A PIPELINE FOR LUNG TUMOR DETECTION AND SEGMENTATION FROM CT SCANS USING DILATED CONVOLUTIONAL NEURAL NETWORKS

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Abstract

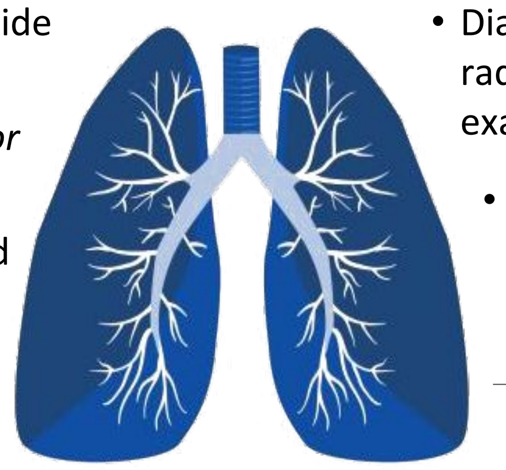
Lung cancer is the **most prevalent cancer worldwide** with about 230,000 new cases every year. Most cases go undiagnosed until it's too late, especially in developing countries and remote areas. Early detection is key to beating cancer. Towards this end, the work presented here **proposes an automated pipeline for lung tumor detection and segmentation from 3D lung CT scans from the NSCLC Radiomics Dataset**. It also presents a new dilated hybrid-3D convolutional neural network architecture for tumor segmentation. First, a binary classifier chooses CT scan slices that may contain parts of a tumor. To segment the tumors, the selected slices are passed to the segmentation model which extracts feature maps from each 2D slice using dilated convolutions and then fuses the stacked maps through 3D convolutions - incorporating the 3D structural information present in the CT scan volume into the output. Lastly, the segmentation masks are passed through a post-processing block which cleans them up through morphological operations. The proposed segmentation model outperformed other contemporary models like LungNet and U-Net. The average and median dice coefficient on the test set for the proposed model were 65.7% and 70.39% respectively. The next best model, LungNet had dice scores of 62.67% and 66.78%.

Motivation

Only 16 % of lung cancer cases are diagnosed at an early (localized) stage
[U.S. National Institute Of Health, National Cancer Institute. SEER Cancer Statistics Review, 1975–2015]

Lung Cancer

- Most common cancer worldwide
- Chance of developing lung cancer in a lifetime - *1 in 15 for men* and *1 in 17 for women*
- **Two million people** diagnosed with lung cancer every year.



Problem

- Diagnosis requires trained radiologists and oncologists to examine diagnostic images.
- Lack of screening programs and personnel in developing countries and rural areas especially in Bangladesh.

Diagnostic Modalities

- Imaging Tests: X-Ray, CT Scan
- Sputum Cytology
- Tissue Sample (Biopsy)

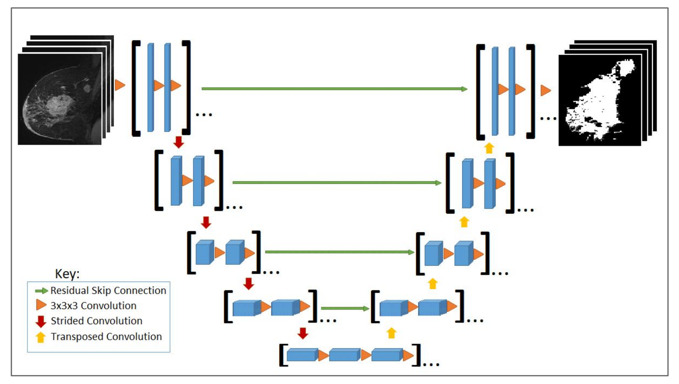
Desired Outcome

- An **automated, end-to-end system** able to diagnose Lung Cancer from CT Scans

Related Works

U-Net

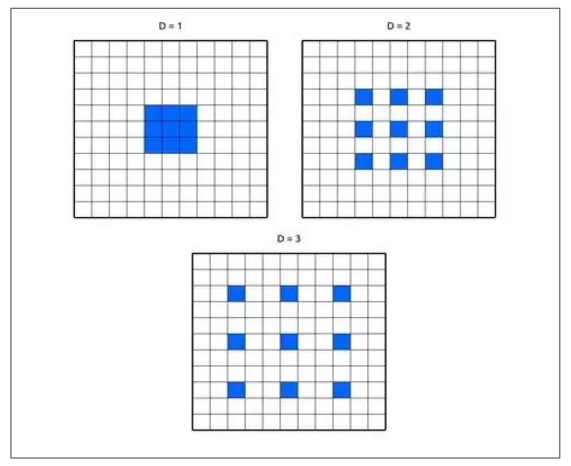
- Proposed by *O. Ronneberger et al.*[1]
- Stack of Convolutional and Pooling blocks that extracts features followed by stack of Upsampling blocks that creates a segmentation mask.
- 3D version uses 3D convolution blocks



U-Net Architecture

LungNet

- Proposed by *M. Anthimopoulos et al.*[2]
- Stack of *Dilated Convolutional* layers that extract features which are fused to create segmentation mask.
- Dilation allows capture of features from a wider area = *larger receptive field*



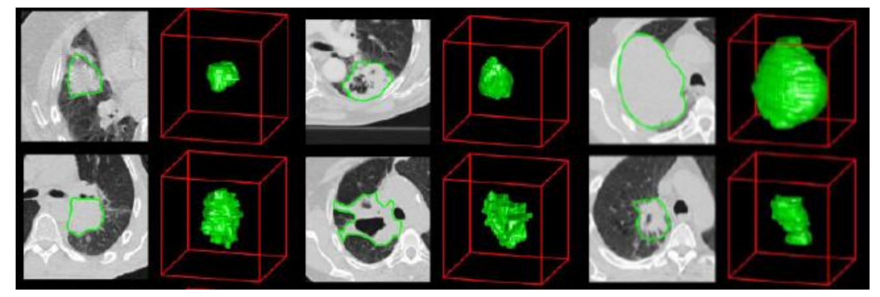
Dilated Convolution Kernel (blue) with dilation rate = D

Data Preparation

- NSCLC-Radiomics Dataset[3,4,5] - 3D CT Scans with tumor regions manually annotated

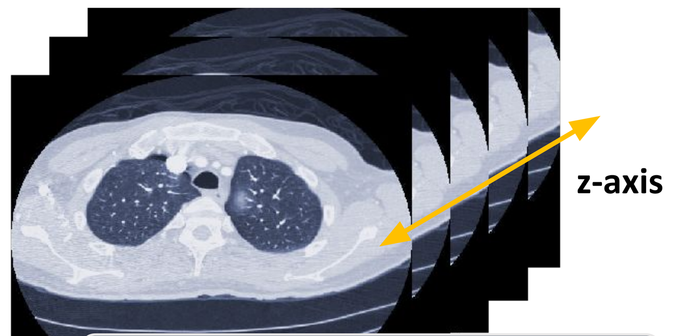
Set	Patients	Axial CT Scan Slices	
		With Tumor	Without Tumor
Train	260	4,296	26,951
Test	40	848	3,630

- Data augmentation - *X/Y Mirroring, Rotations, Elastic Transformation* - 7 fold increase in data
- Three subsets created from total data pool :
  - A : *all Tumor Slices only*
  - B : *A + 10 non tumor slices from each patient*
  - C : *3D stacks of 9 consecutive slices*



Sample Slices from the NSCLC dataset

Pipeline



Input 3D CT Scan

Preprocessing

- Detecting and Cropping out Lung Region (Image Processing)
- Adaptive Histogram Equalization
- Normalization and Resizing

Binary Classifier

- Feature extraction from each 2D slice using LungNet2D
- Binary Classifier labels probable slices containing tumor

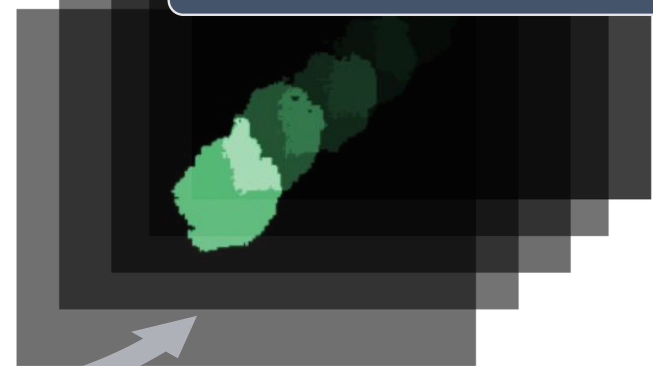
LungNet3D

- 3D Convolutions combine feature maps, extracted from each xy plane, along the z axis
- Outputs 3D masks

Post Processing

- Area based Thresholding to get rid of specks (region < $5mm^2$ removed)
- Morphological Operations to refine segmentation mask

Generated Masks

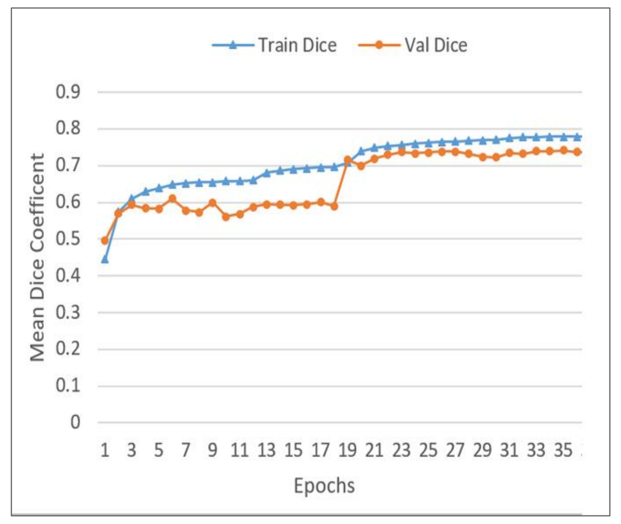


Training

LungNet 3D

$$LossMetric = \ell\{X,Y\} = -log\left(\frac{2*|X\cup Y|+1}{|X|+|Y|+1}\right)$$

- LungNet2D trained first on subset A and then subset B on decimated learning rate
- To transform LungNet2D into the proposed model, LungNet3D :
  - Final Convolutional layers switched to 3D convolutions
  - Instead of single slice input, stacks of 9 slices provided
- LungNet3D trained on subset C



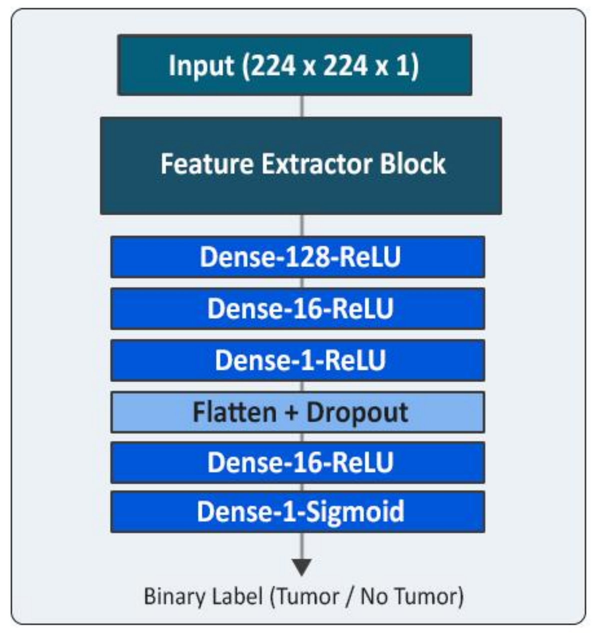
Binary Classifier

$$\ell\{X,Y\} = -[X*log(Y)+(1-X)*log(1-Y)]$$

- The trained LungNet2D model was used as base
- Last Convolutional Final Convolutional layers replaced by fully connected layers
- Trained on subset B to output binary labels (tumor/non-tumor)

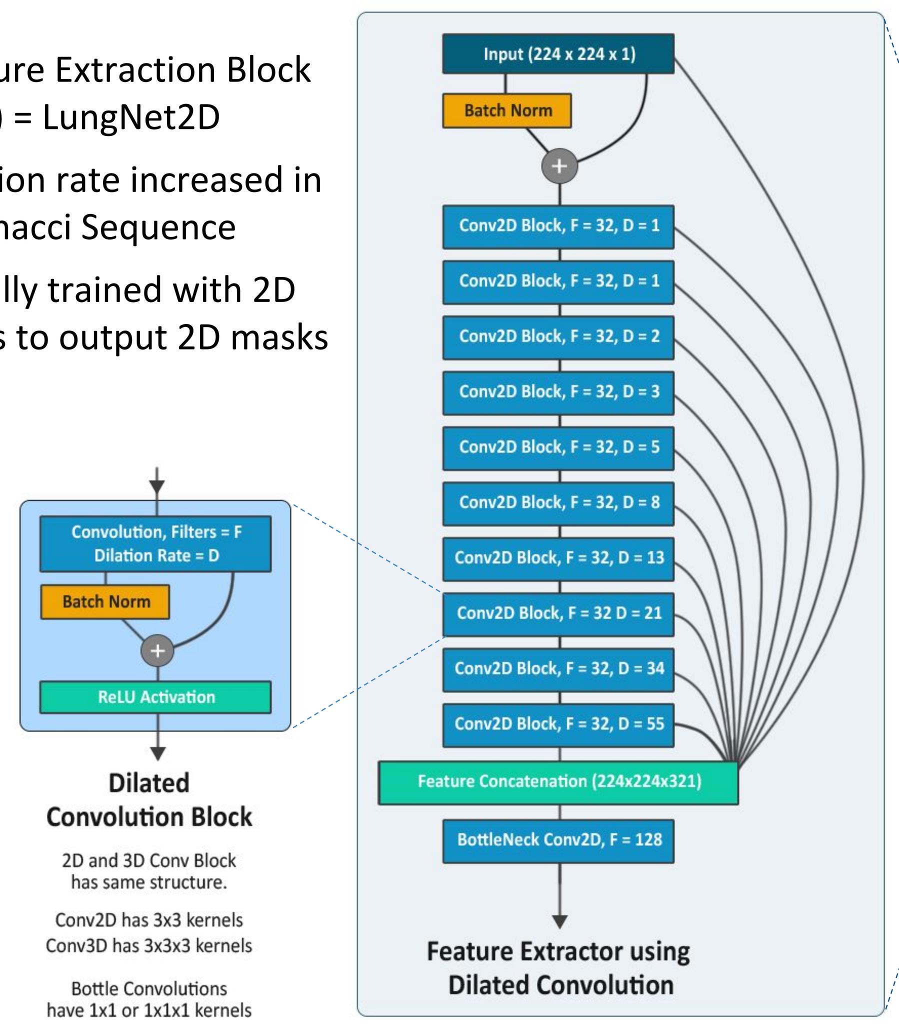
Binary Classifier

- Tumors generally localized in small volume (3-30 slices = 10 ~ 100 mm^3) compared to total lung volume (~ 900 mm^3)
- Frontend binary classifier used to weed out non tumor containing slices
- Positive detection = 8 neighboring slices along the ±z directions passed to Segmentation Model

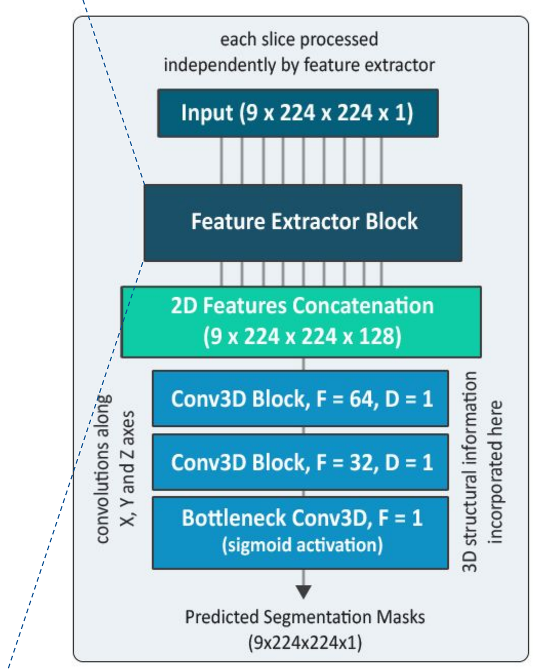


LungNet3D

- Feature Extraction Block (FEB) = LungNet2D
- Dilation rate increased in Fibonacci Sequence
- Initially trained with 2D slices to output 2D masks



- FEB applied to each of the 9 slices in mini stack
- Feature maps are fused through 3D convolution

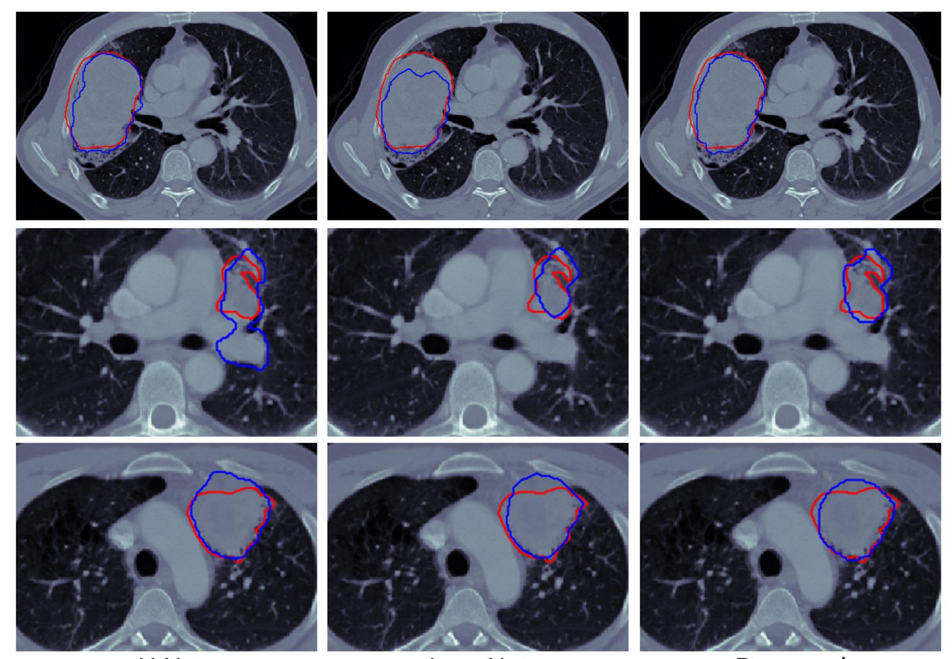


Proposed Segmentation Model

Results

Results on Test Set

Model Arch.	Total Param ($x10^6$)	Mean Dice (%)	Median Dice (%)
U-Net	31	58.5	62.3
LungNet 2D	0.13	62.7	66.8
Proposed	**0.40**	**65.8**	**70.4**



Predicted Masks by different models (Red = Ground Truth, Blue = Predicted)

References: [1] Olaf Ronneberger, Philipp Fischer, and Thomas Brox, "*U-net: Convolutional networks for biomedical image segmentation*", in International Conference on Medical image computing and computer-assisted intervention. Springer, 2015, pp. 234–241.
[2] Marios Anthimopoulos, Stergios Christodoulidis, Lukas Ebner, Thomas Geiser, Andreas Christe, and Stavroula G. Mougiakakou, "*Semantic segmentation of pathological lung tissue with dilated fully convolutional networks*", CoRR, vol. abs/1803.06167, 2018
[3] Hugo JWL Aerts, Emmanuel Rios Velazquez, Ralph TH Leijenaar, Chintan Parmar, Patrick Grossmann, Sara Carvalho, and Philippe Lambin, "*Data from nsclc-radiomics. the cancer imaging archive*", 2015.
[4] Kenneth Clark, Bruce Vendt, Kirk Smith, John Freymann, Justin Kirby, Paul Koppel et al., "The cancer imaging archive (tcia): maintaining and operating a public information repository", Journal of digital imaging, vol. 26, no. 6, pp. 1045–1057, 2013.
[5] Hugo JWL Aerts, Emmanuel Rios Velazquez, Ralph TH Leijenaar, Chintan Parmar, Patrick Grossmann et al., "Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach", Nature communications, vol. 5, pp. 4006, 2014.