Improving the Response rate of RT PCR testing using deep convolutional encoder

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ARTICLE INFO

ABSTRACT

The sensitivity of the RT-PCR test is limited, and the method itself is laborious and time-consuming to carry out. When it comes to making a diagnosis of COVID-19, chest CT scans have the potential to be of assistance. If, on the other hand, the infection does not spread to the lungs, then an abnormality check with a CT scan will not be necessary. Complementary assays have the potential to considerably reduce the frequency of false-positive results when they are used in combining with RT-PCR or CT scans. We propose in this study a decision support system that is based on deep learning and has the capability to evaluate the practically commonly required laboratory parameters for the purpose of identifying COVID-19. Here dataset contains the 1428 radiographs (224 COVID-19, 504 Healthy, 700 Pneumonia) are considered for experimentation.

1. Introduction

The finding that a novel beta coronavirus was the cause of the pandemic led to the virus being given the name Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-COV-2) [1]. Coronavirus Disease 2019 is the name that has been given to the ailment because an infection with SARS-CoV-2 can generate such a diverse array of symptoms in people [2]. This is because SARS-CoV-2 infections can take place in human hosts as well as other animals.

The early signs and symptoms are not very specific and are rather like those of other seasonal viral infections. For example, a high temperature, a dry cough, and excessive fatigue are all symptoms that are common with other seasonal viral infections [3]. The influenza virus may be responsible for causing these symptoms. It is possible that a correct clinical diagnosis cannot be made [4].

To establish a precise etiological diagnosis, it is important to do reverse transcription polymerase chain reaction (RT-PCR) testing to identify the SARS-CoV-2 genome. This is because RT-PCR may detect mutations in the SARS-CoV-2 genome [5].

The use of RT-PCR is subject to a variety of significant restrictions, which can be seen as drawbacks. To begin, utilising the technologies that are currently accessible might take anywhere, and laboratories frequently discover that they are unable to keep up with the demand for their services because of the time commitment involved. Second, there is a potential that some hospitals may not have the resources necessary to carry out tests at all hours of the day [6].

Swabs must be relocated to several different locations as a direct result of this, which makes the process more time intensive and overloads the central labs. The initial retropharyngeal swab RT-PCR result may be mistakenly negative, even though typical symptoms are present. It possible that an oversight occurred throughout the testing process, which would explain this result [7]. Finally, this method comes with a price tag, which may create a significant financial burden not only on healthcare organisations but also on individuals who are in need of this therapy [8].

With such restrictions, a significant number of patients are compelled to wait in the emergency room for a period that is significantly longer than what is required before being admitted to the appropriate unit [9]. Patients who are in critical condition and need endotracheal intubation and mechanical breathing as soon as feasible have a huge barrier since they have reached this point. Even though the healthcare system is currently running at a level that is dangerously close to capacity, these people require the attention of doctors working in emergency departments [10].

The development of a test that is uncomplicated, can be completed in a short amount of time, and can establish whether an individual is susceptible to the SARS-CoV-2 virus or resistant to it could be of significant therapeutic use. Newer, more sophisticated imaging methods have been incorporated into the process of building the algorithms that have been proposed [11].

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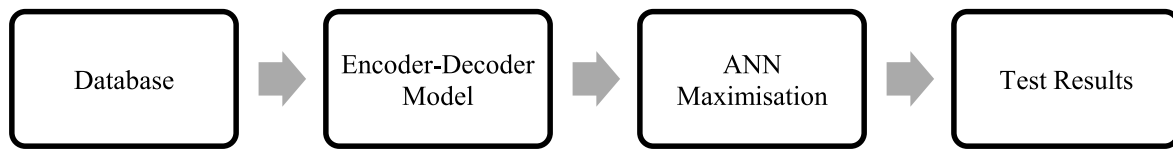
Fig. 1. Proposed model.

The sensitivity of the RT-PCR test is limited, and the method itself is laborious and time-consuming to carry out. When it comes to diagnosis of COVID-19, chest CT scans have the potential to be of assistance. On the other hand, the infection does not spread to the lungs, then an abnormality check with a CT scan is not necessary [12]. Complementary tests have the potential to considerably reduce the frequency of false-positive results when they are used in conjunction with RT-PCR or CT scans.

This study provides a decision support system that is founded on deep learning and possesses the capability to analyse the laboratory parameters that are necessary from practically all patients for the detection of COVID-19.

2. Related Works

To make a definitive diagnosis with RT-PCR, additional RT-PCR testing is required because the findings of between 20% and 30% of these tests are incorrectly positive. In people who are infected with the virus, there is a possibility that a false positive test result could be produced as a result of the following factors: (1) a swab sample of poor quality as a result of insufficient patient material; (2) a swab sample taken at an extremely early or late stage of infection; (3) improper swab sample processing; and (4) technical reasons inherent to the test, such as PCR inhibition or virus mutation [13].

Insufficient patient material can result in a swab sample of poor quality. In addition, CT scans are executed at an earlier stage in the evolution of the disease might not be able to determine the effect that the COVID-19 virus has on the patient lungs at that point in time. It is very challenging for doctors and other medical experts to diagnose the disease in a patient until the virus has completely established itself in the lungs of the individual being treated [14].

A new insight that can enhance clinical practise and the treatment of individual patients, an increasing number of academics have begun looking into medical databases. The findings of this research have resulted in the development of novel treatments and the identification of new ways of diagnosis, both of which contribute to the overall improvement of human health and to the extension of human life expectancy. The use of artificial intelligence (AI) technology into the diagnostic procedure for COVID-19 has given rise to a great number of new research endeavours [15].

Zali et al. [16] said that the CT scans are favoured over RT-PCR for making a diagnosis of COVID-19 in places with a high frequency of the disease. This is since CT scans are less invasive than RT-PCR, require less time to complete, and yield more accurate results.

Kayaaslan et al. [17] investigated patients who had previously had an RT-PCR screening for COVID-19 but had received a negative result. It was hypothesised that these patients were infected with the virus. They arrived at the conclusion that the second RTPCR test was not necessary and that it only offered a minor improvement over the initial test.

Positive RT-PCR results were obtained in 59% of COVID-19 patients, while positive thoracic CT scans were observed in 88% of patients, as stated by the conclusions of the research carried out by Ai et al. [18]. When it came to determining whether or not an individual had COVID-19 infection, Long et al. [19] found that thoracic CT had a sensitivity of 97.2% while RTPCR had a sensitivity of 83.3%. These conclusions were based on the findings of their analysis. In addition to the RT-PCR test, they emphasised the need of utilising CT scans as a

helpful diagnostic tool. CT scans need to be analysed to assist in the early discovery of people who have the ailment and to evaluate how far along they are in the progression of it. The reverse transcription polymerase chain reaction, also known as RT-PCR, requires an extremely lengthy amount of time to obtain results and has a low sensitivity when compared to thoracic CT, which generates data nearly immediately.

In [20], a DL base approach is used to classify and detect the COVID-19 cases from x-ray images. Our model is entirely automated and is capable of categorizing binary class with 100% accuracy using VGG16 and multi-class with 93.75% using a built CNN.

The author in presented a five different image enhancement techniques: histogram equalization (HE), contrast limited adaptive histogram equalization (CLAHE), image complement, gamma correction, and balance contrast enhancement technique (BCET) were used to investigate the effect of image enhancement techniques on COVID-19 detection. A novel U-Net model was proposed and compared with the standard U-Net model for lung segmentation. Six different pre-trained Convolutional Neural Networks (CNNs) (ResNet 18, ResNet 50, ResNet 101, InceptionV3, DenseNet201, and ChexNet) and a shallow CNN model were investigated on the plain and segmented lung CXR images. The novel U-Net model showed an accuracy, Intersection over Union (IoU), and Dice coefficient of 98.63%, 94.3%, and 96.94%, respectively for lung segmentation.

The rate of transmission of the coronavirus pandemic can be slowed or stopped entirely with the assistance of early detection and treatment, which will also help to minimise the severity of the sickness. Numerous researchers have focused their attention on analysing the COVID-19 patient laboratory data to better understand the disease.

3. Proposed method

This research was conducted with the intention of developing a conceptual framework for the classification of COVID-19. To accomplish this goal, chest CT scans and more traditional diagnostic criteria were utilised during the research. The organisational structure of the research project is depicted in Fig. 1.

The following is a list of the actions that must be taken for hybrid CNN models to be successfully executed.

Step 1. The initial phase comprises performing CT scans on patients who either have or do not have COVID-19.
Step 2. The second step is to get the feature vectors from the pooling layer that have previously been pre-trained.
Step 3. Rather of employing the classification layer, we make use of the standard Artificial Neural Network (ANN) technique.
Step 4. In the fourth stage, the improved hyperparameters are implemented into the training of the CNN model as a means of guiding its development.
Step 5. To avoid overfitting the data and to control the error rate the k-fold validation model is used.
Step 6. Result Evaluation

The first thing that was done was to obtain CT scans of each of the patients.

In the second stage, we used the models that had been pre-trained to get the feature vectors of each image that we had previously stored. Multiple iterations of convolution, normalisation, and pooling were

carried out on each individual photo before it was submitted to the CNN models for analysis. Following the completion of these procedures, it was possible to successfully extract feature vectors from each individual image.

When classifying the feature vectors that were obtained through the utilisation of pre-trained models, the softmax layer was utilised as a means of doing so.

As was mentioned in Step 3, ANN were utilised in place of softmax for the classification of feature vectors in the pooling layers. This was accomplished by replacing softmax with ANN.

After adjusting the values of their hyperparameters to achieve optimal performance in the third phase, we moved on to the fourth stage of the process, which consisted of training the CNN models using the training set.

The issue of overfitting was addressed, and error rates were brought back under control after Step 5 utilisation of cross validation on a fivefold basis. The total included training data, which made up 60% of the total, validation data, which made up 20%, and test data, which made up the remaining 20%. This not only led to more accurate findings from the categorization process, but it also made it possible to validate those results.

The results of the classification were acquired and evaluated with the assistance of a technique known as deep convolutional encoder-decoder, which was carried out under the direction of professionals in the medical field.

3.1. Deep convolutional encoder

The DCN network makes use of encoder-decoder frameworks as its backbone to train its nodes in a sequential fashion (Fig. 1).

3.1.1. Encoder network

Encoders are algorithms that take an input and output abstract features that capture all the essential information for later processing, such as segmentation, detection, and classification. Encoders take an input and output abstract features that capture all the necessary information. A substantial chunk of the encoder for a classification network is made up of the convolution and pooling layers. Encoders in the DCN can take advantage of the benefits offered by contemporary classification networks. The extent to which the network is structured is its most valuable feature, as this characteristic plays a significant part in bringing about the outcomes that are wanted to be achieved.

The encoder that is used by the DCN is based on AlexNet, however it has had a few tweaks here and there to improve its performance. It is constructed out of 13 convolutional layers, each of which has two pooling operations and three filters. After the initial layer of processing that involves convolution, this design makes a smooth transition into a layer that is responsible for pooling, and then it moves on to a layer that is responsible for full connectivity.

The architecture of the visual geometry group network (AlexNet) served as the foundation for this framework, but it was modified in some way. Given two data sets, an algorithm known as a convolution can perform mathematical operations such as addition, integration, multiplication, and the derivative when it is given those data sets. The convolution can be represented mathematically as follows:

$$y = x*w \Rightarrow y[i] = \sum x[i-j]w[j] \tag{1}$$

Where.

  x -input data
  w -convolution filter.

The convolution filter, which is also known as the kernel, and the input data x are the two pieces of data. The convolution filter is also known as the kernel. A feature map is generated as a by product of the
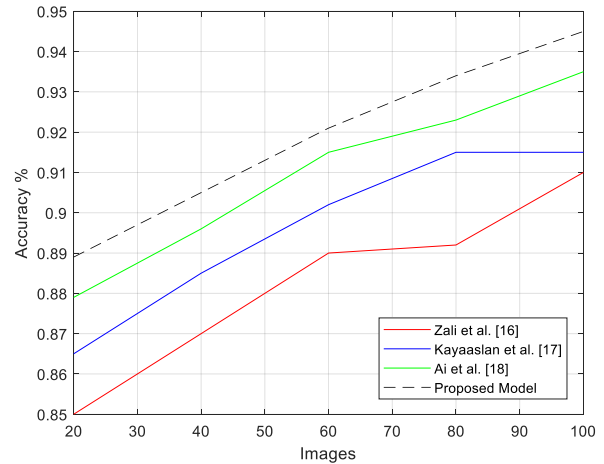

Fig. 2. Accuracy.

convolutional process, which consists of moving the kernel across the whole input data set. This action ultimately leads to the generation of the feature map. It is possible to construct feature maps by combining several different convolutions, each of which has its own individual filter. Combining these feature maps results in the output of the convolution layer, which is created by the layer itself.

After the phase of convolution, activation functions are used to transform the model into a nonlinear representation. This takes place immediately after the convolution phase. Even though the linear function, the sigmoid function, and the tanh are all feasible possibilities for activation functions, the proposed AlexNet uses the rectified linear unit (ReLU) rather than any of the other available options. This is because the ReLU enables substantially faster model training and provides near-global weight optimization. The reason for this is that the ReLU was designed. According to the findings of our investigation, the ReLU activation function can be characterised as follows:

$$f(xi) = \max(0, xi). \tag{2}$$

The layer known as the pooling layer is the one that follows the convolution layer directly after it Equation. (2). This layer decreases the sample size of all the feature maps to speed up the process of overfitting and training the model. The max-pooling strategy, which is implemented in the AlexNet that has been proposed, uses a random selection process to select the maximum value from the pooling window and then uses that value.

In artificial neural networks, the FC layer is responsible for performing operations that are comparable to those carried out by a fully connected layer. The FC layer is responsible for carrying out the classification process using the low-level features that have been automatically extracted by the AlexNet, the convolution layer, and the pooling layer.

In the final stage of classification, the SoftMax activation function is used to assign a probability value to each class in such a way that the probabilities sum up to 1. This ensures that the probabilities always add up to 1. The definition of the SoftMax function and it is feasible that this function could be replaced.

$$S(y = j \vee \varphi(i)) = e\varphi(i) \sum_k e\varphi(i)k. \tag{3}$$

  W- weight matrix.
  X - feature matrix
  φ is generalized as

$$\varphi = \sum_i W_i X_i = W^T X$$

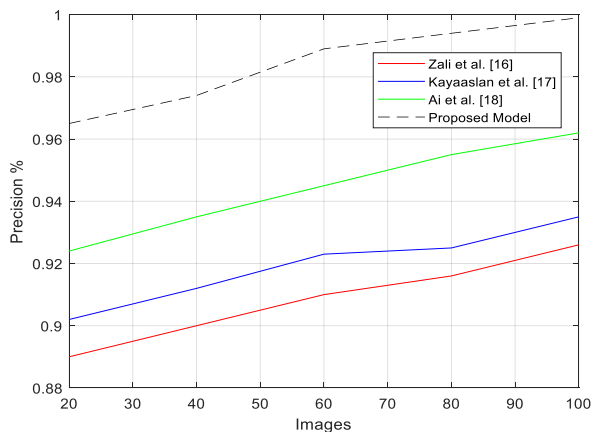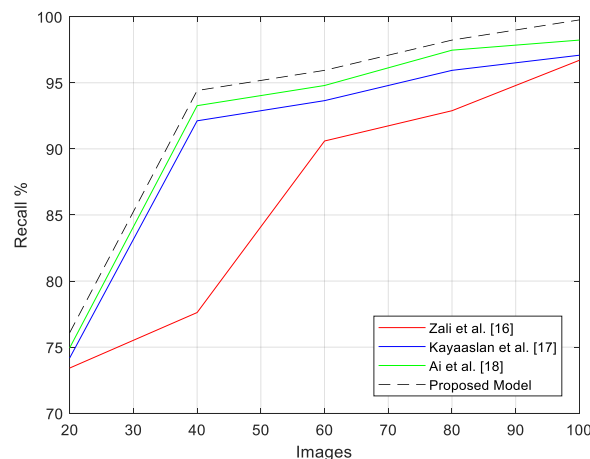**Fig. 3.** Precision.

3.1.2. Decoder network

The process of automatically extracting characteristics and classifying them takes up most of the time that is allotted for the encoding stage. Fig. 3 depicts how we achieve consistency by employing the same AlexNet design for both the encoding and decoding processes.

To rebuild the matching high-level segmented image from the low-level characteristics, the decoder framework makes use of deconvolution in conjunction with an upsampling of the layers. The output feature of the encoder demonstrates the use of a 1×1 convolution to produce a coarse segmentation of the input signal. This segmentation is provided by the encoder. Successive deconvolution layers upsample the output of the layer that came before them to provide features with a high resolution.

The convolution process that takes place inside of the encoder, the size of the output is less than the size of the input. There is a problem with the way the decoding process is carried out. This study utilised a technique known as deconvolution in conjunction with up-sampling to make the input appear the same as the image. Even though the input had a lower resolution than the image, this was accomplished by making the input appear to be up sampled.

To provide a description of the process of transpose convolution, the sparse matrix of the kernel is first multiplied by the output, and then it is transposed to provide a description of the process. The size of the input is raised so that the downscaling of the output, which occurs during decoding because of the convolution features, can be avoided.

4. Results and Discussions

Here dataset contains the 1428 radiographs (224 COVID-19, 504 Healthy, 700 Pneumonia) are considered for experimentation. In addition to the tried-and-true validation procedures for Training and Testing, we also analysed the data with the well-known and extensively used 5-fold cross-validation method. These two methods were utilised in conjunction with one another to verify the reliability of the findings. Using randomization, the dataset was subdivided into five groups (folds) of the same size.

While the remaining samples were utilised in the process of training, a single sample from each group was chosen at random to act as the test or validation dataset. This dataset was then compared to the results of the training process. The accuracy of the model that was developed with the assistance of the data that was included in the validation set.

Every deep learning system that was put into operation had five different models that were designed expressly for it, and the result of each model was an evaluation score. The mean values of the model sensitivity, specificity, overall accuracy, and balanced accuracy were analysed so that we could provide a conclusion regarding the
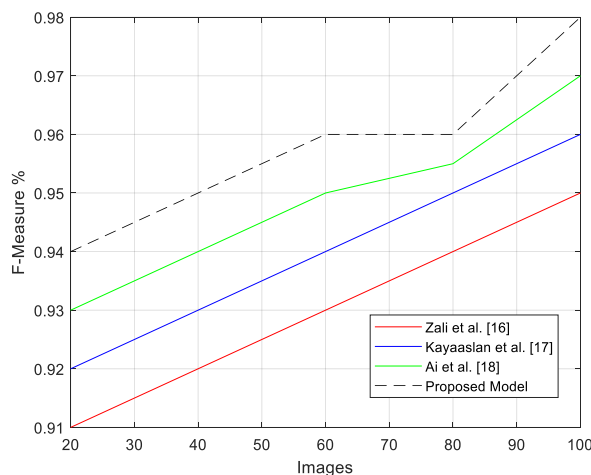

Fig. 4. Recall.

Fig. 5. F-measure.

performance of the models.

$$\text{Accuracy} = (TP + TN)/(TP + TN + FP + FN) \qquad (4)$$

$$\text{Precision} = TP/(TP + FP) \qquad (5)$$

$$\text{Recall} = TP/(TP + FN) \qquad (6)$$

$$\text{F-measure} = (2*TP)/(2*TP + FN + FP) \qquad (7)$$

When compared to the findings obtained by the same deep learning, the latter allows for somewhat superior predicted outcomes. We have concluded that the records distribution between the training and testing dataset should be done using a method that is not random. It takes use of standard clinical data, the likes of which are available in pretty much any hospital that specialises in treating emergencies which shown in Figs. 2–5.

Even though CT scans are superior to X-rays in terms of their ability to detect the changes that are diagnostic of viral pneumonia, it is highly unlikely that every SARS-CoV-2 suspect will access a scanner. This is the case even though CT scans are more effective than X-rays in this regard. Even though there is not yet any evidence, it is possible that people of different races will react to a viral pandemic in several different ways.

5. Conclusions

Although the two tests appear to be complementary to one another, more tests ought to be developed because of the high risk of false positives, the high cost, and the difficulty in separating pneumonia caused by COVID-19 from pneumonia caused by other reasons. It was demonstrated that the AlexNet approach and the method that utilised laboratory parameters were both equally effective at classifying images for COVID-19 detection, with respective accuracy scores of 97% and 98%. This was uncovered because of the investigation that was carried out. The utilisation of laboratory parameters enabled the collection of results that were more accurate. The findings of this research indicate that the diagnostic strategy that was proposed is a practical option that, to obtain more accurate results, can be paired with RTPCR and CT imaging.

Funding Statement

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

https://www.kaggle.com/datasets/tawsifurrahman/covid19-radiography-database

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