

Deep Learning-Based Detection Of Lung Nodules From Ct Scans

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Abstract

Patients with lung cancer frequently have a bad prognosis if the disease is not detected early. In order to visualize interior organs and tissues and identify illnesses, medical imaging is crucial. X-rays, CT scans, and PET scans are commonly used in lung cancer screening; CT scans are preferred since they offer detailed information on lung cancers. Medical imaging is a complicated and time-consuming method of detecting lung cancer. The increasing number of cancer patients, exacerbated by the COVID pandemic, has placed a significant strain on radiologists, who are already in short supply. An Indian report indicates that there is only one radiologist available for every one hundred thousand patients. Consequently, there is a pressing need for automated diagnostic techniques to aid physicians in promptly analysing patients and making swift treatment decisions. Semantic segmentation is crucial for evaluating the disease or identifying any abnormalities in bodily organs. Initially, traditional approaches relied on basic image processing or machine learning techniques, which necessitated extensive manual pre-processing. However, the advent of deep learning has provided a robust and automated solution. Recent advancements in deep learning are pivotal in enhancing the analysis of medical images, facilitating more efficient disease diagnosis, alleviating the workload on radiologists, and supporting physicians in making precise treatment choices.

Keywords: Lung Nodules, Medical imaging, segmentation, Deep learning

INTRODUCTION

Lung cancer continues to be the leading cause of cancer death worldwide. Low-dose computed tomography (CT) scanning of high-risk individuals has been shown to decrease death rates due to lung cancer[1]. Type II errors are the most costly and detrimental in cancer and are most common in lung cancer studies. Diagnosis of lung cancer can involve several issues with reading and interpretation, though many of these may be circumvented by the use of a second reader[2]. The large population of persons at increased risk for lung cancer can make regular screening, with or without the aid of a second reader, a significant workflow and workload problem for radiologists and clinical personnel[3]. Conversely, computer-aided detection (CAD) systems can help radiologists screen for lung cancer by reducing reading times or acting as a second reviewer [9]. Lung cancer is the second most prevalent cancer globally and also the leading killer cancer in the world. In 2020, the report from GLOBOCAN confirms that the incidence of lung cancer is 11.4% and mortality stands at 18%. This ranks it as the second most frequent cancer after breast cancer[5]. Interestingly, 2018 had the highest numbers for lung cancer incidence and mortality, according to the GLOBOCAN report for that year [4]. Figure 1.1 indicates the incidence and mortality rates for the eight most frequent malignancies in 2020. The five-year survival rate for all individuals with lung cancer is 21% globally; the chances are much worse for those diagnosed at a later stage. Early diagnosis is important for enhancing survival chances, although it is typically diagnosed in the advanced stages in lung cancer[7]. According to a study conducted by Indian hospitals in 2020, it was discovered that nearly 90% of India's lung cancer patients were diagnosed with lung cancer in its advanced stage [10].

REVIEW OF LITERATURE

Application of deep learning for early diagnosis and therapeutic assessment of lung cancer consists of literature reviews of deep learning techniques applied to lung cancer segmentation, staging classification, and response to treatment.

The four groups into which the second criterion divides nodules are juxta-pleural nodules, juxta-vascular nodules, well-circumscribed nodules, and nodules with a pleural tail. A sharply defined lesion, also called a solitary pulmonary nodule, is surrounded by aerated lung parenchyma and is typically of regular form. A nodule that is attached to the lung wall or pleura is called a juxta-pleural nodule [6]. A pleural tail nodule has a thin base attached to the lung wall. A juxta-vascular nodule, conversely, is attached to neighbouring blood vessels. Nodules greater than 30 mm are typically regarded as being malignant, suggesting a large tumor or gross tumor mass. Lung cancer can be divided into two main types according to the microscopic features of the cancer cells: small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). The most common type, NSCLC, represents 80–85% of all diagnoses of lung cancer. The TNM staging system determines the stages of both types. But in the case of planning for therapy of small cell lung cancer (SCLC), physicians primarily focus on two stages: limited and extensive[8]. A single lung or a lymph node on one side of the chest may be affected by cancer cells that are exclusive to that side in the limited stage. On the other hand, the widespread stage signifies that the cancer has metastasized to both sides of the chest and possibly other parts of the body. Rapid growth and spread are hallmarks of small cell lung cancer, which can be lethal in a matter of weeks. Consequently, it is imperative for physicians to make critical treatment decisions swiftly. However, it is not uncommon for doctors to also utilize the TNM staging system for SCLC, leading to variations in treatment decisions based on individual patient circumstances.

MATERIALS AND METHODS

Lung cancer is typically identified at advanced stages when the disease has significantly progressed, leading to the formation of large and irregular tumors. To facilitate analysis and enable physicians to formulate suitable treatment strategies, it is essential to segment the lung tumor. In this chapter, we present three methodologies for lung tumor segmentation. Both up-sampling and down-sampling steps utilize 3D convolutional layers with a kernel size of $3 \times 3 \times 3$. All except the final layer apply the ReLU activation function to each convolutional layer. The vanishing gradient issue is effectively addressed by the Rectified Linear Unit, or ReLU, which outputs zero when the input is negative and the input value when positive. In addition, batch normalization is applied after each convolutional layer to reduce the impact of internal covariate shift, which also reduces network overfitting.

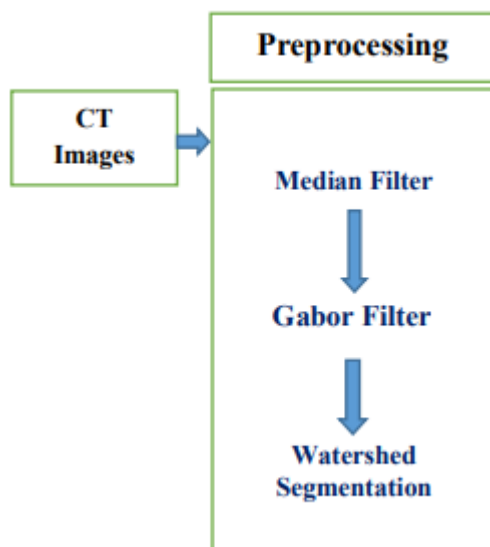


Figure 1: Image Manipulation System

In order to prevent overfitting, the encoder is set to have a dropout rate of 0.1. The encoder applies 3D max-pooling layers with a pool size of $2 \times 2 \times 2$ to reduce the feature map. But the decoder utilizes 3D up-sampling layers with the same pool size to increase the features. Figure 3.1 illustrates the structure of the proposed network. The network takes as input a $256 \times 256 \times 16$ image. The encoder block produces the high-level features, which the decoder blocks up-sample to generate the final tumor masks. To maintain crucial high-level tumor information, the encoder and decoder form skip connections. Also,

there are tight relationships among convolutional layers so that feature maps from all the previous layers can be used as input for every layer and output feature maps of every layer can be used as input for all the following layers. By improving the network's capacity to learn feature maps more precisely, this architecture improves overall performance.

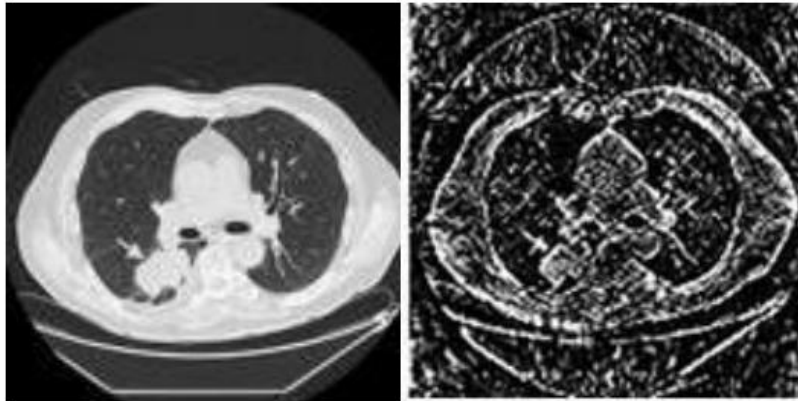


Figure 2: The original image and result of ZCA Whitening

Lastly, a pointwise 3D convolutional layer with a sigmoid activation function and a kernel size of $1 \times 1 \times 1$ is employed to generate tumor volume masks in the input dimensions of the network. Dice loss is employed for loss calculation, and the dice coefficient is employed as the accuracy measure. Following 100 epochs of training, the network shows no additional improvement in the validation dice coefficient.

RESULT AND DISCUSSION

When training precision greatly surpasses validation accuracy, overfitting takes place. This suggests that although the model has successfully committed the training data to memory, it has trouble generalizing to the validation data [11]. It is recommended that validation data be incorporated into the training process in order to alleviate this problem. This enables prompt model modifications by enabling the early termination of training in the event that validation accuracy does not increase. Since retraining the model from scratch takes a lot of effort, this method saves time. In case it is seen that validation accuracy is plateauing, training may be stopped and the model improved through hyperparameter tuning or any other technique to reduce overfitting or underfitting concerns[12].

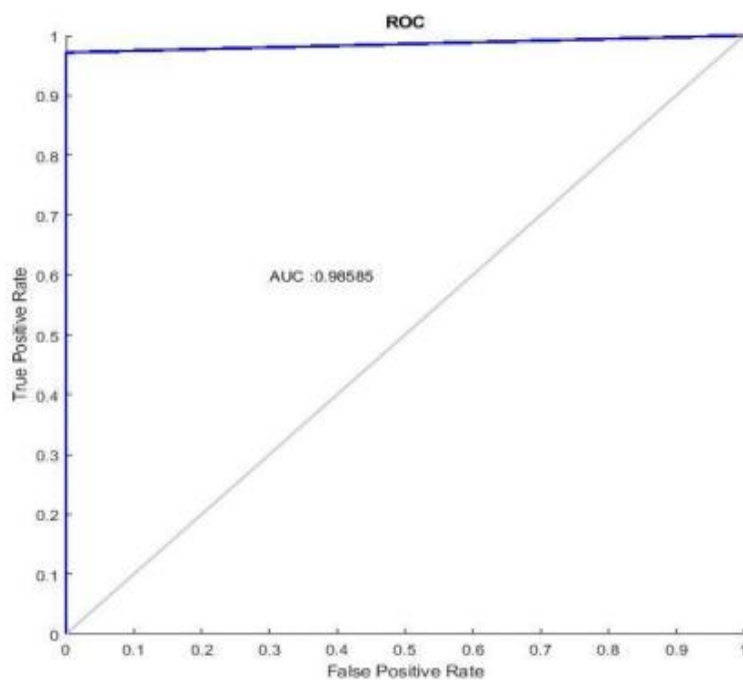


Figure 2: ROC Curve of classification of Lung Images

The 3D patches have a dimension of $256 \times 256 \times 16$ and are created by taking 16 slices from each image, making sure that at least one slice includes the tumor area. The memory constraints imposed on the computer during computation by the GPU are also resolved with this approach [13]. Following clipping to the predefined Hounsfield value range of -1000 HU through +400 HU for the segmentation of the tumors, intensity values of images are normalized in the range from 0 through 1 in order to make them suitable to input into the convolutional neural network. Additionally, the tumor segmentation masks are modified to meet this shape after being scaled from 0 to 1. Following preprocessing, the slices from a single patch are seen together with the matching masks.

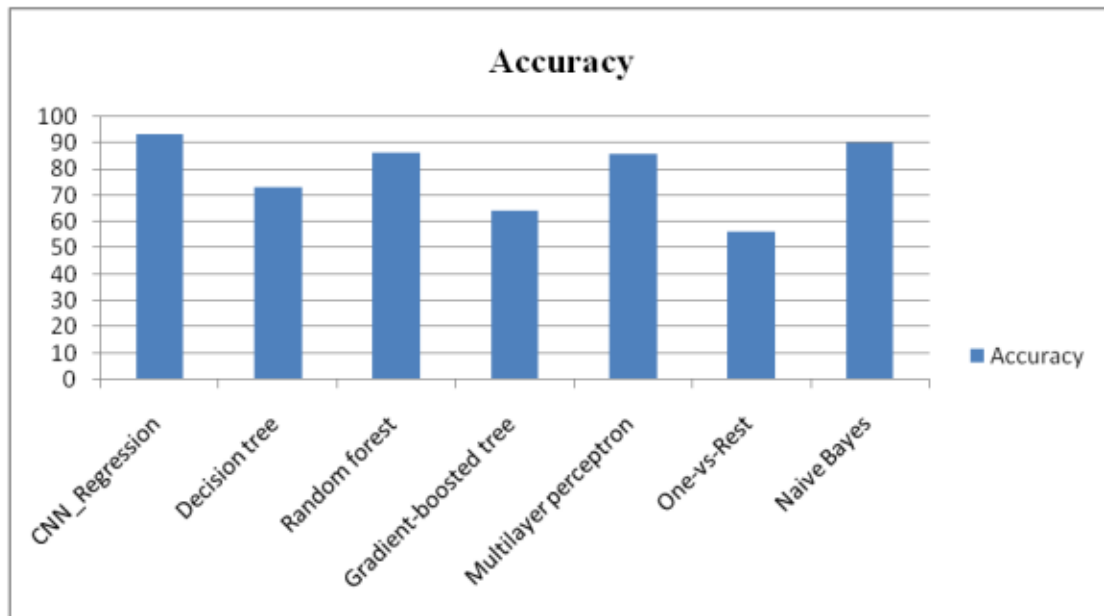


Figure 3: Accuracy achieved form the Classification

In the earlier method, we employed standard convolutional layers characterized by a fixed receptive field [14]. This limitation hindered the effective capture of irregularly shaped tumor regions. In the current approach, we have implemented deformable convolution with a learnable kernel and a deformed receptive field to better address the challenges posed by irregular tumor shapes. Prior to applying the proposed segmentation model, we segmented the lung regions using this approach [15].

CONCLUSION

Diagnosing lung cancer through medical imaging presents significant challenges, particularly with larger tumors that can occupy extensive areas of the lungs and may be located near the lung walls. We have introduced a 3D densely connected convolutional neural network that features dense connections among convolutional layers to effectively segment lung tumors. This network has been assessed using the publicly available NSCLC-Radiomics dataset, achieving a dice score of 67.34%. To mitigate overfitting, various augmentation techniques and batch normalization have been employed. Additionally, a novel pre-processing technique has been implemented to address data imbalance. This technique may be incorporated within computer-aided diagnosis (CAD) schemes for clinical evaluation of lung cancer, thus supporting clinicians in undertaking more comprehensive disease analyses. Even though our system achieves better performance than many of the previous approaches, there can still be further optimization, most importantly in better segmentation for elongated lung tumors. To address this issue, we have developed a strategy utilizing a 3D CNN with deformable convolutions for lung tumor segmentation. The proposed network has been trained and evaluated on two distinct datasets: the NSCLC-Radiomics dataset and another dataset sourced from a local hospital in India. A key feature of our network is its incorporation of deformable convolutions, which leverage a learnable sample matrix to more accurately capture image features.

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