## A Brief Description of My Thesis

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Thesis Title: Pulmonary Nodule Detection Based on Deep Learning

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Lung cancer is an aggressive disease resulting in more than one million deaths per year worldwide. Sometimes there is a suspicious tissue in the lungs, referred to as a lung nodule. In the early stages, lung cancer generally manifests in the form of pulmonary nodules, and to determine if someone will develop lung cancer, we have to look for the early stages of malignant pulmonary nodules. Pulmonary nodules have different types and forms, and even all of them are not malignant or cancerous. This significant difference in the shape of nodules, as well as their small size, makes nodule detection more difficult. An example of CT images is shown in Figure 1.



Figure 1- An example of CT images in three different views. From left to right respectively: axial, sagittal, and coronal views. The lung nodule in these images is marked using a red bounding box.

In my thesis, I have tried to study lung cancer screening based on deep learning. Designing a system for lung cancer screening starts with preparing the data and the labels for training the network. A voxel value in a CT image represents the radiodensity of a tissue and is measured with the Hounsfield meter. Therefore, all pixel values of a CT image should be transferred to the Hounsfield meter. By applying a modified normalization filter, morphological erosion and dilation filter, K-means algorithm, and some other techniques, the lung areas are segmented. Therefore, other tissues that do not contain any information about nodules are removed, and the data is ready to be fed to the model. Additionally, the mask labels are obtained based on the nodule coordinates, the minimum diameter of nodules, and the maximum diameter of nodules. Figure 2 shows an example of lung segmentation.

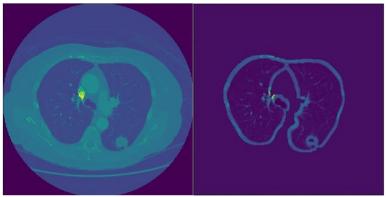


Figure 2- Original CT image and the corresponding segmented lungs (after performing pre-process steps)

In this research, a deep neural network is proposed for lung nodule segmentation using 2D slices of Chest CT images. For the encoder part of this network, the <u>Neural Architecture Search</u> (NASNet) is adopted, which is a powerful feature extractor. For the decoder part, <u>Global Convolutional Network</u> (GCN) as well as <u>Squeeze and Excitation Network</u> (SE) are proposed to help the model to reconstruct the final segmentation map in a more accurate way compared to the existing segmentation models in the field of Medical Image Analysis. GCNs avoid sparse connections and enable densely connections within a large k×k region in the feature map and utilizes a combination of k×1+1×k and 1×k+k×1 convolutions to implement the k×k convolution effectively with a lower number of parameters compared to the trivial k×k convolution. In order to effectively integrate the multi-level features, I propose using a channel attention mechanism by applying the SE block. The Channel attention mechanism enables the network to weight the channels adaptively to get more discriminative features.

Furthermore, a summation of Generalized Dice Loss (GDL) and weighted cross-entropy (WCE) is used as the loss function to train the network. This loss function gives the network the ability to overcome the nodules class imbalance problem. Different data augmentation approaches are also used to solve the overfitting issue. The output of the network is a binary mask in which the lung nodule is identified and segmented. In this way, I was able to solve this localization problem (lung nodule detection) by considering it as a segmentation task and designing a powerful network. The proposed method achieved 69.96 and 80.12 in terms of dice coefficient and sensitivity measures respectively. Figure 3 shows an overview of the proposed architecture for lung nodule segmentation.

The LIDC-IDRI and the LUNA16 datasets are used for training and testing the proposed network, respectively. All the pre-processing steps, network architecture, and post-processing steps are implemented in Python using Tensorflow framework. The PyTable library is used to control the input data flow and keras sequence method for data augmentation. To further improve the speed and efficiency, multi-processing capability of CPU is used in order to parallelize all the processes.

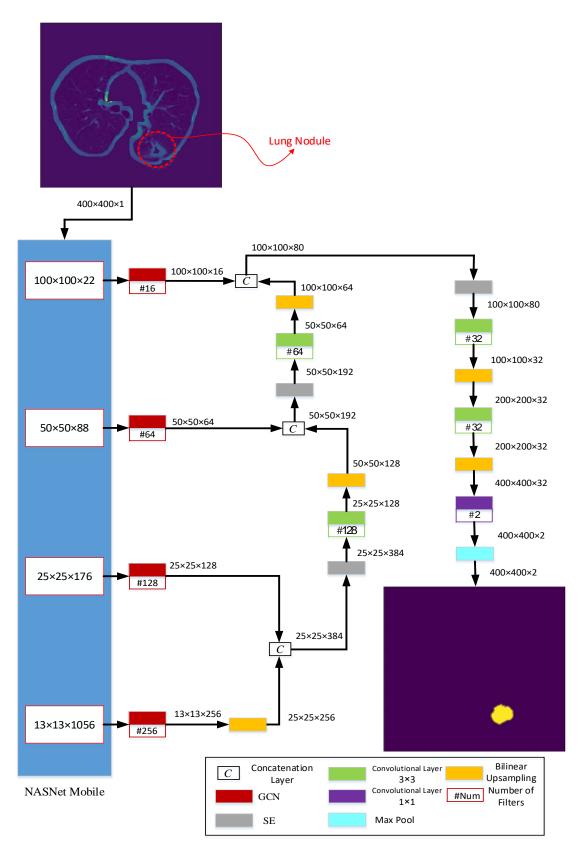


Figure 3-Propsed architecture for pulmonary nodule segmentation