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Accurate detection of coronavirus cases using deep learning with attention mechanism and genetic algorithm

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Abstract
The novel coronavirus disease has caused severe threats to the daily life and health of people all over the world. Hence, early detection and timely treatment of this disease are significant to prevent the coronavirus's spread and ensure more effective patient care. This work adopted an integrated framework comprising deep learning and attention mechanism to provide a more effective and reliable diagnosis. This framework consists of two convolution neural network (CNN), a bidirectional LSTM, two fully-connected layers (FCL), and an attention mechanism. The main aim of the proposed framework is to reveal a promising approach based on deep learning for early and timely detection of coronavirus disease. For greater accuracy, the framework's hyperparameters are tuned by means of a genetic algorithm. The effectiveness of the proposed framework has been examined utilizing a public dataset including 18 different blood findings from Albert Einstein Israelita Hospital in Sao Paulo, Brazil. Additionally, within the experimental studies, the proposed framework is subjected to comparison with the state-of-the-art techniques, evaluated across various metrics. Based on the derived consequences, the proposed framework has yielded enhancements in accuracy, recall, precision, and F1-score, registering approximate improvements of 1.27%, 4.07%, 3.20%, and 2.88%, respectively, as measured against the second-best rates.

Keywords Coronavirus disease · Detection · Deep learning · Attention mechanism · Genetic algorithm

1 Introduction

The novel coronavirus (COVID-19) disease that was detected in Wuhan, China (In December of 2019) has evolved into global public health trouble. For this reason, the COVID-19 disease was declared by the World Health Organization (WHO) as an epidemic in April 2020. With the COVID-19 disease being declared a pandemic, healthcare specialists have highlighted the rules of masks, social distance, and hygiene to inhibit the spread rate of this disease. Based on WHO reports, as of March 2022, this

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virus has infected nearly 441 million people around the world, and more than 5.9 million deaths have been confirmed because of this disease. Moreover, the people living in different countries and territories worldwide have been affected by various aspects such as economic, social life, and education [1]. For all these reasons, improving the success ratio in diagnosing the COVID-19 cases is hugely significant.

Diagnosis, treatment, and isolation of infected patients play a critical role in combating the pandemic. Hence, health care providers have widely used a RT-PCR test as the golden standard for diagnosing the virus [2]. On the other hand, it has been reported that this test has an insufficient sensitivity success in clinical studies. Besides, it has some disadvantages: time-consuming, costly, and sophisticated manual processes [3]. Therefore, efforts are made by experts and researchers to develop alternative test methods in detecting the COVID-19 disease.

Unlike the traditional techniques, smart technologies with artificial intelligence are extensively adopted to diagnose and detect diseases in healthcare applications. Notably, due to ensure more effective and reliable results, deep learning approaches have been applied by many researchers in detecting various diseases using clinical and radiological data. The main reason for utilizing deep learning approaches is that they are capable of capturing complicated and non-linear characteristics from the raw data [4]. Deep learning techniques such as CNN and recurrent neural networks (RNN), including LSTM and GRU, have attracted significant attention for the diagnosis of many diseases. Deep learning procedures are employed to achieve more effective results in classifying many diseases, including colon cancer [5], lung diseases [6] breast cancer [7]. In addition to these, deep learning methods combined with the attention mechanism have been adopted to capture superior patterns in various classifying and predicting problems. Furthermore, the attention mechanism is capable of accurately learning discriminative information by weighting different features from sensors data [8]. As a result, deep learning approaches are able to offer opportunities for stable and reliable analysis in identifying COVID-19 cases.

This work addresses a data-driven technique consisting of deep learning and the attention mechanism to accurately ensure the diagnosis of COVID-19 disease using clinical blood findings. The proposed approach based on CNN, bidirectional LSTM, fully-connected layer, and attention mechanism has been introduced to extract high-level representations from blood findings. The components of the proposed approach consisting of CNN and bidirectional LSTM are applied to learn superior features from raw clinical data effectively. The other component comprising attention mechanism is exploited to explore distinguishing patterns from the learned features. With the learned discriminate information, the classification process is carried out through dense layers. The hyperparameters of the proposed framework, comprising the sizes of unit or filters in each layer, learning rate and dropout rate, are simultaneously tuned by a genetic algorithm. Considering the benchmark studies, the experimental consequences showed that the presented approach had revealed a competitive solution to detect the COVID-19 illness successfully. The research highlights its principal contributions in the following manner:

- An integrated deep learning framework consisting of two CNN, a bidirectional LSTM, two fully-connected layers, and an attention mechanism is introduced to effectively diagnose the presence of COVID-19 disease.
- The framework's attentional mechanism is tested for its ability to uncover discriminative information within features.
- The optimization of network hyperparameters is achieved by employing a genetic algorithm.

- The proposed framework's effectiveness is validated through assessments with various machine learning-based and deep learning-based procedures.

The subsequent sections of the research are arranged as follows. Related works about COVID-19 detection approaches are reviewed in Section 2. The technical background of the presented diagnosis procedure is described in Section 3. Besides, Section 4 gives the details of the experimental setting. Further, the outcomes of the deep learning-based approach are discussed. Finally, the conclusions with potential future investigations are explained in Section 5.

2 Related works

With the pandemic's start in December 2019, multiple academic analyses have been conducted regarding the diagnosis of COVID-19 disease. Firstly, comprehensive review works on the disease diagnosis have been carried out by Subramanian et al. [9] and Islam et al. [10]. The existing studies on the detection of COVID-19 disease can be classified in two fields: conventional machine learning and deep learning techniques [11]. Aljame et al. [12] utilized an ensemble approach consisting of the extra trees, random forest, and logistic regression for COVID-19 diagnosis from the clinical laboratory findings. Besides, Kukar et al. [13] proposed a comprehensive comparison using various blood parameters by different machine learning algorithms related to COVID-19 diagnosis. According to this study, the XGBoost, which is a popular machine learning algorithm, achieves more efficient classification results with less computational time.

Deep learning has been extensively tackled as an effective classification and prediction method in recent years due to successfully learning complicated and nonlinear characteristics from raw data. Especially, various hybrid deep learning approaches that integrate CNN and LSTM methods have been proposed so as to reach more effective performance in the classification of the COVID-19 disease. For instance, an integrated framework based on CNN and LSTM methods introduced by Islam et al. [14] are applied to detect COVID-19 disease from medical images automatically. The developed framework obtained an accuracy of 99.4% and a sensitivity of 99.3%. Aslan et al. [15] tackled a deep learning approach with transfer learning consisting of CNN and bidirectional LSTM for the detection of positive COVID-19 cases utilizing chest X-ray images. Besides, the authors in [16] introduced an enhanced snapshot ensemble approach based on deep learning to classify chest X-ray images associated with COVID-19. Zivkovic et al. [17] introduced a hybrid approach consisting of CNN, XGBoost, and an arithmetic optimization algorithm to diagnose the COVID-19 from X-ray images. Kara [18] presented a deep learning procedure comprising CNN, GRU, and fully connected layers to identify the existence of COVID-19 infection from blood findings.

Furthermore, Shankar et al. [19] introduced an integrated approach consisting of a cascaded recurrent neural network and a barnacle mating optimization algorithm for the diagnosis of COVID-19 using radiological data, and its accuracy rate was achieved as 97.31%. In another work [20], the authors addressed a multi-classification deep learning framework based on CNN and GRU for the diagnosis of three diseases consisting of COVID-19, pneumonia, and lung cancer. Goreke et al. [21] combined a deep learning-based model and an artificial bee colony algorithm to diagnose the presence of COVID-19 disease from clinical findings. Alakus and Turkoglu [22] performed a comparison of classification efficiencies obtained by different deep learning-based techniques regarding the COVID-19 detection. An integrated framework based on deep learning and genetic algorithm addressed by Kara [23] was proposed to predict the influenza-like illness.

The attention mechanism has attracted attention as one of the significant concepts in deep learning applications in recent years. This concept was generated by Bahdanau et al. [24], which aims to increase the performance of deep learning approaches by concentrating on high-representative characteristics. With regard to attention mechanisms in the medical analyzes, Ranjbarzadeh et al. [25] produced a data-driven technique that combines a cascade CNN and a distance-wise attention mechanism to determine the localization and segmentation of the brain tumors accurately. Zhou et al. [26] addressed a deep learning framework with an attention mechanism with the aim of capturing the discriminative features for COVID-19 CT segmentation. Xu et al. [27] offered CNN-based deep learning with the mask attention mechanism to diagnose the COVID-19 disease from radiological images. Taking into account the previously mentioned studies to detect the presence of COVID-19 disease, this research aims to focus on the integration of two CNNs, a bidirectional LSTM, and two FCLs to capture the sophisticated and non-linear patterns from clinical blood data. Furthermore, it is concentrated on utilizing the attention mechanism as a means to extract discriminative information from the features. In this research, the hyperparameters of the proposed framework are simultaneously optimized by a GA aiming to boost the accuracy in the classification process.

3 Theoretical background

This part will introduce the technical particulars regarding the proposed approach and its components consisting of CNN and bidirectional LSTM to detect the presence of COVID-19 disease accurately.

3.1 Convolutional neural networks (CNNs)

CNN, which is a particular kind of deep learning, has achieved great significant solutions in many deep learning applications due to successfully capturing complex and nonlinear features. A typical CNN architecture comprises convolution, pooling, and fully-connected layers. A convolution layer is applied to extract high-level patterns using the convolution kernels in the CNN structure. Moreover, the pooling layers help acquire more specific features by decreasing dimensions [28]. One-dimensional (1D) CNN is generally preferred in applications without image classification instead of 2D or 3D CNN [29].

The input sequence data in a convolutional layer is supposed to be $\boldsymbol{x} = [x_1, x_2, \dots, x_N]$, where N represents the sequence length. The convolution operation is formulated as follow:

$$f_i = \delta(w_f \otimes x_i + b_f) \tag{1}$$

$$x_{k:k+h-1} = [x_k, x_{k+1}, \dots, x_{k+h-1}] \tag{2}$$

where f_i is the extracted featured maps, w_f represents the kernel weight, b_f is the bias, and δ is the activation function. The convolution operation, which denotes the mark $\otimes$, is conducted by using a multiplication between a local part of input data $x_{k:k+h-1}$, and a kernel $\boldsymbol{w} \in \mathbb{R}^{hx1}$, where h denotes the kernel size.

3.2 Bidirectional LSTM

To avoid the issue of exploding/vanishing in conventional RNN methods, LSTM layers have been utilized for sequential time-series data in various real-world applications. These layers comprise three different gates for processing sequential data: the input, forget, and output gates. The calculation of the LSTM layer output is as follows:

$$i^t = \varphi(x^t * w_{i,x} + h^{t-1} * w_{i,h} + b_i) \tag{3}$$

$$o^t = \varphi(x^t * w_{o,x} + h^{t-1} * w_{o,h} + b_o) \tag{4}$$

$$f^t = \varphi(x^t * w_{f,x} + h^{t-1} * w_{f,h} + b_f) \tag{5}$$

$$c^t = c^{t-1} \otimes f^t + i^t \otimes tanh\left(x^t * w_{c,x} + h^{t-1} * w_{c,h} + b_c\right) \tag{6}$$

$$h^t = o^t \otimes tanh\left(c^t\right) \tag{7}$$

where i^t, o^t, f^t, and c^t denote the status of input gate, output gate, forget gate, and memory cell at time step t, respectively. x^t represents the input data. h^{t-1} denotes the output data at the previous time step. Furthermore, φ signifies the sigmoid function, and $\circ$ is the element-wise product. The weight matrices are denoted by w, and the bias vectors by b.

The unidirectional or traditional LSTM layers obtain the information of the current state using only the past time information. Conversely, the bidirectional LSTM layers leverage both the previous and future information to predict the output of the current state [30]. As displayed in Fig. 1, the last outcome of bidirectional LSTM is acquired by using forward and backward layers, and the information of state is calculated as follows:

$$h_t^f = \tau(b_{\mathrm{f}} + W_{h,x}^f \times x_t + W_{h,h}^f \times h_{t-1}^f) \tag{8}$$

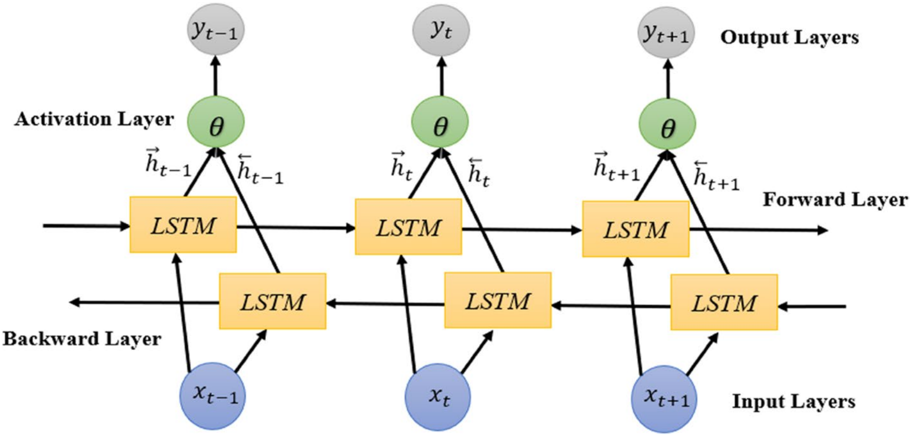


Fig. 1 An example of standard bidirectional LSTM architecture

$$h_t^b = \tau(b_{\mathrm{b}} + W_{h,x}^b \times x_t + W_{h,h}^b \times h_{t+1}^b) \tag{9}$$

$$y_t = \theta\left(W_{h,y}^f \times h_t^f + W_{h,y}^b \times h_t^b\right) \tag{10}$$

where h_t^f and h_t^b represent the forward and backward hidden state, $\tau(\bullet)$ denotes the bidirectional LSTM operations and $\theta(\bullet)$ describes the activation function. Besides, y_t is the output of bidirectional LSTM at time t [31, 32].

3.3 The proposed framework for COVID-19 detection

In the presented framework in detecting the presence of COVID-19 illness using clinical blood findings, two 1D CNN, bidirectional LSTM, attention mechanism, and Dense layers have been employed to learn distinguishing representations from the input data.

Two 1D CNN with different kernel sizes has been adopted to extract superior features from the clinical data effectively. The number of CNN layers is established at 2 through a process of trial and error. The input data of the proposed approach is the dimension of $t \times f$, where t indicates the window size and f describes the feature size. Then, a bidirectional LSTM layer is deployed to successfully extract long-term temporal information from the acquired features obtained by two CNN. The output of the bidirectional LSTM layer is forwarded to an attention mechanism for exploring the discriminative representations from the learned patterns. Next, a FCL is applied to map the characteristics captured in previous layers. Lastly, the other FCL with two neurons is used as the output layer so as to perform the classification of COVID-19 disease. SoftMax function in the last layer is applied and is formulated as follow:

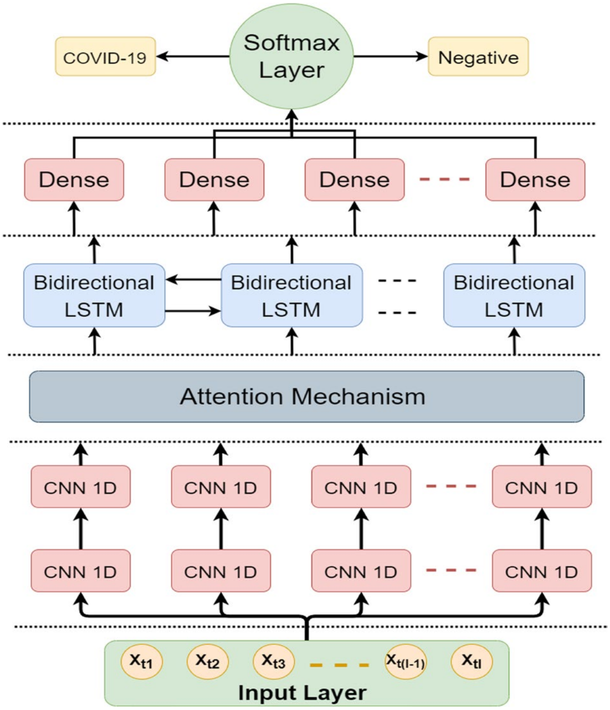
$$\vartheta_i = \frac{e^{z_i}}{\sum_{k=1}^{K} e^{z_k}} (q = 1, 2, \ldots, K) \tag{11}$$

where z_i is the input vector to the function, K represents the number of the classes and ϑ_i is the output vector that contains the probability distributions of the classes. To mitigate overfitting during the training phase, a dropout layer is inserted before each dense layer, and the genetic algorithm optimizes the dropout rate as a decision variable. Figure. 2 depicts the general structure of the presented framework.

In this research, the presented framework comprises three different stages: data preprocessing, training of the network, and testing stages, as demonstrated in Fig. 3. The raw clinical findings are processed to provide more accurate classification results in the data preprocessing stage. Besides, the input data is generated by a sliding window procedure. The training stage is applied to build the optimized network structure utilizing the training dataset. Finally, in the testing stage, the trained proposed framework aims to detect the presence of coronavirus.

This research employs a GA to determine the near-optimal hyperparameters of the proposed network. GA, a meta-heuristic rooted in the principles of natural selection and genetics, falls within the broader category of evolutionary algorithms. This algorithm exhibit strength in systematically exploring large search spaces, enabling the identification of solutions that are near-optimal for complex problem instances [23, 33]. In this paper, the hyperparameters of the proposed approach, encompassing the number of hidden units in

Fig. 2 Network architecture of the presented framework



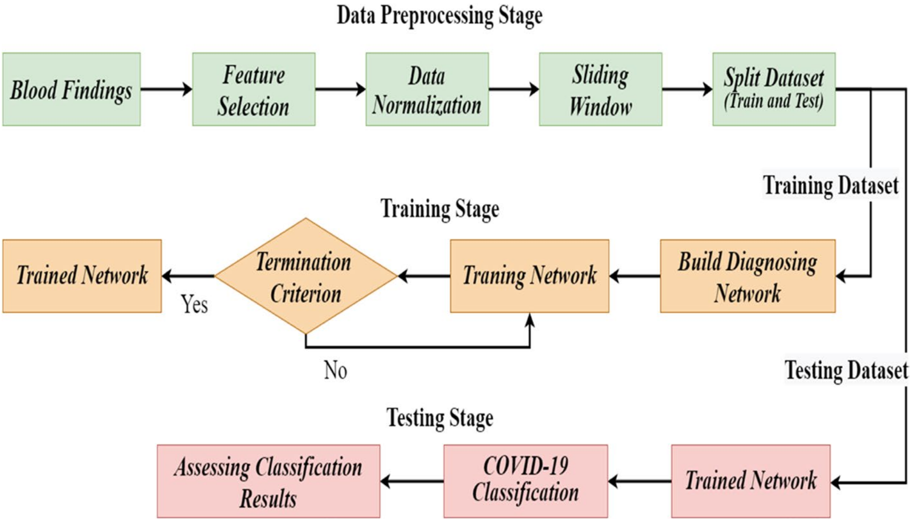


Fig. 3 The presented method flowchart for COVID-19 diagnosis

bidirectional LSTM and fully connected layers, the filter sizes in two CNN layers, as well as the dropout and learning rates, are tuned by means of a genetic algorithm.

4 Experimental setting and results

In this section, it has been introduced the experimental setting and the consequences obtained by the presented framework for the COVID-19 detection.

4.1 Experimental setting

To appraise the performance of the presented approach for COVID-19 disease diagnosis, the dataset introduced by the Albert Einstein Israelite Hospital in Sao Paulo, Brazil, is addressed, which is publicly available via the link https://www.kaggle.com/einsteindata4u/covid19. This clinical dataset, including various blood findings, is acquired from 5644 patients, 559 of whom were infected with the COVID-19 disease. Besides, it has 108 different features and two different labels consisting of negative and positive cases. According to the research of Alakus and Turkoglu [22], the COVID-19 disease is significantly influenced by 18 essential laboratory findings, and it is seen that there exists a lack of data on these specific findings among certain patients. Hence, 18 critical laboratory findings are incorporated, and patients with missing data are excluded from the dataset. After data preprocessing operations, the number of laboratory findings reduced from 108 to 18, and only 600 patients, including 520 negative cases and 80 positive cases, are available in the dataset.

In this paper, the proposed approach's hyperparameters are tuned by the genetic algorithm using the DEAP 1.3.3 library [34]. The tuned hyperparameters comprise the number of hidden in bidirectional LSTM and fully connected layers, the filter sizes in two CNN layers, the dropout and learning rates. Considering the computational time, the size of the units or filters are set as integer values in the range 8 to 64. The dropout rate is set as 0.2, 0.3, and 0.5. Besides, the learning rate is 0.001 or 0.0001. The tuned hyperparameters and others of the network are depicted in Table 1.

Before training the presented approach, the clinical blood data are normalized to be in the range [0, 1] using the Min–Max method as follow:

Table 1 Network parameters

Parameters	Values	Parameters	Values
Filters in CNN	16–16	Activation function	tanh
Kernel sizes	5–3	Loss function	Binary Crossentropy
Hidden units in BLSTM	128	Panding type	same
Hidden units in FCL	64	Optimizer	Adam
Dropout rate	0.3	Learning rate	0.001
Batch size	32	Attention Layer	Dot-product
Number of epochs	250	Number of features	18

$$\overline{x} = \frac{x - \min(x)}{\max(x) - \min(x)} \tag{12}$$

To verify the effectiveness of the presented approach, it is preferred the support vector machine (SVM) algorithm, a deep learning-based fully connected network with two layers, and RNN with two layers. In addition, for the training stage and testing stage, the clinical dataset is split into two different sets with a ratio of 70 to 30 using the train-test split approach. The effectiveness of COVID-19 disease classification techniques is compared the following four metrics: accuracy, recall, precision, and f1-score. These metrics are calculated as follows:

$$Accuracy = (TP + TN)/(TP + TN + FP + FN) \tag{13}$$

$$F1\_score = 2 * TP/(2 * TP + FP + FN) \tag{14}$$

$$Precision = TP/(TP + FP) \tag{15}$$

$$Recall = TP/(TP + FN) \tag{16}$$

where FP, TP, TN, and FN are corresponding to the number of false-positive, true-positive, true-negative, and false-negative samples, respectively. Python 3.8 is utilized to build the presented models in this study.

4.2 Results

In this section, it is introduced the outcomes of the detailed experimental works to evaluate the detection efficiency of the proposed approach for COVID-19 disease. The various benchmark approaches such as baseline techniques and the existing studies in the literature are addressed to validate the classification effectiveness of the proposed framework. In the first experiment, during the training process, the training loss curves of the proposed, RNN and DNN methods are demonstrated in Fig. 4. As illustrated in

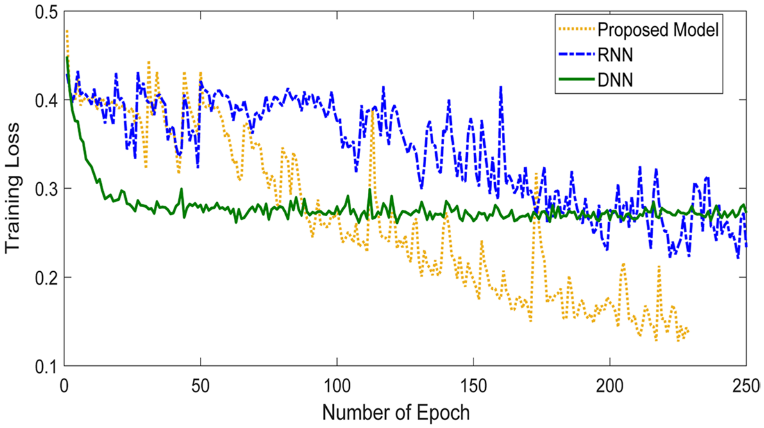


Fig. 4 Evaluation of the training loss curves obtained by different methods

Fig. 4, it is seen that the training loss of each method is minimal level in the past epochs according to the initial epochs. Besides, in the last epoch, it is noticed that the training loss of the suggested technique has decreased more than the other two methods. Thus, the proposed framework provided less training loss at the end of the training phase. The result depicts that the proposed method has successfully converged according to the benchmark methods. The training losses of DNN and RNN have reached almost at the same level in the past epochs. However, the DNN method has converged faster compared to the RNN method.

In order to validate the effectiveness of the presented approach, Table 2 reports an evaluation of prediction outcomes derived from various approach, including baseline methods and state-of-the-art approaches in the relevant literature, in terms of four different metrics. As elucidated in Table 2, the proposed approach yields performance metrics, specifically an accuracy of 91.11%, recall of 91.11%, precision of 90.35%, and F1-score of 90.07%. According to these results, it can be said that the proposed approach gives more acceptable outputs than the baseline methods (DNN, SVM, and RNN) with regard to each comparison metric. In addition, the effectiveness of the presented technique has been evaluated in relation to existing methods discussed in references [22, 35] and [36]. It can be noticed that the presented technique is able to achieve superior classification results compared to the existing related methods. More specifically, compared with the results obtained from methods demonstrating the second highest performance for each metric (Proposed by [36] for accuracy, CNNRNN [22] for recall, precision, f1-score), the proposed approach achieved an improvement of almost 1.27% for accuracy, 4.07% for recall, 3.20% for precision, 2.88% for f1-score. It can be revealed from Table 2 that the proposed method is able to accomplish more accurate classifications in accordance with baseline methods and existing similar studies.

Moreover, Fig. 5 illustrates the confusion matrices obtained by four different approaches, including RNN, SVM, DNN and proposed method, as part of the investigation of the classification performance of the proposed technique. In Fig. 5 (a), it can be seen that the COVID negative cases are detected by the proposed method with a 98.08% success rate and 1.92% error rate. Besides, COVID-19 positive cases are detected correctly with a success rate of 45.83%, while the rate of 54.17% is misclassified. In the RNN method, true-positive and true-negative rates have been observed as 45.83% and 89.74%, respectively. The SVM method is classified as negative in all cases. This means that no COVİD-19 positive cases could be detected. However, it can be revealed that

Table 2 Classification performance of various methods

	Accuracy	Recall or sensitivity	Precision	F1-score
DNN	0.8722	0.8722	0.8444	0.8461
SVM	0.8666	0.8666	0.7511	0.8047
RNN	0.8388	0.8388	0.8473	0.8428
CNN [35]	0.8849	0.7689	0.4151	0.4884
LSTM [35]	0.7850	0.3729	0.3258	0.1936
XGBoost by [36]	0.8771	0.6752	-	0.7145
Proposed by [36]	0.8997	0.7165	-	0.7813
CNNRNN [22]	0.8624	0. 8755	0.8755	0.8755
Proposed model	**0.9111**	**0.9111**	**0.9035**	**0.9007**

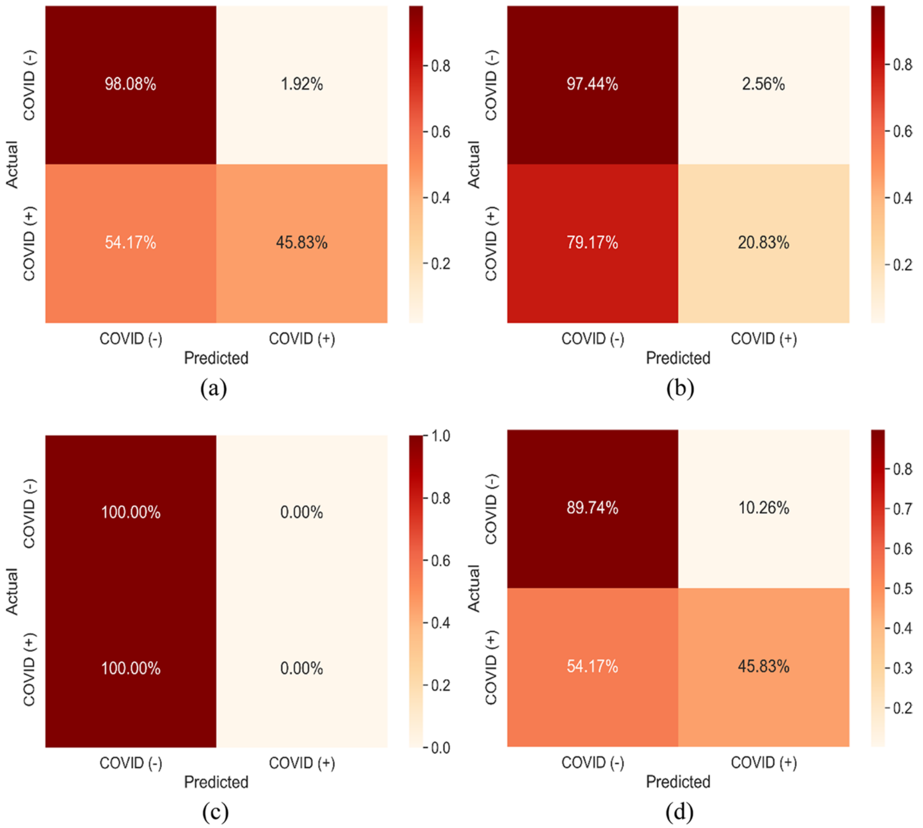


Fig. 5 Comparison of confusion matrices acquired by different methods. (**a**) Proposed, (**b**) DNN, (**c**) SVM, (**d**) RNN

DNN detects COVID-19 negative cases with a rate of 97.44%, and a rate of 20.83% in COVID-19 positive cases. Generally, it is clear that the presented approach provides the best classification with a rate of 98.08% in COVID-19 negative cases compared to other benchmark approaches. In COVID-19 positive cases, the best results with a success rate of 45.83% are achieved by the proposed and RNN methods.

In this research, the classification performances of the situations with or without the attention mechanism in the presented framework are reported according to accuracy, recall, precision, and f1-score in Table 3. The proposed method without the attention mechanism provides an accuracy rate of 90.55%, a precision rate of 89.69%, a recall rate of 90.55%,

Table 3 Comparison of effectiveness under different attention conditions

	With-attention	Without-attention
Accuracy rate	0.9111	0.9055
Precision rate	0.9035	0.8969
Recall rate	0.9111	0.9055
F1-score rate	0.9007	0.8985

and an f1-score rate of 89.85%. Considering the results in Table 3, compared to without the attention mechanism, it is said that the proposed method with the attention mechanism gives better classification results, which effectively captures the discriminative information from clinical blood findings. Overall, the proposed approach has provided a promising solution to accurately detect the presence of COVID-19 disease from clinical laboratory findings taking into account all experimental results. Hence, it can present practical implications for real-world applications, signifying its potential utility across diverse scenarios.

5 Conclusion

This study introduces an integrated deep learning framework, comprising two CNN, a bidirectional LSTM, two fully-connected layers, and an attention mechanism, with the specific aim of effectively discerning the presence of COVID-19 disease. To unravel the complex and non-linear patterns inherent in clinical findings, a combination of two CNNs and a bidirectional LSTM network is applied to effectively discern complex and non-linear patterns. Utilizing an attention mechanism, the exploration of discriminative representations from the acquired patterns is conducted. Furthermore, the genetic algorithm is applied to optimize the hyperparameters of the presented deep learning-based framework.

The effectiveness of the presented framework is experimentally validated utilizing the clinical blood findings. Compared to the machine learning-based and deep learning-based methods, the proposed approach has provided a remarkable solution for diagnosing the presence of COVID-19 disease. In more detail, it is found that the presented method has improved the accuracy, recall, precision, and f1-score by approximately 1.27%, 4.07%, 3.20%, and 2.88% respectively, according to the second-best rates of each performance criteria. It is crucial to note that the proposed approach, while demonstrating promising solutions, faces constraints related to computational overhead, especially in the context of an extensive input data and a comprehensive parameter search space. The identified matter serves as a significant opportunity for improvement in future investigative work. In future research, the focus will be directed towards enhancing classification accuracy by integrating various hyperparameter optimization techniques.

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Data availability The COVID-19 Datasets that support the findings of this study are introduced by in the Albert Einstein Israelite Hospital in Sao Paulo, Brazil. https://www.kaggle.com/einsteindata4u/covid19.

Declarations

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

Informed consent Informed consent was obtained from all individual participants included in the study.

Conflict of interest The authors declare that there is no conflict of interest regarding the publication of this article.

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