
3D Deep Convolution Neural Network Application in Lung Nodule Detection on CT Images

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Abstract

Pulmonary cancer is the leading cause of cancer-related death worldwide, and early stage of pulmonary cancer detection using low-dose computed tomography (CT) could prevent millions of patients being killed every year. However, reading millions of those CT scans is an enormous burden for radiologists. Therefore, an immediate need is to read, detect and evaluation CT scans automatically and fast.

In the paper, we propose a new implementation method in 3D Deep Convolution Neural Network that is suitable for lung-nodule detection. A 3D network performs better than a 2D network as it also captures the vertical information of nodules. Also, leaky ReLUs are used to replace the ReLUs in all activation layers. Furthermore, we don't apply any extra fully connected layers to speed-up the train process and also obtained good result.

The team interpolated the original images and crop out a cube where centered as the given coordinations of all candidates, and apply the common data augmentation methods to balance the positive and negative samples. Finally result is evaluated by a free receive operating characteristic (FROC), and we reach the average sensitivity of 0.932 at 7 different false positive rates.

1 Introduction

Pulmonary cancer is the leading cause of cancer-related death worldwide nowadays, causing more than 1.3 million deaths annually. In order to decrease the death number, scientists and researchers have been made huge effort on it. An effective way to resolve this problem is to apply early detection for the prospective patients. Screening high risk individuals for lung cancer with low-dose CT scans is a promising method. However, after scanning those patients reading millions, we have millions of CT scans awaiting for radiologists to read. Usually, a single radiologists can only read roughly 50 patients' scans, which is very time consuming. Therefore, an immediate need is to read, detect and evaluation CT scans automatically and fast.

The LUNA16 challenge [1] also realized this problem and held a competition that focuses on a large-scale evaluation of automatic nodule detection algorithms on the LIDC/IDRI data set. The LIDC/IDRI data set is publicly available, including the annotations of nodules by four radiologists. The LUNA16 challenge provides a list of candidate nodules (750,000 nodules) from many nodule detectors with specific coordinates. Inside this list, only 1166 nodules are true positives and remaining are all false positives. Our task is to design a powerful classifier to distinguish the minor differences between true and false positives.

2 Data Preprocessing

A key issue is that the original CT images have different voxel length. For example, spacing on z-axis from different CT scans varies from 0.625mm to 2.5mm, same issue exists on the xy plane as well. Thus, before feeding data to our network, we interpolated the original images to same voxel spacing (x: 0.5556mm, y:0.5556mm, z:1mm). Afterwards, using the given coordinate of the center of sphere of all candidate nodules, we crop out a 40*40*24 voxels cuboid from the interpolated images, which is centered at the given coordinates. Finally, we randomly crop out a 36*36*24 cube from the 40*40*24 cube. In this way, we finally get a 20mm*20mm*20mm cube for training afterwards.

Hounsfield value is the unit to represent the relative density of tissues and organs on CT images. In most of the lung CT images, the Hounsfield value varies from -1000 to 1000. For those values greater than 1000, we simply convert them to 1000, the maximum value we set. Same method is applied for values less than -1000.

More importantly, the training dataset has extremely high false positive to true positive ratio (735418:1557). In order to deal with the imbalance labels, we applied common data augmentations for the true nodule positions, such as rotate 90, 180, 270 degrees, shift within 2 pixels on xy plane, zoom out, zoom in, flip respect to x-axis and y-axis. Totally, we increased the true positive sample size 7 times greater.

3 Convolution Neural Network Structure

A 3D DCNN, which captures the full range of contexts of candidates and generates more discriminative features compared with 2D DCNNs, is utilized for false positive reduction. This network contains three small stages. In each of the stage, there are two convolutional layers, followed by a batch normalization layer and a leaky Rectified Linear Unit (leaky-ReLU) activation layer respectively. And a max-pooling layer is connected to the second activation layer. The channels of convolutional layers for stage 1,2,3 are 32,64,128 respectively. Finally, a 2-way softmax activation layer is connected to the last max-pooling layer to classify the candidates from nodules to non-nodules. Moreover, dropout layers are added after max-pooling layers and fully-connected layers to avoid over-fitting, dropout ratio is set to be 0.5. The detailed architecture of the proposed 3D DCNN is illustrated in 1.

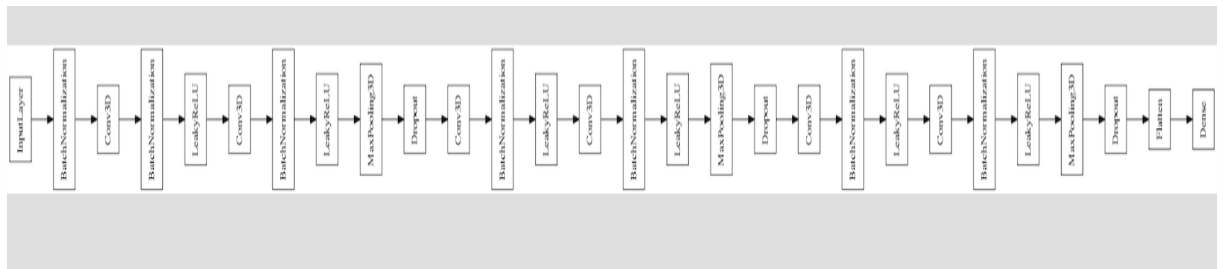


Figure 1: Structure of 3D-DCNN Model

4 Experiments

In this section, we evaluate the performance of our DCNN network system on the LUNA16 Challenge. In the LUNA16 challenge, performance is evaluated using the Free-Response Receiver Operating Characteristic (FROC) analysis [1]. The sensitivity is defined as the fraction of detected true positives divided by the number of nodules. In the FROC curve, sensitivity is plotted as a function of the average number of false positives per scan (FPs/scan). The average FROC-score is

defined as the average of the sensitivity at seven false positive rates: 1/8, 1/4, 1/2, 1, 2, 4, and 8 FPs per scan.

In the cross-validation process. The leaky-ReLU was used in the network and the softmax function was used for logistic regression to yield the prediction probabilities. The weights of the 3D CNNs were initialized from the normal distribution [2] and trained by minimizing the cross-entropy loss with Adam. The learning rate was initialized to 0.0001. Dropout and momentum were used during the training procedure. The method was implemented with Python based on the deep learning library of Keras which is a simplified interface of TensorFlow [3].

5 Evaluation

The evaluation of the result is based on 10-fold cross validation using the provided dataset.

6 References

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