

# COVID-19 Detection Using Segmentation and Classification

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**Abstract**—COVID-19 is a pandemic which has affected the lives of every human on earth. At the time of writing this, there were 90,06,079 confirmed cases in India with 1,32,223 deaths. It is highly contagious that is why along with practicing the guidelines issued by the WHO, we also need to increase the rate at which people are being tested to identify those at risk and isolate them to prevent further spread of the disease. This study aims to provide a method for detection of the novel coronavirus in patients by analyzing the CT scans of their chest. We perform both infection and lung segmentation to identify and differentiate parts of the chest cavity afflicted and classify it as COVID-19 positive or negative. The approach explained here achieves average dice scores as high as 0.96 for infection and 0.98 for lung segmentation respectively and a classification accuracy of 98.4%.

## I. INTRODUCTION

As we evolve as a society and make new technological advancements in healthcare and various other sectors to improve the quality of life, the rate of diseases also rises with it. A major reason for it could be our changed lifestyles. Nowadays, everyone around us seems to be talking about only one thing, Coronavirus. The novel Coronavirus (COVID-19) is a serious worldwide threat although it is neither the first pandemic nor the last. We need some way or the other to tackle it and make ample use of our technological tools to help the entire world's healthcare industry. Researchers all around the world are working collectively towards a vaccine and/or a cure all the while trying to get to know more about this virus. A popular testing procedure which is widely being followed by countries across the globe to test for COVID is called RT-PCR (Reverse Transcription Polymerase Chain Reaction). A major drawback of these tests is the time required to generate results. An alternative is to test the presence of the virus using machine learning to predict who is at the maximum risk of exposure, diagnose patients, understand COVID-19 better, and develop vaccines faster. Detection of the virus at an early stage can help limit the spread of the disease enabling doctors and health professionals to work towards differential diagnoses as soon

as possible. Our team is going to try to help advance this research by working on a deep learning model which will predict whether a person is infected or not by analyzing a CT scan of their chest.

Time and again deep learning has proven to be revolutionary at detecting and analyzing patterns from images. Convolution Neural Networks (CNNs) have given us very good results on similar problems in the past. Advantages of CT Scans over standard X-rays include the fact that they can be used to detect small traces of the virus as they provide a clear three dimensional view of the chest cavity and impart much higher detail to small crevices. Our dataset was sourced from Kaggle containing scans on which we will apply extensive preprocessing before feeding it to our models. After training, our models will try to predict if the person is suffering from COVID-19 and help radiologists segment parts of the infected lung by using image masks on individual slices of scans. Multiple researchers are fervently working towards achieving even higher accuracies so that the testing around the globe can be optimized as quickly as possible. Our primary objective with this project is to ease the burden on the already overworked personnel in the health industry by providing an alternate, yet efficient way to test and diagnose an increased number of people.

## II. RELATED WORK

Researchers have developed various deep learning techniques to examine COVID-19 on the bases of patient reports such as clinical images, X-rays of the thorax, Computerized Tomography Scan (CT scans) for addressing the COVID-19 epidemic. Here we describe some of the recent deep learning-based systems developed in the field of COVID-19 detection.

A deep learning model was used to classify COVID-19.[1] It used a modified version of inception V3 deep learning model as a pipeline for feature extraction. They used capsule neural networks for training and the dataset contains 34,006 CT scan slices (images) belonging to 89 subjects out of which 28,395

CT scan slices belong to positive COVID-19 patients. they got precision of 0.830 and sensitivity of 0.967.

Another model with Harmony-Search and Otsu based systems was proposed by [2]. Their model predicts pneumonia cases from CT scans. Their approach is to extract features for infected sections of CT scans and compare area features of infection and features of lungs then compute the infection/lung pixel ratio. They worked with COVID-19 pneumonia infections dataset of 75-year-old patients and got an average infection rate of 38.52% on axial-view (10 slices), and 39.06% on coronal-view (10 slices).

Another model for detecting COVID-19 through Transfer Learning was proposed by [3]. They used multimodal imaging data from 115 COVID-19 infected X-rays images, 322 Pneumonia patients, 349 COVID-19 CT scans, 397 non-COVID scans, 654 COVID-19, 277 Pneumonia and 172 normal ultrasound images. During preprocessing they used N-CLAHE for normalization, converted to color, then resized the classifier's default size. After augmentation, they applied a VGG19 model on the train and test dataset after splitting it into a 80:20 ratio. They got an F1 score of 0.87 for X-ray, 0.99 for Ultrasounds and 0.78 for CT scans.

Artificial intelligence-based model for detecting COVID-19 pneumonia using chest CT scans was proposed by [4], they used multinational datasets in their model. They used 2724 scans from 2617 patients, including 1029 scans of 922 patients with RT-PCR confirmed COVID-19 and lung lesions related to COVID-19 and Pneumonia. They used 2 kinds of models, the first one is a full 3D model which is used for resampling the cropped lung regions of CT scans and second one is a hybrid 3D model which resamples the cropped lung images to a fixed resolution. They got a validation accuracy of 91.7% and 93.9% on training and testing data respectively on the full 3D model. They got an accuracy of 92.4% and 90.5% on training and testing respectively on the hybrid 3D model.

Another model was made to distinguish between COVID-19 and common pneumonia using CNN on CT scans. They used multi-scale neural networks. They worked on 416 three-dimensional (3D) chest CT scans out of which 206 patients were confirmed COVID-19 positive by RT-PCR. They divided their dataset into three parts: training, validation and testing in the ratio 80:10:10. They achieved an accuracy of 87.5 per slice and AUC of 0.934 in the AI system.

A deep learning-based model for detecting COVID-19 cases using Chest CT Scans was proposed by [6]. They explained various kinds of deep network architectures, using CNN (Convolutional Neural Network) models. First, they explained the SqueezeNet model, in that they discussed the squeeze phase that is used by applying  $1 \times 1$  filters, the ReLU function and how they expand images using  $3 \times 3$  filters and then classification. They also explain about Inception, ResNet, ResNeXt, Xception, ShuffleNet and DenseNet, comparing them using various evaluation metrics. Their conclusion was that by using CT scans they got the best results in DenseNet (accuracy was  $92.9 \pm 2.2$ ).

Another model was proposed by [7] which dealt with infected region segmentation and measurement using CT-scans. They worked with COVID-19 dataset of CT scans containing 275 CT scans which were positive COVID-19 cases with manually labelled ground-truth lesions by a radiologist as they write in [7]. On segmentation they achieved an accuracy around 98.9% in the method proposed by them.

Another model having a neural based framework for predicting COVID-19 cases using CT scans was proposed by [8]. They used a capsule network (CapsNet) for classification. They split their data into three parts: 60% for training, 10% for validation and remaining 30% for testing. Their dataset contained 171 positive COVID-19 cases, 60 Pneumonia, and 76 normal cases. They got an accuracy around 90.82%, sensitivity around 94.55% and AUC as 0.98 for the model with lung segmentation. For the model without lung segmentation they got 90.82% accuracy, 92.7% sensitivity and AUC as 0.95.

A transfer learning method was proposed by [9]. With the use of CNN models, they were able to predict COVID-19 cases by using chest X-rays. For classifying the images, their model used five CNN variants VGG19, MobileNet, Inception, Xception, and Inception-ResNetV2. The dataset included 224 COVID-19 positive case images, 700 images of Pneumonia patients, and 504 images of normal patients. The concept of 10-fold cross-validation was used to split the dataset, for training and evaluation of models. VGG19 was treated as the main model which gave an accuracy of 93.48%, specificity of 92.85%, and the sensitivity was around 98.75%.

Another model based on deep learning to predict COVID-19 cases used X-rays. The feature extraction model used nine pre-trained models, and SVM was used for classification. The dataset contained 158 X-ray images of both COVID-19 positive and COVID-19 negative patients. This model was a combined model of the ResNet50 and SVM model and was statistically superior as compared to other models. Model's accuracy was around 95.38% and F1 score was 95.52%. This method was introduced by Kumar et al. [10]

### III. PROPOSED MODEL

Our model will make use of deep neural networks to perform two main tasks namely segmentation and classification which will further be divided into three subprograms (infection segmentation, binary classification, and lung segmentation).

#### A. Segmentation

We will design a model that will extract features from the inputted CT scans by repeatedly applying convolution and max-pooling layers, thus outputting the segmented mask and the infected lung segment. In the following paragraph we will explain the network implemented by us.

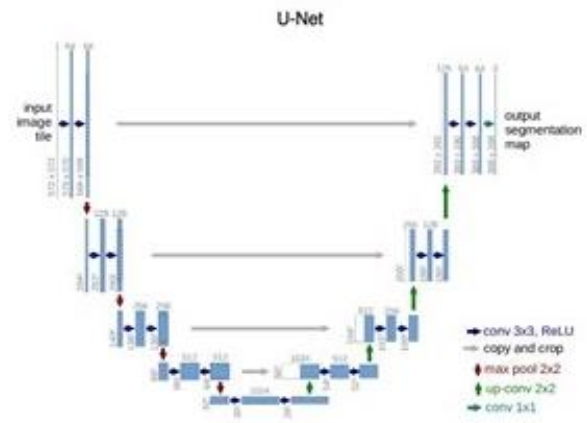
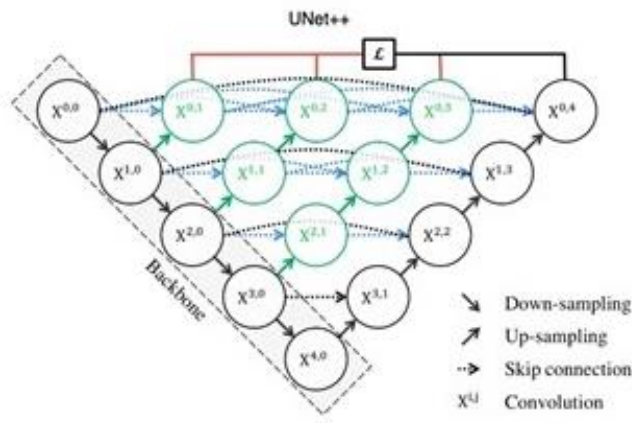


Fig. 1 UNet vs Unet++

UNet++:

UNet++ is a further improved version of UNet. We chose the former because even the slightest errors matter a lot when it comes to medical imaging. Hence, high accuracy is critical in this case. UNet++ is a nested UNet architecture. It achieves better performance by connecting the encoder and decoder using convolution layers and dense block. It differs from UNet in mainly 3 ways:

- Evolved skip pathways – which bridge the semantic gap between coder and decoder sub paths (can be seen in green)
- To improve gradient flow, it uses dense skip connections (which are the blue connections in the figure)
- Achieves model pruning by having deep supervision which leads to an improvement in performance.

Before inputting the CT scans to the model, some necessary pre-processing steps had to be performed:

1) Contrast Limited Adaptive Histogram Equalization (CLAHE): Histogram equalization is an image processing technique used to improve the contrast in an image. Adaptive Histogram Equalization (AHE) differs from Histogram equalization with the fact that AHE calculates various different histograms for different sections in an image and based on those redistributes the contrast in the entire image. In our model we have used a variant of AHE, called CLAHE (Contrast Limited Adaptive Histogram Equalization). The advantage of CLAHE over AHE is that it does not overamplify noise in the image which is the case with AHE. Medical images are known to suffer from contrast problems hence this has been used. The result is an enhanced image which would help in better detection.

2) Cropping: The CT scan is of the entire chest and contains black spaces which contain nothing and parts below the lungs which are not necessary for our model. In order to make the model more efficient and improve training time and reduce the computational complexity, we cropped the various slices to focus only on the lungs thus removing the area in which the presence of COVID would not be found. To crop the images, we draw contour over images and then crop the contour having

the largest area. We also must make sure that the corresponding segmentation map is also cropped by the same limits. Our dataset had a total of 3520 slices out of which 20% from the front and rear had been sliced out because they did not contain any valuable information.

3) Resizing the Images: As we had cropped the images, all images were of different sizes. To make them of the same size we resize the images and the corresponding masks.

4) Normalization: Images and masks were also normalized to a scale from 0 to 1 so that all the inputs to the model were on the same scale.

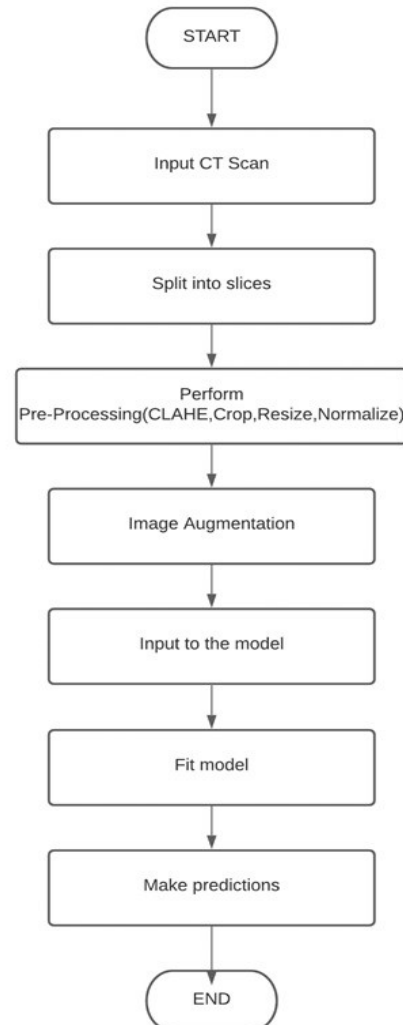


Fig. 2 Workflow of our segmentation script

5) Image augmentation: Image augmentation was performed to increase the amount of data we have so that we have more data to input to our model. The corresponding masks were augmented too.

### B. Classification

In this case when the CT scans are inputted to the model, the model will classify them as COVID positive or COVID negative. For this we made use of a Convolution Neural Network as it is known to have a very good performance with classifying images.

The same pre-processing techniques were applied here too.

CNN models perform well in areas like image recognition, processing, and classification. CNN model uses multiple layers and the training set for training the model and testing data for checking its performance. Each input images passes through a series of convolution layers with filters (Kernels) [17]:

- Convolution layers
- Pooling layers
- Fully connected layer

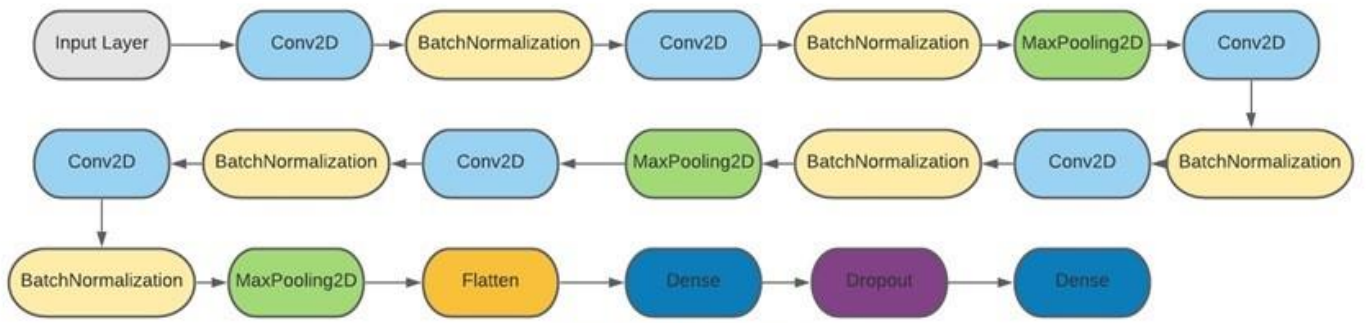


Fig. 3 CNN architecture

These are the basic building blocks of every Convolutional Neural Network [17]. The combinations of these building blocks will define how you want to proceed. Too many layers will form an overfitted model and too few layers will cause the model to underfit. So, we must choose the network architecture according to our dataset and the problem at hand.

For representing each value in the image weighted with its local neighbors by the kernel we use convolution layers [17]. Inside each layer, for extracting features we use various kinds of filters on the given image.

The pooling layer is used for down sampling along the spatial dimensions (width, height) i.e. it reduces the dimension of the feature map but extracts all important features. Adding to its advantages it also reduces noise from the images.

The batch normalization layer is used to stabilize deeper neural networks. It normalizes the activation of the previous layer by re-scaling the inputs. It also helps in optimizing the model.

There are a total of 19 layers in our network.

Using the aforementioned models and preprocessing techniques we have created three python scripts all of which first clean and process the raw data, augment the dataset, compile and train the required model for each of our subtasks, evaluate the trained models using appropriate evaluation metrics and then visualize and store their predictions on the validation set for further analysis and testing. Our first script returns predicted infection masks for new slices, the second predicts whether the patient that the input scan belongs to is COVID positive or not, and finally our third script predicts healthy lung tissue using lung masks calculated by our segmentation models.

## IV. PERFORMANCE ANALYSIS

### A. About the Dataset

From the plethora of options present on the internet, the dataset that we decided to use in our project consists of CT scans which play a very crucial role in the diagnosis of COVID-19. It plays a very big factor in detecting and determining the seriousness of COVID-19 that an individual is suffering from. We had also done a lot of research on the detection of COVID-19 by using X-rays. But the CT-scans were more accurate in the detection of the virus than the X-rays. Hence, the usage of it.

Nowadays, the models which are effective in finding the evidence of COVID-19 and clarify its results can play a very vital role in optimizing diagnosis and its treatment, especially in the areas where there is a shortage of expert radiologists.



Our dataset contains a total of 20 CT scans of patients that have been diagnosed with COVID-19 as well as segmentations of lungs and different infections made by experts.

To make things a little more efficient, we have saved the file paths of different CT scans in a csv file. The files we have used are in NIfTI format (\*.nii). NIfTI (Neuroimaging Informatics Technology Initiative) is a type of file format that is used for neuroimaging. These files are very heavily used in imaging informatics for neuroscience and even in neuroradiology research. Now, to read these following files we have used the nibabel package. With the help of the nibabel (NiBabel) package we can read and write some of the most common medical and neuroimaging file formats. It is the successor of PyNIfTI.

We have used the most common resolution for the CT scans i.e. 512x512. There are a total 3520 slices in a single CT scan. We have used the following 3 annotations for the segmentations:

- Lung Segmentation: It is the different values to account for left and right lungs.
- Infection Segmentation: It is the segmentation of radiological findings that could be COVID-19.
- Lung and Infection Segmentation: It is a combination of both, just to increase the efficiency.

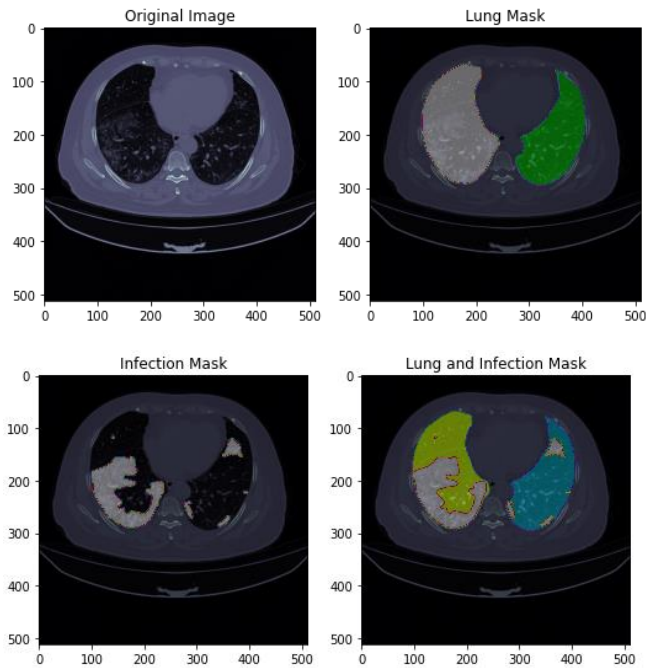


Fig. 4 Representation of a single slice in the dataset

With the inclusion of the original image of the CT scan, we also provide the lung mask image which highlights the entirety of the lung for the user and the infection mask image which shows the infected parts of the lungs that could possibly be COVID-19 by highlighting it. These images very accurately identify their respective results. We also provide the lung and infection mask which is the combination of the

two masks. It increases the efficiency and is very helpful in examining the result.

## B. Quantitative Analysis

Both the Sørensen-Dice coefficient (DICE) and Intersection over Union (IOU) are metrics used to measure the similarity of samples and are commonly used to evaluate the performance of image segmentation models. In terms of TP, FP and FN described elsewhere in this section, we can represent both quantities as:

- $DICE = 2TP / (2TP + FP + FN)$
- $IOU = TP / (TP + FP + FN)$

At the same threshold, IOU is more punishing and has a lower value than the corresponding DICE. Using a combination of both metrics help us determine an optimal threshold for our segmentation tasks and provide us with a good idea of the performance of our segmentation approach that returns image masks on binarized slices of the input CT scans.

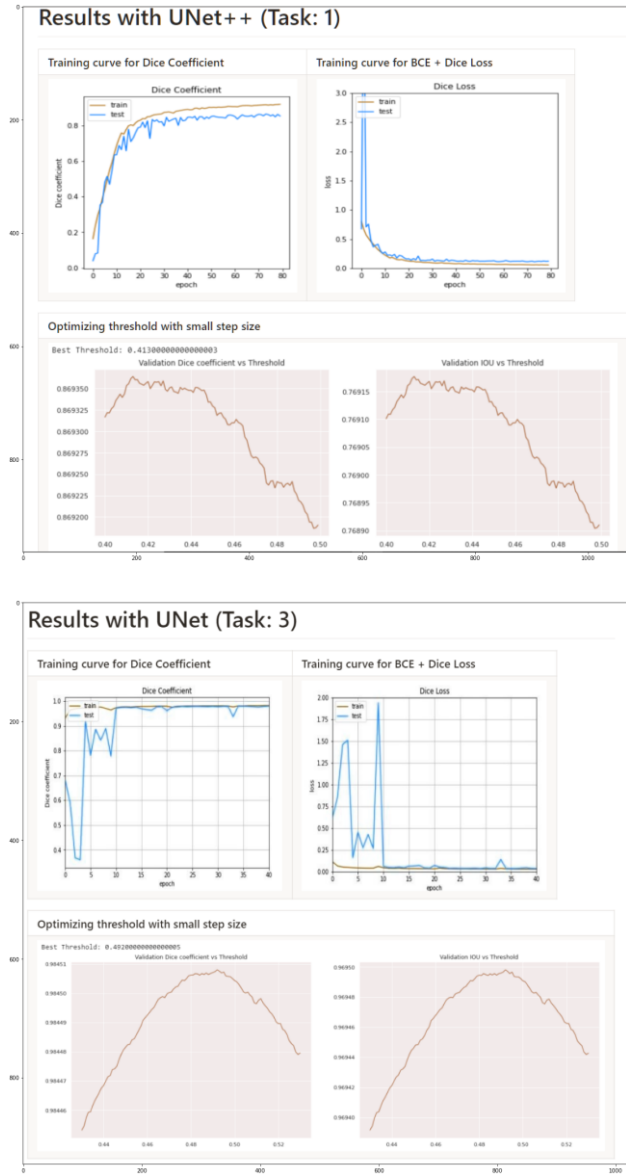
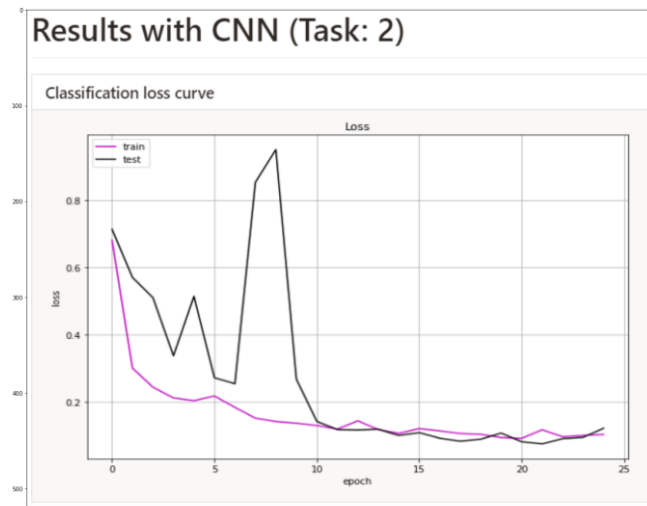


Fig. 5 Segmentation metric graphs

A loss curve is one of the most used plots to debug a neural network during training. It gives us a pretty good idea of the training process and tells us about the direction in which the network learns. As shown in our graph our training sequence has a good learning rate due to us using a blend of cosine annealing and continuous exponential decay. It returns the quantitative loss measure, and the loss function is calculated across every data item at the given epoch. But only the loss on a subset of the entire dataset can be shown by plotting curves across iterations of the dataset. To visualize the outcome, we have plotted the train and test loss curves for a baseline experiment.



A confusion matrix is used to evaluate classification models on validation and testing sets. It is a matrix which contains columns and rows equal to output classes. For binary classification problems, we have a 2x2 matrix where the classes are labelled as positive and negative. It helps in evaluating models by using some variables:

- True Positive (TP)
- True Negative (TN)
- False Positive (FP)
- False Negative (FN)

TP considers those cases which are positive, and the model is predicting correctly. In TN we consider the cases in which the model predicts in the negative class correctly. On the contrary, FP and FN keep a count of those cases in which the model is predicting the opposite of the expected values.

With the help of these terms, we can calculate:

- Accuracy =  $(TP + TN) / (TP + TN + FP + FN)$
- Precision =  $TP / (TP + FP)$
- Recall (sensitivity) =  $TP / (TP + FN)$
- F1-score =  $2 \times (Precision \times Recall) / (Precision + Recall)$

In our confusion matrix class 0 represents normal cases and class 1 represents COVID-19 positive cases. On keeping the threshold at a default value of 0.5 We got 120 cases which our model correctly classified as COVID negative (TN), 29 were not positives and were wrongly classified (FP), 1 was positive and wrongly predicted as negative by the model (FN) and 484 slices were correctly classified as COVID positive (TP).

After finding optimal threshold 0.81 by trial and error, the model's performance increased significantly with 143 TNs, 6 FPs, 5 FNs and 480 TP on the validation set.

Accuracy at the threshold 0.81 was 98.3%, precision was 98.8%, recall was nearly 99% and the F1 score returned was 98.9% which is a marked improvement from the values of these metrics at threshold 0.50 which correspond to 95.2, 94.3, 99.8, and 96.9 percentage for the respective values.

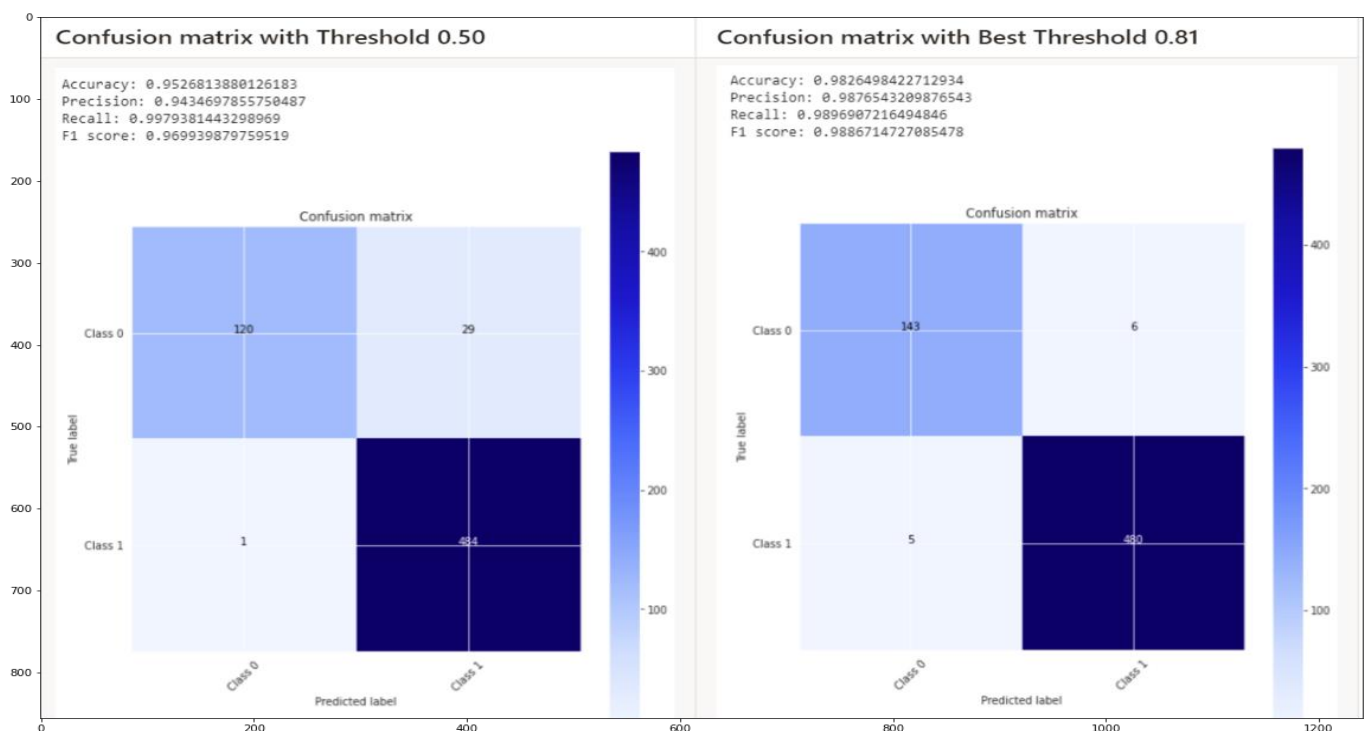


Fig. 6 Confusion matrices for classification

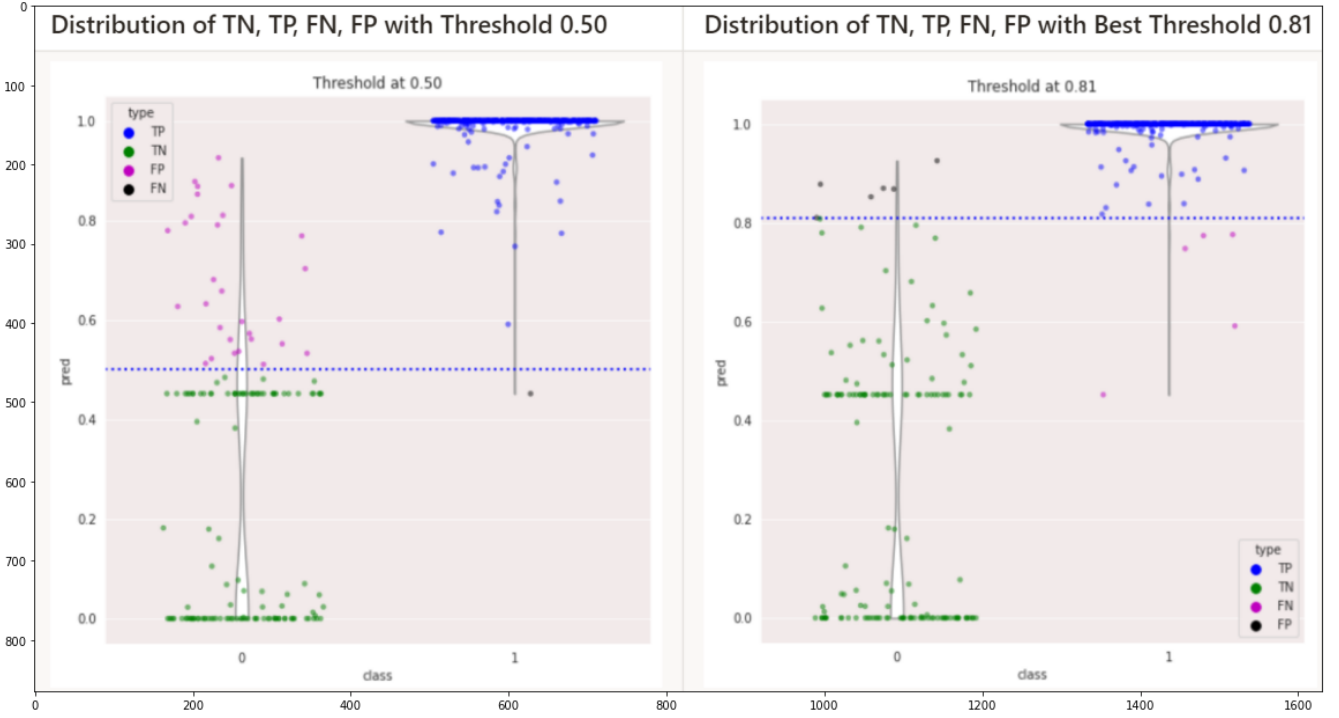


Fig. 7 Cluster plots for classification

## V. RESULTS

The reason our code works surprisingly well on a limited number of scans is primarily because of the preprocessing and augmentation we have applied on individual slices, paying attention to the quality of the training slices selected and allowing the models to be trained against a greater variety of images which greatly reduces the bias that creeps into models trained on smaller datasets. Further improvements can be easily made to the original program by using newer image enhancement algorithms like alpha-trimmed filters, slice-by-slice image masks [11], gamma correction [12] and so on. We can also create a larger augmentation pipeline and/or increase the number of augmented slices generated from each scan. Once an acceptable level of accuracy and precision is achieved, we shift our focus on optimization to reduce the resources consumed by our program and free up space to allow our models to be used on enlarged datasets while maintaining decent runtimes and improved accuracies. Using batch normalization in our models, quickly reaching optimal learning rates using a combination of cosine annealing and exponential decay, using binarized masks instead of false color and reusing weights from suboptimal models for our outputs has helped us drastically improve performance without compromising too much on the accuracy of our final predictions.

For the segmentation of the COVID-19 infection at the lung level, several deep learning models using limited datasets like ours have been recommended. A transfer learning approach [13] using architectures like ResNet50 and InceptionV3 have

claimed 97% accuracy on a set of 100 scans while another approach using multiple VGG16 models [14] have reported best results around 90% accuracy on a similarly limited input. Although our model matches and even outperforms these implementations under our testing conditions, the limited size of the datasets on very deep models will cause overfitting and these results must be validated on a larger database.

In our classification task, we selected a good threshold using simple trial and error by repeatedly running predictions on scans never seen before by our model and returning the values which divided the TP, TN, FP and FN values with the highest accuracy. Other classification models like COVNet [15] that work on distinguishing between COVID-19 and pneumonia have achieved AUROC scores of 0.96 on 4352 scans from 3322 patients. Another method used was inputting pre-selected COVID-19 and other abnormal chest CT scans into EfficientNet B4 [16] after lung segmentation whose final model was reported to have AUROC score 0.95 on 132583 slices sourced from 1186 patients.

As segmentation and classification models both require different parameters to evaluate their respective performances, we compiled a table of all relevant accuracy scores and metrics of every approach we have used in our three tasks and side-by-side comparisons of different models tested on different partitions of the dataset. Predictions made by the models on validation slices were also visualized as seen.

	Dice (Mean of folds)	IOU (Mean of folds)	Precision (Mean of folds)	Recall (Mean of folds)	AUCROC	F1 Score	Accuracy
Infection Segmentation (3-fold)	0.948	0.903	0.947	0.950	-	same as dice	-
Infection Segmentation (4-fold)	0.956	0.917	0.955	0.958	-	same as dice	-
Classification	-	-	0.987	0.989	0.998	0.988	0.982
Lung Segmentation	0.984	0.969	-	-	-	same as dice	-
Note: precision and recall values are as per the best threshold for dice							

Fig. 8 Table of evaluation metrics

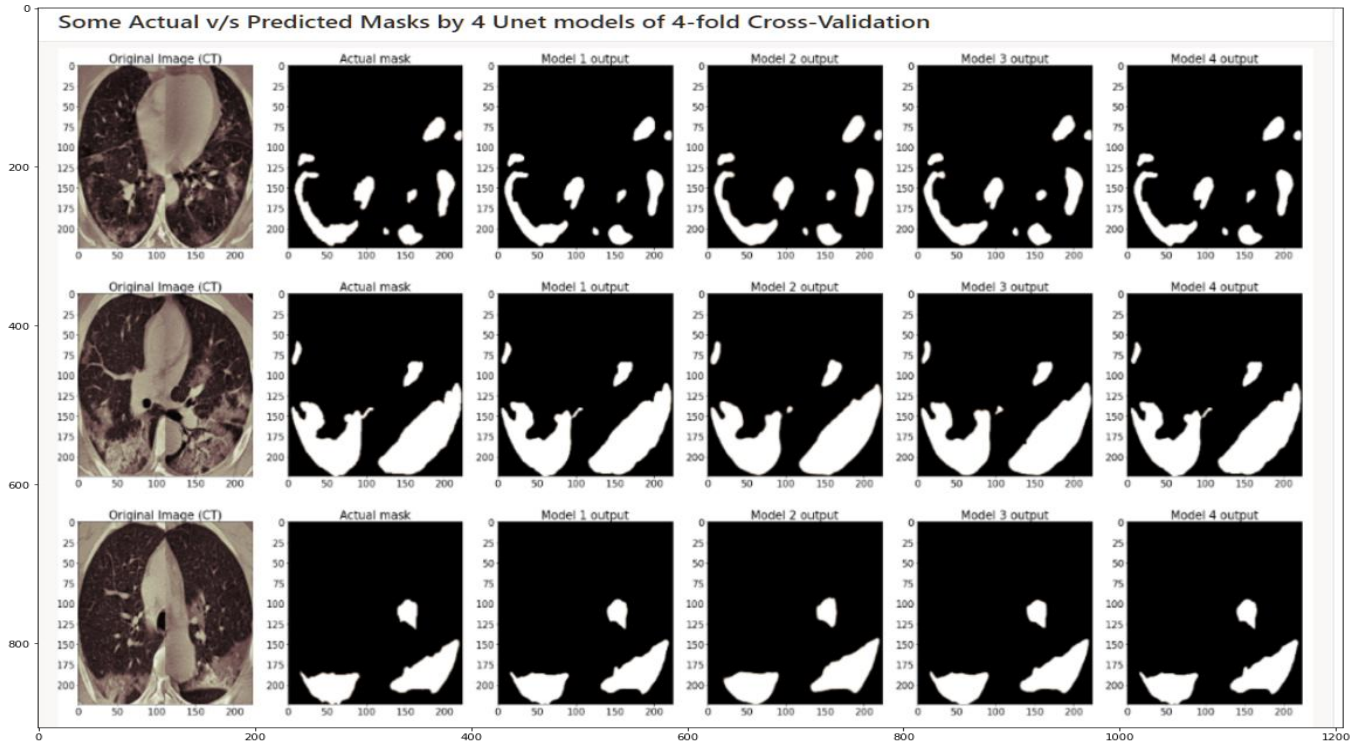


Fig. 9 Predicted infection masks

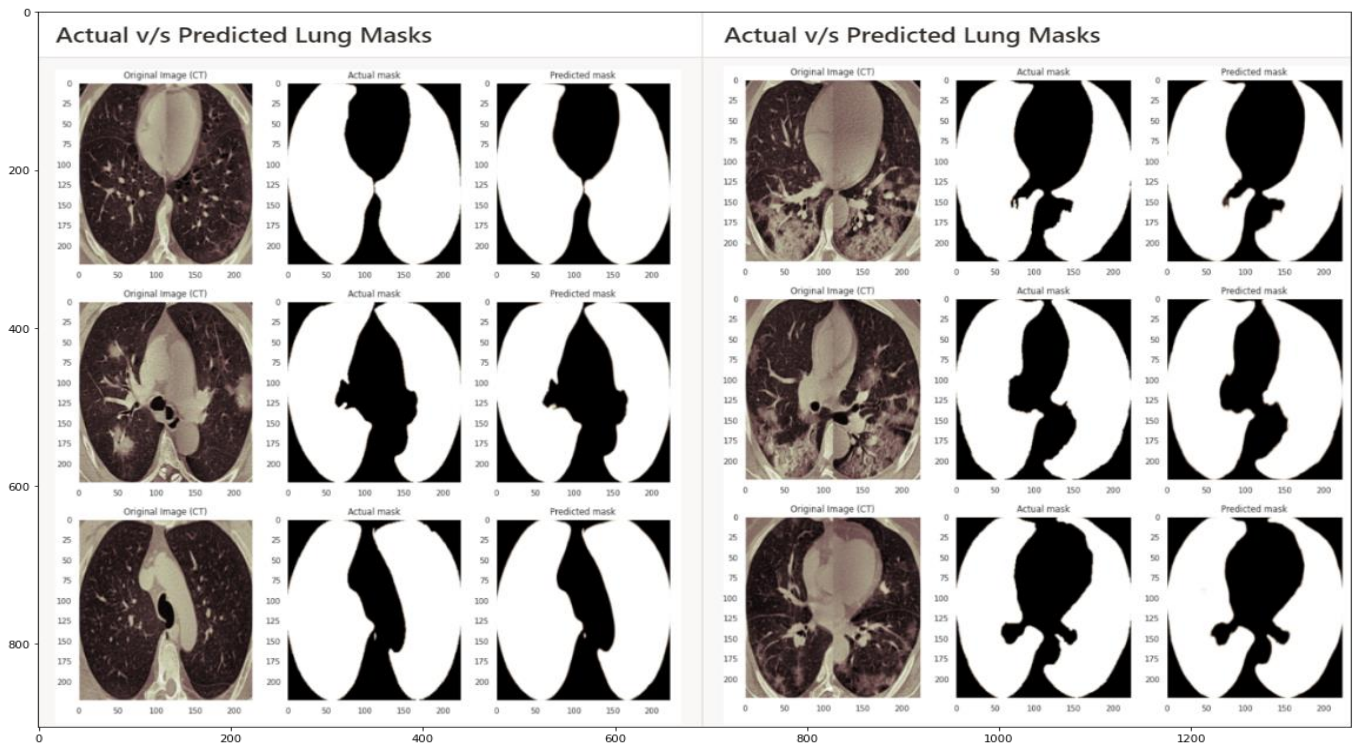


Fig. 10 Predicted lung masks



## VI. CONCLUSION

In this paper we have examined a task-based approach to both detect COVID-19 from chest CT scans and segment severe infection areas from healthy tissue and unnecessary black spaces simultaneously. The augmentation we added on top of the well-defined masks in the dataset helps our program to perform well in the absence of many training examples. Our code shows promise when compared to other similar solutions that work on limited inputs. The combination of UNET++ with user defined CNNs improves overall performance for both segmentation and classification. Further tasks like digital image reconstruction can help existing models improve by using an encoder to extract useful features for the other tasks.

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