JULY 12–16 2020 VIRTUAL JOINT AAPM | COMP MEETING
EASTERN TIME [GMT-4]

Multiple Resolution Residual Network for Automatic Glioblastoma Segmentation in MRI

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INTRODUCTION

Generating highly accurate segmentations of tumors is a crucial step in any radiomics analysis, as the features computed from these regions of interest (ROI) must be robust and reproducible. Segmentation, however, is a major source of variability in the extracted radiomic features and even when the choice of the segmentation method is reliable and yields robust features[1], semiautomatic or interactive methods require manual corrections or inputs from the user and are therefore time-consuming.

As such, a fully automated segmentation approach for tumors such as glioblastoma multiforme (GBM) is necessary for reproducible and consistent radiomics analyses.

AIM

To implement and evaluate two deep network architectures – the commonly used U-Net[2] and our approach, called the multiple resolution residual network (MRRN) – for the segmentation of GBM tumors from magnetic resonance (MR) images.

The impact of our work is to facilitate an automated pipeline for radiomics by reducing inter- and intra-rater variability while increasing reliability and robustness of image features in the workflow.

METHOD

Datasets

- Two datasets were used: 1) 111 FLAIR (Fluid-Attenuated Inversion Recovery) images of internal patients with GBM, and 2) 50 FLAIR images from the TCGA-GBM dataset.[3]
- The training and validation sets consisted of 100 and 11 images, respectively. Both were from our internal dataset.
- The testing set consisted of 50 images from the external cohort.
- All FLAIR MRIs were annotated with expert-validated delineations of the tumor.

Implementation Details

- The networks were trained in 2D using 17,523 images of size 256x256.
- Validation was performed with 840 images of size 256x256.

Evaluation Metrics

- The best model from validation was selected for testing on the TCGA-GBM dataset.
- Performance was measured using the Dice Similarity Coefficient (DSC).

METHOD

Network Architecture

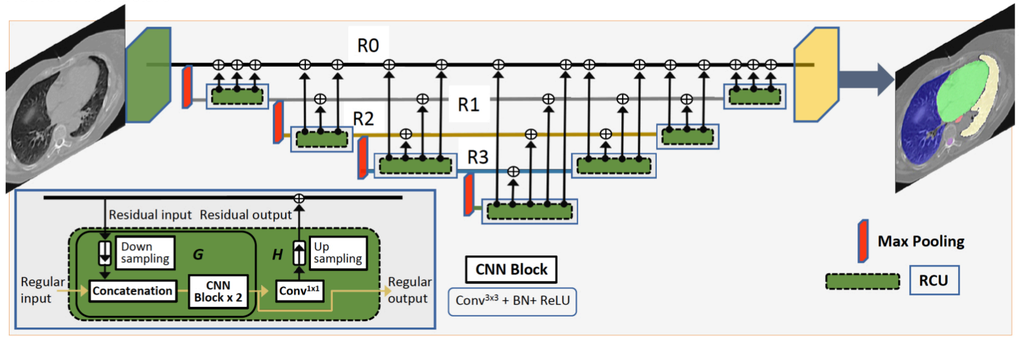

Figure 1. Multiple resolution residual network. Multiple residual feature streams R0, R1, R2, R3 are shown. Convolutional blocks are composed of a sequence of convolutions, batch normalization (BN) and ReLU activations.

- The Multiple Resolution Residual Network[4] (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.

REFERENCES

[1] Tixier F, Um H, Young R, et al. Reliabiltiy of tumor segmentation in glioblastoma: Impact on the robustness of MRI-radiomic features. Med Phys 2019;46:3582-3591

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[3] Clark K et al 2013 The cancer imaging archive (TCIA): maintaining and operating a public information repository J. Digit. Imaging 26 1045–57

[4] Jue Jiang, Yu-Chi Hu, Chia-Ju Liu, Darragh Halpenny, Matthew D. Hellmann, Joseph O. Deasy, Gig Mageras, and Harini Veeraraghavan. Multiple Resolution Residually Connected Feature Streams For Automatic Lung Tumor Segmentation From CT Images. IEEE Trans Med Imaging 2019;38:134-144

RESULTS

Median DSC and interquartile range (IQR) achieved for GBM segmentation

- 0.87 (IQR: 0.85-0.90) with the MRRN
- 0.85 (IQR: 0.81-0.88) with the U-Net

Figure 2 shows four representative cases of GBM segmentations using both methods. As shown, while the U-Net resulted in over-segmentations, our method produced more accurate segmentations.

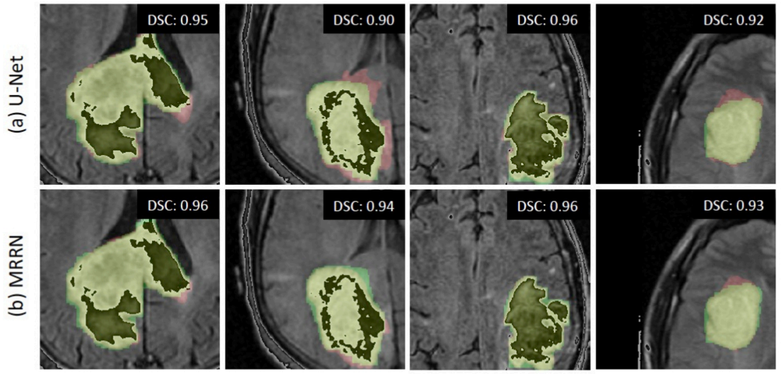

Figure 2. Example segmentations in the testing set for both deep network architectures: (a) U-Net and (b) MRRN. The green masks correspond to expert delineation and red masks to the algorithm segmentations.

CONCLUSION

Our method using the MRRN achieved more accurate segmentations compared to the standard U-Net method. While the U-Net resulted in over-segmentations, our method produced more accurate segmentations.

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