

Semi-Automatic Tumor Boundary Detection in MR Image Sequences

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ABSTRACT

In this paper, we present a semi-automatic approach for the detection of tumor boundary in MR image sequences. An initial slice with an obvious tumor is selected from the image sequence. The tumor is roughly segmented using fuzzy c-means algorithm and its boundary can be further refined by region and contour deformation. For the rest of slices, the initial plan applied for each slice is extracted from the resulting boundary of the previous slice. The tumor boundary is located using region and contour deformation. Performance of our approach is evaluated on MR image sequence. Comparisons with manual tracing show the accuracy and effectiveness of our approach.

1. INTRODUCTION

Managing non-surgical therapy of brain tumor involves periodic monitoring of tumor development in terms of area, volume, shape, etc. Routine magnetic resonance (MR) examination gives only a series of two-dimensional (2D) image slices while subtle changes in the tumor may not be readily noticeable. Although radiologists can manually trace the tumor boundary in each of the 2D image slices for a rough estimation of its volume, it is really a tedious and time-consuming process. Routine application of this process would not be practical. Moreover, the results may not be consistent and repeatable owing to substantial intra-observer and inter-observer variability.

A series of parallel 2D MR images produce a 3D representation of the brain tumor. Successive 2D MR images have some similarities between each other in terms of size, shape, axis, and gray intensity of the tumor. The change in various properties of tumor between one image and the next will be small when the slice thickness is kept within a certain value. In the analysis of successive 2D MR image slices, the traditional way was to process one by one separately. Active contour model [1] and various deformable models [2,3] have been used to deal with this problem. However, the correlation between consecutive images was not taken into consideration. A range of methods [4-7] has been developed for the processing of medical image sequences. Most of them used geometric or shape constraints, which explicitly introduced a priori knowledge on the expected shape of contour. It is not suitable for this problem, as the shape of tumor can be different from case to case. Zhu and Yan [8]

proposed an approach for the detection of brain tumor boundaries in a series of MR image slices using Hopfield neural network. The computation time was very large when it was executed on a workstation or a personal computer. This limited the range of applications.

In this paper, we present a semi-automatic approach for the detection of brain tumor boundary in MR image sequence. An initial slice with an obvious tumor is selected from the image sequence. The tumor is roughly segmented using fuzzy c-means algorithm [12] and its boundary can be further refined by region and contour deformation [9]. For the rest of slices, the initial plan applied for each slice is extracted from the resulting boundary of the previous slice. The tumor boundary is located using region and contour deformation [9]. This method is suitable for this problem, as it can tolerate a rough initial plan. The tumor information between consecutive MR images is utilized, as the shape and position of tumor in one slice are assumed to be similar to that in its neighboring slices. Performance of our approach is evaluated on MR image sequence.

2. METHODS

The approach was to detect boundaries of brain tumors in MR image sequence, which is a sequence of parallel 2D images with known separation between each other. As the brain is a connected entity, it could be assumed that the shape and position of tumor in one slice should be similar to that in its neighboring slices. Based on this assumption, the detected boundary in the current slice can be used as initial plan for the next slice. The major steps of our approach are shown in Figure 1. First, an initial slice is selected from the MR image sequence following the process of initial boundary estimation. Then region and contour deformation [9] is applied to refine tumor boundary. Finally, the tumor boundary is generated and it is also used as initial plan for the next slice.

Initial boundary estimation

In our approach, the first initial plan must be estimated before using the region and contour deformation. The tumor is segmented using fuzzy c-means algorithm [12]. It is a segmentation method to separate objects into different clusters according to various properties. The algorithm is applied twice with the number of cluster setting to two. The first time is to remove the background. The second time

is to extract the brain tumor from the segmented image. The resultant image includes a brain tumor, some tissues, and some noisy structures. Then a binary morphological erosion and dilation process is applied to eliminate tissues and noise from the resultant image. The area of brain tumor is assumed to be relatively larger than that of spurious regions. Binary erosion with an 11×11 -square structuring element is used to eliminate tissues and noise excluding the brain tumor. A conditional dilation is used to restore the part of tumor removed by erosion. The structuring element employed for this process was disc-shaped with a diameter of 15 pixels. Finally, the brain tumor is roughly segmented. The boundary is extracted for further refinement using region and contour deformation.

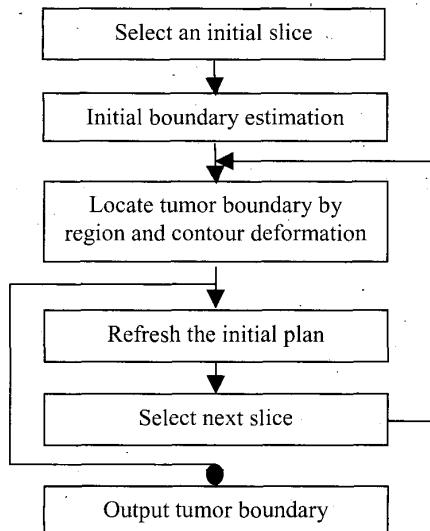


Figure 1. Block diagram of the brain tumor boundary extraction approach

Region deformation

The region deformation [10] is to find a maximum area region with the same gray level distribution using a shrinking-growing method. The Kolmogorov-Smirnov (KS) test method is used to test whether the boundary pixel set and the object pixel set have the same gray level distribution. The Kolmogorov-Smirnov distance D is defined as

$$D = \max_{0 \leq g_s \leq 255} |F_B(g_s) - F_O(g_s)| \quad (1)$$

where F_o and F_B are the gray level cumulative frequency distribution of object and boundary respectively. The hypothesis $F_o = F_B$ is accepted when $D < d$, and d is defined as

$$d = \frac{c}{\sqrt{\frac{A \cdot L}{(A + L)}}} \quad (2)$$

where c is the significance level of the test, A is the area of object, and L is the length of boundary.

When $D > d$, the region plan covers a region different from the tumor. Shrinking is performed to deform the region to meet $D < d$. Hence, the homogeneity of the region can be guaranteed. The shrinking algorithm is the erosion operation. It only deletes the region boundary elements, which has a different gray level distribution. When $D < d$, the region plan covers a region inside the tumor. The region, however, may not cover the whole tumor. To obtain the maximum area, growing is performed until $D > d$. The growing algorithm is the dilation operation. After each shrinking and growing, the new region area is compared with the previous one. If the region area does not change, the process stops; otherwise, the iteration of shrinking and growing continues.

Contour deformation

The boundary obtained from region deformation can be further refined by contour deformation [11]. The "snake" method [1] modeled the contour as an energy-minimizing spline guided by internal and external forces.

$$E_{\text{snake}} = \int_0^1 [E_{\text{int}}(v(s)) + E_{\text{ext}}(v(s))] ds \quad (3)$$

where $v(s) = (x(s), y(s))$ is the parametric equation of the contour, and s is the arc length.

The internal energy E_{int} has two parts.

$$E_{\text{int}} = (\alpha(s)|v_s(s)|^2 + \beta(s)|v_{ss}(s)|^2)/2 \quad (4)$$

where v_s and v_{ss} are the first and second order derivatives, respectively. These two terms are used to control the continuity and smoothness of the contour, with α and β representing the weights.

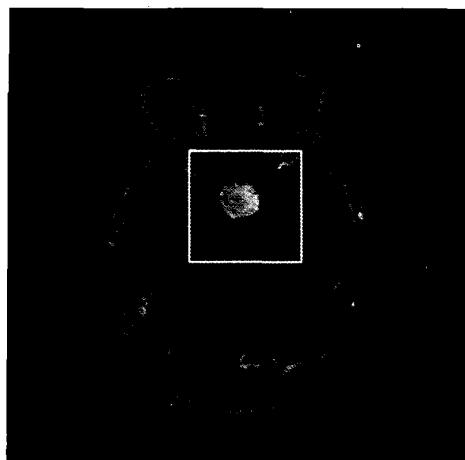
The external energy E_{ext} is from the image edge information. ∇ is the gradient operator and I is the image. $\nabla^2 I$ is the second order derivatives of the image.

$$E_{\text{ext}} = \gamma(s) \log(1 + |G_\sigma * \nabla^2 I|) \quad (5)$$

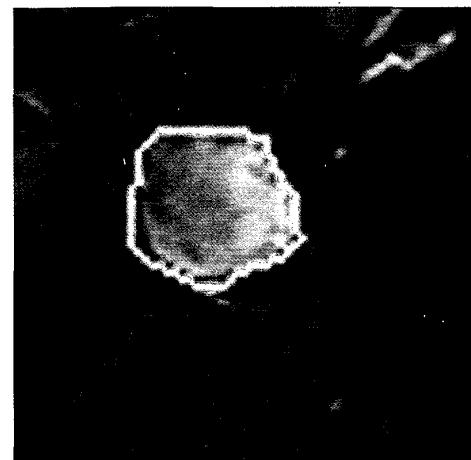
where $\gamma(s)$ is the weight and G_σ is a Gaussian function of the standard deviation σ .

Analysis of results from the approach

Results from the proposed approach were compared with those from manual tracing by our radiologist (P.P.Iu). Double blind method was used in this analysis. One did not know the results from the other when performing one's own part. The result comparison was done afterwards for checking against each other. The percentage overlapped in area was determined for the results obtained from the proposed approach and manual tracing in each image. For the manual tracing, the Paint application from Windows Accessories was used. The image was enlarged to 200% and our radiologist used mouse to draw the tumor boundary with pencil tools in white color.



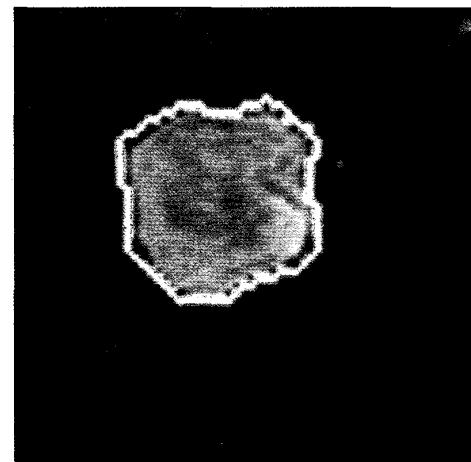
(a)



(a)



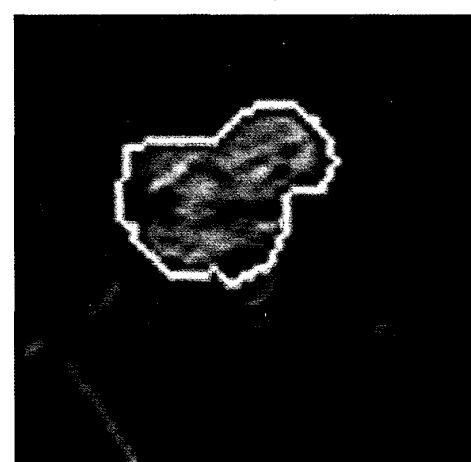
(b)



(b)



(c)



(c)

Figure 2. Selected image slices from the MR image set containing a brain tumor: (a) slice 35, (b) slice 41, (c) slice 49.

Figure 3. Extracted tumor boundaries, superimposed on the original image slices in Figure 2. Only a portion of the image [the rectangular region shown in Figure 2(a)] is shown here: (a) slice 35, (b) slice 41, (c) slice 49.

3. RESULTS

Performance of the proposed approach is shown. A MR image sequence with 74 slices was used. Figure 2 shows several selected images from this sequence (8-bit grayscale, 256 x 256 pixels). The pixel size of each slice is 0.898mm x 0.898mm. The slice thickness is 0.8mm. According to our radiologist's analysis (P.P.Iu), slices 23-60 intersect the tumor. The middle tumor slices appeared relatively obvious and bigger among images of the whole tumor. The initial slice could be selected from one of those images with obvious tumor. Thus it is a better strategy to start from a middle tumor slice and process other slices in two directions: forward and backward. Here, slice 39 was selected as an example. After that, the initial plan was estimated. The boundary located using region and contour deformation was used as initial plan for slices 38 and 40. Our approach could work well for slices 28-50. Figure 3 shows the results of several selected slices from the MR image set. We found that the fast snake method [11] could also work well in the same slice range. To compare with manual tracing, the percentage overlapped in area was over 80% for slices 31-49. The sampling rate of this image set was then reduced to simulate the increase in slice thickness. We increased the step length when selecting the next slice. To simulate the thickness of 3-5 mm, the step length should be 4-6 slices, corresponding to 3.2-4.8 mm. Our approach could work well at any step length from 1 to 6 slices. When step length increased to 4 slices, the fast snake method [11] failed. In the above experiments, the parameters $\alpha(s)$, $\beta(s)$, and $\gamma(s)$ were fixed at 1, 1, and 10 respectively. The values of two other parameters, c and σ , were determined experimentally.

4. DISCUSSION

In our approach, there was no need to trace the initial plans for the region and contour deformation. The first initial plan was generated by our initial boundary estimation method. For the rest of slices, the initial plan applied for each slice was extracted from the resulting boundary of the previous slice. No assumption was made on the gray level distribution of tumor. There was no restriction on the position of initial plan, so it could be far away from the actual boundary of brain tumor. The tumor boundary in each slice was extracted with pixel accuracy in the MR image set. The results of the proposed approach were close to that of manual tracing for the middle part of the tumor. It is reasonable, as the middle part is bigger and clearer than other parts of the tumor. Our approach could work well at larger step length than the fast snake

method [11]. Thus, it is robust for the brain tumor boundary detection in MR image sequence. This helps doctors to monitor different properties of brain tumor at each stage, as it is very difficult to detect minor tumor changes by viewing the MR images. The detected tumor boundary in each slice can also be used for 3D rendering and volume measurement.

5. ACKNOWLEDGMENT

The authors would like to thank Image Processing Group at Guy's Hospital, London, U.K. for providing the MR image set. This work was supported in part by Hong Kong Research Grants Council under Grants HKU553/96M and HKU7036/97E.

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