

Multimodal Brain Tumor Segmentation Using The “Tumor-cut” Method on The BraTS Dataset

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Abstract. In this paper, the tumor segmentation method used is described and the experimental results obtained are reported for the “BraTS 2012 - Multimodal Brain Tumor Segmentation Challenge” of MICCAI’12. “Tumor-cut” method, presented in [1] is adapted to multi-modal data to include edema segmentation. The method is semi-automatic, requiring the user to draw the maximum diameter of the tumor, which takes about a minute user-interaction time per case. The typical run-time for each case is around 10-20 minutes depending on the size of the tumor. Overall Dice overlap with the expert segmentation is 0.36 ± 0.25 for the edema/infiltration and 0.69 ± 0.20 for the tumor region.

1 Introduction

In our “Tumor-cut” paper, the semi-supervised tumor segmentation method is described, in detail [1]. This method, specifically targets gross tumor volume (GTV) of the brain tumors on the contrast enhanced T1-weighted MR images (T1C). Here, we extend our method to multi-modal MRI (T1C + FLAIR) to include edema segmentation, and also evaluated on low-grade non-enhanced tumors. Although, we segment the necrotic areas of the high-grade tumors, quantitative necrotic segmentation results are not reported in this paper due to the lack of the ground truth labels of necrotic regions.

2 Methods

The main steps of the “Tumor-cut” method, presented in [1], is given in Fig. 1. The weight of the regularizer of the level-set is set to 0.2, which is determined in [1] by experiments on both real and synthetic data. The same algorithm is applied on FLAIR volumes to segment the clinical tumor volume ($CTV = GTV + Edema$). This time, the user is asked to draw the maximum diameter of the edema region visible on FLAIR images. The main differences observed between GTV (on T1C) and CTV (on FLAIR) is that the sphericity of the edema area is lower and there occurs more curvatures. For the FLAIR segmentation, to allow results with more curvatures, a four times lower regularizer weight is set arbitrarily, at 0.05. The user-input is gathered by two different maximum diameter lines, drawn separately, one for FLAIR and one for T1C volumes. The resulting maps are combined simply by assigning tumor labels using T1C segmentation and assigning edema label to the difference area of the FLAIR segmentation minus the T1C segmentation.

$$V_{Edema} = \{x \in V_{FLAIR} | x \notin V_{T1C}\}$$

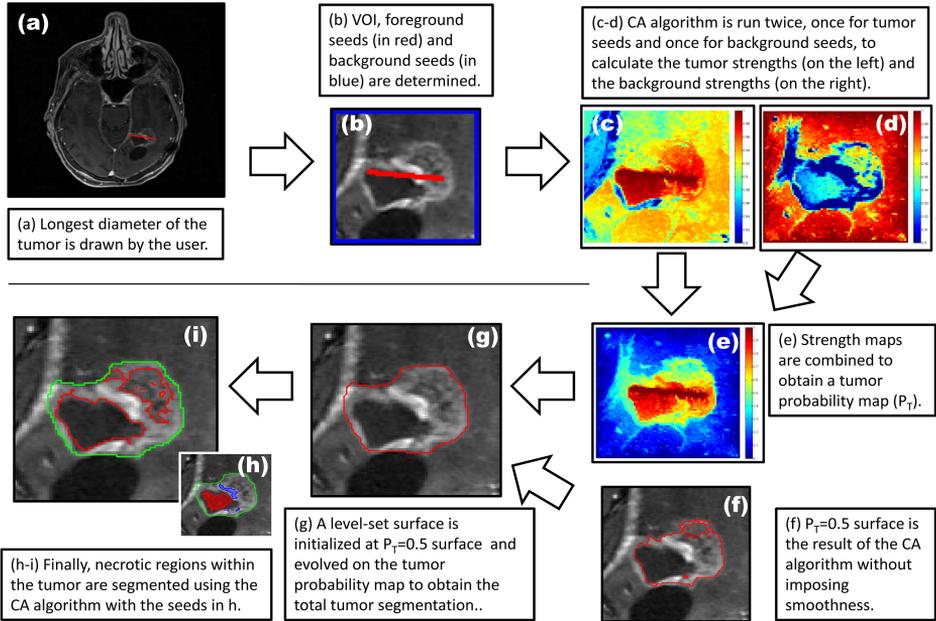


Fig. 1: Flow diagram, which shows the main steps of the "Tumor-cut" algorithm [1].

Table 1: Overall results obtained on the BraTS dataset.

Dice Overlap Edema / Tumor	Jaccard Score Edema / Tumor	Specificity Edema / Tumor	Sensitivity Edema / Tumor	Cohen's Kappa
$0.37 \pm 0.25/0.69 \pm 0.19$	$0.25 \pm 0.20/0.56 \pm 0.23$	$0.99 \pm 0.01/1.00 \pm 0.00$	$0.54 \pm 0.33/0.86 \pm 0.19$	0.27 ± 0.23

3 Results

The method is implemented on Matlab environment, running on a windows 7 workstation, using mex files for core algorithms. For each case, user interaction takes about a minute and typical run-time for each case is around 10-20 minutes, depending on the size of the tumor. The dataset is downloaded from Kitware/Midas web site and the online system provided by the "Virtual Skeleton Database" is used for the evaluation. The Dice overlap results of the runs on each case of the BraTS data set is tabulated in Table 2. For each subset, including high grade and low grade, simulated and patient data, the Dice overlap scores obtained are given as bar charts in Figs 3-6. The overall Dice overlap, Jaccard scores, Sensitivity/Specificity and Cohen's Kappa results with the standard deviations are reported in Table 1.

4 Discussion and Conclusions

Originally we limited the scope of the "Tumor-cut" algorithm to the contrast enhanced gross tumor volumes, which corresponds to the active parts of the high grade tumors in Table 2. For the high-grade cases, the results obtained on the patient dataset (0.73)

PATIENT DATA				SIMULATED DATA			
Case	Edema/Active	Case	Edema/Active	Case	Edema/Active	Case	Edema/Active
LG-1	0.42 / 0.83	HG-1	0.71 / 0.91	Sim-LG-1	0.23 / 0.28	Sim-HG-1	0.53 / 0.97
LG-2	0.34 / 0.55	HG-2	0.65 / 0.63	Sim-LG-2	0.13 / 0.53	Sim-HG-2	0.46 / 0.95
LG-4	0.51 / 0.61	HG-3	0.84 / 0.95	Sim-LG-3	0.08 / 0.50	Sim-HG-3	0.67 / 0.78
LG-6	0.64 / 0.71	HG-4	0.19 / 0.75	Sim-LG-4	0.20 / 0.53	Sim-HG-4	0.40 / 0.66
LG-8	0.20 / 0.78	HG-5	0.56 / 0.33	Sim-LG-5	0.10 / 0.52	Sim-HG-5	0.67 / 0.70
LG-11	0.28 / 0.88	HG-6	0.52 / 0.54	Sim-LG-6	0.11 / 0.64	Sim-HG-6	0.08 / 0.92
LG-12	0.53 / 0.81	HG-7	0.64 / 0.76	Sim-LG-7	0.28 / 0.62	Sim-HG-7	0.69 / 0.90
LG-13	0.31 / 0.48	HG-8	0.66 / 0.94	Sim-LG-8	0.04 / 0.78	Sim-HG-8	0.56 / 0.89
LG-14	0.14 / 0.73	HG-9	0.75 / 0.75	Sim-LG-9	0.06 / 0.54	Sim-HG-9	0.67 / 0.93
LG-15	0.42 / 0.75	HG-10	0.44 / 0.92	Sim-LG-10	0.03 / 0.74	Sim-HG-10	0.54 / 0.98
		HG-11	0.85 / 0.89	Sim-LG-11	0.13 / 0.49	Sim-HG-11	0.39 / 0.92
		HG-12	0.30 / 0.49	Sim-LG-12	0.24 / 0.24	Sim-HG-12	0.71 / 0.78
		HG-13	0.74 / 0.95	Sim-LG-13	0.04 / 0.42	Sim-HG-13	0.67 / 0.70
		HG-14	0.49 / 0.89	Sim-LG-14	0 / 0.70	Sim-HG-14	0.62 / 0.66
		HG-15	0.57 / 0.90	Sim-LG-15	0.14 / 0.51	Sim-HG-15	0.16 / 0.59
		HG-22	0.73 / 0.54	Sim-LG-16	0.30 / 0.29	Sim-HG-16	0.24 / 0.93
		HG-24	0.66 / 0.92	Sim-LG-17	0.10 / 0.38	Sim-HG-17	0.18 / 0.59
		HG-25	0.19 / 0.36	Sim-LG-18	0.15 / 0.69	Sim-HG-18	0.05 / 0.89
		HG-26	0.30 / 0.61	Sim-LG-19	0.33 / 0.60	Sim-HG-19	0.75 / 0.71
		HG-27	0.48 / 0.56	Sim-LG-20	0.06 / 0.60	Sim-HG-20	0.26 / 0.51
				Sim-LG-21	0.04 / 0.83	Sim-HG-21	0.71 / 0.75
				Sim-LG-22	0.20 / 0.57	Sim-HG-22	0.62 / 0.69
				Sim-LG-23	0.30 / 0.22	Sim-HG-23	0.02 / 0.71
				Sim-LG-24	0.08 / 0.66	Sim-HG-24	0.09 / 0.97
				Sim-LG-25	0.03 / 0.81	Sim-HG-25	0.08 / 0.90
Average	0.38 / 0.71	Average	0.56 / 0.73	Average	0.14 / 0.55	Average	0.43 / 0.80

Fig. 2: Table of the Dice overlap results obtained on each case.

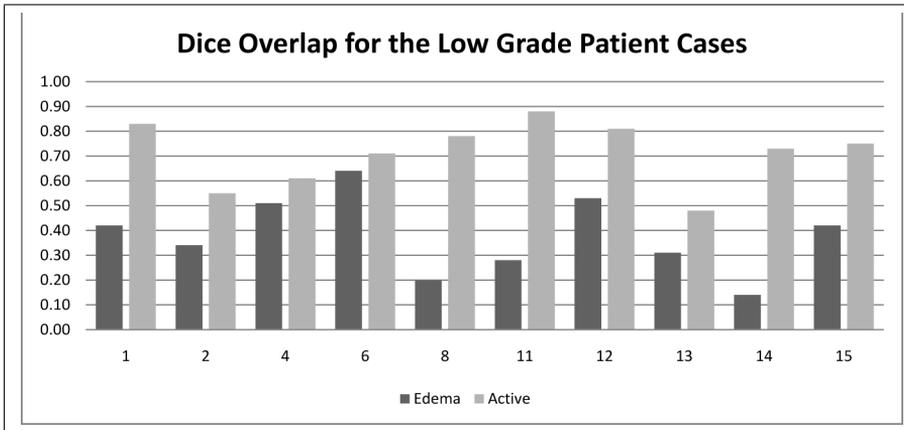


Fig. 3: Dice overlap results obtained on each case of the low-grade patient subset.

and the simulated dataset (0.80) are consistent with the results reported in [1] (0.80 and 0.83). Because the edema region is calculated by subtraction of the two maps, the overlap scores for edema is not independent of the scores for the tumor. For the low-grade simulated data, low performance in some cases is mostly due to the low number of voxels labeled as edema -comparing to patient cases- in the ground truth segmentation, which causes low overlap scores.

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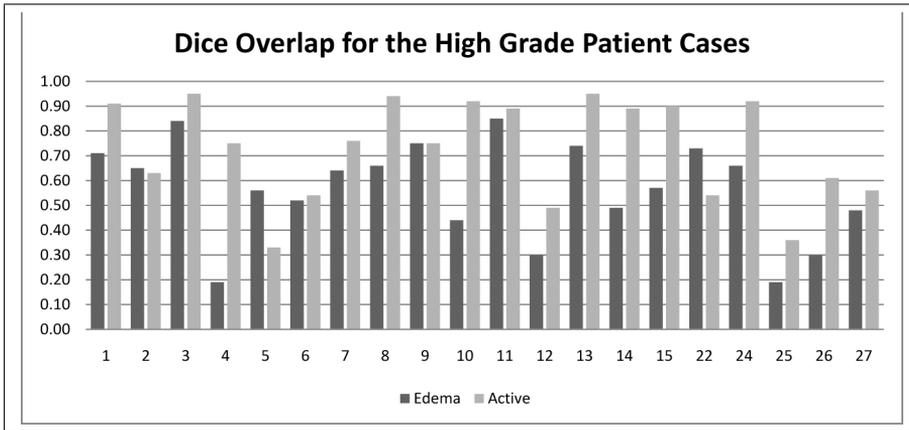


Fig. 4: Dice overlap results obtained on each case of the high-grade patient subset.

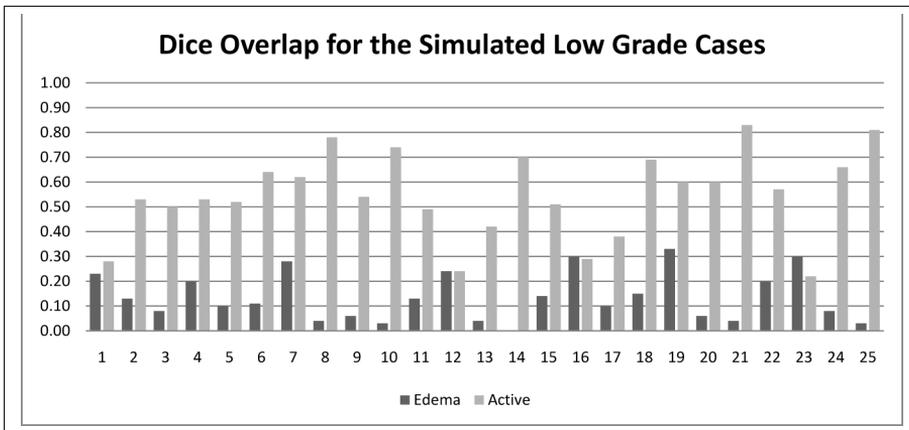


Fig. 5: Dice overlap results obtained on each case of the simulated low-grade subset.

References

1. Hamamci, A., Kucuk, N., Karaman, K., Engin, K., Unal, G.: Tumor-cut: Segmentation of brain tumors on contrast enhanced mr images for radiosurgery applications. *Medical Imaging, IEEE Transactions on* **31**(3) (march 2012) 790–804

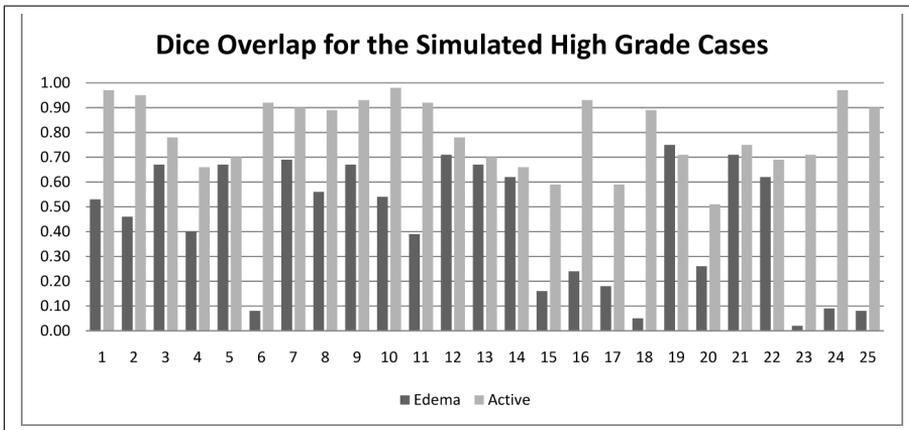


Fig. 6: Dice overlap results obtained on each case of the simulated high-grade subset.