An Optimal Mass Transportation-based Magnetic Resonance Imaging Brain Tumor Segmentation Framework

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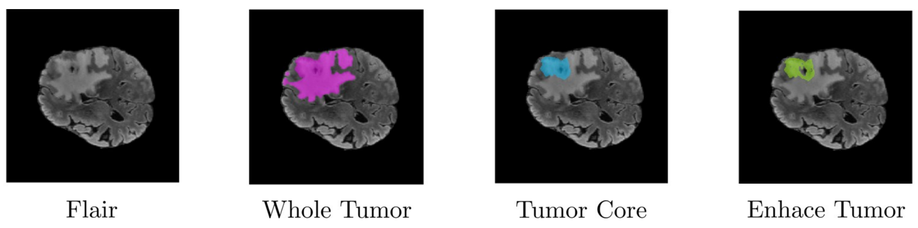
Abstract

This thesis aims to build a brain tumor segmentation framework in MRI images using the deep learning method. For this purpose, we develop a novel 2-Phase framework to enlarge the proportion of brain tumors by using Optimal Mass Transportation (OMT) [1, 2]. Moreover, due to a few training data, we control the density function by different parameters to increase the data diversity. Then we train deep learning models and provide cross-validation results. Overall, the mean cross-validation dice score is 0.9176, and the mean validation (online) dice score is 0.8790 by using SegResNet [3]. Compared with random crop pre-processing, OMT leads the field by a wide margin.

Problem description

Brain tumor segmentation is vital in automatic diagnosis. There are many four different modalities in a brain scan, fluid-attenuated inversion recovery (FLAIR), T1-weighted (T1), T1-weighted contrast-enhanced (T1CE), and T2-weighted (T2). Annotations include the necrotic and non-enhancing tumor core (NCR/NET), the peritumoral edema (ED), and the GD-enhancing tumor. Among the sub-regions to be evaluated are the whole tumor (WT), the tumor core (TC), and the enhancing tumor (ET).

There are two difficulties with brain tumor segmentation. First, due to the large input size for training, we only use small batch sizes. Second, tumor ET is so small and dispersed that models are difficult to detect.

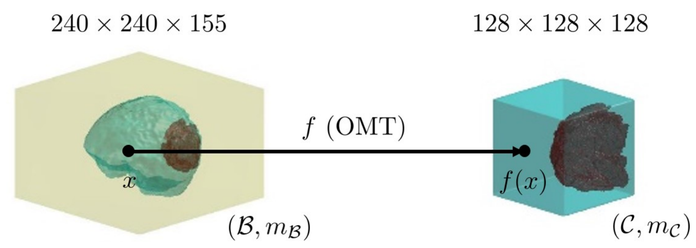


Flair | Whole Tumor | Tumor Core | Enhace Tumor

To deal with the problems above, we propose a novel framework combining OMT and deep learning. OMT has two advantages. First of all, it can deform irregular objects into regular objects, which reduces the shape of model input and speeds up model training. Second, it can enlarge specific regions by controlling density. Based on the advantages above, we designed a 2-Phase framework to detect and segment brain tumors.

OMT Problem. Let $(\mathcal{B}, m_{\mathcal{B}}), (\mathcal{C}, m_{\mathcal{C}})$ be the two measurable spaces which have the same total mass $\int_{\mathcal{B}} \mathrm{d}m_{\mathcal{B}} = \int_{\mathcal{C}} \mathrm{d}m_{\mathcal{C}}$ and let $\mathrm{MP} = \{f : \mathcal{B} \to \mathcal{C} \mid \rho_{\mathcal{B}}(\tau)|\tau| = |f(\tau)|, \forall \tau \in \mathcal{T}(\mathcal{B})\}$ be the set of mass-preserving maps. The OMT problem is to find a map $f^* \in \mathrm{MP}$ that minimizes the transportation cost as the following:

$$f^* = \arg\min_{f \in \mathrm{MP}} \int_{\mathcal{B}} \|v - f(v)\|_2^2 \, \mathrm{d}m_{\mathcal{B}},$$



Results and discussion

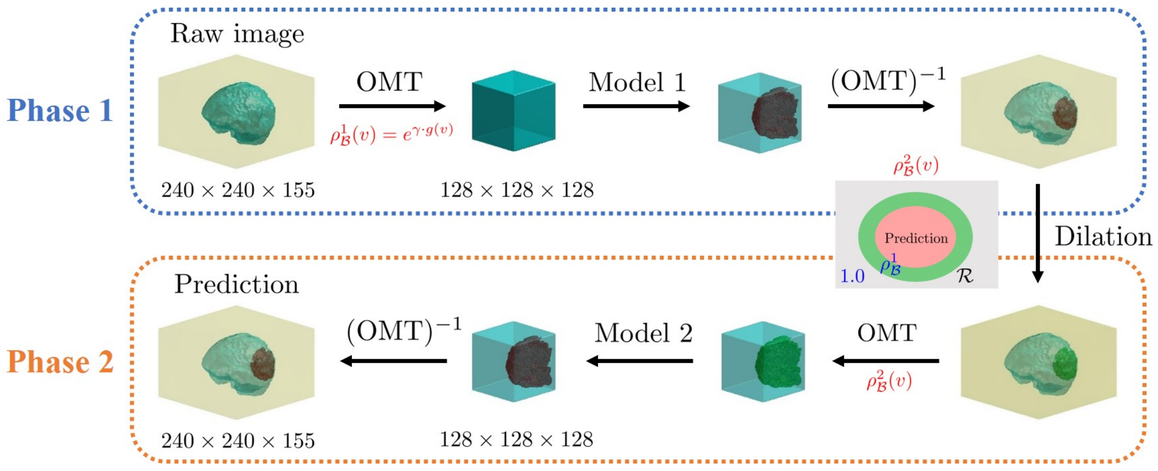
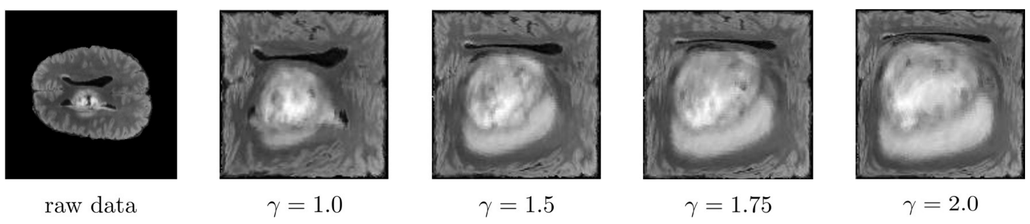


Figure 1: 2-Phase OMT framework.



raw data | $\gamma = 1.0$ | $\gamma = 1.5$ | $\gamma = 1.75$ | $\gamma = 2.0$

Figure 2: Phase 2 OMT image with different γ.

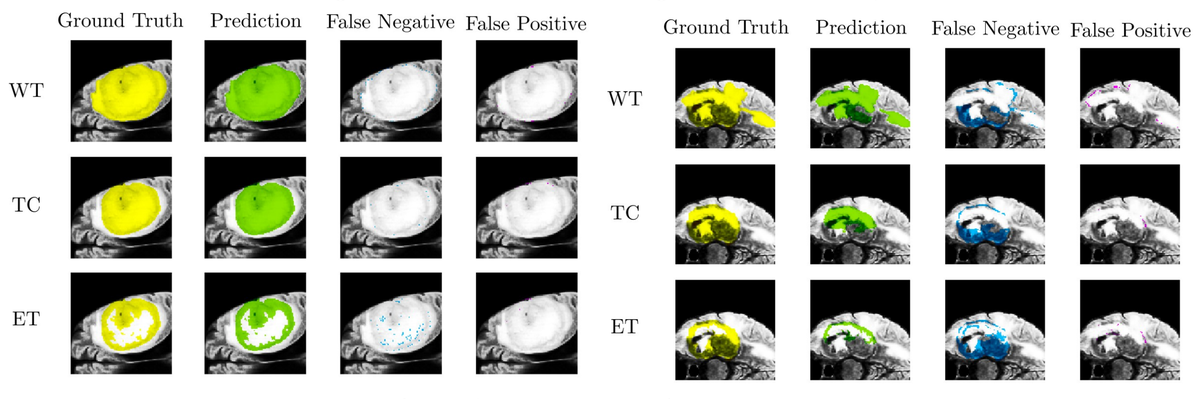


Figure 3: Best case and worst case.

The dataset is provided by MICCAI Brain Tumor Segmentation Challenge 2021. It has 1,251 training data and 219 validation data without labels. We used those data to develop the 2-Phase OMT framework, shown in Figure 1.

In phase 1, we use OMT to map the brain to the cube and predict the WT by ResUNet. Then we expand the 4 pixels by using morphology dilation. It can cover above 99.9% TC and ET. In phase 2, we redefine the density function to enlarge the region's proportion generated from phase 1. Then we predict the WT, TC, and ET by using ResUNet and SegResNet.

We show the average proportion of tumors in raw images, phase 2 OMT images in Table 1 and visualize one case in Figure 2. The proportion of tumors is enlarged as increasing with γ.

Finally, we show the dice score of the models in Table 2. The mean dice score of cross-validation is 0.9176, and the mean dice score of validation (online) is 0.8790. In Figure 3, we show the best case and worst case predictions.

Tumor	Raw image	γ =1.0	γ =1.5	γ =1.75	γ =2.0
WT	6.49%	13.47%	18.27%	20.93%	23.72%
TC	2.42%	5.03%	6.84%	7.84%	8.90%
ET	1.45%	3.04%	4.14%	4.75%	5.40%

Table 1: Tumor average proportion of raw images and OMT images.

Model	Pre-processing	Cross-validation			Validation (online)		
		WT	TC	ET	WT	TC	ET
ResUNet	Random Crop	0.9305	0.9101	0.8610	0.9172	0.8586	0.8090
ResUNet	2POMT	**0.9321**	**0.9146**	**0.8683**	**0.9201**	**0.8667**	**0.8290**
SegResNet	Random Crop	0.9340	0.9082	0.8650	0.9194	0.8542	0.8242
SegResNet	2POMT	**0.9360**	**0.9157**	**0.8812**	**0.9203**	**0.8714**	**0.8452**

Table 2: Dice score of cross-validation data and validation (online) data.

Conclusions

In this thesis, we propose a novel 2-Phase OMT framework for MRI brain tumor segmentation. In pre-processing, we use OMT to transform a brain of 240 × 240 × 155 into a cube of 128 × 128 × 128, which reduces the computation of the deep learning model and training time with keeping the global information of the raw image. Moreover, we design the density function zoom on specific regions to help model detection and make data augmentation by different densities to enhance the model robustness. Compared with random crop pre-processing, the dice score improved significantly.

References

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[3] Myronenko, A.,"3D MRI brain tumor segmentation using autoencoder regularization," BrainLes, MICCAI. pp. 311–320. LNCS, Springer, 2018.