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Kernel sparse representation for MRI image analysis in automatic brain tumor segmentation

Key words: Brain tumor segmentation; Kernel method; Sparse coding; Dictionary learning

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Motivation

1. Because of high spatial resolution and superior soft tissue contrast in magnetic resonance images, MRI images have been used widely in brain tumor segmentation for its non-invasive and harmless.

2. The brain tumor segmentation is challenging due to the complex structure, fuzzy boundaries, and similarity in the intensities of abnormal and normal brain tissue regions.

3. In practice, the segmentation of brain tumor is delineated by experienced clinicians. It is not only time consuming, but also relies on the subjective experience. It is important to develop a valuable and robust tool for brain tumor segmentation.

Main idea

1. The method deploy the *k*-means algorithm on T1-weighted, T2-weighted, and T2-FLAIR-weighted MRI images to cluster all the voxels and select the probable region R1 which fully covers the tumor area and excludes the majority of normal tissues.

2. The *k*-means clustering algorithm is performed on contrast enhanced T1-weighted and T1C-weighted MRI images to determine the probable enhancing tumor region R4 within R1.

3. The regions R1–R4 are segmented precisely using kernel sparse coding method based on four-modality MRI images.

Method

1. MRI images are pre-processed firstly to reduce the noise.
2. The kernel dictionary learning is used to extract the non-linear features to construct five adaptive dictionaries for necrosis, edema, non-enhancing tumor, enhancing tumor tissues and healthy tissues.
3. Sparse coding is performed on the feature vectors extracted from the original MRI images.
4. The morphological filtering is used to fill the area among multiple connected components to improve the segmentation quality.

Major results

The proposed method has good performance on complete tumor, while slightly worse performance on tumor core and enhancing tumor.

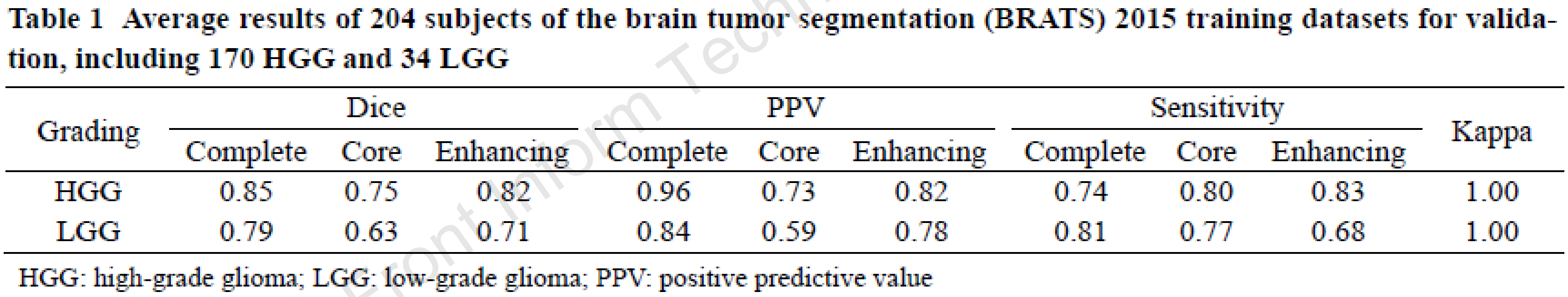

Table 1 Average results of 204 subjects of the brain tumor segmentation (BRATS) 2015 training datasets for validation, including 170 HGG and 34 LGG

Grading	Dice			PPV			Sensitivity			Kappa
	Complete	Core	Enhancing	Complete	Core	Enhancing	Complete	Core	Enhancing	
HGG	0.85	0.75	0.82	0.96	0.73	0.82	0.74	0.80	0.83	1.00
LGG	0.79	0.63	0.71	0.84	0.59	0.78	0.81	0.77	0.68	1.00

HGG: high-grade glioma; LGG: low-grade glioma; PPV: positive predictive value

Major results (Cont’d)

The proposed method is competitive to the other groups in the brain tumor segmentation (BRATS) challenge.

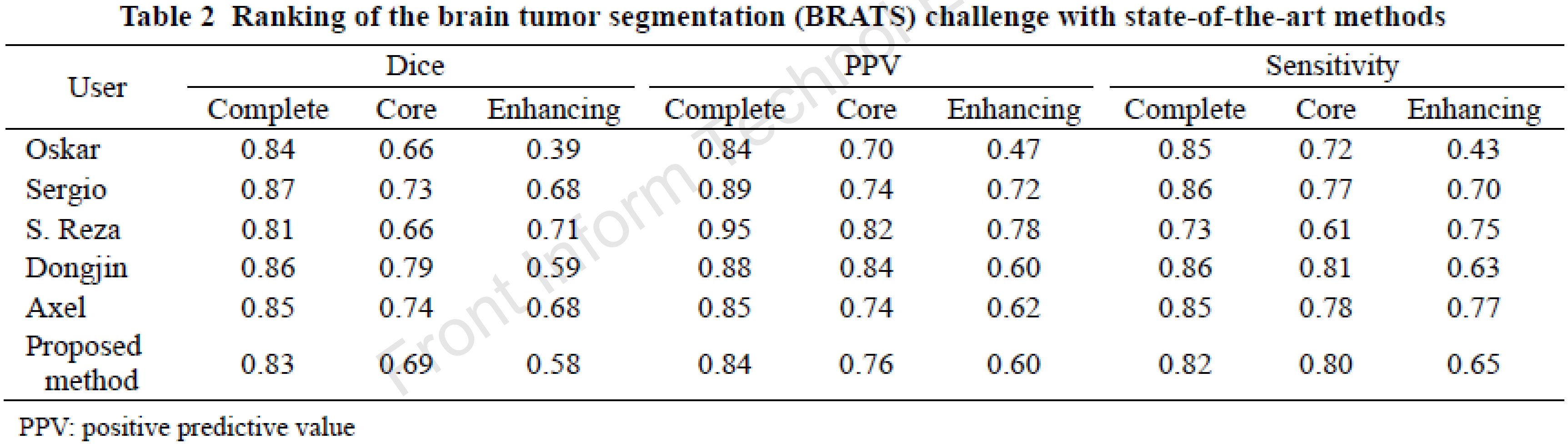

Table 2 Ranking of the brain tumor segmentation (BRATS) challenge with state-of-the-art methods

User	Dice			PPV			Sensitivity		
	Complete	Core	Enhancing	Complete	Core	Enhancing	Complete	Core	Enhancing
Oskar	0.84	0.66	0.39	0.84	0.70	0.47	0.85	0.72	0.43
Sergio	0.87	0.73	0.68	0.89	0.74	0.72	0.86	0.77	0.70
S. Reza	0.81	0.66	0.71	0.95	0.82	0.78	0.73	0.61	0.75
Dongjin	0.86	0.79	0.59	0.88	0.84	0.60	0.86	0.81	0.63
Axel	0.85	0.74	0.68	0.85	0.74	0.62	0.85	0.78	0.77
Proposed method	0.83	0.69	0.58	0.84	0.76	0.60	0.82	0.80	0.65

PPV: positive predictive value

Conclusions

1. The proposed method extracts the non-linear features of MRI images through kernel dictionary learning and sparse coding performed on the feature vectors.

2. The fully-automatic brain tumor segmentation can improve the diagnosis efficiency and reduce the job intensity of physicians.

3. The experiment results are encouraging, and suggest that the proposed method has a better capacity and a higher segmentation accuracy with a low computation cost.