Efficient algorithm for Brain Tumor Segmentation with minimal user interaction

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Abstract— Manual segmentation of brain tumor by doctors is a time consuming task. Therefore, several automatic segmentation algorithms have been developed. Major problem in brain tumor segmentation is to detect the presence of tumors in MR images of the brain and to segment the abnormal pixels from normal pixels. In this paper, the objective is to provide a quick and efficient algorithm for segmentation of solid brain tumors with minimal user interaction to help clinicians and researchers in radiosurgery planning and assessment of the response to the radiotherapy. For this purpose, Cellular Automata(CA) algorithm is presented to effort the initial seed selection and Region of interest(ROI). First, Shortest path problem is solved by combining graph based approach with cellular Automata approach for segmentation. CA algorithm consists of local transition rules which has to be altered in order to find the absolute solution for shortest path problem. For handling the heterogeneous tumor types, a spatially-varying parameter is used and to provide smoothness, a level-set surface is applied over the tumor probability map obtained from CA Transition states. Further, Necrotic region is distinguished from enhanced tumor content with the help of re-examined CA algorithm which can be performed by proper selection of transition rule. Performance comparison is carried out by a measure called Dice Overlap with respect to its sensitivity, robustness and efficiency.

Index Terms— Cellular automata, Brain tumor segmentation**,** Tumor probability map, Level-set surface, Dice overlap.

1 INTRODUCTION

Image Segmentation has been considered as the difficulty of localizing the Region of Interest(ROI).i.e, content of a medical image. Hence, for solving this problem all we need is an interactive algorithm that speed up the segmentation along with enough user interaction. Segmentation of Brain tumor is of high interest because of the advance of medical image guided surgical approaches. Bordering the brain tumor contour is an important step in planning spatially localized radiotherapy which is usually done manually on contrast enhanced T1-weighted magnetic resonance (MRI) images in present clinical methods. For accurate segmentation, information regarding edema region is of high interest in radiosurgery planning which can be acquired from multi-modality images such as T1 or T2 weighted images. But it is impossible to obtain such a higher resolution from single modality images such as Perfusion imaging, Diffusion imaging, etc. And also single modality images are not suitable for geometric measurements.

Population Atlases provide prior information about the tumor by evaluating the deflection from normal brain structure. But, Deformable registration of brain tumor images to the population atlas is an important problem due to the intensity deviations around the tumor and tumor mass effect, which affects the healthy tissue anatomy[2].

Affine registration may also be used for solving the image segmentation problem[3],[4]. But, in case of large deformation of brain tissues, misalignment criteria occurs. There are different performance measures associated with the comparison of various manual expert segmentations which includes Jaccard Index, False Positive Volume Fractions(FPVF), False Negative Volume Fractions(FNVF) and Dice Overlap.

2 RELATED WORK

Based on the Outlier detection, Prastawa and Bullitt provided the average overlap of about 86.7% with an average of 1.5h processing time[3].It is carried out with the brain tumor dataset of three patients.

Region-based active contour models are widely used in image segmentation [5]. In general, these region-based models have several advantages over gradient-based techniques for segmentation, including greater robustness to noise. However, when using level-set surfaces in 3D, classical active contours had the problem of initialization. Because the tumor class does not have prior spatial information, many tiny structures, especially blood vessels, are categorized as tumor since they also enhance with contrast.

Ho et al. used fuzzy classification of pre- and post-contrast T1 images to obtain a tumor probability map to evolve a level-set surface [6]. Liu et al. have adapted the fuzzy connectedness framework for tumor segmentation by constructing a rectangular volume of interest selected through identifying the first and last slice of the tumor and specifying a set of pixels in the tumor region [7]. Interactive algorithms have become popular for image segmentation problem in recent years.

Graph based seeded segmentation framework includes some generalizations such as random walker (RW) [12], graph-cuts (GC) [11], shortest paths, and power watersheds [13] have been clarified as special cases of a general seeded segmentation algorithm. This combined framework solves a minimization problem involving a graph's edge weights confined by probabilities or adjacent vertex variables. In [8], the association between GC, RW, and shortest paths was shown to depend on different norms:L_1 (convergence q=1 for GC);L_2

(q=2 for RW); L_∞(q=infinity for shortest paths), in the energy that is optimized. Geodesic distances between foreground and background seeds were also consolidated into other shortest path-based segmentation algorithms by [9] and [10].

Cellular Automata algorithm is basically a computer algorithm that is discrete in space and time and operates on a lattice of pixels. Cellular Automata were introduced by Ulam and Von Newmann[14]. Cellular Automata can be successfully applied in various Image processing applications such as Noise removal, border detection, Image Enhancement, segmentation and Filtering.

3.PROPOSED METHODOLOGY

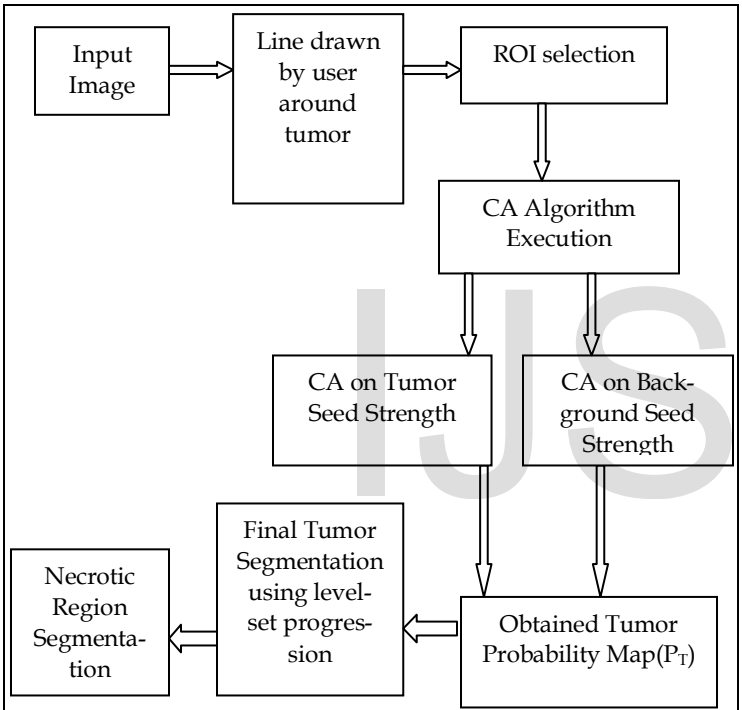

Figure 1:Block Diagram of Proposed Method

3.1 Steps of the Algorithm

Tumor-Cut algorithm consists of the following steps to perform the segmentation of solid Brain tumor with enough user interaction:

Step1: User draws line that forms a bounding square box around the visible parts of the tumor in order to determine the Region of Interest(ROI).

Step2: By using this line drawn, Foreground and background seeds are evaluated.

Step3: To acquire strength maps for both Background and Foreground at each pixel, CA algorithm is executed on the ROI twice, i.e., each for background and foreground seeds.

Step4: Two strength maps, i.e., foreground and background maps are then united to acquire the total tumor probability map P_T.

Step5: An inherent Level-set surface is embedded over the tumor surface with its initialization at P_T=0.5 in order to obtain the convergence to the final tumor segmentation map.

Step6: Conclusively, CA based OTSU thresholding method is used to distinguish the necrotic and the enhanced tumor tissue content.

3.2 Seed Selection

Our seed selection algorithm employs the same idea to follow the familiar clinical routine to which the clinicians are used to: the Region of interest (ROI), 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 ROI and the seeds are computed as follows:

1) The line is cropped from each end and thickened to three pixels wide to obtain tumor seeds.

2) ROI is selected as the bounding box of the sphere having a diameter longer than the line.

3)One-pixel-wide border of this ROI is considered as background seeds.

The ROI is completely bounded by the background seeds, each path connecting inside and outside the ROI 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.

3.3 Re-examined CA algorithm Framework

A Cellular Automata is basically a computer algorithm that is discrete in space and time. It operates on a lattice of cells or sites or pixels. According to the local update transition rule, each pixel or cell changes its state synchronously, depending on its neighbours. The state of every cell is only dependent on the state of its local neighbours and hence, they are parallel, continuous and homogenous. Update rules are similar for each and every cell or pixel.

Usually cellular automata is used for finite state set(discrete), but CA also supports infinite or continuous state sets when the states are in real numbers. Grow cut method uses a continuous state CA to conjointly label the images using user equipped seeds. The cells are analogous to image pixels and MRI gray scale intensities are considered as image features. The state set for each image pixel is represented as $S<\Theta,l,\hat{C}>$ where Θ stands for "Strength" value in a continuous interval [0,1], 'l' for label and $\hat{C}$ for image feature vector. The automata is initialized by electing corresponding labels at seeds with a strength value be-

tween 0 and 1.1 reflects the labelled seeds and 0 for unlabeled seeds.

In the tumor segmentation application, the cells or nodes in CA framework refers to the MRI volume pixels in 3-D. The automata algorithm is initialized with user defined tumor and background seeds and iterated by the following transition rule:

$l_i^{t+1}=l_i^t$ and $x_i^{t+1}=g(i,i^*)x_{i^*}^t$ where $i^*=\arg\max_{j\in N_i} g(i,j)x_j^t$ --(1)

Where g is a pixel similarity or transition function confined to [0,1], which is similar to the edge weight function w_{ij} in the Graph theoretic seeded segmentation framework. A typical symmetric edge weight function depending on the image features, is given by the absolute intensity difference or gradient magnitude between neighboring nodes i and j

$$g(i,j)=e^{-||I_i-I_j||} \quad --(2)$$

where I_i denotes the MR image intensity at node i. In the seeded tumor segmentation application over contrast enhanced T1-weighted MRI for heterogeneous tumors, which mostly consist of a ring enhancing region around a dark necrotic core, most of the tumor seeds fall in the necrotic region. This sometimes causes the segmentation algorithm to get baffled at necrotic to enhancing tumor transition borders. To overcome such problems, prior knowledge that tumor pixels are brighter in post-contrast T1 weighted images can be used. This can be achieved by modifying the transition function g(i,j) by admitting a spatially-varying parameter

$$g(i,j)=\begin{cases} e^{-\beta||Ii-Ij||}, if\ Ii>Ij\ and\ Ij=Tumor \\ e^{-||Ii-Ij||}, otherwise \end{cases} \quad --(3)$$

The inspiration here is based on the observation that the enhancing tumor cells are brighter than the normal cells, and more centrally located necrotic core is darker. Therefore, by adjusting the parameter β, the weight reduction of a tumor state while passing through a ramp up gradient is adjusted to be lower than other tumor categories. Although, some of the properties derived for the algorithm is no more valid, as due to asymmetric edge weight values, we can no longer annotate the algorithm in the undirected graph framework.

3.4 Level Set Progression on obtained tumor Probability Map

In segmentation of brain tumors from post-contrast T1 images, Smoothing is an important precedent, because of three main reasons: (i)An area surrounded by tumor tissue is considered as a tumor region even the intensity characteristics are likely to be healthy, (ii)It is possible to include misclassified necrotic regions to tumor region, which are usually surrounded by enhanced tissue and (iii)It is possible to eliminate nearby vascular structures that are enhanced by application of the contrast agent.

CA algorithm has the benefit of finding distance of each pixel or cell to the nearest seed in a simultaneous iteration. However, the resulting strength map has only one-sided information, that is the distance to the other label classes is not available. In order to create a probabilistic map, which can be used in an implicit surface (e.g., a level set surface) progression, the algorithm is run for each class with corresponding class seeds (tumor and normal) separately. Geodesic distances to the label class seeds can be calculated by D=-ln(x). Finally, the tumor probability map is obtained by combining the geodesic distances for tumor (D_T) and background (D_B) as

$$P_T=D_B/(D_T+D_B) \quad --(4)$$

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 selecting a higher probability of being a tumor when the distance to the background seeds is large, and being a background when the distance is small. After acquiring the tumor probability map using the foreground and background strength maps, an inherent 3-D level-set surface is initialized over the volume V whose inside is given by $\{(X,Y,Z):P_{TUMOR}>0.5\}$. The central idea of level-set surface is to represent the evolving contour using a signed function, where its zero level correspond to the actual contour or outline of tumor. The level-set embedding is carried out over the tumor surface by

$$\delta s/\delta t=(u-v)(u+v-2P_T)N \quad --(5)$$

where u, v are the means inside and outside the surface, and N is the unit normal vector to surface S.

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, however by using a local Gaussian kernel to define interior and exterior regions around the proliferating surface in order to estimate 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 essential part of the proposed method, as the clinical segmentation, particularly in radiation therapy, mainly contours the tumor borders using contouring for radiotherapy planning as opposed to pixel by pixel labeling of the tumor carried out in some cases. Therefore, our interactive tumor segmentation includes an appropriate intelligent smoothing of the tumor borders based on the labeling results obtained from a graph-theoretic approach

3.5 Necrotic Region Segmentation

In CE-T1 MR images, necrotic parts of the tumor are examined as 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. Instead of using sim-

ple thresholding, connectedness was imposed by using the CA algorithm with two thresholds as follows: Initially the pixels lower than a necrotic threshold are labeled as necrotic seeds and higher than an enhanced threshold are labeled as enhanced seeds. Thus, necrotic regions are differentiated from that of the enhanced tumor tissue content for detailed therapy response with the help of CA based OTSU thresholding method.

4 RESULTS

This section provides the results of Tumor segmentation for radiosurgery applications using Cellular Automata Algorithm.

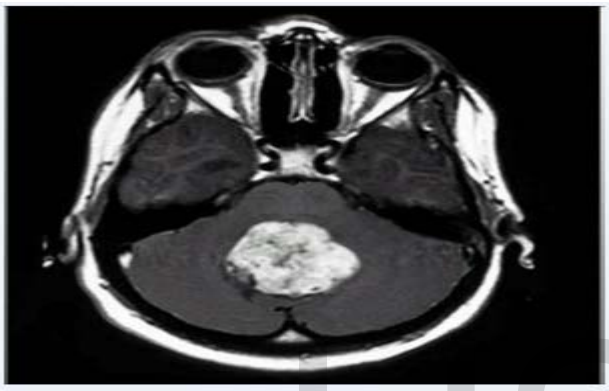

Figure 2:Original Image

In figure 2, medulla MRI image is considered as an input image with tumor in which the Region of Interest(ROI) is selected by the user itself by drawing a bounding square box around the visible parts of tumor. The cropped part of that ROI is shown in figure 3.

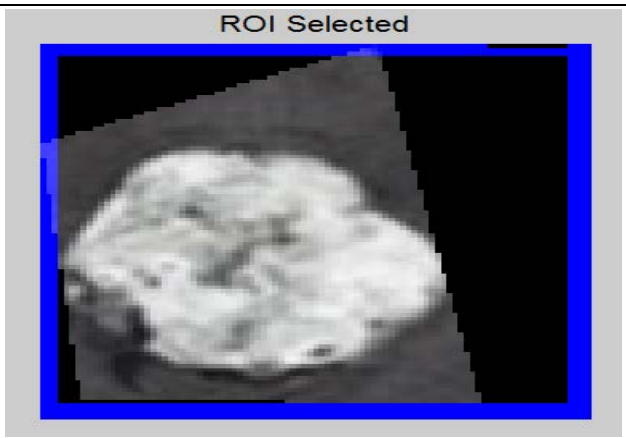

Figure 3:ROI Selection

In figure 4 and 5, the tumor and background strengths are calculated by applying CA algorithm for both tumor and background seeds separately. Then the obtained tumor and background strengths are combined to acquire a total tumor probability map, as shown in figure6.

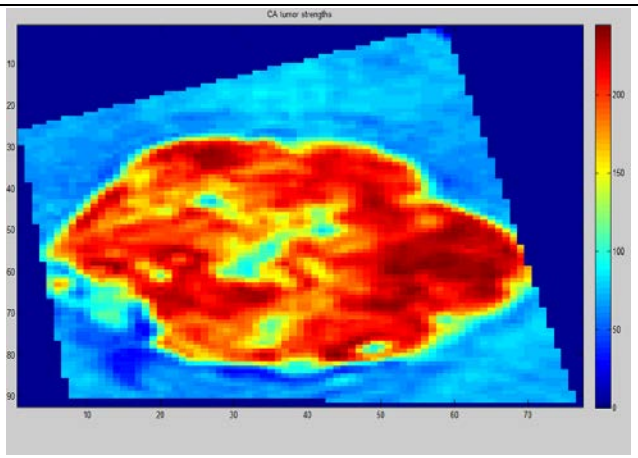

Figure 4:CA Tumor Strength

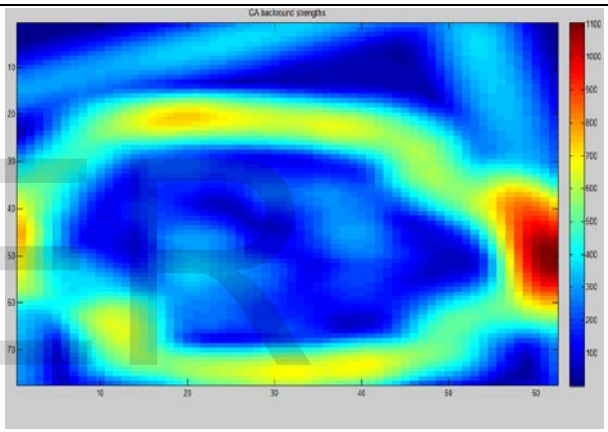

Figure 5:CA Background Strength

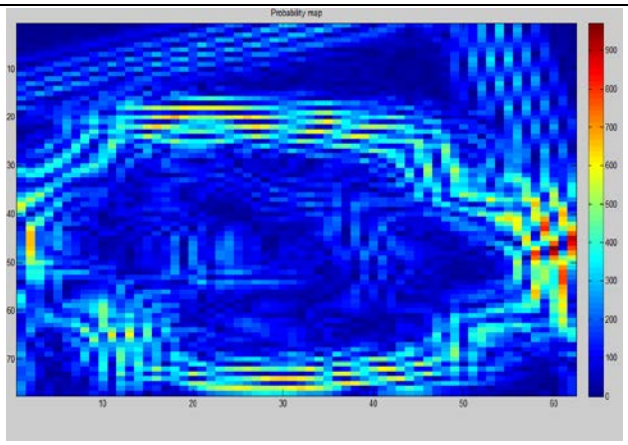

Figure 6:Tumor Probability Map

In figure 7, the final segmented image is aacquired using the level-set evolution on the tumor surface with the help of constructed tumor probability map from the CA states. Dice overlap is a performance measure which is used to quantify the overlap between obtained segmentation maps and the

true segmentations. The CA method provides an overlap performance of about 83% in brain tumor segmentation.

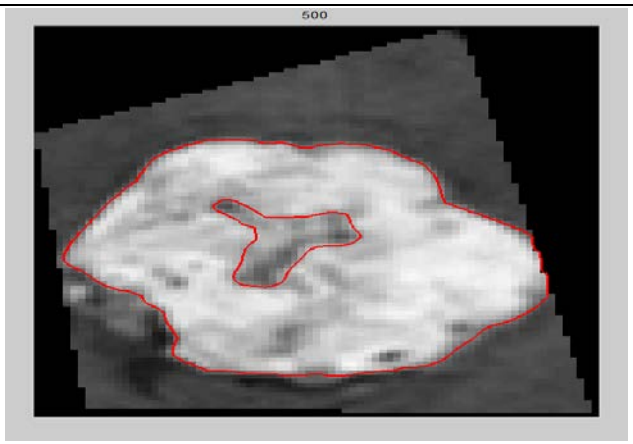

Figure 7:Segmented Image

Figure 8:Necrotic region segmentation

5. CONCLUSION

Manual segmentation of brain tumor by doctors is a time consuming task. Therefore, several automatic segmentation algorithms have been developed. The Literature was made on the area and the problem was identified. With the help of improved Cellular Automata algorithm, Volume of Interest and seed selection was Standardized. Here, a segmentation algorithm is presented for the problem of tumor delineation which exhibit varying tissue characteristics. Strengths of the proposed method include its simple interaction over a single slice and less sensitivity to the initialization, 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. In order to help for the detailed assessment of radiotherapy response, the necrotic parts within the tumor region have been distinguished using the CA algorithm. For the targeted clinical application of radiosurgery planning, using a single modality is an advantage due to the computational efficiency and ease of use. It is found that the result is promising and gives 80-90% Overlap performance.

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