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MRI Brain Tumor Segmentation and Necrosis Detection Using Adaptive Sobolev Snakes

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Abstract

Brain tumor segmentation in brain MRI volumes is used in neurosurgical planning and illness staging. It is important to explore the tumor shape and necrosis regions at different points of time to evaluate the disease progression. We propose an algorithm for semi-automatic tumor segmentation and necrosis detection. Our algorithm consists of three parts: conversion of MRI volume to a probability space based on the on-line learned model, tumor probability density estimation, and adaptive segmentation in the probability space. We use manually selected acceptance and rejection classes on a single MRI slice to learn the background and foreground statistical models. Then, we propagate this model to all MRI slices to compute the most probable regions of the tumor. Anisotropic 3D diffusion is used to estimate the probability density. Finally, the estimated density is segmented by the Sobolev active contour (snake) algorithm to select smoothed regions of the maximum tumor probability. The segmentation approach is robust to noise and not very sensitive to the manual initialization in the volumes tested. Also, it is appropriate for low contrast imagery. The irregular necrosis regions are detected by using the outliers of the probability distribution inside the segmented region. The necrosis regions of small width are removed due to a high probability of noisy measurements. The MRI volume segmentation results obtained by our algorithm are very similar to expert manual segmentation.

Keywords

Active contour; tumor segmentation; necrosis detection; MRI analysis

1. Introduction

MRI based brain tumor segmentation is a problem of extracting the three-dimensional shape of the tumor from an MRI volume scan, which is vital in a variety of clinical applications. The obtained 3D shape can be shown independently, or overlaid on each MRI slice. The

extracted shape model can be analyzed further by clinical researchers or neurosurgeons to plan the surgical procedure and/or evaluate the disease progression. The presence detection of dead tissue (necrosis) is also very important for tumor evaluation.

Robust tumor segmentation methods have attracted a lot of attention in the last decade.¹ Many methods have been proposed to solve the problem, e.g., see²⁻⁴ and the references therein. Most of these methods need some sort of manual initialization, and major human expert intervention in the process of segmentation. Other methods use learned *a priori* data, and are more appropriate for specific types of tumors.

We present the incorporation of probabilistic approach to tumor detection into the framework of region based active contour segmentation. The proposed robust tumor segmentation algorithm uses a manually selected region inside the tumor as an acceptance class model and band around the tumor as a rejection class for evaluating the background model. The selection has been done only in a single MRI slice.

The probability density function of the tumor is then computed using 3D anisotropic diffusion⁵(see Figure 2, brighter color corresponds to higher probability). Finally, the Sobolev snake evolution produces the final tumor segmentation.

2. Algorithm Description

The algorithm has two goals: extracting three dimensional shape of the tumor from the MRI volume, and identifying the regions within the tumor where necrosis occurred. To identify the boundaries of the tumor, we need to select the regions of highest probability for a tumor. We are selecting manually in a single MRI slice the region of tumor, and the region surrounding the tumor which does not include tumor pixels (see Figure 1). From the former we learn on acceptance class of intensity distribution $p_a(i)$, and from the later we are learning on rejection class intensity distribution $p_r(i)$. Both p_a and p_r are normalized to a sum of one.

Let's denote the MRI volume data by $I(x, y, z)$. For a given pixel (x, y, z) the probability of being in the acceptance class is:

$$P(x, y, z) = \frac{p_a(I(x, y, z))}{p_a(I(x, y, z)) + p_r(I(x, y, z))} \quad (1)$$

Due to inhomogeneous imaging data and noise effects, the obtained probability function is not smooth enough, thus additional operation of anisotropic diffusion⁵ was applied to estimate better the probability distribution.

The estimated distribution is provided by a numerical solution of the following differential equation:⁵

$$\frac{\partial P}{\partial t} = \text{div} (c(x, y, z; t) \nabla P) \quad (2)$$

where $c = e^{-\frac{\|\nabla P\|^2}{K^2}}$, and the constant parameter K controls the sensitivity to high gradients.

The result for a single slice can be seen in Figure 2.

The obtained probability 3D map is used for the segmentation of the tumor. We have proposed to use adaptive Sobolev snake algorithm⁶ for extracting tumor boundaries.

2.1 Adaptive Sobolev Snakes

In this subsection, we outline the idea of adaptive Sobolev snake. More information about the algorithm and the implementation can be found in Nakhmani and Tannenbaum⁶ and the references therein.

Let $C(s)$ be a closed boundary, where s is a parametrization. The boundary evolves in the imagery data I domain to minimize some predefined energy E :

$$C_{optimal} = \arg \min (E(C)) \quad (3)$$

A popular in applications region-based energy has been defined by Chan and Vese:⁷

$$E^{C-V}(C) = \int_{inside(C)} |I - c_{in}|^2 + \int_{outside(C)} |I - c_{out}|^2 \quad (4)$$

where c_{in} and c_{out} are the mean intensity values inside and outside the boundary C respectively.

Chan and Vese assumed that the inside and outside intensities are different, and chosen the energy that is minimized when these two intensities are separated. Note that we use a particular case of the energy proposed by Chan and Vese; we intentionally avoid using the penalty on an area size and contour length, since the target of interest may have different sizes and boundaries.

The force derived from the energy is designed to minimize the energy E in the case of perfect segmentation. The force is computed by:

$$F^{C-V} = -\nabla E \quad (5)$$

The snake governed by the force (5) is a regular Chan-Vese snake. The computation of the force depends on a choice of inner product. Note that the force for each snake point depends only on the intensity at this point, thus it is sensible to noise. To overcome this problem, Sundaramoorthi *et al.*⁸⁻¹⁰ proposed to use H^{-1} Sobolev metrics to compute the gradient, and obtained:

$$F^{Sobolev}(s) = (K_{\lambda} * F^{C-V})(s) \quad (6)$$

where $*$ denotes circular convolution with the kernel:

$$K_{\lambda}(s) = \frac{1}{L} \left(1 + \frac{(s/L)^2 - (s/L) + 1/6}{2\lambda} \right); s \in [0, L] \quad (7)$$

We have proposed to use adaptive λ parameters⁶ for Sobolev snake evolution. We know that λ determines the width of the smoothing kernel K_{λ} , and the Sobolev snake acts like Chan-Vese snake for small λ , and translated rigidly for large λ . Based on these heuristic arguments, we propose to compute this parameter by:

$$\lambda = \frac{\mu}{|c_{in} - c_{out}|} \quad (8)$$

where μ is constant. This will allow to overcome the problem of low contrast regions segmentation by preserving the boundary shape in such regions.

To find the numerical solution we need to initialize the algorithm with some initial boundary. This initialization has been done by using the mask $P(x, y, z) > 0.5$, i.e., more than 50% probability that the pixel belongs to the acceptance class. Starting from that boundary, the evolution of Sobolev snake produces the final tumor segmentation.

2.2 Necrosis Detection

When the tumor boundaries are available, the regions of necrosis can be extracted. In terms of intensity, those regions does not fit well into the acceptance class model. One major problem of necrosis detection is the problem of noisy measurements. Spur dark pixels may appear at different locations within the tumor, but they are not reliable, and cannot be count as a necrosis regions. This problem is more significant near the boundaries of the tumor.

In our algorithm we detect only large enough regions of necrosis with the width larger than one pixel. We identify regions within the tumor that have low probability ($P < 0.5$), and use morphological opening to remove small regions. Finally, we remove the regions with the width of one pixel. Those regions are detected by applying four linear filters:

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 1 \end{bmatrix} \quad \begin{bmatrix} 0 & 1 & 0 \\ 0 & 0 & 0 \\ 0 & 1 & 0 \end{bmatrix} \quad \begin{bmatrix} 0 & 0 & 1 \\ 0 & 0 & 0 \\ 1 & 0 & 0 \end{bmatrix} \quad \begin{bmatrix} 0 & 0 & 0 \\ 1 & 0 & 1 \\ 0 & 0 & 0 \end{bmatrix}$$

If at least one of those filters produces zero output, this means that the region has width of one, and the appropriate pixels are removed from the necrosis mask.

3. Results

We have tested our algorithm on different brain MRI volumes, and two representative examples have been shown in this section.

In the first example, the initial acceptance and rejection classes were selected as in Figure 1. The results of segmentation (which in our 3D case can be called active interface

segmentation) are shown in Figure 3 for the selected MRI slices. The white contour shows the tumor segmentation, and the red contours within the tumor boundaries show the necrosis. It can be seen that the segmented regions reasonably follow the real tumor boundaries (as determined by an expert).

The entire 3D tumor boundaries model was extracted and visualized with the help of 3D Slicer¹¹ (see Figure 4).

The second example shows the result of tumor and necrosis segmentation of glioblastoma (see Figure 5) for selected frames. In both examples it can be seen that tumor boundary not always follow exactly the bright regions of the image where tumor is located. The reason for that is in internal smoothness constraints that we have in our algorithm. Without those constraints, the result of segmentation would be very noise sensitive.

4. Conclusions

We have proposed an algorithm for semi-automatic brain tumor volume segmentation for MRI brain data. The proposed method allows detection and segmentation without prior anatomical data or learned models. Manual human intervention into the process of segmentation is minimal, and the results match quite nicely the expert segmentations. The proposed method is robust to noise, low contrast, and variations in the initial manual selection.

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Figure 1.
Example of Rejection and Acceptance class selection for on-line learning of the background and foreground model (Slice 80).

Figure 2. Probability density function (Slice 80). Brighter color corresponds to higher probability of tumor, except necrosis regions.

Figure 3.
The result of segmentation for the selected MRI slices.

Figure 4.
Reconstruction of 3D tumor boundary model.

Figure 5.
The result of segmentation for the selected MRI slices.