
COVID AFFECTED LUNG SEGMENTATION AND CLASSIFICATION

A Minor Project Report
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CERTIFICATE

This is to certify that the Minor Project Report entitled **Covid Affected Lung Segmentation and Classification** submitted by **Shubham (222SP025)** as a record of the Minor Project presented by him is accepted in partial fulfillment of the requirements for the award of Master of Technology (Signal Processing and Machine Learning) in the Department of Electronics and Communication Engineering, National Institute of Technology Karnataka, Surathkal.

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ABSTRACT

Detection and segmentation of lung with lung abnormalities is a difficult task as abnormal lung are often large in size, irregular in shape and grow against surrounding structures of similar density and intensity. For normal lung, segmentation can be performed by making use of excellent contrast between air and surrounding tissues. But it fails when lung affected by high density pathology. So, the lungs with high density pathology have to be detected. Active contour model based lung and infection segmentation technique is proposed here which accurately detect and segment the covid affected lung from the CT lung images. Proposed method automatically detects the interior contours, from the CT lung images.

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1 Introduction

The eruption of the severe acute respiratory syndrome COVID-19 continues to grow where over (686,791,545) worldwide cases of confirmed infections are reported at the end of April'27 2020, according to Worldometer.

To control the spread of this virus, screening large numbers of suspected cases for appropriate quarantine and treatment has become an urgent priority. Most tests to check for COVID-19 relied on tests done at a laboratory for pathogen testing, which is the most accurate test possible. Still, it is time-consuming with significant false-negative results [1].

Patients suspected of having respiratory infection or pneumonia are admitted to the hospital under consideration of specific diagnostic procedures with laboratory and other non-laboratory tests to identify the cause, location, and severity of the infection. The laboratory tests include standard procedures, like blood gas analysis tests, complete blood count (CBC), and pleural effusion [2], in a procedure that needs transporting samples from the hospital to the lab, which takes up valuable time. On the flip side, the non-laboratory tests are the computer-assisted imagery analysis techniques used to inspect/registrate the lung regions using digital chest radiography (or standard 2D X-ray) or CT scan. On the contrary to the conventional 2D X-ray; which uses a fixed X-ray tube that does not provide much detail. 3D CT scan is a nondestructive scanning technology that has the advantage of providing a very detailed view of the lung of bone, soft tissue, and blood vessels [2]. Advantages of CT imaging include low cost, wide availability, high spatial resolution with current multi-slice scanners, short scan time and higher sensitivity. Disadvantages include: Inferior soft tissue contrast compared to MRI and X-ray-based radiation exposure [3].

2 Literature Review

Various methodologies in computer vision have been proposed to deal with different sides to combat the COVID-19 pandemic, including segmentation and classification methods [4]. These approaches can be classified into two fundamental classes: Classical Machine Learning and Deep Learning methods [5].

In general, Image segmentation has become an increasingly important task in radiology research and clinical practice. The goal of segmentation is to separate regions or objects of interest from other parts of the body to make quantitative measurements. More specifically, obtaining further diagnostic insights, including measuring the area and volume of segmented structures. The main challenges of segmentation algorithms exaggerates due to intensity in-homogeneity, presence of artifacts and closeness in the gray level of different soft tissue.

Various aspects of segmentation algorithms have been explored for many years. Existing segmentation approaches can be classified into three main classes: manual, semi-automatic, and fully-automatic. Manual segmentation methods are time-consuming, monotonous, and can be affected by inter and intra-observer variability. Semi-automatic approaches are already widespread and integrated with publicly available software packages. Finally, fully-automatic procedures do not need user intervention. Each of these methods has its advantages and limitations. However, even now, the investigators try to make segmentation steps as easy as possible with the help of automatic software tools. Still, the problem of segmentation remains challenging [6], because (1) no general solution can be applied on a large and continually growing number of different regions of interest (ROI), (2) vast variations of ROI properties, (3) different medical imaging modalities. Lastly (4) associated changes of signal homogeneity; mainly variability and noise for each object [7]. Besides, as noted in Shi et al. [8] (a) while plenty of AI systems have been proposed to assist in diagnosing COVID-19 in clinical practice, there are only a few works related to infection segmentation in CT scans. (b) most of COVID-19 imaging data-sets focus on diagnosis, only one data-set providing segmentation labels, and (c) the qualitative evaluation of infection and longitudinal changes in CT scans could thus offer useful and vital information in fighting against COVID-19. However, these methods are not applicable when we have a tiny data-set. In this paper, we have focused on a segmentation system to automatically quantify infection regions of interest (ROIs) and measure the volume of the infection area.

3 Methodology

Fig:1 represents the workflow of this project as shown below

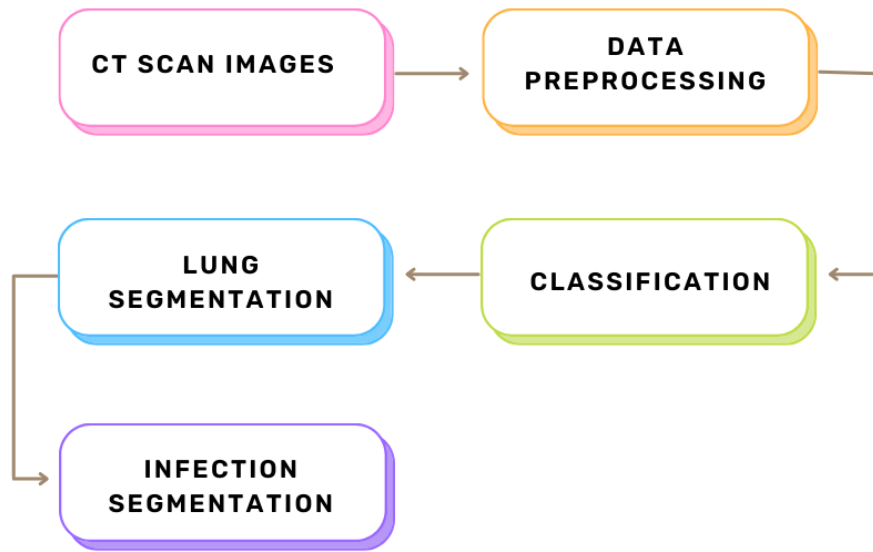


Figure 1: Workflow diagram

3.1 Dataset:

CT scans play a supportive role in the diagnosis of COVID-19 and is a key procedure for determining the severity that the patient finds himself in.

Models that can find evidence of COVID-19 and/or characterize its findings can play a crucial role in optimizing diagnosis and treatment, especially in areas with a shortage of expert radiologists.

This dataset [9] contains 20 CT scans of patients diagnosed with COVID-19 as well as segmentations of lungs and infections made by experts.

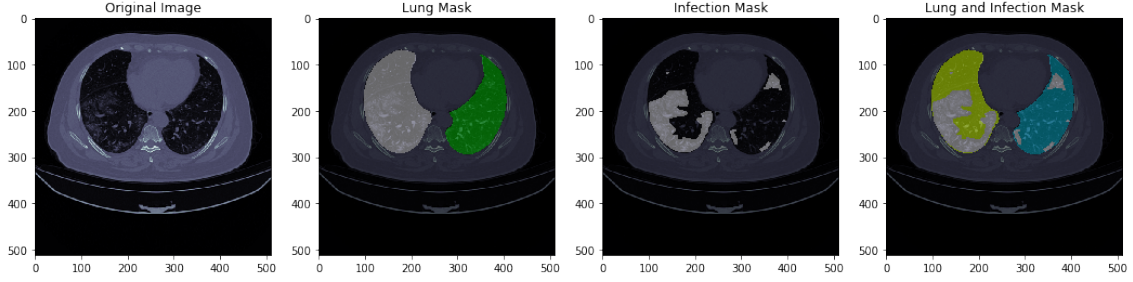


Figure 2: Dataset Collection

3.2 Data Preprocessing

The data pre-processing step includes the contrast enhancement as well as cropping the CT-scan images such that they focus only on the lung part. To achieve this we have used Contrast Limited Adaptive Histogram Equalization (CLAHE) algorithm enhancer for contrast improvements.

1. Improving contrast of the images

We will use the createCLAHE fuction from OpenCV to balance out the histogram in a uniform way. Basically, we will try to improve the contrast in such a way that the dark regions are visible and the lighter regions are made clear in a dynamic format.

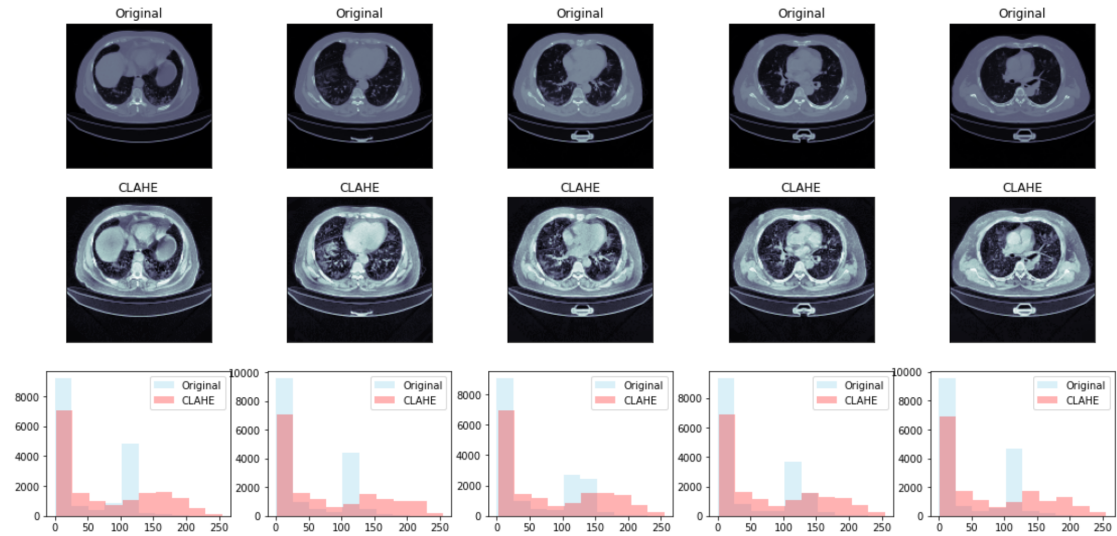


Figure 3: CLAHE Contrast enhancements

2. Cropping the image

The area of interest for this project is the area where lungs are located. Area other than that is of no use so we will crop out the image and store only the area in which we are interested in.



Figure 4: Dataset cropping process

To crop the images, firstly we binarised the image and performed bio-medical imaging techniques such as erosion and dilation. Here we have used K-means to find the clusters and drew bound box around it and cropped the CT-scan.

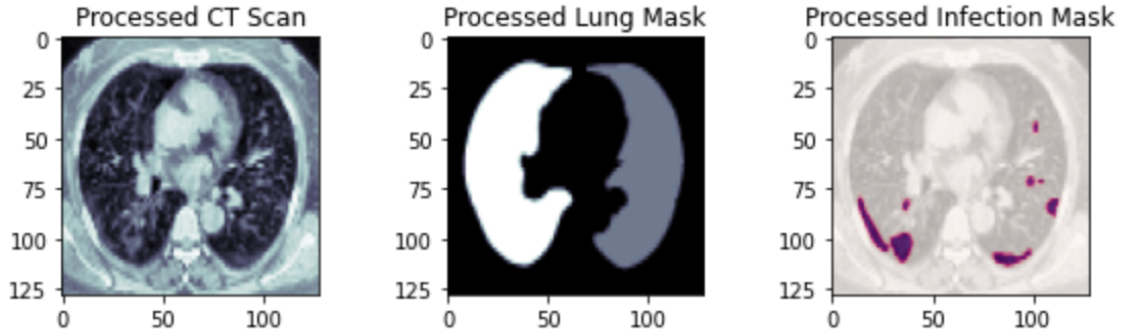


Figure 5: Final preprocessed dataset

3.3 Classification

The pre-processed 2d ct-scans are labeled as Covid-19 positive or negative based on their infection masks. The labeled dataset is then used to train a CNN model which gives a value between 0 and 1. Threshold is decided using ROC curve and the prediction is converted to binary values. A confusion matrix is created which is used to calculate precision, recall and F1 score.

We have defined a 2D convolutional neural network (CNN) model using the Keras API. The model takes grayscale images with a width and height of 128 pixels as input. The model is built using the functional API, which means that each layer is defined and then connected to the previous layer.

Here is a summary of the layers in the model:

- **Input layer:** Takes input images with shape (128, 128, 1) where 1 represents a single grayscale channel.
- **Convolutional layers:** The model has four convolutional layers, each followed by a max pooling layer and batch normalization layer. The convolutional layers have 64, 64, 128, and 256 filters, respectively, and use a 3x3 kernel. The activation function used for each convolutional layer is Rectified Linear Unit (ReLU).
- **Global Average Pooling layer:** This layer takes the output of the last convolutional layer and calculates the average value for each feature map.
- **Dense layers:** The output of the global average pooling layer is connected to a dense layer with 512 units and the activation function is ReLU. A dropout layer with a dropout rate of 0.3 is then applied to help prevent overfitting.
- **Output layer:** The final dense layer has a single output unit with a sigmoid activation function. This is because the model is designed to perform binary classification, where the output represents the probability that an image belongs to a certain class.

Overall, this model architecture is suitable for image classification tasks where the input images have a relatively low resolution (128x128 pixels).

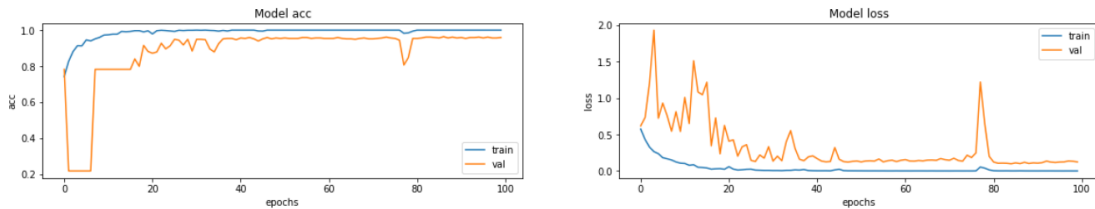


Figure 6: Model accuracy and loss curve

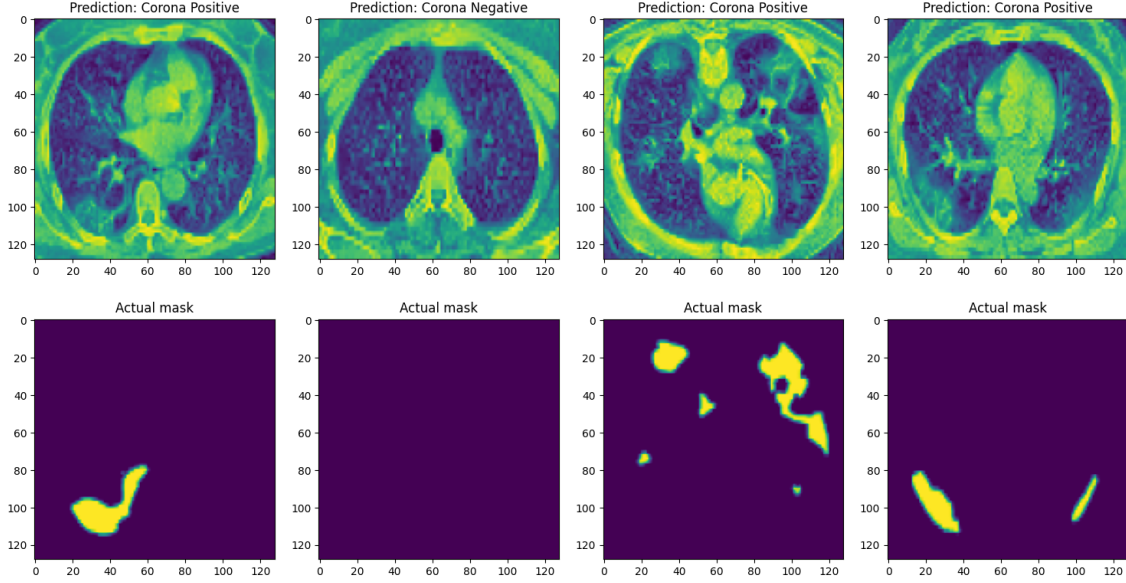


Figure 7: Covid Infected Classification Result

3.4 Lung Segmentation

The pre-processed 2d ct-scans and the lung masks are used to train a CNN model which marks the lung area in the ct-scans. A U-net architecture is implemented for this task. Dice coefficient is used to judge the efficiency of the model. Exponential decay is used to change the learning rate during training.

The model is designed to take in grayscale images with dimensions of 128x128 pixels.

The first layer is the input layer, which takes in the 128x128 grayscale image. The input is then passed through four convolutional layers. Each convolutional layer applies a set of filters to the input image and applies an activation function (ReLU) to the output. The first convolutional layer has 16 filters, the second has 32, the third has 128, and the fourth has 256.

After each convolutional layer, a max pooling layer is applied, which reduces the dimensionality of the feature maps output by the convolutional layer.

After the fourth convolutional layer, a dense layer with 256 neurons and a ReLU activation function is applied to further process the output.

The output is then passed through three up-sampling layers, each followed by a convolutional layer. The up-sampling layers increase the size of the feature maps and the convolutional layers apply a sigmoid activation function to generate the lung segmentation output. The final convolutional layer has a single filter to identify the lungs in the input image

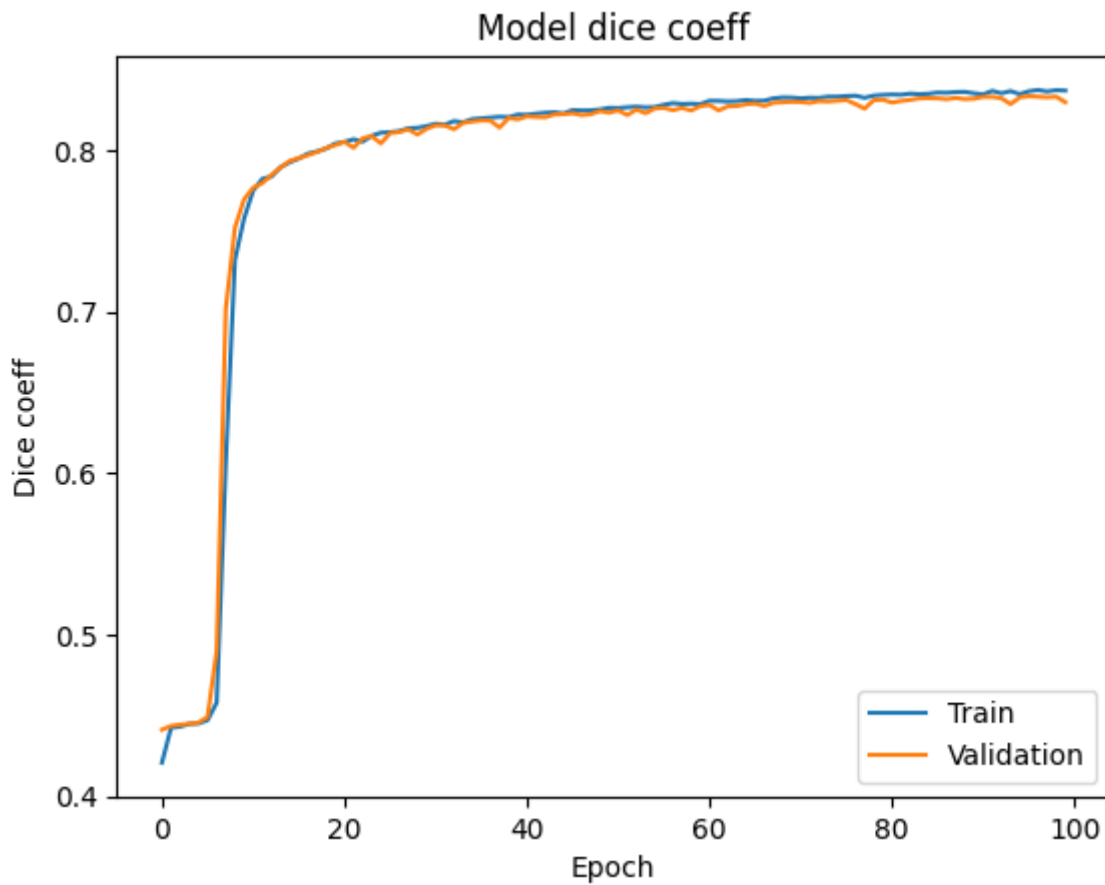


Figure 8: Model Dice coefficient

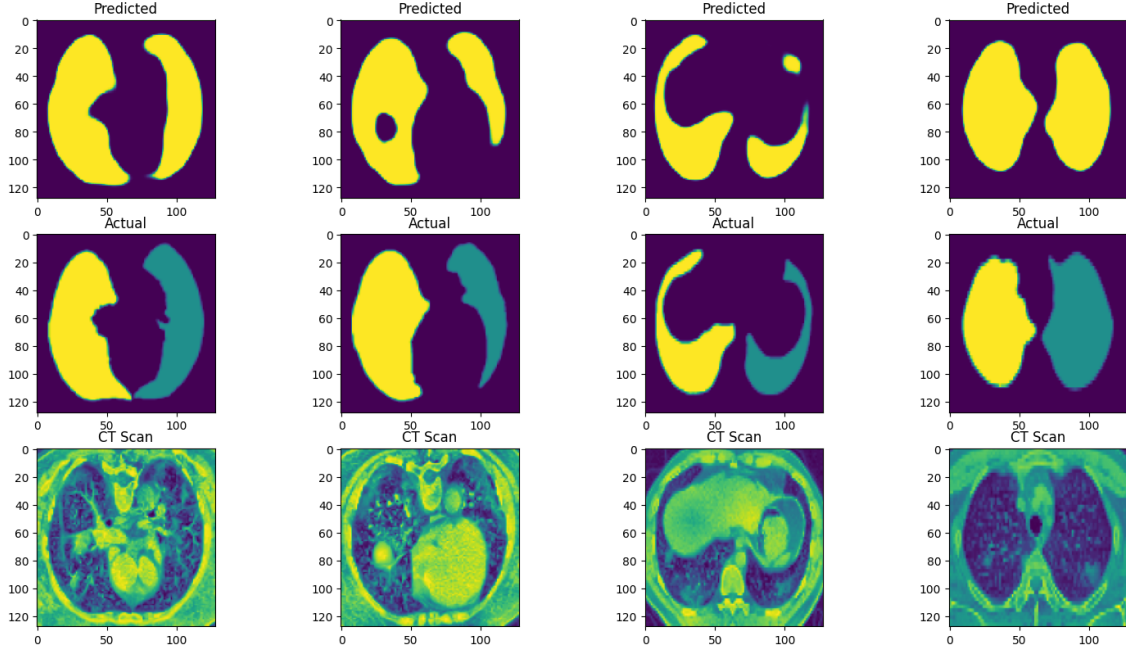


Figure 9: Lung Segmentation

3.5 Infection Segmentation

We have implemented a U-net with dice coefficient along with Cosine Annealing Learning Rate Schedule for state of the art segmentation achieving a dice-coefficient of 0.8238 and validation-dice-coefficient 0.7622.

The infection segmentation function defines a UNet model for lung infection segmentation using CT scan images. The model consists of four encoding blocks and four decoding blocks. Each encoding block has two convolutional layers followed by batch normalization, ReLU activation, max pooling, and dropout layers. The output of each encoding block is concatenated with the output of the corresponding decoding block before passing it to the next decoding block. Each decoding block has a transposed convolutional layer, followed by two convolutional layers with batch normalization and ReLU activation. The final layer is a 1x1 convolutional layer with sigmoid activation, which outputs the segmentation mask.

The model is compiled with the binary cross entropy dice loss function, and the Adam optimizer with a learning rate of 1e-4. The model is trained for 100 epochs with a batch size of 16. The learning rate is decreased using the CosineAnnealingLearningRateSchedule callback.

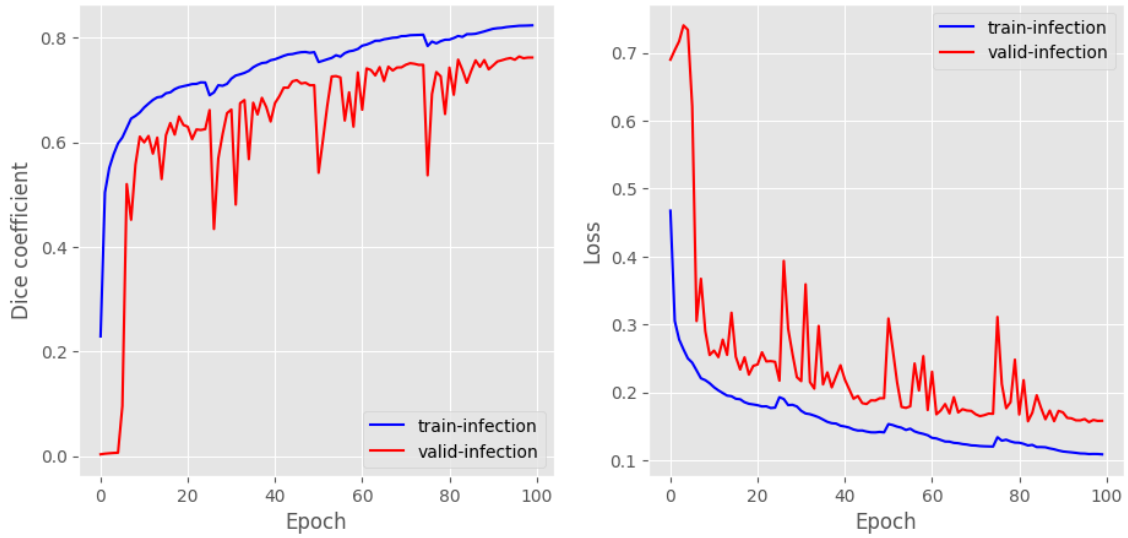


Figure 10: Model Dice Coefficient and Loss

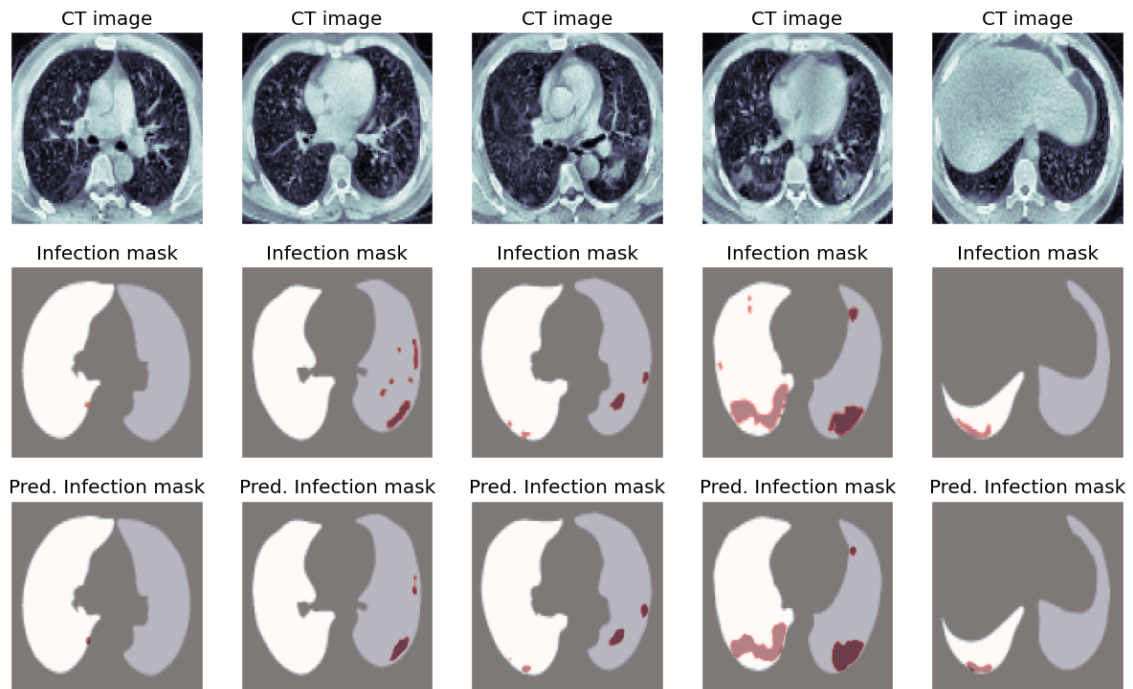


Figure 11: Infection Segmentation output

4 Result and Discussion

As stated in earlier section, we have used Kaggle dataset to evaluate our model. Firstly we have preprocessed the data to enhance the contrast using CLAHE architecture. After that we cropped the lung image removing the unnecessary area, keeping only the region of our interest (ROI).

After preprocessing we have classified the data into covid positive and covid negative based on the 2D CNN model.

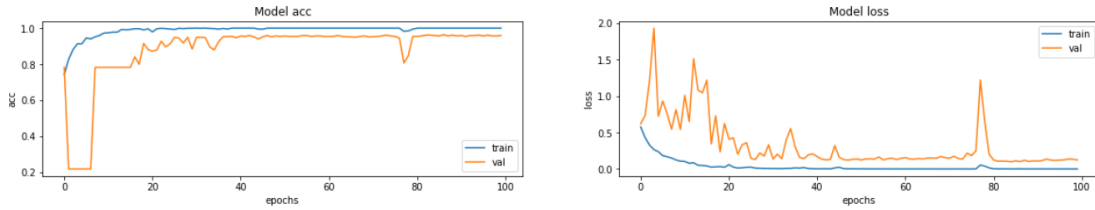


Figure 12: Classification Model accuracy and loss curve

In the next step we have segmented the lung image using the UNet architecture with dice-coefficient of 0.8370 and validation-dice-coefficient of 0.8297.

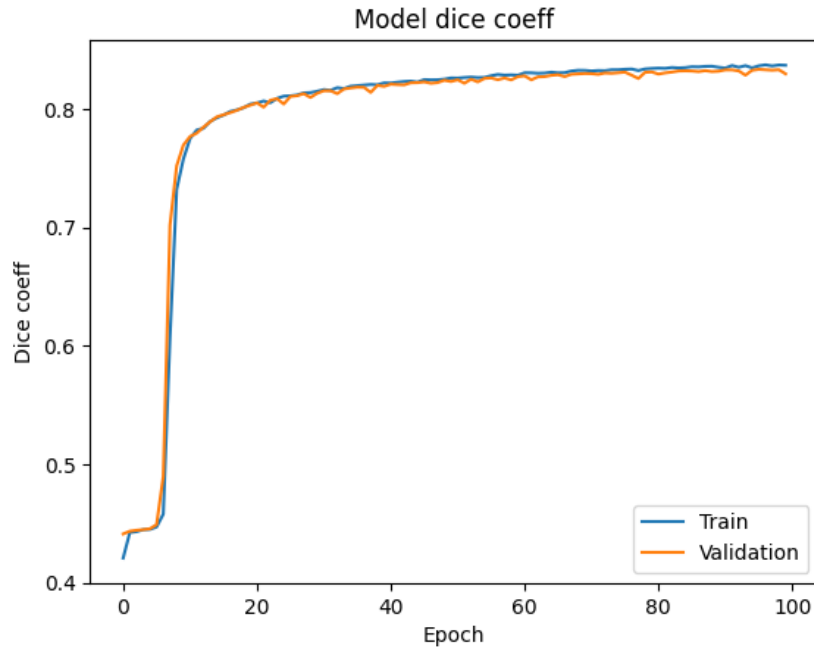


Figure 13: Lung Segmentation Model Dice coefficient

In the last step we have segmented the infection using UNet architecture achieving a dice-coefficient of 0.8238 and validation-dice-coefficient 0.7622.

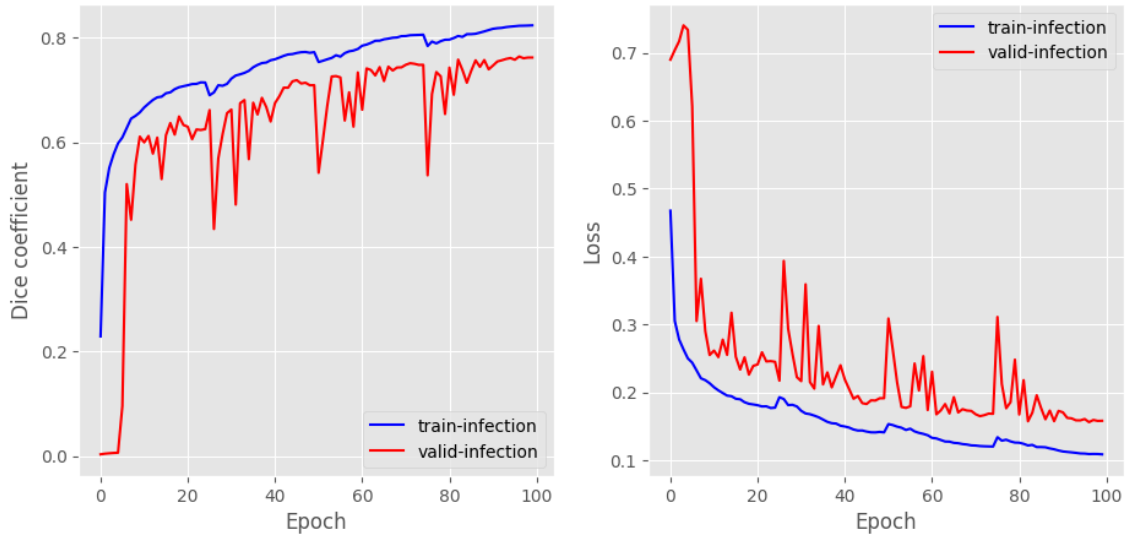


Figure 14: Infection Segmentation Model Dice Coefficient and Loss

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