A Fast Approach to Lung Segmentation in X-ray CT Images

José Silvestre Silva\textsuperscript{1}, Augusto Silva\textsuperscript{2,3} and Beatriz Sousa Santos \textsuperscript{2,3}

\textsuperscript{1}Departamento de Física
Universidade de Coimbra
Rua Larga
3004-516 Coimbra
PORTUGAL
email: jsilva@ci.uc.pt

\textsuperscript{2}Departamento de Electrónica e Telecomunicações
Universidade de Aveiro
Campo Universitário
3810 Aveiro
PORTUGAL
email: asilva@ieeta.pt
email: bss@ieeta.pt

\textsuperscript{3}IEETA - Instituto de Engenharia Electrónica e Telemática de Aveiro
Campo Universitário
3810 Aveiro
PORTUGAL

\textbf{Abstract}: This paper describes a method for the segmentation of pulmonary regions on thoracic cross-sectional images obtained by X-ray computer tomography. Relying on priori information about the general location and morphology of the lungs, our method is based on the interpretation of the histogram, mapping each peak to a group of anatomical structures. We also applied morphologic filtering to bypass misleading effects of pulmonary blood vessels. This method has been applied to several CT images from different patients and, since it is intrinsically non-iterative, proved to be much faster than the more general method of active contours.

\textbf{Keywords}: image segmentation, computed tomography, chest CT, histogram mapping, morphologic filtering.

\section{1. INTRODUCTION}

X-ray Computer Tomography (CT) is one of the most efficient medical diagnostic methods and has currently a widespread usage. This imaging modality provides detailed cross sectional images of thin slices of the human body [1]. State of the art CT machines, featuring fast helical scanning capabilities, allow a large target volumetric acquisition, with a tighter control of longitudinal resolution. The gathered data set is thus more suitable to be processed and visualized in 3D, as compared to the traditional “stack of slices” approach constrained by a lower, and normally predefined, longitudinal resolution [2-4].

In this context, the development of efficient (i.e. fast and accurate) methods for lung segmentation, as a pre-processing step, continues to deserve an increasing interest; the reasons are twofold:

- accurate lung segmentation is important to perform accurate (geometrical and/or densitometric) measurements;
- fast lung segmentation is important due to the great amount of information that has to be processed in order to generate 3D visualization and measurements.

In this work we describe a method for the fast 2D segmentation of pulmonary regions based on an ingenious region removal approach and common anatomical prior information.

\section{2. OBJECTIVES}

Our image data set consisted on a stack of chest CT slices and it was our objective to develop an algorithm for the detection of pulmonary contours on the overall set of CT images based on a 2D approach. It should be efficient enough to be embedded in a future application for 3D visualisation and measurement of the lungs. It should also be optimised to spend the less computational resources as possible.
3. METHODS

To identify the pulmonary regions [5-7], we have considered two possibilities, corresponding to two radically different approaches. The first method closely follows the active contour algorithm [8]. It starts from a connected set of seed points easily defined in the interior of each lung and then iteratively expands towards the final lung contours. The expansion process is mathematically controlled by equations resulting from an energy minimization task. The second possibility corresponds to identifying through appropriate thresholding the outer pulmonary structures (ribs, muscles, blood vessels, mediastinum, etc), that normally correspond to much brighter areas. Those image regions with a density comprised by the thresholding window form a connected region involving the lungs. After calculating the interior contour of this connected region, we easily reach the lungs contours.

The first method, requires a significant degree of interaction not only for the selection of the seed points, but also for the particular choice of weight parameters that play a major role in the spatial evolution of the contour. Moreover, it is intrinsically iterative which contributes to slow down the overall procedure. While requiring an ultimate medical expert validation, the second method may be executed in only one passage, without cycling or interactive calculus. We henceforth proceeded with this method carrying on experiments using real CT images.

The studied images were in digital format (256×256 pixels). For practical reasons, the dynamic range was scaled to the interval [0 – 255]. This conversion does not influence the segmentation process since what is searched for depends on strong density transitions between pixels.

Our algorithm begins by defining a thresholding window on the histogram. The brightest value, corresponding to bone tissue, determines the upper grey level window limit. Moving towards darker values, the first local maximum corresponds to outer pulmonary structures; the second local maximum corresponds to mediastinic structures together with blood vessels. The window lower limit is finally determined by the next local minimum (value near zero, slightly on the left of the two peaks already mentioned). The result of this simple windowing procedure is a mask (boolean image) that leads, in a first passage, to an automatic pre-segmentation of lung regions.

From our segmentation task perspective, spurious white spots corresponding to blood vessels inside the pulmonary regions should be regarded as noise and thus be removed by some suitable method. A morphologic filter [9] was then applied, to eliminate isolated white spots, in a way that the final binary image exhibits a single white connected region.

The resulting binary image has only a white region and several dark regions: two of them correspond to the lungs. The main remaining problem consists on rejecting the outer black regions in the binary image. This was simply achieved by a morphologic fill operation using the mask vertices as starting points.
Calculating the area of the dark regions and retaining the two largest values is enough to unambiguously identify the two lungs. The final step is simply a contour detection and tracking procedure around the predefined masked pulmonary regions. The final result can be observed in figure 4. For the sake of visibility of more detailed anatomical features, the pulmonary contours appear superimposed on the CT image after global histogram equalization.

Figure 4 - Equalised image with superimposed pulmonary contours.

The algorithm was implement in MATLAB 5.3 using, whenever possible, vectorized data structures and pre-existing image processing functions [10]. The typical computational time for one image segmentation on a Pentium II 350MHz was about 2 to 3 seconds.

4. RESULTS

Results similar to those shown in figure 4 were obtained with many other real chest CT images provided by a CT scanner running at the Medical Imaging Department of the Coimbra University Hospital (figures 5 to 8). The method is robust enough to handle the more challenging CT slices either from the apex or the basal levels.

Figure 5 – Image from upper third pulmonary region.

Figure 6 – Image from middle third pulmonary region.

Figure 7 – Image from middle / last third pulmonary region.

Figure 8 – Image from last third pulmonary region.
Figure 9 – Image with both pulmonary regions connected.

Figure 10 – Image with one airway included in left lung.

Although this method works on most images, it exhibits an imperfect behavior in some images. The first problem is that the method isn’t robust enough to handle images were both lung regions are connected, the method takes both pulmonary regions as one global region (see figure 9). The second problem is the inclusion in the sought for regions of spurious airway structures such as trachea and bronchi, when they are too near of a lung; these organs appear as large black spots on the image, as seen in figure 10.

Nevertheless, this algorithm proved to be effective in most of 90 tested images from 3 patients.

5. CONCLUSIONS

The proposed method for lung segmentation in chest CT images seems to be fast and accurate enough to provide a good quality data set for further quantitative analysis and visualization procedures.

An improved version of this method is under development in order to take in account the referred problems.

It should be stressed that the higher performance obtained with this method as compared to the active contours methodology is mainly a consequence of the rather significant prior anatomical information that has been incorporated in our algorithm. However, we believe that the overall performance can still be improved exploiting, for example, 3D spatial coherence as the segmentation procedure evolves from slice to slice.

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