Enhanced Detection of COVID-19 using Deep Learning and Multi-Agent Framework: The DLRPET Approach

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***Abstract*—The ongoing global pandemic caused by novel coronavirus (COVID-19) has emphasized the urgent need for accurate and efficient methods of detection. Over the past few years, several methods were proposed by various researchers for detecting COVID-19, but there is still a scope of improvement. Considering this, an effective and highly accurate detection model is presented in this paper that is based on Deep learning and multi-Agent concepts. Our main objective is to develop a model that can not only detect COVID-19 with high accuracy but also reduces complexity and dimensionality issues. To accomplish this objective, we applied a Deep Layer Relevance Propagation and Extra Tree (DLRPET) technique for selecting only crucial and informative features from the processed dataset. Also, a lightweight ResNet based Deep Learning model is proposed for classifying the disease. The ResNet model is initialized three times creating agents which analyses the data individually. The novelty contribution of this work is that instead of passing the entire training set to the classifier, we have divided the training dataset into three subsets. Each subset is passed to a specific agent for training and making individual predictions. The final prediction in proposed network is made by implementing majority voting mechanism to determine whether an individual is COVID-19 positive or negative. The experimental outcomes indicated that our approach achieved an accuracy of 99.73% that is around 2% higher than standard best performing KISM model. Moreover, proposed model attained precision of 100%, recall of 99.73% and F1-score of 98.59 % respectively, showing an increase of 5% in precision, 4.73% in recall and 4.59% in F1-score than best performing SVM model.**

Keywords—COVID-19; deep learning; SVM; ResNet; disease classification; biomedical applications; multi-agent

I. Introduction

Since the outbreak of COVID-19 disease in 2019, two major sections of our society i.e., health care and economy have seen the worst phases [1]. This disease is basically a continuation of a number of earlier catastrophes brought on by extremely contagious respiratory viral diseases. The first case of COVID-19 was found in Wuhan city of China that was caused by SARS-CoV-2 virus and quickly expanded to other countries causing healthcare emergency. The structure of COVID-19 virus is positive single strand RNA which shares genetically characteristics with SARS and Bat SARS corona viruses [2]. Every virus has a size of between 50 nm to 200 nm and comprises of some basic proteins like Spike, Envelop, Membrane and nucleocapsid which are represented by Alphabetical letters S, E, M and N respectively [3,4]. The virus envelop is created by utilizing the S, E and M proteins while as, N protein is responsible for holding the RNA genome of the virus [3]. As per the study conducted recently, it has been observed that bats serve as one of the prevalent natural hosts of virus [6], and intermediate host is Malayan Pangolin. However, the virus is also transmitted from one person to another through respiratory droplets released by infected person during coughing or sneezing. These droplets could transmit the infection by additionally contaminating surfaces in the environment. People who have been exposed to coronavirus developed moderate to serious respiratory symptoms and may need assistance with ventilation support. To interrupt the process and stop the disease from spreading, numerous countries have restricted their borders [9]. Despite this, it is imperative to quickly identify infected persons in order to put an end to this fast spread. One of the biggest challenges faced by doctors is that asymptomatic persons can also spread the disease [10]. Even though symptomatic patients are main source of transmission, however the risk of transmission is further increased by the undetected asymptomatic patients. The handling of COVID-19 involves the avoidance, identification, command, and cure of the disease. All of these processes have an impact on the others [11].

With the aim of addressing the current issues, a number of computer aided diagnostic (CADs) techniques utilizing the concept of Artificial Intelligence (AI) [12] were used for effectively detecting COVID-19 in earliest stages. By using training data, AI algorithms can identify individuals who are at higher risk for developing COVID-19 [13], characterize its epidemiological research, and simulate how the disease spreads. Furthermore, these intelligent models can also aid in developing new medicines and vaccines, along with this they perform screening of compounds that have potential for vaccines [23]. Moreover, AI based chat-bots were also utilized in different health centers, so that they can advise a far larger number of individuals than call center [14], reducing the strain on healthcare emergency number. Additionally, AI might control the global outbreak by employing thermal imaging to search public areas for those who may be sick as well as by implementing social isolation and lockdown procedures. Thus, by utilizing AI methods including Machine Learning (ML) and Deep Learning (DL), medical institutions may not just speed up the diagnosing procedure but also aid in establishing more effective containment plans, improved results for patients, and increasingly intelligent public health decision systems for better healthcare.

A. Motivation and Contribution

The urgent necessity to address the pandemic-related global health issue is what motivates the development of improved COVID-19 detection methods. In order to make sure that COVID-19 has little effect on healthcare providers and community, it is crucial that cases are quickly and accurately identified. Diagnostic techniques now in use have drawbacks, such as inconsistent reliability and a tendency to put a pressure on testing facilities. Researchers are working to develop novel detection models that improve diagnostic accuracy and efficacy by utilizing cutting-edge technology like artificial intelligence and deep learning. By employing these techniques, we could hasten diagnosis especially in areas with limited resources and also aid medical professional in making decisions to support efforts for curbing the spread of virus. The creation of reliable COVID-19 detection models also reflects the determination of scientific researchers to successfully confront the big challenges provided by the epidemic and is in line with their ideology of harnessing technology for public health benefits. With the aim to improve the detection rate of COVID-19 detection models, a new and effective approach is presented in this paper that can not only handle high dimensionality of complex datasets but also increase the detection rate as well. The major research contributions are mentioned below:

- To provide a COVID-19 prediction model that utilizes laboratory outcomes instead of using chest X-ray, CT scan images.
- To provide an effective solution for handling high dimensionality dataset with proposed deep LRP and Extra Tree operated feature selection model that ensure selection of the informative and crucial features.
- To propose a light weight ResNet based classification model for COVID-19 detection that contributes to healthcare field by providing faster training and resource friendly solutions.

After analyzing the related literature, it is clear that already a lot of DL models have been presented for detecting the COVID-19 persons. However, one of the biggest limitations in these models is that they don't possess extremely high accuracy rates because of the inability to recognize patterns and relationships among various features.

However, there are some models that exhibit high accuracy rates but their overall structure is so complex and intricate that it becomes difficult to implement them in real world. Furthermore, we also observed that majority of the works were based on image processing techniques, and very less work has been done on analytical data. The detailed analysis for reviewed works with their advantages and disadvantages are given in Table I. Keeping these limitations in mind, a new and unique model is proposed in this work that can address above mentioned limitations and achieves high accuracy results. Section II consists of our proposed methodology, followed by the Simulating Setup and Results Evaluation Matrices in Section III, Section IV consist of result analysis and conclusion.

TABLE I. OVERALL FINDING OF REVIEWED STUDIES

Author	Advantages	Limitations
Al Shehri et al.2022	Proposed a combined CNN and Darknet based architecture and to achieve higher detection rate	Need more Resource requirements, and lacks in training network with informative data only instead of direct images.
Oyelade, O. N. et al. 2021	Proposed a pre-processing mechanism to support the classification models	Lacks in exploring models in larger datasets, and feature selection may be included to achieve higher rates with less resource requirements.
Sakib, S. et al.2020	A unique dataset is generated by using 4 public datasets.	Use of GAN based networks need higher resource for training models.
Kogilavani, S. V. et al.2022	An analysis of different existing CNN architectures is conducted in study	Lacks in exploring new classification method in order to achieve better classification rates.
Alom, M. Z. et al.2020	Segmentation based model is proposed to get informative area from X-ray Images to improve classification rates.	Faced issues with smaller datasets, false positive detections were higher in suggested model.
Alazab, M. et al.2020	Implemented classification and forecasting models to handle COVID-19 spread.	Main focus was on working with Chest X-ray images, other clinical factors or environmental factors were not considered and recommended for future works.
Gaur, L. et al.2023	Evaluated 3 Pre-trained CNN networks for mobile applications.	Restricted to explore new deep learning architecture those can be lighter and less complex.
Irmak, E 2020.	Proposed a CNN network and achieved an accuracy of 99.20%	Work is restricted to smaller dataset and area biased information, additionally need to explore more datasets.
Rajawat, N. et al 2022.	Proposed a ROI extraction based informative selection scheme for training Classifier	It is restricted to variety of data and requires more clean images to achieve better classification rates.
Xue, Y. et al.2023	Implemented CNN based model with data augmentation to handle smaller dataset issue.	Facing issue of larger feature set and suggested feature selection methods for future use.

II. OUR PROPOSED WORK

With the aim to improve the accuracy rate of COVID-19 detection model, an effective and unique model is proposed in this manuscript that is based on Deep Learning (DL) and Multi-agent techniques [5]. The proposed model undergoes through seven stages of Data preparation, Feature Selection, Data Splitting, Agent formation, Training of Agents, voting mechanism and finally performance assessment. During the first phase of proposed approach, all the necessary data related to COVID-19 is taken from an online repository which is then processed for attaining a meaningful dataset in second phase [7] [8]. In the third phase, only important and crucial attributes are selected from the available feature set by implementing DL model in order to minimize complexity and dataset dimensionality issues. During the next phase, the data is categorized into training and testing data in the proportion of 80:20. After this, agents are formed in the model by dividing training data into three subsets. In the fifth phase, the proposed DL architecture [14] is initialized three times so that they can be trained using three different agents. The main contribution of our work is that DL architecture is proposed that is based on agents wherein each agent is passed a separate dataset [15]. This was not the case in earlier detection models wherein the entire dataset was passed to classifier for training and testing its performance [16]. The results attained by three DL models are then combined in sixth stage by employing voting mechanism [17] and finally, performance is reviewed in the last phase of proposed work.

A. Dataset Preparation

In the proposed work, COVID-19 information dataset available on GitHub is utilized that contains all the necessary information regarding the disease. The samples of the repository were collected from a hospital that is situated in Sao Paulo Brazil. The dataset contains a total of 18 samples collected from 600 patients. Among these patients, 520 are unknown to us and remaining 80 are COVID infected. The dataset can be accessed on https://github.com/burakalakuss /COVID-19-Clinical [18]. Additionally a close examination of dataset is performed to identify potential biases and demographic imbalances. The analysis results that the considered dataset is not having factors including age, gender, socio-economic status etc. that means model does not require explicitly evaluation or adjustment for potential biases or demographic imbalances. Since the utilized dataset contains lot of null or missing values that can lower the accuracy of prediction rate and can also cause over fitting issues. Therefore, data pre-processing technique is implemented [19]. Pre-processing is the process of refining the dataset so that all unnecessary or redundant information is removed from it. It aids in enhancing the accuracy of disease detection system. In our work, we have implemented Mean Imputation Method for filling the null values. It is considered as one of the frequently used techniques for filling up the null values wherein blocks are filled by calculating the mean value of same column.This process not only handled the issue of null entities but also eliminates the requirements of data augmentation step. It also showcases the capability of method to enhance dataset entities with any augmented data.

Furthermore, the strings present in the dataset were converted into numeric values by employing a Level encoder technique [20]. The label encoding process involves assigning a unique integer to each category in the variable. The features present in the dataset are represented by numeric codes in the given feature space which ultimately helps the proposed algorithm to understand and comprehend patterns and their relationships. After applying these pre-processing techniques, we were left with dataset that comprises of only 43 columns which represents more informative dataset than raw dataset. Nevertheless, it must be noted here that there might be a possibility that these columns still contain irrelevant data which might enhance the intricacy of model, therefore, it is important to refine this data further by employing Feature Selection techniques.

B. Feature Selection using DLRPET

Feature selection is of paramount importance in various data-driven tasks, including COVID-19 detection. It involves selecting a subset of relevant features from the processed dataset while discarding irrelevant or redundant ones. The need of implementing FS techniques arises by the fact that high dimensional features lead to computational complexity and increases the risk of overfitting. By implementing an effective FS technique, the dimensionality of the model is reduced which in turn makes the detection process more efficient. Moreover, it also enhances the data quality as all irrelevant data is removed from the dataset and only those attributes are preserved that aid in improving detection accuracy rate. In our work, we have employed Deep Learning based architecture for selecting crucial and important features. Furthermore, the proposed DL based FS method is further optimized by employing two effective FS techniques named as, LRP and Extra Tree. Hence, the name of our proposed features selection technique as Deep LRP Extra Tree (DLRPET).The reason of incorporating Layer wise relevance propagation ad Extra tree in DL network is that it allows the model to attribute the relevancy of model's output back to the input features. Additionally tree based phase need lesser memory as they are more memory efficient [39].The combined model calculates the contribution and importance of feature setto final prediction that assist the model to select best set of input features. The working of proposed DLRPET is initiated by defining the initialization or configurational parameters for the DL architecture that are mentioned in Table II.

TABLE II. DL INITIALIZATION FACTORS

Sr. No.	Parameters	Values
1	No of layer	4
2	Optimizer	Adam
3	Loss	Binary cross entropy
4	Metrics	Accuracy
5	Epochs	50
6	Batch size	32

Before introducing the concept of LRP and Extra tree on the DL feature selection algorithm, we trained it on the processed dataset for analyzing the patterns of features and their relationships. The proposed DL based FS technique comprises of four layers of input, Dense_1, Dense_2 and output layers. The first layer considers the dataset attained after implementing pre-processing technique. This data is then received by first dense layer that constitutes a total of 43 units, which depicts its dimensionality. Moreover, it also comprises of RelU activation function that adds the concept of non-linearity to the network. The refined data is then passed through second dense layer with same configuration, which helps the model to learn more intricate features and their relationships. Finally, the output is received by the last layer of DL model which comprises of only 1 unit and sigmoid activation function. Once the DL model is initialized, the concept of LRP and extra tree is introduced in it for selecting optimal features. The two techniques are implemented at each layer of DL network for calculating the feature importance. Based on this feature importance, the outputs generated by LRP and ET are integrated to create a final feature vector with most effective features. The process of FS starts when LRP is configured for getting the weights and biases from trained DL model which are then summed up for extracting the positive values. The relevance score for each attribute using LRP is calculated by using Eq. (1).

$$\mathrm{r_{values}} = \frac{\mathrm{p_{values}}}{\sum_1^n \mathrm{p_{values}}} \quad (1)$$

In the next phase of FS, Extra tree technique is applied on every DL layer for evaluating feature importance or $\mathrm{f_{values}}$. It is calculated by using the Gini Impurity calculation which is given by

$$G_{imp} = \sum_k p_{mk}(1 - p_{mk}) \quad (2)$$

where, $p_{mk}$is probability of belonging to class k at m node . The feature importance in Extra tree is calculated by "Gini" impurity reduction.

$$\mathrm{f_{values}} = \sum_t \sum_m G_{imp}(t) - \left(\frac{\sum_t G_{imp}(t) \times Sample_t}{Sample_{total}}\right) \quad (3)$$

Where t is individual tree in ExtraTree, and m is each node in given tree, $Sample_t$ is sample count in tree t, and $Sample_{total}$ is count of sample in while dataset.

The relevance score and feature importance generated by LRP and ET are then integrated for selecting highly effective and informative features, by using the formula given in Eq. (2).

$$\mathrm{C_{values}} = \mathrm{f_{values}} + \mathrm{r_{values}} \quad (4)$$

By using this formula, we attained a total of 10 crucial features in the proposed work whose details are given in Table III, along with their numeric values.

TABLE III. FEATURE ATTAINED BY DLRPET MODEL

Attributes	Non-Null	Count	Data Type
patient_age_quantile	5644	Non-null	int64
sars-cov-2_exam_result	5644	Non-null	int64
Hematocrit	5644	Non-null	float64
serum_glucose	5644	Non-null	float64
respiratory_syncytial_virus	5644	Non-null	int64
mycoplasma_pneumoniae	5644	Non-null	float64
neutrophils	5644	Non-null	float64
urea	5644	Non-null	float64
proteina_c_reativa_mg/dl	5644	Non-null	float64
potassium	5644	Non-null	float64

C. Data Separation

After selecting the features in previous phases, the data is separated into the training and testing datasets keeping the proportion of separation to 80 and 20. This approach involves allocating 80% of the dataset to the training set, where the model learns patterns and relationships within the data, and the remaining 20% to the testing set, which is used to assess the model's performance and generalization to new, unseen data. This ratio strikes a balance between providing the model with sufficient data to learn complex patterns and reserving a portion for evaluation, helping to prevent overfitting, and ensuring that the model's performance is assessed on independent data. This separation facilitates a rigorous assessment of the model's ability to make accurate predictions on new instances, validating its effectiveness before deploying it in real-world applications.

D. Lightweight ResNet and Agent-based Classification Model

In the next phase of proposed work, an effective DL based classification model is presented for identifying and categorizing COVID-19 individuals. The reason for using the DL based model in the proposed work is that it is able to handle huge datasets of covid-19 quite efficiently without losing any important information. Here, we have utilized an advanced version of CNN architecture named as, ResNet that comprises of various residual connections. The primary contribution of our work is to propose ResNet classification model in which concept of multi-agents is utilized for increased performance.

The basic functionality of proposed classification model is that training data is divided into three subsets and at the same time the proposed DL classification model is initialized three times, creating 3 agents of Model 1, model 2 and model 3 respectively. The three data subsets are then passed to the three agents separately and each model gives its own prediction. The proposed model is different from current COVID-19 detection models in the fact that standard models pass entire training data to the classifier for training and then generates outcomes on testing data, while as, in our case, each subset of training data is passed to different models or agents to produce the respective predictions. The final prediction is then made by employing ensemble learning based voting mechanism. Now, before further delving deeper into the proposed model, we must know why ResNet is employed in proposed work over other DL networks. The answer to this question is very logical and simple. During the training phase of DL model comprising of various layers, the convergence process might be a challenging process due to vanishing of gradients. This issue hinders the propagation of gradients through the network, causing slow convergence or unstable optimization, which ultimately results in degraded performance of the overall network. This issue needs to be resolved in our model as we aim to achieve high detection accuracy with lowest complexity. Through analysis, we studied that ResNet is one of the effective DL models that can mitigate vanishing gradient problems during training phase. As mentioned earlier, the vanishing gradient problem occurs when a deep neural network struggles to propagate gradients across layers, resulting in extremely slow or even stagnant learning. This issue makes the training of a DL model extremely stressful and challenging.

In our work, ResNet is used for tackling this problem by employing skip or shortcut connections, also referred as residual connections. Such connections enable the training process to effectively skip some layers by allowing details from previous layers to be fed instantly to later ones. This aids in navigating gradients successfully and guards against the loss of crucial training data. Our ResNet design basically comprises of eight important layers (input, reshape, conv2D, batch normalization, Activation, residual block, global average pooling and dense layers) which are designed in such a way that it effectively analyses data and aids in improving accuracy rate of detection model, as shown in Fig. 1.

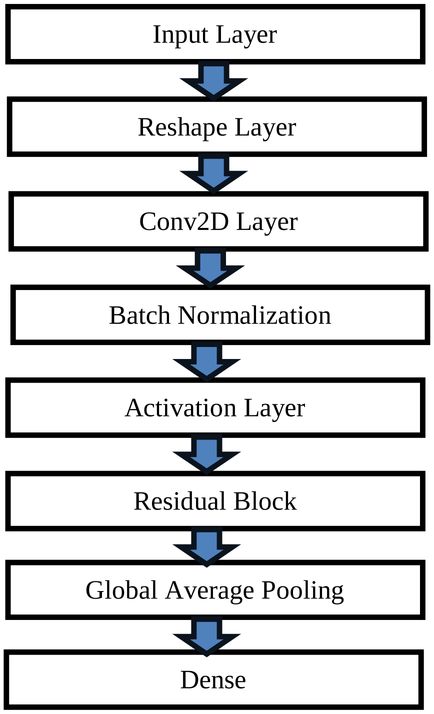

Fig. 1. Architecture of ResNet model.

It must be noted here that residual blocks are added in the proposed ResNet architecture for creating a deeper network without suffering from vanishing gradient problems. The input data is passed through two residual blocks, each consisting of two Conv2D layers with a shortcut connection. The output is then globally average pooled to reduce spatial dimensions, and finally, a Dense layer with a SoftMax activation is used for classification into two classes. Also, the total parameters used in the proposed model were 9794, out of which 9634 are trainable parameters and remaining 160 are non-trainable parameters.

By following this architecture, we were able to develop a lightweight ResNet classification model with least number of parameters that are able to learn complex representations from the data. Moreover, the addition of residual blocks in the proposed model enables training of deeper networks efficiently. This specific ResNet model is designed to handle 1D input data. The details of proposed model classification model are shown in Table IV.

The brief description of each layer used in proposed lightweight ResNet model is explained below:

1) Input layer: The first layer of our model receives 1D input data that contains only 10 features, attained by applying DLRPET FS technique. This layer assumes that shape of input data is 100 x10.

2) Reshape layer: This layer is added in the proposed model for changing the shape of input data while keeping the number of elements constant. In the proposed network, the input data is reshaped to have the dimensions of 100, 10, 1.

3) Conv2D layer: The reshaped data is then received by the first Conv2D layer in which 16 filters of size 3x3 are present. This layer extracts the meaning and complex patterns from the reshaped input data.

4) Batch normalization layer: Moreover, Batch normalization is performed after each convolutional operation for normalizing the activations of intermediate layers within each mini-batch of training data. It helps mitigate issues related to internal covariate shift and enables more effective training of deep networks.

5) Activation layer: Furthermore, to add the concept of non-linearity ReLU activation function is also applied in the proposed architecture, which allows the model to learn and represent complex relationships in data.

6) Residual blocks: In our approach, two residual blocks have been added by using the ResNet_block function. Both residual blocks comprise of two conv2D layers along with a shortcut connection. The functionality of each residual block is explained below:

a) The data received by the previous layer is accepted through convolutional layer that comprises of num_filters filters and kernel_size. After this, batch normalization is performed on output of first convolutional layer for normalizing activations. Moreover, RelU activation function is used for adding non-linearity to this layer.

TABLE IV. LAYER WISE DETAILS OF PROPOSED MODEL

Layer Type	Output Shape	Number of Parameters	Description
Input	(None, 100, 10)	0	Input layer that accepts 2D data of size 100x10.
Reshape	(None, 100, 10, 1)	0	Reshapes the input to 4D format for convolutional layers.
Conv2D	(None, 100, 10, 16)	160	Initial convolutional layer with 16 filters of size 3x3.
Batch Normalization	(None, 100, 10, 16)	64	Batch normalization to normalize activations.
Activation (ReLU)	(None, 100, 10, 16)	0	ReLU activation function to introduce non-linearity.
Residual Block	(None, 100, 10, 16)	Varies	Two Conv2D layers with shortcut Connection and ReLU.
Global Avg Pooling	(None, 16)	0	Global Average Pooling reduces spatial dimensions to 1x1.
Dense	(None, 2)	34	Output layer with 2 units and SoftMax activation.

b) In the next phase, another convolutional layer is implemented with same num filters and kernel size on output of previous layer, which is followed up by batch normalization technique.

c) After this, we have introduced the concept of shortcut connections in the network which performs a convolutional operation with 1x1 filters) on the input if strides > 1. The output of shortcut connection is then subjected to batch normalization.

d) In the next layer, the output generated by two convolutional layers and shortcut connection is added element-wise. Finally, RelU activation function is applied to the sim for adding the non-linearity concept to it.

7) Global average pooling layer: After the stack of residual blocks, the model applies global average pooling to reduce the spatial dimensions to (batch size, numbed of filters). This step averages the values along the spatial dimensions, retaining only the number of filters. It offers several benefits, including dimensionality reduction, regularization, and improved interpretability.

8) Output layer: Finally, the data is received by the output layer which comprises of two units specifically for binary classification problem. It also uses SoftMax activation function which aims to classify the input data into one of two classes in this layer.

Our proposed Lightweight ResNet architecture is also compatible for small and medium sized datasets. Moreover, it can also be used in tasks wherein the deeper networks may not be a suitable option due to resource constraints. Once the model architecture is defined, it is initialized three times to create three agents (Model_1, Model_2 and Model_3) in the proposed work. The configurational parameter of the three agents remains same as depicted in Table V. The main reason for creating agents in the proposed work is to enhance the classification accuracy rate of our model by training it on different subset of training data. As depicted by the table, the featured dataset is divided into training and testing sets of 80:20. Furthermore, we have used sparse categorical cross entropy loss function in the proposed work for training the model.This loss function aids in optimizing the parametric values of our network whose value must be decrease with the increase in epoch size.

TABLE V. RESNET CONFIGURATIONAL PARAMETERS

Training Parameters	Values
Training data	80%
Testing data	20%
Optimizer	Adam
Loss	Sparse categorical cross entropy
Metrics	accuracy
No of Class	2
Epoch	8
Batch size	32

Additionally, we have also utilized Adam optimizer in the proposed work with a learning rate of 0.001 for training the network. However, unlike the traditional model wherein entire training dataset was utilized for training a classifier, we divided the training data into three subsets. Each data subset is then passed to the three agents which passes the data through number of layers described above and produces their respective predictions. The final prediction for determining the individual as COVID-19 positive or negative is achieved by implementing majority voting mechanism. During this phase, the class predicted by the majority of agents is chosen as the final prediction. The idea behind voting mechanism is that by aggregating the predictions of diverse models, the overall predictive performance can be improved, often resulting in more accurate and robust predictions.

III. SIMULATING SETUP AND RESULTS EVALUATION MATRICES

The efficacy of proposed COVID-19 detection approach is examined and also put in comparison with few traditional models in Google Colab Platform, wherein these codes can be executed easily in a Jupyter Notebook environment too. The system on which this software was used possess i5 processor with 8GB RAM and 500 GB HDD. The experimental outcomes were attained in terms of Accuracy, precision, recall and F1-Score, as shown in Eq. (5) to Eq. (8). Moreover, we have also analyzed the performance of proposed approach in context of True Positive Rate (TPR), confusion matrix and accuracy attained by proposed approach during training and validation scenarios.

$$Accuracy = \frac{(TP+TN}{(TP+TN+FP+FN)} \times 100\% \tag{5}$$

$$Precision = \frac{TP}{(TP+FP)} \times 100\% \tag{6}$$

$$Recall = \frac{TP}{(TP+FN)} \times 100\% \tag{7}$$

$$F1 - score = 2 \times \frac{Precision * Recall}{(Precision + Recall)} \tag{8}$$

As we have discussed in earlier sections that proposed DL classification model is initialized three times for validating its performance on three data subsets or agents created from training dataset. The hyper parameters given in Table I and IV are selected in an unbiased way, in order to select the parameters a maximum of 10 runs of simulation are conducted while changing the parameters with in defined range of parameters that includes epochs from 5 to 100, batch size from 8 to 128, and different optimizers including Adam, Gradient Descent, etc. After systematic review the final values of hyper parameters are selected a given Table I and IV. So firstly, we will be analyzing the accuracy of three DL models during their training and validation process. Fig. 2 shows the graph attained for accuracy for Model 1 in which epochs are represented on x-axis and accuracy is depicted on y-axis respectively. The first subset or data agent is passed to model 1 and its accuracy is observed during training and testing phases. The graph reveals that accuracy increases with the increase in epoch size in both cases of training and validation. Initially, the model is not be able to capture complex patterns present in the data, but as it sees more examples it starts adjusting its parameters and becomes better at fitting the training data.

Similarly, we have also observed the accuracy curve obtained for proposed DL and multi-agent-based classification model during its training and testing phases, as shown in Fig. 3. In second model, the second subset or data agent is passed to it to check its effectiveness in context of accuracy. It has been observed that training curve for Model 2 is very low initially because it has not explored lot of data samples, however, as the epoch size increases the accuracy of training curve also increases; depicting that model is getting trained effectively on this data. Similar, is the case with validation curve of model 2 but the only difference is that it shows better accuracy results even during initial phases. This is because the model is already trained on training subset and hence is giving good results on unseen data as well. Additionally, Fig. 4 showcases the accuracy rate obtained by Model 3 on third data agent during its training and validation phase. The given graph simulates that accuracy rate increases with increase in epochs for training and validation phases. This indicates that our third model is able to capture complex and intricate patterns of COVID-19 patients effectively as it is exposed to more epochs, which ultimately enhances its accuracy as well.

Fig. 2. Accuracy attained for model 1 during training and validation.

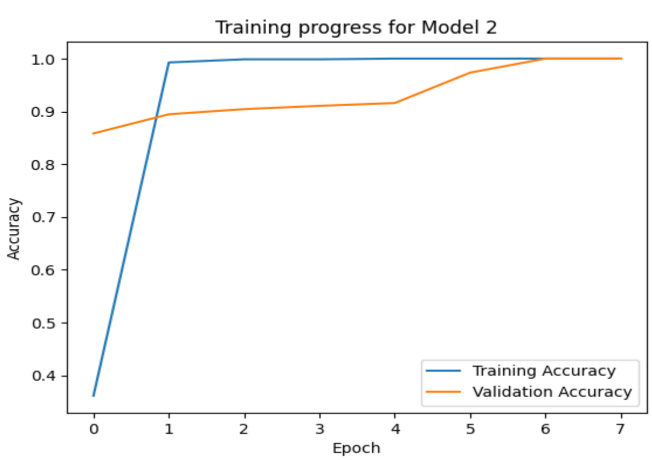

Fig. 3. Accuracy attained for Model 2 during training and validation.

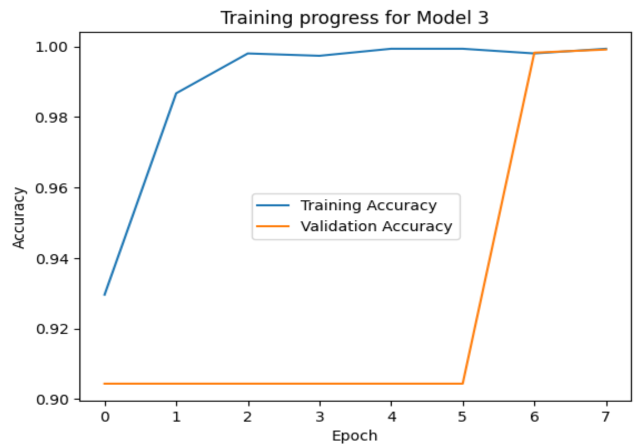

Fig. 4. Accuracy attained for Model 3 during training and validation.

These training and validation accuracy curves of the proposed model are not only giving information of how network is performing during training for each epoch, but also validate our claim of being light weight. The training curve of all the three models represents that proposed model trained faster with less number of epochs. Fig. 2, 3, and 4 shows that while training, although very a smaller number of epochs (8 Epochs) are given for training but still the proposed model is using only 25% of the given epochs that is around 2 epochs to get a stable point of accuracy curve. This shows that the proposed model need less time requirement and it early understands the data patterns to support the lightweight property of model.

To further validate the effectiveness of proposed approach, we evaluated its TPR performance with respect to False Positive Rates (FPR), as demonstrated in Fig. 5. The TPR graph, also known as the Receiver Operating Characteristic (ROC) curve, is a graphical representation that illustrates the performance of a binary classification model across different thresholds. In the beginning, the TPR is typically low, while the FPR is also low. This corresponds to a threshold where the model is very conservative in making positive predictions. However, as the threshold becomes more permissive, the model starts classifying more instances as positive. This leads to an increase in both TPR and FPR. The TPR rises because the model captures more true positive cases, as it becomes less stringent in making positive predictions. However, the FPR also increases, indicating that the model is more prone to mistakenly classifying negative instances as positive. The point where the curve is closest to the top-left corner represents the ideal balance between high TPR and low FPR.

Also, the ability of the proposed model to correctly predict the COVID-19 and non-COVID-19 patients is determined by confusion matrix (see Fig. 6). This matrix gives detailed breakdown of how many instances of each class were correctly or incorrectly classified by proposed model. From the simulation it is analyzed that total false positive came out in testing phase are 0 in count and false negative are 3 in count. Although it is an effective score but still there are few misclassifications seen, the reason behind that is expected to be the relation among the varying entities that arise a different pattern to be identified for considered class. Further by examining the confusion matrix, we can easily evaluate the performance of proposed model under other parameters. In nutshell, we can say that the confusion matrix gives a clear picture of how well a model performs on different classes.

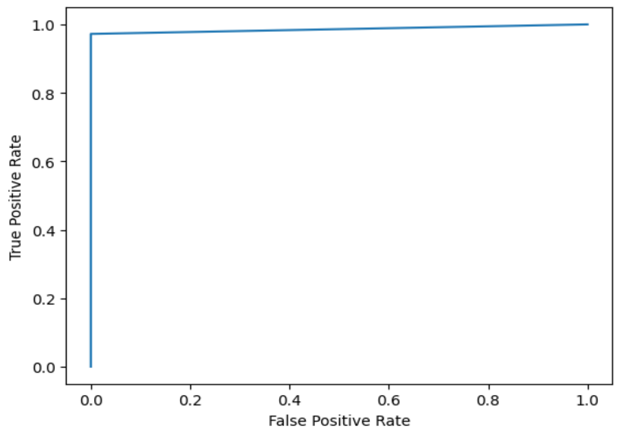

Fig. 5. TPR obtained in proposed approach.

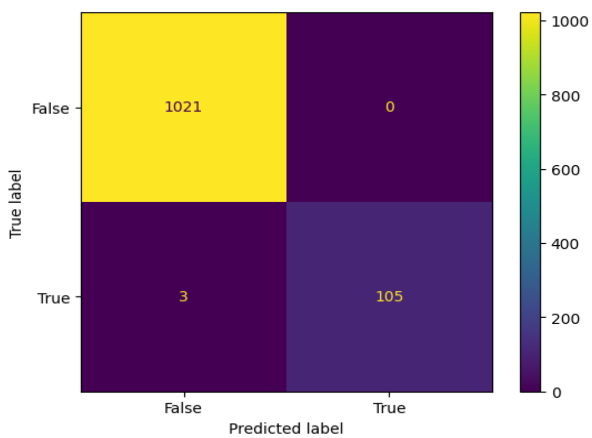

Fig. 6. Confusion matrix obtained in proposed model.

Furthermore, to prove the supremacy of our approach, we compared its performance with standard RF, Bernoulli and SVM models in context of their accuracy rate for classifying COVID and non-COVID patients. The comparative graph for accuracy is depicted in Fig. 7, wherein different techniques and their accuracy rate is represented on x and y-axis respectively. The simulated graph reveals that there is an increment of around 5.57%, 7.23% and 4.73% in accuracy of proposed approach when compared with standard RF, Bernoulli and SVM models respectively [40]. This increased accuracy rate in proposed model is attained because our DL classification model can learn intricate patterns for three different data agents without enhancing its complexity. Likewise, we have also evaluated the performance of proposed approach with standard COVID-19 detection models in terms of their precision rate. The comparative graph obtained for the same is shown in Fig. 8. After carefully examining the given graph, it is observed that standard Bernoulli model is exhibiting lowest precision value of 86% whereas, it was improved by RF and SVM models that achieved 95% precision rate. On the contrary, our approach is showcasing a precision of 100%, which specifies that all positive predictions made by a binary classification model are correct. This is an ideal scenario because it indicates that the model is not producing any false alarms for negative instances, which can be particularly important in COVID-19 detection. Furthermore, these results reveal by employing the proposed DL classification model precision rate is improved by around 5% then best performing standard models i.e., RF and SVM respectively. Moreover, the performance of proposed approach is also examined and validated by comparing it with conventional models in terms of their recall percentage. Fig. 9 showcases the comparison graph obtained for recall. The given graph simulates that again recall value was lowest in Bernoulli model with only 93%, followed up by RF and SVM model with 94% and 95% respectively. This lowest recall rate in standard model depict that they are not able to comprehend data effectively which degrades their performance. However, in our proposed approach, the recall rate is exceptionally high at 99.73% which marks an increment of 4.73% then SVM model. This high recall rate in proposed model determines that our approach is successfully able to capture majority of the instances that belong to positive cases.

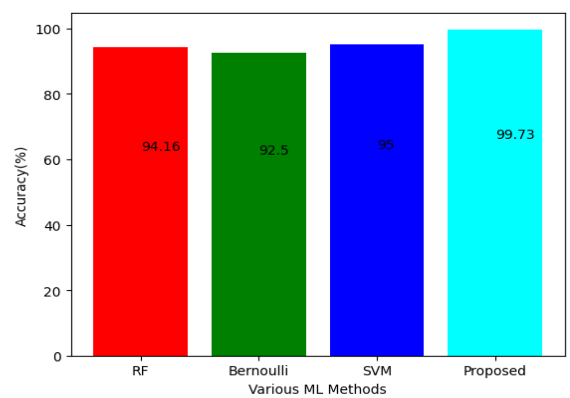

Fig. 7. Comparative graph for accuracy.

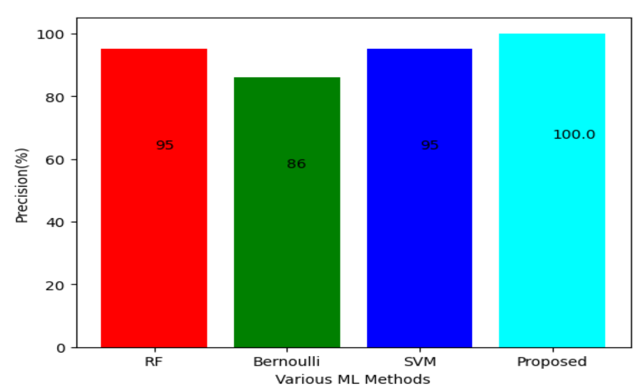

Fig. 8. Comparative graph for precision.

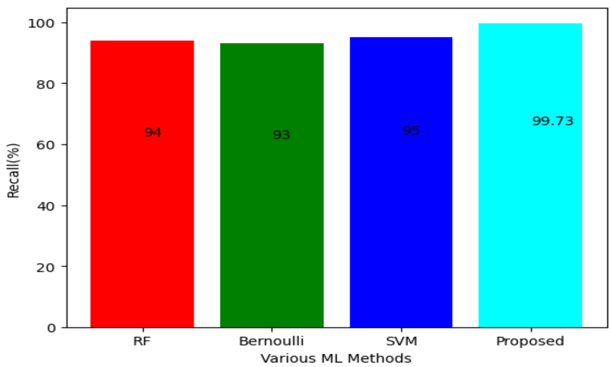

Fig. 9. Comparative graph for Recall.

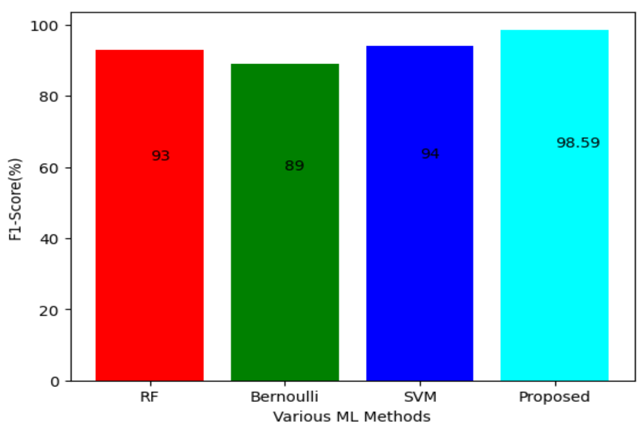

Fig. 10. Comparative graph for F1-Score.

Finally, the effectiveness of proposed approach is also validated by putting it in comparison with standard models in terms of F1-Score, as shown in Fig. 10. The x and y axis of the given graph calibrates to different detection techniques and their F1-Score respectively. Upon examining the graph carefully, we observed that Bernoulli is the worst performing model with 89% while as, RF and SVM achieves F1-Score of 93% and 94% respectively. While as, when we analyzed the F1-Score in proposed model, we observed an upward trend of 98.59%, showcasing the supremacy of proposed approach over other similar approaches. The exact value of each parameter is mentioned in table also and is shown in Table VI.

In addition to this, the proposed scheme is compared with other state of art techniques used for identifying the COVID-19 from the statistical data. Below Table VII gives the details if the outcomes analyzed with other methods and our proposed scheme.

TABLE VI. COMPARATIVE ANALYSIS OF DIFFERENT PARAMETERS

Algorithm	Accuracy	Precision	Recall	F1-Score
RF	94.16	95	94	93
Bernoulli	92.5	86	93	89
SVM	95	95	95	94
Proposed	99.73	100	99.73	98.59

TABLE VII. COMPARATIVE ANALYSIS WITH OTHER STATE OF ART METHODS

Algorithm	Accuracy	Precision	Recall	F1-Score
ANN [19]	86.90	87.13	87.13	87.13
CNNRNN[20]	86.24	87.55	87.55	87.55
CNNLSTM [21]	92.30	92.35	93.68	93
KISM [22]	97.87	81.82	100	90
Su X et al.[23]	92.82	93.41	93.41	93.41
Proposed	99.73	100	99.73	98.59

In this phase a comparison with different methods used to classify the COVID-19 with similar dataset and type of dataset is conducted. The analysis shows that ANN [19] achieved accuracy was 86.90%. Additionally, few recently developed models including KISM [22] and Su X et al. [21] are achieving an accuracy of 97.87 % and 92.82 %, even deep learning-based models CNNRNN, and CNNLSTM given in [20][21] are achieving 86.24 % and 92.30 % of accuracy respectively. However, in proposed scheme, a score of 99.73%accuracy is achieved which is around 2% more than standard highest scorer KISM [22]. Similarly, proposed method outperformed models given in [21], [22] and [23] by attaining highest value of precision, and F1-Score that are 100% and 98.59% respectively. The details values for individual algorithm are given in Table VI.

IV. RESULTS ANALYSIS AND CONCLUSION

The results attained by proposed model showcases that by implementing multi-agent-based DL model for identifying and classifying individuals into COVID positive or negative, the accuracy of detection rate increases. When compared to previous models, we observed that proposed models' accuracy rate is 99.73% which is 5.57%, 7.23% and 4.73% more than standard RF, Bernoulli and SVM models. Moreover, proposed model shows an accuracy improvement of 12.83% than ANN [41], 1.86% than KISM [42] and 6.91% than Su X et al. [43] approaches respectively. Similarly, our approach was able to improve the precision, recall and F1-Score rates also due to its ability to capture complex and intricate patterns of COVID-19 effectively. The results proved that proposed model attained a precision rate of 100% which signifies that it is able to predict every instance correctly. Moreover, this precision score indicates that there is an improvement of 14% then Bernoulli model, 5% then RF and SVM and 12.87%, 18.18% and 6.59% than ANN [41], KISM [42] and Su X et al. [43] models respectively. Similar trend is observed for recall and F1-Score parameters which showed an overall increment of 4.73% and 4.59% over best performing standard model (SVM).Through machine learning in COVID-19 detection, diagnosis, and treatment, we can improve multi-agent systems for better healthcare [44, 45].These analytical records prove that proposed system is more robust and accurate in determining and classifying the individuals as COVID-19 infected and normal. In this manuscript, an effective COVID-19 detection model is presented that is based on DL and Multi-agent techniques. The primary goal of the proposed work is to increase the detection accuracy rate while minimizing the complexity and dimensionality issues. To prove the efficacy and supremacy of our approach, we compared its performance with standard detection methods in Google Colab Platform. The simulated results reveal that our method attained accuracy rate of 99.73%, surpassing traditional RF, Bernoulli, SVM, ANN, KISM, CNNLSTM, CNNRNN and Su X et al. models which attained only 94%, 92%, 95% , 86.9%, 97%, 92%, 86% and 92.8% accuracies. Moreover, the proposed model also attained a high precision of 100% which means it is correctly predicting classes, while as, it was only 95% in RF and SVM, 86% in Bernoulli, 87% in ANN and CNNRNN, 81% in KISM, 92 % and 93% in CNNLSTM and Su X et al., methods. Furthermore, we have observed an increment of 5.73%, 6.73%, 4.73%, 12.6%, 12.18%, 6.05% and 6.32% for recall values when compared with RF, Bernoulli, SVM, ANN, CNNRNN, CNNLSTM and Su X et al. methods.

In addition to this, our approach is outperforming traditional model in terms of F1-Score also by attaining a score of 98.59%. These results simulate that our proposed model is more efficiently and effectively able to detect COVID-19 patients. Despite the fact that proposed approach is giving best results than other similar models, it is important to identify its inherent limitation caused by data scarcity. As proposed model is trained on laboratory finding based dataset, lacking data variability for input information, the generalization of proposed model is still necessary to explore to its fullest. Therefore, future research can focus on working with joining different datasets to achieve larger and generalized informative datasets for effective training and testing of the model.

REFERENCES

[1] R. Khalilov, M. Hosainzadegan, A. Eftekhari, A. Nasibova, A. Hasanzadeh, &P. Vahedi, “Overview of the environmental distribution, resistance, mortality, and genetic diversity of new coronavirus (COVID-19),” *Advances in Biology & Earth Sciences,* vol. 5, no. 1, 2020.

[2] A.E. Gorbalenya, S.C. Baker, R. S. Baric, R. J. De Groot, C. Drosten, A.A. Gulyaeva, and J. Ziebuhr, “The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2,” *Nat Microbiol. 2020,* vol. 5, pp. 536–44, 2020.

[3] S. Akhai, S. Mala, & A. A. Jerin, “Understanding whether air filtration from air conditioners reduces the probability of virus transmission in the environment,” *Journal of Advanced Research in Medical Science & Technology,* vol. *8*, no. 1, pp. 36-41, 2021.

[4] S. Akhai, S. Mala, & A.A. Jerin, “Apprehending air conditioning systems in context to COVID-19 and human health: A brief communication,” *International Journal of Healthcare Education & Medical Informatics,* vol. *7*, no. 1&2, pp. 28-30, 2020.

[5] L.P. Samaranayake, C.J. Seneviratne, & K.S. Fakhruddin, “Coronavirus disease 2019 (COVID-19) vaccines: A concise review,” *Oral diseases,* vol. 28, pp. 2326-2336, 2022.

[6] N. Subramanian, O. Elharrouss, S. Al-Maadeed, & M. Chowdhury, “A review of deep learning-based detection methods for COVID-19,” *Computers in Biology and Medicine,* vol. 143, no. 105233, 2022.

[7] Organization for Economic Co-operation and Development, “Enhancing public trust in COVID-19 vaccination: The role of governments,” *OECD Publishing*, 2021: Accessed on: Feb 09, 2023. [Online]. Available: https://www.oecd.org/coronavirus/policy-responses/enhancing-public-trust-in-covid-19-vaccination-the-role-of-governments-eae0ec5a/

[8] R. Keni, A. Alexander, P.G. Nayak, J. Mudgal, and K. Nandakumar, “COVID-19: emergence, spread, possible treatments, and global burden,” *Frontiers in public health*, pp.216, 2020.

[9] A. Filipić, I. Gutierrez-Aguirre, S. Primc, M. Mozetič, & D. Dobnik, “Cold plasma, a new hope in the field of virus inactivation,” *Trends in Biotechnology,* vol. 38, no. 11, pp. 1278-1291, 2020.

[10] U.K.H. Ecker, S. Lewandowsky, J. Cook, “The psychological drivers of misinformation belief and its resistance to correction,” *Nat Rev Psychol,* vol. 1, pp. 13–29, 2022. https://doi.org/10.1038/s44159-021-00006-y.

[11] R. Liu, H. Han, F. Liu, Z. Lv, K. Wu, Y. Liu, & C. Zhu, “Positive rate of RT-PCR detection of SARS-CoV-2 infection in 4880 cases from one hospital in Wuhan, China, from Jan to Feb 2020,” *Clinic achimicaacta,* vol. 505, pp. 172-175, 2020.

[12] S. Akhai, “From Black Boxes to Transparent Machines: The Quest for Explainable AI,” *Available at SSRN 4390887*, 2023. doi: http://dx.doi.org/10.2139/ssrn.4390887

[13] W. Al Shehri, J. Almalki, R. Mehmood, K. Alsaif, S.M. Alshahrani, N. Jannah, & S. Alangari, S, “A Novel COVID-19 Detection Technique Using Deep Learning Based Approaches,” *Sustainability,* vol. 14, no. 19, 2022.

[14] O.N. Oyelade, A.E.S. Ezugwu, & H. Chiroma, “CovFrameNet: An enhanced deep learning framework for COVID-19 detection,” *IEEE Access,* vol. 9, pp. 77905-77919, 2021.

[15] S. Sakib, T. Tazrin, M.M. Fouda, Z.M. Fadlullah, & M. Guizani, “DL-CRC: deep learning-based chest radiograph classification for COVID-19 detection: a novel approach,” *IEEE Access*, vol. 8, pp. 171575-171589, 2020.

[16] S. V. Kogilavani, J. Prabhu, R. Sandhiya, M.S. Kumar, U. Subramaniam, A. Karthick, & S.B.S. Imam, “COVID-19 detection based on lung CT scan using deep learning techniques,” *Computational and Mathematical Methods in Medicine*, 2022.

[17] M.Z. Alom, M.M. Rahman, M. S. Nasrin, T.M. Taha, & V.K. Asari, “COVID_MTNet: COVID-19 detection with multi-task deep learning approaches,” *arXiv preprint arXiv*, vol. 2004, no. 03747, 2020.

[18] Dataset: Accessed: Oct 30, 2023. [Online]. Available: https://github.com/burakalakuss/COVID-19-Clinical.

[19] J. Sharma, C. Giri, O.-C. Granmo, and M. Goodwin, “Multi-layer intrusion detection system with ExtraTrees feature selection, extreme learning machine ensemble, and softmax aggregation,” EURASIP Journal on Information Security, vol. 2019, no. 1. Springer Science and Business Media LLC, Oct. 22, 2019. doi: 10.1186/s13635-019-0098-y.

[20] A. Kareem, K. Hameed, et al., “Realizing an effective COVID-19 diagnosis system based on machine learning and IOT in smart hospital environment," IEEE Internet of things journal, vol. 8, no. 21, pp.15919-15928, 2021.

[21] TBA Ibrahim Turkoglu, “Comparison of deep learning approaches to predict COVID-19 infection,” Chaos, Solitons & Fractals, vol. 140, no. 2020, 2021.

[22] Y. Fan, M. Liu, G. Sun, “An interpretable machine learning framework for diagnosis and prognosis of COVID-19,” PLoS ONE, vol. 18, no. 9, 2023. https://doi.org/10.1371/journal.pone.0291961

[23] X. Su, Y. Sun, H. Liu et al., “An innovative ensemble model based on deep learning for prediction COVID-19 infection,” Scientific Reports, vol. 13, no. 1, 2023.