Modified Tumour Cut Algorithms For MRI Image Segmentation of Brain Tumours

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Abstract—**The brain tumour segmentation methods rely on the intensity enhancement. Among them, a clustering method have been investigated and used. In this paper, CA (Cellular Automata) based seeded tumour segmentation algorithm is proposed. Which determine the Volume of Interest (VOI) and seed selection. First, establish the connection of the CA-based segmentation to the graph-cut method to show that the iterative CA framework solves the shortest path problem. This paper describe segmentation method consist of two phases. In the first phase, the MR Image is acquired from patient database and contrast enhancing the image. In the second phase, the CA algorithm run twice for background seed (healthy cell) and foreground seed (tumour cell) for probability calculation. Furthermore, apply Graph- Cut (GC) method to differentiate necrotic and enhancing tumour tissue content, which gains importance for a detailed assessment of radiation therapy response.**

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

I. INTRODUCTION

The brain is a soft, delicate, non replaceable and spongy mass of tissue. Brain tumour is a techniques to efficiently solve a wide variety off brain Brain tumour is due to group of abnormal cells that grows inside of the brain or around the brain. It can also indirectly damage healthy cells by crowding other parts of the brain and causing inflammation, brain swelling and pressure within the skull. So it is an important to detect the tumour probability in earlier stage and to remove it so as to protect the healthy cells.

Image segmentation represents a method of separation a portion of image into separate area. The ultimate aim in a large number of image processing applications is to extract important features from the image data, from which a description, interpretation, or understanding of the scene can be provided by the machine .In the brain itself, comprising a necrotic (dead) part and an active part, the edema or swelling in the nearby brain, As all tumour do not have a clear boundary between active and necrotic parts there is need to define a clear boundary between brain tissues. In the first phase CA algorithm perform the clustering of class seeds and probability calculation.

Here explore the use of cellular automata (CA) for clustering of seeds and segmentation. where CA have been used to perform a wide variety of image processing tasks such as noise removal, edge detection, morphology detection, ridge-valley detection, convex hull detection etc. Outlining the brain tumour contour is a major step in planning spatially localized radiotherapy (e.g., Cyber knife, iMRT) which is usually done manually on contrast enhanced T1-weighted magnetic resonance images (MRI) in current clinical practice. There are various attempts for brain tumour segmentation in the literature which use a single modality, combine multimodalities and use priors obtained from population atlases. Energy minimization along with image smoothing is performed with the graph cuts method [1]. Different types of algorithms

Need for the Project

Brain tumour 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 tumour segmentation. In recent years a great effort of the research in field of medical imaging was focused on brain tumours segmentation. Brain tumours may be of any size, variety of shapes, may appear at any location, and may appear in different image intensities.

Objective

In this present a fast and robust practical tool for segmentation of solid tumours with minimal user interaction to assist clinicians and researchers in radio surgery planning and assessment of the response to the therapy. Segmentation of brain tissues in gray matter , white matter , and tumour on medical images is not only of high interest in serial treatment monitoring of "disease burden" in oncology imaging, but also gaining popularity with the advance of image guided surgical approaches. Outlining the brain tumour contour is a major step in planning spatially localized radiotherapy [3] .

Here CA algorithm to establish the connection of the CA-based segmentation [6] 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 application is in the clinical radio surgery planning, where

manual segmentation of tumours are carried out on contrast enhanced T1-MR images by a radio-oncology expert, here modify the CA segmentation towards the nature of the tumour properties undergoing radiation therapy by adapting relevant transition rules.

II. DESCRIPTION

Overview of the Process is as follows.

A. 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 and frame grabbers.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.

B. 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.

C. Tumour Seed Selection

The 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 tumour seeds [5] and the background seeds are determined by using the line already drawn by the user to measure the longest diameter of the solid tumour. Similarly focusing on tumour segmentation problem, the seed selection procedure starts with a single line drawn by the user along the longest visible diameter of the tumour. Afterwards, the VOI and the seeds are computed. The line is cropped by 15% from each end and thickened to three pixels wide to obtain tumour seeds.

D. VOI Selection

Volume of Interest is selected as the bounding box of the tumour having a diameter 35% longer than the line. 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 labelling 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 colour between the background colour and the foreground colour.

E. Clustering

In clustering similarity between points is defined in terms of some distance metric. It is the process of organizing objects into groups whose members are similar in some way. A cluster is therefore a collection of objects which are 'similar' between them and are 'dissimilar' to the objects belonging to other clusters.

F. Grow cut Clustering

Cellular automata are dynamic systems that evolve on a discrete grid of cells that interact locally to produce information at a global scale. In general, any discrete system undergoing deterministic local interactions can be modelled as a cellular automaton (CA). CA consists of some pre-defined state transition rules, which determine the value of each cell based on the value of its neighbourhood cells. In case of image clustering, the state transition rules are applied iteratively to update the value of each pixel in an image 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).

G. Obtain Tumour Probability map

Strength maps are combined to obtain the probability map. The intuition with this probability construction is that probability of being a tumour is proportional to its distance normalized to the closest background seed. This leads to choosing a higher probability of being a tumour when the distance to the background seeds is large, and vice versa.

Therefore, the tumour probability map is obtained by combining the distances for [8] tumour (D_T) and background (D_B). Geodesic distances to the class seeds can be calculated by

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

$$P_{Tumor} = \frac{D_B}{D_{T} + D_B} \qquad (2)$$

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 (tumour and healthy) separately.

H. Graph-cut surface

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

a graph-theoretic approach [2]. Smoothing is an important prior in segmentation of brain tumours from post-contrast T1 images, because of three main reasons: First, an area surrounded by tumour tissue is considered as a tumour region even the intensity characteristics are likely to be healthy. Secondly, it is possible to include misclassified necrotic regions to tumour 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. This is a process that is expected to simulate the expert's manual contouring. The qualitative effect of adding the Finally, it is possible to exclude nearby vascular structures that are enhanced by administration of the contrast agent. This is a process that is expected to simulate the expert's manual contouring. The qualitative effect of adding the smoothing step over the CA result is shown in Figure , which exemplifies how the borders are smoothed after level set evolution over the tumour probability map displayed.

I. Enhancing/Necrotic Segmentation

Quantification of the necrotic regions within a whole tumour is an important problem in assessment of the tumour progress, necrotic of the tumour can occur as a result of the radio surgery as well as by the tumour progress itself like in high grade gliomas. However, aim in this study is to quantify the necrotic and enhanced parts of the tumour using solely contrast enhanced T1 weighted MRI volumes.

III. PROPOSED METHODS

Here proposed algorithm is cellular automata (CA) algorithm and Graph-cut method, which 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 Grow-cut for image segmentation, this showed the potential of the CA algorithm on generic medical image problems. However, Grow-cut was not designed for specific structures, such as tumours, 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 adhoc way of smoothing was introduced. Moreover Graph-cut proposed for enhancing the necrotic regions from the tumour probabilistic map.

A. Cellular Automata

The CA model consists of a grid of cells (or voxels in our case) that influences a set of neighbouring cells according to transition or evolution rules. In our segmentation application, some cells will be assigned labels (user seeds) and these cells will attempt to propagate their labels to neighbouring cells. At label boundaries, neighbours will compete with each other based on the transition rules [7]. Mathematically speaking, we can define our cellular automata as a triple, $CA = (S;N;\partial)$ where S is a nonempty set of states, $N \in R3$ is the neighbourhood, and $\partial:S^N \to S$ is the local transition rule. The area of computation is our volume, $v \in V \in R3$, where v represents a voxel in our volume. We define our neighbourhood system as the von Neumann neighbourhood (6-voxel neighbourhood)

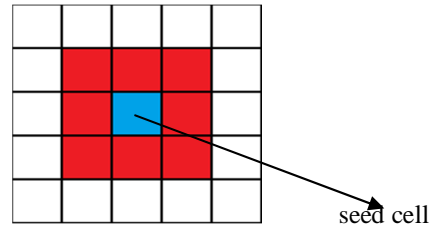$$N(v) = \| u-q \| = \sum_{i=1}^{3} |v_i - q_i| \qquad q\ v \in R^3 \qquad (3)$$

Fig. 2 . CA model

- Array dimension
- Neighbourhood structure
- Transition rule

B. Tumour Cut Algorithm

Steps of the proposed cellular automata based tumour segmentation algorithm is First, (a) the user draws a line over the largest visible diameter of the tumour; (b) using this line, a VOI is selected with foreground(red)-background(blue) seeds; (c)–(d) tumour 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 voxels; (e) two strength maps are combined to obtain the tumour probability map; (f) Graph-cut is used to evolve the surface which converges to the final segmentation map (g). Finally, (i) the necrotic region of the tumour is segmented using a CA-based method with the chosen enhanced and necrotic seeds in (h).

A pseudo code of tumour probability

```
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
```

end for
// Combine strengths for tumor and background to
    Tumor probability map
$P_T = \ln(xB_g) / (\ln(xB_g) + \ln(x_T))$
  End
       where q* is new neighbouring cell

The CA based framework using low level image features such as colour/gray level, pixel intensity values to derive state transition rules. In this paper, selected feature is Intensity of seed cells. The initial level and the number of seed points are derived randomly from the space of positive integer values. The state of cell is given by a 3 tuple (l, θ, I) where l is the label of seed cell, $\theta \in (0, 1)$ is the strength of the cell, 0 indicate normal cell, 1 indicate tumour cell, I is the pixel intensity .The strength of a cell is a function of image features and is used to define the state transition function for updating the labels of cells at each time step. Pixels with initial random labels are assigned the cell strength 1. The state transition rule between two pixels p and q is defined using a monotonically decreasing function g as

$$G(I_p - I_q) \quad \theta_q > t \quad\quad\quad (4)$$

Where $g(x) = 1 - [x / \max| I |]$

Currently, the threshold parameter t, which determines the level of quantization of pixel intensity values, is assigned manually. Automatic parameter selection using top-down information is a subject of future work. In addition, equivalence classes are constructed corresponding to each label, which are updated when two labels merge. The algorithm is iterated until the local label update stops occurring. For a given image **X**, the equivalence class for pixels p with labels l is defined as
$$[l] = \{ P \in \mathbf{X} \mid P \sim l\} \quad\quad\quad (5)$$
The state transition function defines the state of the central cell at time $t+1$ with respect to the values of cells in its neighbourhood at time t.

IV . RESULT AND CONCLUSIONS

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 as shown below. The input images are contrast enhanced. During training phase input image is labelled as foreground (Green) and background (Blue). In this CA based method, threshold values are selected for probability calculation of tumour seeds. Then graph-cut surface is initialized for smoothening the tumour region. Finally necrotic or dense tissue regions within the tumours are segmented.
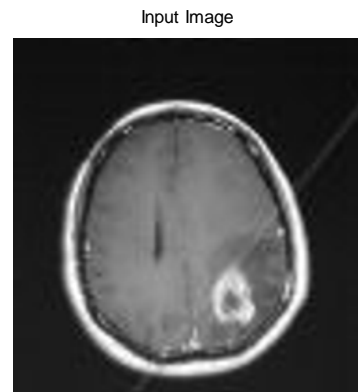
Input Image

Fig.3. Input Brain MR Image

B. OUTPUT

Enhanced contrast Input Image and seed selection

Here performing manually labelling of background seed (white) and tumour seed (red).
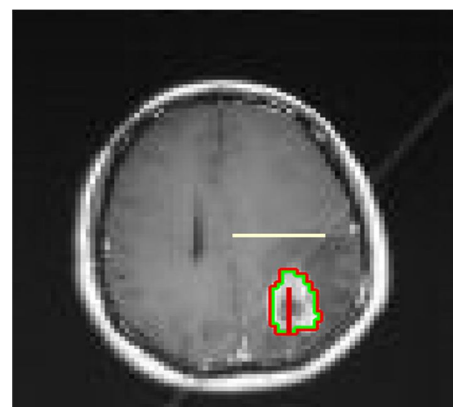

Fig. 4. Contrast Input Image and labelling seed

1). PROBABILITY MAP

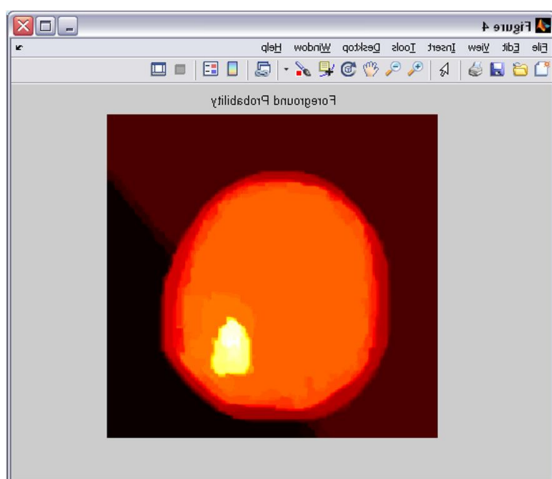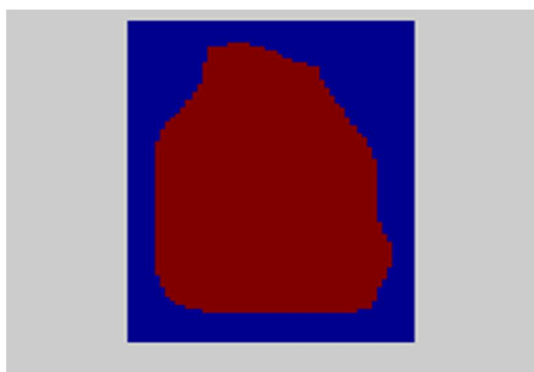Here run CA algorithm twice for background seed clustering and tumour seeds.

Fig . 5. Foreground probability map

2). TUMOR SEGMENTATION

therapy becomes important, so applied the CA based tumour segmentation to partition the tumour tissue further into its necrotic and enhancing parts. Here a validation study over a synthetic tumour database is performed. The probability maps constructed from each modality could be combined to obtain the final segmentation.

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V. SCOPE FOR FURTHER STUDIES

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 tumour analysis . In future this work will pave the way to reach automatic assessment of the tumour response to therapy, due to reasonable and acceptable success rate of algorithm.

VI. CONCLUSION

In this paper presented a segmentation algorithm for the problem of brain tumour which exhibit varying tissue characteristics .Here attempts presented to quantify changes in necrotic and enhancing tumour tissue contents. As the change in necrotic and enhancing part of the tumour after radiation