SEGMENTATION OF BRAIN TUMOR MULTI-PARAMETRIC MRI SCANS USING ARTIFICIAL NEURAL NETWORKS

Zhirko M., Titko V., Grakova N.

Department of Intellectual Information Technologies, Belarusian State University of Informatics and
Radioelectronics

Minsk, Republic of Belarus

E-mail: {mzhirko, vtitko27}@gmail.com, grakova@bsuir.by

In this paper, we present an automated method for brain tumor segmentation. A deep learning-based segmentation algorithm is expected to be able to solve diagnosis making, treatment planning, and resembling tasks. The automated method will help specialists to make more specific analyses in a relatively short amount of time. The analysis, made by this method is considered to have quite a good accuracy. The project is made open-source so that everyone is able to use it and do a contribution to make it better. Convolution Neural Networks (CNNs) are widely used for computer tomography (CT) images. Reliable, fast, and fully automated brain tumor segmentation is based on a Dense V-Network. An ample clinically acquired multi-parametric MRI dataset is used for the training, validation, and testing of our model. We conclude that deep-learning-based segmentation represents an acceptable method for brain tumor abdominal CT segmentation whose accuracy can surpass current methods.

INTRODUCTION

Segmenting abdominal images can facilitate clinical workflows in multiple domains, encompassing diagnostic interventions, treatment planning, and treatment delivery. Due to its clinical prevalence, brain tumor CT has been the focus of such research, along with three methods: statistical models (SM), multi-atlas label fusion (MALF), and registration-free methods.

Manual segmentation of 3D abdominal images is labor-intensive and impractical for most clinical workflows, therefore the need for automatic segmentation tools has emerged. In registration-free methods, the challenges consist of constructing variable- and deformation-invariant features ("hand-tuned"or learned) that characterize anatomy from training data sets that are not registered. However, these techniques have been shown to yield less accurate multi-organ segmentation than the registration-based approaches.

I. RELATED WORK

The main methodologies for brain tumor segmentation include the usage of different algorithms. For example, statistical approaches, that involve point distribution models or conditional shape modeling. Or multi-atlas label fusion methods could be used. But those methods are limited by image registration accuracy. It happens because of the huge variability of brain tumors. They could differ in size, shape, position, and appearance.

To avoid that problem we can use registration-free methods. Some of those could be based on voxel-by-voxel classification. Other approaches could use handcrafted features or feed-forward neural networks. But lots of recent works involve classifiers which are based on fully convolutional neural networks (FCNN).

With fully convolutional neural networks, there are two main approaches. In the first approach we're segmenting volumetric medical images slice-by-slice. Research shows that it works well, but results between adjacent slices of the same MRI or CT aren't always consistent. This problem can be partly solved with the passing of the previous slices mask as additional input to FCNN. But still, it doesn't make the whole use of data structure. 3D FCNN was proposed to solve this issue.

The second approach uses the whole volumetric medical image as an input to 3D FCNN. With help of 3D layers (convolution, pooling, up-sampling, etc.), this model can successfully exploit the volumetric nature of this data. The training algorithm for this network is very similar to the training algorithm of a simple neural network. Also, as experiments show, those type of networks doesn't need a lot of data. In the original U-Net paper, the authors used just 30 images.

II. DATA

Ample multi-institutional routine clinically acquired multi-parametric MRI (mpMRI) scans of glioma, with pathologically confirmed diagnosis and available MGMT promoter methylation status, are used as the training, validation, and testing data for this method. All Brain Tumor Segmentation (BraTS) mpMRI scans describe native (T1) and post-contrast T1-weighted (T1Gd), T2-weighted (T2), and T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) volumes, and were acquired with different clinical protocols and various scanners from multiple data contributing institutions.

All the imaging datasets have been manually annotated, by one to four raters, following the same annotation protocol, and their annotations were approved by experienced neuro-radiologists. Annotations comprise the GD-enhancing tumor, the peritumoral edematous/invaded tissue, and the necrotic tumor core. The ground truth data were

created after their pre-processing, i.e., co-registered to the same anatomical template, interpolated to the same resolution (1 mm3), and skull-stripped.

III. Our Method

For our task we used the Dense V-network. This method uses a fully convolutional neural network, which is inspired by U-Net architecture. The critical features of this approach are the following:

- A batch-wise spatial dropout;
- Dense feature stacks;
- V-network downsampling and upsampling;
- Dilated convolution;
- Explicit spatial prior.

IV. Training

The network was trained for 42 epochs using Adam optimizer with an initial learning rate equal to 0.003. Dice function was used as a loss function, because it considers the loss information both locally and globally, which is critical for high accuracy.

In order not to struck in a local minimum of the loss function, we multiplied the learning rate by a factor of 0.5, when validation loss didn't improve for 5 epochs straight.

Dataset was randomly split into train and validation sets (70% and 30% out of total data respectively). Every MRI image size was set to (184, 184, 128). The batch size was set to 2. Loss changing during the training process is presented on plot 1
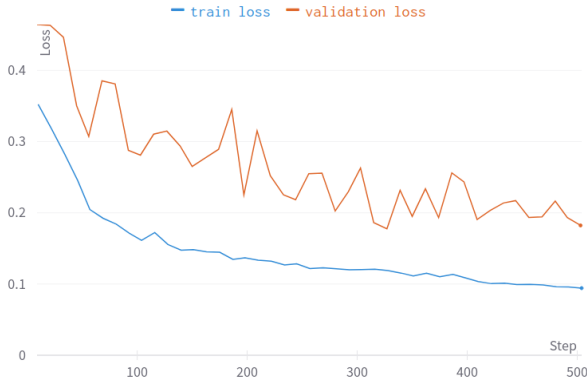

Рис. 1 – Model train and validation loss during training process

V. Results

Metrics result is provided in table X. Dice score significantly (on 0.16) drops on validation images. It happens because of the variability of different MRI images. Not only do brains and tumors differ in shape and size. Even the MRI images themselves have different resolutions and orientations. In further research, this problem can

be solved by applying more augmentations, and by more sophisticated data preprocessing.

Таблица 1 – Dice score

Data split	Dice value
train	0.8956
validation	0.7359

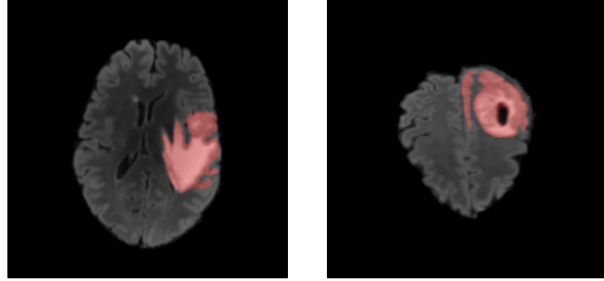Examples of segmentation on two different MRI images are provided below.

Рис. 2 – Examples of tumor segmentation

VI. Conclusion

Segmentation of brain tumors is proposed to facilitate intraprocedural navigation of brain tumor interventions. The proposed deep learning-based Dense V Net can segment brain tumors more accurately than previous methods. However clinically acceptable segmentation accuracies have yet to be defined for guiding abdominal interventions and depends on the intervention and guidance system. The automatically generated segmentations of abdominal anatomy have the potential to support image-guided navigation in brain tumor endoscopy procedures.

1. Cerrolaza J. J. et al. Automatic multi-resolution shape modeling of multi-organ structures //Medical image analysis. – 2015. – Т. 25. – №. 1. – С. 11-21.
2. Okada T. et al. Abdominal multi-organ segmentation from CT images using conditional shape–location and unsupervised intensity priors //Medical image analysis. – 2015. – Т. 26. – №. 1. – С. 1-18.
3. Ronneberger O., Fischer P., Brox T. U-net: Convolutional networks for biomedical image segmentation //International Conference on Medical image computing and computer-assisted intervention. – Springer, Cham, 2015. – С. 234-241.
4. Dolz J. et al. Deep CNN ensembles and suggestive annotations for infant brain MRI segmentation //Computerized Medical Imaging and Graphics. – 2020. – Т. 79. – С. 101660.
5. Menze B. et al. Multimodal brain tumor image segmentation. benchmark: change detection //Proceedings of MICCAI-BRATS. – 2016.
6. Zhou X. et al. Three-dimensional CT image segmentation by combining 2D fully convolutional network with 3D majority voting //Deep Learning and Data Labeling for Medical Applications. – Springer, Cham, 2016. – С. 111-120.