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Automatic segmentation of the lungs using multiple active contours and outlier model

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Abstract— **This paper presents a method for the automatic segmentation of the lungs in X-ray computed tomography (CT) images. The proposed technique is based on the use of multiple active contour models (ACMs) for the simultaneous segmentation of both lungs and outlier detection. The technique starts by grey-level thresholding of the images followed by edge detection. Then the edge points are organized in strokes and a set of weights summing to one is assigned to each stroke. These weights represent the soft assignment of the stroke to each of the ACMs and depend on the distance between the stroke points and the ACM units, on gradient direction information and also on the stroke size. Both the weights and the ACMs energy minimization are computed using the generalized expectation-maximization (EM) algorithm. Initialization of the ACM's is fully automatic. Experimental results show the effectiveness of the proposed technique.**

I. INTRODUCTION

X-ray computed tomography (CT) is the most commonly used diagnosis technique for the analysis of the pulmonary region and the number of CT evaluations of the lungs has been steadily increasing. In most pulmonary CT image analysis applications the first step is the segmentation of the lungs. Some examples include airway analysis [11], emphysema detection [10], evaluation of lung ventilation [12] and the detection of lung nodules [14], [15]. Several algorithms have been proposed for the segmentation of the lungs. Most methods start with grey-level thresholding followed by region segmentation based on a sequence of morphological operations [8], [9], [14]. For instance in [9] the step of grey-level thresholding is performed using optimal thresholding to select the threshold automatically. Then connected components labelling is performed, the background air is eliminated by deleting regions that are connected to image borders and only the two larger regions are retained. In some images there is a superposition of the lungs region which requires an additional step for their separation. This task of lung separation is usually one of the most computational intensive. in [9] the left and right contours are separated by identifying the anterior and posterior junctions by dynamic programming. Lung separation in [8] is performed by a heuristically based region splitting procedure according to a thickness measure. Some methods include a priori anatomical knowledge [11], [12] which makes them more powerful but at the cost of more computational load. For instance in [12] anatomical knowledge stored in a semantic network is used to guide the low level image processing and a lung separation step based on dynamic programming is also included. Recently, an algorithm using marker based watershed transform was proposed [13] that eliminates the tasks of finding an optimal threshold and separating the attached left and right lungs. However, the identification of internal and external markers which is based on morphological operations relies on heuristics. In [2] two independent ACM's based on geodesic gradient vector flow are used. Although this method works well on concavities it is unable to bridge anatomical structures such as the trachea or bronchi in case of adverse initialization. In this paper we present a method for the automatic segmentation of the lungs in thoracic CT images. The proposed technique is based on the use of multiple active contour models (ACMs), an algorithm recently proposed in [1] in which multiple ACM's compete for the boundaries of multiple regions, thus alleviating the well known problem of ACM's initializations. The algorithm proposed in this paper includes two major contributions: 1) it uses a different observation model which makes it less sensitive to initialization and more robust to outliers, 2) initialization of the ACM's is fully automatic. A new outlier model is developed that takes into account the strokes size in order to reject the smaller strokes corresponding to the smaller nearby anatomical structures. In addition, the observation model is also improved and features are extended to include the gradient direction as well as the edge locations. These modifications make the method more robust thus allowing a fully automatic initialization which is based on the detection of dark circles on a white background with the Hough Transform. This paper is organized as follows: section II formulates the problem, section III describes the proposed algorithm for lung segmentation, section IV presents experimental results and section V concludes the paper.

II. SEGMENTATION WITH MULTIPLE ACTIVE CONTOUR MODELS

A. Problem Formulation

Let y be the set of all edge points detected in an image and let us assume that y is organized in connected components, called strokes, $y^j, j = 1, ..., N$ where $y^j = \{y_1^j, ..., y_n^j\}$ is the set of edge points belonging to the j-th stroke. The number of ACM's, L, is assumed to be known and we add an extra model to account for outliers. We denote it the outlier model, $x^{outlier}$. Let x^k be the k-th active contour model, $k = 1, ..., L$ defined by a sequence of 2D points $x_i^k, i = 1, ..., M^k$;

the number of points for each snake is adjusted by insertion and deletion in order to keep the distance between two consecutive points constant and therefore different ACM's may have different number of points. x^k can either be an open or closed contour. We will assume that the strokes detected in the image are independent:

$$p(y|x) = \prod_j p(y^j|x) \tag{1}$$

and that the distribution of each stroke is a mixture of L+1 densities:

$$p(y^j|x) = \sum_k \alpha_k p(y^j|x^k) + \alpha_{outlier} p(y^j|x^{outlier}) \tag{2}$$

where the α_k's are the mixing proportions verifying $\alpha_k \geq 0$, $\alpha_{outlier} \geq 0$ and $\sum\limits_k \alpha_k + \alpha_{outlier} = 1$.

Our aim is to estimate the L ACM's using the MAP criterion:

$$x^* = \arg\max_x p(x|y) = \arg\max_x \left[\log p(y|x) + \log p(x)\right] \tag{3}$$

As discussed in [1] this can not be solved analytically so the EM algorithm is used.

B. Observation Model

We assume each stroke has i.i.d. edge points, each modelled by a mixture of M^k densities centered in the snake elements:

$$p(y^j|x^k) = \prod_n p(y_n^j|x^k) = \prod_n \frac{1}{M^k} \sum_i \varphi_\sigma(y_n^j, x_i^k) \tag{4}$$

This model is related to the elastic net model [3] and associates every edge point with a given snake element. This model is less sensitive to initialization than the previous model used in [1]. Since in the thresholded images the lungs appear as black regions against a white background we use directional snakes [4] and define the contribution of each feature to the potential function introduced as follows:

$$\left\{ \begin{array}{ll} \varphi_\sigma(y_n^j, x_i^k) = N(y_n^j, x_i^k, \sigma^2 I) & \left|\theta_N(x_i^k) - \theta_G(y_n^j)\right| \leq \pi/2 \\ 0 & otherwise \end{array} \right. \tag{5}$$

where $N(y, \mu, R)$ denotes the normal density function with mean μ and covariance R, $\theta_N(x_i^k)$ is the contour's outward normal direction at snaxel x_i^k and $\theta_G(y_n^j)$ is the gradient direction at edge point y_n^j. This approach makes sure that only those edge points with the correct gradient direction will attract the ACM's. For the case of the outlier model, the contribution of each feature to the potential is a constant. Previously we used the same constant for every stroke, $V = \phi_\sigma(|3\sigma|^2)$ and our outlier model had the ability to classify the strokes that were distant from all the ACM's as outliers. We now propose using a different value for each stroke, V^j.

$$p(y^j|x^{outlier}) = \prod_n p(y_n^j|x^{outlier}) = \prod_n N^j V^j = \left(N^j V^j\right)^n \tag{6}$$

If V^j is set inversely proportional to the size of the corresponding stroke, N^j, then the smaller strokes will also tend to be classified as outliers, and the ACM's will be able to bridge the small outlier strokes. Therefore we used $V^j = \exp(-KN^j)$ where K is a positive constant.

C. Prior Model

We adopt the following prior:

$$\log p(x) = \sum_k \left(E_{\text{int}}(x^k) + \sum_{l \neq k} E_{\text{inter}}(x^k, x^l) \right) \tag{7}$$

where $E_{\text{i}}(x^k)$ is a regularization energy that expresses the assumption that each contour is smooth and $E_{\text{inter}}(x^k, x^l)$ is another regularization energy that expresses the interaction between different active contours. For $E_{\text{int}}(x^k)$ we used:

$$E_{\text{int}}(x^k) = \sum_i \left(\left\|x_i^k - x_{i-1}^k\right\| - l_0\right)^2 \tag{8}$$

where l_0 is the desired spacing between successive snake elements, set by the user. Setting $l_0 \neq 0$ prevents the active contour from shrinking collapsing into a point. For $E_{\text{inter}}(x^k, x^l)$ we used:

$$E_{\text{inter}}(x^k, x^l) = \sum_i \sum_m \varphi(|x_m^l - x_i^k|^2) \tag{9}$$

where $\varphi(d)$ is a distance measure that can be tailored to fit a particular application. Any kind of geometrical relation between contours can be defined, for example the contours can attract or repel each other, they may be required not to intersect or to be concentric.

D. Estimation of the multiple ACM's

In the EM algorithm it is assumed that y is incomplete data and that the complete data includes binary labels $z_j, j = 1, ..., N$ with $z_j = \{z_j^1, ..., z_j^{L+1}\}$, that indicate which model generated the stroke; $z_j^k = 1$ means that stroke y^j was generated by model x^k. The complete log likelihood is given by:

$$logp(y, z|x) = \sum_j \sum_k z_j^k \log p(y^j|x^k) \tag{10}$$

Instead of maximizing (3), the EM algorithm alternates between two steps. In the E-step it finds the conditional expectation of the complete log likelihood with respect to the unknown x given the observed data y and the current estimate, $\hat{x}$.

$$Q(x, \widehat{x}) = E\left[\log p(y, z|x)|y, \widehat{x}\right] \tag{11}$$

$$\begin{aligned} Q(x, \widehat{x}) &= E\left[\sum_j \sum_k z_j^k \log\left[\alpha_k p(y^j|x^k)\right]\right] \\ &= \sum_j \sum_k w_k^j \log\left[\alpha_k p(y^j|x^k)\right] \end{aligned} \tag{12}$$

where w_k^j is a set of weights summing to one assigned to each stroke. The weights w_k^j represent the soft assignment of stroke y^j to the active contour x^k. The weights are given by:

$$w_k^j = p(z_j^k = 1|y^j, \widehat{x}) = \frac{\alpha_k p(y^j|x^k)}{\sum\limits_m \alpha_m p(y^j|x^m)} \tag{13}$$

In the M-step the estimation of the active contour is obtained by the maximization of:

$$U(x, \widehat{x}) = Q(x, \widehat{x}) + \log p(x) \quad (14)$$

The maximization is performed by the gradient algorithm:

$$x_{t+1}^{k} = x_{t}^{k} - \gamma \nabla_{x}(Q(x, \widehat{x})) \quad (15)$$

where ∇_x represents the gradient. This equation can be rewritten as follows:

$$x_{t+1}^{k} = x_{t}^{k} - \gamma_{\text{int}} f_{\text{int}} - \gamma_{\text{ext}} f_{\text{ext}} - \gamma_{\text{inter}} f_{\text{inter}} \quad (16)$$

where $f_{\text{ext}}(x_i^k)$, $f_{\text{int}}(x_i^k)$ and $f_{\text{inter}}(x_i^k)$ are external, internal and interaction forces. More details are given in [1].

III. PROPOSED ALGORITHM FOR THE SEGMENTATION OF THE LUNGS

The first step of the proposed algorithm is gray-level thresholding using Otsu's [7] method which computes the optimal threshold that maximizes between-class variation. The thresholding operation usually separates the lungs and the outer chest walls and in some images also the trachea, esophagus or bronchi. Usually there are small white spots inside the lungs regions corresponding to blood vessels. After thresholding, the edges of the binary image are detected and sets of connected edge points (strokes) are detected. The nearby smaller anatomical structures and the white spots inside the lungs originate strokes that we wish to discard as outliers (Fig. 1). At this point the directional information of the edges is also calculated and will be used to improve the segmentation performance.

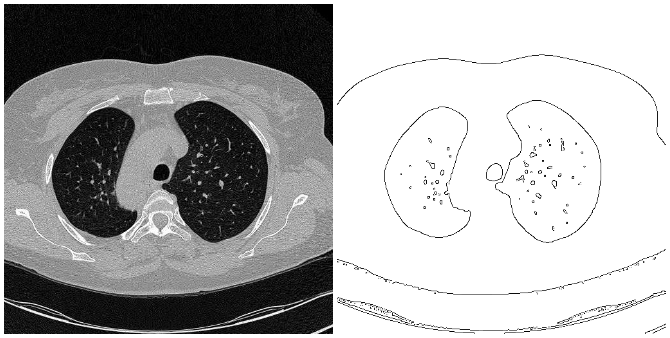

Fig. 1. Edge detection step. a) Original image b) Corresponding edges.

For the simultaneous segmentation of both lungs two ACMs are used (L=2). In case there are other thoracic structures of interest in the images, the trachea for example, more ACMs can be used.

A. Initialization

The initialization is fully automatic. Since the competition between the multiple ACMs makes them quite robust we are able to use a crude initialization with two parallel circles with the same radius. These two circles are found with the Hough Transform (HT) using a very coarse quantization for the circles center coordinates (a, b) and also for the radius *r*. The circle detection tries to find dark circles on a bright background and therefore exploits the geometrical relationship between the center coordinates (a, b) and the edge direction ϕ obtained in the edge detection stage. This relationship, together with the knowledge of the expected range of radii, makes it possible for every edge point (x, y) to vote in the parameter space across a line segment normal to the tangent. The line segment is defined by the points (x, y) and (x_1, y_1) which are calculated as follows:

$$\begin{aligned} x_1 &= x + r_{\max}\cos(\phi) \\ y_1 &= y + r_{\max}\sin(\phi) \end{aligned} \quad (17)$$

where $r_{\max}$ is the maximum value allowed for the radius. The circles are found by searching the 3D accumulator space for two peaks with the same *b* coordinate for the circle center and also the same radius. This search for the maxima is exhaustive but it is fast since the number of cells is quite small because of the coarse parameter quantization. Initialization can be located either inside, outside or across the lungs region.

B. Lung Superposition

In the case of lung superposition, after the algorithm's convergence there will be a separation between the ACM's because there are no edges at the lungs junction and both lungs are competing for the same strokes. Therefore, in order to connect the ACM's at the junction, we add interaction forces between the ACM's. We use the long range attraction forces and short range repulsion forces also used by [6] which are derived from the intermolecular dynamics potential function known as the Lennard-Jones function:

$$f_{\text{inter}}(x_i^k, x_j^m) = A\left\|r_{ij}\right\|^{-n} - B\left\|r_{ij}\right\|^{-m}$$

where $\|r_{ij}\|$ is the distance between snaxels x_i^k and x_j^m and n, m, A and B are constants. We use the default A = B = 1.0, m = 1, n = 3. An example of lung separation is given in section IV.

IV. RESULTS

This section presents examples to illustrate the performance of the proposed method. The input data consists of stacks of chest CT slices with X-ray attenuation ranging from -1024 to 3071 Hounsfield units, corresponding to a 12 bit quantization. Images are 512x512 with slice thickness of 1.0 millimeters. Edges were obtained with the Canny edge detector and strokes were obtained with a connected components labelling algorithm. The external forces acting on each model unit were multiplied by independent gains as suggested in [5] in order to speed up convergence. The gain factors γ_{int} and γ_{inter} were chosen manually. The first example illustrates performance of the algorithm in the middle pulmonary region and shows the robustness of the method with respect to the initialization. Fig. 2 a) and b) shows the initial contours and the final contours obtained by the algorithm. Although there is a large degree of intersection between the two ACM's produced by the automatic initialization step, still the method is able to recover due to the competition between the two ACM's. In addition the algorithm is able to classify the trachea as an outlier as well as the spurious strokes located inside the lungs.

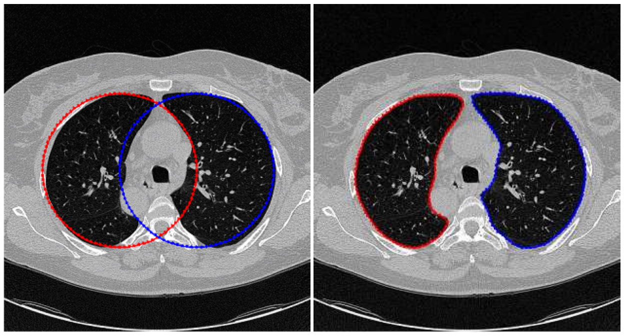

Fig. 2. Lung segmentation in the middle pulmonary region. a) Automatic initialization b) Final Segmentation.

The second example illustrates the performance of the algorithm in the lower pulmonary region and shows that the method can deal with pronounced concavities and different shapes for each lung. Fig.3 a) and b) show the initial contours on the left and the final contours on the right.

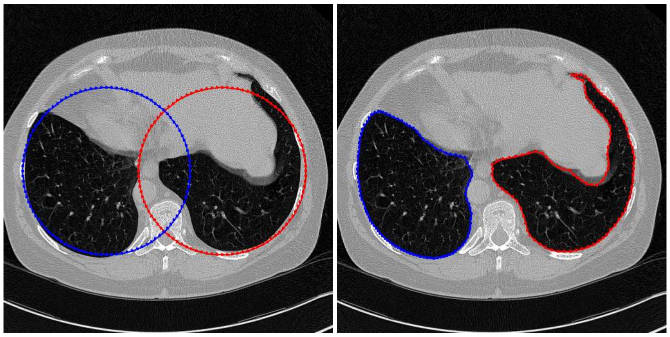

Fig. 3. Lung segmentation in the lower pulmonary region. a) Automatic initialization b) Final Segmentation.

The third example illustrates the performance of the algorithm in the case of lung superposition. Fig.4 a) shows the segmentation results obtained without interaction forces and Fig.4 b) shows the final segmentation with joined contours after the use of interaction forces between the ACM's.

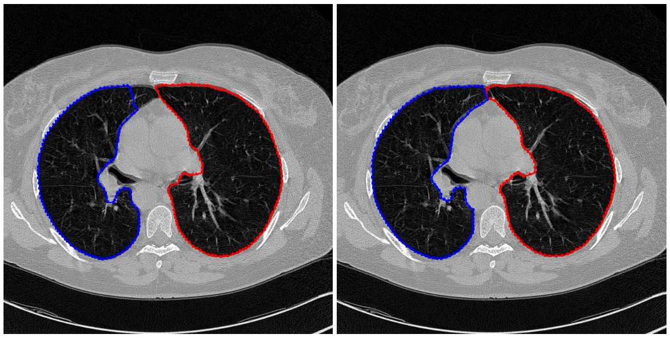

Fig. 4. Lung superposition. a) Segmentation before interaction forces b) Final Segmentation.

V. CONCLUSIONS

This paper proposes a method for the automatic segmentation of the lungs in X-ray computed tomography (CT) images using multiple active contour models and an outlier model. The method segments both lungs simultaneously and also accounts for outlier features detected in the image. No user intervention in required to initialize the contour since the initialization is fully automatic. Optionally more thoracic structures other than the lungs can be segmented. Future work will include the extension of the proposed methods to 3D for the analysis of the complete CT data set.

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