# A Modified Dense-UNet for Pulmonary Nodule Segmentation

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**Abstract.** Lung cancer continues to be a major health concern worldwide, taking countless lives every year. Although the detection of lung nodules has been made versatile by using CT scans, radiologists require certain assistance to make this process faster and more efficient. This need led to the introduction of Computer Aided Diagnosis (CAD) and then, deep learning into the healthcare field. In this work, we have proposed a modified 2D Dense-UNet model for the segmentation of lung nodules from the CT scan images. The model is trained and tested on the LUNA16 dataset which is publicly available. Through the addition of Squeeze & Excitation (SE) blocks and the GeLU activation function in its dense layers, some improvement has been observed in the basic model. Furthermore, we have also compared our suggested model's performance to that of various other 2D deep learning networks on the basis of their Dice Coefficient (DSC).

**Keywords:** Pulmonary Nodule Segmentation, Deep Learning, Convolutional Neural Network, UNet, Squeeze and Excitation

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## 1 Introduction

Throughout the world, lung cancer is a serious health problem. Not only is it the primary cause of cancer-related demises globally [20], but also it is the second most common type of cancer [3]. According to estimates, every year India reports about 13.9 Lakhs new cases of lung cancer till 2022 [1]. Due to the low diagnosis rate of 15% [2], there is an increment in the fatality rates.

If lung cancer is recognized in its earlier stages, the rate of survival is incremented from 10-15% to a promising 60-80%. Lung cancer has been diagnosed and detected using chest X-rays and CT pictures. The common method for detecting lung cancer is through CT scan images of the lungs. Although it is versatile, the number of scans produced here is large and takes time to analyze. Moreover, there are cases when minute nodules present in the lungs might be missed. Thus, in order to aid radiologists in lung cancer identification and diagnosis, CAD was introduced in this field.

Throughout the years, the application of CAD for the purpose of lung cancer detection using CT images has been researched. It presented many advantages such as greater speed of numerical calculation which further enabled precise measurements, an ever-growing base of diagnostic information and the resistance to fatigue. Multiple factors of the image including grayscale distribution, texture features and volume of the lung nodule are analysed to aid the differential diagnosis of the lung nodules.

Segmentation of lung nodules is a crucial step involved in the detection of lung cancer and is also challenging as the nodules have size and shape similarities with their surroundings. It involves the extraction of the shape or profile of the lung nodule for quantification like measurement, composition and malignancy analysis. This medical image processing technique aims to detect and distinguish irregular or round-shaped lesions from the lungs, which could possibly indicate cancer. Deep learning (DL) models [17] utilize different algorithms and networks to perform this.

In recent times, DL-based methods are being researched for lung nodule segmentation due to their better accuracy as compared to basic ML techniques. DL-based models can be applied to a vast amount of data and can be optimized easily. They utilize Convolutional Neural Networks (CNN) [12, 19] which contour the nodule voxels. CNN comprises neurons that self-optimize through learning. They are employed in the area of image pattern recognition, allowing us to encrypt particular image-specific features into the architecture. This makes it suitable for the task of nodule segmentation from CT images.

UNet is one of the most used structures. It is a CNN built mainly to perform the segmentation of medical images. The decoder and the encoder units present in this symmetrically combine to form a U-Shaped architecture. A lot of research has been done to use UNet as the base and then developing architectures which give efficient segmentation results, but most of the work done till now is 3D UNet inspired. Although 3D captures more information and gives good results it requires high processing speed and equipment to run on large scale efficiently and is also costly which can be a limitation to it being accessible to larger masses. Thus, we worked towards improving the segmentation problem in 2D by introducing different layers and blocks in the 2D UNet architecture to get better results for pulmonary nodule segmentation.

We used the publicly available LUNA-16 dataset and following is a summary of main contributions of our work:

1. We propose a Squeeze-and-Excitation Dense-UNet (SE Dense-UNet).
2. Introduction of dense layers and connections improves density and the network performance as each of the layers has access to the features learned by the previous layers
3. Addition of SE block in the decoder layer enables the model to capture the interdependencies existing between the channels in the feature maps, which further aid in identifying more informative and descriptive features.

This paper is divided into the following sections: Introduction, Related Works, Data and Methods, Results, and Conclusion & Future Work.

## 2 Related Works

Research over the years has shown that UNet is amongst the most efficient fully convolutional networks for segmenting biomedical images and thus has been used as a base by many researchers for developing powerful models for lung nodule segmentation. To enhance its performance various changes have been proposed and tested by different researchers on both its 2D and 3D architecture. Proposed improvements range from morphological changes in data preprocessing, adding layers, trying different optimizers, and integration of techniques. With the aim to enhance the performance of 2D UNet, Liangsheng Wu et al.[23] suggested methods to be undertaken during preprocessing in order to obtain better segmentation results for pulmonary nodules. Tiequn Tang et al.[21] suggested a network with complementary features which used several approaches to bring out both low-level and high-level local features and then combined them. An enhanced model built on the UNet network was presented by Guofeng Tong et al.[22]. The network was upgraded primarily by recreating the dataset and adding convolutional, pooling, and upsampled layers. They also added a residual network, which enhanced the benefits of network training. Niranjan Kumar S. et al.[11] tried different optimizers with UNet for segmentation to find the best results. They applied Adadelta, SGD(Stochastic Gradient Descent), Adam, and Adagrad optimizers. The most efficient results were obtained by the Adam optimizer. Zeeshan Ali et al.[4] made use of densely connected dilated convolutions; their method aimed to improve the feature learning mechanism and thus build an efficient end-to-end segmentation algorithm. Nikhil Varma Keetha et al.[9] proposed U-Det, an end-to-end resource-efficient model. To boost segmentation efficiency, this model employed the Mish activation function, mask class weights, and a bidirectional feature network between its decoder and encoder. In order to optimize feature transmission and network utilization while also accelerating feature extraction, Ying Zhou et al.[26] suggested an approach that combined the MobileNetV2 network and switched from conventional to deep separation convolution [15, 8]. Through the combination of Atrous convolution blocks with densely and compactly riched convolution blocks, the strategy suggested by Muazzam Maqsood et al.[14] ensured that the coverage and loss data were not sacrificed and the range of filters was broadened. Zhitao Xiao et al.[24] in 2020 described the 3D-Res2UNet approach for the segmentation of pulmonary nodules, which is built on Res2Net and 3D-UNet.

The UNet network is utilised as a foundation for constructing models not only for lung nodule segmentation, but also for a variety of other segmentation challenges in the medical area. For the purpose of segmenting the liver and tumors, Xiaomeng Li et al.[13] developed a new hybrid densely connected UNet that combined a 3D DenseUNet for hierarchically accumulating volumetric contexts with a 2D counterpart for effectively obtaining intra-slice attributes. For segmentation technology of Multiphoton Microscopy(MPM), a novel Dense-UNet deep learning segmentation model was suggested by Sijing Cai et al.[5]. This model used dense concatenation to accomplish feature reuse and deepen the depth of the network design. A modified UNet network (SD-UNet) was suggested by Shuangcai Yin et al.[25], combining a global context with data from multiple scales to efficiently enhance COVID-19 infections segmentation impact. Dense atrous spatial pyramid pooling (Dense ASPP) and Squeeze-and-attention (SA) components were combined in this network. Pengfei Cheng et al.[7] proposed a two-stage Dense-U-Net deep learning method for automatic segmentation and localization of CT vertebrae. In the first step, vertebrae were located using a 2D-Dense-U-Net that detected the centroids of the vertebrae using 2D slices and dense labels. The second step used 3D-Dense-U-Net to segment a particular vertebra within a ROI located based on the centroid. Finally, a spine was created by joining all of the segmented vertebrae together and resampling it at the initial resolution. Martin Kolarík et al.[10] aimed to test the concept that the segmentation U-net type networks could have residual and dense interconnections. Deep neural networks for classification frequently use this concept. In accordance with the primary 3D U-Net, they developed and evaluated the Dense-UNet and ResidualUNet networks. Their findings showed that employing dense and residual interconnections might assist to provide considerably better outcomes, but it was computationally expensive in regards to both memory and time needed.

## 3 Data and Methods

This section describes the data and the model architecture we have used to perform the segmentation of the lung nodules. The Figure1 provides a diagrammatic representation of the proposed methodology.

### 3.1 Dataset

For training and testing our model, we used the publicly available LUNA16 dataset. It consists of 888 CT scan images generated from the LIDC/IDRI database which have thickness of slice less than 2.5mm. This dataset includes the annotations from the LIDC database that have been accepted by at least 3 of the 4 radiologists and have a nodule diameter of 3 mm or more, totaling 1186 nodules.

### 3.2 Preprocessing

The unwanted objects present in the CT images can lead to poor performance of the model if used whilst training. We used the LUNA16 dataset for training and testing our model. Every CT scan present in this dataset is a 3D medical image that consists of multiple slices representing the different cross-sectional views of the lungs. Since the dataset consisted of MHD files, the SimpleITK python library was used to read the dataset and extract lung images of 512 x 512 dimension. OpenCV library is used for a variety of preprocessing techniques which have been discussed in detail below:

1. Applying CLAHE: Contrast Limited Adaptive Histogram Equalization was performed to balance the contrast in CT images using the cv2.createCLAHE function.

2. Binary Thresholding: To convert photos to binary form, binary thresholding is used. The threshold value was determined by using K-means clustering to divide the images into 2 clusters based on bright and dark pixels, and then taking the mean of the centroid of the clusters as the threshold value.

3. Erosion and Dilation: Images obtained after binary thresholding are passed through dilate and erode methods present in the OpenCV library to remove noise, blood vessels and bumps from the images. Dilation enlarges the images whereas erosion shrinks the images.

4. Filling Holes: After erosion and dilation lung images are extracted by removing the region which is close to the boundary of the image as the lungs are situated near the center. Then, using the findContours, drawContours, and other methods present in the OpenCV library, holes in these images are filled using the Contour filling approach.

5. Extracting lungs and nodule masks: Lungs (ROI) are finally segmented with the help of masks obtained after drawing Contours. Nodule masks are

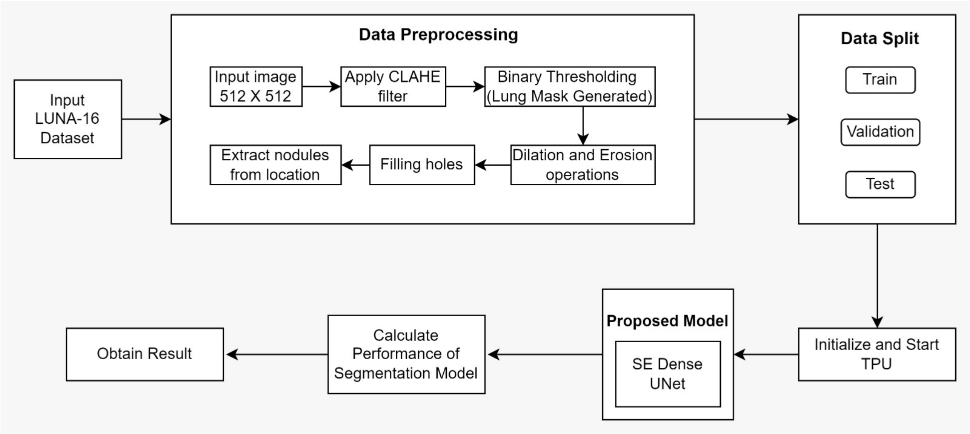

**Figure 1:** Proposed Methodology

extracted by taking nodule location from the annotations file and extracting a circular region around the spot.

Figure 2 shows the images obtained after some preprocessing steps: (a) is the original CT scan image from the dataset (b) image is obtained after applying CLAHE (c) image is obtained after binary thresholding (d) image is obtained after filling holes using contours and (e) is the final segmented lung ROI.

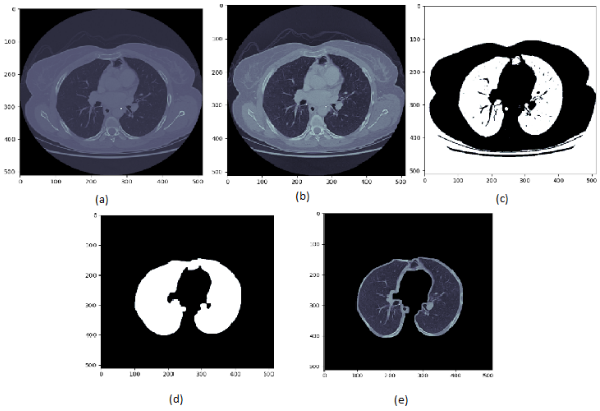

**Figure 2:** Images obtained during preprocessing

### 3.3 Structure of SE Blocks Used

In recent years, the application of SE blocks to various deep learning models has increased. This is mainly to better the ability of the neural networks to map the dependencies existing between the channels. Due to the usage of 2D images in the model, it becomes necessary to preserve as many necessary features as possible. Moreover, these blocks provide access to global information. In Figure 3, the structure of the SE blocks added in the decoders of the model is shown. At first, the squeeze operation was performed which had a convolutional layer as input. Here, the spatial dimension of the feature maps was reduced while also preserving the channel dimension. Every channel was then squeezed into a single numerical value through 2D Global Average Pooling, which represented the significance of that channel in capturing features.

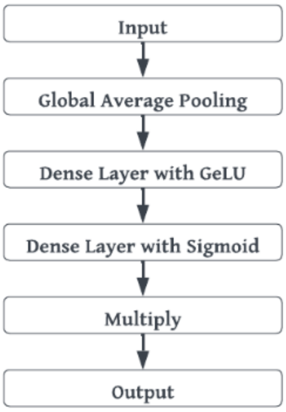

**Figure 3:** Structure of SE Block used

Further, two dense layers were applied. In order to introduce non-linearity, the first dense layer used the GeLU activation function while also reducing the complexity of the channel by a particular ratio. We used the ratio of 16. Then, the second dense layer utilizes the sigmoid activation function that generates a set of scalar weights for each channel. The original feature maps are then multiplied with these weights to produce a refined set of features. This is the excitation operation.

### 3.4 Structure of SE Dense-UNet

In this paper, we propose a 2D SE Dense-UNet architecture which is inspired by the original UNet model. Its architecture is shown in Figure 4. UNet is a CNN architecture which was designed primarily to perform image segmentation. It consists of two major parts - the encoder and the decoder, which are connected to each other through a bottleneck layer. There are many convolutional and pooling layers present in the encoder which reduce the dimensions of the image while maintaining the important features. The decoder, on the other hand, consists of up-convolution and concatenation layers. It merges the information gathered from the encoder layers and also, restores tries to restore the original spatial resolution of the image. Although this UNet architecture proved to be versatile in certain cases, it suffered from a major drawback. There were certain objects that were more complex or large to fit into the encoder & decoder architecture of the UNet. This inspired the Dense-UNet architecture.

There is dense connectivity present in the Dense-UNet. This essentially means that all the layers in this architecture are connected to every other layer. Thus, the information is shared between all the layers and the architecture is utilized more efficiently. We recognized that there are certain limitations within the Dense-UNet architecture. It has high computational cost and even suffers from overfitting in certain cases. Hence, we propose the introduction of Squeeze & Excitation (SE) blocks in the decoder. Through the selective weighing of channels in each feature map, these blocks reduce the number of parameters needed to represent the data. Not only that, it can increase the capacity of the channel to deal with complex segmentation tasks through its ability to adaptively adjust the feature maps. Every CT slice in the input dataset is of dimensions 512 by 512 and is a grayscale image.

There are in total five blocks present in the encoding path. These consist of two 3X3 2D convolution layers which are separated by a concatenation layer. The second 2D convolution layer is followed by the concatenation layer which performs its operation on the output generated by that layer. In order to improve performance, the GeLU activation function is used on these 2D convolution layers. The function is described below:

$$\begin{aligned} GELU(x) &= xP(X \leq x) = x\Phi(x) \\ &= x \cdot \tfrac{1}{2}[1 + erf(x/\sqrt{2})] \end{aligned}$$

$if X \sim N(0,1)$

The purpose of using GeLU over ReLU were:

1. It has smooth function, meaning it is differentiable and continuous throughout the input range. This ensures that small changes in the input ensures that there would be changes in the output as well.

2. While the ReLU activation produces zero output for negative inputs, GeLU produces non-zero output. This feature is essential for segmentation since certain image features may have negative intensity values that are needed for accurate segmentation.

A Dense layer is then added which takes input from the concatenation layer and uses ReLU activation function. In order to reduce overfitting in the neural network, we pass the input from the dense layer to a dropout layer having 0.4 dropout rate. This is summarized below:

1. 2D Convolutional Layer with GeLU activation
2. Concatenation Layer
3. 2D Convolutional Layer with GeLU activation
4. Concatenation Layer
5. Dense Layer
6. Dropout Layer with rate of 0.4
7. 2D MaxPooling Layer

The dimensions of the output generated by these five encoder blocks are 32X32, 64X64, 128X128, 256X256, and 512X512 respectively and the number of channels continues to be 1 throughout these blocks. While the encoding path extracts important features from the CT scan images, the decoding path essentially takes these features and develops their respective segmentation masks.There are four decoder blocks in this path.

First, an upsampling layer is introduced in the block. This layer concatenates the output which is generated from the 2D transpose convolution layer (or the deconvolutional layer). Then we pass the output generated from the upsampling layer through a SE block. Through the introduction of the SE block in our model, there is an improvement in the channel interdependencies. These are then followed by two convolutional layers which are separated by a concatenation layer. Second convolutional layers output is passed through another concatenation layer. Finally, in the decoder block the dropout layer is added with a dropout rate of 0.4. The last output layer consists of a simple 2D convolutional layer with sigmoid activation.

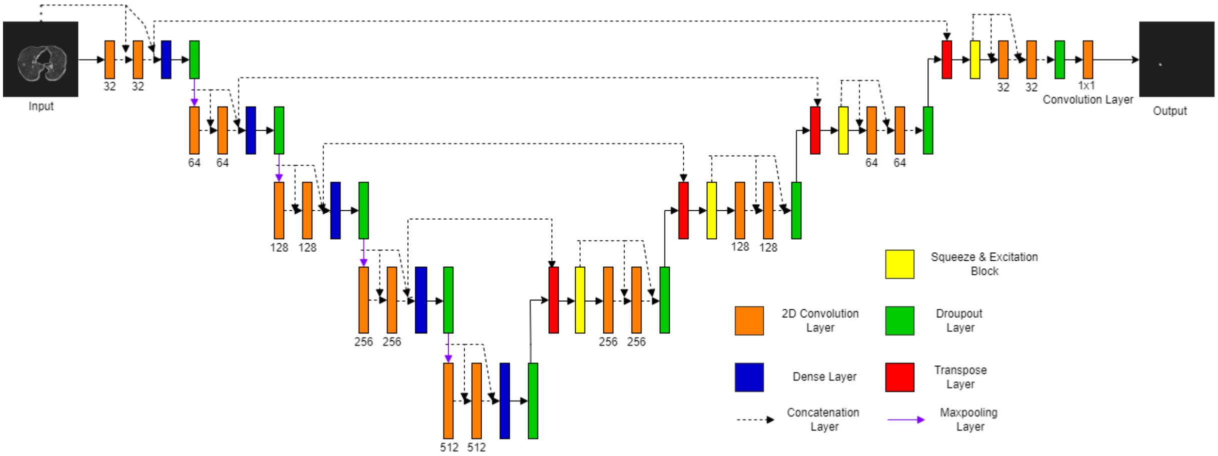

**Figure 4:** Model Architecture

This is summarized below:

1. 2D Transpose Layer
2. Concatenation Layer
3. SE Block
4. 2D Convolutional Layer with GeLU activation
5. Concatenation Layer connected to the corresponding convolutional layer in encoder
6. 2D Convolutional Layer with GeLU activation
7. Concatenation Layer connected to the corresponding convolutional layer in encoder
8. Dropout Layer with rate 0.4

The dimensions of the output generated in these four decoder blocks are 256X256, 128X128, 64X64, and 32X32 respectively and the number of channels remains one.

# 4 Results

## 4.1 Experimental Setup

The proposed model was trained using the Tensor Processing Units (TPU) accelerator available on Kaggle Notebooks. They perform faster and more efficient large matrix operations which minimizes the time-to-accuracy while training large and complex neural networks. In comparison to GPUs, their speed is better because of which, they were preferred to train our model. The Kaggle Notebook environment is built on the Google Cloud Platform (GCP) and provides users with a Jupyter notebook interface. There was about 16 GB RAM and 73 GB disk space available on Kaggle when used with TPU. We used the Kaggle TPU V3.8 for training the model with the Adam optimizer at a learning rate of 2e-4 for 1000 epochs.

## 4.2 Model Performance

Since the LUNA16 dataset is large and unbalanced, dice coefficient (DSC), Jaccard Index (IoU), dice loss and binary accuracy have been used for the modelâs performance evaluation. The preprocessed LUNA16 dataset was split into 10% validation data, 10% testing data, and 80% training data. The maximum Dice Score was obtained after training the model with the Adam optimizer at a learning rate of 2e-4 for 1000 epochs. Dice Loss was 14.39%, Binary accuracy was 99.98% and IoU was 73.65%

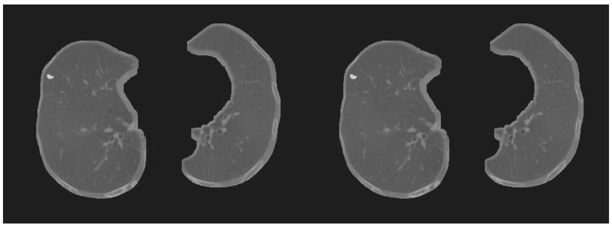

**Figure 5:** Actual vs Predicted Values

The actual location of the nodule and the one predicted by our model is shown in Figure 5. On the left, the shape and location of the nodule inside the lung observed by the radiologists are shown whereas the right shows the predicted ones. In Figure 6, the DSC of the validation and training dataset is shown whilst the model was training, where the green graph line is for the validation data and the blue is for the training data.

There is a gradual increase in the value of the dice coefficient, but it starts to fall in the same region after a certain number of epochs causing the line to become somewhat straight. The same goes for the plot for IoU in Figure 7, showing the IoU values for the validation and training dataset. The reason for the straight line after gradual increase could be the limitation in the dataset or even, not enough learning rate.

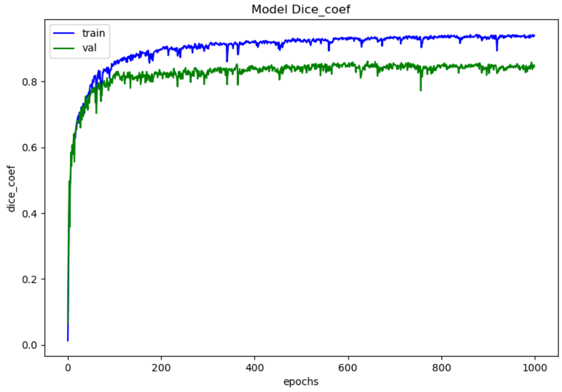

**Figure 6:** Epochs vs DSC for our work

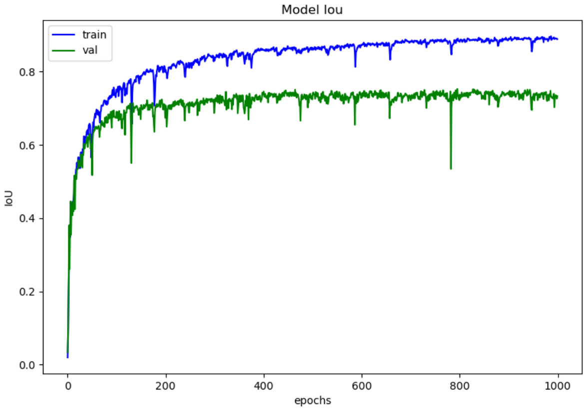

**Figure 7:** Epochs vs IoU for our work

The dice loss for the validation and training datasets is shown in Figure 8. There is a steady reduction in value, and then there isn't much change. after some epochs.

### 4.3 Comparison with other models

We compared our model's performance with some other 2D deep learning segmentation models. Table 1 provides a summary of the models proposed and the DSC obtained from the works done by other researchers for lung nodule segmentation. From the table, we can conclude that our model performs better than the mentioned works.

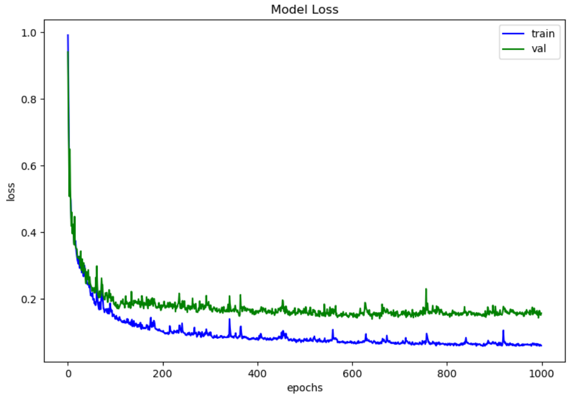

**Figure 8:** Epochs vs Dice Loss for our work

**Table 1:** Comparision with other 2D deep learning segmentation models in terms of their DSC

| *Work* | *Algorithm* | *DSC*(%) |
|---|---|---|
| *Ronneberger et al.*[18] | *UNet* | 77.15 |
| *Ali et al.*[4] | *Dilated Convolution* | 81.1 |
| *Cao et al.*[6] | *DB − ResNet* | 82.74 |
| *Wu et al.*[23] | *UNet with Dice Loss* | 83.24 |
| *Our Work* | *Dense − UNet* | 84.68 |
| *Our Work* | *SE Dense − UNet* | 85.77 |

## 5 Conclusion & Future Work

In our work, we proposed a SE Dense-UNet model for 2-D lung nodule segmentation. The LUNA-16 dataset on which the model was trained went through a series of preprocessing steps to obtain lung ROI and nodule mask. The Adam optimizer was used to train it for 1000 epochs, and the GeLU activation function was employed in its convolution layers. For improving the density of the network, the Dense layer was introduced in the encoder to avoid over-fitting, Dropout layers were added in both the decoder and the encoder with a dropout rate of 0.4 and to track the loss experienced by it, the dice loss function was used. Our model on evaluation gave a DSC of 85.77%, IoU of 73.65% and binary accuracy of 99.98%.

In the future, work can be done to implement a 3-D version of our model exploring volumetric segmentation for a more holistic representation of lung nodules. We can then evaluate its performance on 3D dataset to assess its potential in clinical applications. One can further look into the model's potential for generalization and possible applications in a wider variety of medical segmentation scenarios. As mentioned, there are certain limitations to the extent our model could be trained. Thus, work can be done to pre-process the data more efficiently. Furthermore, our work can be extended for the classification of the segmented nodules as benign and malignant. Adapting the model for specialized tasks could enhance its utility in targeted clinical applications.

Working in tandem with radiologists, clinicians, or medical institutions will be beneficial in the future for a thorough assessment of the SE Dense-UNet model in a clinical context. After getting their input, one canÂ evaluate how well the model works with the diagnostic procedure and work on makingÂ iterative improvements based on real-world observations. Another potential future application is the creation of user-friendly interfaces to improve accessibility for radiologists and medical practitioners.

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