# Automatic Segmentation of Brain Tumors on Non-Contrast-Enhanced Magnetic Resonance Images using Fuzzy Clustering

**Y-M. Liu[1], C-C. Liao[1,2], F. Xiao[1,3], J-M. Wong[1], and I-J. Chiang[1,4]**

[1]Institute of Biomedical Engineering, National Taiwan University, Taipei, Taiwan, [2]Department of Neurosurgery, Taipei Hospital, Department of Health, Taipei, Taiwan, [3]Department of Neurosurgery, National Taiwan University Hospital, [4]Institute of Biomedical Informatics, Taipei Medical University, Taipei, Taiwan

## Introduction

Manual brain tumor segmentation from magnetic resonance imaging is a difficult and time-consuming task for physicians. For this reason, an automated brain tumor segmentation method is desirable. Currently, segmentation of gadolinium-enhanced tumor is feasible via combining semi-supervised clustering with knowledge-based analysis [1]. However, the accuracy of supervised segmentation techniques depends on the performance of human experts. Moreover, approximately 10% of all brain tumors can not be enhanced in magnetic resonance (MR) images after a contrast agent has been administered, making segmentation extremely difficult [2]. Therefore, we define a non-contrast-enhanced brain tumor segmentation with an unsupervised clustering algorithm, Fuzzy C-Means (FCM) and there is no need for manual data labeling. There are tumor segmentation studies based on non-contrast-enhanced T1-weighed (T1), T2-weighed (T2) and proton density weighed (PD) images [2, 3]. Our study is based on T1 and T2 images only. Even though FCM is quite popular, the neighborhood condition is not considered in FCM. Region merging used in this study just makes up for that weakness. The purpose of this study is to segment brain tumor with non-contrast-enhanced MR imaging via unsupervised FCM clustering combined with region merging and knowledge-based analysis.

## Material and Methods

The MR images in this study were acquired from a medical center in central Taiwan. Patients with meningioma were imaged in T1 and T2 images (256×256 pixels). Because T1 and T2 images have different intensity on same tissues, we performed a multi-spectral histogram for pixels clustering. Based on the concept of split and merge, the system split pixels into clusters by FCM [4], and merged by region merging to obtain tumor. Fig. 1 shows the primary stages of this system. FCM iteratively calculated the fuzzy membership to classify multi-spectral histogram by minimizing the cost function. Generally, the cluster number would be eight, including bone marrow, white matter, gray matter, CSF, edema, tumor ,background and other normal tissues. However, in order to obtain good segmentation, we increased the cluster number to 32. As the pixels were classified, there are two steps to find the seed region for mergence. First, labeled the cluster pixels by 4-connected neighborhood, the feature vector of each pixel was changed to that of the cluster prototype, reducing the complexity. Then, the largest distinctive region of each cluster became the seed region. Merge is to absorb the neighborhood regions with similar feature to seed region. In this study, once the intensity of neighborhood regions were similar to seed region on both T1 and T2 images, the neighborhood region would be absorbed by seed region. The results of the merging process were classified into 4 types: tumor, brain, background, and other normal tissues. Finally, knowledge-based analysis such as eccentricity, solidity and so on, then we can select tumor from the 4 categories. To evaluate the segmentation results, they were compared to the tumor "ground-truth" (GT) which manually labeled by physicians on contrast-enhanced T1.

## Results

Our system had been tested on 25 patients with meningioma. Tumor regions identified with our system were then compared to tumor regions of GT on a pixel level by three measures, including true positives (TP), false positives (FP) and false negatives (FN). GT equals the summation of TP and FN. To represent overall performance of this system, two metrics were used, percent match (PM) and the correspondence ratio (CR) shows in below respectively. $\mathrm{PM} = (\mathrm{TP}/\mathrm{GT}) * 100\%$; $\mathrm{CR} = [\mathrm{TP} - (0.5 * \mathrm{FP})]/\mathrm{GT}$.

In our system, the total PM varies from 29.1% to 100% with a mean and standard deviation of 0.842 and 0.193, respectively while the total CR varies from 0.22 to 0.94 with a mean and standard deviation of 0.716 and 0.203, respectively.

## Conclusions

This system detects tumor with two non-contrast-enhanced MR images, T1 and T2 only. Compared to some tumor segmentation systems using contrast-enhanced images, our system is more convenient and faster. Moreover, the overall quantitative results of this system are satisfactory. This statement represents that tumorous pixels were not only highly match between GT and our system, but has a fair level of correspondence between GT and our system. Therefore, this system has a great potential of being a clinical MR images analysis tool for helping human experts to obtain tumor location and volume estimation or even to plan therapy in the future.

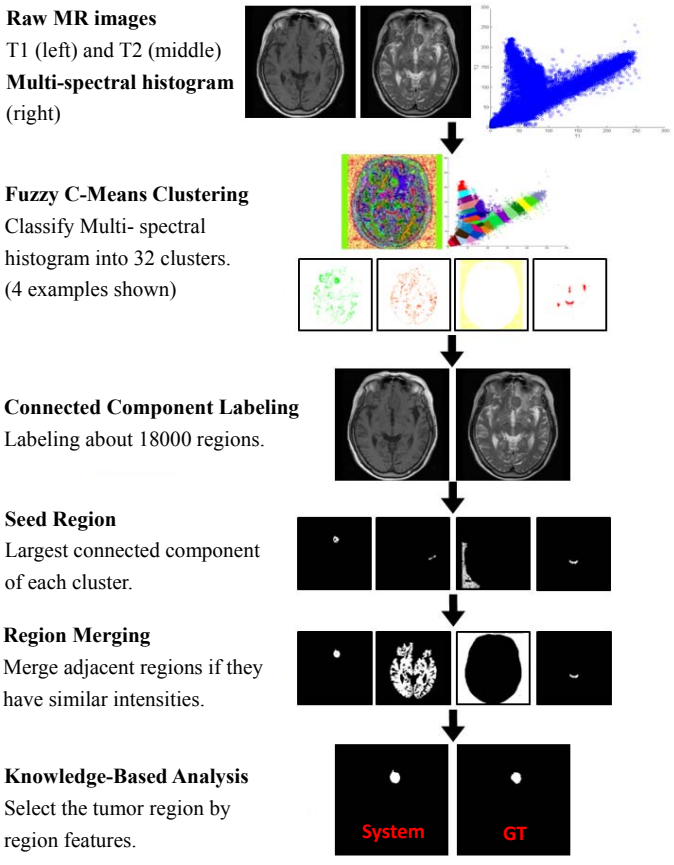


Fig. 1: System overview

## References

[1]. Zhou J, et al., Comput Biol Med, 2003, 33:407-424.
[2]. Fletcher-Heath LM, et al., Artif Intell Med, 21:43-63.
[3]. Clark MC, et al., IEEE Trans Med Imaging, 1998, 17:187-201.
[4]. Bezdek JC, et al., Med Phys, 1993, 20:1033-1048.