

# Brain Tumor Segmentation by a Cascaded Framework

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## Introduction

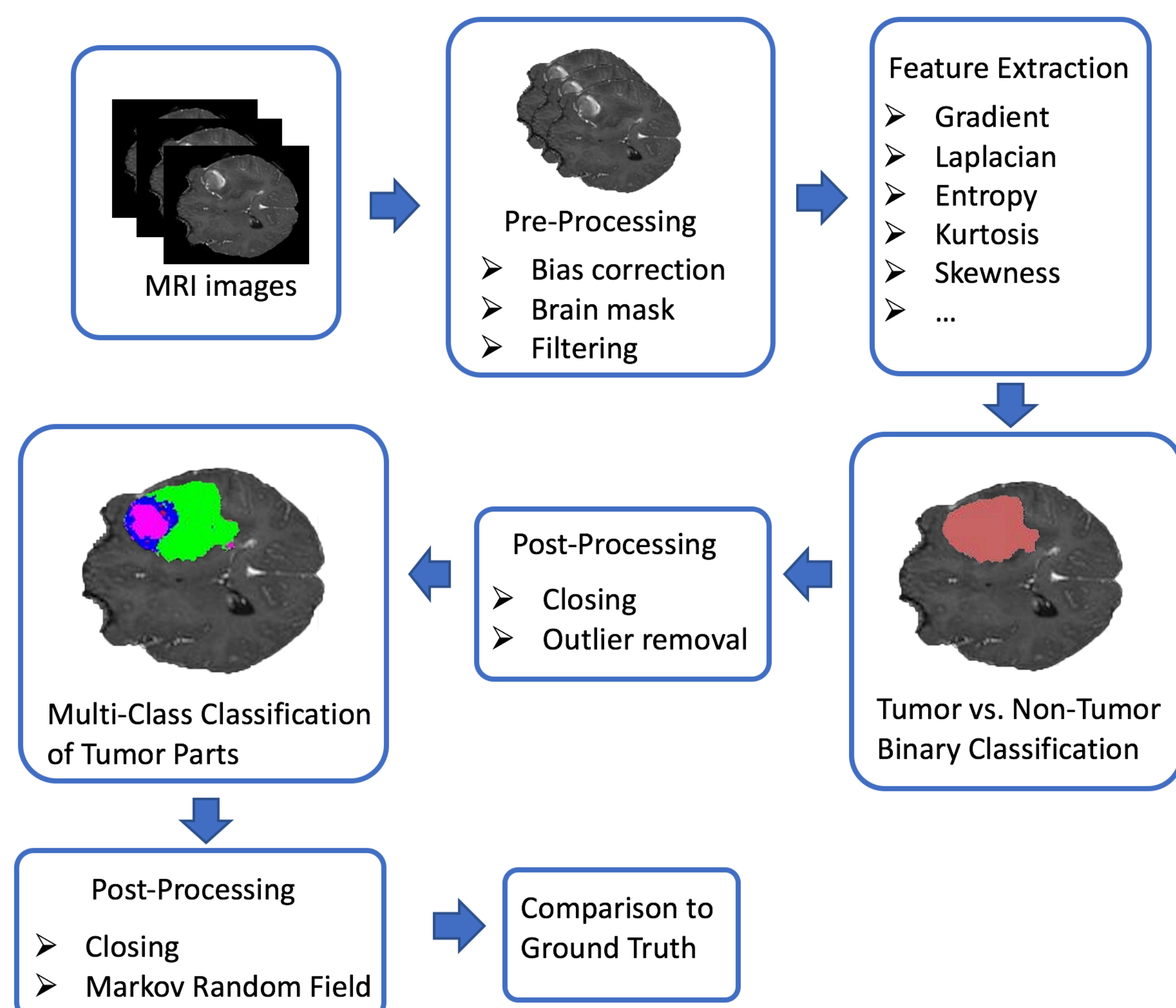
Brain tumor segmentation from magnetic resonance images (MRI) is of high value in healthcare, especially in radiosurgery and radiotherapy planning.

In this project, we aim at segmenting brain tumors from multi-modal imaging data. It's a challenging computer vision task in medical image processing because of the unpredictable appearance and shape. Many different segmentation strategy have been proposed in the literature. We explored some of the state-of-art method and choose a cascaded brain tumor segmentation approach[1] to identify tumor from brain MRI scan images and make some improvement of this method. Finally, we will run the algorithm on different datasets to demonstrate the effectiveness.

## Framework

The goal of brain tumor segmentation is to detect the location and extension of the tumor regions, namely active tumorous tissue (vascularized or not), necrotic tissue, and edema (swelling near the tumor).

A cascaded framework is shown following. After pre-processing and feature extraction of input MRI images, a classifier is applied to distinguish brain tissue into tumor and non-tumor regions. A post-processing step is then carried out to extract large connected components of the tumor tissue. A second level of classification is then performed to distinguish between different tumor types. Two classification methods was used, one class SVM and random forest.



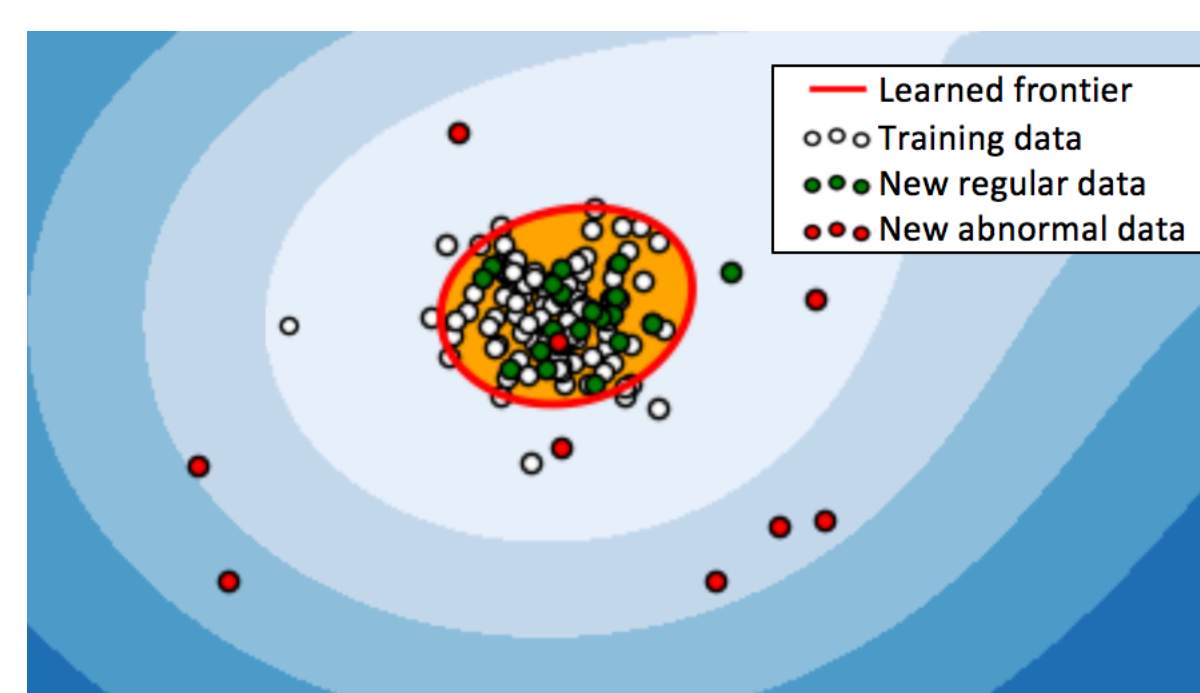
### One-Class SVM:

One-class SVM[4] has been widely used for outlier detection. Only positive sample are used in training. The basic idea of one-class SVM is to use a hypersphere to describe data in the feature space and put most of the data into the hypersphere.

$$\min_{R \in \mathbb{R}, \xi \in \mathbb{R}^I, c \in F} R^2 + \frac{1}{\nu I} \sum_i \xi_i$$

$$s.t. \|\Phi(X_i) - c\|^2 \leq R^2 + \xi_i, \quad \forall i \in \{1, \dots, I\} : \xi_i \geq 0$$

$$f(X) = R^2 - \|\Phi(X) - c\|^2$$

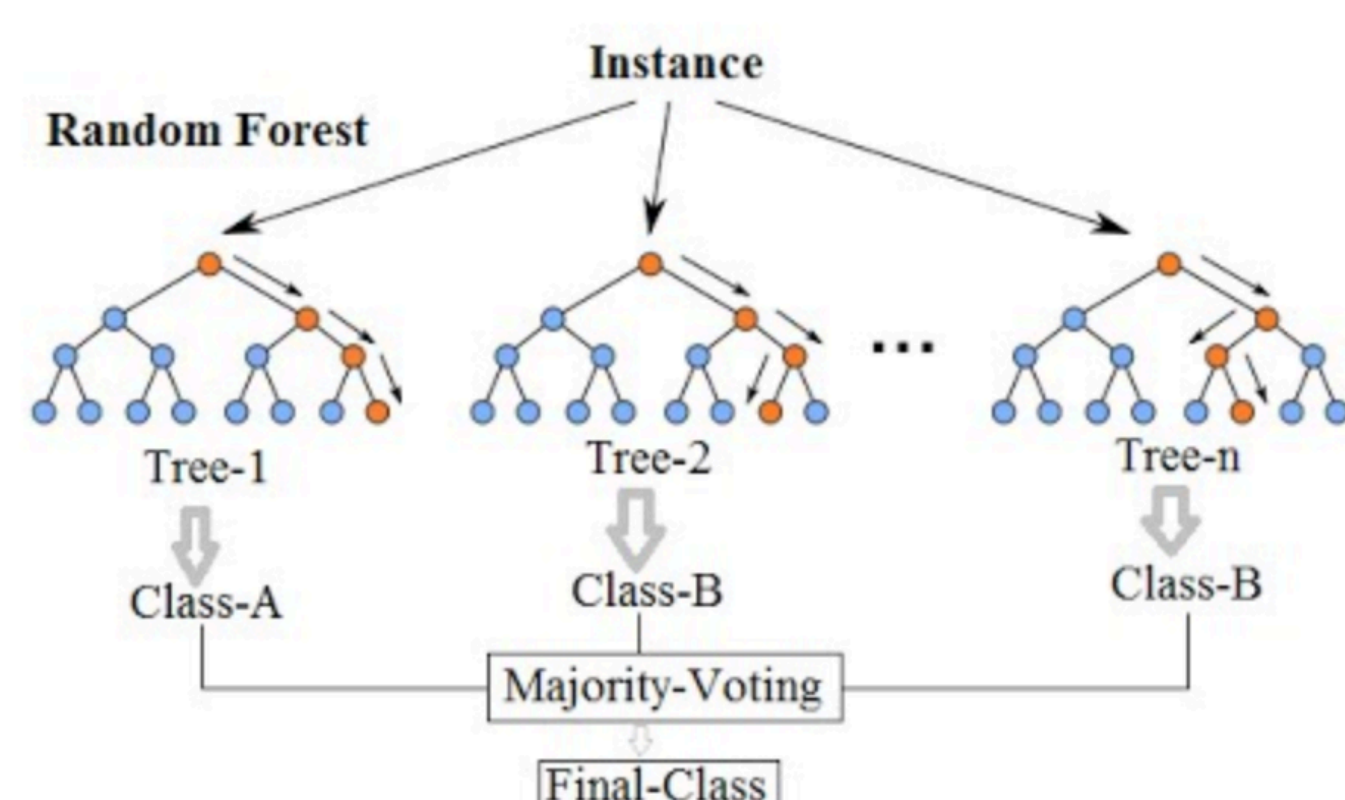


### Random Forest:

Random forests[6] are an ensemble learning method for classification, regression and other tasks, that operate by constructing a multitude of decision trees at training time and outputting the class that is the mode of the classes (classification) or mean prediction (regression) of the individual trees.

$$IG(X, S) = H(S) - \sum_{t \in T} p(t) H(t)$$

$$\hat{f} = \frac{1}{B} \sum_{b=1}^B f_b(x')$$



## Experiment Results

We used the BraTS challenge 2015 dataset[2], which contains about 300 high- and low- grade glioma cases. Each data set has T1 MRI, T1 contrast-enhanced MRI, T2 MRI, and T2 FLAIR MRI volumes. Annotations comprise the whole tumor, the tumor core (including cystic areas), and the Gd-enhanced tumor core.

We first use shell script to process the BraTS dataset and use N4ITK in ANTs toolkit to do pre-processing in batches. Pre-processing result is shown in Fig.1. Then, we feed the extracted features to the cascaded framework and get the result which is shown in Fig.2. Table 1 shows the classification accuracy.

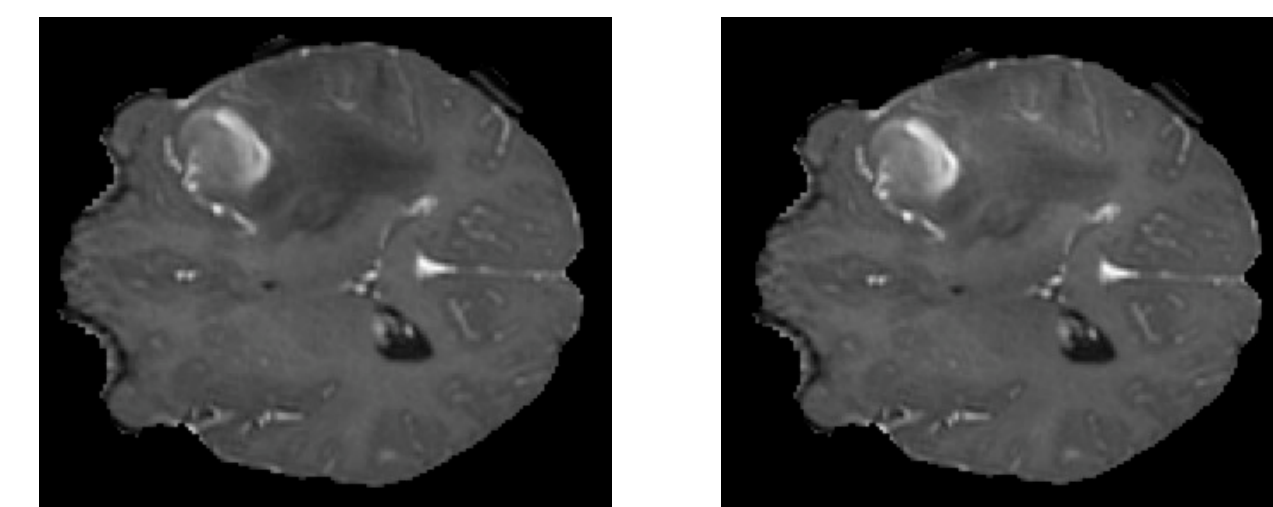


Fig.1 Origin image(left), image after bias correction[5] (right)

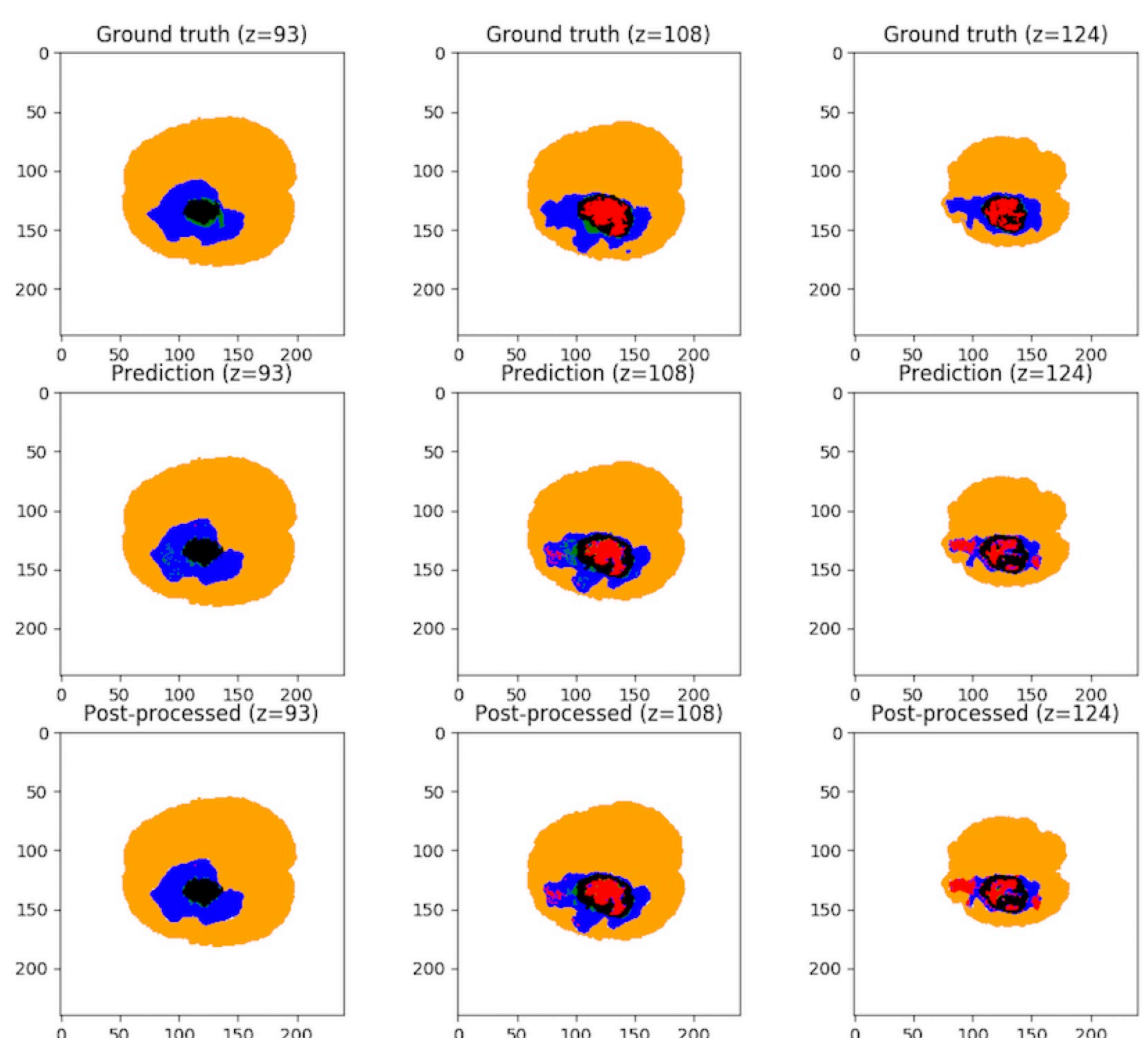


Fig.2 Result image (first row: ground truth, second row: prediction, third row: post-processed)

Table 1: Cascaded random forest method classifier result

Cascaded RF method	Mean	Std	Min	Max
Whole Tumor	0.8052	0.1327	0.4634	0.9388
Tumor Core	0.7062	0.1620	0.3074	0.9346
Enhancing Tumor	0.7543	0.1697	0.2663	0.9221

## Conclusion

We implemented and improved a cascaded framework for classifying tumor cells. One-class SVM and random field are performed separately to do classification. In One-class SVM, we treat tumor cells as outlier since number of normal cells is much greater than tumor cells. We use one-class SVM to classify tumor and non-tumor cells. By employing simple morphological operation, we can fine tune the intermediate results and feed to the second random forest classifier to do more fine-grained classification. The experiment demonstrate the effectiveness of our framework.

## Reference

- [1] Malmi, E., Parambath, S., Peyrat, J.-M., Abinshed, J., Chawla, S.: CaBS: a cascaded brain tumor segmentation approach.
- [2] BraTS Challenge dataset, <https://www.virtualskeleton.ch/BraTS/Start2015>
- [3] Zhang Y, Wu L. An MR brain images classifier via principal component analysis and kernel support vector machine[J]. Progress In Electromagnetics Research, 2012
- [4] K. Heller, K. Svore, A. Keromytis, and S. Stolfo. One class support vector machines for detecting anomalous windows registry accesses. In Workshop on Data Mining for Computer Security (DMSEC), 2003.
- [5] Tustison, Nicholas J., et al. "N4ITK: improved N3 bias correction." *IEEE transactions on medical imaging* 29.6 (2010): 1310-1320.
- [6] Gareth James; Daniela Witten; Trevor Hastie; Robert Tibshirani (2013). An Introduction to Statistical Learning. Springer. pp. 316–321