# Malignancy Estimation of Lung Nodules using Multiview CNNs

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## **ABSTRACT**

Recently, malignancy estimation has been a crucial step in lung cancer diagnostics. In this work, we formulate malignancy estimation as a classification problem and perform the experiments on the LIDC dataset using deep convolutional neural networks. Unlike other methods, we sample multiple views from 3D volume of lung nodules and apply a max voting heuristic on softmax for final classification. Experimental results shows that our model outperforms prior work with a mean of 88.5% accuracy on 5-fold cross validation.

### 1. INTRODUCTION

As of 2017, lung cancer accounts for most number of deaths in the world [16]. It can be identified early by CT scans in the form of lung tumors. An important problem while diagnosis is estimating the malignancy of the lung nodules. Knowing the probability of a nodule being malign is important since it is required to estimate the frequency of follow-up computed tomography scanning. In this work, we try to tackle this problem using deep CNNs.

Most of the current methods have predominantly utilized 2D slices from volumetric data. Some of the classical approaches have used texture features[4], 2D and 3D Haralick features for the task of nodule classification into benign and malignant. Recently, some methods have utilized deep learning for lung nodule classification [5], for example a 2D CNN approach has been adopted in [6], [7], [8] for lung nodule classification, where in [8] they adopted multi-scale nodule patches and learns class specific features by concatenating feature responses from the last layer for each scale. In contrast to these, only classifying into benign and malignant, we aim to estimate the malignancy of a nodule. For this work, we utilize the LIDC [3] dataset that has nodule malignancy associated with each lung nodule annotation.

While intuitively it seems logical to build 3D shape classifiers directly from 3D models, [17] shows a counterintuitive result that 2D image renderings of 3D shapes can dramatically outperform the classification accuracy. One reason for this result is the relative efficiency of the 2D versus the 3D representations. In particular, while a full resolution 3D representation contains all of the information about an object, in order to use a voxel-based representation in a deep neural network that can be trained with available samples and in a reasonable amount of time, it would appear that the resolution needs to be significantly reduced. Therefore, we use 2D CNNs in classifying the malignancy of lung nodules. Our contributions in this project are:

- We propose a multiview voting based deep CNN architecture for malignancy estimation in lung nodules.
- We train and test the end-to-end 2D CNN and evaluate the performance with different strategies.

# 2. RELATED WORK

There is an extensive notion of prior work on understanding lung nodule malignancy. Traditionally, lung nodules were classified by extracting hand-crafted features or descriptors [11] and applying regression or ready-made classifiers. These features include morphological features, voxel grouping, and pixel intensity based thresholding [13, 8]. In [4], the nodules are segmented based on appearance-models. The method uses k-nearest neighbour classifier by using shape analysis. A similar approach is taken in [5, 18]. [5] uses 2D texture features such as Gabor and Local Binary patterns, while [18] uses active 3D contours and texture features from neighbouring voxels. These methods use SVM and Linear Discriminant Analysis (LDA) respectively.

With the recent release of a large data set, LIDC-IDRI [1], deep learning based models have become the most powerful methods in accurate estimation of lung nodule malignancy. Several works [21, 6, 2, 3, 14, 15, 19, 7] proposed deep CNNs for nodule classification to automatically learn the features. [14] proposed multi-view CNNs for false positive nodule detection. [20] combined multi-view CNNs with Fischer vector encodings to obtain hybrid features for classifying lung nodule shape. We take this approach to estimate malignancy of lung nodules.

# 3. METHODOLOGY

We formulate the malignancy prediction as a classification problem, in contrast to previous methods [12, 13] that have formulated it as a regression.

## 3.1 Data preparation

Multiple annotations for the same nodule is present in the LIDC dataset. We treat each such annotation separately as a single data point, however, we label each annotation for the same nodule with the average rating for that nodule. To obtain which annotations belong to the same nodule, we form the adjacency matrix for the annotations. Two annotations are labeled adjacent in the graph if the minimum pairwise euclidean distance between the contour boundary points is smaller than a certain threshold. Finally, clusters are obtained as connected components in the graph obtained from this adjacency matrix. Then, we dissect the 3D (50x50x50) volume into multiple views as shown in Fig. 1 (a) of 2D 50x50 image sizes. We used a total number of 178084 lung nodule images in training. We have four classes for the images, which are "Highly Unlikely (HU)", "Moderately Unlikely (MU)", "Moderately Suspicious (MS)", and "Highly Suspicious (HS)". Important to say that at the end we reduce number of classes to two, which are "Unlikely" and "Suspicious" by summing up HU with MU and MS with HS respectively. Such summation is done by using corresponding confusion matrix.

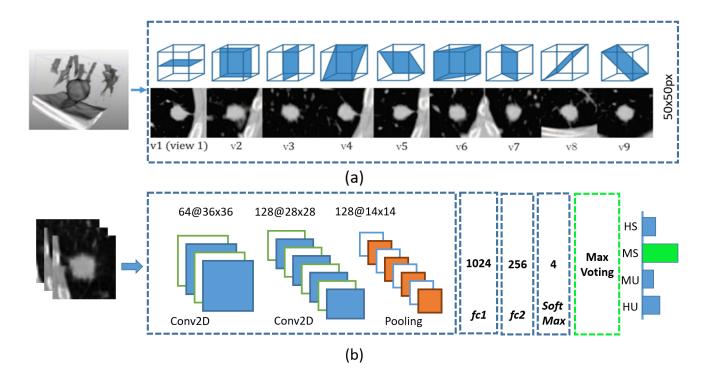


Figure 1: Data generation and Network Architecture. a) Generating multiple views. b) Network with 2 Fully connected layers followed by softmax and Max voting.

### 3.2 Network Structure

Fig. 1 (b) partially shows our CNN architecture. The figure lacks dropouts, one convolutional layer, and one pooling layer for the sake of saving space. We experimented with end-to-end CNN classifier with first 50x50 pixels input, then classical convolutional and pooling layers, finally 3 fully connected layers, within which the first two are used to extract nodule features and the last is used as input for the soft-max classifier. All the layers have rectified linear unit (ReLU) as activation function. We tweaked number of epochs, batch size, filter sizes, number of layers, and dropout. We also experimented with number of views (90, 180, 270, and 360). We found that the accuracy is improved with increased number of views. We used 360 views in our final model.

# 4. RESULTS

We split the dataset into training and testing parts in order to do 5-fold cross validation. Instead of splitting by

Architecture	Accuracy
Naive Multi-view (ours)	86.8
Max Voting (ours)	88.5
Sarfaraz (Transfer learning)[6]	80
Sarfaraz (Multi task learning) [6]	90
Sarfaraz [7]	82.47
Mario [2]	82.4

Table 1: Comparison of mean accuracy for 5-fold cross validation versus Previous methods

nodules, we divided the dataset by patient id since this is a more practical testing scenario. The network was built using Keras with tensorflow background framework and trained using Adadelta Optimizer. Batch sizes of 10, 25, 50, 100, 200 and 400 were used. We were using NVIDIA GeForce GTX GPU for training and inference, which gave us a significant speedup compare to conventional CPU.

Table 1 shows the performance of our model with the prior work. We compare our mean accuracy of 5-fold cross validation. Our model outperforms [2] and [7] by more than 6%. Also, we get comparable results with [6]. Although [6] achieves 90% accuracy with multi task learning, they have used extra annotations. Our model achieves 88.5% without having to use any such extra information.

### 5. CONCLUSION

In this work, we proposed a multiview and max voting based deep CNNs for classifying lung nodule malignancy. Our results outperforms the prior work marginally by 4%. Here, we only utilize LIDC dataset, since our method did not take any other information with the training data except for its malignancy labels, therefore other datasets like LungTime [18] can also be added into our estimation networks. For the future work we would like to add more data into our experiments and hope to increase the accuracy further. A mixture of experts [9] or a multi scale approach [10, 12] over these architectures is expected to perform even better and our future experiments will combine these multiple architectures into a single network to fully utilize the information at multiple scales.

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