Automated Detection of COVID-19 from CT Scans using Convolutional Neural Networks

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Abstract: COVID-19 is an infectious disease that causes respiratory problems similar to those caused by SARS-CoV (2003). In this paper, we propose a prospective screening tool wherein we use chest CT scans to diagnose the patients for COVID-19 pneumonia. We use a set of open-source images, available as individual CT slices, and full CT scans from a private Indian Hospital to train our model. We build a 2D segmentation model using the U-Net architecture, which gives the output by marking out the region of infection. Our model achieves a sensitivity of 0.96 (95% CI: 0.88-1.00) and a specificity of 0.88 (95% CI: 0.82-0.94). Additionally, we derive a logic for converting our slice-level predictions to scan-level, which helps us reduce the false positives.

1 INTRODUCTION

Coronaviruses are a large family of RNA viruses that are usually known to cause respiratory tract illnesses like the common cold. They appear crown-like due to their spiked surface and are categorized into 4 major groups: alpha, beta, gamma, and delta. Most coronaviruses affect animals and can be transmitted between animals and humans (Kong and Agarwal, 2020). COVID-19 is the latest addition to the list of animal-to-human transmissions, preceded by SARS and MERS. COVID-19 is an infectious disease that has affected more than 6.8 million people in the world as of June 8, 2020. The most common clinical manifestations include fever (83% of patients), cough (82% of patients), and shortness of breath (31% of patients) (Chen et al., 2020b). The hallmarks of COVID-19 include bilateral distribution of minute patchy shadows and ground-glass opacity in the nascent stages. The progression of this disease is marked by the spread of these opacities and infiltrates to both the lungs (Wang et al., 2020b). The World Health Organization has published several testing protocols for detecting the disease (Wang et al., 2020a). The most commonly used reference test for the diagnosis of COVID-19 is the real-time reverse transcription-polymerase chain reaction (RT-PCR) (Gundlapally et al.,).

Reverse Transcription Polymerase Chain Reaction (RT-PCR) test is the key approach used for diagnosing COVID-19. However, it has some limitations; their shortcomings include the complex process used for specimen collection, the amount of time required for the analysis, and variability in the accuracy of the tests (Bullock et al., 2020). Apart from this, a major hurdle in controlling the spread of the disease is the accuracy and shortage of testing kits (Zhao et al., 2020a). Hence, computer-based detection assisted by an expert in the loop with minimal infrastructure is proposed as an alternative to testing kits and vaccines. Computer-aided detection has helped in detecting, localizing, and segmenting out a varied set of diseases using medical imaging analysis. In particular, machine learning is being used for medical imaging analysis by developing deep-learning systems that extract the spatio-temporal representative features from an image, analyze them, and decide the diagnostic outcomes (Wang et al., 2020b).

The most common, economical, and easy-to-use medical imaging and diagnostic technique is chest radiography or chest X-rays. This technique plays an important role in the diagnosis of lung diseases. Expert radiologists use chest X-ray images (CXRs) to detect pathologies like pneumonia, tuberculosis, atelectasis, infiltrates, and early lung cancer (Qin et al., 2018). But, detecting COVID-19 using CXRs is challenging due to the less evident visual features in CXRs caused by the overlapping of ribs and soft tissues and low contrast (Zhang et al., 2020). The limited availability of annotated images adds to the difficulty. The RT-PCR test is very specific but has a lower sensitivity of 65-95%, which means that the test can be negative even when the patient is infected (Fang et al., 2020)(Ai et al., 2020). These short-

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comings can be resolved by using chest CT scans, a cross-sectional imaging modality with high accuracy and speed, instead of CXRs. A recent study of the coronavirus infection on the cruise ship "Diamond Princess" showed evidence of the lung parenchymal pattern (classic for COVID-19) on CT studies of the chest in 54% of the asymptomatic cases (Inui et al., 2020).

Most of the recent literature reported that COVID-19-positive patients had characteristic features highly evident in the CT scan images (Xie et al., 2020). These features included different degrees of ground-glass opacities with or without crazy-paving sign, multifocal organizing pneumonia, and architectural distortion in a peripheral distribution (Ai et al., 2020). COVID-19 eventually develops into chronic pneumonia, and thus the visual symptoms it has are similar to those of bacterial and viral pneumonia. In CT scans, the ground-glass opacities are more similar to consolidation (Wang et al., 2020b). Studies have proven that chest CT has a higher sensitivity for the diagnosis of COVID-19 as compared with RT-PCR tests taken from swab samples (Ai et al., 2020). To curb human-to-human transmission and isolate the affected from the healthy, it is essential to detect the presence of COVID-19 at an early stage. This is where CT assists in the detection of minor infections (Anthimopoulos et al., 2016).

In this paper, we propose a prospective technique based on artificial neural networks wherein our model predicts the CT scan as COVID-19 positive or negative. This screening tool can help prioritize the treatment for patients with COVID-19 visual manifestations in their CT scans.

2 RELATED WORK

In the past few years, deep learning has evolved as a technique with its capabilities extending from classification and object detection to segmentation in medical image analysis. Some studies showed better results than expert radiologists. Rajpurkar et al. (Rajpurkar et al., 2017) proposed and presented a DenseNET-121 model for pneumonia detection which performed binary classification on CXRs using CNNs. This paper used F-1 score as the primary metric but failed to specify the prevalence of the set. Qin et al. (Qin et al., 2018) proposed pneumonia and pulmonary edema classification by extracting textural features. Parveen et al. (Parveen and Sathik, 2011) used an FCM clustering algorithm to detect pneumonia, where they showed that the lung area of the chest appeared like a black or dark gray shaded region when it became infected with pneumonia.

Recently, there have been many developments in detecting COVID-19 from CXRs and CTs. Xu et al. (Xu et al.,) proposed a 3D deep learning model that categorized CT scans as either COVID-19 pneumonia-positive or viral pneumonia-positive. They trained a location-attention classification model and used the predicted probabilities to give a prediction calculated by a Bayesian function. Their best model gave a recall of 86.7% and it needed further validation on multi-clinical studies. Chen et al. (Chen et al., 2020a) built a model using UNet++ (Zhou et al., 2018), a powerful architecture for medical image segmentation, and used a 3-consecutive slice and quadrant-based post-processing approach to mark a scan as positive or negative. This post-processing approach helped them reduce the number of false positives. Several studies have addressed diagnosis as a binary classification problem, i.e., healthy vs. COVID-19-positive (Bullock et al., 2020). For example, Wang et al. (Wang et al., 2020b) used a modified Inception neural network architecture and attained an accuracy of 79.3%. This model was trained on the CTs having severe pathological infections and it hence needs to be tested for all pathological stages to validate this in real-world scenarios. Shan et al. (Shan et al., 2020) developed a deep learning system that automatically quantified infection regions of interest (ROIs) and their volumetric ratios with respect to the lung. Li et al. (Li et al., 2020) put forth a 3D deep learning model, where they combined the 2D local and 3D global features using a max-pooling operation and predicted the class using the probability score from the softmax activation. One of the significant limitations of this paper is that the model seems to give 90% sensitivity on their test set, but hasn't been tested on the out-of-sample test set. In our paper, we overcome this limitation. Jianpeng et al. (Zhang et al., 2020) proposed a deep-learning architecture to differentiate COVID-19 cases from non-COVID-19 cases from CXRs. Their model is composed of three components: a backbone network, a classification head, and an anomaly detection head. The backbone network extracts the high-level features and feeds them to the rest of the heads. Zhou et al. (Zhou et al., 2020) use a U-Net with attention mechanism to utilize rich contextual features from the U-Net encoder, they train their model using focal tversky loss for small lesion segmentation. The model has been trained and evaluated on a small dataset of around 829 slices. Yan et al. (Yan et al., 2020) propose a Feature Variation block which enhances the global intensity of the pixels around the lung region and uses Progressive Atrous Spatial Pyramid Pooling to handle manifes-

tations at various scales. This model achieves state-of-the-art performance on 3D U-Net models attaining dice coefficient of 0.726 on datasets from China and Germany.

Several other approaches used a 3-category classification method, differentiating healthy patients from pneumonia and COVID-19. Xu et al. (Xu et al.,) used classical ResNet architectures, adding fully-connected layers at the end, and took the classification approach to solve the problem. He et al. (He et al., 2016) used ResNets for feature extraction, and Song et al. (Song et al., 2020) used the Feature Pyramid Networks (Lin et al., 2017), which are the backbone in U-Nets, for learning fine-grained features in the images.

Gurujit et al. (Randhawa et al., 2020) identified an intrinsic COVID-19 genomic signature and used it together with a machine learning-based alignment-free approach for an ultra-fast, scalable, and highly accurate classification of whole COVID-19 genomes.

3 DATA

We used COVID-19-positive and non-COVID data from GitHub (Zhao et al., 2020b) and consolidation and healthy CT scans from a private Indian hospital. The data obtained contained 275 CT scans labeled as COVID-19-positive. The ground truth in these images was decided on the basis of their RT-PCR test results. These CT images had different sizes from 143 patient cases (Zhao et al., 2020a). The scans differed in voxel sizes but had the same aspect ratio. In total, the data contained 5212 slices and was split at patient-level into training, validation, and test sets. Each set had a prevalence of 20% of positive cases. As the available open-source data had resolutions varying from 256x256 to 768x768, we resize the input to 512x512 pixels. This input size was the median size of the images in the dataset and sufficed our computational requirements. This model was trained using a GPU with 16GB RAM. The original images were in the unsigned int8 format, in the range of [0, 255]. We converted these images to floating-point 16, in the range of [0, 1]. The output masks were in the binary form [0, 1] at pixel-level, where 1s indicated the region of interest. Table 1 shows the detailed distribution of data.

Qualified radiologists inspected the CT slices one-by-one and classified each slice into one of two classes: COVID and NON-COVID. The COVID class contained slices where typical findings including bilateral pulmonary parenchymal ground-glass and consolidative pulmonary opacities, sometimes with a rounded morphology and a peripheral lung distribution (Chung et al., 2020) were observed. Ground-glass opacification was defined as hazy increased lung attenuation with preservation of bronchial and vascular margins, and consolidation was defined as opacification with obscuration of margins of vessels and airway walls (Hansell et al., 2008). Notably, lung cavitation, discrete pulmonary nodules, and lymphadenopathy were marked as negative. Other slices where above manifestations were not seen were marked as NON-COVID. For COVID slices, the radiologists also highlighted the region of interest where the manifestations were observed using polygon masks.

Table 1: Slice-Level Dataset splits.

Dataset	COVID-19	NON-COVID	Total slices
Training	657	2628	3285
Validation	120	477	597
Test	266	1064	1330

Figure 1 shows an example of the annotation. We used positive slices from COVID positive CTs and negative slices from healthy scans for training our model, this helped us overcome the challenge of using any false negatives to train the model. All the images in Table 1. were annotated by the radiologists, converted to masks and used as ground truth for training and evaluating the model.

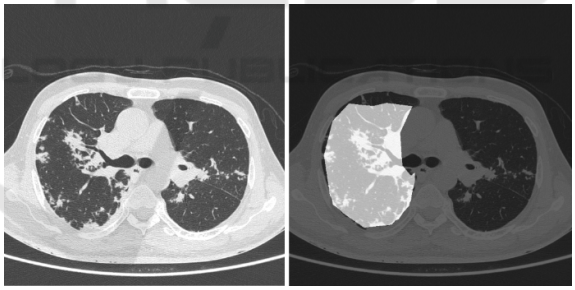

Figure 1: (Left) original image and (right) annotated ROI.

4 METHODOLOGY

In this section, we give a brief overview of our training and the inference algorithms.

We used U-Net (Ronneberger et al., 2015) for medical image segmentation, which uses the concept of deconvolution (Zeiler and Fergus, 2014). U-Nets are built on the architecture of fully convolutional networks. The most important property of U-Net is the shortcut connections between the layers of equal resolution in the encoder path and the decoder path. These connections provide essential high-resolution features to the deconvolution layers (Hesamian et al., 2019).

Here, we used Xception (Chollet, 2017) as the encoder for U-Net. Xception with its depthwise separable convolutions and residual connections, has proven to give better performance as compared to other models with similar parameters (Chollet, 2017).

Initially, we used ImageNet weights to train the model, but the model predicted a cluster of pixels instead of coherent masks. As we did not have a CT model for the same architecture, we used transfer learning by fine-tuning a network pre-trained on CXRs for the same problem but a different task (Shin et al., 2016). Transfer learning tends to give better performance when the tasks of source and target network are more similar; yet even transferring the weights of far and distant tasks has been proved to be better than random initialization (Yosinski et al., 2014).

Here, we have tried to solve the problem of distinguishing COVID-19 cases from non-COVID-19 by using weights from our COVID-19 vs healthy model, as pre-trained weights for this model already gave a sensitivity of 0.9 with a specificity of 0.8. We then built a CT model for consolidation vs healthy and later fine-tuned our model for COVID-19 vs non-COVID-19.

In the training stage, we use binary cross entropy as the loss function and the standard Adaptive Adam Optimizer with a batch size of 4. We set the maximum epochs to 50 and set the learning rate to 10^{-4}, which is decayed on the plateau after patience of 4 epochs. We resize each training image to a fixed size of 512×512 pixels. To alleviate the overfitting of our model on the training data from a particular source, we try to include data from varied sources. One of the drawbacks of having a 2D CT model is that the inference tends to be slow. Since our model has a sensitivity of 0.964, we plan to use specific slices for inference.

5 RESULTS

We tested our model using varied sets of data from different sources. We initially evaluated the model on our test set, consisting of 1330 images, in which COVID-19-positive samples had a prevalence of 20%. Our model gave a sensitivity of 0.963 (95% CI: 0.94-0.98) and a specificity of 0.936 (95% CI: 0.92-0.95). The dice coefficient on positive samples was 0.561. Figures 2 and 3 show the superimposed masks on one of the slices.

Apart from this, we evaluated the model on a total of 140 scans with a prevalence of 20% for positive cases. These scans were tested on data from three

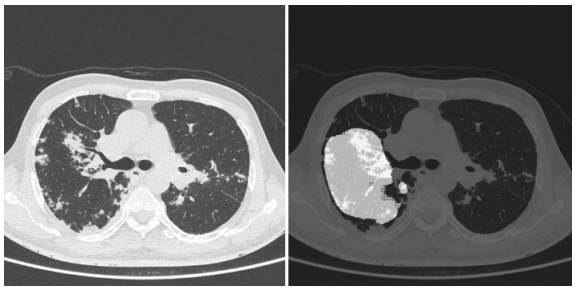

Figure 2: (Left) original image and (right) corresponding predicted mask.

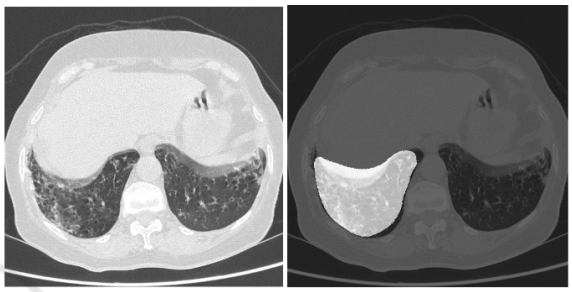

Figure 3: (Left) original image and (right) corresponding predicted mask.

sources. One source contained scans from Italy and China, while the remaining came from two separate private Indian hospitals. After passing these images through our model, we sorted the slices as per the position of the slice in the CT scan. We observed a pattern wherein the consecutive slices had the same predictions, which is expected from a radiology perspective. Figure 4 provides an example of the predictions for a positive CT scan. Here we see the expected pattern of consecutive slices, predicted as positive by the model.

Hence, we convert the slice-level prediction to scan-level prediction using the logic that if 15 consecutive slices in a scan are marked as positive, then we mark the scan as positive (Chen et al., 2020a). Table 2 shows the results obtained at scan-level.

Table 2: Scan-Level performance of the model on the test set.

Performance Metric	Value	95% C.I.
Sensitivity	0.964	(0.88,1)
Specificity	0.884	(0.82,0.94)
F1-score	0.794	(0.68,0.89)

6 DISCUSSION

The diagnosis of COVID-19 using CXRs and CT scans has gained significance since the ubiquitous

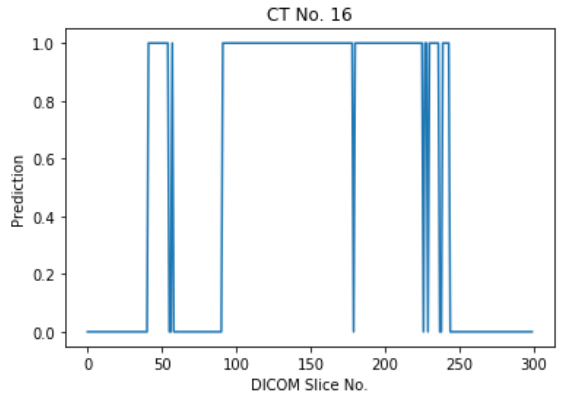

Figure 4: (Left) original image and (right) corresponding predicted mask.

spread of this disease. But, chest CT scans usually tend to show the region of infection more clearly than CXRs (Kong and Agarwal, 2020). A limitation of this study is that the patterns considered for COVID-19 were few in number– notably consolidation and ground glass opacity. These patterns might vary regionally where pleural effusion could be observed in COVID-19 infected patients. These patterns can even overlap with other pathology manifestations.

Another limitation is we have not considered the clinical history of the patient. The real-world utility of this tool can be enhanced once it considers the radiological and clinical parameters to determine the ultimate outcome. Our current implementation is a 2D model built at slice-level. Since a CT study could have the number of slices running into thousands, this 2D model certainly adds to the time complexity of processing the whole scan. Although we are satisfied with the performance our model currently shows on the data from diverse distributions, deploying the model in production is a challenge, given the time complexity.

In the future, we plan to implement a 3D model that will take the whole CT scan as input and give out masks for the infected areas. The primary challenge with this approach will be the requirement of a lot of annotated data to give an equivalent performance. Additionally, we propose a model that differentiates between COVID-19 and chronic and viral pneumonia and address the challenges associated with it, like fine-grained, accurate annotations and large amounts of data for all the specified categories. In conclusion, chest CT has proved to have a higher sensitivity than RT-PCR tests (Ai et al., 2020). Our analysis suggests that chest CT can be a potential alternative for COVID-19 screening and evaluation, especially in epidemic situations where the spread is uncontrollable, and diagnosis needs to be done with celerity.

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