AUTOMATED TUMOR SEGMENTATION USING LEVEL SET METHODS

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Abstract: In the framework of detection, diagnostic and treatment planning of the tumours, the Positron Emission Tomography (PET) and Magnetic Resonance Imaging (MRI) have become the most efficient techniques for body and brain examination. Radiologists take usually several hours to segment manually the region of interest (ROI) on images to obtain some information about patient pathology. It is very time consuming. The aim of our study is to propose an automatic solution to this problem to help the radiologist's work. This paper presents an approach of tumour segmentation based on a fast level set method. The results obtained by the proposed method dealing with both PET and MRI images are encouraging.

1 INTRODUCTION

PET (Positron Emission Tomography) and MRI (Magnetic Resonance Imaging) scans are both standard imaging tools that physicians use to pinpoint disease states in the body and the brain. A PET scan demonstrates the biological function of the body before anatomical changes take place, while the MRI scan provides usually information about the brain tumor. Accurate and automatic tumor segmentation is a very important issue in many applications of medical image system for quantitative studies. As known, manual tracing by an expert of a tumor in 3D is not only exceedingly time consuming, but also exhausting for experts leading to human errors. Therefore, an automatic segmentation is necessary.

Many segmentation methods have already been used in medical imaging field. A simple method is the thresholding. (Malyapa et al., 2002) used a binary threshold to segment tumorous areas in the pelvis region. This method allows the user to obtain results very quickly but it is not very accurate. The seeded region growing is one of segmentation methods. It consists of choosing seeds, and growing them according to a criteria. One solution adopted by (Adams et al., 1994) is to choose the seeds as the local minima and maxima and then to grow them until the regions touch themselves. But when one need to delineate just one region, one cannot venture to fill the entire image. That is why (Zoroofi et al., 2004) have chosen the seeds upon the histogram and then let grow until the criteria was no longer verified. This work has been used to the segmentation of a non-necrotic femoral head. Mathematical morphology segmentation based on watersheds (Roerdink et al., 2001)is proposed in (Mancas et al., 2004)to segment PET /CT images. The principle of the watershed technique is to transform the gradient of a grayscale image into a topographic surface. An iterative watersheds is used in (Mancas et al., 2004). A very common way to segment medical images is to use an atlas of the humain body as a priori knowledge. (Bondiau et al., 2005), (Erhardt et al., 2001) and (Lorenzo et al., 2004) have used such approach respectively on the brain, the hip and the heart atlases. The statistical methods have been also studied to deal with the medical images, because of noise presenting in images. (Ruan et al., 2000) propose a statistical segmentation based on Random Markov Fields to segment brain RM images. The fuzzy segmentation offers an interesting point of view to take into account ambiguities of objets to segment. As shown in (Dou et al., 2004), membership functions are modelled to express the fuzzy signals of the brain tumor observed in differ-

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ent types of images. Among various image segmentation techniques, active contour model [2] has emerged as a powerful tool for semi-automatic object segmentation. The basic idea is to evolve a curve, subject to constraints from a given image,for detecting interesting objects in that image. It consists in the resolution of systems of partial differential equations for which interface propagation phenomenon has to be described. The active contour models are often implemented based on level set method ((Sethian, 1999)), which is a powerful tool to capture deforming shape. But it has the disadvantage of a heavy computation requirement even using the narrowband evolution. The fast marching method is proposed for monotonically advanced fronts ((Sethian, 1999)), and is extremely faster than level set evolution. Generally, there are three key problems needed to be solved to implement the curve evolution methods. The first one is the initialization of the seed points. The second one is the formulation of the speed function. And the last one is the determination of the stopping criterion.

The level set methods have been widely applied in medical imagery (Suri et al., 2002) in different domains : the brain (Xie et al., 2005), the bone (Morigi et al., 2004), the vascular trees (Farag et al., 2004) and so on... The most common way to initialize the level set is the manual selection of a ROI which seems to be relevant ((Xu et al., 2000), (Farag et al., 2004) and (Xie et al., 2005)). Sometimes a simple mouse click combined with a fast marching approach (Fan,) is used. In this case the final contour determined by the fast marching step is the initial front of the level set. Those methods are semi-automated while we are focused on the automated methods. (Morigi et al., 2004) proposed an automated method but the imaging system is not the same as the subject of our study.

Our work consists of detecting tumors from the whole body image volume acquired by a PET/CT device. We have no *a priori* knowledge on the location of the tumor zone to detect. A contour evolution model using a level set method with an initialization based on thresholding is proposed in this paper.

The paper is organized as the following. Firstly, an overview of our study is described. Secondly, the principle of the level set method and its implementation will be exposed. The different steps of our approach and the associated results are then presented. Finally we will conclude and give some perspectives.

2 OVERVIEW OF THE STUDY

2.1 Segmentation Framework

Our aim is at detecting the tumorous areas in the body and in the brain from PET images and MRI images. Any *a priori* knowledge about locations of the tumors are taken into account. As the PET images are usually noisy and bad contrasted, the methods based on the image intensity or gradient are not efficient in these cases. The statistical methods cannot be neither used efficiently due to the small size of the tumor : they are too small to get statistical properties comparing with all images. The solution of the evolving contours is interesting in this case because they can grow to the expected size of the tumorous areas with help of geometrical and intrinsic properties.

For segmenting the 3D images, we complete it through a 2D slice-by-slice process. The proposed framework consists of 3 steps: seed detection giving a set of seeds which are susceptible belonging to the tumor; seed selection allowing to obtain one seed considered as the initial tumor contour; contour evolution according to an active contour model.

The seed detection consists of finding ROIs using intensity information. The areas of high glucose activity lead to high gray levels observed in PET images. A thresholding of images can be carried out to obtain the ROIs. The problem is how to choose the threshold. As known, the histogram can give the information about the distribution of grey levels. The maximum of the histogram is firstly found, which represents body tissus. Supposing that the number of pixels belonging to tumor regions has less than that of the pique of histogram. The threshold is then defined as the gray level on which the number of pixels equals to the maximum multiplied by a proportionality factor α which is given by experiences.

After the thresholding of images, several seeds are obtained in which some of them do not belong to the tumor. The big regions representing some anatomical regions which give high intensity, and very small regions due to noise, are detected as seeds. The big regions can be easily moved out from the seeds. A dilatation, morphological mathematics operator, is carried out to eliminate the small seeds. This seed selection step allows us to delete aberrant seeds and to keep that of tumorous areas. From the obtained initial contours (seeds), a level set method is used to grow them to find the tumor contours. In the next section, this method is presented in details.

3 CONTOUR EVOLUTION BASED ON LEVEL SET METHOD

The level set method has been introduced by (Osher et al., 1988) in order to solve the partial differential equations. It refers to the theory of the curve evolution. The algorithm proposed by Sethia ((Sethian, 1999) has been widely applied to many domains ((Fan,), (Xu et al., 2000))

3.1 Theory

Considering a curve represented by a level set function Φ, which is defined as a distance function :
For a point p, if $\Phi > 0$, p is outside the contour,
if $\Phi = 0$, p is on the contour,
if $\Phi < 0$, p is inside the contour.

From a geometric point of view, the evolution of a contour can be described as follows :

$$\frac{\partial x}{\partial t} = VN \tag{1}$$

with x a point of the contour, V the speed function, N the normal vector of the curve at x. The evolution of the curve depends on the normal vector N of the curve and the curvature K at each point of the curve, with :

$$N = \frac{\nabla\Phi}{|\nabla\Phi|}$$

$$K = \nabla\frac{\nabla\Phi}{|\nabla\Phi|} = \frac{\Phi_{xx}\Phi_y^2 - 2\Phi_x\Phi_y\Phi_{xy} + \Phi_{yy}\Phi_x^2}{(\Phi_x^2+\Phi_y^2)^{3/2}}$$

To describe the evolution of the curve we need to initialize it. The initial curve is defined as zero level set :

$$\Phi((x(t)),t=0) = 0 \tag{2}$$

To associate the zero level set to the evolving curve at each time and to derive the motion equation for this level set function, the zero level set has to te be re-initialized at each time step :

$$\Phi((x(t)),t) = 0 \tag{3}$$

After derivation of the equation 3 :

$$\Phi_t + V\nabla\Phi((x(t)),t) = 0 \tag{4}$$

where $V = x'(t)\cdot N$ is defined as a speed function. This speed function is the key of the implementation of the level set method.

3.2 Speed Function

The speed function V depends on :

- local properties given by local geometrical information (curvature, normal of the curve),
- global properties depending on the form and the position of the front,
- independent properties defined as a fluid velocity that transport passively the front.

Based on these properties, the speed function can be expressed as follows :

$$V = V_{prop} + V_{curv} + V_{adv} \tag{5}$$

with $V_{prop} = V_0$ constant speed propagation
$V_{curv} = -\varepsilon K$ curvature dependent speed
$V_{adv} = U(x,y,t)\cdot N$ advection speed

Since the speed function decreases to zero at the boundary of the area to segment, the components of the speed function are proposed as follows:

$$\varepsilon = \varepsilon_c V_{pij} \text{ with } \varepsilon_c \text{ constant }, \tag{6}$$

$$V_{pij} = \frac{1}{1+Gij} \text{ with } G_{ij} \text{ the image gradient at pixel } (i,j)\ , \tag{7}$$

$$U_{ij} = \beta\nabla V_{pij} \text{ with } \beta \text{ constant }. \tag{8}$$

ε_c and *beta* are constant parameters to be defined according to used images. For further details on the implementation of the speed function, see (Sethian, 1999) and (Xu et al., 2000).The stopping criteria depends on the speed function, therefore indirectly on the intrinsic parameters of the images. The evolution of contours stops when the speed function V = 0.

3.3 The Narrow Band

The problem of this method is that it takes a long time to compute if the update of the level set function is made on the entire image. The solution proposed by (Chopp, 1993) is to compute the level set function in a narrow band around the front. The level set function is only updated when it reaches the boundary of the narrow band. This narrow band approach can reduce importantly the computing time. It has been used in shape recognition by (Malladi et al., 1994) and analyzed by (Adalsteinsson et al., 1995) with success. Therefore, the narrow band is also adopted to the our method in the process of evolution.

4 EXPERIMENTAL RESULTS

4.1 Data

The data PET, we use for our experimentation, consist of three PET image volumes corresponding to three patients who reach some tumors. The size of the images is of 144x144 pixels and their resolution is above 7mm per pixel for both PET and Ct images. One volume is composed of about 190 slices. Visually, the three tumors observed in images are well segmented, confirmed by hospital experts. The MRI images are acquired on a 1.5T GE (General Electric Co.) machine using an axial FLAIR. The image volume consists of 512 (pixels) x 512(pixels) x 24 (slices) with a voxel size of 0.470.47 5.5 mm3. Three volumes of one patient acquied during a medical treatment at three time points are used in our experience. Six months separates each time point. The volume variations can be then calculated from segmentation results.

4.2 Choice of Parameters

Different values of the parameters have studied and tested before validate these ones : $\alpha = 0,0025$ for the seed detection parametrization, $\varepsilon_c = 0,05$ and $\beta = 0,005$ for the level set parametrization. Those values are chosen according to the images to be dealed with. They can keep the same if the images to be treated are acquired from the same imaging machine.

4.3 Segmentation

Ten PET slices of a patient who reaches a lung tumor are presented here (figure 1). For giving a good visualization, the gray levels are inverted. The tumor appears dark. The results obtained in different steps are shown from the figure 2 to 4:

- seed detection,
- seed selection,
- tumor segmentation with the level set method.

The seed detection (figure 2) allows us to determine ROIs which could be contained by tumorous areas. It is achieved thanks to the gray level information of the entire image volume. We know that higher gray levels represent areas of higher glucose activity and the tumors have abnormal glucose activity. But as foreseen the ROIs obtained are not necessarily tumors. The seed selection (figure 3) can help the decision of seed as explained previously.

The level set method is carried out image by image for all the voulme from the initialization given by the seed selection. We can see on figure 4 that the tumor is well segmented. The same approche is performed on MRI data. For example, for one patient, the variation is decreased about 15.42 percent six months after. This measure provides a very important information for the experts to evaluate the medical treatment.

5 CONCLUSION AND FUTURE WORKS

This paper presents a work on the automatic segmentation of tumorous areas for whole body and brain. The tumors are well segmented even if it remains in the results healthy regions. Two possibilities have been evoked to solve this :
- Improving the seed detection by using a multi-scale binarization method (see (Jolion, 1994) and (Trier et al., 1995)) for example. Indeed the question of seed detection has been briefly considered to test the level set method.
- Implementing a very robust classification method. A SVM classification has already evoked : previous works on medical image classification, lead in the laboratory, gave encouraging results (AitAouit, 2004).
If the initialization step is not robust enough, the classification step is necessary to select tumor contour.

Finally the level set should be implemented as a real 3-dimensional method in order to consider the whole 3D information. That allows to ameliorate the performances of the coutour evolution.

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Figure 1: patient 3 stack sample illustrating a lung tumor.

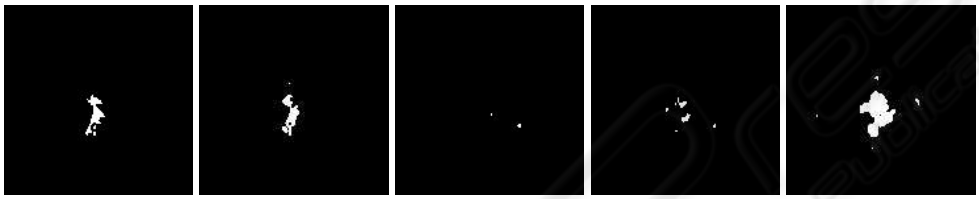

Figure 2: Seed detection on this sample.

Figure 3: Seed treatment.

Figure 4: level set segmentation.