

4 Results and Discussion

In order to evaluate the proposed segmentation and severity recognition model, several metrics have been measured such as accuracy, sensitivity, specificity, and dice coefficient (F). Besides the most important metric for segmentation is the Jaccard Index or the Mean Intersection-Over-Union (mIOU).

The following equations (1-6) present the metrics formulas that have been used for model evaluation:

$$Accuracy = \frac{TP + TN}{TN + TP + FN + FP} \quad (1)$$

$$Sensitivity = \frac{TP}{TP + FN} \quad (2)$$

$$Precision = \frac{TP}{TP + FP} \quad (3)$$

$$Specificity = \frac{TN}{TN + FP} \quad (4)$$

$$F1 = \frac{2TP}{2TP + FP + FN} \quad (5)$$

$$IOU = \frac{TP}{TP + FP + FN} \quad (6)$$

Where TP: True Positive, TN: True Negative, FP: False Positive, FN: False Negative. Table 1 summarizes the evaluation metrics of the proposed model.

Table 1. Evaluation metrics of the proposed model

Metric	Proposed segmentation model
Accuracy	0.926±0.00
Sensitivity	0.919±0.13
Specificity	0.938±0.15
Precision	0.842±0.08
F1	0.839±0.12
IOU	0.746±0.09

As shown in Table 1, the proposed segmentation shows a high performance for detecting the infected cells to recognise the level of the COVID-19 infection. The proposed model in [30] shows performance using U-Net 0.678, 0.836, 0.265, and 0.308 of Sensitivity, Specificity, Precision, and IOU respectively. The higher result of the proposed method may relate to the pre steps before training the model including clearing images, using high quality images, and tuning the network parameters.

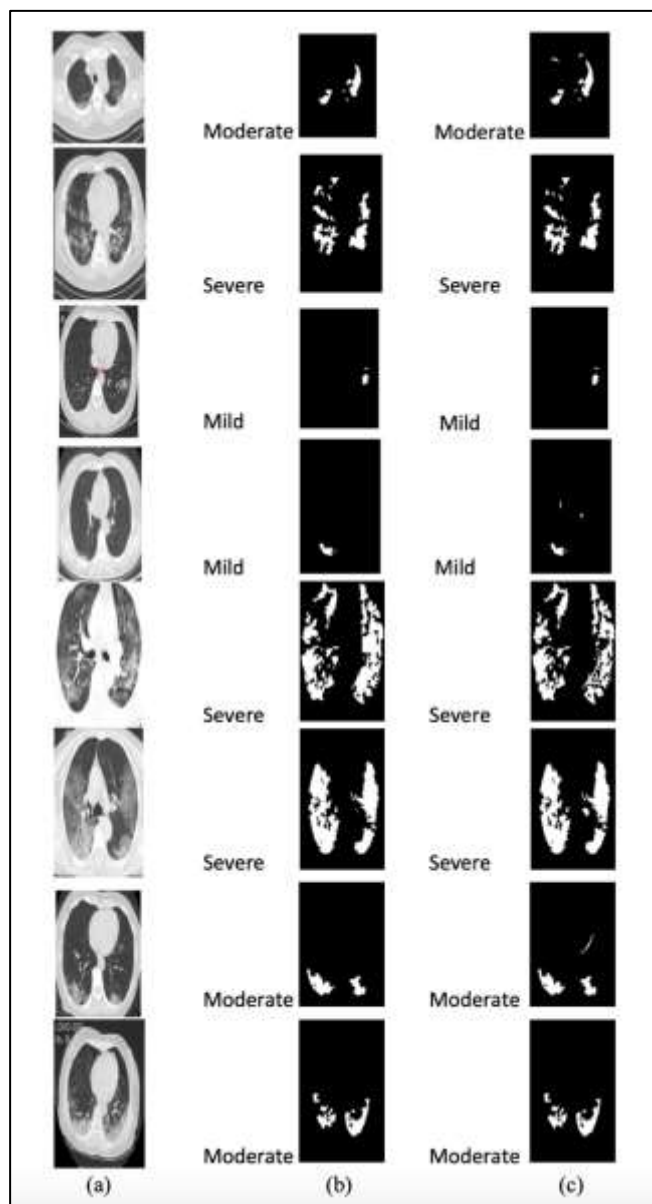


Fig. 4: Visual illustration of the proposed segmentation model (a): CT Image (b): Ground Truth (c): Segmentation and recognition result

Figure 4 shows some cases of lung infection recognition including the ground truth which has been recognized by an expert clinical biologist.

Figure 4 demonstrates a strong match between the ground truth and the proposed method result for infected lung tissue segmentation and recognition for COVID-19 CT-scan images testifying to the deep learning model's promising performance in infected cell detection and segmentation.

As shown in lung images there is a high similarity between the infected cells and the blood vessels, however, the model succeeded in recognizing using a robust deep learning network. Figure 4 depicts two cases where the model failed to accurately highlight the infected cells exactly as the

ground truth which has not been affected by the severity degree of the diagnosis.

Due to the blood vessel and infection regions having comparable intensities, it is more difficult to accurately identify the infected cells, which makes the miss-segmentation more obvious in mild cases of COVID-19 patients.

Recently, an AI system aimed to develop and enhance an automatic intelligent system for classifying chest X-ray images to detect and identify the COVID-19 virus using machine learning into infected and normal, [32]. The concentration in this work is based on infected images only.

5 Conclusions

Segmentation is necessary for an accurate diagnosis and tracking of pneumonia lesions caused by COVID-19 in CT images. Although deep learning holds tremendous potential for automating this procedure, a substantial quantity of high-quality annotations is hard to come across. To overcome this challenge, a novel semantic segmentation and severity recognition framework is proposed to detect the severity level of COVID-19 after diagnosis of the infection. Overall, semantic segmentation is a powerful technique in computer vision that enables a detailed understanding of images at the pixel level, with numerous applications across different domains.

Adequate segmentation of the lungs is essential for determining the infected tissues and severity of COVID-19. Deep learning provides several types of networks that can be trained using labeled images in which the model detects the infected tissues to recognize the severity degree based on the infected area.

The proposed framework revealed encouraging findings in the segmentation of COVID-19 images of contaminated lung tissue. Nonetheless, there are some challenges related to this research that need to be addressed in further studies. One of these limitations is the nature of the CT-scan imaging which is carried out several times with several angles as slices, so in some slices, the image is recognized as mild, and in different slices for the same patient is recognized as moderate or severe. Moreover, to develop this work to be used in clinical practice the model should be integrated with another model that identifies the image as infected or normal before using the proposed criteria to distinguish the level of the infection.

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