An effective detection of COVID-19 using adaptive dual-stage horse herd bidirectional long short-term memory framework

Durga Prasad Mannepalli | Varsha Namdeo

Department of Computer Science and Engineering, Sarvepalli Radhakrishna University, Bhopal, Madhya Pradesh, India

Correspondence
Durga Prasad Mannepalli, Department of Computer Science and Engineering, Sarvepalli Radhakrishna University, Bhopal, Madhya Pradesh, India.
Email: dp.mannepalli@gmail.com

Abstract
COVID-19 is a quickly increasing severe viral disease that affects the human beings as well as animals. The increasing amount of infection and death due to COVID-19 needs timely detection. This work presented an innovative deep learning methodology for the prediction of COVID-19 patients with chest x-ray images. Chest x-ray is the most effective imaging technique for predicting the lung associated diseases. An effective approach with adaptive dual-stage horse herd bidirectional LSTM model is presented for the classification of images into normal, lung opacity, viral pneumonia, and COVID-19. Initially, the input images are preprocessed using modified histogram equalization approach. This is utilized to improve the contrast of the images by changing low-resolution images into high-resolution images. Subsequently, an extended dual tree complex wavelet with trigonometric transform is introduced to extract the high-density features to decrease the complexity of features. Moreover, the dimensionality of the features reduced by adaptive beetle antennae search optimization is utilized. This approach enhances the performance of disease classification by reducing the computational complexity. Finally, an adaptive dual-stage horse herd bidirectional LSTM model is utilized for the classification of images into normal, viral pneumonia, lung opacity, and COVID-19. The implementation platform used in the work is PYTHON. The performance of the presented approach is proved by comparing with the existing approaches in accuracy (99.07%), sensitivity (97.6%), F-measure (97.1%), specificity (99.36%), kappa coefficient (97.7%), precision (98.56%), and area under the receiver operating characteristic curve (99%) for COVID-19 chest x-ray database.

Keywords
classification, deep learning, feature extraction, feature selection, optimization, preprocessing
INTRODUCTION

The novel corona virus disease named as COVID-19 occurred in Wuhan, China, in December 2019 and made a severe community health issue in global. COVID-19 creates only few symptoms in 99% of the people in earlier stage and in the rest it is very critical. Moreover, this is a very infectious disease, and the physicians are more at threat. The huge family of viruses called corona viruses not only affects the humans but also affects various species such as animals and birds. The animal corona viruses once after affecting the human, it can transfer the virus from human to human and currently it is named as COVID-19.

The first stage of detection is the recognition of disease symptoms and specialized signs support to predict the infection of corona virus in individuals. Based on the type of corona virus, symptoms vary from person to person. Unlike SARS, the corona virus not only affects the respiratory system but also affects other organs of human body such as the liver and kidneys. Some of the people are getting early symptoms and some are not getting any symptoms until it leads to severe stage. This is the major cause of the disease and there is a necessity of effective methodology for early-stage prediction.

Chest x-ray is the very essential methodology for the analysis of lung diseases globally because it is the common reliable technology and also not an expensive methodology for the diagnosis. Moreover, chest x-ray produces lowest radiation to patients compared to other imaging techniques. But correct prediction with x-ray images is difficult and it needs better knowledge and experience. The specialist physicians are predicting the COVID-19 only by way of seeing the chest x-rays of patients. Different studies proved that the abnormalities caused by the corona virus in the chest are similar to that of lung opacity. So the methodology to effectively differentiate lung opacity and corona virus is the major need in disease prediction.

Nowadays, COVID-19 prediction is done by chest x-ray of patients by specialized physicians. The prediction of pneumonia in x-ray image is easy but the COVID-19 identification on the same image is a difficult one. Machine learning methodologies are needed to accurately identify COVID-19. There are numerous researches describing COVID-19 prediction but the automatic machine learning methodology using disease prediction is very limited. The absence of effective detection technique makes the need of accurate detection in affected patients. The machine learning–based approaches generally depend on constant expansion of computer mechanisms.

Recently, various image processing machine and deep learning methodologies are presented in prediction of COVID-19 by disease classification with x-ray images. The initial identification of this infectious disease can help to control disease transmission. Some of the existing approaches for the identification of COVID-19 are random forest (RF), decision tree (DT), logistic regression (LR), naïve Bayes (NB), K-nearest neighbor (K-NN), and support vector machine (SVM). To improve the prediction accuracy deep learning techniques are introduced, such as deep learning neural network and convolutional neural network (CNN). CNN is the important classifier for the accurate identification of disease in images. The major contributions of the presented approach are described as follows:

- To improve the performance of the presented approach, adaptive dual-stage horse herd bidirectional LSTM (ADHH-BiLSTM) model–based classification is presented. The presented approach classifies the images into normal, viral pneumonia, lung opacity, and COVID-19.
- To decrease the error in the classification approach, optimization approach is utilized, and it is suitable for reducing the overfitting issues and computational complexity issues.
- To predict COVID-19 accurately, extended dual tree complex wavelet transform with trigonometric transform is utilized for effective feature extraction. The effective feature extraction is important for accurate differentiation of the classes.
- To reduce the dimensionality of the features, adaptive beetle antennae search (ABAS) optimization is utilized. This approach will enhance the performance of classification of disease.
- To prove the efficiency of the presented technique different performance measures will be analyzed with the different existing approaches.

The organization of this paper is described as: Section 2 characterizes the recent related works; Section 3 characterizes the detailed description of the presented methodology; Section 4 describes the results and their corresponding discussion; and Section 5 concludes the paper correspondingly.

RELATED WORK

In this section, various existing approaches to COVID-19 detection using computed tomography (CT) and x-ray images are reviewed. Moreover, the advantages and limitations of the existing approaches are analyzed, and the
limitations are solved in the presented approach. Studies recognize COVID-19 with chest x-rays based on multiple or binary classification. According to the reviews of related works, the deep learning–based network is highly recommended for the recognition of COVID-19.

Narin et al.\textsuperscript{26} presented a deep CNN framework for automatic estimation of corona virus. The five CNN models, such as ResNet50, ResNet 101, ResNet 151, Inception V3, and Inception-ResNet V2, were presented for the identification of corona virus–affected patients with x-ray images. Moreover, the presented approach detects the class of diseases such as normal and COVID-19. Rasheed et al.\textsuperscript{27} developed a novel approach for the identification of COVID-19 in x-ray images. LR and CNN classifiers were utilized. Furthermore, principal component analysis (PCA) was introduced in this technique for the dimensionality reduction and to increase the classification accuracy. The deep neural network with generative adversarial network was further utilized for enhancing the classification accuracy and reducing the overfitting errors.

Ibrahim et al.\textsuperscript{28} presented a pneumonia prediction with deep learning–based technique in x-ray images through COVID-19 pandemic. Here, the deep learning technique with pretrained AlexNet model exploited the better classification of COVID-19 and normal images. The non-COVID-19 classes includes pneumonia caused by virus otherwise bacteria. The introduced model was trained to achieve two-stage classifications only. The developed framework provides better accuracy but still there was a possibility of improvement in accuracy. Amyar et al.\textsuperscript{29} introduced an innovative multitask deep learning–based technique to jointly identify the COVID-19 patients by images. The three combined tasks such as segmentation, classification, and reconstruction were utilized for disease prediction. Moreover, the presented technique comprises of general encoder technique for separated features representation with these three tasks. For the reconstruction, two decoders with multi-layer perceptron model were utilized. Further classification was performed corresponding to the data.

Apostolopoulos et al.\textsuperscript{30} presented a deep learning–based methodology to extract the effective features from x-ray images, which helps to differentiate the diseases. This framework extracts the high-dimensional features and then makes the classification decision based on the extracted features. This differentiates the x-ray images into COVID-19 and normal classes. The framework was compared with the existing CNN for proving the effectiveness of developed approach. Hassantabar et al.\textsuperscript{31} introduced CNN and deep neural network (DNN) methods for the prediction of COVID-affected persons which depend on CT and x-ray images. Here, fractal features were extracted using the DNN, and CNN framework was also utilized for the accurate identification of corona-affected patients through lung x-ray images. To analyze the efficiency of disease prediction, the novel CNN and DNN approaches were compared in terms of binary classification using metrics such as miss rate, accuracy, fallout, similarity, and so on.

Toğacı et al.\textsuperscript{32} developed a COVID-19 identification framework using deep learning algorithms with optimization and fuzzy color stacking techniques. Here, the images were preprocessed using fuzzy color technique. Further, the stacked dataset was trained by MobileNet V2 and SqueezeNet based deep learning models. By employing the social mimic optimization methodology, the efficient features were chosen from the feature sets obtained from the deep learning models. Afterward, features were united and categorized by utilizing SVM approach. Gupta et al.\textsuperscript{33} presented a deep learning classification approach for the accurate identification of COVID-19 patients on x-ray images. The integrated stacked DNN (InstaCovNet-19) was introduced in this work for the prediction of corona virus–affected people. To accomplish the effectiveness in disease prediction, different models such as ResNet 101, Inception V3, Xception, MobileNet, and NASNet were utilized in the training process. Moreover, the developed framework classifies COVID-19 and pneumonia based on the causes of their abnormalities in x-ray images.

Das et al.\textsuperscript{34} introduced an ensemble learning with CNN for automatic detection of COVID-affected patients in x-ray images. The ensemble-based learning structure, comprising ResNet 50 V2, DenseNet 201, concatenated network, and Inception V3, was utilized in the presented framework. These networks were independently trained to achieve the accurate classification of images. The images were categorized into positive otherwise negative classes in the x-ray images to identify the corona-affected patients. The average accuracy (91.62%) obtained was very lower. Rehman et al.\textsuperscript{35} developed a self-activated CNN framework for multiple class COVID-19 recognition. Two-way classification process was considered in the presented approach. In one way, a deep learning–based CNN was considered. In second way, transfer learning was considered with deep CNN for getting deep features. Finally, the classification was performed with the machine learning–based classification approach. The developed approach obtained the accuracy of 87.89%. The resultant accuracy performance can be enhanced further by considering the significant methodology.

Das et al.\textsuperscript{36} presented a deep transfer learning–based model for the effective prediction of COVID-19 in chest x-ray images. Xception network was utilized to train the network weights in larger datasets as well as fine-tuning was done. The overall performance was evaluated based
on three class such as pneumonia, COVID-19 (positive), and other infection except pneumonia and COVID-19. Chouhan et al.\textsuperscript{37} introduced an innovative transfer learning approach for the detection of pneumonia in x-ray images. Here, the features were extracted by utilizing the deep learning framework. Afterward, the ensemble classifier network is utilized for the recognition of pneumonia. The introduced approach for pneumonia recognition attained the accuracy of 96.4%. This achieved performance can be improved further and the COVID-19 detection was suggested in future.

Chimmula and Zhang\textsuperscript{38} developed a time-series prediction using LSTM framework in detecting the transmission of COVID-19 in Canada. Initially, the input data were analyzed to predict the key features on the number of new reported cases comparing with previous infections. Recovery rate was used as an important feature in building the LSTM model. The Canadian dataset is used to train the LSTM framework and the performance on accuracy obtained was 93.4% with RMSE 34.83. Moreover, the error was very high as 51.46 when the LSTM model trained on Italian dataset. Aslan et al.\textsuperscript{39} presented the detection of COVID-19 infection using hybrid BiLSTM network. The detection procedure involves the combination of dual architectures. Lung segmentation was performed using artificial neural network to acquire the robust features. The pretrained AlexNet model was used along with BiLSTM network, which allows the temporal features and helps attain higher classification in COVID-19 detection against other state-of-art approaches. The major drawback was limited detection accuracy of 98.70% and the performance was tested with only one database.

Joloudari et al.\textsuperscript{40} presented the diagnosis of COVID-19 in the images of CT scan using deep neural network-global feature extractor (DNN-GFE). The DNN-GFE approach was developed to perform accurate diagnostics in categorizing normal and sick individuals. The image normalization procedure was utilized to generate images of good quality and to enhance the COVID-19 diagnosis. The accuracy of classification obtained with the CT images was 96.71%, whereas the existing classifiers DT-GFE (84.57%) and RF-GFE (85.62%) gained lower results. Khoeimeh et al.\textsuperscript{41} developed a model for predicting COVID-19 in CT images combining CNN-autoencoders (CNN-AE). The chance of survival was analyzed accurately with CNN-AE considering the clinical features. Data augmentation (DA) process was followed to balance the number of samples of diverse classes from the dataset. The overall accuracy obtained was 96.05% with DA which has outperformed traditional CNN without DA (92.49%).

Sharifrazi et al.\textsuperscript{42} presented accurate COVID-19 detection in x-ray images using fusion (CNN + SVM + Sobel)-based architecture. Initially, the images were preprocessed with the Sobel filter to obtain the accurate edges. Next, these images were fed to the deep learning CNN classifier and SVM, which allows a 10-fold cross-validation strategy. The accuracy of classification gained with the x-ray image analysis was 99.02%. The use of Sobel filter has improved the classification performance compared to the accuracy gained with sigmoid function (92.94%). Ayoobi et al.\textsuperscript{43} developed a time series forecasting using deep learning (DL) in identifying the new cases on COVID-19 and death rates. Here the real-time forecasting was encountered by analyzing the prediction of every $n$ day ($n = 1, 3, 7$). The data were collected from the WHO website. The DL models used for the analysis were convolutional LSTM, Gated recurrent unit (GRU), and LSTM. The average error was evaluated with the dataset gaining LSTM (0.492), Con-LSTM (0.71), and GRU (0.494). The statistical analysis was done using the Friedman test.

Alizadehsani et al.\textsuperscript{44} introduced COVID-19 detection in CT images with the uncertainty-aware semi-supervised classification (SC) approach using limited labeled and large unlabeled COVID-19 data. The classification using the semi-supervised limited labeled data (LLD) was processed for detecting COVID-19 automatically. To enhance the classification accuracy, Sobel detector was used. The performance of SC-LLD was analyzed with accuracy (99.60%), specificity (99.80%), and sensitivity (99.39%). The classifier accurateness was evaluated and compared with supervised CNN model and gained lower performance as accuracy (69.87%), specificity (46.40%), and sensitivity (94%). Hemdan et al.\textsuperscript{45} presented a framework on DL techniques for the automated COVID-19 detection as well as forecasting. This paper discusses various DL methods for automatic diagnosis of COVID-19, which make use of x-ray images.

The increasing number of COVID-19 patients makes high need of accurate detection of corona patients. The medical practitioners all over the world need an effective model for the accurate identification of COVID-19 disease. In the existing approaches, different techniques are utilized for the prediction of pneumonia. But still, detection of various strains of pathogens by utilizing molecular testing is still not up to the standard level for the diagnosis. Moreover, medical practitioners collecting the specimen are also affected. So, the machine learning technique–based methodologies are utilized for disease prediction. This provides accurate prediction and also safety to the physicians. Moreover, the difficulties in the prediction of COVID-19 in existing techniques can be overcome by the presented approach. The x-ray images with deep learning methodologies can provide fast and accurate detection of disease. Moreover, the majority of
the approaches introduced in existing techniques are only concentrated on two classes such as normal and COVID-19. But the presented approach classifies the images into normal, or lung opacity or viral pneumonia, or COVID-19.

3 | PROPOSED METHODOLOGY

This work presented an effective detection of COVID-19 using adaptive dual-stage horse herd BiLSTM framework. Initially, the input images are preprocessed using modified histogram equalization (MHE) for enhancing the contrast of an image. Afterward, extended dual tree complex wavelet transform with trigonometric transform is utilized for extracting the effective features. Subsequently, ABAS optimization is utilized to lessen the dimensionality of the features and to choose the optimal set of features. Finally, adaptive dual-stage horse herd BiLSTM structure is utilized for the accurate prediction of COVID-19, normal, viral pneumonia, and lung opacity in x-ray images. The schematic diagram of the presented methodology is depicted in Figure 1.

3.1 | Image preprocessing using MHE

Histogram equalization is an important technique used to enhance the contrast of an image. In this study, an improved version of histogram equalization called MHE is proposed for performing image preprocessing. The equalization of histogram changes the pixel’s intensity in uniform through the equal distribution of pixel values. By this way, the low-contrast regions of the image are improved. The histogram equalization process depends on the cumulative probability density function. It is the cumulative sum of the probabilities that lies in its domain. First, consider an image \( I(y,z) \) consists of \( N \) pixels and a gray level of \( [0,L-1] \). Then the probability distribution function is described as,
Here, \( p_M \) represents the number of level \( k \) seen in the image. Subsequently, the cumulative density function of the values of histogram is expressed in Equation (2).

\[
\text{Cdf}(k_M) = \sum_{k=-\infty}^{\infty} p(n), \text{ for } k_M = 0,1,\ldots,L-1. \tag{2}
\]

Then the histogram equalization process plots an input level \( k_M \) into an output level \( k_M \). The output levels of histogram equalization is described as,

\[
\bar{k}_M = (L-1) \times \text{Cdf}(k_M). \tag{3}
\]

Subsequently, the output level increment is expressed in Equation (4) as,

\[
\Delta \bar{k}_M = (L-1) \times \bar{p}(k_M). \tag{4}
\]

Equation (4) signifies the distance among \( \bar{k}_M \) and \( \bar{k}_M + 1 \). This provides the direct connection between the probability density function of the considered input image in gray level \( k_M \). Then the MHE is the weighted average of input and the uniformly distributed histogram as per Equation (5).

\[
\bar{H}_m = \left( \bar{k}_M \times H_{in} \right) + \left( \bar{k}_M \times \bar{H}_v \right). \tag{5}
\]

Here, the involvement of input histogram in the modified histogram is described in Equation (6),

\[
\bar{k}_M^* = \frac{1}{1+\lambda}. \tag{6}
\]

The histogram equalization is modified by changing the level of histogram based on the contrast level of input image. This process effectively enhances the contrast of an image for further processing.

### 3.2 Feature extraction using extended dual tree complex wavelet transform with trigonometric transform

The extended dual tree complex wavelet transform with trigonometric transform–based feature extraction is described in subsequent equations. This extended dual tree complex wavelet with trigonometric transform (EDTCWT) is the improved form of dual tree complex wavelet transform.\(^{47}\) In this, complex wavelet \( \psi(t) \) and complex scaling functions \( \phi(t) \) are expressed in Equation (7),

\[
\psi(t) = \psi_L(t) + j\psi_H(t), \tag{7}
\]

\[
\phi(t) = \phi_L(t) + j\phi_H(t). \tag{8}
\]

Here, the top and bottom tree are considered as \( L \) and \( H \) correspondingly. The output coefficients of tree \( L \) and \( H \) can be considered as real and imaginary parts of complex wavelet (CW) coefficients. Equations (7) and (8) are obtained by satisfying the subsequent necessities.

The extensions to two dimensions are obtained by the two-dimensional (2D) complex wavelet expressed in Equation (9), and also the 2D complex separable scaling function expressed by Equation (12).

\[
\psi_1(y,z) = \phi(y) \times \psi(z), \tag{9}
\]

\[
\psi_2(y,z) = \psi(y) \times \phi(z), \tag{10}
\]

\[
\psi_3(y,z) = \psi(y) \times \psi(z), \tag{11}
\]

\[
\phi(y,z) = \phi(y) \times \phi(z). \tag{12}
\]

Thus, the 2D EDTCWT is developed separately through the two trees utilized for the rows of an image and the two trees are columns of an image. The resultant wavelet coefficients are associated with the simple addition and subtraction functions to obtain a wavelet coefficient. After this extraction of features, trigonometric transform is applied to attain the effective combination of features to identify the COVID-19 disease accurately in images. The 2D discrete trigonometric transform is described as,

\[
p_{ij} = \frac{2}{N \sin(2\pi N)} \sum_{m=0}^{N} \sum_{n=0}^{N} g_{m,n} \cos \left( \frac{2i\pi m}{N} - \phi \right) \times \cos \left( \frac{2i\pi n}{N} - \psi \right). \tag{13}
\]

The inverse operation of trigonometric transform is described in subsequent Equation (14),

\[
g_{m,n} = \frac{2}{N \sin(2\pi N)} \sum_{j=0}^{N-1} \sum_{i=0}^{N-1} p_{ij} \sin \left( \frac{2i\pi m}{N} + \psi \right) \times \sin \left( \frac{2i\pi n}{N} + \phi \right). \tag{14}
\]

This combination of extended dual tree complex wavelet transform with trigonometric transform extracts the features used to differentiate the output class.
3.3 | ABAS optimization

In this section, the working principle of ABAS is explained, especially weight factor is adopted to enhance the random searching ability of basic ABAS optimization algorithm. ABAS optimization\(^{16}\) is a recent optimization approach motivated by the beetle’s hunting activity. The beetle swarm has two antennas to find the food via smell. If the intensity of the smell is higher in the left antenna, then the swarm will search the food on left side. Similarly, if the smell intensity is higher in right side, then the beetle will search the food on right side. In similar way, dimensionality of the features is reduced. The higher important features are chosen and discarding the lower important features in the similar optimization process. This reduces the redundant features present in the features set. Initially, beetle searches the food in random direction and it is described in a random vector as per Equation (15),

\[
\bar{B} = \frac{\text{Rand}(d, 1)}{||\text{Rand}(d, 1)||}. \tag{15}
\]

Here, Rand represents the random function, \(d\) represents the search space dimension, and \(||\cdot||\) represents the norm function.

In this phase, the random search is optimized by using the increased number of iterations. Here, the optimization process tends to the local optimum due to the random search function and also reduced multiplicity of population. Hence, to improve the diversity of population and also to obtain the better dimensionality reduction in the extracted features, the weight factor is computed using Equation (16) and it is updated in Equation (15) instead of random function. The adaptive weight factor is calculated using Equation (16)

\[
W_m = \exp\left(\frac{N}{N_{\max} - 1}\right). \tag{16}
\]

Here, \(W_m\) signifies the weight factor at \(k\)th iteration, \(N_{\max}\) signifies the maximum number of iteration, \(N\) signifies the current iteration, and \(N \leq N_{\max}\). The random function is updated with this weight factor. The spatial coordinates of the left and right side antennas are described in Equations (17) and (18),

\[
y_r^k = y^{k-1} + \epsilon^k \bar{B} \text{sign}\left(\left|\bar{F}(y^k_L) - \bar{F}(y^k_R)\right|\right). \tag{19}
\]

Here, \(\epsilon\) represents the step size of the beetle. To solve the local optimal issue, step size and the antenna length are updated by the subsequent model in Equation (20),

\[
d^k = 0.95^{k-1} + 0.01, \tag{20}
\]

\[
\epsilon^k = \epsilon^{k-1}. \tag{21}
\]

Here, \(d^k\) represents the distance among two antennae in the \(k\)th iteration and \(\epsilon^k\) represents the step size. The process is stopped after attaining the optimal set of features at maximum iterations (\(I_{\max}\)).

3.3.1 | Feature selection using ABAS optimization algorithm

The process of feature selection is very critical because the presence of high-dimensional data causes overfitting and increases the training time. In our proposed approach, an ABAS optimization algorithm is utilized for the selection of features with reduced dimensionality. Majorly, the reduced dimension of optimal feature vectors assists for avoiding the overfitting problem of classifier model. In the ABAS optimization algorithm, each feature vector and their error value can be considered as beetle and smell intensity, respectively. Also, fitness value is evaluated, which assesses the optimality of each feature vector and in every iteration the feature vectors that offer better value than the previous one is considered as global optimum.

The objective function of feature selection is considered into a minimization problem using error values and ratio of selected feature vectors. Any feature vector that can minimize the objective function can be treated as more optimal. The proposed ABAS optimization algorithm uses the error minimizing fitness function mentioned in Equation (22).

\[
\text{Fitness} = \alpha E_R + \beta_1 \frac{|S_{PV}|}{|T_{PV}|}. \tag{22}
\]

Here, \(E_R\) is represented as error rate and the number of feature vector chosen in the current iteration is denoted as \(|S_{PV}|\), \(|T_{PV}|\) indicates the total number of feature vectors. \(\alpha\) and \(\beta_1\) also considered as random numbers, ranging between 0 and 1 whose sum is equal to 1. This feature process reduces the redundant features present in the feature set and provides an optimal set of features with reduced dimensionality. The dimensionality
reduced selected set of features are given as an input to dual-stage horse herd BiLSTM to accurately identify the COVID. This effective feature set is used to improve the accuracy level of the classification process.

### 3.4 Classification using adaptive dual-stage horse herd BiLSTM framework

The classification model presented in this study is the improved model of conventional LSTM framework. The presented BiLSTM section consists of input layer, embedding layer, BiLSTM layer, deep attention layer, and output layer. In the input layer, the selected features are given as an input for further processing. The schematic representation of layers in the dual-stage deep attention–based BiLSTM is depicted in Figure 2. Table 1 illustrates the hyperparameter and training details of ADHH-BiLSTM.

#### 3.4.1 Input layer

In the input layer, the selected features are considered as an input to the layer. The dimensionality reduced features selected by the ABAS optimization algorithm is given as an input to the dual-stage horse herd BiLSTM. In the input layer, the selected features set $Z_1, Z_2, Z_3, \ldots, Z_T$ is given as an input to the BiLSTM framework.

#### 3.4.2 Embedding layer

In this layer, each selected input features are plotted into a lower dimensional vector.

\[
\tilde{E}_T = Z_T V_{\text{size}}. \tag{23}
\]

Here, $V_{\text{size}}$ represents the size of feature vectors $|V_{\text{size}}|$ and the value 1 at index $\tilde{E}_T$ and 0 for other positions; $Z_T$ signifies the features set. The features are embedded in this layer using Equation (23). Afterwards, embedded information is given to the next layer as a vector.

#### 3.4.3 Dual-stage BiLSTM layer

The BiLSTM layer is used to attain the high level of features after the embedding layer. In this layer, forward and backward directional process is utilized to attain the higher level of features. In the proposed dual-stage BiLSTM, two BiLSTM layers are utilized to advance the process and to obtain the accurate prediction of output classes. Moreover, the BiLSTM framework are the improvement of the unidirectional LSTM networks through presenting a forward and backward directional process for deep learning the features. It is effective to learn the feature data both from the previous and the next. This BiLSTM layer comprises of forward and backward process. The output concatenation of this layer is described in Equation (24),

![Schematic diagram of dual-stage horse herd BiLSTM](image)

**TABLE 1** Hyperparameter and training details of ADHH-BiLSTM

| Parameters                              | Values |
|-----------------------------------------|--------|
| Number of hidden units                  | 125    |
| Gate activation function                | Sigmoid |
| State activation function               | tanh   |
| Number of horses ($N$)                  | 50     |
| Optimizer                               | ADHH   |
| Learning rate                           | 0.001  |
| Maximum Epoch                           | 200    |
| Mini batch size                         | 512    |
| $d^r, d^h, d^f$                          | 0.5, 0.2, 0.1 |
| $r^i, r^f$                              | 0.1, 0.05 |
| Dropout rate                            | 0.5    |
| Maximum Iteration                       | 100    |
\[ \Pi_T = H_k \oplus H_k. \]  

(24)

Here, the forward and backward pass outputs are combined through element-wise addition. Furthermore, \( H_k \) denotes the forward pass outputs and \( H_k \) denotes the backward pass outputs. Here, dual-stacked BiLSTM layer process is performed for deep learning process.

### 3.4.4 Attention layer

The concatenated two-stage BiLSTM outputs are given to attention layer for the accurate output class prediction. This output decision process is further enhanced by the weight optimization using adaptive horse herd optimization. The output attained in the previous layer is characterized as \( \Pi_T \), in which \( T \) denotes the length. In this layer, the BiLSTM outputs are multiplied by the optimized weights. Here, the optimized weight is attained through the horse herd optimization algorithm and results in accurate disease prediction. The activation function is described as per Equation (25),

\[ F_t = \sigma(W_f Y_T + W_f H_T + b_f). \]

(25)

Here, \( \sigma \) signifies the activation (sigmoid) function, \( W_f \) signifies the weight vectors, \( Y_T \) signifies an input series, \( H_T \) represents the hidden state output of previous layer, and \( b_f \) denotes bias. Here, the weight vectors are optimized by the horse herd optimization.

### 3.4.5 Weight optimization

The major inspiration of horse herd optimization algorithm is the hierarchical organization of horse herds. In the hierarchical order, Horse A will be the dominant than Horse B and Horse B will be the dominant one than Horse C in a hierarchical order. In the similar way of hierarchical process, weights are optimized in the BiLSTM framework. However, the behavioral pattern of horses depends on the stages, namely grazing (G), sociability (S), hierarchy (H), imitation (I), roam (R), and defense (D) mechanism. Initially, hierarchical order is initially evaluated by the fitness values of the horses from herd. The range of age for the considered horse is \( \alpha, \beta, \delta, \gamma \). Consider, \( N \) horses and \( Q \) is a function.

\[ \text{Herds} = \{h_1, h_2, ..., h_N\}, \]

\[ Q = \text{Herds} \rightarrow \{1, 2, 3, ..., N\}. \]

If \( \text{fitness}(h_y) < \text{fitness}(h_z) \), where \( y \neq z \) and \( y, z \in \{1, 2, ..., N\} \), then

\[ Q(h_y) > Q(h_z). \]

(28)

If \( \text{fitness}(h_y) = \text{fitness}(h_z) \), where \( y \neq z \) and \( y, z \in \{1, 2, ..., N\} \), then

\[ [Q(h_y) - Q(h_z)](y - z) > 0. \]

(29)

The order of each horse is computed by Equation (30)

\[ O(h_y) = \frac{Q(h_y)}{N}. \]

(30)

Here, \( O(h_y) \) represents the order of horse. The weighted average of the locations of all the horses from the herd are equivalent to the center of every herd. The center of every herd is evaluated by Equation (31),

\[ h_{\text{center}} = \frac{\sum_{y=1}^{N} y_h y_{rank}}{\sum_{y=1}^{N} y_{rank}}. \]

(31)

The Euclidean distance among the location of stallion and the center of the herd is evaluated through Equation (32),

\[ d_{(\text{stallion, herd})} = \sqrt{\sum_{z=1}^{N} (\text{stallion}_z - h_{\text{center}})^2}. \]

(32)

Here, \( d \) represents the dimensions of the search space. If the particular horse fits to the set herd of horses, then the velocity is updated by Equation (33),

\[ V_{y,z}^{K+1} = V_{y,z}^{K} + H_{y,\text{rank}} \times (h_{\text{center},z} - x_{y,z}^K). \]

(33)

\[ V_{y,z}^{K+1} = V_{y,z}^{K} + W_f \times (h_{\text{center},z} - x_{y,z}^K). \]

(34)

Here, \( W_f \) signifies the weight factor. It is adapted instead of random number between 0 and 1. Here, \( K \) denotes the current iteration and the \( K + 1 \) represents the new iteration. The horse memory matrix consists of number of rows that is equivalent to the horse memory pool value and \( P \) columns.

\[ M_y^{K+1} = \begin{bmatrix} M_{1,y,1}^{K+1} \cdots M_{K+1,y,1}^{K+1} \\ \vdots \\ M_{HMP,y,1}^{K+1} \cdots M_{HMP,y,1}^{K+1} \end{bmatrix} K + 1. \]

(35)
The equation used to update the memory matrix cells are described as,

\[ O_W = M_{N,y,z}^{K+1} = x_{y,z}^{K+1} \times N_D(0, S_d). \]  

(36)

Here, \( N_D \) represents the normal distribution and \( S_d \) represents the standard deviation. The global best position is obtained in \( K + 1 \) iteration. The horse herd optimization is an appropriate one for the optimal weight updating in BiLSTM framework. The obtained global best positions \( (O_W) \) are considered as an optimal weight to update the dual-stage BiLSTM framework.

### 3.4.6 Output layer

Finally, the BiLSTM outputs are multiplied with the optimized weights \( (O_W) \) in attention layer and results in the final output, and it is characterized in Equation (37),

\[ O_{class} = \pi_{T,out} \times O_W. \]  

(37)

Finally, multiplying the optimized weights with the BiLSTM outputs attains accurate output prediction. It is described in Equation (38),

\[ \pi_{T,out} = \frac{\overline{H}_t + \overline{H}_t}{\overline{H}_t \times \overline{H}_t}. \]  

(38)

Moreover, \( \overline{H}_t \) represents the forward pass outputs and \( \overline{H}_t \) represents the backward pass outputs. The outputs attained in Equation (38) is updated in Equation (37) for attaining the accurate final output. Finally, the proposed dual-stage horse herd BiLSTM framework accurately classifies the images into COVID, lung opacity, normal, and viral pneumonia classes.

### 4 RESULTS AND DISCUSSION

The experimental results of a presented COVID-19 prediction using adaptive dual-stage horse herd BiLSTM framework is performed in the working platform of PYTHON. The dataset utilized for this work is COVID-19 chest x-ray database. The performance of this proposed approach is analyzed by comparing the existing approaches such as adaptive neuro fuzzy inference system (ANFIS), CNN, VGGNet, deep transfer learning, ResNet 50, AlexNet, ResNet 101, GoogleNet, InceptionNet V3, ResNet 152, in regards to different effective performances like accuracy, sensitivity, specificity, kappa statistics, F-measure, precision, receiver operating characteristic (ROC) curve, AUC score. The sample input images are depicted in Figure 4. The output detected COVID, normal, lung opacity, and viral pneumonia classes are depicted in Figure 5.

#### 4.1 Dataset description: COVID-19 chest x-ray database

The dataset used in this study is the COVID-19 chest x-ray database. This is a public data source obtained from https://www.kaggle.com/tawsifurrahman/covid19-radiography-database. The researcher’s team from Qatar University, and the University of Dhaka formed a dataset of chest x-ray images for COVID-19 positive cases with normal, lung opacity, and viral pneumonia class images. The dataset has COVID-19 positive cases are 3616, normal cases are 10 192, lung opacity category images are 6012, and the viral pneumonia-affected images are 1345. The images present in this database are in the form of portable network graphics (PNG) file format. The dataset acquired for training the model was very small in size and imbalanced. To resolve the issue of containing very-limited sized x-ray image dataset, it has been enlarged by employing DA method to increase its size and also to create the feature-rich model training. Image flipping and rotation at various angles have been employed to make additional data for dataset balancing of the minority class. After data balancing, 80% of images are used for training and the remaining 20% is used for testing.

#### 4.2 Performance metrics

In this section, an effective performance metrics such as accuracy, sensitivity, kappa statistics, F-measure, AUC, ROC curve, and specificity are computed for the examination of the proposed methodology effectiveness. These performance metrics are described in subsequent subsections.

#### 4.2.1 Accuracy

It is evaluation that the output this measure reflects how close the measured value is to the actual value. It is the ratio of accurately predicted class labels among the entire image data. The accuracy measure is computed by Equation (39),

\[ \overline{A}_Y = \frac{\overline{t}_{positive} + \overline{t}_{negative}}{\overline{t}_{positive} + \overline{t}_{positive} + \overline{t}_{positive} + \overline{t}_{negative}}. \]  

(39)

Here, \( \overline{A}_Y \) represents the accuracy, \( \overline{t}_{negative} \) signifies the true negative (people who truly do not have the virus),
positive signifies the true positive (people who truly have the virus), $f_{\text{positive}}$ signifies the false positive (people who is not sick is predicted falsely as sick based on the test), and $f_{\text{negative}}$ signifies the false negative (people who is truly sick is predicted falsely as not sick based on the test).

### 4.2.2 Sensitivity

This metric computes the performance of correct prediction of positively labeled classes in the images. This computation is described in Equation (40),

$$\Sigma_e = \frac{t_{\text{positive}}}{t_{\text{positive}} + f_{\text{positive}}}.$$  \hspace{1cm} (40)

Here, $\Sigma_e$ signifies the sensitivity measure.

### 4.2.3 Specificity

This metric is similar to the sensitivity measure but this computes the performance of negatively labeled class prediction. It is evaluated by Equation (41),
Here, $SP$ signifies the specificity measure.

**4.2.4 | Kappa coefficient**

Kappa statistics measure is used to assess the consistency of the classification approach. It is assessed through the confusion matrix values. The increased value of this measure is equivalent to the quality of the approach. It is expressed in Equation (41),

$$SP = \frac{t_{negative}}{t_{negative} + f_{negative}}.$$  

Here, $SP$ signifies the specificity measure.

**4.2.5 | Precision**

This measure evaluates the performance of accurate prediction of labeled positive classes among all the positives. Precision of the presented methodology is computed by Equation (43),

$$PR = \frac{t_{positive}}{t_{positive} + f_{positive}}.$$  

Here, $PR$ signifies the precision measure.

$$\bar{K}_p = \frac{2 \times (t_{positive} \times t_{negative} - f_{negative} \times f_{positive})}{(t_{positive} + f_{positive}) \times (f_{positive} + t_{negative}) + (t_{positive} + f_{negative}) \times (f_{negative} + t_{negative}).}$$  

Here, $\bar{K}_p$ signifies the kappa statistics measure.
4.2.6 | F-measure

This performance evaluation is the harmonic mean of precision and the sensitivity. The enhanced output of this performance provides the balance among the sensitivity and precision evaluations of the proposed work. This F-measure computation is expressed in Equation (44),

\[
F_M = 2 \times \frac{PR \times Se}{PR + Se}.
\]  

(44)

Here, \(PR\) signifies the precision measure and \(Se\) signifies the sensitivity measure.

4.2.7 | AUC score

This measure provides the probability of ranking the effectiveness of presented methodology. The higher performance of the AUC (area under the ROC curve) is the better efficiency of presented technique at the differentiation of negative and the positive classes. This performance measure is evaluated in Equation (45),

\[
\text{AUC} = \frac{1}{2} \left( \frac{T_{positive}}{T_{positive} + F_{positive}} + \frac{T_{negative}}{T_{positive} + F_{negative}} \right).
\]

(45)

4.2.8 | ROC curve

This measure is utilized for the prediction of classification performance. It is computed based on the two parameters such as true positive rate (TPR) and false positive rate (FPR). Here, the computations of TPR and FPR is expressed in the subsequent equations,

\[
T_{PR} = \frac{T_{positive}}{T_{positive} + F_{positive}},
\]

(46)

\[
F_{PR} = \frac{F_{positive}}{F_{positive} + T_{negative}}.
\]

(47)

Here, \(T_{PR}\) signifies the TPR and \(T_{PR}\) signifies the FPR.

4.3 | Performance analysis

In this section, performances of the presented methodology is examined with the different existing techniques with different effective performance metrics. The confusion matrix of the presented work with four different classes such as normal, COVID-19, viral pneumonia, and lung opacity is depicted in Figure 6.

The comparison metrics of the presented and the existing different approaches are mentioned in Table 2.

In Table 2, the presented work performance is assessed with various metrics such as accuracy, specificity, kappa statistics, sensitivity, and F-measure are provided. This proved that the presented methodology is providing more significant enhancement than the different existing approaches.\(^{36}\) The computational time performance proposed approach with some popular deep learning classifier models are tabulated in Table 3.

According to Table 3, the proposed approach computational times are compared with the other deep learning models. By using the feature selection and hyper parameter tuning of classifier with a small x-ray image dataset, the proposed approach running time is low. Moreover, the prediction time is 0.86 s for proposed approach, which is one of the best prediction times among the other models in this COVID-19 classification task.

The training and testing accuracy and loss curves of the proposed deep learning–based approach with respect to epochs 75, 150, and 200 are shown in Figures 7–9. As shown in these figures, the accuracy values of the training and testing phases has increased when the number of epoch increased. On the other side, the loss of the training and testing phases has decreased when the number of epochs increased. Therefore, these evaluations show that the proposed deep learning model–based approach has significant improvement for COVID-19 classification.

In Figure 10, the performance evaluation in regards to precision is provided with the different existing approaches such as Inception V3, Resnet 50, Resnet 101, Resnet 152, and Inceptionresnet V2.\(^{26}\) Here, the presented methodology attains enhanced precision.

FIGURE 6 Confusion matrix of presented classification

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which is more significantly improved than the other existing approaches. This proved that the presented approach is providing better performance than the other existing approaches. The performance of the proposed methodology in regards to different performance metrics are mentioned in Table 4.

In Table 4, the performance metrics of the presented approach with four different classes are provided. This proves that the presented approach attains enhanced performance in all the performance metrics. Moreover, the performance evaluation of the presented approach in terms of ROC curve is depicted in Figure 11.

Figure 11 provides the performance evaluation in regards to ROC measure with the various existing schemes such as CNN, AlexNet, Googlenet, deep transfer learning, Inceptionnet V3, ANFIS, VGG Net, and ResNet 50. The ROC curve is depicted based on the obtained AUC score and the higher the value of this means the better performance. The presented approach attains higher ROC (AUC = 0.99) than the different existing approaches.
The accuracy performance is validated for each class and compared with the exiting approaches, as presented in Table 5.

In Table 5, the performance comparison on accuracy is compared for each class. Here, the presented approach provides improved performance for each class: normal (98.8%), COVID-19 (99.27%), lung opacity (99.06%), and viral pneumonia (99.13%). This proved that the presented ADHH-BiLSTM approach attains more significant enhancement than the existing ResNet 50 and AlexNet approaches. Table 6 displays the proposed classification accuracy by analyzing with preprocessed and non-preprocessed images.

**Figure 8**  Accuracy and loss curves of proposed model, epoch = 150. (A) Training and testing accuracy curves, epoch = 150. (B) Training and testing loss curves, epoch = 150

**Figure 9**  Accuracy and loss curves of proposed model, epoch = 200. (A) Training and testing accuracy curves, epoch = 200. (B) Training and testing loss curves, epoch = 200

**Figure 10**  Performance analysis in regards to precision
4.3.1 Cross validation: Fivefold cross validation

In this, amount of data in the dataset is divided into five parts. Here, one part is considered as a testing and the remaining parts are considered for the training process. Here, the 20% of the data is utilized for testing purpose. The first part is considered for testing and the remaining parts are considered for training. Similarly, each part is considered for testing for validating the performance of the approach. The schematic diagram of fivefold cross validation is depicted in Figure 12.

Performance of the presented approach in COVID-19 detection based on fivefold cross validation is examined, and it is presented in Table 7.

4.3.2 Dropout for reducing the overfitting

To reduce the overfitting in the presented networks, the input and the recurrent connections are removed from the activation and the weights are updated at the time of network training. This process decreases the overfitting and enhances the network performance. The data in the input connection of every LSTM layer connection are not included in weight update and node activation. The dropout value is considered in between the range of 0 and 1. Here, 0 represents the “no dropouts” and 1 represents the “no connection.” In the presented technique, dropout rate is considered as 0.5 to attain the accurate results.

Table 8 illustrates the comparison on accuracy metric with different existing methods. The performance of proposed ADHH-BiLSTM approach is compared in terms of accuracy with other deep learning models and gained superior performance in the COVID-19 detection with chest x-ray images. This proves the effective nature of the proposed classification model over other architectures.

5 CONCLUSION

This work presented an effective COVID-19 prediction using adaptive dual-stage horse herd BiLSTM framework. To achieve this effectively, this work utilized effective combination of approaches. Here, the MHE approach is utilized for enhancing the contrast of an image. Moreover, extended dual tree complex wavelet with trigonometric transform is used for better discriminant feature extraction and the adaptive optimization approach is utilized for reducing the dimensionality of the features. Finally, the developed ADHH-BiLSTM framework

| Techniques | Normal | COVID-19 | Lung opacity | Viral pneumonia |
|------------|--------|----------|--------------|-----------------|
| ResNet 50  | 96.9   | 97.10    | 89.6         | 93.7            |
| AlexNet    | 96.9   | 94.5     | 82.5         | 97.4            |
| Proposed   | 98.8   | 99.27    | 99.06        | 99.13           |
effectively detects the normal, COVID-19, viral pneumonia, and lung opacity classes. The performance results of the presented work is compared with the different existing approaches based on different performance metrics: accuracy (99.07%), sensitivity (97.6%), specificity (99.36%), kappa coefficient (97.7), F-measure (97.1%), precision (98.56%), and AUC (99%). This proved that the

| TABLE 6 | Proposed diagnostic results of non-preprocessed images with preprocessed images |
|----------|--------------------------------------------------------------------------------|
| Technique | Non-preprocessed image output | Preprocessed image output |
| Proposed  | 97.34 | 99.07 |

**FIGURE 12** Schematic diagram of fivefold cross validation

**TABLE 7** Performance evaluation based on cross validation in COVID-19 detection

| Network model | Accuracy (%) | Specificity (%) | Sensitivity (%) | F-measure (%) | Kappa coefficient (%) |
|---------------|--------------|-----------------|-----------------|--------------|-----------------------|
| Fold 1        | 99.07        | 99.24           | 97.57           | 96.7         | 97.4                  |
| Fold 2        | 98.93        | 99.30           | 97.6            | 97.5         | 97.7                  |
| Fold 3        | 99.21        | 99.36           | 97.72           | 96.5         | 98.0                  |
| Fold 4        | 99.14        | 99.42           | 97.9            | 97.1         | 97                    |
| Fold 5        | 99.0         | 99.48           | 97              | 97.7         | 98.4                  |
| Average       | 99.07        | 99.36           | 97.6            | 97.1         | 97.7                  |

**TABLE 8** Comparison on accuracy metric with different existing methods

| Author name and reference | Technique used | Dataset used       | Accuracy (%) |
|---------------------------|----------------|--------------------|--------------|
| Proposed                  | ADHH-BiLSTM    | Chest x-ray        | 99.07%       |
| Das et al.36              | Deep transfer learning | Chest x-ray | 97.40%       |
| Narin et al.26            | Inception V3, ResNet 50, ResNet 101 ResNet 152, Inception-ResNet V2 | Chest x-ray | 96.1%        |
| Apostopolus et al.30      | VGG-19         | Chest x-ray        | 93.48%       |
| Ibrahim et al.28          | Deep Learning  | Chest x-ray        | 93.42%       |
| Hassantabar et al.31      | DNN            | Chest x-ray        | 83.84%       |
| Togaçar et al.32          | MobileNet V2 and SqueezeNet | Chest x-ray | 98.25%       |
| Das et al.34              | Ensemble learning + CNN | Chest x-ray | 91.62%       |
| Rehman et al.35           | CNN            | Chest x-ray        | 96.67%       |
| Chouhan et al.37          | Ensemble model | Chest x-ray        | 96.39%       |
| Aslan et al.39            | Hybrid BiLSTM  | Chest x-ray        | 98.70%       |
| Sharifrazi et al.42       | CNN + SVM + Sobel | Chest x-ray | 99.02%       |
presented approach attains more enhanced performance than the different existing approaches.

DATA AVAILABILITY STATEMENT
Data sharing not applicable to this article as no datasets were generated or analyzed during the current study.

ORCID
Durga Prasad Mannepalli https://orcid.org/0000-0002-1546-1710
Varsha Namdeo https://orcid.org/0000-0002-0538-2453

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