WATERSHED TRANSFORM FOR AUTOMATIC IMAGE SEGMENTATION OF THE HUMAN PELVIC AREA

Alzenir O. Silva, Juliana F. Camapum Wanderley, Alan N. Freitas, Hansenclever de F. Bassani, Rodrigo A. de Vasconcelos and Flávia M. O. Freitas

Departamento de Engenharia Elétrica, Universidade de Brasília, juliana@ene.unb.br

ABSTRACT

In this work, we propose a new system for automatic image segmentation of organs of the human pelvic area. The algorithm is based on multi-region growing followed by watershed transform. The main contributions are the method of seed pixels selection and predicate of the multi-region growing algorithm and the segmentation results achieved. The system was tested in 400 images and its efficiency was measured by two different statistical methods, correlation and the *t-test*. The clinical application of the proposed technique is the radiotherapy treatment, which depends on the delineation of the treated area. The organs of interest are the rectum, bladder and seminal vesicles.

1. INTRODUCTION

The radiotherapy treatment planning requires the delineation of the therapy structures that will be submitted to the radiation beams. When executed manually, this delineation is a slow process and can result in human errors. This process needs precision, minimizing the radiation on healthy areas, close to the target tissues.

The objective of this work is to help the clinical oncologist in this complex task by providing an accurate and reliable automatic method for segmentation of therapy relevant structures from the human pelvic area. The images were acquired by X-ray Computed Tomography (CT) scans. The regions of interest are rectum, bladder and seminal vesicles.

The method consists of applying the watershed in the mosaic image. Beucher [1] [2] uses the gradient and the watershed to get the mosaic image while Bueno [3] calculates the mosaic image through the multi-region growing algorithm. The main problem of the multi-region growing algorithm is how to choose the seed pixels and the homogeneity criteria, known as the predicate. In this project, we propose a new technique to solve these problems, which will be independent of the CT equipment where the image was taken.

2. REVIEW

2.1. Watershed Transform

In order to understand the watershed transform, we make an analogy between the image function and a topographic relief (Figure 1). The gray level maximum values are the top of the mountains and the regions between these maximum values are the valleys or catchment basins (CB). Each regional minimum is a flooding source and it is associated with a catchment basin. The CBs are flooded in a constant rate. The watershed lines are the points where two CB meet, from different flooding sources.



Figure 1. Image function seen as a topographic relief, m are regional minima and b are the valleys (catchment basin).

The most applied watershed algorithms in medical image processing are the ones from Vicente & Soille [4], which are based on immersion simulations, and the ones from Meyer [5], which are based on hierarchical queues.

The watershed transform cannot be applied directly to the image or the image gradient because this results in over-segmentation (Figure 2).

Beucher [1] [2] [6] [7] proposed two solutions to this problem based on homotopy modification of the image gradient: one is achieved through morphological reconstruction (Beucher Paradigm) and the other by creating a mosaic image through the watershed transform. The mosaic image is an image composed of constant gray level (homogenous) patches.

3. SEGMENTATION MODEL

The segmentation model implemented in this work can be explained in three steps. First, we overcome the oversegmentation problem by creating a mosaic image through multi-region growing. After that, the gradient of the mosaic image is computed. Finally, we apply the watershed algorithm proposed by Meyer.



Figure 2. Segmented image after applying the watershed in the gradient image – over-segmentation.

In Figure 3 and Figure 4, we show the result of applying the multi-region growing in a CT image of the pelvic area.



Figure 3. Lines extracted from two images: the input image (full line) and the mosaic image (dotted line).



Figure 4. (a) Input image (b) mosaic image through multiregion growing.

3.1. Multi-Region Growing

In the classic region-growing algorithm, the region grows from a single seed and the growing is led through a predefined homogeneity criteria. This method can be extended to the multi-region growing region where several regions are computed simultaneously. The success of this algorithm depends on the seed pixels selection and the homogeneity criteria.

In the literature we can find methods, which are based on morphological filters by reconstruction. They look for homogeneity regions [8]. Other methods analyze the image histogram and manually select the gray levels of the highest peaks [3] [9] as the seed pixels.

We decide to implement a new peak detection algorithm based on image histogram. This algorithm provides the seed pixels and the homogeneity criteria to the multi-region growing. Consequently, we do not need to define any parameter. This algorithm was tested in several images of different CT equipments and proved to be totally automatic.

3.1.1. Seed Pixels Selection (markers)

The markers selection, known as seed pixels, is computed from the image histogram. The following steps were implemented:

- 1) Build the image histogram.
- 2) Determine all the peaks (P) of the histogram.

3) Select, in sequence, some or all the peaks P between the ones that were determined in step 2, following the rule:

3.1) For each *P* calculate g(pi)

$$g(p_i) = freq_i \times dist_i^2 \tag{1}$$

where p_i is the peak *i* of the histogram, $freq_i$ is the height of the peak and

$$dist_{i} = \begin{cases} 1, \text{ if } p_{i} \text{ is the first peak} \\ \text{horizontal distance to the nearest} \\ \text{selected } p_{i}, \text{ otherwise} \end{cases}$$
(2)

The horizontal distance is calculated by the absolute value of the difference between the gray level of the peak been tested and the nearest peak from the ones which have already been selected.

3.2) The peak p_i which maximizes the function $g(p_i)$ is selected.

4) All the pixels in the image with gray level of the selected peaks p_i from P are chosen as seed pixels.

Figure 5 shows an example of the steps described above. We consider the graphic as an image histogram. The horizontal values are the gray levels. The vertical values are the frequencies of each gray level. In the second line, $g(p_i)=freq_i$, and p_1 is the first selected peak (gray level 2). In the third line, $dist_i$ is the distance of each peak p_i from the selected peak p_1 and the peak which maximizes $g(p_i)$ is p_4 . In the end, the selected peaks have gray levels 2, 32 and 19. As a result, all the image pixels with gray levels 2,32 and 19 are classified as seed-pixels. These pixels will initiate the multi-region growing algorithm.

3.1.2. Homogeneity Criteria

Consider f(x,y) as the gray level of the pixel (x,y). The homogeneity criteria (H_{pi}) is defined as

$$H_{p_i}(x, y) = \begin{cases} \text{True, if } v_i \le f(x, y) \le v_{i+1} \\ \text{False, otherwise} \end{cases}$$
(3)

where the peak p_i been tested is located between one valley on the left v_i and one valley on the right v_{i+1} . The computation of the gray level of the valleys is presented in Equation 4:

For each peak p_i select a gray level I between p_i and p_{i+1} that minimize the function $h_i(I)$, as defined in the equation below.

$$v_{i} = \underset{I}{MIN} \left(h_{i}(I) \right)$$

$$h_{i}(I) = freq_{i} \times \left| I - \frac{(I_{i} + I_{i+1})}{2} \right|$$
(4)

Where: *I* is a gray level between the gray levels of two selected peaks p_i and p_{i+1} ; $freq_i$ is the frequency of *I*; $\frac{(I_i + I_{i+1})}{2}$ is the middle value between p_i and p_{i+1} and; $\left|I - \frac{(I_i + I_{i+1})}{2}\right|$ is the distance of *I* to the middle point

between p_i and p_{i+1} ;



Figure 5. Selection of histogram peaks as seed pixels.

The method described above resulted in a very efficient peak detection algorithm, which led to a successful segmentation algorithm. We tested images from two different CT equipments and images taken from the breast and pelvic area. In the next section, we present the statistical results that validate our segmentation.

4. RESULTS

4.1. Statistical Measures

We have tested an image database of 400 images of X-ray CT scans. The image format is DICOM (Digital Imaging Communications in Medicine) and the dimension is 512x512. Radiologists accomplished the manual segmentation.

The signature of the contour was calculated to estimate the error. It is represented by a function (ρ,θ) created by the distance measure ρ of the contour to the center point for different values of angle θ (Figure 6). The angles were taken in intervals of 10 degrees, resulting in 36 samples.

Two statistic analyses were undertaken in the manual and automatic samples. The *t*-*test* [10] [11] is calculated by the following equations.

$$t = \frac{/\bar{M} - \bar{A}/}{S_D}$$
(5)
$$\boxed{\begin{bmatrix} N_M \\ \sum_{i=1}^{N} (M_i - \bar{M})^2 \end{bmatrix}} + \begin{bmatrix} N_A \\ \sum_{i=1}^{N} (A_i - \bar{A})^2 \end{bmatrix} (1 + 1)$$
(6)

 $S_D = \sqrt{\frac{1}{\sum_{i=1}^{i} (M_i - M_i)} \sum_{i=1}^{i} (M_i - M_i)} \times \left(\frac{1}{N_M} + \frac{1}{N_A}\right)$ (6) Where M_i and A_i are the manual and automatic samples,

Where M_i and A_i are the manual and automatic samples, \overline{M} and \overline{A} are the mean of the manual and automatic samples; N_M and N_A are the amount of manual and automatic samples and $(N_M + N_A-2)$ is the degree of freedom of the *t-test* statistic.



Figure 6. (a) The bladder contour (manual and automatic segmentation), (b) signature graphic (ray ρ x angle θ).

The critical interval to |t| is |t| < 1,67, with degree of freedom 70, t(70), and the trust level of 90% [11].

The other statistic measure is the correlation, calculated from Pearson (r) index [10][11]. The best result is the one closer to 1.

$$r = \frac{\sum_{i=1}^{N} (A_i - \bar{A})(M_i - \bar{M})}{\sqrt{\left(\sum_{i=1}^{N} (A_i - \bar{A})^2\right) \left(\sum_{i=1}^{N} (M_i - \bar{M})^2\right)}}$$
(7)

4.2. Statistical Tables and Segmentation Examples

Statistic measures from *t-test* and correlation for the bladder segmentation can be seen in Table 1.

Figure 7, Figure 8 and Figure 9 show results from our segmentation algorithm when applied to the human pelvic area to extract the contour of the treated structures: bladder, rectum and seminal vesicles. The complete

statistical table and segmentation results can be seen in Silva [13].

Table 1 . <i>T-test</i> and correlation resultsfor bladder segmentation.		
Image	t	Correlation (r)
Img 20	0.8739	0.9922
Img 22	1.1705	0.9429
Img 24	0.1961	0.9381
Img 146	0.4274	0.9217
Img 211	0.6593	0.9782



Figure 7. Bladder segmentation - (a) input image and (b) image after applying our segmentation algorithm.



Figure 8. Rectum: (a) manual segmentation by clinician and (b) automatic result of our segmentation algorithm.



Figure 9. Seminal vesicles: (a) manual segmentation by clinician and (b) automatic result of our segmentation algorithm

5. CONCLUSIONS

The statistic measures showed the high accuracy of our segmentation, what make it useful for automatic delineation of organs from medical images.

The multi-region growing algorithm implemented in this work is quite independent of the input image, what is a great advantage of the automatic segmentation algorithm proposed. It was possible to segment the regions of interest (bladder, seminal vesicles and rectum in the case of pelvic images) from medical images with varying contrast and dimension. The seed selection and homogeneity criteria are robust leading to a successful segmentation.

Unfortunately, there are limitations such as when an organ is connected to another organ or when the contrast is very poor for organs in the neighborhood.

6. REFERENCES

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