Design of Epidemic Model For Covid-19 Disease Prediction Using Deep Learning

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KEYWORDS

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ABSTRACT

Promising technologies are available in the developing field of Public Health Surveillance (PHS) to help public health authorities make decisions more quickly by expediting the process of monitoring, analysing, and using unofficial sources. The cornerstone of public health practice is public health surveillance. Influencing policy decisions, spearheading new program initiatives, improving public relations, and helping organisations assess their research expenditures all depend on surveillance data. Public health experts may find that mathematical models are an effective tool in controlling epidemics, which might result in a significant drop in the number of cases and deaths. Moreover, decision-makers can optimise prospective control strategies, including as vaccination campaigns, lockdowns, and containment measures, by using mathematical models to produce long- and short-term forecasts. This work suggests the evolution of epidemics.

1. Introduction

Public health information systems, which are intended to include a wide range of data sources essential to public health action, serve as the foundation for public health monitoring [1]. Public health information systems range from simple systems that gather data from a single source to digital systems that take data in multiple forms and involve intricate surveys [6]. Computer technologies have the potential to improve these systems. Digital technology is still advancing public health monitoring in spite of its drawbacks [2]. For instance, by 1991, all of the health departments in the United States had been computerised by the National Electronic Telecommunications Systems for Surveillance (NETSS) to facilitate the methodical collection, processing, and exchange of data on ailments that needed to be reported. Subsequently, the CDC put into place the National Electronic Disease Surveillance System (NEDSS) to improve and manage the current surveillance systems and enable individuals to react promptly to health risks [12]. Once the nationwide monitoring system is put into place, public health experts and government agencies will be able to recognise and react to epidemics and acts of bioterrorism instantly [3]. The way we organise information, communicate, and approach science has changed as a result of computers and data. Massive dataset curation has revolutionised many industries, enabling previously unthinkable advances. But data by itself is meaningless; instead, we should work to gain information and insights that can be put to use to improve people's lives and impact decisions. The potential of new computer technology to improve the efficacy, capacity, and quality of public health monitoring systems is a topic of much discussion. Using "e-Health," a potentially dynamic health information system, is one example. The term "e-health" is relatively new and refers to medical practice that uses electronic processes and communication [11]. An additional strategy makes use of search engine data to identify outbreaks. Researchers used data from Google Trends (GT) over a 5-year period to study the extremely contagious disease measles in several European nations, and they were able to make an early prediction that was at least two months ahead of time. A recent study on the potential of internet surveillance systems to help spot epidemics early provides another example [4]. The research findings indicate that internet information sources facilitate expedited epidemic identification, reduce expenses, and augment transparency in reporting. Future public health monitoring projects should prioritise advancements in electronic data transmission and integration, patient confidentiality, data protection, and system security, as the number and diversity of systems increase. The revolutionary field of computer vision is enabled by both machine learning (ML) and deep learning (DL). Clinical professionals can receive assistance in interpreting medical imaging data and save interpretation times by using machine learning techniques in computer-aided detection and diagnosis [9]. More data sources from various health imaging systems are anticipated to be included in this AI-driven diagnostics as machine learning becomes more widely available and its analytical capabilities grow.

Framework Of The Proposed Model

The majority of current pandemic models take into account the number of infected but non-quarantined individuals as the infection source for daily new infected cases in the future when evaluating the coronavirus development trend [5]. On the other hand, the infection rate varies depending on the stage of the coronavirus infection. Traditional models reflect the growing trend of an epidemic inefficiently because they assume that all COVID-19 infected individuals have the same rate of virus transmission. According to this article, the majority of newly confirmed coronavirus cases under preventative and control approaches have recently been infected by patients who already have coronavirus infection [14]. However, it can be difficult to detect those who are asymptomatic and hence have the ability to spread the infection. Thus, there is a precise correlation between newly infected cases on day t and reported cases within the last k days. Moreover, there exists a direct correlation between the date of infection and the rate of infection in patients. Due to government initiatives and media attention that can halt the illness's spread, the rate of infection in recently confirmed cases may fluctuate over time on day t during the previous k days. This research uses the ratio of all infected cases at time t to all infected cases throughout different time periods prior to time t to estimate the infection rate based on this assumption. In order to forecast the rate of infection of infected individuals at different times, the proposed model used grouped multiparameter variables to assess the impact of confirmed coronavirus cases at different intervals previous to time t on coronavirus infected cases at time t [7]. The development pattern of the infectious disease is then examined using this improved model. Additionally, the SIQRV epidemiological model is optimised using the hybrid approach of the Evolution Strategy and LSTM network in order to assess the infection rate deviation and calculate the number of infected patients. ES is first used to compute the transmission rate of infection, and the tolerable mortality rate serves as the fitness function, which served as the foundation for the city lockdown settings. [8].

2. Methodology

One of the deep neural network models, the LSTM model [13], processes a sentence word by word until the end. At that point, a hidden layer within the network presents the full sentence semantically. The LSTM model sought to determine the sentence's important keywords and undesired terms. The identified keywords are checked to see if they relate to the same topic, and if so, the same cells may be engaged. Document retrieval is aided by the automatic keyword detection and subject assignment features. Sentence embedding vector computation, a crucial step in determining query and document similarity, is made easier with the aid of LSTM. The proposed model generates a sentence embedding vector, which is helpful for the job of document retrieval. The model is constructed with several layers. TensorFlow is used to implement the embedding layer, and the result.

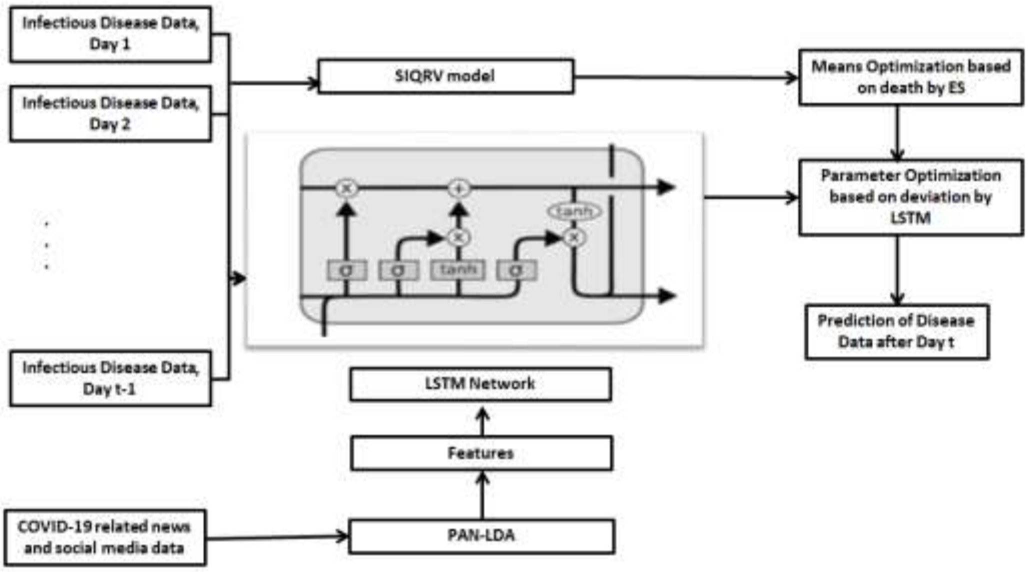
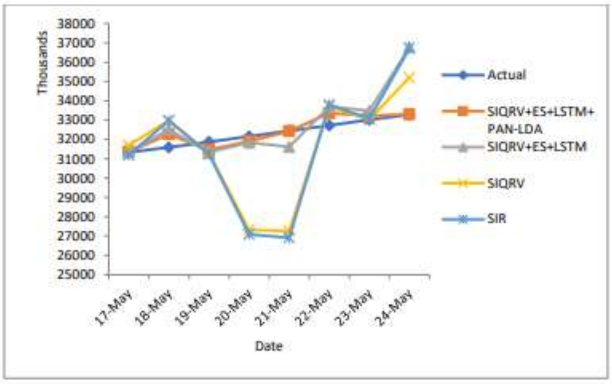


Figure 1: overall proposed framework

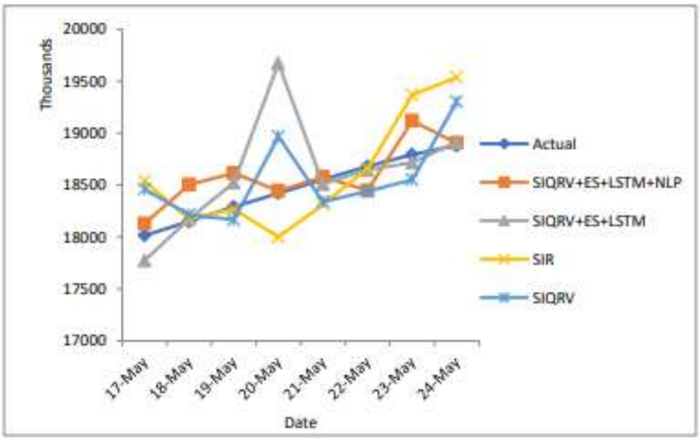
This paper, which is split into two sections, mainly employed ES to optimise model parameters. The first section describes how to optimise lockdown circumstances in a metropolis by utilising the ES. Initially, a starting point value is set for the model, with allowable death serving as the evaluation criterion. A three-day fatality rate of more than 0.045 is deemed unsatisfactory by regulatory criteria. A city's lockdown will be based on the most recent version of the LSTM model parameter, which is saved and updated when the unacceptable high death rate is reached. Run the model with minimal mortality as the fitness function and modify the neural network parameters using an evolutionary method all at once. A twice-evolutionary method is used to develop the ideal neural network parameters, or control measures [10]. Other model parameters are also adjusted using the LSTM method, and to determine if the model has achieved minimal error, historical and model data—that is, the total number of confirmed cases and fatalities—are compared. Additionally, the anticipated number of contaminated instances.

3. Results and discussion

Individuals incubation at different infection time intervals have different infection rates. The infection rate of cases reported on day t may be affected differentially by each newly confirmed patient in the last k days. We look at the effects and time laws governing the spread of epidemics.



(a)



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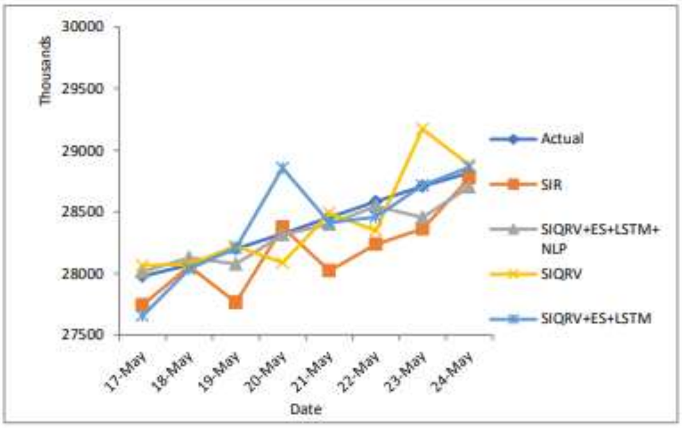

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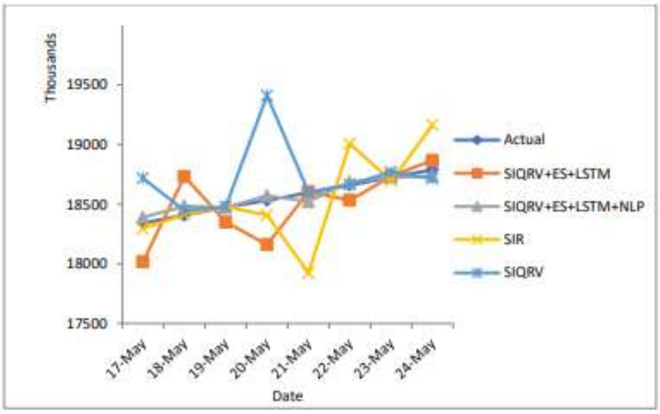

(d)

Figure 3: Actual and Predicted Confirmed Cases for(a) Maharashtra(b) Kerala(c) Karnataka(d) Delhi

In order to make COVID-19 trend forecasts, an epidemiological model called Deep-SIQRV—which is based on machine learning and deep learning methodologies—was developed. It discovered that the infection rates of reported cases fluctuate across different time intervals. The model focusses on the effects of decreasing immunity brought on by vaccinated people becoming susceptible again. The infection rate and other model parameters were optimised by this suggested model using the LSTM network and ES.

4. Conclusion and future scope

The PAN-LDA model was utilised in this study to examine and separate news articles and social media posts pertaining to COVID-19, after which they were encoded as semantic characteristics. These attributes are then used to update the infection rate of the suggested Deep-SIQRV model, which was included into the LSTM network. This research, which aims to predict the COVID-19 trend, claims that infected cases at different times contribute differentially to vulnerable persons. Investigations are conducted into the impact of confirmed cases from a few days before day t on newly confirmed cases on day t. We propose a grouped multiparameter approach that separates current case infection rates into discrete time-based groups. The model's predicted outcomes show a strong degree of agreement with the actual data, suggesting that the suggested model performed a better job of correctly predicting the virus's development trend and transmission law. Additionally, adding language-related data, like relevant news articles and social media posts, improves the prediction model's accuracy. This study demonstrates that developing a revolutionary pandemic prevention system requires a high degree of data realisation efficiency.

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