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Level-set segmentation of brain tumors using a threshold-based speed function

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ABSTRACT

The level set approach can be used as a powerful tool for 3D segmentation of a tumor to achieve an accurate estimation of its volume. A major challenge of such algorithms is to set the equation parameters, especially the speed function. In this paper, we introduce a threshold-based scheme that uses level sets for 3D tumor segmentation (TLS). In this scheme, the level set speed function is designed using a global threshold. This threshold is defined based on the idea of confidence interval and is iteratively updated throughout the evolution process. We propose two threshold-updating schemes, search-based and adaptive, that require different degrees of user involvement. TLS does not require explicit knowledge about the tumor and non-tumor density functions and can be implemented in an automatic or semi-automatic form depending on the complexity of the tumor shape. The proposed algorithm has been tested on magnetic resonance images of the head for tumor segmentation and its performance evaluated visually and quantitatively. The experimental results confirm the effectiveness of TLS and its superior performance when compared with a region-competition based method.

1. Introduction

The accurate estimation of tumor size is important for clinical reasons, e.g., for treatment planning and therapy evaluation. Although maximum tumor diameter is widely used as an indication of tumor size, it may not reflect a proper assessment of this tumor attribute because of the 3D nature and irregular shape of the tumor [1,2]. Tumor volume, on the other hand, may be an appropriate representation of tumor size. One way to obtain an estimate of tumor volume is via segmentation. Such schemes implicitly acquire the tumor volume by extracting the tumor surface. Surface extraction has been obtained either directly by 3D tumor segmentation or indirectly via a pseudo-3D approach, i.e., reconstruction of the 3D surface from the extracted 2D contours [3]. Since the former approach generally achieves higher accuracy, it is the main focus of our research.

There are several proposed approaches in the literature for tumor segmentation and volume estimation. Fuzzy-connectedness is a useful method that has been adapted for measuring the tumor volume in MR images [4,5]. Markov random fields (MRFs) are also popular models for many medical image processing tasks such as segmentation [6,7]. Lee et al. [8] evaluated the use of support vector machine (SVM) classification method and MRFs for brain tumor segmentation and claimed the superiority of SVM-based approach. Recently, Corso et al. [9] applied the extended graph-shifts algorithm for image segmentation and showed its application in tumor segmentation. Also, in a more recent publication [10] the Bayesian generative model was incorporated into the graph-based image segmentation and was applied to brain tumor segmentation.

Active surfaces/contours are other popular methods that are widely used for the segmentation of 3D objects, implicitly in the form of a level set function or explicitly as a snake function. In the recent years, the level set method has become popular due to its ability to handle complex geometries and topological changes. The level set is in fact a shape-driven tool which, using a properly defined speed function, can grow or shrink to take the shape of any complex object of interest. Unlike the traditional deformable models, the level set method does not depend on the parameterizations of the surface [11]. This makes it very attractive and flexible in shape modeling and image segmentation. Another attractive advantage of the level set method is that, given an initial zero level set (initial hypersurface), the entire segmentation procedure is fully automatic. Moreover, unlike other methods, the extension of the algorithm to 3D is straightforward and does not require additional machinery. These properties make the level set one of the state of the art methods for segmentation, especially 3D segmentation. Therefore, the focus of the paper is on level set-based approaches.

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However, there are difficulties in using level sets that make them less desirable in some circumstances. One problem is that the level set formulation entails the tuning of several parameters. The difficulty in adjusting such parameters for specific applications has led to several approaches. In some methods, the interactive rates for solving the level set partial differential equation give the user immediate feedback on the parameter settings; the user can therefore tune the parameters and control the shape of the level set in real time [12–14]. The disadvantage of these methods is that they increase user interaction and provide good segmentation results only if the user is sufficiently familiar with the level set formulation and the object of interest. Another method, proposed by Leventon et al. [15], provides a more generic and automated segmentation of tumor through the combination of level set evolution with statistical shape constraints. In this method, *a priori* shape information is incorporated into a geodesic active contour so that the model parameters are estimated, and the curve then evolves based on that estimation. The problem with this approach is that it may be difficult to obtain statistical prior knowledge in many cases, especially for tumor segmentation.

One of the main parameters in the level set equation is the speed function, whose design is perhaps the most important step in the level set approach. The speed function can be defined based on the results of various clustering algorithms such as K-means clustering and fuzzy classification [16–18]. In these approaches a clustering step is performed and the deformable model then grows on top of the clustered pixels. However, in some other approaches classification and level set growing are performed simultaneously. Ho et al. [19] proposed region competition in the evolution of the level set, in which the difference between pre- and post-contrast enhanced magnetic resonance (MR) images is used to adjust the speed function. In their method, the histogram of the difference image is fitted by parametric distributions for both the enhanced parts and the noisy background. Using this fitted distribution, the difference image is mapped to the tumor posterior probability for use in the speed function. This idea can be extended based on non-parametric density estimation by kernel expansion or Parzen windowing [20]. The main drawback of such algorithms is their dependency on the accurate estimation of tumor and non-tumor probability density functions. On one hand, the parametric estimation of density functions may not provide sufficient accuracy because tumors do not generally have uniform intensities. On the other hand, non-parametric density estimation methods such as Parzen windowing require sufficient training samples for both regions. The additional complexity of estimation due to such algorithms motivates us to use density-independent schemes.

Many level set algorithms may be distinguished on the basis of their speed functions. Some approaches, for example, require user interaction while others rely on prior estimation of the tumor density function. We propose a level set method for 3D brain tumor segmentation which employs a speed function that does not require density function estimation and is obtained by minimal user interaction [21]. The basic idea is to use a global threshold to form the speed function. The initial threshold is calculated using the level set initialization and is then iteratively updated throughout the process of segmentation. Upon reaching the tumor boundary, the variation of the threshold declines because of the contrast between tumor and non-tumor intensities, and the process stops. This algorithm can be implemented in an automatic or semi-automatic form depending on the complexity of the tumor shape. A further advantage is that it can be applied to either pre- or post-contrast T1 MR images and does not require both these images at the same time.

The challenge of our scheme lies in the trade-off between the rate of convergence and the accuracy of segmentation. A high convergence rate is achieved when the variation of threshold with respect to the iteration number is large. This, however, may lead to low accuracy in segmentation or even destabilization of the algorithm. On the other hand, a small variation of the threshold can guarantee convergence, although at a reduced rate. In this paper, we study this trade-off and propose an appropriate threshold calculation algorithm.

The key contributions of this paper are:

- We introduce the TLS method, which calculates a global threshold for tumor segmentation, thereby making density estimation of the tumor and non-tumor unnecessary.
- We propose an algorithm to update the threshold iteratively.

The rest of the paper is organized as follows. Section 2 introduces the TLS algorithm, an iterative approach for finding and updating the threshold, and the stopping criterion. The initialization of the level set and the design of the speed function are also presented. In Section 3, a detailed discussion of threshold updating is provided in addition to the presentation of a modified TLS for non-homogeneous tumors. The simulation results in Section 4 demonstrate the effectiveness of our algorithm. Section 5 concludes the paper.

2. Threshold-based segmentation using level set

We assume that the histograms of the tumor and adjacent non-tumor[1] regions slightly overlap. Such an assumption often holds in MR images. Without loss of generality, we assume that the tumor region has mean intensity value greater than that of the background. In such a situation, it is very likely that there exists a threshold which discriminates between tumor and non-tumor voxels. Using the level set, TLS specifies an algorithm to find a proper threshold and a method to update it on an iterative basis. The initial value of the threshold is based on the level set initialization performed by the user inside the tumor region. TLS specifies a speed function on the basis of such a threshold. An important feature of our approach is that explicit knowledge of the density functions of tumor and non-tumor regions is not required.

Fig. 1 shows two real instances in which appropriate thresholds can be chosen from the shaded intensity ranges, which are where the final (converged) thresholds are very likely to lie. Intuitively, when the densities of the tumor and non-tumor regions are more widely separated, this range is expected to be wider, as can be seen in Fig. 1(b). In the figures, the tumor and non-tumor regions are selected based on the manual segmentations and are inside the volume of interest.

A brief description of the TLS approach is presented in Fig. 2. To speed up the algorithm, we propose the use of narrow band [22,23] in the level set evolution process and restrict processing to the volume of interest. TLS requires an appropriate estimate of the threshold to segment the tumor properly, and this is obtained via the concepts of confidence interval and confidence level. In the following sections, we explain these ideas and their application to threshold estimation. The level set evolution equation is presented and its speed function designed on the basis of our threshold updating approach. Level set initialization and the TLS stopping criterion are also discussed.

2.1. Confidence interval

The confidence interval (CI) can be defined for any distribution as an interval in which a certain percentage, the confidence level (CL), of observations is located. For a symmetric distribution such

[1] The area around the tumor boundary and inside the cuboid that encompasses the volume of interest.