Asian Journal of Computer Science and Technology
ISSN: 2249-0701 (P) Vol.5 No.1, 2016, pp.10-16
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DOI: https://doi.org/10.51983/ajcst-2016.5.1.1764

Image Mining Automata Based Seeded Tumor C-Taxonomy Algorithm for Segmentation of Brain Tumors on MR Images (BITA)

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(Received 12 January 2016; Revised 23 January 2016; Accepted 10 February 2016; Available online 18 February 2016)

Abstract **- In this paper, CA algorithm is used to 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 with proper choice of transition rule. An algorithm based on CA is presented to differentiate necrotic and enhancing tumor tissue content to assist clinicians and researchers in radiosurgery planning and assessment of the response to the therapy. Proposed segmentation framework is composed of three stages. First VOI is selected with foreground & background seeds using the line drawn by the user over the largest visible diameter of the tumor. In second stage, tumor CA algorithm is run on the VOI for the foreground & background seeds to obtain strength maps. Two strength maps are combined to obtain tumor probability map & level set surface is evolved on tumor probability map to impose spatial smoothness. Finally necrotic regions of the tumor is segmented using CA based method with chosen enhanced & necrotic seeds.**

Keywords: **Tumor segmentation, Cellular Automata (CA), Magnetic Resonance Imaging (MRI), Necrotic region, Radiotherapy, Seeded segmentation.**

I.INTRODUCTION

Brain tumor segmentation from MR images is a difficult task and image analysis based on intensity and shape.There are many issues and challenges associated with brain tumor segmentation. In recent years a great effort of the research in field of medical imaging was focused on brain tumors segmentation. Brain tumors may be of any size, variety of shapes, may appear at any location, and may appear in different image intensities.

Segmentation of brain tissues in gray matter [1], white matter [2], and tumor [3] 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 which is usually done manually on contrast enhanced T1- weighted magnetic resonance images (MRI) in current clinical practice [4].In this paper, a fast and robust practical tool for segmentation of solid tumors with minimal user interaction to assist clinicians and researchers in radio surgery planning and assessment of the response to the therapy is presented.

II.RESEARCH METHODOLOGY

Image segmentation has often been defined as the problem of localizing regions of an image relative to content However, recent image segmentation approaches have provided interactive methods that implicitly define the segmentation problem relative to a particular task of content localization.[5]. There are various attempts for brain tumor segmentation which use a single modality, combine multi modalities. Region-based active contour models are widely used in image segmentation. In general, these region-based models have several advantages over gradient-based techniques for segmentation, including greater robustness to noise. However, classical active contours had the problem of being "only as good as their initialization," even when using level-set surfaces in 3D. Interactive algorithms have become popular for image segmentation problem in recent years. Graph based seeded segmentation framework has been generalized such that graph-cuts (GC) [6], random walker (RW) [5], shortest paths, and power watersheds [7] have been interpreted as special cases of a general seeded segmentation algorithm, which solves a minimization problem involving a graph's edge weights constrained by adjacent vertex variables or probabilities. In [8], the connection between GC, RW, and shortest paths was shown to depend on different norms: (GC); (RW); (shortest paths), in the energy that is optimized. Geodesic distances between foreground and background seeds were also incorporated into other shortest path-based segmentation algorithms.

III.PROBLEM IDENTIFICATION RESEARCH

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. CA algorithm shows potential on generic medical image problems.

IV.SOLUTION OF RESEARCH PROBLEM

In this paper, the CA algorithm is introduced to 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 with a proper choice of the transition rule. Next, as our application is in the clinical radiosurgery planning, where manual segmentation of tumors are carried out on contrast enhanced T1-MR images by a radio-oncology expert, we modify the CA segmentation towards the nature of the tumor properties undergoing radiation therapy by adapting relevant transition rules. Finally, a smoothness constraint using level set active surfaces is imposed over a probability map constructed from resulting CA states.

V.IMPLEMENTATION RESEARCH

A. Cellular Automata in Image Segmentation

A cellular automata is basically a computer algorithm that discrete in space and time and operates on a lattice of cells [11]. Since it was first proposed by Von Neumann and Ulam [12],Cellular Automata has attracted researchers from various fields in both physical and social sciences because of its implicity and potential in modeling complex systems.

Each individual cell is in a specific state and changes synchronously depending on the states of some neighbors as determined by a local update rule [13]. They are parallel, local and homogeneous, since the state of any cell depends only on the states of the local neighbors at the previous time step and the update rules are same for every cell.

Formally, a cellular automaton (CA) is a triple $A=(S,N,\delta)$ where S is a nonempty set, called the state set, N is the neighborhood, and $\delta: S^N \rightarrow S$ is the local transition function (rule); S^N which is the argument of δ , indicates the states of the neighborhood cells at a given time, while S which is its value, is the state of the central cell at the next time step [11].

There are various attempts of using CA in image processing problems including image enhancement, sharpening and smoothing, image filtering, edge detection and image segmentation (Grow-cut). Grow-cut method uses a continuous state cellular automata to interactively label images using user supplied seeds. The cells are corresponding to image pixels, and the feature vector is RGB or gray scale intensities[14]. Cellular automata were introduced they have been progressively used to model a great variety of dynamical systems application domains.

VI.RESEARCH METHODS

A.Tumor Cut Algorithm

Steps of the cellular automata based tumor segmentation algorithm is as follows.

1) Image Acquisition: To Access the real medical images like MRI, PET or CT scan and to take up a research is a very complex because of privacy issues and heavy technical hurdles. The first stage in any vision system is the image acquisition stage. In this stage, images can be acquired from cameras. Magnetic resonance imaging (MRI) is a non- invasive medical test that helps physicians diagnose and treat medical conditions. MRI uses a powerful magnetic field, radio frequency pulses and a computer to produce detailed pictures of organs.

2) Pre-processing: MRI brain images cannot be fed directly as the input for the proposed technique. The input image is subjected to a set of pre-processing steps so that the image gets transformed suitable for further processing. The digital image data for a spatial database requires several pre- processing procedures. The goal of digital image processing is to increase both the accuracy and the interpretability of the digital data during the image processing phase.

3) *VOI & Seed Selection*: Seed selection algorithm employs the same idea to follow the familiar clinical routine to which the clinicians are used to: the volume of interest (VOI), the tumor seeds and the background seeds are determined by using the line already drawn by the user to measure the longest diameter of the solid tumor. Similarly, focusing on tumor segmentation problem, the seed selection procedure starts with a single line drawn by the user along the longest visible diameter of the tumor. Afterwards, the VOI and the seeds are computed as follows: 1) The line is cropped by 15% from each end and thickened to three pixels wide to obtain tumor seeds; 2) VOI is selected as the bounding box of the sphere having a diameter 35% longer than the line; 3) One-voxel-wide border of this VOI is used as background seeds Since the VOI is completely bounded by the background seeds, each path connecting inside and outside the VOI is blocked by a seed. Then, the result of labeling using only the data inside the region is equivalent to using the whole volume whereas the computation time is significantly reduced. Edge detection uses the difference in color between the background color and foreground.

4) *Tumor and Background Strength*: Tumor CA algorithm is run on the VOI for each two sets of seeds (for the foreground and background) to obtain strength maps for foreground (c) and background (d) at each voxel. One obvious drawback is that the user draws the line on only a single slice of the tumor volume, hence it is not guaranteed that the depth of the tumor will also coincide with theVOI.

5) Obtaining Tumor Probability map: Strength maps are combined to obtain the probability map. The intuition with this probability construction is that probability of being a tumor is proportional to its distance normalized to the closest background seed. This leads to choosing a higher probability of being a tumor when the distance to the background seeds is large, over analysis Processing and vice versa.

Therefore, the tumor probability map is obtained by combining the distances for tumor (D_T) and background (D_B). Geodesic distances to the class seeds can be calculated by

$D = -\ln(x)$ (1)

$P_{Tumor} = D_B/D_T + D_B$ (2)

Finding distance of each cell to the nearest seed in a simultaneous iteration.. In order to create a probabilistic map, which can be used in an active surface (e.g., a level set surface) evolution, the algorithm is run for each class with corresponding class seeds (tumor and healthy) separately.

A.CUT ALGORITHMS OR C-TAXONOMY

A pseudo code of tumor probability is given as follows for all
∀l ∈{Tumor, Background}
//Initialize
for ∀p ∈ P
if p is a seed of class l, xo l,p=1 , else xo l,p=0
end for
Do until convergence
//For each cell…..
for ∀p ∈ P
// Neighbors try to attack current cell
for ∀q ∈ N(P)
find q:q with maximum g(p,q). xt l,,p*
xt+1 l,,p = g(p,q). xt l,,p**
end for
// Copy previous state xt l,,p = xt+1 l,,p
end for end do

6) *Level Set Evolution on Constructed Tumor Probability Map*: Smoothing is an important prior in segmentation of brain tumors from post-contrast T1 images, because of three main reasons: First, an area surrounded by tumor tissue is considered as a tumor region even the intensity characteristics are likely to be healthy. Secondly, it is possible to include misclassified necrotic regions to tumor region, which are usually surrounded by enhanced tissue. Finally, it is possible to exclude nearby vascular structures that are enhanced by administration of the contrast agent. After obtaining the tumor probability map using the foreground and background strength maps, an implicit 3-D level-set surface is initialized over the volume whose inside is given by $\{(X,Y,Z): P_{Tumor>0.5}\}$. The level set function whose zero-level set represents an initial estimate of the tumor surface,S, is evolved on P_{Tumor} with a piecewise constant region assumption of [10], however by using a local Gaussian kernel to define inner and outer regions around the propagating surface in order to compute regional statistics of the map, which constitute the inside and outside sample means in this case. When the surface evolution converges, the final tumor segmentation map is obtained.

The level-set-based smoothing over the constructed tumor probability map constitutes an important part of the proposed method, as the clinical expert segmentation, particularly in radiation oncology, mainly outlines the tumor borders using contouring for radiotherapy planning as opposed to pixel by pixel labeling of the tumor carried out in some validation studies. As a result, our interactive tumor segmentation includes an appropriate intelligent smoothing of the tumor borders based on the labeling results obtained from a graph- theoretic approach.

7) Enhancing/Necrotic Segmentation: Quantification of the necrotic regions within a whole tumor is an important problem in assessment of the tumor progress. In CE-T1 MR images, necrotic parts of the tumor are observed s hypo-intense for there is no blood flow into these regions where enhanced parts are hyper-intense. Without any prior information, segmentation using an intensity threshold can be applied by assigning necrotic label to the voxels lower than the chosen threshold and enhanced label to those that are higher. Threshold,is chosen using expectation maximization[15] and Otsu's methods [16]. Instead of using simple thresholding, connectedness was imposed by using the CA algorithm with two thresholds as follows: Initially the voxels lower than a necrotic threshold are labeled as necrotic seeds and higher than an enhanced threshold are labeled as enhanced seeds. Next, the voxels at remaining mid-intensities are labeled by assigning the label of he nearest seed using the CA algorithm. An algorithm to choose the two thresholds is devised as follows: First the number of necrotic voxels and the number of enhanced voxels are roughly calculated by using Otsu'smethod. Then the necrotic and enhanced thresholds are determined such that%25 of the necrotic volume is assigned as necrotic seed and %25 of the enhanced volume is assigned as enhanced seed.

VII . RESULTS AND DISCUSSION

A. Input

In the experimental setup 256x256 input images extracted. During testing Brain Image including healthy and diseased cells are taken for analysis. The images are taken are that of MRI scan. The test image can be of any size. The input image is shown in fig.1. The input images are contrast enhanced during training phase.Input image is labeled as foreground (Green) and background (Blue). In this CA based method, threshold values are selected for probability calculation of tumor seeds. Then graph-cut surface is initialized for smoothening the tumor region. Finally necrotic or dense tissue regions within the tumors are segmented.

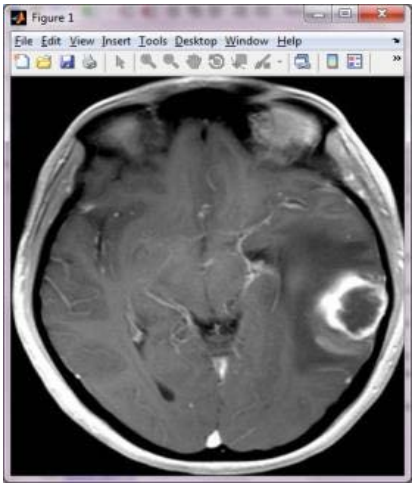

Fig. 1 Input Brain MR Image

B. Output

In this step, image is processed & VOI & seeds are selected as shown in Fig.2.

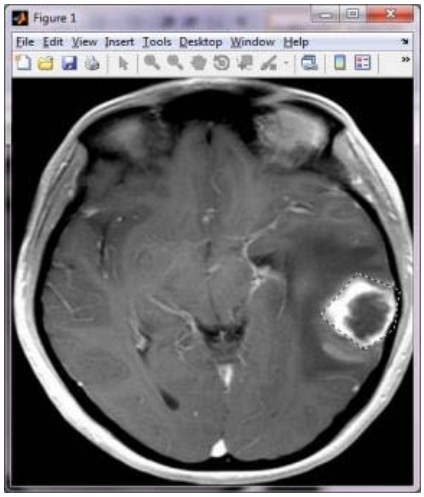

Fig. 2 VOI & seed selection

Tumor CA algorithm is run twice on the VOI for the foreground and background seeds to obtain strength maps for foreground and background as shown in Fig.3 & Fig.4.

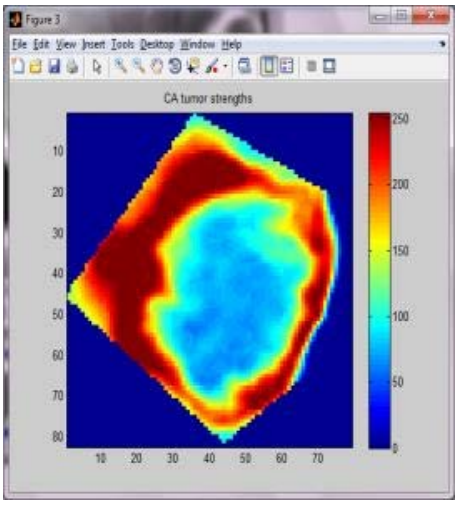

Fig.3 Tumor Strength

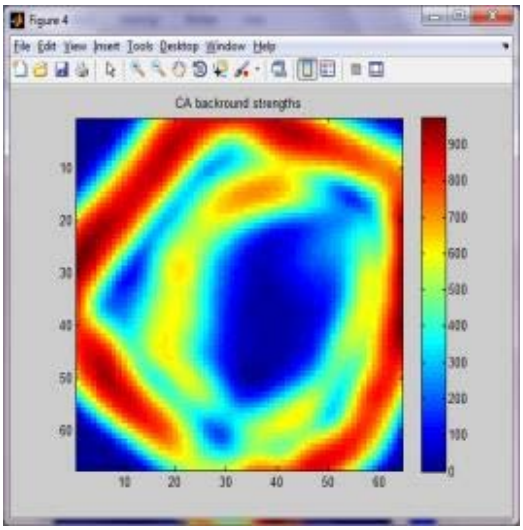

Fig.4 Background Strength

Tumor Probability map is constructed from the two strength maps as shown in Fig.5

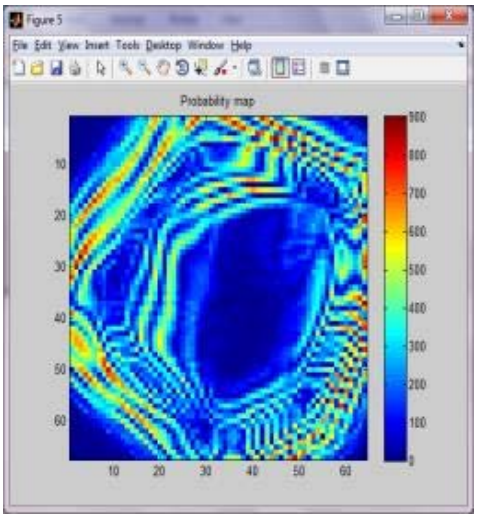

Fig.5 Tumor Probability map

The level-set-based smoothing over the constructed tumor probability is constructed as shown in Fig.6.

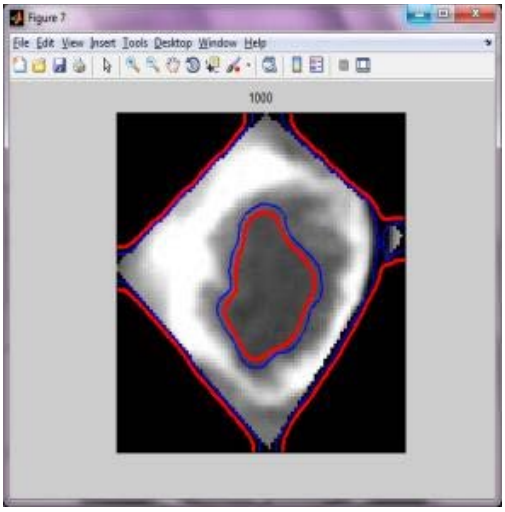

Fig.6 smoothing image

Finally necrotic and enhanced thresholds are determined using CA algorithm as shown in Fig.7.

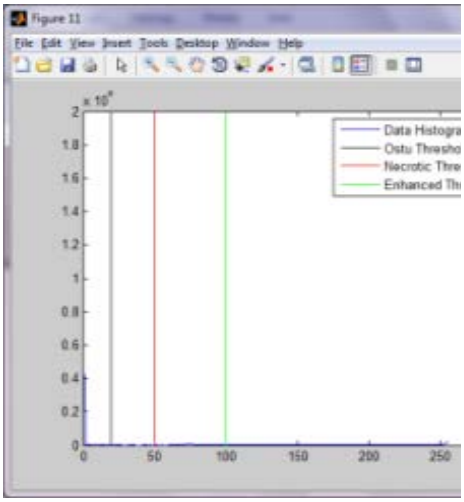

Fig.7 necrotic and enhanced thresholds

VIII. FUTURE SCOPE

CA algorithm have shown promising results in various applications in computer vision and can be successfully applied in other medical image analysis tasks, such as analysis of tomography images of lungs, mammography mass detection and prostate tumor analysis. In future this work will pave the way to reach automatic assessment of the tumor response to therapy, due to reasonable and acceptable success rate of algorithm.

IX. CONCLUSION

In this paper segmentation algorithm is presented for the problem of brain tumor which exhibit varying tissue characteristics .Here attempts presented to quantify changes in necrotic and enhancing tumor tissue contents. As the change in necrotic and enhancing part of the tumor after radiation therapy becomes important, so applied the CA based tumor segmentation to partition the tumor tissue further into its necrotic and enhancing parts.The probability maps constructed from each modality could be combined to obtain the final segmentation.

ACKNOWLEDGMENT

This paper is made possible through the help and support from everyone, including: My wife M.suganya and Daughter S.S.Inakshi and My sir S.Syed Nazimuddeen and S.Irshath Ahamed , and in essence, all sentient beings. I sincerely thank to my parents, family, and friends, who provide the advice and financial support. The product of this paper would not be possible without all of them.

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