#0948 Automatic segmentation of glioma based on MRI K-space data

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Introduction

Nowadays, Magnetic Resonance Imaging (MRI) plays a pivotal role in gliomas diagnosis, analysis, and surgery planning. Nevertheless, the accuracy of MRI segmentation is enormously restricted by the quality of images. Therefore, we demonstrate a new method that can directly make segmentations from K space data. And the results show that our method achieves the state of the art.

Materials and Methods

Dataset: BraTS 2018 dataset. 285 cases (210 HGG and 75 LGG) which have all four MRI modalities (T1, T1c, T2, and FIAIR) rigidly aligned, resampled to 1x1x1 mm isotropic resolution, and skull-stripped.

Network: Deep Residual Unet

Details: We firstly made 18923 2D slices from 285 3D datasets. We concatenated 4 available 2D MRI modalities into the 4 channel image as an input. The output of the network is 3 nested tumor subregions. Then we simulated fully sampled k space data from the input image by trajectory and make the k space image size 8x160x160. The eight channels represent the real and imaginary parts of the four MRI modalities. Afterward, we took 20% data as the test dataset. And we also used 10-fold cross validation on the remaining dataset.

Discussion and conclusion

In this work, our new semantic segmentation method for brain tumor segmentation from 2D K space data has achieved the state of the art performance. For increasing the accuracy, we also experimented with several data augmentation techniques such as flipping and padding for increasing the generalization ability of our model. Moreover, we have also tried the post-processing techniques such as CRF. However, the results after adding the techniques do not act better since K space data do not demonstrate the same property as images. The only method we tried that makes the results better is increasing the network depth. So we added some resnet on the model for avoiding the vanishing gradient.

Results

The used training time is approximately 3 days. Our results are shown in Table 2. Compared with the results on the Brats2018 website, our method has a better performance on details and segmenting edges. Our BraTS 2018 testing dataset results are 0.8573, 0.8789, and 0.7765 mean dice for WT(whole tumor), TC(tumor core), and ET (enhanced tumor core). It demonstrates that our method has achieved the state of the art compared with other results.

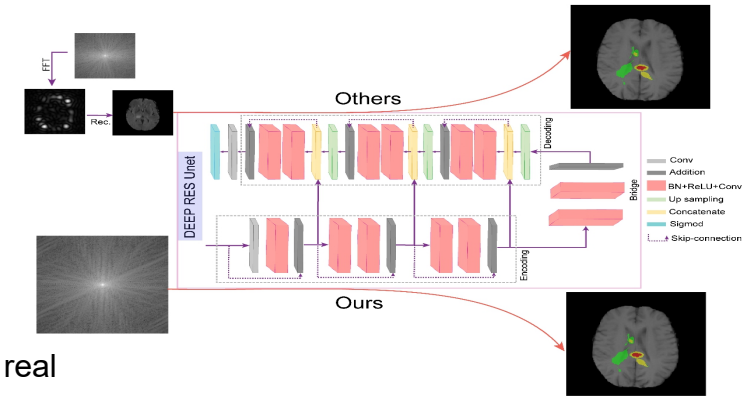

Figure 1. Comparision between traditional segmentation process and ours

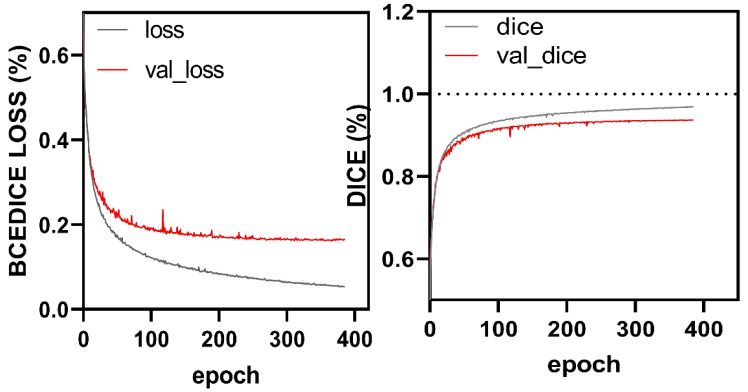

Figure 2. Tranining Process over epoch

Table 1 Quantitative results of our work

Testing dataset	Dice			Hausdorff（mm）		
	WT	TC	ET	WT	TC	ET
	0.8573	0.8789	0.7765	2.5649	1.6146	2.7187

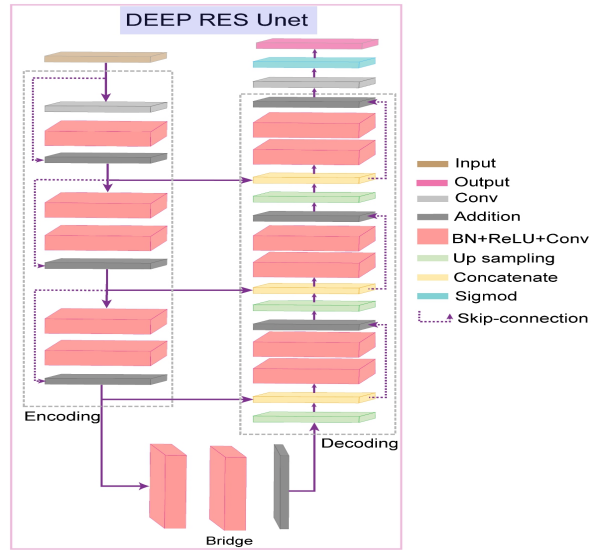

Figure 3. Main architecture of deep residual Unet

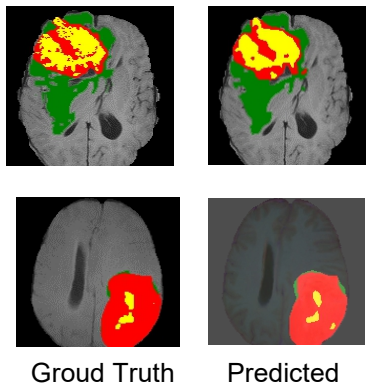

Figure 4. A The whole tumor (WT) part contains all visible labels, the tumor core (TC) part contains red and yellow labels, and the enhancing tumor core (ET) class is shown in yellow.