they were not shareable. Despite the World Health Organization's push to expedite clearance for COVID-19-related developments, regulatory organizations like the United States Food and Drug Administration (FDA) can be slow, and traditionally, they have been slow with AI technology, though efficiency has improved in recent years.

Table.3. shows the associated ML challenges in the diagnosis of COVID-19.

Data is critical for the AI model's building, particularly in the process of neural network construction, when a vast quantity of data is necessary for training and verification. In the age of contemporary information technology, there are several routes for data collecting, which has been of enormous assistance to artificial intelligence technology in the battle against the pandemic. However, the new Coronavirus emerged in late 2019, and the World Health Organization (WHO) proclaimed it a pandemic in March 2020, [19]. The data collecting period was brief, thus there should be a significant proportion of incorrect data. In addition, as shown in Fig. 5, we gathered information from Hopkins on the present global disease spread.

According to Fig.5., the present locations of the world's new coronary pneumonia infections are mostly concentrated in North America, South America, and Europe, with Asia and Africa having a relatively modest number of infections. Furthermore, the prevalence and death rates of COVID-19 vary by geography. This demonstrates that the distribution of the novel coronavirus varies by area. Even though data from several locations may be utilized to construct a model in the process of symptom identification, establishing a generic model in the process of spreading prediction should be challenging.

(Challenges	Perspectives
0	Improve the accuracy of the AI diagnosis	In the diagnosis of COVID- 19, combine chest imaging with clinical symptoms, exposure history, and laboratory investigations.
0	Reduce the false- negative diagnosis rate	Spare capacity for CT and X- ray imaging scans, with the added benefit of quick COVID-19 diagnosis.

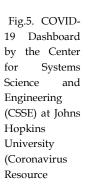
Table.3. Machine learning-based challenges and perspectives on COVID-19 detection

Many researchers have displayed the outcomes of lung picture identification in the current research, however, because the activated heat map has similar colors in aberrant locations, it may indicate comparable consequences for diverse lung illnesses. This was highlighted in Yan et al's, [2020] study, which

compared COVID-19 to common pneumonia infections, as seen in Fig. 5. Only using photos recognized by the AI model, it is impossible to differentiate COVID-19 infected patients.

There may be technological, legislative, and sociological impediments to the broad deployment of AI-based COVID-19 diagnostic tools, but these obstacles are not insurmountable. In reality, the epidemic has presented a once-in-a-lifetime chance to bring together broad groups of eager volunteers to address the issue. Academic and nonprofit workers have led collaborative efforts that have resulted in enlarged and open-access datasets. Coswara and COUGHVID, for example, from both universities, have completely shared their techniques, code, and data, [1445]. Such a global initiative is dependent on the common principles of open-source and transparent datasets and algorithms, as well as a dedication to the vision of making AI-based diagnostics a global reality by overcoming regulatory and societal hurdles.

Cumulative cases (a)









Incidence rate (c)



Case Fatality ratio) (d)



Using cutting-edge technologies is not enough to install a COVID-19 AI diagnostic system. This goal can only be achieved by assembling a varied and multi-national team of specialists and volunteers dedicated to opensource algorithms and standardized data gathering for the greater welfare of mankind, [15, 16]. To combat the spread of COVID-19, it is advised that AI technology be integrated with other technologies. For example, by combining the Internet of Things and artificial intelligence technologies, services such as remote monitoring, data collecting and telemedicine may be realized. The integration of artificial intelligence technologies and cloud computing can increase results accuracy and give medical treatments and other services more swiftly.

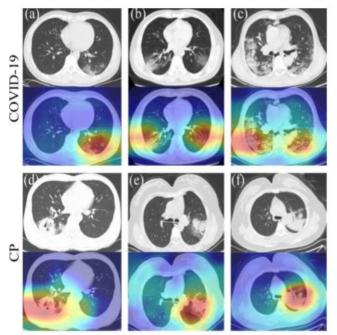


Fig.6. AI system recognition results. (COVID-19: Coronavirus disease 2019; CP: Common pneumonia, Yan et al [20].)

CONCLUSION

AI is being utilized to help with several areas of the COVID-19 epidemic, including epidemiology, molecular research and medication development, medical diagnosis and therapy, and socioeconomics. The combination of AI and COVID-19 can help to diagnose positive patients more quickly. To learn about the dynamics of a pandemic relevant to AI, we conduct a literature search of different AI technologies and their associated challenges. This demonstrates that artificial intelligence technology plays a significant role in coronavirus suppression, yet no model or artificial intelligence technology has an absolute edge in every element. Although AI technology is quick and accurate

in symptom detection, it still has flaws such as limited illness categorization capacity and symptom misjudgment (such as false-negative patients), and doctors' role remains dominating. We have also discussed the mathematical models for predicting COVID-19 among people. A good mathematical model, according to mathematical modelers, represents the data it employs. The lack of noiseless undelayed consistent data is currently the most significant challenge for mathematical models. Data adulteration appears to be occurring mostly as a result of variances in case registration criteria and the unpredictability of Covid-19 symptoms. The Continuum (SIR) family of models appears to be quickly expanding, with everincreasing concerns and variables, resulting in increased differential equation complexity.

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