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Multiple Resolution Residual Network for Automatic Thoracic Organs-At-Risk Segmentation in CT

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INTRODUCTION

Radiotherapy treatment (RT) planning requires highly accurate segmentation for precise tumor targeting while reducing unnecessary dose to critical normal organs.¹ However, clinically used manual delineations are often time consuming to produce and exhibit high inter- and intra-rater variability.²

Current methods for automatic segmentation of thoracic organs-at-risk (OARs) still pose a challenge for small structures like the esophagus due to the loss of resolution in the deeper layers. In order to deal with these limitations, the goal of the current work was to implement a deep learning method that simultaneously combines information from multiple feature streams computed at different image resolution levels to preserve different levels of spatial context for the segmentation of structures of varying sizes.

AIM

To implement and evaluate a multiple resolution residual network (MRRN) for the segmentation of multiple normal organs-at-risk (OARs) from computed tomography (CT) images for aiding with thoracic radiotherapy treatment (RT) planning.

METHOD

Datasets

- Two datasets were used: 1) 239 planning CT scans of internal patients with locally advanced non-small cell lung cancer (LA-NSCLC), and 2) 48 CT scans from the 2017 AAPM Thoracic Auto-Segmentation Challenge³, of which 36 were provided for training ahead of the challenge and 12 during the online testing phase of the challenge.
- Our training cohort consisted of a mix of both datasets, resulting in 250 scans.
- The validation set consisted of 25 scans from the internal cohort.
- The testing set consisted of the 12 online scans from the challenge.
- All CTs were annotated with expert delineations of the heart, left and right lungs, esophagus, and spinal cord.

Implementation Details

- The network was trained in 2D using 28,401 images of size 256x256.
- The network was implemented using the Keras and Tensorflow library and trained on Nvidia GTX 1080Ti with 12GB memory.
- The network was optimized using the ADAM algorithm with an initial learning rate of 1e-4 and cross-entropy loss for 50 epochs with a batch size of 10.

Evaluation Metrics

- The segmentation accuracy compared to expert delineations was measured using the Dice Similarity Coefficient (DSC).

METHOD

Network Architecture

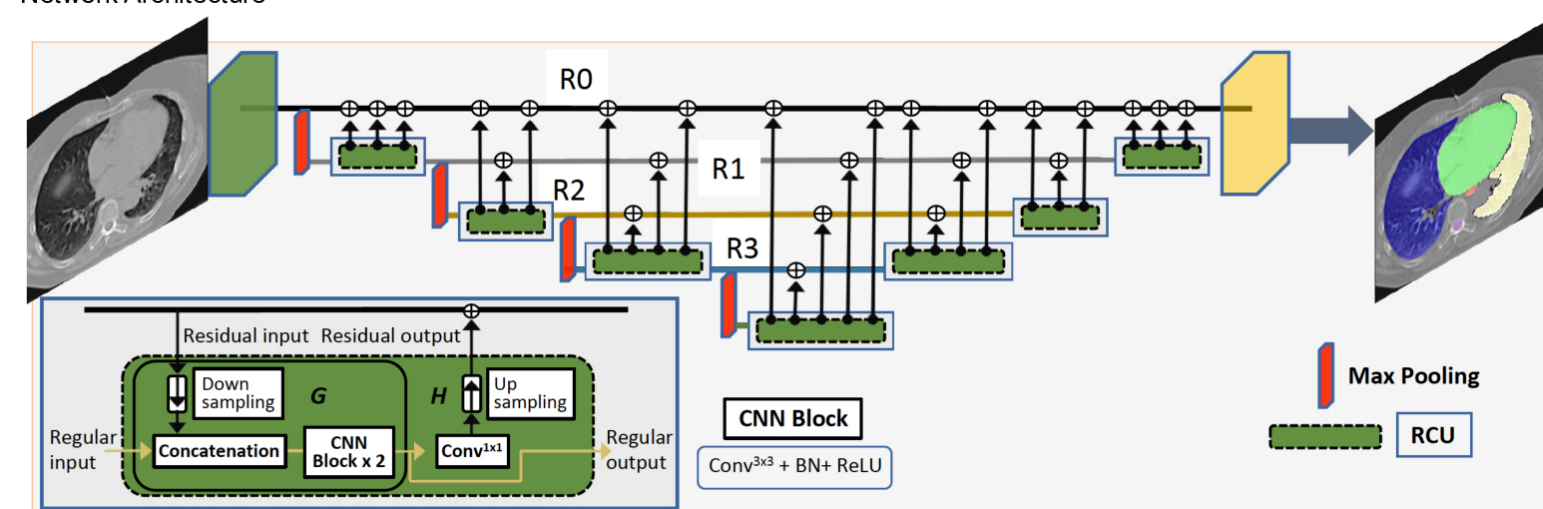


Figure 1. Multiple resolution residual network. Multiple residual feature streams R0, R1, R2, R3 are shown. Convolutional blocks are composed of a sequence of convolutions, batch normalization (BN) and ReLU activations.

- The Multiple Resolution Residual Network⁴ (MRRN) helps enlarge the semantic context in the image by simultaneously combining multiple feature streams (e.g. R0, R1, R2, R3 in **Figure 1**) extracted from various image resolution and feature levels through a series of residual connection units (RCU).
- The RCU takes in a residual input from one of the preceding higher resolution feature streams, which is down-sampled, and features from the immediately preceding CNN layer or RCU. These two inputs are then passed through CNN blocks before the residual output is passed back to the feature stream, after up-sampling, and the regular output is passed to the RCU or CNN layer.

CONCLUSIONS

We evaluated a multiple resolution residual network for segmenting multiple normal organ structures from thoracic CT images. Our approach outperformed the best-performing method in the 2017 AAPM Thoracic Auto-Segmentation Challenge for hard-to-segment structures like the esophagus and achieved comparable results for the heart, left and right lungs, and spinal cord.

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RESULTS

Median DSC and interquartile range (IQR) achieved with the MRRN

- 0.93 (IQR: 0.92-0.94) for the heart
- 0.97 (IQR: 0.96-0.97) for the left and right lungs
- 0.76 (IQR: 0.73-0.80) for the esophagus
- 0.89 (IQR: 0.87-0.90) for the spinal cord

When compared with three best-performing methods in the 2017 AAPM Thoracic Auto-Segmentation Challenge, our approach produced the most accurate segmentations for the esophagus. The accuracy was comparable between the four methods for the remaining analyzed organs (**Table 1**), expressed as mean DSC \pm standard deviation.

Figure 2 shows a representative case from the online testing phase of the 2017 AAPM grand challenge. As shown by the yellow-colored overlap between the two masks (red and green), our method produced a reasonably accurate segmentation for all five structures.

Table 1. DSC achieved for thoracic OARs in the AAPM online testing set.

Method	2D/3D	Heart	Left Lung	Right Lung	Esophagus	Spinal Cord
MRRN	2D	0.93 \pm 0.02	0.97 \pm 0.01	0.96 \pm 0.02	0.76 \pm 0.06	0.88 \pm 0.022
Elekta	2.5D/3D	0.93 \pm 0.02	0.97 \pm 0.02	0.97 \pm 0.02	0.72 \pm 0.10	0.88 \pm 0.037
UVa	3D	0.92 \pm 0.02	0.98 \pm 0.01	0.97 \pm 0.02	0.64 \pm 0.20	0.89 \pm 0.042
Mirada	2D	0.91 \pm 0.02	0.98 \pm 0.02	0.97 \pm 0.02	0.71 \pm 0.12	0.87 \pm 0.110

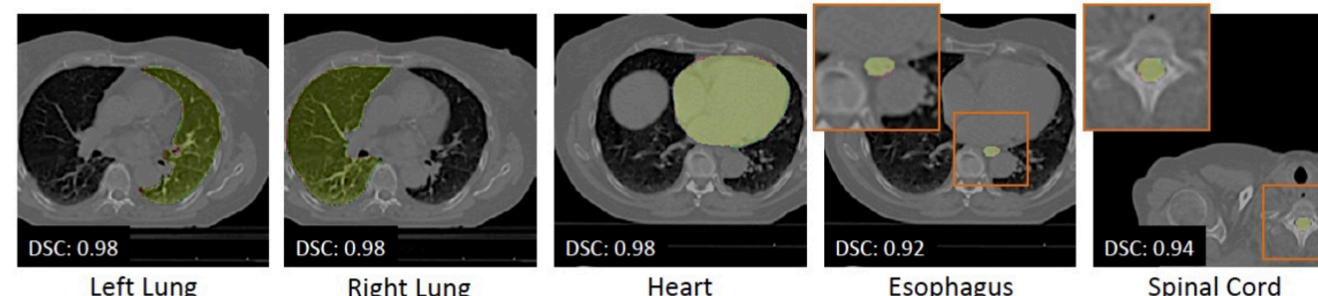


Figure 2. Example segmentations generated with the MRRN for the analyzed organs in the AAPM online testing set. The red masks correspond to algorithm segmentations and green masks to expert delineations.

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