Novel Method for Automatic Segmentation of Infiltrative Glioblastoma

Kelvin Wong[1,2] and Stephen Wong[1,2]

[1]*Department of Systems Medicine and Bioengineering, Houston Methodist Research Institute, Houston, TX, United States,* [2]*Department of Radiology, Weill Cornell Medical College, New York, NY, United States*

Introduction

Glioblastoma Multiforme is the most lethal and common brain cancer in adult. Organized by NCI, public databases of genomics, proteomics and other omics data and clinical imaging of GBM are available which are prime resources to understand the cancer biology and how it impacts disease progression. Quantitative extraction of information from patient's image data can potentially bridge the knowledge gap between the macro and micro-scale. In addition, automatic segmentation of various components of glioblastoma from patients' MRI are vital to unbiasedly extracting knowledge from complicated imaging data due to variability in imaging parameters.

Currently, major effort such as BRAin Tumor Segmentation (BRATS) Challenge, attempts to segment large number of GBM cases into edema, Gd-enhanced tumor core, non-enhancing tumor, and necrosis/cyst/hemorrhage (combined). Notably, segmenting the enhancing infiltrating tumor is not part of the challenge due to the difficulties in identifying them. Some may even mistaken the infiltrative tumor as non-enhancing tumor. However, preclinical mouse models MRI studies of infiltrative anaplastic astrocytoma and patient derived xenograft of pediatric and adult GBM all show consistent low Gd-enhancement in these tumors. We also observed the same phenomenon in a small subset of pathologically confirmed GBM cases.

To investigate the prevalence and extent of low Gd-enhancement tumor in GBM, we developed an algorithm to automatically segment the tumor into edema, necrosis/cyst, Gd-enhanced tumor core as well as low Gd-enhancement regions. The method is applied to the GBM collection in The Cancer Imaging Archive (TCIA).

Methods

The automatic segmentation method is implemented by a combination of in-house software and SPM12 (Wellcome Trust Centre for Neuroimaging, University College of London, UK). A custom tissue probability map was generated by excluding the cerebellum in SPM12. Tissue segmentation was performed on the Axial spin-echo T1 MRI to generate gray matter, white matter and cerebrospinal fluid map and the gray/white matter maps were combined to a brain tissue mask. Axial spin-echo FLAIR MRI and Axial spin-echo T1 post-contrast MRI were normalized with non-contrast Axial spin-echo T1 MRI to obtain a relative enhancement maps with the normal brain tissue having a value of unity in both FLAIR and T1 post-contrast MRIs. Coil inhomogeneity inherent in all the images are effectively cancelled and minimal non-brain tissue is included after using the mask. A lower bound thresholds of 1.4-fold and 1.3-fold were used to determine the FLAIR enhancement regions and T1 enhancement regions and a lower bound threhsold of 1.1-fold was used to identify the low Gd-enhancement region. After 1.1-fold threshold, a representative sample T1 enhancement image is shown in Figure 1. A Density-based spatial clustering of applications with noise (DBSCAN) method with a intensity regularized hybrid Euclidean distance matrix to regularize the change of intensity as well as the scattering of points. The result is shown in Figure 2.

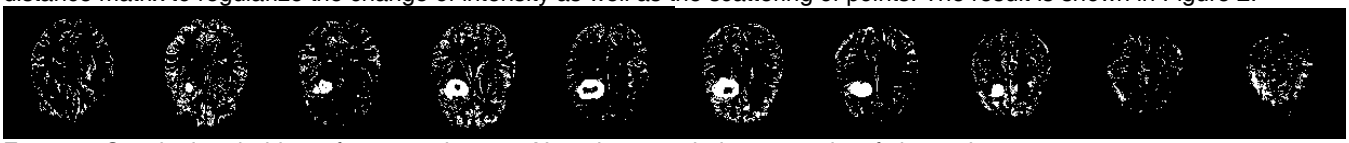

Figure 1. Simple thresholding after normalization. Note the noisy behavior in identify low enhancement region in images.

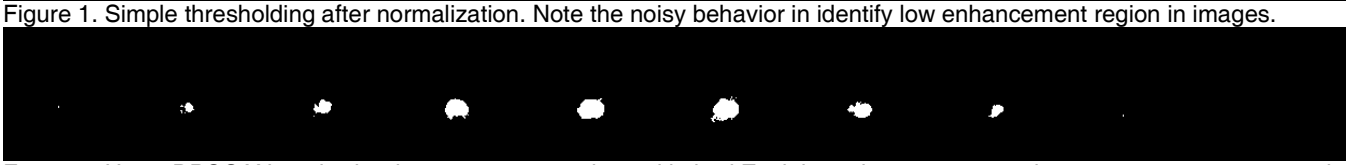

Figure 2. Using DBSCAN method with an intensity regularized hybrid Euclidean distance matrix, the tumor region is extracted.

Results

A representative tumor segmentation is shown in Figure 3. A total of 25 cases were processed from one site in TCIA. Two cases were excluded. One is due to adjacent image suppression artifacts and one Axial T1 image acquired without image intensity filter correction.

Conclusion

We demonstrated in a small cohort of GBM cases (n=25) in TCIA that low enhancement regions can be reliable detected a well as segment the different regions of a GBM tumor.

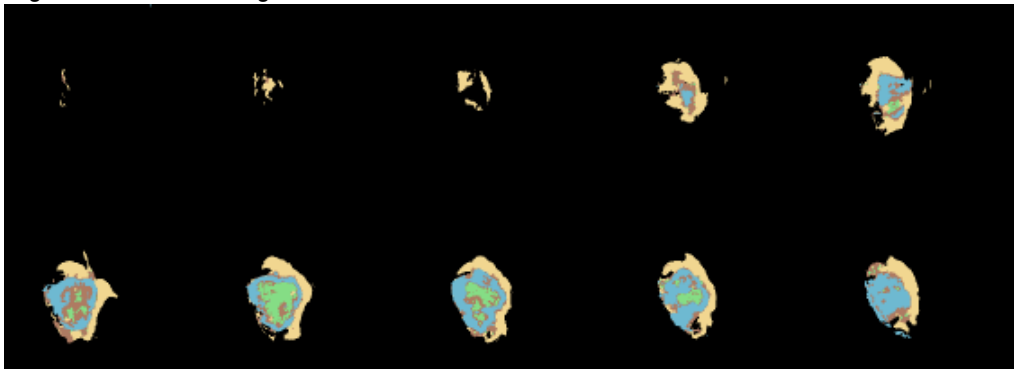

Figure 3. Another case of GBM tumor segmentation. Green is necrosis. Light brown is edema. Blue is high enhancement tumor region. Brown is low-enhancement tumor region.