



Extended VGG16 Deep-Learning Detects COVID-19 from Chest CT Images

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ABSTRACT: Coronavirus disease 2019 (COVID-19), is a rapidly spreading disease that has infected millions of people worldwide. One of the essential steps to prevent spreading COVID-19 is an effective screening of infected individuals. In addition to clinical tests like Reverse Transcription-Polymerase Chain Reaction (RT-PCR), medical imaging techniques such as Computed Tomography (CT) can be used as a rapid technique to detect and evaluate patients infected by COVID-19. Conventionally, CT-based COVID-19 detection is performed by an expert radiologist. In this paper, we will completely and utterly discuss COVID-19. We present a deep learning Convolutional Neural Network (CNN) model that we have developed to detect chest CT images with COVID-19 lesions. Afterwards, based on the fact that in an infected individual, more than one slice is involved, we determine and apply the best threshold to detect COVID-19 positive patients. We collected 5,225 CT images from 130 COVID-19 positive patients and 4,955 CT images from 130 healthy subjects. We used 3,684 CT images with COVID-19 lesions and their corresponding slices from healthy control subjects to build our model. We used 5-fold-cross-validation to evaluate the model, in which each fold contains 26 patients and 26 healthy subjects. We obtained a sensitivity of $91.5\% \pm 6.8\%$, a specificity of $94.6\% \pm 3.4\%$, an accuracy of $93.0\% \pm 3.9\%$, a precision of $94.5\% \pm 3.5\%$, and an F1-Score of 0.93 ± 0.04 .

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1- Introduction

1- 1- Background

Coronavirus Disease 2019 (COVID-19) is a highly contagious disease that spreads mainly from person to person with the appearance of respiratory distress [1]. It has been widespread worldwide since December 2019 and so far, it has infected more than 115 million people. Imaging of the chest can be used to detect lung involvement, initiate treatment, isolate infected individuals, and attenuate the chain of infection [2]. As a conventional laboratory technique, the real-time Reverse Transcriptase-Polymerase Chain Reaction (RT-PCR) test has been used for diagnosing COVID-19 positive cases [3]. While this test is widely used worldwide, according to current clinical experiences, it has a high probability of early false negatives for the determination of viral RNA in sputum or nasopharyngeal swabs. Additionally, several studies have demonstrated a highly variable positive rate, depending on how the specimen was collected, and a reduction in positive rate overtime after symptom onset. In addition to RT-PCR, medical images such as Computed Tomography (CT) images may provide a significantly more trustworthy, useful, and rapid technique to classify and evaluate COVID-19, specifically in epidemic regions. In contrast to conventional X-ray images, CT produces detailed images of the chest through the slices.

Therefore, these detailed slices can be used by physicians to determine the exact site of infection and evaluate the extent of the disease [4]. However, the chest CT-based COVID-19 classification involves an expert radiologist and considerable time, which may be scarce when COVID-19 infection is growing at a rapid rate. Additionally, it is found that the COVID-19-infected patients may show patterns on chest CT images not easily detectable by the human eye [5, 6]. Thus, an automatic, rapid detection tool is necessary for the screening of the COVID-19 pneumonia, using chest radiography and chest CT [6-8]. Deep Learning (DL) is proposed to automate the screening of the CT scans, detect infections, and evaluate the extent of the disease [9].

The main contributions and novelties of this paper are:

- Developing an automatic method for detecting COVID-19 patients using CT images.
- Using CT images from a realistic, national dataset with ground truth in the development and evaluation of the proposed method.
- Using a pre-trained CNN to overcome the need for big data in the training phase.
- Investigating various pre-trained networks (ResNet, Inception V3, VGG16, DenseNet, and Xception), and the identifying VGG16 as the simplest and the most accurate technique.

The remainder of the paper is organized as follows. First,

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we review recent literature related to the COVID-19 detection from CT images. Next, we present our methods and results. Later, we discuss the results, describe the limitations of the proposed approach, and explain future works.

1- 2- Related Works

In order to diagnose COVID-19 and segment the related infections from chest x-ray images or CT scans, several deep learning approaches have been proposed [10]. However, in most CT-based studies, two factors reduce the generalization of the results: (i) each slice is treated independently, and (ii) a single dataset is used for training and testing of the models [4]. One of the basic tools to classify the COVID-19 patients from the other types of pneumonia using CT chest images is the Support Vector Machine (SVM) model. For instance, N. Yang et al. [11] constructed an SVM model for this classification using radionics features obtained from textural and histogram features of the infections. Using this method, they achieved a classification accuracy of 88.33% between COVID-19 and other types of pneumonia, a sensitivity of 83.56%, a specificity of 93.11%, and an area under the ROC curve of 0.947, which shows the effectiveness of their method for the diagnosis of COVID-19. Additionally, M. Barstugan et al. [12] used an SVM model for this purpose using the features extracted by Gray Level Co-occurrence Matrix (GLCM), Gray Level Run Length Matrix (GLRLM), Gray-Level Size Zone Matrix (GLSZM), Local Directional Pattern (LDP), and Discrete Wavelet Transform algorithms (DWT). They used 150 CT images and four different window sizes of 16×16, 32×32, 48×48, and 64×64. After implementing 2-fold, 5-fold, and 10-fold cross-validations, the best classification accuracy was reported as 99.68% obtained from the GLSZM feature extraction method and 10-fold cross-validation.

Weakly-supervised deep learning (WSDL) methods have also been proposed to classify COVID-19 and non-COVID-19 patients using chest CT images [13]. S. Hu et al. [1] applied a WSDL method on 450 chest CT images of COVID-19, Community-Acquired Pneumonia (CAP), and non-pneumonia (NP) patients. The results of classifying COVID-19 from NP cases showed a mean accuracy of 96.2%, precision of 97.3%, sensitivity of 94.5%, specificity of 95.3%, and area under the ROC curve of 0.970 (there seems to be a typographic error in these results since the accuracy should be between sensitivity and specificity). In another effort, Wang, et al. [14] developed a WSDL framework to classify the COVID-19 cases and localize the infected regions using 499 CT volumes for training and 131 CT volumes for testing. They segmented lungs by a pre-trained UNet, and fed them into a 3D deep neural network to predict the probability of COVID-19. The infected regions were localized by combining an unsupervised identification of the connected components with the activation regions of the classification network. This study achieved an accuracy of 97.6% and the area under the ROC curve of 0.959, which are close to but somewhat inconsistent with the results of the above study.

In the study of A. Amyar et al. [15], a chest CT dataset of 449 COVID-19 cases, 98 patients with lung cancer, 397

cases with other types of pathology, and 100 healthy subjects were used to develop a multi-task deep learning model for the classification of COVID-19 and localization of the infected regions. This model was composed of an encoder, two decoders for reconstruction and segmentation, and a Multi-Layer Perceptron (MLP) neural network for classification. As the evaluation results, the Dice Similarity Coefficient (DSC) and area under the ROC curve were considered and reported, which were higher than 0.78 and 0.93, respectively. Moreover, He et al. [16] developed a Multi-task Multi-instance Deep Network (M²UNet) for the segmentation of the lung lobes and the assessment of COVID-19 severity in 666 CT images of COVID-19 patients. This algorithm included a patch-level encoder, a segmentation subnetwork, and a classification subnetwork that achieved a classification accuracy of 0.985, a sensitivity of 0.783, a positive predictive value (PPV) of 0.799, and a DSC of 0.785.

Convolutional Neural Networks (CNN) can also be effective for the classification of COVID-19 patients using chest CT images. Singh et al. [5] used a CNN model to classify COVID-19 cases into two groups of infected and not-infected. The initial parameters of the CNN model were tuned using a Multi-Objective Differential Evolution (MODE) model. The results showed an accuracy of 0.933 and outperformed the competitive models of Artificial Neural Network (ANN), Adaptive Network-based Fuzzy Inference System (ANFIS), and CNN in terms of accuracy, F score, sensitivity, specificity, and Kappa statistics by 1.98%, 2.09%, 1.83%, 1.68%, and 1.93%, respectively.

Other studies have focused on developing pre-trained deep network models. Yu et al. [17] used four of these pre-trained models (ResNet-50, ResNet-101, Inception-V3, and DenseNet-201) with multiple classifiers (linear discriminant, linear SVM, cubic SVM, KNN, and Adaboost decision tree) to classify severe and non-severe COVID-19 patients, using 246 and 483 chest CT images of the two groups, respectively. After validating the results with the holdout, 10-fold, and leave-one-out cross-validation, the DenseNet-201 with cubic SVM model showed the best accuracy of 95.20% and 95.34% for the 10-fold and leave-one-out validations, respectively. Moreover, in the study of X. Deng et al. [18], five Keras-related deep learning models (ResNet50, InceptionResNetV2, transfer learning, Xception, and VGGNet16) were developed for the classification of COVID-19 cases using a dataset of 767 chest CT images and 5857 chest X-rays. The results achieved the highest classification accuracy of 75% and 84%, respectively for the CT images and X-rays, which are lower than those of the above study. In [19], M. Loey et al. selected five different CNN models (ResNet50, GoogleNet, VGG-19, VGG-16, and AlexNet) for the classification of COVID-19 infected patients, and CGAN was also used for classical data augmentation that can effectively improve the classification performance [20]. The results revealed that ResNet50 outperformed the other methods with an accuracy of 82.91%, a sensitivity of 77.66%, and a specificity of 87.62%. Pre-trained VGG-19 has also been an effective tool for this classification [21]. P. Gifani et al. [22] used 15 pre-trained CNNs for the

Table 1. Summary of previous research on COVID-19 detection using chest CT.

Author (Year) [Reference no.]	Model	Image Classes	Accuracy%
Yang (2020) [11]	SVM	COVID-19, Pneumonia	88.3%
Barstugan (2020) [12]	SVM	COVID-19 infected patches vs. non-infected patches	99.7%
Hu (2020) [1]	Inspired by the VGG architecture	COVID-19, CAP, Normal	96.2%
Wang (2020) [14]	DeCoVNet	COVID-19+ vs. COVID-19-	97.6%
Amyar (2020) [15]	MLP	COVID-19, Lung cancer, Other types of pathology, Normal	86.0%
He (2021) [16]	M ² UNet	COVID-19 with different severities (mild, moderate, severe, and critical)	98.5%
Singh (2020) [5]	MODE-based CNN	COVID-19 infected vs. not-infected	93.3%
Yu (2020) [17]	DenseNet-201 with cubic SVM	COVID-19 severe vs. non-severe	95.3%
Deng (2020) [18]	ResNet50, VGG16	COVID-19, Normal	75.0%
Loey (2020) [19]	ResNet50	COVID-19 infected vs. not-infected	82.9%
Gifani (2020) [22]	Majority voting of EfficientNet, Inception, and Xception	COVID-19+ vs. COVID-19-	85.0%
Hasan (2020) [23]	LSTM	COVID-19, pneumonia, Normal	99.7%
Sun (2020) [24]	AFS-DF	COVID-19, CAP	91.8%
Abdar (2020) [25]	VGG16	COVID-19, Normal	90.0%

classification of COVID-19 and non-COVID-19 cases on a dataset of 349 and 347 CT scans labeled as being positive and negative COVID-19, respectively. They showed that the majority voting of five models with EfficientNet (B0, B3, and B5), Inception_resnet_v2, and Xception has the highest performance compared to the individual transfer learning structures and among the other models based on the accuracy, precision, and recall metrics which were 0.85, 0.857, and 0.854, respectively.

In another study for the classification of COVID-19, pneumonia, and healthy subjects, Hasan et al. [23] applied a combination of deep learning methods on Q-deformed entropy handcrafted features of a dataset comprising 321 patients. The analysis steps on each CT lung scan were pre-processing, histogram thresholding, feature extraction based on deep learning and a Q-deformed entropy algorithm, and classification of features using a Long Short-Term Memory (LSTM) neural network classifier. The highest accuracy achieved by combining all extracted features was 99.68%. Additionally, Sun et al. [24], proposed an adaptive feature selection guided deep forest (AFS-DF) algorithm for this classification. They used 1495 CT images of COVID-19 and 1027 of Community-Acquired Pneumonia (CAP) patients. After using a high-level representation of the features to learn the model, and a feature selection based on the trained deep

forest model, the performance metrics of accuracy, sensitivity, specificity, and area under the ROC curve were found to be 91.79%, 93.05%, 89.95%, and 96.35%, respectively.

In our recent work [25], we acquired a dataset of 10,979 chest CT images from 131 COVID-19 patients and 150 healthy subjects. We then identified 1,966 CT images with COVID-19 infections detected by an expert radiologist, along with 1,735 similar CT images of the healthy subjects, for the training of a CNN model with the maximum focus on the infected regions. Such regions were segmented by an attention R2U-net with a dice value of 0.79 [26]. Our base model was VGG16 plus some pooling, dropout, and dense layers to generate the two-class output and achieve reasonable accuracy. After implementing five-fold cross-validation, the model revealed a precision of 92%, a sensitivity of 90%, a specificity of 91%, an F1-Score of 0.91, and an accuracy of 90%. A heatmap is an effective tool that can be generated to reveal where the developed model is focusing on while making the predictions [27, 28]. Our model's heatmaps showed a successful focus on the infected regions of COVID-19 due to the clean training dataset, preprocessing steps, and developed model. A summary of the previous research works associated with the COVID-19 detection using chest CT images is presented in Table 1.

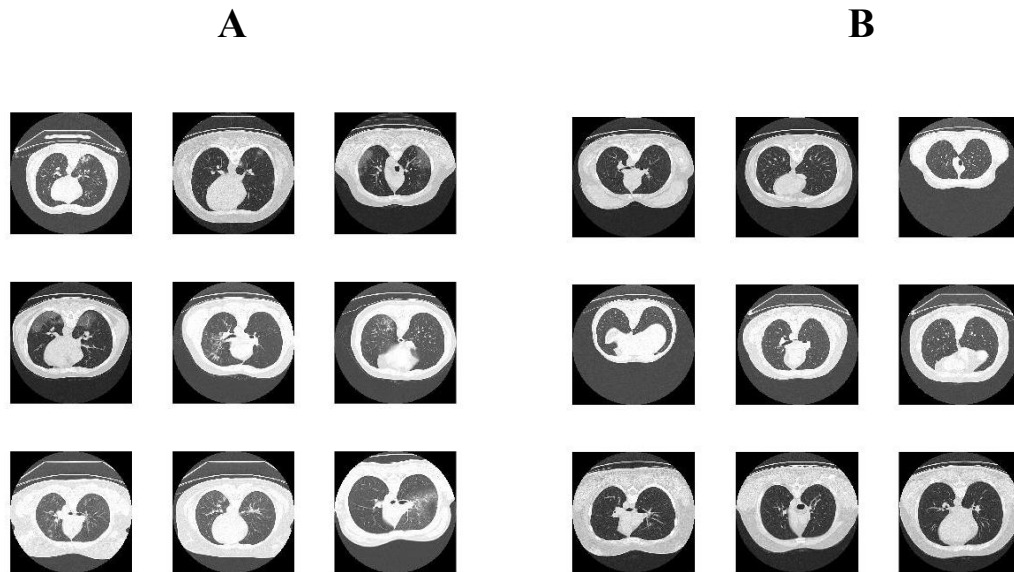


Fig. 1. Sample chest CT images of COVID-19 positive patients (A), and nonCOVID-19 cases (B).

2- Materials and Methods

2- 1- Patients and Data

In this study, we collected 5,225 CT images from 130 COVID-19 positive patients and 4,955 CT images from 130 healthy subjects (i.e., a total of 10,180 CT images from 260 cases, acquired in the Alinasab Hospital of Tabriz, Tabriz, Iran). In each CT slice, our expert co-investigator segmented regions of infection. We used these slices and their segmentation masks in preprocessing and training of the model to increase the performance and generalization of the model. Moreover, to minimize irrelevant differences between the images of the two groups and allow the model to focus on the relevant differences (infections). For the healthy subjects, we used the slices that anatomically matched the slices of the COVID-19 patients that contained infections. In total, 1,957 CT slices with COVID-19 infections, along with 1,727 similar slices from healthy subjects, were used to train and evaluate the model. Sample CT slices of nonCOVID-19 and COVID-19 cases are shown in Fig. 1 (A) and Fig. 1 (B), respectively.

2- 2- Image Preprocessing

The following preprocessing steps were applied to the images:

Step 1. Hounsfield Unit Transformation:

An intensity transformation was applied to all images to map the image intensities onto the Hounsfield unit, so that all images are treated the same (i.e., processed in the same, standard intensity range).

Step 2. Extracting Lungs:

Each image was first binarized by intensity thresholding to classify the pixels that represented the lungs from those that represented outside of the lungs. The connected

components were identified and labeled by size. Two or three big connected components corresponded to the lungs and background. The connected component corresponding to the background was used as a mask to delete the irrelevant pixels from the images. The connected components corresponding to the lungs were used as a mask to preserve the lung pixels and use them in the following steps. The resulting images are called lung images.

Step 3. Histogram Equalization:

Histogram equalization was applied on the lung images using a transformation created by the histogram of the infected regions. This step produced an intensity transformation for each image to widen the histogram of the infection regions, making it easier for the model to detect the infections.

Step 4. Stretching Contrast of Images:

Finally, another intensity transformation was applied to stretch the whole image contrast so that the images are generally more informative to the model.

Sample preprocessed CT images of the COVID-19 cases, and non-COVID-19 cases are shown in Fig. 2 (A) and Fig. 2 (B), respectively.

2- 3- Deep Transfer Learning

The necessity of using a very large training dataset makes it extremely time and memory-consuming to train the CNN models. We used pre-trained networks to overcome this difficulty (i.e., we used deep transfer learning and updated the model weights using our dataset). We applied multiple pre-trained deep learning networks such as DenseNet [29], Inception V3 [30], Xception [31], VGG16 [32], and ResNet [33]. Most of these models have a very deep and complicated network with several layers. Thus, we needed a large dataset

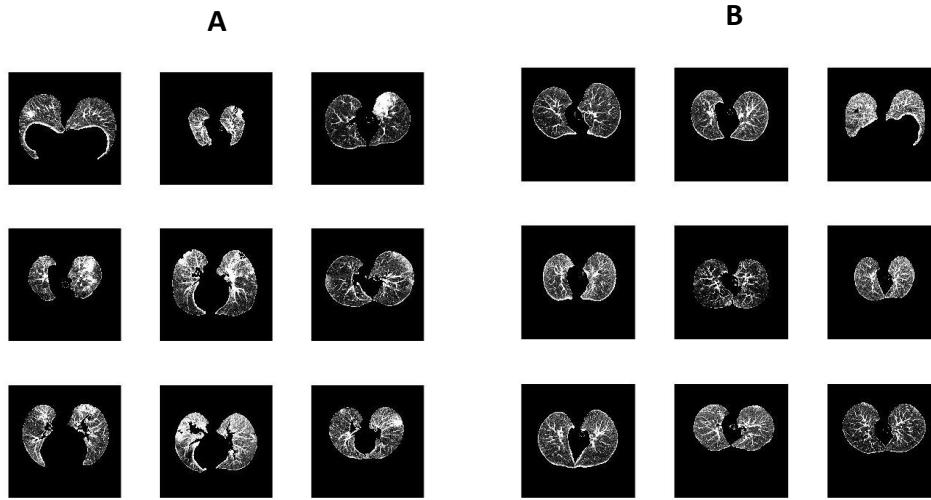


Fig. 2. Sample lung images of COVID-19 patients after preprocessing (A), and nonCOVID-19 cases after preprocessing (B).

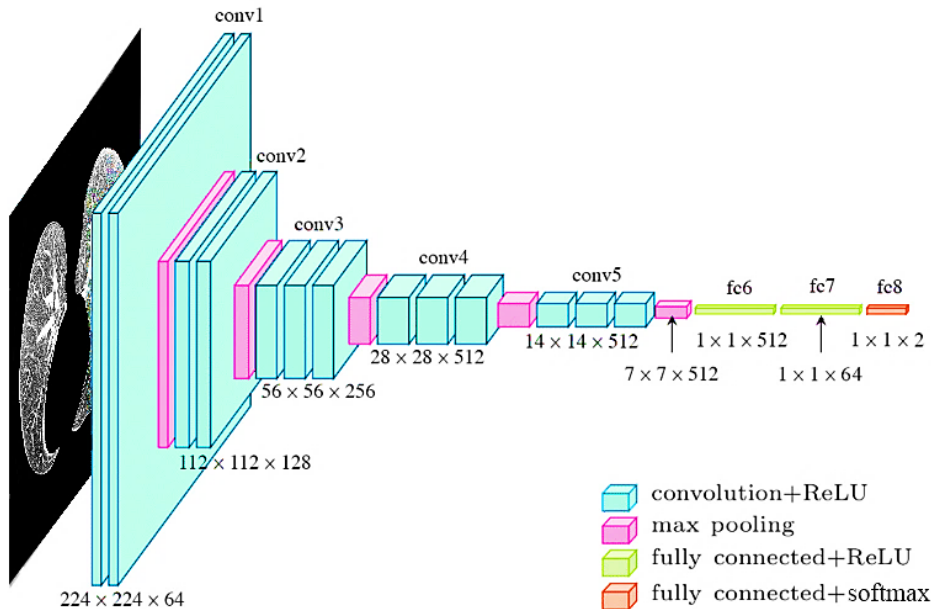


Fig. 3. The deep model architecture with VGG16 as the base model.

to train our model even when we used transfer learning. Due to this limitation, we chose VGG16 as our base model since it was less complicated than the others. The implementation included the following steps:

Step 1: Used the preprocessed images as the input to the model (shape = $224 \times 224 \times 3$).

Step 2: Froze all weights of VGG16.

Step 3: Fetched the last convolution layer's output of VGG16.

Step 4: Applied global max pooling.

Step 5: Applied a flatten layer and a dense layer with an ReLU activation function (units = 512).

Step 6: Applied a 50% drop-out layer.

Step 7: Applied a dense layer with the ReLU activation function (units = 64).

Step 8: Applied a 50% drop-out layer.

Step 9: Applied a dense layer for classification with a softmax activation function.

The Adam algorithm was chosen for optimization with an initial learning rate equal to 0.001 and 5×10^{-5} decay. The batch size was set to 64, and the number of training epochs was set to 20. The model architecture is shown in Fig. 3.

We used five-fold cross-validation to evaluate the performance of our proposed method. To this end, based on

Fold 1	Subset 1	Subset 2	Subset 3	Subset 4	Subset 5
Fold 2	Subset 2	Subset 3	Subset 4	Subset 5	Subset 1
Fold 3	Subset 3	Subset 4	Subset 5	Subset 1	Subset 2
Fold 4	Subset 4	Subset 5	Subset 1	Subset 2	Subset 3
Fold 5	Subset 5	Subset 1	Subset 2	Subset 3	Subset 4

Training data

Validation data

Testing data

Fig. 4. Five-fold cross-validation data partitioning: patients were randomly assigned to the subsets.

Table 2. The performance of the developed model.

Metric	Precision	Sensitivity	Specificity	F1 Score	Accuracy
Value	92.0%±2.1%	88.5%±2.8%	91.2%±2.6	0.90±0.02	89.6%±1.6%

the number of cases the CT data was randomly partitioned into five subsets, each including 26 patients and 26 normal subjects. Fig. 4 shows a schematic of this data partitioning, and how we used the subsets for training, validation, and testing of the model. The training data was used to train the model, the validation data was used to set the hyperparameters of the model, and the test data was used to evaluate the model performance.

As shown in Fig.4, three subsets of the data were used for training in each fold of our five-fold cross-validation; one subset for validation, and one subset for testing. This means that in each fold, 60% of the data was used for training, 20% for validation, and 20% for evaluation.

3- Results

After training the model, we used the standard statistical analysis methods to estimate the performance of the model. First, the True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) rates were calculated for each epoch, and later we calculated evaluation metrics like sensitivity, precision, specificity, accuracy, and F1 score based on this parameter. These quantities are defined in Eqs. (1)-(5), where TP, TN, FP, and FN are defined as:

True Positive (TP): The COVID-19 lung image is correctly classified.

True Negative (TN): The healthy lung image is correctly classified.

False Positive (FP): The healthy lung image is misdiagnosed.

False Negative (FN): The COVID-19 lung image is misdiagnosed.

$$precision = \frac{TP}{TP + FP} \tag{1}$$

$$Sensitivity = Recall = \frac{TP}{TP + FN} \tag{2}$$

$$Specificity = \frac{TN}{TN + FP} \tag{3}$$

$$F1score = 2 \times \frac{recall \times precision}{recall + precision} \tag{4}$$

$$Accuracy = \frac{TP + TN}{Totalsample} \tag{5}$$

The results of the model evaluation and the calculated performance metrics are presented in Table 2. According to the results, the VGG16 network achieved an accuracy of 89.6%±1.6% to detect patients infected by COVID-19. The sensitivity of 88.5%±2.8% shows the ratio of correctly detected COVID-19 patients' CT images to all patients' CT images that had COVID-19 lesions. The resulting

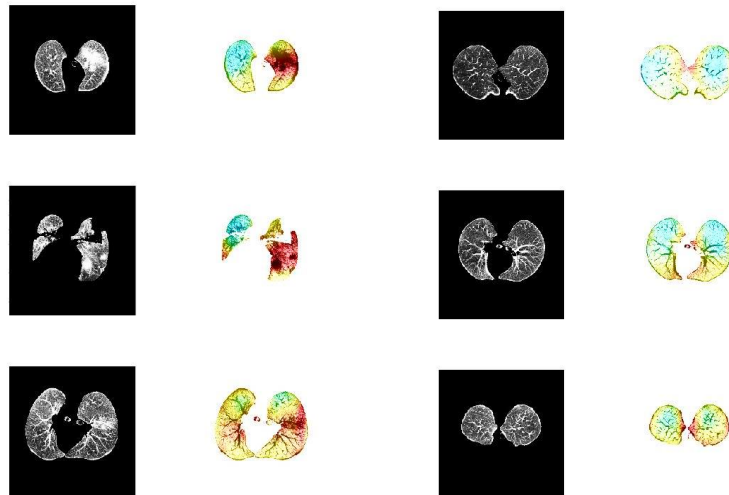


Fig. 5. COVID-19 lung images (left) and normal lung images (right) with their heatmaps.

92.0%±2.1% precision means that 92.0%±2.1% of the images detected as COVID-19 infected images were those of the COVID-19 patients.

Moreover, to identify the regions with critical information for the network, we generated and plotted the heatmaps. To do so, we implemented the steps described in [34] as follows.

Step 1: Computed the output of the model and the last convolutional layer output for the input image.

Step 2: Computed the gradient of the predicted class relative to the last convolutional layer.

Step 3: Multiplied the gradient matrix by the last convolutional layer output (matrix).

Step 4: Normalized the result and add it to the original image.

In Fig. 5, the left side shows sample results of COVID-19 cases, and the right side shows sample results of healthy cases.

In a real situation, a whole CT scan without any slice selection is available. To simulate a practical situation, we repeated our testing with the whole 3D CT-scan slices of the test subjects and obtained higher accuracy. We set a threshold to the number of infected slices to detect infected persons from the healthy cases. Based on the fact that person infected with COVID-19 has more than one slice involved, we investigated to find the best threshold to detect infected individuals based on the number of infected slices.

To find the threshold, we used 5-fold cross-validation. Here, we applied the model on all CT images (not only the images that showed COVID-19 lesions). It should be noted that in the construction of the deep neural network (e.g., in the first fold), we used one group of patients and normal cases (26 patients and 26 normal cases) as the test data, which

included 666 CT images. However, here we used all images of these cases, which included 2,027 CT images. To use all CT images in all folds, we divided the data into five groups and in each fold, and we used four groups for training and finding the best threshold, while using the remaining group to evaluate the threshold.

Table 3 shows FN, FP, and accuracy after setting the threshold from one to ten. Fig. 6 shows the accuracy of the model for different thresholds. The parameters we used here are defined as follows:

True Positive (TP): The COVID-19 positive patient is correctly classified.

True Negative (TN): The nonCOVID-19 case is correctly classified.

False Positive (FP): The nonCOVID-19 case is misdiagnosed.

False Negative (FN): The COVID-19 positive patient is misdiagnosed.

Based on the results, we set the threshold equal to seven to detect infected persons (i.e., if a person had seven or more infected slices, they would be placed in the patient's group, and if a person had fewer than seven infected slices, they would be placed in the normal group). Note that this threshold is obtained based on our dataset using accuracy as the performance measure; it may be different for another dataset and another performance measure. Using this threshold, the accuracy of COVID-19 identification was obtained to be 93.0%, which is higher than COVID-19 CT image identification which was 89.6%. Various metrics regarding the performance of the developed model are shown in Table 4. Note that all performance measures are higher than the CT image classification. Sensitivity has raised from 88.5% to 91.5%,

Table 3. Obtained FN, FP, and Accuracy for various thresholds.

Threshold	False Negative	False Positive	Accuracy
1	0	69	0.734 ± 0.025
2	2	43	0.826 ± 0.013
3	4	22	0.900 ± 0.031
4	6	17	0.911 ± 0.021
5	7	13	0.923 ± 0.033
6	9	10	0.926 ± 0.031
7	11	7	0.930 ± 0.044
8	16	6	0.915 ± 0.037
9	21	3	0.907 ± 0.035
10	23	2	0.903 ± 0.047

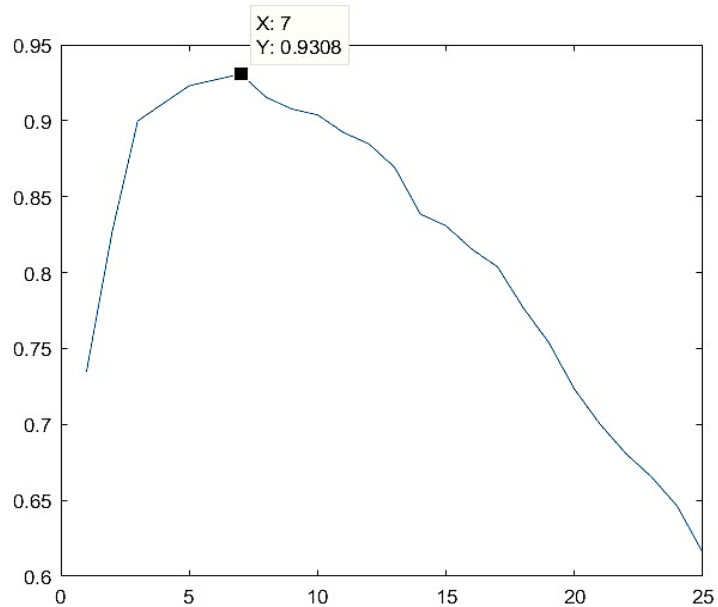


Fig. 6. Accuracy values used to find the best threshold.

Table 4. The performance of the developed model with threshold 7 for subject-by-subject evaluation.

Metric	Precision	Sensitivity	Specificity	F1 Score	Accuracy
Value	94.5%±3.5%	91.5%±6.8%	94.6%±3.4%	0.93±0.04	93.0%±3.9%

precision raised from 92.0% to 94.5%, specificity raised from 91.2% to 94.6%, F1-Score raised from 0.90 to 0.93, and accuracy raised from 89.6% to 93.0%.

We observed that our proposed network with a properly-set threshold, provides reasonable accuracy to detect CT images with COVID-19 infections. Compared to using alternative thresholds, it provides a more accurate classification to detect COVID-19 positive patients. The network can thus be used to distinguish COVID-19 patients from healthy subjects. Additionally, since the heatmaps showed that our proposed network decided based on the pixels infected by the virus, this network can also be used for detecting the regions of infection in chest CT images.

4- Discussion

COVID-19 is a new coronavirus pandemic that affects the daily life of people around the world. An approach to prevent disease spread is screening. When screening is performed in the first phases of the disease, the person can prevent others from being infected using health recommendations. However, conventional ways of screening have difficulties. For instance, insufficient automated toolkits are available, and their use is time and cost-consuming.

In this study, we developed a convolutional neural network to identify an individual infected by COVID-19 using CT images. By investigating the images and based on specialists' recommendations, we observed ground-glass opacities in an infected person's lung CT. This characteristic could discriminate COVID-19 lung images from non-COVID-19 lung images, using the popular VGG16 network. Afterwards, we found the best threshold for the number of infected slices to identify COVID-19 positive patients. The results showed that the best model had an accuracy of 93.0%. Additionally, according to heatmaps, the model could identify the infected areas in the lung CT images, and use them to classify the data.

It should be noted that in this work, we used our national data that we were confident about. Most of the public datasets that we found were either Chest Radiography (CXR), or included patient data from various sources, which were heterogeneous, and normal subject data from Kaggle that was homogeneous. Additionally, in some of the public datasets, the age ranges of the patients were different from the normal subjects. The network trained using such data would not detect the COVID-19 patients, but it would detect the normal subjects, or different age groups. In fact, when we fine-tuned our network on such data, we obtained 100% accuracy.

5- Limitations and Future Work

Considering the novelty of COVID-19, there are several limitations associated with its automatic detection. A major limitation is the lack of a large dataset to secure the generalization of the models for practical applications. For future work, a more advanced backbone architecture of deep learning networks can be employed, and handcrafted features can be extracted based on prior knowledge. Generative Adversarial Networks (GANs) can be developed to increase the number of images for training and increasing the performance of the model. Attention-based multiple instances learning can be used instead of training on individual slices, putting the patient-specific slices into a bag and train on bags. Therefore, the network learns to assign weights to individual slices in a COVID-19 bag and automatically sample those high weighted slices for infection detection [1,10]. Deep learning methods can be used not only to classify and segment the infections but also to predict the disease progression and the treatment outcome [35].

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