



Cellular Automata Based Brain Tumor Segmentation on Weighted Magnetic Resonance Images

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ABSTRACT

A fast and robust practical tool is presented for segmentation of solid tumors with minimal user interaction to assist clinicians and researchers in radiosurgery planning and assessment of the response to the therapy. Particularly, cellular automata (CA) based seeded tumor segmentation method on contrast enhanced T1 weighted magnetic resonance (MR) images, which standardizes the volume of interest (VOI) and seed selection, is proposed. First, we establish the connection of the CA-based segmentation to the graph-theoretic methods to show that the iterative CA framework solves the shortest path problem. In that regard, we modify the state transition function of the CA to calculate the exact shortest path solution. Furthermore, a sensitivity parameter is introduced to adapt to the heterogeneous tumor segmentation problem, and an implicit level set surface is evolved on a tumor probability map constructed from CA states to impose spatial smoothness. Sufficient information to initialize the algorithm is gathered from the user simply by a line drawn on the maximum diameter of the tumor, in line with the clinical practice. An algorithm based on CA is presented to differentiate necrotic and enhancing tumor tissue content, which gains importance for a detailed assessment of radiation therapy response. Validation studies on both clinical and synthetic brain tumor datasets demonstrate 80%–90% overlap performance of the proposed algorithm with an emphasis on less

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sensitivity to seed initialization, robustness with respect to different and heterogeneous tumor types, and its efficiency in terms of computation time.

Index Terms—Brain tumor segmentation, cellular automata, contrast enhanced magnetic resonance imaging (MRI), necrotic tissue segmentation, radiosurgery, radiotherapy, seeded segmentation, shortest paths

INTRODUCTION

Brain tumor segmentation: Segmentation of brain tissues in gray matter, white matter, and tumor on medical images is not only of high interest in serial treatment monitoring of

“disease burden” in oncologic imaging, but also gaining popularity with the advance of image guided surgical approaches. Outlining the brain tumor contour is a major step in planning spatially localized radiotherapy (e.g., Cyberknife, iMRT) which is usually done manually on contrast enhanced T1-weighted magnetic resonance images (MRI) in current clinical practice. On T1 MR Images acquired after administration of a contrast agent (gadolinium), blood vessels and parts of the tumor, where the contrast can pass the blood–brain barrier are observed as hyper intense areas. There are various attempts for brain tumor segmentation in the literature which use a single modality, combine multi modalities and use priors obtained from population atlases.

Contrast enhanced magnetic resonance imaging (MRI):

Modalities which give relevant information on tumor and edema/infiltration such as Perfusion Imaging, Diffusion Imaging, or Spectroscopic Imaging provide lower resolution images compared to T1 or T2 weighted sequences, and the former are generally not preferable for geometric measurements. One of the main reasons to use multimodality images such as T2 weighted MRI is to segment edema/infiltration region which is generally not observable in T1 images. Although the glial tumors infiltrate beyond the enhanced margin and edema/infiltration region might be of interest to fractionated radiotherapy in general, it is not possible to distinguish edema and infiltration, so usually this region is not included in primary target planning of radiosurgery, particularly in Cyberknife.

On the other hand, population atlases provide an important prior to improve segmentation by measuring the deviation from the normal brain. Deformable registration of brain images with tumor to the population atlas is an extremely challenging problem and still an active research area due to intensity variations around the tumor mainly caused by edema/infiltration, and the tumor mass effect, which also deforms the healthy tissue morphology. In some studies, affine registration has been used for this purpose; however misalignment issues arise, especially where there is a large deformation of the brain structures.

Although it was reported that the shortest paths and RW produce relatively more seed-dependent results, it can be argued that the global minimum of an image segmentation energy is worth as good as the ability of its energy to capture underlying statistics of images, and a local minimum may produce a solution closer to the ground truth than that of a global minimum. Hence, with good prior information provided as in the case of a seeded image segmentation problem, efficiently finding good local minima becomes meaningful and worthwhile. On the other hand, cellular automata (CA) algorithm motivated biologically from bacteria growth and competition, is based on a discrete dynamic system defined on a lattice, and iteratively propagates the system states via local transition rules. It was first used for image segmentation, which showed the potential of the CA algorithm on generic medical image problems.

Radiosurgery:

The first treatment of choice, depending on the location and size of the tumor, is surgical removal of as much of the lesion as possible (also called resection). Surgery can also

reduce symptoms caused by swelling in the skull, thus reducing the need for medication. Improvement in surgical techniques in recent years has made surgery much safer; however, surgery always has risks that you and your loved one should discuss with the oncologist and neurosurgeon. Surgery may be followed by radiotherapy (see below) to help prevent the formation of new tumors. In deciding whether surgery is right for your loved one, your doctor will consider the size, location and type of the tumor, overall health, and medical history.

Medical image analysis typically involves heterogeneous data that has been sampled from different underlying anatomic and pathologic physical processes. In the case of glioblastoma multiforme brain tumor (GBM), for example, the heterogeneous processes in study are the tumor itself, comprising a necrotic (dead) part and an active part, the edema or swelling in the nearby brain, and the brain tissue itself. To complicate matters, not all GBM tumors have a clear boundary between necrotic and active parts, and some may not have any necrotic parts. Medical image analysis typically involves heterogeneous data that has been sampled from different underlying anatomic and pathologic physical processes.

Radiotherapy:

Patients with more than one tumor, or with one tumor that is not readily accessible, are typically treated with radiation therapy. Radiation Therapy is the use of painless x-rays directed to damage or destroy tumor cells. Radiation may be used after surgery to prevent the tumor from coming back (recurrence), or to destroy tumor tissue that could not be completely removed. In cases where surgery is not an option, radiotherapy may be used instead of surgery to destroy tumor tissue or to relieve symptoms. Radiation is painless, and is typically given in 15-minute visits over several weeks. Radiation has the potential to cause various side effects, depending on your treatment plan. Ask the radiation oncologist about potential side effects of treatment.

Automatic segmentation has the potential to positively impact clinical medicine by freeing physicians from the burden of manual labeling and by providing robust, quantitative measurements to aid in diagnosis and disease modeling. One such problem in clinical medicine is the automatic segmentation and quantification of brain tumors. We consider the GBM tumor because it is the most common primary tumor of the central nervous system, accounting for approximately 40% of brain tumors across patients of all ages, and the median postoperative survival time is extremely short (8 months) with a 5-year recurrence-free survival rate of nearly zero.

Cellular automata (CA) algorithm motivated biologically from bacteria growth and competition, is based on a discrete dynamic system defined on a lattice, and iteratively propagates the system states via local transition rules. It was first used by Vezhnevets *et al.* [19] (Grow-cut) for image segmentation, which showed the potential of the CA algorithm on generic medical image problems. However, Grow-cut was not designed for specific structures, such as tumors, which display heterogeneous content such as necrotic and enhancing tissue. Moreover, anatomic structures typically have relatively smooth boundaries, however, Grow-cut tends to produce irregular and jagged surface results, and only an *ad hoc* way of smoothing was introduced.

Limited therapy options require a careful diagnostic for patients with brain tumors. A multitude of available brain imaging sequences gives rise to patient data sets that include multi-parametric, multi-modal, and multi-temporal volumes even in standard clinical settings. Quantitative analysis of a lesion in these data poses a challenging computational problem. In this paper, a fully automated method is presented for channel-specific tumor segmentation in such multi dimensional images. Tumors may be modeled as outliers relative to the expected shape [4, 5] or image signal of healthy tissues.

Magnetic resonance imaging (MRI) provides indispensable information about anatomy and pathology, enabling quantitative pathologic and clinical evaluations. Segmentation is an important image-processing step by which regions of an image are classified according to the presence of relevant anatomic features. For example, segmentation of MRI of the brain assigns a unique label (e.g., white matter, gray matter, lesions, cerebrospinal fluid, to each voxel in an input gray-scale image). Segmentation methods typically yield binary or categorical classification results. However, continuous classification schemes (e.g., volume size, distance between the volume surfaces, percentage of overlap voxels, percentage of highly discrepant voxels, and probability-based fractional segmentation) are increasingly becoming commonplace. The performance of segmentation methods has a direct impact on the detection and target definition, as well as monitoring of disease progression. Thus, the main clinical goal of surgical planning and quantitative monitoring of disease progression requires segmentation methods with high reproducibility because of the limited number of images available per patient.

A brain tumor is a collection of damaged cells that multiply out of control within the brain. Also called a neoplasm, growth, mass or lesion, a brain tumor is classified as either primary or secondary (metastatic), and can be benign or malignant. Primary brain tumors develop and generally remain in the brain. Secondary brain tumors, or metastatic brain tumors, are cancers that develop elsewhere in the body and spread to the brain. The most common cancers that spread to the brain are lung and breast cancers.

Literature Survey

Sean Ho, Elizabeth Bullitt, and Guido Gerig developed a new method for automatic segmentation of anatomical structures from volumetric medical images. Driving application is tumor segmentation from 3-D MRIs, which is known to be a very challenging problem due to the variability of tumor geometry and intensity patterns. A pre- vs. post-contrast difference image is used to calculate probabilities for background and tumor regions, with a mixture-modelling fit of the histogram. The level-set procedure was successfully run on several tumor datasets, and compared with hand segmentation by an in-house expert rater. The output of each segmentation is a binary image on the same voxel grid as the original MRI.

Marcel Prastawa et al described a framework for automatic brain tumor segmentation from MR images. The detection of edema is done simultaneously with tumor segmentation, as the knowledge of the extent of edema is important for diagnosis, planning, and treatment. The only required input for the segmentation procedure is the T2 MR Image channel. Tumors have a partially enhancing tumor that causes a large deformation of the normal structures. Tumors contain a large, partially enhancing tumor inside the brain stem.

Niloy Ganguly et al reported a detailed survey of the various modelling applications of CA. The survey also provides a vivid sketch of the different theoretical developments which have taken place over the years in the CA research held. These developments have established the immense potential of CA in modelling different applications, thus spreading the appeal of cellular automata over a wide cross-section of researchers.

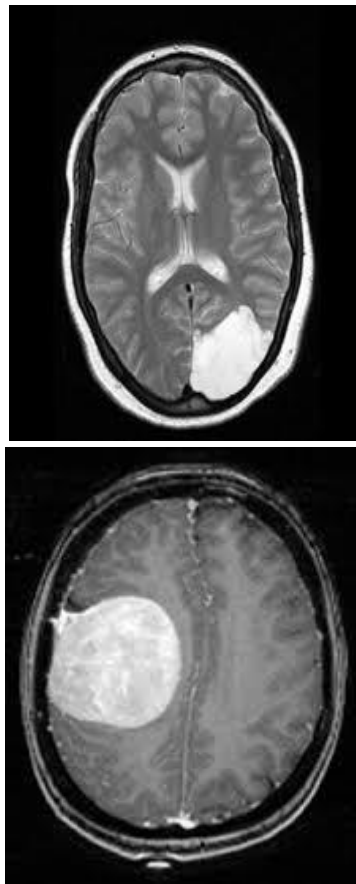


Figure 1: brain tumor images

Methodology:

Tumor segmentation techniques can be performed given below steps,

- Seed Selection Based on Tumor Response Measurement Criteria
- Adapting Transition Rule to Tumor Characteristics
- Level Set Evolution on Constructed Tumor Probability Map
- Enhancing/Necrotic Segmentation

A pseudo code of the tumor-cut algorithm is given below:

```

// For each cell ...
for  $\forall p \in P$ 
  // Copy previous state
   $l_p^{t+1} = l_p^t$ 
   $\theta_p^{t+1} = \theta_p^t$ 
  // Neighbors try to attack current cell
  for  $\forall q \in N(p)$ 
    if  $g(\|\vec{C}_p - \vec{C}_q\|_2) \cdot \theta_q^t > \theta_p^t$ 
       $l_p^{t+1} = l_q^t$ 
       $\theta_p^{t+1} = g(\|\vec{C}_p - \vec{C}_q\|_2) \cdot \theta_q^t$ 
    end if
  end for
end for

```

RESULTS & DISCUSSIONS

The performance measures, Dice overlap, mean, median, and maximum surface distances and the volume percent error between the ground truth segmentation and the results of the algorithm are reported in Table I for the synthetic dataset. The standard deviations show the extent of performance for different realizations of the initialization. The Dice overlap is on the average 83%. Due to the challenging case 5, the volume error is increased.

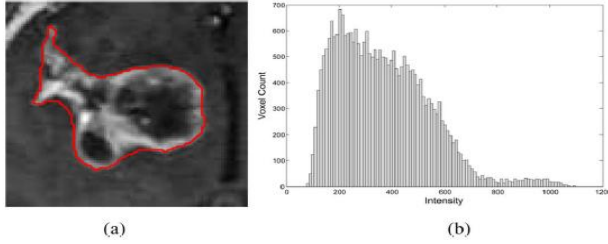


Fig 2 (a) Tumor contour calculated by the proposed method, overlaid on a sample MRI slice. **(b)** MRI intensity histogram of the 3D tumor volume.

Synthetic tumors	Volume error(%)	Max distance(m m)	Mean distance(m m)
1	7.3±5.5	7.6±1.6	1.3±0.3
2	14.8±7.2	8.0±2.3	0.9±0.2
3	4.0±0.4	3.7±0.0	0.4±0.0
4	16.1±0.2	2.9±0.4	0.5±0.0
Average	44.8±76.7	6.8±3.6	1.7±2.1

Table 1: Performance criteria over 4 different tumor images

CONCLUSION

A segmentation algorithm for the problem of tumor delineation is presented which exhibit varying tissue characteristics. As the change in necrotic and

enhancing part of the tumor after radiation therapy becomes important, also applied for the Tumor-cut segmentation to partition the tumor tissue further into its necrotic and enhancing parts. Validation studies is presented over a synthetic tumor database and two real tumor databases. Strengths of the proposed method include its simple interaction over a single slice and less sensitivity to the initialization (demonstrated by lower coefficient of variation values), its efficiency in terms of computation time, and robustness with respect to different and heterogeneous tumor types. Choosing the contrast enhanced T1 modality limits the

application to the tumors that are enhanced with the contrast agent, excluding the edema/infiltration region around the tumor.

REFERENCES

- [1] M. Prastawa E. Bullitt, S. Ho, and G. Gerig, “A brain tumor segmentation framework based on outlier detection,” *Med. Image Anal.*, vol. 8, no. 3, pp. 275–283, 2004.
- [2] B.Menze,K.V.Leemput,D.Lashkari,M.-A.Weber,N.Ayache,andP.Golland, “A generative model for brain tumor segmentation in multimodal images, “*Med. Image Comput. Comput.Assist. Intervent.*, vol.13, pp. 151–159, Sep. 2010.
- [3] S. Ho, E. Bullitt, and G. Gerig, “Level-set evolution with region competition:Automatic 3-D segmentation of brain tumors,” in *Proc. ICPR,2002*, vol. 1, p. 10532.
- [4] N. Ganguly, B. K. Sikdar, A. Deutsch, G. Canright, and P. P. Chaudhuri, A survey on cellular automata Centre for high performance computing, Dresden Univ. Technol., Dresden, Germany, Tech. Rep., 2003
- [5] V. Vezhnevets and V. Konouchine, “Growcut-interactive multi-label n-d image segmentation by cellular automata,” presented at the Graphicon, Novosibirsk Akademgorodok, Russia, 2005.
- [6] J. Kari, “Theory of cellular automata: A survey,” *Theoretical Comput. Sci.*, vol. 334, no.1–3, pp. 3–33, 2005.
- [7] A. Hamamci, G. Unal, N. Kucuk, and K. Engin, “Cellular automata segmentation of brain tumors on post contrast MR images,” in *MICCAI*. New York: Springer, 2010, pp. 137–146.
- [8] M. Prastawa, E. Bullitt, and G. Gerig, “Synthetic ground truth for validation of brain tumor MRI segmentation,” in *MICCAI*. NewYork: Springer, 2005, pp. 26–33.
- [9] N. Archip, F. Jolesz, and S. Warfield, “A validation framework for brain tumor segmentation,” *Acad. Radiol.*, vol. 14, no. 10, pp. 1242–1251, 2007.
- [10] M.-R. Nazem-Zadeh, E. Davoodi-Bojd, and H. Soltanian-Zadeh, “Atlasbasedfiber bundle segmentation using principal diffusion directions and spherical harmonic coefficients,” *NeuroImage*, vol. 54, pp. S146–S164, 2011.