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An Effective Approach to SARS-CoV-2 Diagnosis by Developing the CNN Algorithm

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Abstract

Today, SARS is a viral infection of the respiratory system that causes damage to the alveoli. The virus that causes severe acute respiratory syndrome belongs to the family of coronaviruses, commonly known as COVID, which is the same family of viruses that cause common colds. The increasing use of artificial intelligence (AI) and machine learning (ML) nowadays provides excellent opportunities to support and improve medical services in societies. In this paper, a developing model of deep learning (DL) is designed and implemented to classify SARS-CoV-2 disease images into two classes: COVID and non-COVID, with an accuracy of 99%. From a performance and accuracy perspective, the artificial convolutional neural network (CNN)-based detection model that was developed achieved better performance than the pre-trained VGG16 model and other learning models with a similar purpose. As a result, this designed model is able to aid medical professionals by providing a tool that facilitates the detection of this sickness and, consequently, the provision of appropriate medical care.

Keywords: Magnetic Resonance Imaging (MRI), Deep Learning (DL) Effective Approach, Developing CNN Algorithm, VGG16 Model, SARS-COV-2 Disease.

نهج فعال لتشخيص مرض السارس من خلال تطوير خوارزمية الشبكة العصبية التلافيفية

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الخلاصة

يعتبر مرض السارس اليوم عدوى فيروسية تصيب الجهاز التنفسي وتسبب تلف الحويصلات الهوائية. ينتمي الفيروس المسبب لمتلازمة الجهاز التنفسي الحادة الوخيمة إلى عائلة الفيروسات التاجية ، المعروفة باسم كورونا ، وهي نفس عائلة الفيروسات التي تسبب نزلات البرد. يوفر الاستعمال المتزايد للذكاء الاصطناعي والتعلم الآلي في الوقت الحاضر فرصًا ممتازة لدعم الخدمات الطبية وتحسينها في المجتمعات. في هذه الورقة

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، تم تصميم وتنفيذ نموذج مطور للتعلم العميق (DL) لتصنيف صور مرض SARS−COV−2 إلى فئتين ؛ كوفيد ، وغير كوفيد. بدقة 0.99٪ . من حيث الأداء والدقة ، تفوق نموذج الكشف المستند إلى الشبكة العصبية التلافيفية الاصطناعية (CNN) المقترح على نموذج VGG16 المدربين مسبقًا ونماذج التعلم المماثلة الأخرى. ونتيجة لذلك ، فإن هذا النموذج المطور قادر على مساعدة المهنيين الطبيين من خلال توفير أداة تسهل اكتشاف هذا المرض ، وبالتالي توفير الرعاية الطبية المناسبة.

1. Introduction

After a few years, SARS-CoV-2 was discovered as the causative agent of Coronavirus Disease 2019 (COVID-19), which helped to reinforce the common signs and symptoms of COVID-19, such as cough, fever, and shortness of breath. This was demonstrated by seasonal upper respiratory infections [1] and [2]. Diagnostics identify SARS-CoV-2 infection using viral nucleic acids, antigens, or serology. A chest CT or MRI confirms disease symptoms [3]. Since infection frequently compromises the cardiovascular, nervous, renal, liver, and immune systems, COVID-19 can cause mortality [4]. To decrease transmission, social distancing, face masks, contact isolation, and hand hygiene have been used in conjunction with contact tracing, clinical assessment, and viral testing for SARS-CoV2 [5] and [6]. The name SARS is used as an acronym for Severe Acute Respiratory Syndrome (SARS), which is one of the contagious respiratory diseases that can lead to severe illness.

This disease occurs when a person is infected with one of the viruses known as coronaviruses. Coronaviruses are common viruses that infect the upper respiratory system, and many types of coronaviruses can attack the human body [7], [8], and [9]. The effects of SARS-CoV-2 on the human lung have been studied using a variety of diagnostic imaging techniques, including CT, MRI, and others. To monitor the progression of SARS-CoV-2 disease in the clinic, MRI is the imaging modality of choice because of its high degree of standardization and widespread availability. However, due to the large amount of data contained within each MRI image (both in terms of volume and resolution), analyzing an MRI scan is a time-consuming process for medical professionals [10] [11].

The term "DL" or "Deep Neural Network" refers to artificial neural networks (ANN) with multiple layers [12]. DL is a class of learning techniques developed to represent data with complex structures by combining numerous non-linear transformations [13]. It has become increasingly common to use DL models when dealing with a wide range of problems, but medical image processing is one area where this trend has grown particularly quickly [14]. DL models have received a lot of interest in disease detection studies in the past few years, largely because it is believed that these models are more accurate than traditional ML approaches [15].
However, detecting SARS-CoV-2 disease is difficult and requires a lot of selective feature representation in order to make a diagnosis [16]. The term "computer vision" is used to describe a subfield of AI that focuses on the analysis of visual input and how a computer can learn and understand from this analysis [17]. The DL algorithm family known as CNNs has been shown to be especially effective in a variety of vision-related tasks, including image recognition and classification, video analysis, medical image analysis, and more [18] [19]. The DL approach used for the construction of this model is CNN. This model also includes a maximum pooling layer and four convolutional layers [20].

While deep neural networks are being trained, batch normalization is employed to speed up the process and make the network more stable. This might necessitate using learning rates that are far higher than usual, which could hasten the learning process even further. The regularization impact of batch normalization reduces generalization error and may even make

the use of dropout for regularization unnecessary. CNNs collect and acquire higher-level characteristics from an image's raw pixel data using a variety of filters, which the model may subsequently employ for categorization. There are three parts to a CNN: Convolutional layers apply a picture with a specific assortment of convolution filters. The layer applies a series of mathematical operations to each sub-area to create a single mark on the final feature map. After that, ReLU activation functions are often used on the output of convolutional layers to introduce nonlinearities into the model. Convolutional layers extract picture data, which is then downsampled by pooling layers to lower the dimensionality of the feature map and speed up processing.

The max-pooling approach, which isolates subregions of the feature map, preserves the highest value, and discards all other values, is a common pooling algorithm. The characteristics recovered by the convolutional layers and downsampled by the pooling layers are classified by dense or fully connected layers. Every node in a dense layer is connected to every other node in the layer below it [21][22][23].

1.1 Related Works

DL algorithms have been successfully used in a variety of works in many spheres of life. The same advanced technology has recently been widely used to reduce the negative effects of various diseases through early identification and diagnosis [24], [25], and [26]. During the coronavirus pandemic, the application of DL algorithms to the detection of lung illnesses and other prediction fields saw an exceptional increase [27]. A deep bidirectional recurrent neural network (BRNN) model based on long short-term memory (LSTM) and gated recurrent unit (GRU) cells was used to distinguish the genome sequence of SARS-CoV-2 from that of other strains of coronavirus, such as SARS-CoV and MERS-CoV, as well as the common cold and other acute respiratory infection (ARI) viruses. The GRU-BRNN model had an overall classification accuracy of 96.8%, compared to 95.8% for the LSTM model. This was in contrast to the LSTM BRNN model's overall classification accuracy of 95.8%. The results of this study demonstrated that the proposed GRU-BRNN model has a greater capacity for classifying SARS-CoV-2 [28].

[29] introduced a DL classification method, xDNN, and tested it on a CT scan dataset containing SARS-CoV. 80% of the data was used for training and 20% for validation. xDNN was compared to other cutting-edge technologies, including black-box deep neural networks and support vector machines. The method achieved 97.38% accuracy using an explainable DL algorithm (xDNN) on this dataset and built an active DL-based fusion model with swarm intelligence (EDLFM-SI) to identify and categorize whether a person has been exposed to the SARS-CoV-2 virus. Moreover, the EDLFM-SI technique includes a number of steps, including feature extraction, data augmentation, preprocessing, and classification. Also, a combination of feature extractors based on the capsule network (CapsNet) and MobileNet is used. In addition, the water strider algorithm (WSA) is used to adjust the DL models' hyperparameters. Last but not least, a cascaded neural network (CNN) classifier is used to identify SARS-CoV-2. Several simulations are run on the COVID-19 CT data set and the SARS-CoV-2 CT scan data set to demonstrate the increased performance of the EDLFM-SI approach.

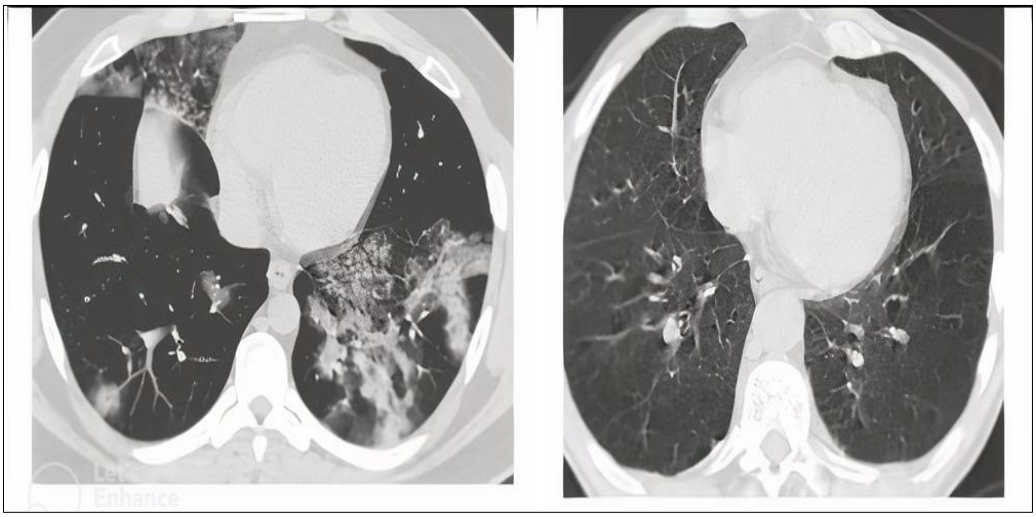
Through its impressive results in the simulation, the EDLFM-SI technique proved to be unrivaled among recent approaches. [30] suggested a deep learning convolutional neural network-based method for classifying viruses and other species from genome sequences (CNN). The length of the genome sequence is not constrained by the suggested approach. The findings demonstrate that the unique concept successfully separates the sequences of SARS-

CoV-2 from those of other viruses. The National Center for Biotechnology Information (NCBI) provided 1557 SARS-CoV-2 instances for the study, and the Virus-Host DB provided 14,684 distinct virus samples. The tests were conducted using forty-eight different architectures because a CNN has a number of adjustable parameters. Since a CNN may be tuned in many ways, tests were conducted using 48 distinct network topologies, the best of which accurately classified viruses into their respective realms at a rate of 91.94 ± 2.62% and SARS-CoV-2 at a rate of 100% in the Riboviria domain. [31] assessed the DL model to identify and forecast illnesses. This method utilized 548 CT images from Radiopedia data from internet sources: 232 from 12 COVID-19-infected patients, 186 from 17 influenza A patients, and 130 from 15 healthy candidates. The CT imaging reference data indicates a model accuracy of 79.39% [32].

1.2 SARS-Cov2 dataset

The SARS-CoV-2 computed tomography (CT) scan dataset comprises a total of 2482 CT scans, collected from real patients who visited hospitals in Sao Paulo, Brazil. Out of these, 1230 scans belong to patients who are not affected by the pathogen, and 1252 scans belong to positive COVID patients. Figure 1 shows samples from each of the disease groups associated with SARS-CoV-2. To evaluate the performance of the convolutional neural network (CNN) models, two binary classifications were conducted. The SARS-CoV-2 dataset of MRI pictures was divided into 80% for training (1986 image) and 20% for testing (496 image) during the experiment by using the k-fold cross-validation method.

The dataset is publicly available on the website for free access [33].



(a) **(b)**

Figure 1: Samples of SARS-CoV-2 disease classes: (a) COVID and (b) non-COVID [33]

1.3 Performance Measurements

The degree of fit of the offered models is evaluated by calculating the accuracy, recall, precision, and F1-score as shown in Eq(1), Eq(2), Eq(3), and Eq(4), respectively (represented by True Positive (Tpo), True Negative (Tne), False Positive (Fpo), and False Negative (Fne).

$$Accuracy = \frac{True_{Pos}+True_{neg}}{True_{Pos}+True_{neg}+False_{pos}+False_{neg}} \quad (1)\ [34]$$

$$Recall = \frac{True_{Pos}}{True_{Pos}+False_{neg}} \quad (2)$$

$$Precision = \frac{True_{Pos}}{True_{Pos}+False_{pos}} \quad (3)$$

$$F1-score = 2\frac{PM.RM}{PM+RM} \quad (4)\ [35]$$

1.4 Results

The proposed deep CNN model-based detection can be seen in Figure 2.

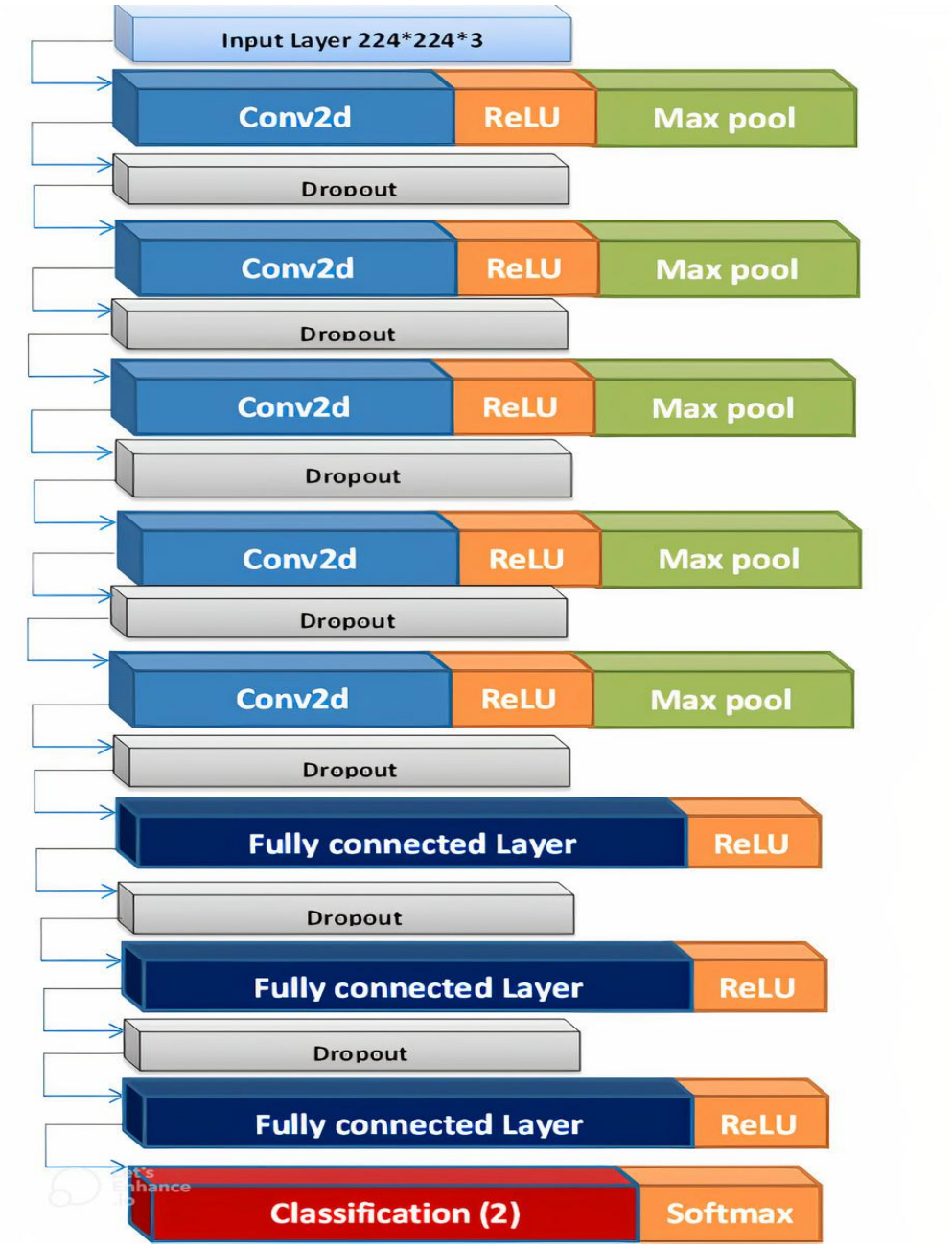


Figure 2: The layers of the developed CNN model

The newly created CNN model comprises three max-pooling layers, eight two-dimensional convolutional layers (Conv2d) with 3x3 kernel sizes, and five dense layers that are fully connected. Specifications of the newly developed CNN model are presented in Table 1.

Table 1: The architecture details of the proposed Deep CNN model

Layer (type)	Output Shape	No. of Parameters
img_input (Input Layer)	(None, 224, 224, 3)	0
layer_1 (Conv2D)	(None, 224, 224, 32)	896
layer_2 (MaxPooling2D)	(None, 112, 112, 32)	0
dropout (Dropout)	(None, 112, 112, 32)	0
Batch normalization	(None, 112, 112, 32	128
layer_3 (Conv2D)	(None, 112, 112, 64)	18496
layer_4 (MaxPooling2D)	(None, 56, 56, 64)	0
Dropout_1 (Dropout)	(None, 56, 56, 64)	0
layer_5 (Conv2D)	(None, 56, 56, 128)	73856
layer_6 (MaxPooling2D)	(None, 28, 28, 128)	0
dropout_2 (Dropout)	(None, 28, 28, 128)	0
layer_7 (Conv2D)	(None, 28, 28, 256)	295168
layer_8 (MaxPooling2D)	(None, 14, 14, 256)	0
dropout_3 (Dropout)	(None, 14, 14, 256)	0
layer_9 (Conv2D)	(None, 14, 14, 512)	1180160
layer_10 (MaxPooling2D)	(None, 7, 7, 512)	0
dropout_4 (Dropout)	(None, 7, 7, 512)	0
fc_1 (Flatten)	(None, 25088)	0
lyaer_11 (Dense)	(None, 512)	12845568
dropout_5 (Dropout)	(None, 512)	0
lyaer_12 (Dense)	(None, 128)	65664
dropout_6 (Dropout)	(None, 128)	0
lyaer_13 (Dense)	(None, 64)	8256
dropout_7 (Dropout)	(None, 64)	0
predictions (Dense)	(None, 2)	650
Total params: 14,672,834 Trainable params: 14,672,834 Non-trainable params:64		

The lung MRI images are first reduced in size to 224 x 224 before being fed into the CNN model. There are many layers in this model. The fundamental convolutional layers of this model convolve the input lung MRI image using learned filters, and the Rectified Linear Unit (ReLU) function of nonlinear activation is employed to give the essential feature mappings. Following the third, fifth, and eighth convolutional layers, max-pooling layers are used to reduce the size of features, the number of parameters used, and the number of calculations the network has to do. This is done while keeping the important features more compact as you move from lower to higher layers and making the network more resistant to geometric changes and some distortions. When these layers are added, the feature maps are downsampled, and each block that doesn't meet is replaced with its highest value. While the convolutional and max-pooling layers of the created CNN model acquire data from small patches in an image of the lung, the dense layers of the model allow classification using the obtained discriminative features. After three max-pooling layers, dense layers, and eight convolutional layers, a two-dimensional feature map is collapsed into a one-dimensional feature vector. Since dense layers connect all of the feature bits from the preceding layer to

the output layer, they are effective for learning non-linear correlations between features. The SARS-Cov2 stages are ultimately divided into two classes using the SoftMax activation layer by selecting the labels with the highest prediction probabilities. As stated in Table 2, different hyperparameters are used in this model.

Table 2: The hyperparameters for the proposed model

Layer (type)	Description
No. of convolution layer	5
Filter size	(3,3) (32,64,128,256,512)
No. of Max poling layer	5 (2,2) stride 2
No. of fully connected layer	3 (1024,128,64)
Dropout Rate	(0.2,0.3,0.4,0.5)
Optimizer	Adamax
Learning Rate	0.002
Beata1	0.9
Beata2	0.999
Epsilon	$1e-8$
Loss function	categorical_crossentropy
Batch size	32
Number of epoch	80
Activation function	Relu

The newly generated model is tested against the pre-trained VGG16 model. A new CNN model can identify SARS-Cov2 sickness stages with 0.99% accuracy and 0.01 loss. While the pre-trained VGG16 model had an accuracy of 0.97% and a loss of 0.03%, the current model had a loss of 0.05%. Figures 3 and 4 show the loss and accuracy (per epoch) curves for the models that were presented using the SARS-Cov2 MRI image dataset for training and testing (val).

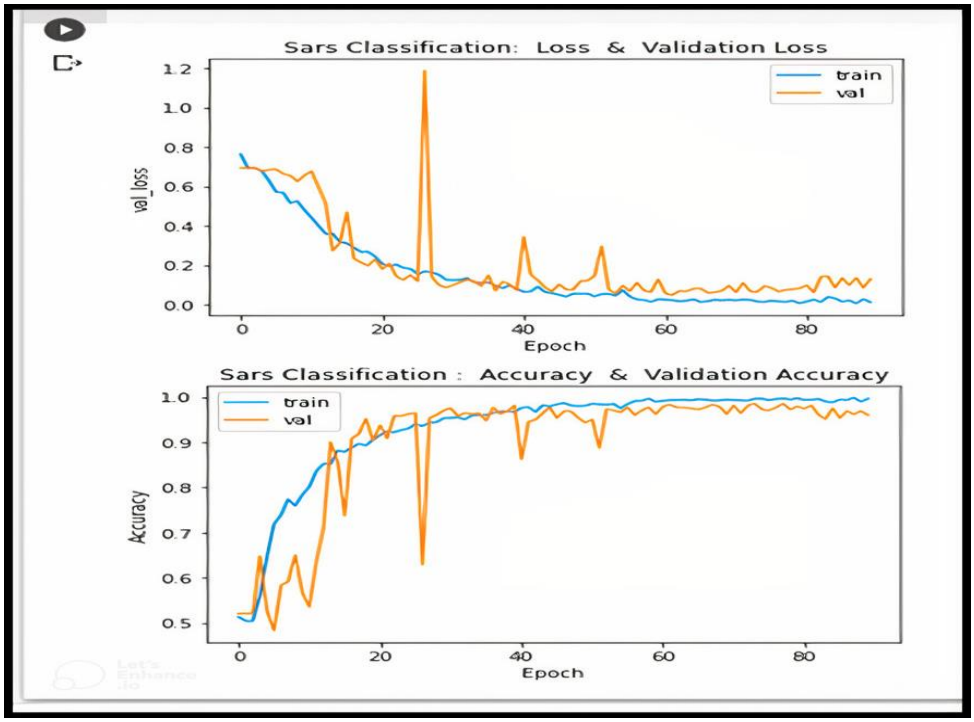


Figure 3: Accuracy and val-loss of CNN

Table 3: CNN and VGG16 model recall, precision, and F1-score computations

Classes	CNN		
	Precision	**Recall**	**F1-score**
covid	1.00	0.99	0.99
Non-covid	0.99	1.00	0.99
Accuracy			0.99
Macro Average	0.99	0.99	0.99
Weighted Average	0.99	0.99	0.99
Classes	**Vgg16**		
	Precision	**Recall**	**F1-score**
covid	0.95	0.99	0.97
Non-covid	0.99	0.95	0.97
Accuracy			0.97
Macro Average	0.97	0.97	0.97
Weighted Average	0.97	0.97	0.97

The results presented in Table 3 demonstrate that the developed CNN model works better than the VGG16 model when it comes to recognizing SARS-Cov2 disease, with the former maintaining higher values that are closer to one in recall, accuracy, and F1-score.

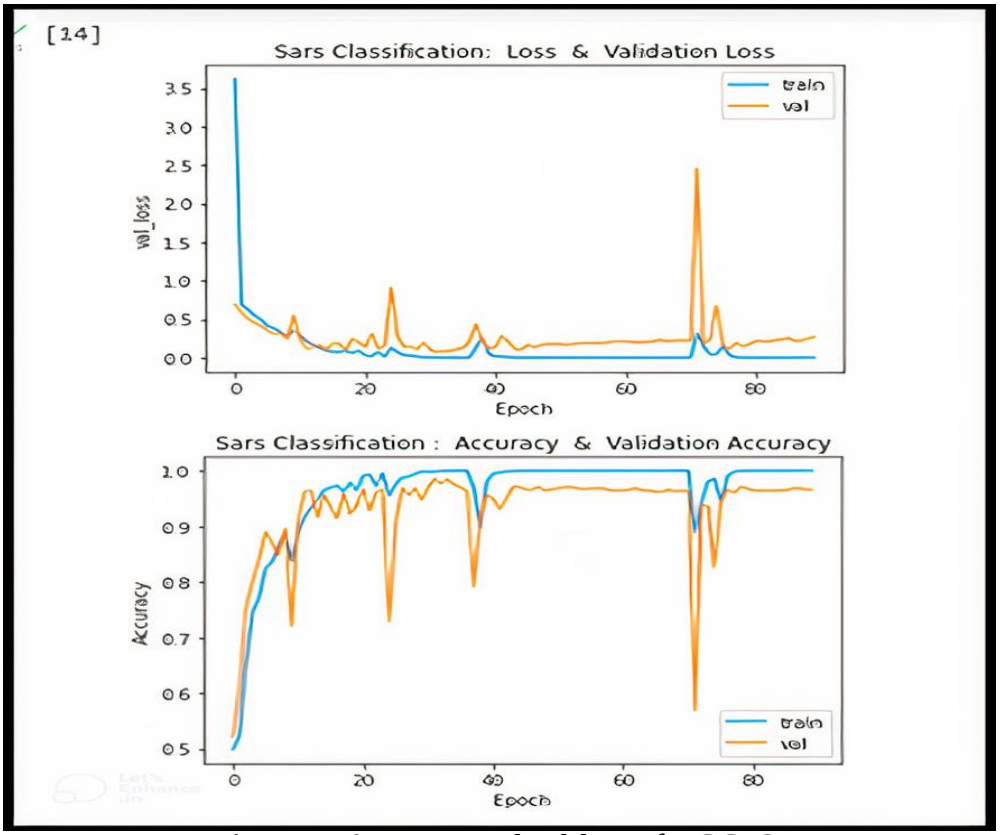
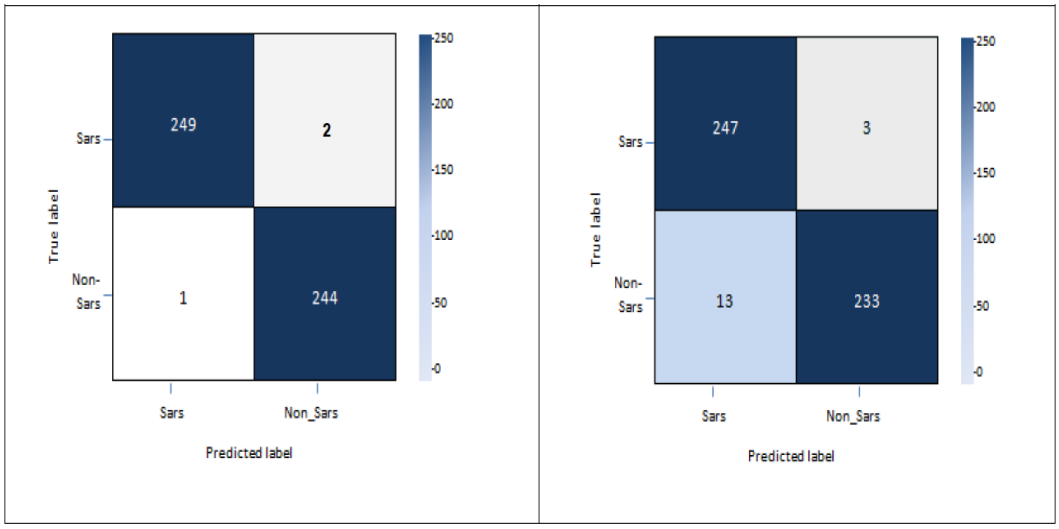


Figure 4: Accuracy and val-loss of VGG16

Figures 5 (a) and (b) demonstrate the confusion matrix of the presented models for detecting SARS-Cov2 disease on the set of tests.



(a) (b)

Figure 5: (a) CNN confusion matrix and (b) VGG16mode confusion matrix

1. 5 Conclusion

The SARS-CoV-2 pandemic is progressing at an alarming rate. The speed and strength of recovery can be affected by a nation's health, humanitarian, social, and economic policies. Currently, testing for this new virus is intensifying rapidly. COVID-19 diagnostic testing is crucial for discovering the virus, comprehending its epidemiology, controlling the ailment, and preventing its spread. For quicker screening strategies in the global fight against the epidemic, comprehensive operating procedures and the harmonization of existing diagnostic tests are required. Similarly, academic scientists and biotechnologists are charged with identifying more strains of SARS-CoV-2 to enhance mass-based specificity, antibody sensitivity, and antigen-based assays. Importantly, virus detection technology can facilitate the creation of extremely sensitive, simple, scalable, quick, and cost-effective COVID-19 detection tests that efficiently supply diagnostic capacity on demand during a pandemic. The CNN model for this study classifies lung MRI images after recognizing their features. This model predicted SARS-CoV-2 disease on MRI images with an accuracy of 0.99%. The performance of the previously trained VGG16 was compared. The proposed model performed well and may help clinicians predict SARS-CoV-2 disease. A future study will use the model as an independent framework in several open-source datasets to screen and identify SARS-CoV-2 disease types.

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