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Classification of Lung Diseases and Infection Localization from Chest X-Ray Images using Deep Learning

[1] Md. Ariful Islam, [2] Pintu Chandra Shill

[1] [2] Khulna University of Engineering and Technology, Khulna, Bangladesh
Corresponding Author Email: [1] islam2207554@stud.kuet.ac.bd, [2] pintu@cse.kuet.ac.bd

Abstract*— Over the recent years, chest diseases have become a severe problem that has a significant impact on people's lives all around the world. If these diseases are not detected in time, they can be fatal and cause death. Chest radiography (CXR) is a cost-effective method of identifying and diagnosing diseases. However, identifying chest anomalies from CXR images is time-consuming and needs professional radiologists. Automatic biomedical image segmentation helps speed up disease detection and diagnosis. So, a fully automated system is necessary, and there is a lot of work regarding this. Rapid advancements in deep learning have produced groundbreaking outcomes in this area. Modern networks like U-Net and SegNet, however, frequently perform poorly in difficult domains. This paper proposes a fully automated system for chest disease detection along with a segmentation module. We have combined the classification and segmentation tasks into a single model and have developed a novel architecture that is based on Nested UNet architecture. Besides, this work also quantifies the infection rate of a chest and localizes the infected region of the chest due to COVID-19. The proposed approach uses a transfer learning enriched pre-trained encoder to learn enough from the limited amount of data. It has modified skip connections to reduce semantic gaps between the corresponding levels of the encoder-decoder layer. The proposed architecture has comparatively fewer parameters than most of the recent works. As a result, it has a lightweight design and is less likely to overfit. With an iterative procedure, the created network improved lung area segmentation performance, achieving an Intersection over Union (IoU) of 93.59% and a Dice Similarity Coefficient (DSC) of 97.61%. Additionally, with 97.67% Intersection over Union (IoU) and 87.61% DSC, COVID-19 infections of varied shapes were perfectly localized. Finally, the proposed model has obtained an excellent chest disease detection performance with an accuracy of 92.86% which is satisfying. The remainder of the study outlines a novel method for automating the detection and segmentation of chest diseases from CXR pictures using deep learning, transfer learning, and a special Nested U-Net architecture.

Index Terms*— Lung Nodule, CT Scan, Deep Learning, viral Pneumonia, Pulmonary Function Test.

I. INTRODUCTION

Lung disease is common throughout the world. These include chronic obstructive pulmonary disease, pneumonia, asthma, tuberculosis, fibrosis, etc.[1] Timely diagnosis of lung disease is essential. Lungs are responsible for taking in oxygen from the air we breathe and expelling carbon dioxide, a waste product of cellular metabolism. The lungs also play a crucial role in regulating the acid-base balance of the body by removing excess carbon dioxide. Early detection and diagnosis of these diseases are critical for effective treatment and management. Chest X-rays are a widely used imaging modality for diagnosing lung diseases. Additionally, identifying the infected region(s) in chest X-ray images can be a daunting task, even for experienced radiologists.

Deep learning techniques have shown tremendous potential in various image segmentation and classification tasks, including medical image analysis[2]. With deep learning methodologies, AI researchers have made considerable progress in improving the quality of automated diagnostic medical imaging systems. Many intriguing paths are now opening up as a result of their pioneering work that could potentially assist in identifying chest diseases. There are places where the number of doctors is not sufficient. These automatic systems can play a vital role as a helper system in the absence of a doctor or expert. Chest X-rays are the most common diagnostic imaging tool used in the detection and diagnosis of lung diseases. X-ray images are easy to obtain, non-invasive, and inexpensive. However, the interpretation of chest X-ray images can be difficult, and it requires specialized training. Radiologists must have an in-depth understanding of the anatomy and physiology of the lungs to identify the various patterns and abnormalities present in the image. Additionally, identifying the infected region(s) in chest X-ray images can be challenging. The identification of the infected area(s) can be obscured by the presence of other structures, such as the heart or diaphragm.

Traditional methods for the diagnosis of lung diseases rely on manual analysis of chest X-ray images by a radiologist. This process is time-consuming and can lead to errors, especially when dealing with large volumes of images. Impact of lung segmentation on the diagnosis and explanation of COVID-19 in chest X-ray images [3]. A deep learning architecture can provide a faster and more accurate diagnosis of lung diseases. By identifying the infected area(s) in chest X-ray images, track the changes in the infected region(s) over time, providing insights into the efficacy of the treatment. The deep learning architecture can help in

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reducing healthcare costs associated with the diagnosis and treatment of lung diseases. Traditional methods for the diagnosis of lung diseases require specialized training and expertise, which can be expensive. Additionally, misdiagnosis or delayed diagnosis can lead to further complications and increased healthcare costs. A deep learning architecture can provide a faster and more accurate diagnosis of lung diseases, reducing the need for further testing and hospitalization.

Numerous researchers have conducted studies to investigate the relationship between machine learning systems and the prediction of diagnostic information from X-ray images [4-5]. The identification of lung illness using fundamental image processing techniques also takes a significant amount of time. Following the fruitful development of GPUs and CNNs, both the performance of CAD (which is used for diagnosing lung illness) and the decision support arrangement received a significant boost. For the purpose of diagnosing lung cancer and other lung disorders, a number of deep-learning models have been proposed in a number of studies [6, 7, 8, 9]. In reference [6], a three-dimensional deep convolutional neural network (CNN) with multiscale prediction techniques is developed for the purpose of identifying lung nodules from segmented pictures. However, the research presented in Reference [6] is unable to categorize different diseases, and the multiscale prediction algorithms are only used for analyzing tiny nodules. In reference [7], a full CNN is suggested as a method for reducing the number of false positives that occur during the classification of lung nodules. This technique is limited in that it can only evaluate the characteristics of the CT scan images in order to lessen the likelihood of making an incorrect diagnosis. In reference [7], the Luna 16 dataset was utilized.

The importance of artificial intelligence (AI) is discussed in Reference [8], which provides an overview of the current state of the art in the categorization and evaluation of chest X-rays. In addition, this issue is described in the study [8], which also organizes a novel 108,948 front view database called ChestX-ray8, in which the 32,717 X-ray photos are of different patients. Deep Convolutional Neural Networks are used by the authors of Reference [8] to validate results on this lung data, and they achieve some encouraging results. According to the article [9], having a dataset with a large number of labels is the pinnacle of success in terms of classification tasks and prediction. The research presented in Reference [9] provides a large dataset referred to as the Chex portion. This dataset includes 224,316 radiography chest pictures collected from 65,240 patients. The authors of [9] use CNNs to assign labels to this dataset based on the prospective information provided by the model. In order to evaluate the results of this model, lateral and frontal radiographs are taken. In addition to this, a benchmark dataset can be found in reference [9].

This study proposes a deep learning framework by combining a visual geometry group-based neural network (VGG), data augmentation, and spatial transformer network (STN) with a convolutional neural network(CNN). This scheme is automatic biomedical image segmentation that helps speed up disease detection and diagnosis. This study combines the classification and localization tasks into a single model and has developed a novel architecture that is based on Nested UNet architecture. Besides, this work also quantifies the infection rate of a chest and localizes the infected region of the chest. The proposed approach uses a transfer learning enriched pre-trained encoder to learn enough from the limited amount of data. It has modified skip connections to reduce semantic gaps between the corresponding level of the encoder and decoder layer. The proposed architecture has comparatively fewer parameters than most of the recent works. As a result, it has a lightweight design and is less likely to overfit. With an iterative procedure, the created network improved lung area segmentation performance, achieving an Intersection over Union (IoU) of and a Dice Similarity Coefficient (DSC)[10].

II. RELATED WORKS

Chest X-rays are one of the most common medical imaging modalities used to diagnose various diseases. Recently, deep learning techniques have shown promising results in the field of X-ray-based disease detection. By training deep neural networks on large datasets of X-ray images, it is possible to automate the disease detection process and improve the accuracy and speed of the diagnosis. In this chapter, we present a thorough survey of existing literature on chest disease detection and infection localization to compare and contrast with our proposed method. The literature review will also highlight the challenges and limitations of current approaches, and provide insights into the potential future directions of this research. By conducting a comprehensive review of the existing literature, this section will provide a foundation for the proposed research and help to place the current work in context.

The most revolutionary advancement in deep learning is the Convolution Neural Network (CNN). CNNs were first suggested by Fukushima et al.[11] in his seminar paper on the ”Neocog-nitron.” To conduct end-to-end picture segmentation, Long et al.[12] introduced a fully convolutional network (FCN), which is slightly different from CNN. FCN separates the image into segments by making pixel-level predictions. Using improved FCN, Palit et al.[13] established a model for biological cell segmentation that dramatically reduces image segmentation time while also significantly increasing accuracy. The watershed method and FCN were integrated by Li et al.[14] to increase segmentation effectiveness. FCN is straightforward and effective, yet it still has significant flaws. For instance, the FCN repeatedly employs the pooling operation during the down-sampling procedure. This causes it to lose picture information and

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produce an inadequate segmentation result. Inspired by the FCN, researchers came up with a new kind of architecture called encoder-decoder architecture. Similar to classification networks, the network's encoder section is where feature extraction takes place. The decoder network tries to recreate the feature using the encoder's extracted features. The enhanced complete convolutional encoder-decoder network, known as U-Net, was put forth by Ronneberger et al. As resources are few and expensive in the medical picture arena, U-Net's ability to learn from small amounts of data is a big advantage[16]. U-Net's requirement to bypass connections between corresponding encoder-decoders is one of its most striking features. The decoder component can recover the spatial information lost during the pooling processes using these skip connections, which speeds up learning [17]. The network does not, however, take into consideration the semantic differences between the two feature maps that were combined. However, several recent initiatives have been impacted by U-Net because of its revolutionary contributions to the field of biological image segmentation.

Later, SegNet, another encoder-decoder design, was suggested by Badrinarayanan et al.[18]. SegNet's use of a reduced version of the VGG-16 network trained on the ImageNet dataset as the encoder is notable. The pooled indices are saved during max-pooling in the encoder and used in the decoder afterward. That makes the architecture computationally effective and aids in the preservation of context information. [18] [19].

III. METHODOLOGY

There are some major issues when creating medical image datasets. Some of these are privacy issues, the need for professional annotation, advanced image acquisition pipelines, and expensive imaging equipment. As a result, there are few public medical image benchmark datasets. Each of these datasets contains only a few images. Two different datasets COVID-QU-Ex Dataset and COVID-19 Radiography Dataset, were selected to evaluate the segmentation and classification performance as shown in Fig. 1. The COVID-QU-Ex Dataset consists of 33,000 Chest X-ray data together with binary infection masks of three different classes containing 11,955 Covid-19, 11,261 Non-Covid Viral or Bacterial Pneumonia infections and 10,704 Normal cases. On the other hand, the COVID-19 Radiography dataset contains 21165 overall images and their corresponding binary lung mask images. In this dataset, 4 classes have 3616 Covid-19 positive, 10,192 Normal, 6012 Lung Opacity Non-COVID lung infection, and 1345 Viral Pneumonia images.

Inspired by MultiResUNet, modifications of the skip connections will reduce semantic gaps between long skip connections. The pre-trained weights will be used to initialize the encoder part of the proposed model. The Center block will consist of the convolutional block from VGG16 and pass it into the decoder parts of the network. This is simply a bridge between the two parts of the network as shown in Fig. 1. Also, the classification module originates from this block of two novel architectures, one for whole lung segmentation and classification and another for segmenting infection areas as shown in Fig. 2. We will also consider the transfer learning technique. The Decoder block produces the predicted output segmentation mask.

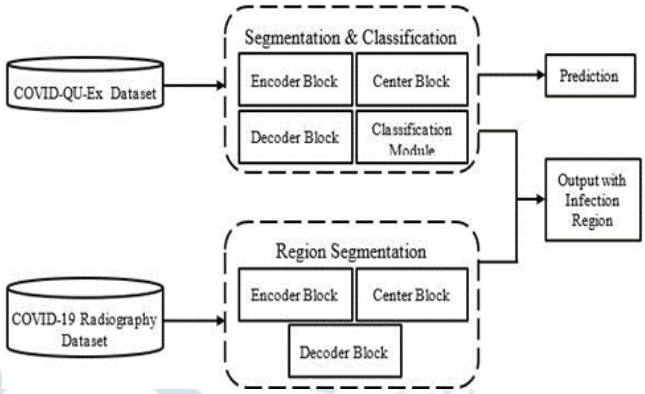

Fig. 1. Proposed network for Lung disease detection and infected region localization

The classification module for the Segmentation-Classification model uses the concept of VGGNet architecture. In convolutional neural networks(CNNs), feature extraction is done automatically by the network, which learns filters that can be used to extract relevant features from the images. The VGG19 pre-trained model is followed by three CNN blocks during the feature extraction stage. Extracted features from encoders will be used for the classification module. A dense layer with 3 neurons will produce the probability of each class as the classification result. The class achieving the highest predicted probability will be the final classification result.

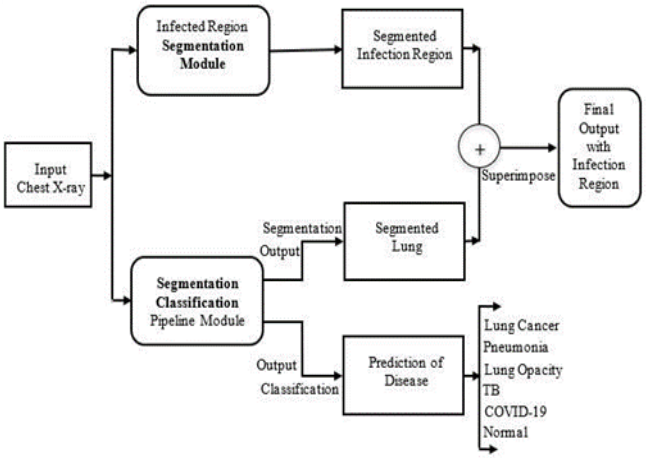

Fig. 2. Overall block diagram for proposed segmentation classification model.

For segmenting the infection areas, we will follow the same system except for the Classification Module. The Decoder Phase will produce output ranging from 0 to 1. As our task is to classify each pixel of the input image into two

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classes, we used this function to generate the output segmentation mask. To reduce the semantic gaps mentioned previously, we will skip the connection. Re-designed skip pathways transform the connectivity of the encoder and decoder sub-networks as shown in Fig. 1. In U-Net, For segmenting the infection areas, we will follow the same system except for the Classification Module. The Decoder Phase will produce output ranging from 0 to 1. As our task is to classify each pixel of the input image into two classes, we used this function to generate the output segmentation mask. To reduce the semantic gaps mentioned previously, we will skip the connection. Re-designed skip pathways transform the connectivity of the encoder and decoder sub-networks as shown in Fig. 1. In U-Net, the feature maps of the encoder are directly received in the decoder. Still, in UNet++, they undergo a dense convolution block whose number of convolution layers depends on the pyramid level. In our proposed model, in the skip pathway, each convolution layer is preceded by a concatenation layer that fuses the output from the previous convolution layer of the same block, which brings the semantic level of the encoder feature maps closer to that of the feature maps awaiting in the decoder and the corresponding up-sampled output of the lower block.

we formulate the skip pathway as follows: let $x^{i,j}$ denote the output of node $X^{i,j}$, where i indexes the down-sampling layer along the encoder and j indexes the convolution layer of the dense block along the skip pathway. The stack of feature maps represented by $x^{i,j}$ is computed as

$$i,j\,\mathcal{H}(x^{i-1,j}), j = 0,\ i > 0$$

$$x = \{\mathcal{H}([x^{i,j-1}, \mathcal{U}(x^{i+1,j-1})]),\ j > 0$$

Where function H(·) is a convolution operation followed by an activation function, U(·) denotes an up-sampling layer, and [ ] denotes the concatenation layer. Basically, nodes at level i = 0 receive only one input from the pre-trained layer of the encoder, and nodes at level j = 0 and i > 0 receive only one input from the previous layer of the encoder; nodes at level j>0 receive two inputs, both from the encoder sub-network and the last input is the up-sampled output from the lower skip pathway.

The Segmentation-Classification model will generate the entire semantic segmented lung mask, which will show the boundaries of the lungs in the Chest X-ray image. On the other hand, the Infection Region Segmentation model will generate the segmented infection region mask, which will show the boundaries of the infected area within the lungs. By superimposing these two masks as shown in Fig.2, the system can localize the infection area in the lungs by extracting the borders of both masks. This will allow the system to determine the exact location of the infection within the lungs. Finally, the extracted areas from both segmented masks will be superimposed on the original Chest X-ray image. To perform disease classification feature architecture was used that comprised 19 CNNs with 3 convolution filters and 1 stride. In the feature extraction step, the output was turned into a one-dimensional data vector, which was then used as an input in the classification stage after being modified through the flattening layer. The remaining components of the categorization step are comprised of three thick layers. It is a thick layer with six neurons and the SoftMax activation function that generates the final classification output as shown in Fig. 2. This can be achieved using a variety of deep learning architectures such as U-Net, Mask R-CNN, or SegNet. Once the lung regions have been segmented, use a classification model to classify the images based on the presence or absence of lung diseases. Evaluate the segmentation and classification models separately to ensure they are performing well. Use metrics such as dice coefficient, precision, recall, and F1- score for segmentation and accuracy, precision, recall, and AUC-ROC for classification. Fine-tune the models and hyperparameters based on the evaluation results to optimize performance. One popular approach is to use a fully convolutional network FCN architecture, which is specifically designed for pixel-wise classification tasks such as segmentation. The FCN can be trained using annotated datasets and can achieve high accuracy in lung segmentation tasks.

IV. EXPERIMENTS AND RESULTS ANALYSIS

The comparison of the proposed model with several baseline models or traditional machine learning approaches to assess its superiority. These results demonstrate the potential of the proposed model to be a valuable tool for medical professionals in analyzing Chest X-rays and making accurate diagnoses. After Monitoring the model's performance on the validation dataset during training to avoid overfitting and was capable of adjusting hyperparameters (learning rate, batch size). After training, evaluate the model's performance on the testing dataset using various metrics, such as accuracy, precision, recall, F1-score, ROC-AUC, and confusion matrix. If the dataset is imbalanced or exhibits bias (e.g., certain diseases are more prevalent), use appropriate techniques like oversampling, under-sampling, or re-weighted loss functions to mitigate these issues. Based on the analysis, fine-tune the model or explore other architectures to improve performance.

A. Lung Segmentation and Disease Classification Model

The proposed Lung Segmentation and Disease Classification model has the ability to perform two tasks, The first task is to segment out the lung portion from the chest X-ray. On the COVID-19 Radiography Dataset, this proposed model gained the top position obtaining the dice score of 97.61% and the Jaccard index of 93.59%. Table III illustrates that the performance of our suggested model is superior to that of the majority of the other models that make use of this dataset. This is demonstrated by the fact that our model outperforms the majority of the other models. By evaluating the relative performances with the following models, we can see that our proposed model obtained the

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highest Jaccard Index among these models but U-Net++ with transfer learning obtained the highest dice coefficient score as it contains a larger number of parameters than the proposed model. But as a lightweight model, our proposed model performs almost better than the other models for the segmentation task. Combine the lung segmentation and disease classification models into a unified pipeline. The segmented lung regions can be used as input for disease classification Comparison between different models for the segmentation task using the COVID-19 Radiography Dataset is summarized in Table I.

TABLE I. Comparison of Different Architectures for Lung Segmentation

	UNET	UNET (TL)	UNET ++	UNET++ (TL)	Our Method
IoU (%)	89.63	91.60	91.73	93.47	93.59
Dice (%)	94.20	95.41	95.65	97.63	97.61

The second stage that the Lung Segmentation and Disease Classification model that has been suggested will take is to classify the specific disease that is shown on the chest X-ray. This will be done in accordance with the suggested model. By competing against other models using the COVID-19 Radiography Dataset, this suggested model was able to attain the best level of accuracy achievable. It was the winner of the competition. The following dataset was subjected to an investigation and comparison with four additional separate models, which are as follows: U-Net without transfer learning, U-Net with transfer learning, U-Net++ without transfer learning, and U-Net++ with transfer learning. Due to the greater number of parameters it possesses compared to the model that was proposed, U-Net++ with transfer learning achieved the highest recall. U-Net++ was able to achieve maximum precision without the use of transfer learning because it has more convolution layers, each of which is capable of extracting better features than the model that was presented. As a result of analyzing how well the following models compare to one another, we can see that the model that we have provided has the highest level of accuracy among all of these models. However, U-Net++ with transfer learning had the maximum recall. This is likely due to the fact that it has a greater number of parameters than the model that was recommended. Having said that, when it comes to the classification problem, the model that we have proposed, in spite of the fact that it is a lightweight model, performs almost as well as the other models do. Table II gives a summary of comparisons done between multiple models for the purpose of the classification task while utilizing the COVID-19 Radiography Dataset. These comparisons were made using the COVID-19 Radiography Dataset.

TABLE II. Comparison of Different Architectures for Disease Classification

Comparison (%)	UNET	UNET (TL)	UNET ++	UNET++ (TL)	Our Method
Precision	89.09	89.18	**90.12**	89.86	89.75
Recall	89.97	89.11	89.64	**89.79**	89.55
Accuracy	91.70	92.79	90.48	92.06	**92.86**

Table III demonstrates that the performance of our suggested model is superior to that of the majority of the other models that use this dataset.

Table III. Comparison of The Proposed Segmentation-Classification Model With Existing Works

Papers	Segmentation DSC	Accuracy	Classification Sensitivity
Yeh et al. [46]	0.88	-	82%
Tabik et al. [37]	0.885	76%	73%
Robert et al.[38]	0.95	84%	82%
Proposed Model	**0.97**	**92.86%**	**89.75%**

B. Infection Region Segmentation Model

The Infection Region Segmentation Model that has been suggested has the capability to isolate the area of the lungs that is infected as a result of any disease using images from the chest X-ray. This model was able to achieve the highest possible score on the COVIDQU- Ex Dataset, which was 87.61%, and it also had an accuracy of 98.23%. The following dataset was subjected to an investigation and comparison with four additional separate models, which are as follows: U-Net without transfer learning, U-Net with transfer learning, U-Net++ without transfer learning, and U-Net++ with transfer learning.

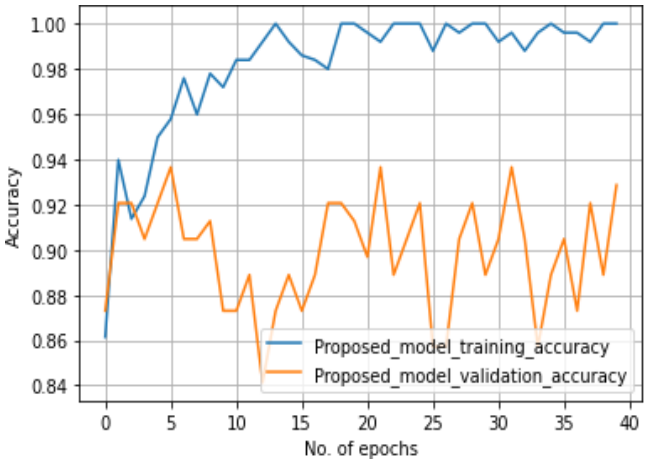

Fig. 3. Progression graph of Classification Module for the proposed model of the accuracy over the number of epochs

The relative performances of the following models are being evaluated, and we can see that our proposed model

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obtained the highest dice coefficient and accuracy among these models; however, U-Net++ with transfer learning obtained the highest Jaccard Index scores because it contains a greater number of parameters than the proposed model does. This is because the proposed model contains fewer parameters than U-Net++ with transfer learning does. However, in spite of the fact that it is a very simple model, the one that we have suggested does the segmentation task nearly as effectively as the models that were shown previously. Table IV presents a summary of the comparison that was done between the various models for the segmentation job while employing the COVID-QU-Ex Dataset. This comparison was done so that the COVID-QU-Ex Dataset could be used.

Table IV. Comparison of Different Architectures for Infection Localization

	UNET	UNET (TL)	UNET ++	UNET ++(TL)	Our Method
IoU (%)	93.67	95.42	96.41	**97.70**	97.67
Dice (%)	73.50	76.52	77.68	84.94	**87.61**
Accuracy	94.53	96.35	95.19	96.03	**98.23**

Table V. Comparison of Proposed Infection Model With Existing Works

Papers	Accuracy	DSC	IoU
Anas et al. [[1]	97.99%	**88.10%**	83.1%
Covid-MANet [47]	97.01%	86.15%	76.94%
Proposed module	**98.23%**	87.61%	**97.67%**

Table V. shows that our proposed infection segmentation model performs better than most of the existing models using this dataset.

V. CONCLUSION

We began by conducting research on the most recent architectural designs, SegNet and UNet. During the down-sampling process, it has been discovered that certain boundary information is lost in architectures such as Seg-Net. The significant semantic gap that is produced by long skip connections results in a loss of accuracy in the UNet design. UNet++ is offered as a means of closing the semantic gap. However, the computing cost may be high, especially when dealing with extensive or complicated datasets. Because of this, it might be challenging to train and use UNet++ models in applications that run in real-time. UNet++ models are susceptible to overfitting, especially in situations when there is a shortage of training data. Additionally, we have outlined the one-of-a-kind difficulties associated with biomedical picture segmentation. We presented a new lightweight architecture that incorporates transfer learning technology, modified skip connections, and a classification module in order to solve all of the problems that have been outlined above. As a result of having fewer parameters than UNet++ does, this architecture is more efficient than the latter. Because of this, the suggested model is less likely to result in overfitting when given a small training dataset, which is something that frequently occurs in the field of biomedical imaging. Additionally, the trimmed version can be employed in the event of tasks that are easier, and in that scenario, the number of parameters is reduced an even greater amount. We demonstrated that our model has a greater capability for exact segmentation boundaries, that it can reduce the number of false positives and false negatives, and that it has a greater capacity for rapid learning through a variety of in-depth tests. The robustness of our model may also be seen through its performance over the dice coefficient and the Jaccard index.

After that, we performed an in-depth analysis of our suggested architectural design. We conducted in-depth experiments with all three components to demonstrate their usefulness in accurate and exact disease categorization as well as chest X-ray picture segmentation. Our model was trained just as successfully as the earlier architectural iterations.

We monitored the performance using metrics such as the Jaccard Index and dice on the segmentation output, as well as precision, recall, and accuracy on the classification output. As a result of our experiment, we discovered that the categorization module, when applied to UNet, assists the model in achieving greater precision, recall, and accuracy; however, this also results in a tiny reduction in IOU and dice. The Nested path in UNet++ allows the model to improve its segmentation performance by raising the score of the evaluation metrics. This can be seen in the table below. However, it is a complex architecture, and it takes an excessive amount of time to converge. Additionally, someone may have difficulty deploying the model to a platform with restricted resources.

Learning that can be applied to new situations significantly contributes, as well, to the overall improvement in score. By utilizing the transfer learning strategy, the model is also able to achieve convergence at a faster rate. It is clear to observe that incorporating transfer learning into the UNet and UNet++ architectures results in a significant reduction in the amount of time required for the training phase. Additionally, the infection region segmentation module performed exceptionally well in this proposed model. In addition to that, the percentage of the chest that is affected is displayed. We can determine whether or not our model is accurate by comparing the predicted mask to the real mask and examining the results. In addition to this, the matrices demonstrate the infection region segmentation and localization module's reliability as well as its efficiency. Therefore, the significance of our proposed architecture is investigated, and its efficacy in detecting chest diseases and locating infection regions was demonstrated through this case study.

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