A Hierarchical 3D U-Net for Brain Tumor Substructure Segmentation

J Yang[1], R Wang[1,2,3], Y Weng[2,3*], L Chen[2,3], Z Zhou[4]
1 School of Artificial Intelligence, Xidian University, Xi'an, CN.
2 UT Southwestern Medical Center, Dallas, TX.
3 Medical Artificial Intelligence and Automation (MAIA) Lab, University of Texas Southwestern Medical Center, Dallas, TX.
4 University Of Central Missouri, Warrensburg, MO.

UT Southwestern
Medical Center
Radiation Oncology

XIDIAN UNIVERSITY

UNIVERSITY OF CENTRAL MISSOURI — LEARNING TO A GREATER DEGREE

INTRODUCTION

Glioma is a commonly malignant brain tumor with a high mortality and morbidity. With the rapid development of Magnetic Resonance Imaging (MRI), physicians can utilize multimodal MRI images to better diagnose and make more effective treatment plan. To achieve this goal, accurate and efficient brain tumors segmentation is of great importance. However, manually contouring brain tumors is time-consuming, and physician's experience strongly influence segmentation results. As such, it is necessary to develop an automated brain tumor segmentation algorithm. Inspired by the multi-task deep learning approach, a hierarchical three-dimensional U-Net (hU-Net) model is developed in this study, which integrates the prior knowledge into the segmentation. The experimental results demonstrated that more accurate segmentation results can be obtained.

AIM

The accurate segmentation of brain gliomas has played an important role in tumor diagnosis, tumor characterization, and surgical planning. The gliomas always contain three substructures: whole tumor (WT), tumor core (TC) and enhancing tumor (ET). particularly, WT contains TC, whilst TC contains ET. Inspired by the multi-task deep learning approach, we aim to develop a hierarchical three dimensional U-Net (hU-Net) model which can exploit this prior information to improve the segmentation accuracy.

METHOD

The proposed hU-Net model consists of three hierarchical cascade U-Net blocks.
• The first U-Net segments substructure WT.
• The second U-Net block segments substructure TC.
• The third block segments substructure ET.
• The segmented mask was made into a voxel-wise product with the original input image.
The results were then used as the input of next U-Net block. Three basic U-Net blocks were connected and the loss function was calculated, respectively. Finally, we utilized the multi-task deep learning paradigm to optimize the whole network. The whole framework is illustrated as follows.
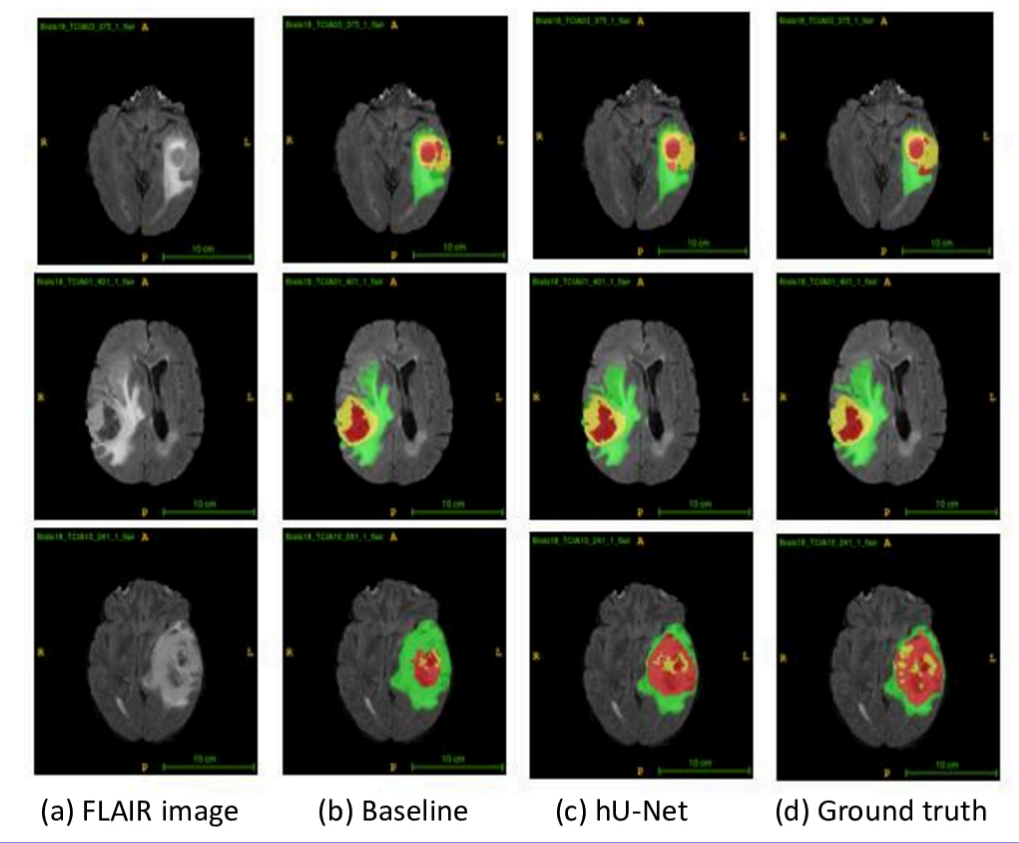

RESULTS

(a) FLAIR image   (b) Baseline   (c) hU-Net   (d) Ground truth
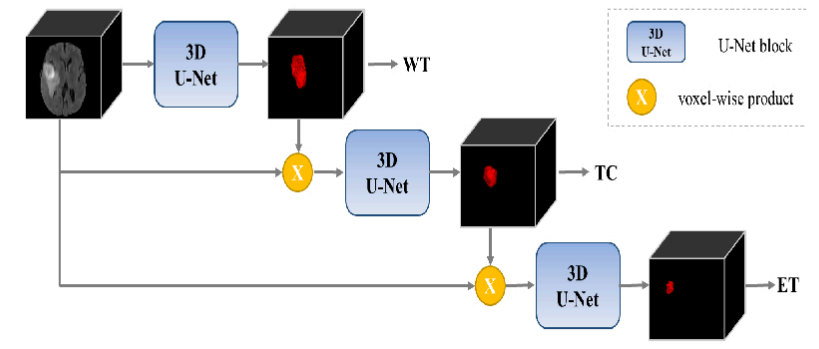
Table : The substructure segmentation results of baseline and hU-Net.

Model Dice	Baseline			hU-Net		
	WT	TC	ET	WT	TC	ET
Test_average	0.8099	0.7276	0.7111	0.9031	0.8551	0.7426
TCIA01	0.9764	0.4921	0.5832	0.9730	0.8716	0.6199
TCIA03	0.9105	0.8757	0.8096	0.8971	0.9205	0.8519
TCIA10	0.9209	0.9545	0.8997	0.9422	0.9628	0.9248

DATASETS

The BraTS2018 dataset from Multimodal Brain Tumor Segmentation Challenge 2018 were used in this study. It contains 285 patients, including 75 low-grade gliomas and 210 high-grade gliomas. All patients had four sequences: 1) native (T1); 2) post-contrast T1-weighted (T1Gd); 3) T2-weighted (T2); and 4) T2 Fluid Attenuated Inversion Recovery (FLAIR) volumes.

We selected 228 patients for training and remaining 57 patients for testing. Every image was normalized by the mean value and standard deviation of the training set.

CONCLUSIONS

We compared our hU-Net method with the U-Net. For the proposed hU-Net, the average dice coefficient can achieve 0.90, 0.86, and 0.74 for three substructures WT, TC and ET, respectively. Compared with U-Net, our method obtained an improvement of 9.32%, 12.75%, and 3.15% for each type.

The proposed hU-Net is capable of modeling hierarchical structure of gliomas for brain tumor segmentation. The quantitative and visual segmentation results demonstrated that hU-Net can obtain better performance.

REFERENCES

[1] Urban G, Bendszus M, Hamprecht F, Kleesiek J. Multi-modal brain tumor segmentation using deep convolutional neural networks. MICCAI BraTS (brain tumor segmentation) challenge. Proceedings, winning contribution. 2014 Sep:31-5.

[2] Ronneberger O, Fischer P, Brox T. U-net: Convolutional networks for biomedical image segmentation. InInternational Conference on Medical image computing and computer-assisted intervention 2015 Oct 5 (pp. 234-241). Springer, Cham.

[3] Kamnitsas K, Bai W, Ferrante E, McDonagh S, Sinclair M, Pawlowski N, Rajchl M, Lee M, Kainz B, Rueckert D, Glocker B. Ensembles of multiple models and architectures for robust brain tumour segmentation. InInternational MICCAI Brainlesion Workshop 2017 Sep 14 (pp. 450-462). Springer, Cham

[4] Menze BH, Jakab A, Bauer S, Kalpathy-Cramer J, Farahani K, Kirby J, Burren Y, Porz N, Slotboom J, Wiest R, Lanczi L. The multimodal brain tumor image segmentation benchmark (BRATS). IEEE transactions on medical imaging. 2014 Dec 4;34(10):1993-2024..

CONTACT INFORMATION

rfwang@xidian.edu.cn