

RESEARCH ARTICLE

Enhancing CNN-LSTM neural networks using jellyfish search algorithm for pandemic modeling

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Summary

This paper presents a comprehensive three-step approach (CNN-JSO-LSTM) for predictive modeling using a pandemic such as COVID-19 as a test case. Initially, a Convolutional Neural Network (CNN) is employed to extract crucial features pertinent to the pandemic. Subsequently, the Jellyfish Search Optimizer (JSO) algorithm is applied for feature selection, identifying the most relevant factors. These chosen features are then inputted into a Long Short-Term Memory (LSTM) network, responsible for classifying samples into “healthy” and “diseased” categories. Our method enhances LSTM performance using the Jellyfish Search optimizer, resulting in exceptional prediction accuracy. Our experiments achieved remarkable metrics, with an accuracy of 95.32%, high sensitivity (94.87%), and precision (94.28%), surpassing alternative methods. In conclusion, our study presents a promising and highly accurate approach for pandemic prediction, harnessing deep learning and swarm intelligence techniques. These findings suggest a potential for more effective pandemic management and intervention strategies.

KEYWORDS

CNN neural network, COVID-19, deep learning, feature selection, jellyfish search (JS) optimizer algorithm, LSTM neural network, pandemic prediction

1 | INTRODUCTION

The COVID-19 pandemic, caused by SARS-CoV-2, has emerged as a global crisis, akin to previous infectious diseases such as SARS-CoV-1 and MERS-CoV, all inflicting severe respiratory illness. This novel disease was first identified in Wuhan, China, in December 2019. Owing to its highly contagious nature, the World Health Organization (WHO) swiftly declared COVID-19 a Public Health Emergency on January 30, 2020, culminating in its formal designation as a global pandemic on March 11, 2020. By March 6, 2022, this pandemic had claimed the lives of approximately 6 million people worldwide, underscoring its profound impact on public health and global stability.¹

The unprecedented threat posed by SARS-CoV-2 has spurred a global quest to understand the virus, its transmission dynamics, and potential containment strategies. The rapid proliferation of COVID-19 worldwide and its far-reaching economic and societal implications necessitate innovative approaches to disease detection and control.²

Detecting and diagnosing COVID-19-infected individuals is a critical imperative in mitigating the pandemic. While Reverse Transcription Polymerase Chain Reaction (RT-PCR) provides a reliable diagnostic method based on gene sequencing, it has limitations. This technique typically takes four to 6 h to deliver results, rendering it impractical for mass testing and may yield false negatives, thereby contributing to viral transmission.^{3,4} The urgency of early COVID-19 detection to curb transmission and alleviate hospital congestion necessitates alternative diagnostic solutions.

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Medical imaging, particularly Computed Tomography (CT) scans and x-ray imaging, has emerged as an effective means to diagnose COVID-19, offering a valuable solution to overcome some of the limitations of RT-PCR.⁵ These imaging modalities have shown promise in detecting lung infections caused by COVID-19, yet their interpretation is challenging. Radiologists and clinicians may not consistently identify the early signs of COVID-19 in x-ray images, and diagnostic errors in analyzing lung CT scans remain a concern.⁶

The COVID-19 symptoms vary, with fever, dry cough, shortness of breath, and headache being the most common. However, a significant percentage of cases may be asymptomatic, posing a heightened threat to public health. With vaccines and precise pharmaceutical treatments unavailable, diagnostic and preventive measures are pivotal in curbing the pandemic.^{7,8}

Amid this backdrop, innovative technologies have played a significant role in disease diagnosis, prevention, and control. Artificial intelligence (AI), particularly deep learning and machine learning, has gained prominence in the medical domain, offering the potential to streamline and enhance COVID-19 diagnosis. AI-based medical systems have leveraged CT and x-ray images to diagnose COVID-19, some built upon pre-trained models using transfer learning.^{9,10} Additionally, machine learning and data science have been instrumental in classifying and predicting the spread of COVID-19, while machine vision technology has bolstered epidemic control.^{10,11}

To analyze the interconnections between COVID-19 and the fields of Machine Learning (ML) and Deep Learning (DL) across approximately 3000 articles up to the year 2024, VOSViewer software was employed to visualize a comprehensive network graph. This graph elucidates the intricate relationships and thematic clusters that have emerged within the scholarly discourse, highlighting the pivotal role of ML and DL techniques in understanding, predicting, and managing aspects of the COVID-19 pandemic. Through the visualization, key topics, methodologies, and trends can be discerned, demonstrating how advanced computational approaches have become integral in the fight against COVID-19. The articles, extracted from the Scopus database, represent a wide array of research efforts that span epidemiological analysis, vaccine distribution optimization, diagnostic tools development, and enhancement of treatment strategies. The resulting network graph serves as a testament to the interdisciplinary nature of contemporary research efforts and offers insights into the evolving landscape of technological applications in public health crises (Figure 1).

For the image, imagine a detailed and intricate network graph visualized in VOSViewer,¹² showcasing nodes representing critical terms related to COVID-19, Machine Learning, and Deep Learning. Each node's size corresponds to the term's prevalence within the dataset, while lines connecting the nodes indicate the strength and frequency of their co-occurrence in the literature. The graph is color-coded to differentiate between thematic clusters, such as diagnostic models, predictive analytics, and treatment strategies, illustrating the diverse applications of ML and DL in addressing the pandemic's challenges. This visual representation provides a clear and insightful overview of the research landscape, emphasizing the interconnectedness of these fields in advancing our response to COVID-19.

Efforts to predict the spread of COVID-19 have been marred by challenges, particularly the heavy reliance on CT scan images, which may yield significant prediction errors. This paper introduces an innovative approach integrating deep learning and swarm intelligence methods to enhance prediction accuracy. Our method leverages social network and medical center data for a more holistic prediction. In the initial step, a Convolutional Neural Network (CNN) extracts features from Twitter data and medical center information. Subsequently, the output of the CNN is subjected to feature selection using the mermaid algorithm. In the final step, we employ an optimized Long Short-Term Memory (LSTM) network enhanced by the Jellyfish Search (JS) optimizer algorithm for classifying samples as "healthy" or "diseased."

This paper aims to improve the accuracy and timeliness of COVID-19 spread prediction with the intention of saving lives. It introduces a novel approach that combines deep learning methods and swarm intelligence, representing a significant advancement in the field. The contributions of this work include the utilization of a CNN neural network for extracting COVID-19-related features, the introduction of a binary version of the Jellyfish Search (JS) optimizer algorithm for feature selection integrated with the CNN network, and the optimization of LSTM network prediction accuracy through optimal parameter tuning using the Jellyfish Search (JS) optimizer algorithm.

The paper is organized into several sections. Section 2 reviews prior work on COVID-19 prediction. Section 3 details our proposed method, including its formulation and modeling for pandemic prediction. Section 4 presents our method's implementation, analysis, and comparative evaluation with other approaches. Finally, Section 5 offers the results and outlines future research directions.

2 | RELATED WORKS

COVID-19 is an infectious disease that evolved from the coronavirus family virus. In March, the WHO declared COVID-19 to be a global pandemic. The widespread spread of COVID-19 has caused 223 countries to report cases of COVID-19. Reports show that millions worldwide have lost their lives due to the COVID-19 disease. The infected cases and the death rate of COVID-19 are increasing rapidly. The COVID-19 disease has caused the death of millions of people in many countries.¹³

Early detection of coronavirus infections is crucial for epidemic control, resource planning, and prompt treatment of patients. Detecting the initial stages of the virus aids in isolating individuals and swiftly addressing chronic patients. However, the diagnostic process for this disease poses challenges due to the high testing costs, particularly affecting both developed and underdeveloped nations. Machine learning and other learning methodologies are pivotal in diagnosing and forecasting various diseases, as referenced in Reference 13. Notably, CNN and DNN are particularly influential in predicting COVID-19 among deep learning approaches. The most impactful machine learning and deep learning techniques for

with predictive DL methods. In Reference 23, they presented an intelligent early warning system for Twitter data analysis using machine learning (ML). They used the pre-training technique of natural language processing to analyze tweets. In addition, they proposed a linear regression model for predicting COVID-19. Empirical results show that using Twitter data to provide surveillance and forecasting of COVID-19 in the United States is necessary to support the decision-making of health departments. In Reference 24, they presented a method of predicting COVID-19 tweets based on the hybrid word embedding method. During the COVID-19 outbreak, social media platforms such as Twitter provided valuable and massive data to evaluate health-related decisions better. The authors of this research suggested that by using supervised machine learning approaches, users' emotions effectively predict disease outbreaks and provide early warnings. In their method, the collected tweets are preprocessed in the first step. In the second step, various features are extracted from posts using several commonly used techniques, such as TF-IDF, Word2Vec, Glove, and FastText. They used the combination of syntactic features (TF-IDF) with semantic features (FastText and Glove) for feature extraction. Experimental results show that FastText, TF-IDF, and SVM perform better than other models. The tests showed that the SVM method has the best performance, with an accuracy of 88.72%. This study shows that hybrid methods have proven their ability to extract features from tweets. In Reference 25, it is proposed to monitor the information published on the social network during the COVID-19 pandemic using machine learning techniques. In their method, TF-IDF is used for feature selection; then, they presented several machine learning models to predict people's opinions about COVID-19 disease. The experimental results show that SVC is better than other methods in terms of performance and accuracy in predicting users' opinions about COVID-19. In Reference 26, they suggested predicting the symptoms of COVID-19 in social networks through machine learning. Social media are an excellent data source for analysis because they allow people to share feelings, ideas, and even symptoms. This research has analyzed the performance of eight machine-learning algorithms to predict the symptoms of COVID-19. Experiments showed that the random forest algorithm and convolutional neural network are more accurate than other methods in predicting the symptoms of COVID-19. In Reference 27, they proposed using a machine learning approach to predict the probability of recovery of COVID 19 patients based on a healthy diet pattern. Studies show that much of the world's population dies daily from this terrible virus. However, it has been determined that many people also recover from this scary disease. The most important thing behind the recovery against this virus is the strength of the human body's immunity. Unfortunately, immunity is not the same for all people. Human immunity depends on eating habits. They have tried to predict the probability of recovery of COVID-19 patients in South Asian countries based on a healthy diet pattern. They used machine learning methods such as random forest (RF), support vector machine (SVM), and K-nearest neighbor (KNN). Their studies showed that the random forest has the most accuracy in predicting the recovery of patients with COVID-19. In Reference 28, they proposed predicting COVID-19 disease in people with 14 clinical characteristics by machine learning methods. Today, the RT-PCR test is a practical method to confirm the infection of COVID-19. The RT-PCR tests are limited due to the lack of resources, the time-consuming, and the need for specialized laboratories. Most previous studies have focused on chest CT and x-ray images using deep learning algorithms due to the doses of x-ray radiation in CT scan images, high costs, and the small number of available devices. Therefore, a cheaper and faster diagnostic model is needed to identify the positive and negative cases of COVID-19. They developed six prediction models for the diagnosis of COVID-19 using six different classifiers based on 14 clinical characteristics. This study included 114 cases from Taizhou Hospital in Zhejiang Province, China. The results showed that the CR classification method is the most accurate classification for predicting the positive and negative of COVID-19, and its accuracy is 84.21%. Their proposed method will help countries in the early diagnosis of COVID-19, especially when RT-PCR kits are insufficient to test the infection. This issue is vital in developing countries that suffer from the lack of RT-PCR tests and specialized laboratories. The Jellyfish Search Optimizer is a bio-inspired optimization algorithm that utilizes the behavior of virtual jellyfish for exploration in the search space. It promotes diversity and parallel random searches to find optimal solutions for various problems. This algorithm can enhance the performance of machine learning models and neural networks by optimizing parameters and hyperparameters.²⁵ However, the Jellyfish Search (JS) optimizer, has not been extensively explored in the literature for COVID-19 prediction. This article aims to bridge that gap by incorporating the JS optimizer into the proposed prediction model.

3 | THE PROPOSED METHOD

Machine learning techniques are employed to forecast the future status of the pandemic, categorizing it into blue, yellow, orange, and red states. Among these methods, machine learning and deep learning play a pivotal role in predicting the onset of the COVID-19 pandemic. The proposed approach combines deep learning, machine learning, and swarm intelligence to predict the pandemic. This method encompasses feature extraction utilizing a CNN neural network and feature selection via a meta-heuristic approach, along with enhanced predictions using an improved LSTM neural network. Additionally, the LSTM output is refined through majority voting.

3.1 | The framework of the proposed method

Figure 2 illustrates the framework of the proposed approach designed to predict the emergence of the COVID-19 pandemic. This predictive method, based on the conceptual framework, consists of several phases: data gathering from diverse sources like social networks, medical facilities, online

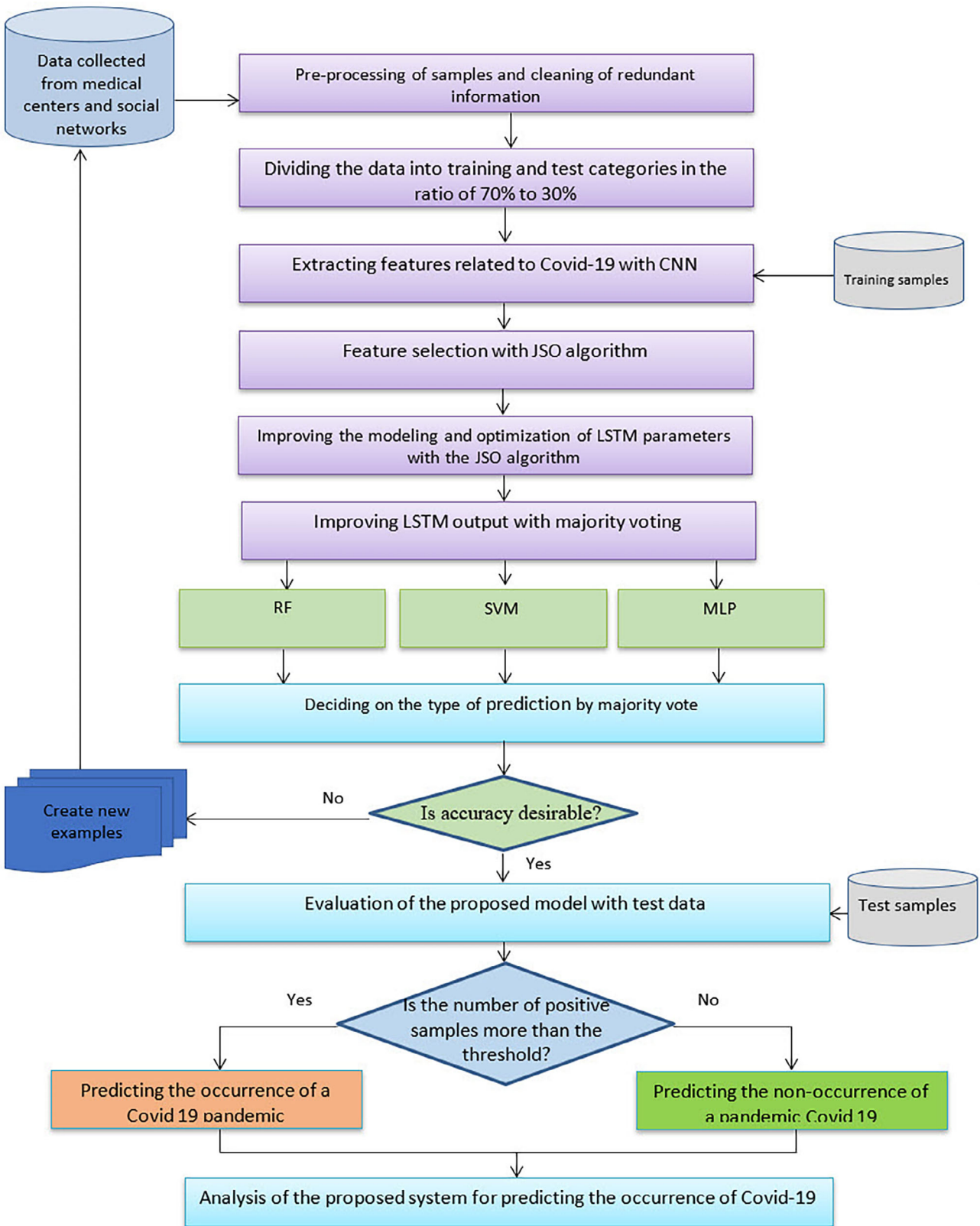


FIGURE 2 Framework of the proposed method.

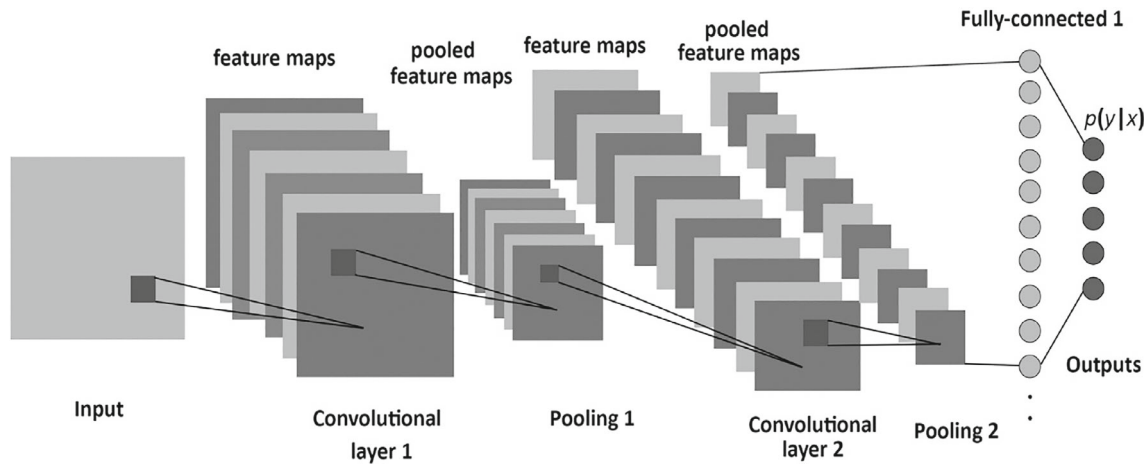


FIGURE 3 Convolutional neural network(CNN) structure for feature extraction.²⁹



FIGURE 4 The structure of a feature vector.³⁰

databases, etc.; data preprocessing and normalization to facilitate feature extraction and selection; optimization of the feature selection stage through swarm intelligence techniques and LSTM enhancements via architectural modifications; optimization of LSTM network parameters using novel meta-heuristic methods; integration of a majority voting phase within the LSTM output to minimize COVID-19 pandemic prediction errors; application of majority voting in conjunction with support vector machine, artificial neural network, and random forest methods to enhance prediction outcomes; in cases where the votes from these three learning methods align and differ from LSTM, the voting result supersedes the LSTM output; assessment of the proposed methodology and an increase in sample volume to enhance prediction model accuracy; and, when the accuracy of the proposed method is deemed suitable, evaluation with test samples to validate the prediction model. Furthermore, comparing positive sample numbers to the total samples is used to predict and issue an alert for an impending epidemic outbreak when the positive samples surpass a predefined threshold.

3.2 | Feature extraction and feature selection

The dataset collects from social networks, medical centers, etc. The CNN neural network is used to extract the primary features of the COVID-19 pandemic. Figure 3 shows the structure of the convolutional neural network for feature extraction.

In the proposed method, the CNN neural network extracts an initial set of features from the data. The features extracted by the CNN neural network are determined as the input of the feature selection phase in the next step. JSO algorithm is used for feature selection in the proposed method. Each feature vector is a member of the JSO algorithm. Suppose a feature vector is encoded as X_i . The feature vector X_i is the i th member of the JSO algorithm. In the first step, several random feature vectors are generated as the initial JSO population. The initial population of randomly generated feature vectors formulates by Equation (1):

$$P = \begin{bmatrix} (X_{11}, X_{12}, X_{13}, \dots, X_{1d}) \Rightarrow X_1 \\ (X_{21}, X_{22}, X_{23}, \dots, X_{2d}) \Rightarrow X_2 \\ (X_{31}, X_{32}, X_{33}, \dots, X_{3d}) \Rightarrow X_3 \\ \vdots \\ (X_{n1}, X_{n2}, X_{n3}, \dots, X_{nd}) \Rightarrow X_n \end{bmatrix} \quad (1)$$

In this equation, n random feature vectors are generated in the first step. Each feature vector has d features related to the COVID-19 disease. Each feature vector, as shown in Figure 4, has zero and one element, which indicates the non-selection of the feature and selection, respectively.

Each feature vector uses the cost function to predict and classify the samples of COVID-19. A multilayer neural network is used to evaluate the feature vectors. The merit of a feature vector or a member of the JSO algorithm depends on the average prediction error and the number of selected features. The appropriate cost function for evaluating feature vectors is presented in Equation (2):

$$\text{Cost}(X_i) = w_1 E(X_i) + w_2 \frac{|X_i|}{d}. \tag{2}$$

In the objective function, $E(X_i)$ is the error in the prediction and classification of COVID 19 samples. $|X_i|$ The number of features selected in the feature vector is X_i . Coefficients w_1 and w_2 are two random values between zero and one. The sum of these coefficients is equal to one, so the objective function is formulated as Equation (3):

$$\text{Cost}(X_i) = w_1 E(X_i) + (1 - w_1) \frac{|X_i|}{d}, \tag{3}$$

$E(X_i)$, or the prediction error of the COVID-19 disease, is formulated in Equation (4).

$$E(X_i) = \frac{\sum_{i=1}^n (y_i - y'_i)^2}{n}, \tag{4}$$

y_i shows the class type of the i th sample in terms of whether or not it is affected by COVID-19. y'_i is the predicted value of the i th sample. n is the number of evaluation samples. The final cost function for feature selection is formulated in Equation (5).

$$\text{Cost}(X_i) = w_1 \cdot \frac{\sum_{i=1}^n (y_i - y'_i)^2}{n} + (1 - w_1) \frac{|X_i|}{d}. \tag{5}$$

Minimization of this cost function by a feature vector shows the competence of a feature vector in predicting COVID-19. Each feature vector is updated under the influence of water waves or active and passive movements of the JSO algorithm. The direction of movement of water waves in the JSO algorithm is formulated as Equation (6):

$$\vec{trend} = \frac{1}{nPop} \cdot \sum \vec{trend}_i = \frac{1}{nPop} \sum (X^* - e_c X_i). \tag{6}$$

The e_c is the tendency of solutions to move towards the optimal solution or food. X^* is the most optimal solution or the best feature vector. $nPop$ is the number of feature vectors. Formulated the direction of movement of jellyfish or feature vectors according to Equation (7).

$$\vec{trend} = X^* - \beta \times rand(0, 1) \times \mu. \tag{7}$$

The feature vectors are updated based on water waves, and Equation (8) is used for this purpose. Equation (8) can be expanded like Equation (9):

$$X_i(t + 1) = X_i(t) + rand(0, 1) \times \vec{trend}, \tag{8}$$

$$X_i(t + 1) = X_i(t) + rand(0, 1) \times (X^* - \beta \times rand(0, 1) \times \mu). \tag{9}$$

In the JSO algorithm, feature vectors have passive and active searches. In the passive search, each vector searches for the lower and upper bounded features of the problem space, as in Equation (10).

$$X_i(t + 1) = X_i(t) + \gamma \cdot rand(0, 1) \times (U_b - L_b). \tag{10}$$

In the active search mode, a jellyfish such as X_i randomly selects a feature vector such as X_j and considers two different states. In the first case, the merit of the feature vector X_i is higher than the feature vector X_j . In the second case, the merit of the feature vector X_i is lower than the feature vector X_j . To update the feature vector in the first case, Equation (11) is used, and in the second case, Equation (12) is used:

$$X_i(t + 1) = X_i(t) + rand \cdot (X_j(t) - X_i(t)), \tag{11}$$

$$X_i(t + 1) = X_i(t) + rand \cdot (X_i(t) - X_j(t)), \tag{12}$$

1. Define the objective function:

$$\text{MinCost} = w_1 * \text{Error}(X_i) + (1 - w_1) * |X_i| / d$$
 2. Initialize parameters:
 - Set MaxIt (Maximum Iterations)
 - Set $t = 1$ (Current Iteration)
 3. Generate an initial population of random feature vectors.
 4. Evaluate the initial population using the cost function.
 - Select the most optimal feature vector (X^*).
 5. Repeat until the stop criterion is met ($t > \text{MaxIt}$):
 - a. For each individual i in the population ($n\text{Pop}$):
 - i. Calculate the time control $c(t)$.
 - ii. If $c(t) \geq 0.5$:
 - The jellyfish follows the ocean current.
 - Determine the ocean current direction:

$$\text{trend} = X^* - \beta * \text{rand}(0, 1) * \mu$$
 - Calculate the new location of jellyfish:

$$X_i(t+1) = X_i(t) + \text{rand}(0, 1) * (X^* - \beta * \text{rand}(0, 1) * \mu)$$
 - iii. Else:
 - The jellyfish moves inside a swarm.
 - If $\text{rand}(0, 1) > (1 - c(t))$:
 - * Jellyfish exhibits type A motion (Passive motions).
 - * Define the new location of the jellyfish.
 - Else:
 - * Jellyfish exhibits type B motion (Active motions).
 - * Determine the direction of the jellyfish.
 - * Calculate the new location of the jellyfish.
 - b. Evaluate the new population using the cost function.
 - Update the most optimal feature vector (X^*) if necessary.
 - c. Increment the iteration counter ($t = t + 1$).
6. Use the optimal feature vector for LSTM network learning.
7. Enhance LSTM error reduction through majority voting.
8. Evaluate the proposed model with test data.

FIGURE 5 Feature selection pseudocode.

The coefficient $c(t)$ determines the type of movement of the algorithm for active and passive search and is formulated in Equation (13).

$$c(t) = \left| \left(1 - \frac{t}{\text{Max}t} \right) \times (2 \cdot \text{rand} - 1) \right|. \quad (13)$$

Equation (13) defines the variables ' t ' and ' $\text{Max}t$ ' as the current and maximum counters within the JSO algorithm. Figure 5, the pseudocode illustrates selecting passive and active movements to update the feature vectors. The steps for feature selection using the JSO algorithm are outlined as follows:

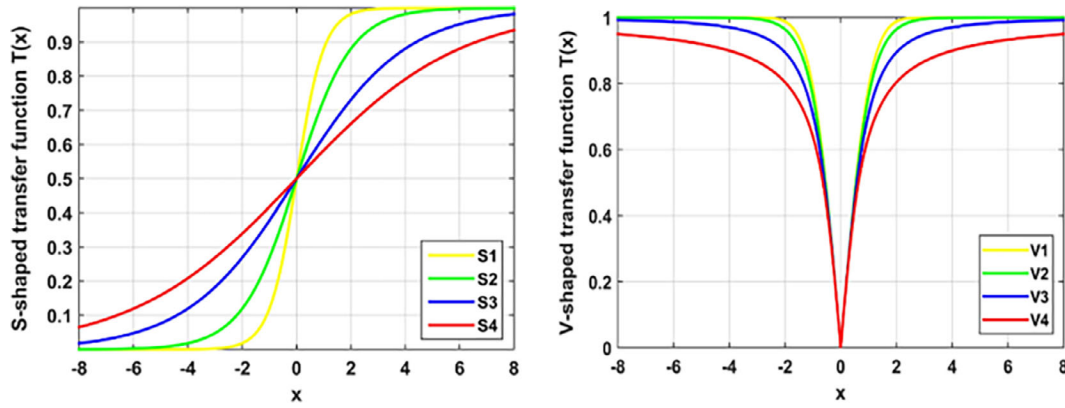


FIGURE 6 From left to right, S and V function to binarize feature vectors.³¹

1. An initial population of random feature vectors is generated as the starting point for the JSO algorithm.
2. The initial population undergoes evaluation using a cost function to identify the most optimal feature vector for predicting the COVID-19 pandemic.
3. Active and passive search phases of the JSO algorithm are executed, directing feature vector updates in line with the wave-based movements.
4. In each iteration, the optimal feature vector for COVID-19 prediction is recalculated.
5. In the final iteration of the JSO algorithm, the optimal feature vector is employed to train the enhanced LSTM model through the JSO algorithm.
6. The error in the improved LSTM output is mitigated by applying majority voting.

$$T(x_i^k(t)) = \frac{1}{1 + e^{-x_i^k(t)}}, \tag{14}$$

$$T(x_i^k(t)) = \left\lfloor \frac{2}{\pi} \arctan\left(\frac{2}{\pi} x_i^k(t)\right) \right\rfloor. \tag{15}$$

In each step of the proposed method, the feature vectors are binarized again with S and V transformation functions. Figure 6 shows the diagram of S and V transformation functions. The equation of two transformation functions, S and V, are formulated as Equations (12) and (13), respectively:

After the process of normalizing the values of the features by the transfer function S and V as in Equation (16), each feature of feature vector is converted to zero or one by the threshold value:

$$x_i^k(t) = \begin{cases} 1 & \theta \leq T(x_i^k(t)) \\ 0 & \theta > T(x_i^k(t)) \end{cases}. \tag{16}$$

3.3 | Pandemic prediction

LSTM is a recurrent neural network (RNN). LSTM network cells have short-term memory units. The LSTM neural network controls the status cell using a forget gate, input gate, and output gate. Figure 7 shows the structure and components used in the LSTM network.

In LSTM structure, f_t , i_t , and o_t three gates are designed to control information flow. f_t controls the information of memory cells from time $t-1$ to time t . It controls the input information to the memory cells at time t . o_t controls the information of the memory cells at time t until the hidden state h_t . Equations (17), (18), and (19), respectively show the formulation of f_t , i_t , and o_t in the LSTM network.

$$f_t = \sigma(w_{fc} \cdot C_{t-1} + w_{fh} \cdot h_{t-1} + w_{fz} \cdot x_t + b_f), \tag{17}$$

$$i_t = \sigma(w_{ic} \cdot C_{t-1} + w_{ih} \cdot h_{t-1} + w_{iz} \cdot x_t + b_i), \tag{18}$$

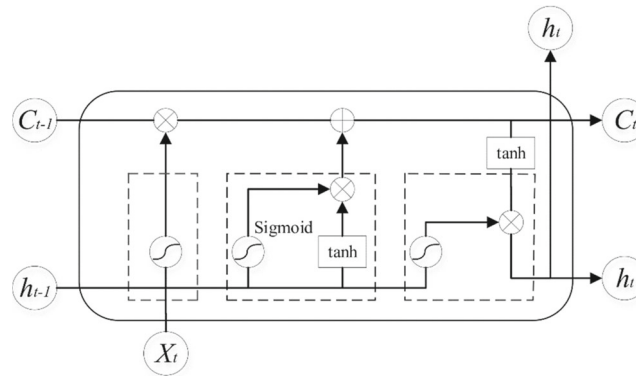


FIGURE 7 LSTM neural network structure.³²

$$o_t = \sigma(w_{O_c} \cdot C_{t-1} + w_{O_h} \cdot h_{t-1} + w_{O_x} \cdot X_t + b_0). \quad (19)$$

In these equations, w_{f_c} , w_{f_h} , and w_{f_x} are the weight matrix between gate f_t and memory cell C_{t-1} . In this method, b_f is the gate bias of f_t . Other weight matrices are derived from the following: C_t and C_{t-1} represent the values of the memory cells at time t and time $t-1$. b_f , b_i and b_o represent the bias and σ is the activation function.

The proposed approach involves training an enhanced LSTM neural network with optimal features while employing a majority voting mechanism incorporating random forest, support vector machine, and decision tree algorithms to refine the LSTM outputs. The primary aim of this majority voting process is to minimize the output errors produced by the LSTM. This methodology optimizes the LSTM parameters to enhance the algorithm's efficiency and reduce errors. It is worth noting that an excessive number of nodes in the LSTM can lead to prolonged training times and potential model non-convergence, whereas using too few nodes significantly compromises the LSTM's learning capability. Therefore, we apply optimization methods to fine-tune the LSTM parameters, mainly focusing on the number of nodes in the input layer, the second layer, and the batch size.

To optimize these LSTM parameters, we incorporate the Jellyfish Swarm Optimization (JSO) algorithm. In Figure 8, the flowchart illustrates the steps for LSTM network optimization within our proposed method:

1. First, LSTM parameters are represented as members of the JSO algorithm.
2. An initial population is generated, comprising random LSTM parameter sets, which are subsequently evaluated using a prediction error index.
3. The most optimal LSTM parameters, or "jellyfish," are selected based on these evaluations.
4. By considering the $C(t)$ parameter in the JSO algorithm, we determine the type of LSTM parameter updates using wave equations and active and inactive behaviors.
5. The JSO algorithm equations are iterated to optimize the LSTM parameters continually.
6. In the final iteration of the JSO algorithm, the most optimal parameters are employed for LSTM predictions.

Furthermore, machine learning algorithms such as MLP, RF, and SVM are utilized to optimize the LSTM prediction type. Specifically, suppose the outputs from these three machine learning methods predict a pandemic occurrence while the improved LSTM predicts otherwise. In that case, adjustments are made to the LSTM output to align with the consensus prediction.

4 | EXPERIMENTS AND ANALYSIS

This section implements the proposed method on tweets and data from medical centers. In this section, the dataset and evaluation indicators are introduced, and then the results of the tests are discussed.

4.1 | Data set

This paper uses several datasets to analyze and evaluate the proposed method. The dataset³³ is one of the datasets related to medical centers that was presented in 2020. This dataset has analyzed the information of 5644 Negative and Positive samples. About 10% of samples are infected with

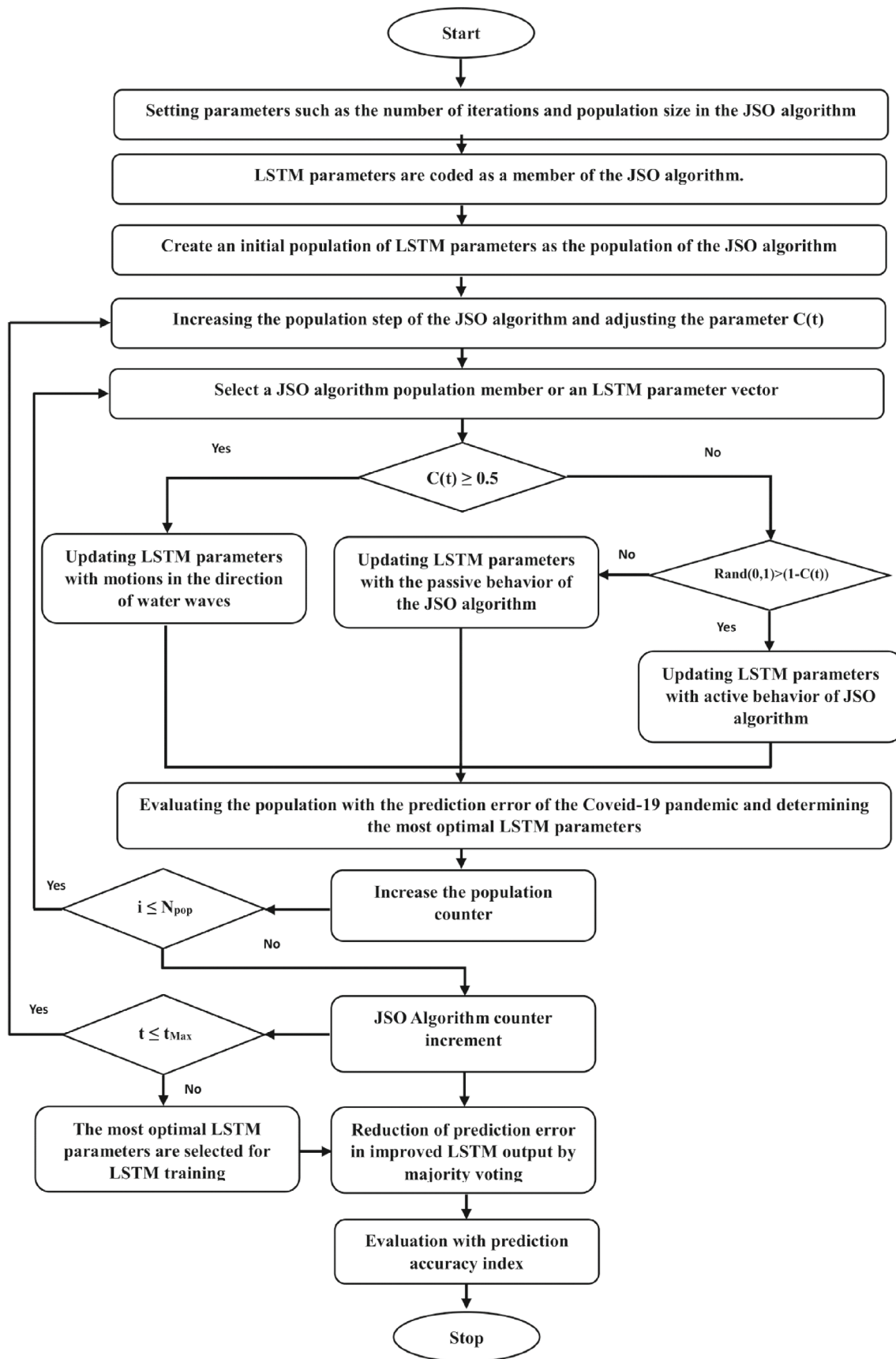
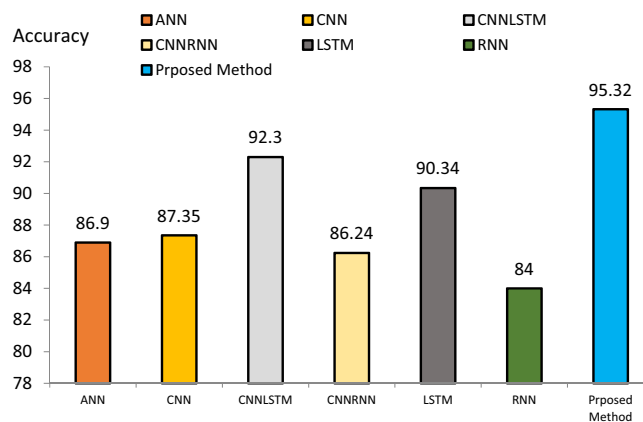
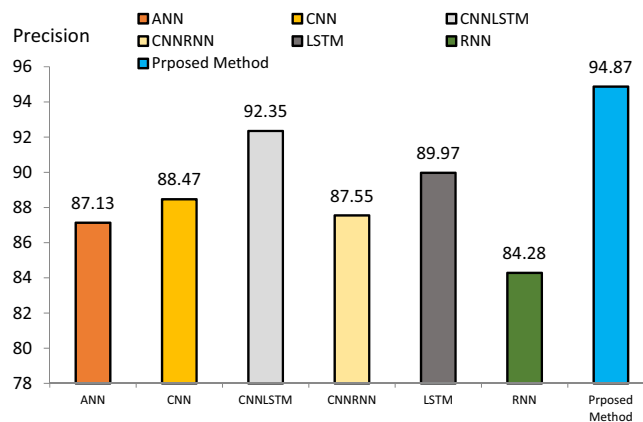


FIGURE 8 Flowchart of the proposed method for optimizing LSTM parameters in the prediction of COVID-19.

TABLE 1 Comparison of precision, accuracy, and sensitivity index with hospital dataset.

Method	Sensitivity	Precision	Accuracy
ANN	87.13	87.13	86.90
CNN	88.67	88.47	87.35
CNNLSTM	93.68	92.35	92.30
CNNRNN	87.55	87.55	86.24
LSTM	89.98	89.97	90.34
RNN	84.27	84.28	84.00
CNNJSO	92.11	93.95	93.24
LSTMJSO	92.25	92.02	92.18
Proposed Method (CNN-JSO-LSTM)	94.28	94.87	95.32

**FIGURE 9** Comparison of the prediction accuracy of the diagnosis of COVID-19.**FIGURE 10** Comparison of the prediction precision of the diagnosis of COVID-19.

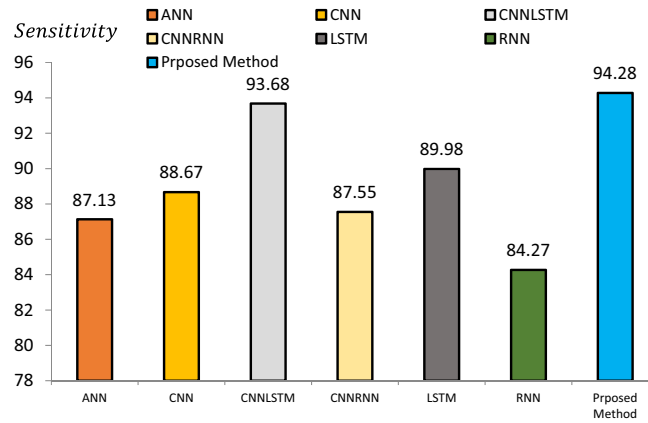


FIGURE 11 Comparison of the sensitivity of the prediction of the diagnosis of COVID-19.

the virus; 10%, between 2.5% and 6.5%, need special care in the hospital. Experiments have also been conducted to evaluate the proposed method on the dataset related to Twitter to analyze user’s opinions about COVID-19.*

4.2 | Evaluation

This article uses accuracy, sensitivity, and precision indicators to evaluate the proposed method. The rule of each evaluation index is formulated in Equations (20)–(22)³⁴:

$$Acc = \frac{TP + TN}{TP + TN + FP + FN} \times 100\%, \tag{20}$$

$$Sensitivity = Recall = \frac{TP}{TP + FN} \times 100\%, \tag{21}$$

$$precision = \frac{TN}{TN + FP} \times 100\%. \tag{22}$$

True Positives (TP), True Negatives (TN), False Negatives (FP), and True Negatives (TN) are used to calculate the accuracy, sensitivity, and precision.

4.3 | Analysis

The implementation software is Matlab 2021. The beta and omega coefficients in the JSO algorithm are set to 3 and 0.1, respectively. The size of the population and the number of repetitions of the JSO algorithm are 10 and 50, respectively. The experiment is repeated 30 times, and the average of the evaluation index is calculated. The number of training and test data in the experiments equals 70% and 30% of the data, respectively. The data’s normalization limit is also limited to [0,1]. The number of hidden layers in the multilayer neural network equals 2. Table 1 compares the proposed method’s accuracy, sensitivity, and precision evaluation index with several deep learning methods such as ANN, CNN, CNNLSTM, CNNRNN, LSTM, and RNN.

According to the tests, the proposed method’s accuracy, precision, and sensitivity index in diagnosing the disease of COVID-19 are equal to 95.32%, 94.87%, and 94.28%, respectively. Experiments show that the proposed method has more accuracy, precision, and sensitivity in predicting COVID-19 than ANN, CNN, CNNLSTM, CNNRNN, LSTM, and RNN methods. The comparison of the proposed method with the accuracy, precision, and sensitivity is shown in the diagram of Figures 9–11.

The accuracy of ANN, CNN, CNNLSTM, CNNRNN, LSTM, and RNN for predicting COVID-19 is 86.90%, 87.35%, 92.30%, 86.24%, 90.34%, and 84%. The comparison of learning methods with the proposed method shows that the proposed method is the most accurate, and the CNNLSTM method is in second place. The accuracy index for predicting COVID-19 in ANN, CNN, CNNLSTM, CNNRNN, LSTM, and RNN methods is 87.13%, 88.47%, 92.35%, 87.55%, 89.97%, and 84.28%. The proposed method (CNN-JSO-LSTM) is more accurate than the others methods in predicting COVID-19. The worst performance in the accuracy index for predicting COVID-19 is the RNN network. The sensitivity index of ANN, CNN,

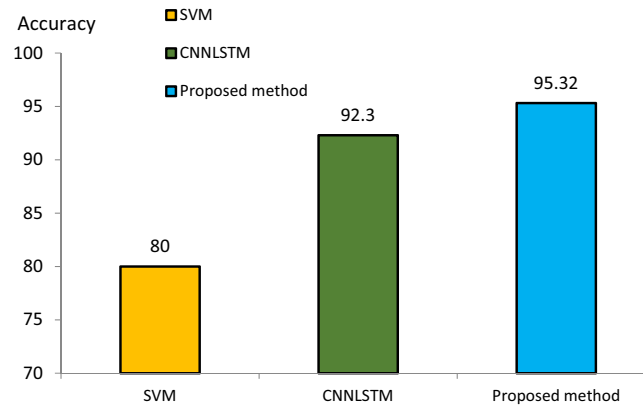


FIGURE 12 Comparison of accuracy with machine learning and deep learning methods for predicting COVID-19.

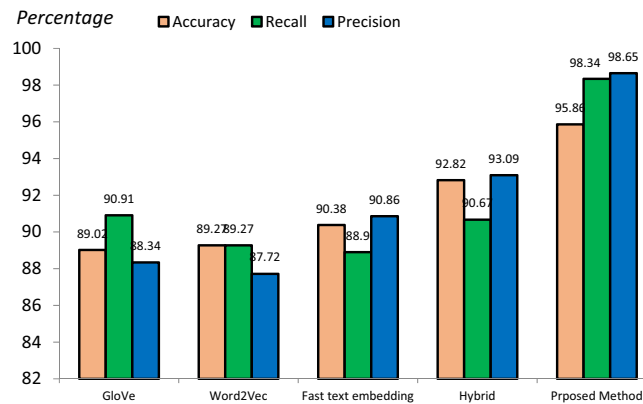


FIGURE 13 Comparison of the proposed method in predicting COVID-19 with the CapsNet method.

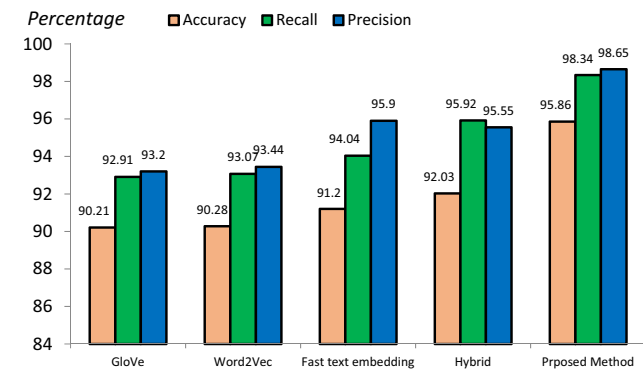


FIGURE 14 Comparison of the proposed method in predicting COVID-19 with the GRU method.

CNNLSTM, CNNRNN, LSTM, and RNN for predicting COVID-19 is equal to 87.13%, 88.67%, 93.68%, 87.55%, 89.98%, 84.27%, while the sensitivity index in the proposed method for The prediction of COVID-19 is 94.28%.

In the graph of Figure 12, the proposed method is compared in the accuracy index with two studies in China and Brazil for predicting COVID-19. In a study conducted in China, an SVM was used to predict COVID-19. In another study, data from Brazilian medical centers used a combination of CNN and LSTM.

The proposed method for predicting the COVID-19 disease has an accuracy of 95.32%. The accuracy of the SVM and CNNLSTM methods is equal to 80% and 92.3%, respectively. The proposed method has improved the accuracy by 3.02% compared to similar architecture such as CNNLSTM. The results were compared in the Twitter social network to evaluate the proposed method. In the diagram of Figures 13–15, the proposed method is compared with CapsNet, GRU, and Ensemble deep learning methods in terms of accuracy, sensitivity, and precision.

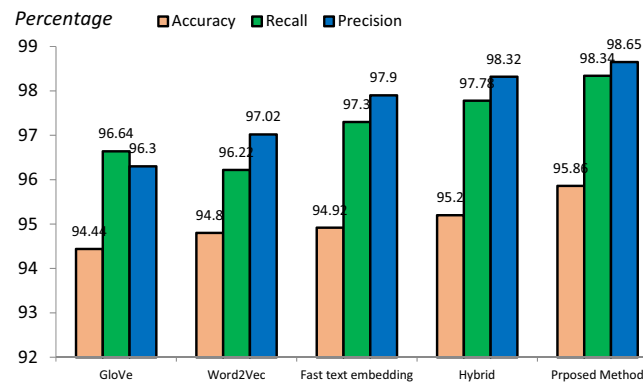


FIGURE 15 Comparison of the proposed method in predicting COVID-19 with the Ensemble method.

GloVe, Word2Vec, Fast text embedding, and Hybrid methods were used in these comparisons. In the diagram of Figure 12, the CapsNet deep learning method is used to predict, and at the same time, GloVe, Word2Vec, Fast text embedding, and Hybrid feature extraction methods are used for it. The comparisons show that the CapsNet method has the highest accuracy and precision index in extracting the combined feature. The proposed method of Word2Vec, Fast text embedding, and Hybrid in combination with CapsNet has more accuracy. The accuracy, sensitivity, and precision of the proposed method for predicting tweets in which people are infected with COVID-19 and have given negative comments are 95.86%, 98.34%, and 98.65%, respectively. If the GRU prediction technique type is selected, then the predictive method is less accurate than this method. Experiments showed that the GRU method is more accurate than the CapsNet method. The proposed method is also more accurate in predicting the disease of COVID-19 than the combined method of GRU and CapsNet.

5 | CONCLUSION

In recent years, the global pandemic, such as the COVID-19 outbreak, has caused substantial loss of life and posed significant challenges to public health. Deep learning methods, including CNN and LSTM, show potential in predicting the spread of such pandemics; however, they need help optimizing their parameters. This research introduces an innovative hybrid approach to improve the architecture of CNN and LSTM networks for pandemic prediction. This approach utilizes data from both Twitter and medical centers and involves a multistep process. Initially, data undergoes preprocessing, followed by feature extraction carried out by the CNN network. Subsequently, the feature selection task is performed using the Jellyfish Search Optimizer (JSO) algorithm. The selected features are fed into the LSTM network, where the JSO algorithm optimizes its parameters. Experimental results using hospital-related data showcase the effectiveness of this proposed method, achieving an accuracy of 95.32%, sensitivity of 94.87%, and precision of 94.28% in forecasting pandemic occurrences. Remarkably, this method outperforms several other models, including Artificial Neural Networks (ANN), CNN, CNN-LSTM, CNN-RNN, LSTM, and RNN. When applied to Twitter data, the approach exhibits even higher accuracy, sensitivity, and precision at 95.86%, 98.34%, and 98.65%, respectively, surpassing models like Gated Recurrent Unit (GRU) and Capsule Networks (CapsNet) in analyzing social media tweets for pandemic prediction. While the proposed method offers improved accuracy compared to standalone CNN and LSTM networks, it involves a more complex implementation. Future endeavors may involve applying the model to predict weather conditions and refining CNN parameters to minimize output errors in this deep-learning technique.

DATA AVAILABILITY STATEMENT

Data sharing not applicable to this article as no datasets were generated or analysed during the current study.

ENDNOTE

*<https://github.com/gabrielpreda/COVID-19-tweets>.

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