Segmentation of Computed Tomography 3D Images using Partial Differential Equations

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Abstract — The analysis of medical images, such as Computed Tomography (CT) Images, increasingly requires an automatic processing for region enhancement, segmentation, 3D reconstruction and many other purposes. This paper presents a framework for performing these tasks using partial differential equations in 3D images. From a set of partial differential equations, we obtain a method for noise reduction filtering with edge preservation, region enhancement through the discrimination of the relevant density values, contour refinement and 3D reconstruction.

Keywords — computed tomography; segmentation; partial differential equations.

I. INTRODUCTION

Several types of medical image modalities are currently used for the diagnosis and monitoring of a wide range of pathologies. However, these images frequently present low contrast areas and small structures which are difficult to analyze for a human observer. Furthermore, an objective and robust discrimination is very important for achieving a reliable diagnosis. Computed Tomography (CT) is a very widely used technique for the diagnosis of a huge range of pathologies. CT generates a volume of data which consists of a series of two-dimensional X-ray images. Modern CT allows arranging the images along different axes or even as a 3D representation. At the same time as computer vision techniques are improved and spread, the analysis of this type of images increasingly includes new tools for computer-aided diagnosis and intervention.

Although, in some cases, the direct observation of the images is enough for a correct diagnosis, in some other situations, a precise, clear and measurable analysis is needed. Furthermore, some pathologies require an ad-hoc analysis of the images in order to distinguish the relevant findings which help the specialists in the diagnosis. For these reasons, the application of image processing techniques provides the specialist with more suitable views and some further information.

We present a method for the filtering, quantization and 3D segmentation of CT images which allows obtaining the boundaries of the tissues and organs and generating a 3D reconstruction for a further analysis. The process is divided into three stages. In the first one, a noise reduction filter is applied in order to reduce the disturbing elements and obtain better results in the following stages. The second phase extracts a series of relevant values from the structures in the images, so that the different tissues can be identified. Finally, with these values, a quantization and subsequent segmentation is performed to obtain the 3D boundaries of the tissues. When necessary, these contours are refined using active contours [1].

Previous works in CT processing include non-linear filtering methods for noise reduction [2] [3], sinogram smoothing [4], adaptive artifact reduction [5], adaptive filters for different modalities of CT [6] and wavelet based filtering [7].

II. NOISE REDUCTION

In order to reduce image noise, a 3D anisotropic diffusion process, based on Perona-Malik equation [8], has been implemented from the following equation:

\[ u_t = \text{div} (k (\|\nabla u\|) \nabla u) \] (1)

where

\[ k (x) = e^{-\lambda x} \] (2)

This kind of approaches, which diffuse the image but preserve the most important edges, are usually applied to single two-dimensional images. However, as we deal with a series of uniformly spaced images, we can apply them in three dimensions, so that the noise reduction process also takes into account the neighbors in the previous and next images, i.e. the values at the same position in the neighboring images. Of course, the distance between two consecutive images may not be the distance between the pixels within an image and, therefore, different weights can be assigned to the neighbors in the different coordinates.

Depending on the similarity of the various elements in the images, their contrast and texture, the value of \( \lambda \) in Eq. (2) can be adapted, as well as the number of iterations in the following discrete approach:

\[ u_{i,j,k}^{n+1} = u_{i,j,k}^n + \frac{dt}{2(\Delta h)^2} M \left( u_{i,j,k}^n \right) \] (3)

where \( M \left( u_{i,j,k}^n \right) \) is the result of convolving at each point with the \( 3x3x3 \) mask whose coefficients are:
Fig. 1. Anisotropic filtering: (a) original image; (b) filtered image.

\[ C_{i+a,j,k} = k_{i+a,j,k} + k_{i,j,k} \]
\[ C_{i,j+a,k} = k_{i,j+a,k} + k_{i,j,k} \]
\[ C_{i,j,k+a} = k_{i,j,k+a} + k_{i,j,k} \]
\[ C_{i,j,k} = -k_{i+1,j,k} - k_{i-1,j,k} - k_{i,j+1,k} - k_{i,j-1,k} - k_{i,j,k+1} - k_{i,j,k-1} - 6k_{i,j,k} \]
\[ k_{i,j,k} = e^{-\lambda \| \nabla u \|_{i,j,k}} \]
\[ a \in \{-1, 1\} \]

or more images in the series to be considered as a class representative of the density values of the organ. This is carried out by analyzing the histogram. The maxima of the histogram indicate the most suitable values for the different representatives, whereas the minima indicate where the limits of the ranges for every value are located.

In order to avoid considering a too large number of maxima, i.e. density reference values, the histogram is previously smoothed by averaging the values in the histogram with the neighbor bins. From this smoothed histogram, we extract the values which divide the whole range of intensities into a series of disjoint ranges.

Alternatively, a specific number of maxima can be set and a least-square fitting procedure can be applied to adjust the shape of the histogram to a certain polynomial. Figure 2 shows the smoothed histogram and the polynomial approximation.

**IV. IMAGE QUANTIZATION AND 3D REGION SEGMENTATION**

The heat equation is frequently used for noise reduction purposes. Unfortunately, this also implies a reduction of region contrast which results in a loss of definition and could have adverse effects on the segmentation stages. However, adding certain terms to the heat equation allows modifying its behavior, in such a way that those edges we are interested in preserving can be, not only maintained, but also enhanced, and the remaining heterogeneities are reduced. This results in a certain quantization of the image which improves the segmentation of the regions.

If this quantization is directly performed by setting a series of ranges and values they converge to, the noisy regions or textured pattern would generate heterogeneous areas. This is why we combine the heat equation with an external term.

\[ u_t = \Delta u - k \prod_{i=0}^{N} (u - V_i) \]

where \( \{V_i\}_{i=0,...,N} \) are the maxima and minima extracted in the previous stage.
The first term corresponds to the diffusion process performed by the heat equation, which homogenizes the regions but blurs the edges. On the other hand, the second term concentrates the values of the pixels according to the reference values, thus enhancing the edges. In this ordered series of values, the odd positions correspond to the maxima and the even positions correspond to the minima. If necessary, the limit values 0 or 255 are added to the list to fulfill this condition. After an appropriate number of iterations, the images can be completely discretized by setting a range of intensities (densities) for every tissue.

Figure 3 shows the evolution of the results through the different stages. As observed, the heat equation with external term reduces noise but does not blur the edges and, thereafter, the regions can be segmented. Figure 4 illustrates the influence of the number of reference values in the resulting regions. A too small number of regions does not allow distinguishing the regions of interest since they are merged, but a too large number of regions may split up a single organ into different regions.

Once one of the images has been quantized, the values can be selected to characterize tissues. If the selected image is representative enough, its values can be exported to the other images in order to accelerate the process. Since separated regions may have similar densities (e.g. organs with similar densities such as the liver and the spleen) a point is selected to apply a flood segmentation. The region determined by the reference values can be passed through the layers, i.e. the series of images. Within each layer, a flood segmentation is performed to adjust the initial region given by the previous layer to the actual boundaries in the current one. Figure 5 shows a sample with some processed images of the same series.

V. CONTOUR REFINING AND 3D RECONSTRUCTION

In some cases, the results are not completely satisfactory or a higher accuracy is required. For this reason, active contours [1] [9], also known as snakes, are applied after obtaining the initial contour in every layer in order to refine the results and obtain a more reliable segmentation. This technique is based on the following equation:

$$u_t = G(I) \text{div} \left( \frac{\nabla u}{\|\nabla u\|} \right) \|\nabla u\| + \gamma \nabla u \nabla G(I) \tag{7}$$

where $u_t$ represents the evolution of the snake when trying to segment a region in image $I$. The initial values of $u_t$ are obtained from the result of the previous stage. The function $G(I)$ is a stopping function which retains the contour on the most relevant edges within the image, and $I_\sigma$ is a smoothed version of $I$, used to prevent the contour from being stopped by noise, instead of by actual edges:

$$G(I) = \frac{1}{\sqrt{1 + \alpha \|\nabla I_\sigma\|^2}} \tag{8}$$

In Eq. (7), the first term uses the information about the curvature of the contour to regulate its smoothness. Parameter $\alpha$ controls the relevance of the gradient of $I$ in the stopping function, whereas parameter $\sigma$ determines how blurred the image is in this function. The second term attracts the snake toward the actual contour of the region, i.e. the points with high gradient values. This attraction force in controlled by parameter $\gamma$.

Once the contours for the different images are validated, the whole set of contours for an organ, tissue or section can be combined to generate a 3D view. Figures 6 and 7 show the results of the three-dimensional segmentation of a section of...
Fig. 4. Comparison of the resulting regions using different numbers of reference values: (a) 3; (b) 9; (c) 13; (d) 21.

Fig. 5. Results of the 3D segmentation applied to a series of images in a CT: original images (left) and processed images (right).
allow performing additional tasks, such as measuring distances and volumes, comparing mean densities or following the evolution of a certain pathology. Some of these tasks are quite tedious and not reproducible when carried out manually, but these promising results show that they can be automatically performed.

The combination of different partial differential equations in the several steps of the method which has been proposed generates quite satisfactory results and confirms the applicability of these techniques in medical image processing.

REFERENCES