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Lung Nodule Segmentation using Deep Learning and Advanced UNet Model

Pragati D, Pawar^{1*}, Sanjay L. Badjate², Sanjay M. Gulhane³

- ^{1*} Department of Electronics & Telecommunication Engineering, Jawaharlal Darda Institute of Engineering and Technology, Yavatmal, India; e-mail: pragatipawar6227@gmail.com
- ² S. B. Jain Institute of Technology, Management & Research, Nagpur, India.
- ³ Pravara Engineering College, Loni, India.

ABSTRACT

Cancer is known as one of the world's top reason of mortality in human beings. Lung cancer, notably, has the highest mortality rate. Thus, timely detection of nodule or tumor is a critical and significant job in saving lives. One of the hot topic in current research field is automatic detection of lung nodules. Many methods have been implemented using computer vision-based technologies in the past, but achieving the desired precision still remains a difficult job. In this research, we adopt Convolutional Neural Network (CNN) based UNet image segmentation model and improved its architecture by incorporating convolution mechanisms. Moreover, this scheme uses binary cross entropy as loss function during training process. The proposed mechanism is tested on LIDC-IDRI dataset. The experimental analysis shows the augmented performance of proposed approach when compared with existing segmentation techniques. The qualitative and quantitative comparative analysis shows that the suggested scheme substantially improves the efficiency of segmentation performance.

Keywords: Lung nodules detection, image processing, deep learning, CNN, LIDC-IDRI.

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INTRODUCTION

hese days, people are experiencing diverse malignant growth in brain, lungs, liver, etc. called as tumors. A majority of individuals are experiencing cancer or cellular breakdown in the lungs [1]. The mortality caused by cellular breakdown in the lungs are more than the mortality due to some other malignant growth. The survival rate of lung patients can be extended to half of the overall diseased which presently is 14% [2]. The recovery rate is essentially improved now-a-days however, there are possibilities to expand this survival rate which would be more than the current rate. To accomplish it, the inner examination of the body through imaging techniques is required so the tumor cells can be seen and taken out [2]. Different strategies are utilized to take the pictures from inside the body like X-beams, Computed Tomography (CT) checks, Magnetic Resonance Imaging (MRI) and so forth [3]. Cancer cell growth in the Lungs cause 1.3 million deaths every year and is considered

Corresponding Author : Pragati D, Pawar, Department of Electronics & Telecommunication Engineering, Jawaharlal Darda Institute of Engineering and Technology, Yavatmal, India; e-mail: pragatipawar6227@gmail.com

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as a main source of malignancy demise overall [4]. Location and treatment at a beginning phase are needed to viably conquer this disease. CT scan was as off late embraced as a mass-screening method for pulmonary disease detection, empowering fast improvement in the capacity to distinguish tumors early. Because of the advancement of CT examining innovations and increased demand, radiologists are

©The Author(s). 2022 Open Access This article is distributed under the term of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/ licenses/by/4.0/), which permits unrestricted use, distribution, and non-commercial reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if change were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0) applies to the data made available in this article, unless otherwise stated. overpowered with the information they need for analysis. Regular screening with low-radiation CT has been proven in the National Lung Screening Trial to help reduce mortality from cellular breakdown in the lungs In any event, radiologists' examination of CT data for the purp ose of detecting the presence of lung tumours and their severiy is a timeconsuming process. Because of the high risks associated with fake negatives, having CT image reports evaluated by several specialists is appealing.

To improve work process and lessen outstanding task at hand for radiologists working on distinguishing and diagnosing tumor in the lungs, a few Computer-Aided Detection and Diagnosis systems have been created by specialists in industry and the scholarly community [6].

Lately, profound CNN has risen as a main strategy for consequently recognizing and segmenting lung tumors and have made incredible progress [7]. Cutting edge systems for tumor recognition frequently use the 3DRegion Proposal Network (RPN) [8] for tumor screening [7, 9, 10], trailed by a 3D classifier to decrease false positives [11, 12]. Albeit one phase detector has likewise been introduced in [13], and their hit standard was unique in relation to what was proposed earlier for the same task [14]. Additionally, the refinement offered by the additional classifiers could address a few errors caused by the detection methods. Regarding tumor segmentation, U-Net [15] and V-Net [16] like architectures are broadly embraced in clinical images segmentation [17]. Practically speaking, a CAD framework for lung nodule discovery and segmentation mostly comprises of a few autonomous subsystems that are optimized independently.

There exist a few constraints on dealing with each task independently. To start with, it is time and resource exhaustive task to train a deep CNN model. Though, every stage in neural network layer is intended for specific purposes, they share the basic methodology of fetching out features which describe tumor in lungs. Second, the outcome efficacy of the entire framework may not be ideal, on the grounds that independently training so many layers avoid correspondence between them and learning characteristic feature representations. Naturally, the segmentation mask of the tumor ought to give a solid picture of the tumor features to the neural network to learn distinguished features, which may thus improvise the efficacy of nodule or tumor identification [18]. We employ Deep Learning, a cutting-edge framework, to enhance the detection of malignant pulmonary nodules. Deep learning is based on the use of 'deep' neural networks (DNNs) with many hidden layers. This technique has emerged as the dominant way for a range of complicated pattern recognition problems in recent years. The use of DNNs for CADe is still in its early phases of development.

However, preliminary research into the usefulness of deep learning has revealed a relatively low amount of false positives when compared to usual findings produced by classical segmentation approaches [19]. Furthermore, research has shown that DNNs have a lot of promise for use in a number of CADe applications that use volumetric medical data [20]. Two of these studies looked at the use of convolutional neural networks for pulmonary nodule classification [21-23], however the use of large 'deep' neural networks in this context has only been proven using off-the-shelf, pre-trained networks [20].

In rest of the article, we describe brief literature review in section II where existing techniques for nodule segmentation are discussed, section III describes the proposed methodology to obtain the improved segmentation. The outcome of proposed approach is discussed in section IV where we compare the performance of proposed approach. Finally, section V presents the concluding remarks.

LITERATURE SURVEY

Tang et al. [1] presented a novel scheme based on Deep CNN, comprising of two phases that are completely 3D from start to finish and uses the best in class approach for object identification. In the first phase, probable tumor regions are detected through a U-Net based 3D Faster Recurrent CNN model that is pre-trained on hard negative mining method. Second, the false positive is reduced by applying 3D Deep CNN classifiers that are pre-trained on complex instances created during screening of tumor-like objects. At last, they proposed a technique with combine both models from the two phases to deliver the ultimate prediction result.

Ding et al. [5] also presented a Deep CNN based scheme for lung nodule/tumor recognition. They initially utilize a de-convolutional architecture with Faster Region-based CNN for identification of tumor-like objects on axial slices. Subsequently, a 3D Deep CNN was applied for the ensuring least false positive alarms.

Zhu et al. [7] introduced a completely automatic pulmonary Computed Tomography (CT) nodule detection

system called Deep Lung. This scheme comprises of two elements, tumor recognition (recognizing the areas of tumors) and classification (recognizing tumor is benign or malignant). This work considers the 3D characteristics of lung CT. Further, dual path network is developed to for tumor identification and classification. Specifically, this scheme uses a 3D faster region with CNN to detect the tumor where it uses 3D dual path blocks and U-Net type of encoder and decoder modules to viably train from tumor features. For tumor classification, Gradient Boosting Machine (GBM) with 3D DPN features was presented. The tumor classification sub network was approved on a public dataset from LIDC-IDRI, on which it attained higher accuracy than standard techniques and outperformed the expectations of experienced medics, based on modality of the picture. In the Deep Lung framework, tumor-like objects were distinguished first by the tumor recognition sub network, and tumor finding is led by the classification sub network.

Zhu et al. [9] presented a unique scheme that uses deep 3D Convolution Network framework called DeepEM that is amplified with Expectation-Maximization (EM) method. The EM method helps to extract weakly supervised labels from medical records to identify tumor in lungs.

Tang et al. [11] introduced another fully 3D deep CNN architecture i.e. Nodule Net, to identify nodule locations in the lung with decreased false positives and tumor segmentation performed altogether in a multi-tasks style. To have an isolation between various tasks and motivate feature diversification, they consolidate two significant operations: (1) decoupled feature maps to identify tumors and reduce false positive rate, and (2) an improved segmentation subnet to increase the accuracy of tumor segmentation.

Zuo et al. [24] set forward a multi-resolution CNN to mine features of different stages and resolutions from various depth layers in the NN for pulmonary tumor-like objects classification. This work is many times confronted by the radiological heterogeneity of the CT scans and the varying magnitudes of pulmonary tumors. Using of knowledge transfer mechanism, the technique can be partitioned into three stages. To begin with, first they transfer knowledge from the source CNN model (used for edge identification) and enhance the model to another multi-resolution model which is appropriate to classify the image. At that point, the information is transferred from source training progress to consider entire side-output branches in

the model of the side-yield branches in calculation. Also, an improvement is performed in the objective equation and the loss function to be calculated imagewise instead of pixel-wise. At last, instance generation and data improvisation were carried out to train and evaluate a classifier that is customized for pulmonary tumor candidates.

Cao et al. [25] present a Dual-branch Residual Network called DB-ResNet, which is an information driven model. Their scheme combines two new methods to improve the prediction ability of the model: (1) the proposed model can at the same time catch multi-view and multi-scale features of various tumor objects in CT scan reports; (2) they join the intensity feature with of the features obtained through CNN. They presented a pooling strategy, called the Central Intensity-Pooling (CIP) layer to mine the intensity features of the block's center voxel, and subsequently utilize the convolution network to acquire the convolutional features of the block's center voxel. Also, they developed a weighted sampling technique based on the boundary of tumors to select those voxels through the weighting score, to enhance the model's accuracy.

Singadkar et al. [26] presented a novel methodology based on Deep Deconvolutional Residual Network (DDRN) to segment tumor from the lungs CT image. This methodology depends on two prime functions. First, the proposed DDRN is fully trained and it checks the various different kinds of tumors from the 2D set of lung CT images. Summation-based long skip linking from convolutional to deconvolutional layer of the NN saves the spatial data lost during the pooling activity and extracts complete resolution features.

Nagi et al. [27] introduced a fully automatic segmentation methodology. Primarily, the lung portion is mined based on the ideal grayscale threshold. Subsequent stage, a new crossover 3D tumor-like objects recognition technique is introduced that includes Active Contour Model (ACM), 3D neighborhood linking and mathematical characteristics based rules. A crossover feature vector is made, by joining structural texture feature and Histogram of Oriented Gradient which is diminished by Principle Component Analysis (HOG-PCA) features, for every detected tumor-like objects. Subsequent to feature extraction, classification operation is carried out using four distinct classifiers i.e. SVM, kNN, Ada Boost and Naive Bayes.

Nasrullah et al. [28] introduced a novel deep learning system with diverse strategies for the precise diagnosis of cancerous tumor. Because of the recent successes of deep CNN in image processing, they had utilized two deep three-dimensional (3D) adaptive mixed connection network (CMixNet) frameworks for pulmonary tumor identification and classification. Identification of tumor was done on efficiently-learnt CMixNet features and U-net type of encoder-decoder framework via faster R-CNN. The characterization of the cysts was carried out on the learnt features from the modeled 3D CMixNet structure via a gradient boosting machine (GBM). The final decision was taken in conjunction with physiological symptoms and clinical pathogenesis to decrease false positives and misdiagnosis outcomes due to multiple forms of errors.

Xu et al. [29] presented a scheme named MSCS-DeepLN that examines malignancy of the lung tumor and fixes problems in parallel. To determine the malignancy of the cyst, three lightweight models are trained and integrated. As the basis of each lightweight model, 3D-CNN were used to derive the lung cyst features from CT images and maintain spatial heterogeneity of the lung tumor. The multi-scale feedback from CT images helps the sub-networks to learn and retain complex multi-level contextual features. Their suggested technique utilizes an AUC approximation technique as the penalty term to tackle the imbalance problem. The error in this penalty term is created from each major and minor class pair during training, so that negative and positive could contribute equally to update this model.

PROPOSED MODEL

Previous sections illustrate various aspects of pulmonary nodule segmentation and detection followed by a brief literature review where numerous existing techniques are deliberated. The convolution neural network reported its distinctive role in medical image segmentation. Due to compelling benefits of CNN, we adopt the CNN based methodology for pulmonary nodule segmentation.

INTRODUCTION TO CNN

We present a brief discussion about CNN in this section. An improved version of the multilayer perceptron is known as CNN. These networks' most essential components are the convolutional and subsampling layers. These layers can be arranged in the stacked manner to learn hierarchy of the features. The convolution layer extracts the feature maps of its previous layer which is connected by filters. The input is denoted as $C^{(m-1)}$, output is denoted as $C^{(m)}$ and $C_i^{(m)}$ denotes the feature map for m^{th} layer. The output of current layer can be expressed as:

$$C_{j}^{(m)} = F_{W,b} \left(C_{i}^{(m-1)} * w_{(i,j)}^{m} + b_{j}^{m} \right) \quad (1)$$

Where F_{wb} denotes the nonlinear activation function,* denotes the convolution, $w_{(i,j)}^m$ denotes the linking of kernels for *i*th input map and *j*th output map in the current layer. Several nonlinear activation functions exist such as hyperbolic tangent, sigmoid, and rectified linear function. Furthermore, these networks use a subsampling layer after convolution layer which introduces invariance property and reduces computational complexity. Generally, pooling layer is used as subsampling layer. In this work, we use average pooling which creates a group of 3x3 pixels, centered at the pooling unit, the distance between pooling set is considered as two pixels. The final convolution layer is followed by the Softmax classifier which uses Softmax loss function. For any binary classification problem, the kernel convolutions generate the prediction outcome which into multinomial distribution for the considered class labels. Finally, the predicted outcome is normalized. The Convolution networks use shared weights which helps to utilize the same filter for each pixel in the layer. The process reduces the memory requirement and improves the performance.

Let us consider that the training set is constructed using *n* labeled samples presented as { $(x^1, y^1), (x^2, y^2), ..., (x^n, y^n)$ } where *y* denotes the class labels as $y^i = 0$ or 1 and i = 1, 2, ..., n. We denote θ as a function which has a set of parameters including Softmax parameters, kernel, and bias parameters. To model the logistic regression, a cost function is formulated which need to be minimized with respect to as:

$$E(0) = -\frac{1}{n} \Big[y^{i} \log F_{\theta}(x^{i}) + (1 - y^{i}) \log (1 - F_{\theta}(x^{i})) \Big]$$
(2)

However, sometimes the Softmax generates the large values hence we incorporate a weight decay function to penalize the large values which regularize the classification. The partial derivatives are computed using back-propagation and cost function is minimized using gradient based optimization.

U-NET ARCHITECTURE FOR IMAGE SEGMENTATION

Currently, image segmentation is considered as a challenging task which is adopted widely in various

applications such as biomedical field. U-Net is a promising CNN based architecture for image classification and object segmentation based on their corresponding classes inside the image. This architecture is composed of using two paths i.e. contracting path which gathers the context information and a symmetric expanding path to improve the localization of objects.



Figure 1: Basic U-Net architecture for image segmentation

Above given figure 1 shows U-Net architecture for image segmentation [30-31] which contains convolution, ReLU and max pooling modules. In this architecture, the blue box contains the feature map and number of channel corresponding to the feature map is presented above the box. Similarly, the white box represents the features which are obtained from the previous blocks and arrows represent the different features. Left part of the network is known as contracting path and right side of the network is known as the expanding path of the network. As a result, the considered architecture consists of two blocks of 3x3 unpadded convolutions. After each convolution layer a rectified linear unit activation function is applied and 2x2 max-pooling operation function with two strides which contains down sampling operations.

Similarly, the expanding path performs up sampling of the feature maps. Moreover, it uses a 2x2 convolution to reduce the channel by half. Further, it concatenates the feature maps, 2x2 up-convolution, and 3x3 convolution followed by the ReLU.

The proposed approach uses stochastic gradient descent, these networks require input pictures and their related segmentation maps. To compute the energy function, a pixel-wise soft-max is merged with the cross-entropy loss function and applied to the final feature map. The cross-entropy is expressed as:

$$E = \sum_{x \in \Omega} w(X) \log \left(p_{l(x)}(x) \right)$$
(3)

where $l: \Omega \to \{1, ..., K\}$ denotes the true label, $w: \Omega \to R$ denotes the weight map. Further, morphological operations are applied to estimate the separation border and then weight map is computed as:

$$w(x) = w_{c}(x) + w_{0} \exp\left(-\frac{(d_{1}(x) + d_{2}(x))^{2}}{2\sigma^{2}}\right)$$

Where $w_c: \Omega \to R$ represents the weights of the attributes. These weight parameters are used to balance the class frequencies, $d_1: \Omega \to R$ distance to the nearest cell in considered environment, and $d_2: \Omega \to R$ is the distance to second nearest cell computed simultaneously.

PROPOSED U-NET ARCHITECTURE FOR TUMOR SEGMENTATION

This subsection presents the description of proposed U-Net architecture for pulmonary nodule tumor segmentation. The proposed architecture is depicted in below given figure 2.



Figure 2: Proposed U-Net architecture for pulmonary nodule tumor segmentation

This model represents an end-to-end mapping of image slices to the segmentation of nodule. During training process, we consider a loss function to learn the model parameters from training data by minimizing the loss function. In this work, we use a weighted cross entropy loss function, defined as:

$$L = -\frac{1}{N} \sum_{i=1}^{N} \sum_{c=1}^{3} w_i^c y_i^c \log P_i^c$$
(5)

Where P_i^c denotes the probability of voxel *i* to belonging to the class *c* i.e. whether the predicted voxel belongs to the background, nodule, y_i^c denotes the ground truth of detected voxel, and w_i^c denotes the weighting factor.

The Table-1 given below gives the description of the proposed U-Net architecture for pulmonary nodule tumor segmentation.

Table-1: U-Net Architecture Description

Layer	Shape	Parameter	Connection	
Input	(64 64 1)	0		
(Input Layer)	(04, 04, 1)	0		
Conv1_1	(64, 64, 32)	320	input	
(Conv 2D)	(
conv1_1_bn	(64, 64, 32)	128	conv1_1	
conv1_2	(64, 64, 32)	9248	conv1_1_bn	
conv1_2_bn	(64, 64, 32)	128	conv1_2	
pool1	(32,32, 32)	0	conv1_2_bn	
conv2_1	(64, 64, 64)	18496	pool	
conv2_1_bn	(32,32,64)	256	conv2_1	
conv2_2	(32,32,64)	36928	conv2_1_bn	
conv2_2_bn	(32,32,64)	256	conv2_2	
p0012	(16,16,64)	0	conv2_2_pn	
conv3_1	(16,16,128)	/3856	pool2	
CONV3_1_DN	(16, 16, 128)	512	conv3_1	
conv3_2	(16,16,128)	14/584	conv3_1_bn	
conv3_2_bn	(16,16,128)	512	conv3_2	
p0013	(8,8,128)	0	conv3_2_bn	
conv4_1	(8,8,256)	295168	pool3	
conv4_1_bn	(8,8,256)	1024	conv4_1	
conv4_2	(8,8,256)	590080	conv4_1 bn	
conv4_2_bn	(8,8,256)	1024	conv4_2	
p00l4	(4,4,256)	0	conv4_2_bn	
conv5_1	(4,4,512)	1180160	p0014	
conv5_1_bn	(4,4,512)	2048	conv5_1	
conv5_2	(4,4,512)	2359808	conv5_1_bn	
conv5_2_bn	(4,4,512)	2048	conv5_2	
conv2d_transpose _17	(8,8,256)	524544	conv5_2_bn	
dropout_41	(8,8,256)	0	conv2d_transpose	
concat6	(8 8 512)	0	conv4_2_bn	
concato	(0,0,312)	0	dropout_41	
conv6_1	(8,8,256)	1179904	concat6	
conv6_1_bn	(8,8,256)	1024	conv6_1	
conv6_2	(8,8,256)	590080	conv6_1_bn	
conv6_2_bn	(8,8,256)	1024	conv6_2	
conv2d_transpose _18	(16,16,128)	131200	conv6_2_bn	
dropout_42	(16,16,128)	0	conv2d_transpose _18	
oncat7	(16,16,256)	0	conv3_2_bn dropout_42	
conv7_1	(16,16,128)	295040	concat7	
 conv7_1_bn	(16,16,128)	512	conv7_1	
 conv7_2	(16,16,128)	147584	 conv7_1_bn	
conv7_2_bn	(16,16,128)	512	conv7_2	

conv2d_transpose _19	(32,32,64)	32832	conv7_2_bn	
dropout_43	(32,32,64)	0	conv2d_transpose _19	
concat8	(32,32,128)	0	conv2_2_bn dropout_43	
conv8_1	(32,32,64)	73792	conv8_1	
conv8_1_bn (Batch Normalization)	(32,32,64)	256	conv8_1_bn	
conv8_2 (Conv2D)	(32,32,64)	36928	conv8_2	
conv8_2_bn (Batch Normalization)	(32,32,64)	256	conv8_1_bn	
conv2d_transpose_20 (Conv2DTran)	(64,64,32)	8224	conv8_2_bn	
dropout_44 (Dropout)	(64,64,32)	0	conv2d_transpose	
concat9 (Concatenate)	(64,64,64)	0	conv1_2_bn dropout_44	
conv9_1 (Conv2D)	(64,64,32)	18464	concat9	
conv9_1_bn (Batch Normalization)	(64,64,32)	128	conv9_1	
conv9_2 (Conv2D	(64,64,32)	9248	conv9_1_bn	
conv9_2_bn (Batch Normalization)	(64,64,32)	128	conv9_2	
dropout_45 (Dropout)	(64,64,32)	0	conv9_2_bn	
conv10 (Conv2D)	(64,64,1)	33	dropout_45	

RESULTS AND DISCUSSION

In this section, we present the outcome of proposed approach and compared the obtained performance with existing techniques. The proposed model is implemented using Python 3.7 installed on windows operating system. The system has 16GB RAM and 4 GB NVIDIA graphic card. We use publically available Lung Nodule Analysis 2016 grand challenge data to train the network using proposed deep learning architecture. This data is obtained from LIDC-IDRI dataset repository. In this experiment we have considered 888CT images. The ground truth data is constructed with the help of four experienced radiologists in a two-phase annotation process.

We measure segmentation performance in terms of Dice similarity coefficient (DSC) which is a measurement of difference between ground truth and segmented outcome of proposed approach. This can be computed as:

$$DSC = \frac{2 \times V(G_t \cap S_v)}{V(G_t) + V(S_v)}$$
(6)

Where G_t denotes the ground truth, S_v denotes the segmentation outcome, and v is the volume size. We compare the performance of proposed approach with active contours, Central Focused Convolution Neural Networks (CFCNN), U-Net with simple diameter information, Multi-view Convolution Neural Networks, Graph cuts, Watershed, and Markov random field, and

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Hand-crafted features. Below given table-2 shows the comparative analysis in terms of Dice coefficient. These outcomes are obtained without ablation with 80% data used for training and 20% used for testing.

Table.2. Comr	parative Anal	vsis in Term	s of Dice	Coefficient
Table-2. Comp	Jai a live Anai	y 313 111 101 111	2 01 DICE	COEITICIEIT

Techniques	Dice Coefficient	
CFCNN	0.81	
Simple U-Net	0.79	
Multi-view Convolution Neural Networks	0.78	
Hand-crafted features	0.74	
V-Net	0.96	
Roy et al. [31]	0.93	
Singadkar et al. [32]	0.95	
Proposed Model	0.98	

Below given figure shows the quantitate analysis of proposed approach for lung nodule segmentation where we compare thee predicted output with the ground truth.



Figure 3: Qualitative outcome of proposed model

CONCLUSION

In this work, we focus on lung nodule segmentation using computer vision-based applications. The CNN based applications have reported a significant performance improvement hence we adopt CNN based UNet model for nodule segmentation. The proposed model uses several convolution layers in a fully connected CNN model. Moreover, we have incorporated weighted binary loss function to improve the learning performance. An extensive experimental study is carried out on publicly available lung nodule segmentation challenge dataset. When compared to existing methodologies, the proposed strategy provides better results, according to the comparison analysis.

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