Automatic Region Based Segmentation and Analysis of Lung Volumes from CT Images

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Abstract
Lung segmentation is an important step in modern radiological diagnostics. In this paper we propose an automatic method for lung segmentation with previous preprocessing of the lung computed tomography images. Our algorithm starts with segmentation with the initial thresholding to create binary image. After creation of the binary image, the threshold is used to set all the pixels under the selected value to the background. This will eliminate the table and other non anatomical pixels from the images. The algorithm is looking for the first pixel on the CT image, and after it is found, the region growing commence, and the lung region is segmented containing right and left lung and airway. Morphological operators are used to enhance the image edges, as well to include the missing tissue due to their high attenuation. The results were compared with the volume found by human observer's segmentation, and for measure of similarity we used Pearson correlation coefficient, and with the P=0.996657, we can conclude that there is a significant correlation between our method and the gold truth.

Keywords
3D Lung Segmentation, Region Growing, Lung Quantification

I. Introduction and Previous Work
CT (Computed Tomography) for imaging the human body is present since 1975, and originally, CT is not considered a good technique for imaging the thorax. Low resolution images have led to great partial volume effect, and large differences in attenuation values between air and tissue have distracted radiologists to accurately detect small lesions. 20 years ago, advanced axial resolution has enabled high-resolution computed tomography (HRCT). 1mm thick scans can show anatomical detail of the lungs similarly to pathologic sampling. Current scanners allow full acquisition of isotropic lungs with millimeter precision within a single breath. Compared with other modalities, CT is the preferred method for monitoring lung disease.

A large number of research studies is dealing with the segmentation of lung tissue. A lot of researchers are using the basic techniques of image processing such as filtering, the region growing approach and connected components analysis and mathematical morphology for segmentation [1-4]. Segmentation of the lung has become of interest to the scientific community, as an important prerequisite for all types of computer-aided analysis of the lung in the lung CT images. Various algorithms from different authors can be found for medical image segmentation such as thresholding [5], region growing [6-7]. Different window width and level settings can also effect the image reconstruction [8]. Denison et al. [9] presented one of the first region based approach, with the 2d region growing method, which required manual seed placement. All these methods work only on 2D slices, and not on 3D volumes. Since the beginning of the century, research efforts in the area have been intensified significantly. Silva et al. [10] and Hu et al. [11] are one of the first that proposed the methods for the segmentation, as well as Kuhnigk et al. [12], Zheng et al. [13], and Armato and

Sensakovic [14]. All of these methods follow the scheme of gray-level thresholding, connectivity analysis, and post-processing for lung separation and closure of the lung, or pulmonary involvement of high-density structures in the lung mask. The last step in the majority of lung segmentation is the inclusion of higher-density lung structures than previously calculated threshold parenchyma. For this step, the kernel-based morphological closing filters are used for the most part. Armato et al. [14] made use of so-called closure rolling ball algorithm, which can be described as the process of rolling the ball a certain radius to the unclosed lung surface.

II. Materials and Methods
First step in creation of the CAD system for segmentation of the anatomical structures is to preprocess the images. The preprocessing of the images is used to eliminate the non anatomical pixels, like patient table and medical devices from the CT images. By this process we want to exclude all pixels that are not going to be used in the segmentation process. Threshold is determined by choosing arithmetic mean between water (0 HU) and air (1000 HU), and adding 10%, that was empirically established with the test data. By converting the image with threshold of -550 HU, we created a binary image with exclusion of all the pixels below this value. The areas with the longest area are detected, the patient thorax and the patient table. By keeping the biggest area, only anatomical pixels retained on the segmented image.
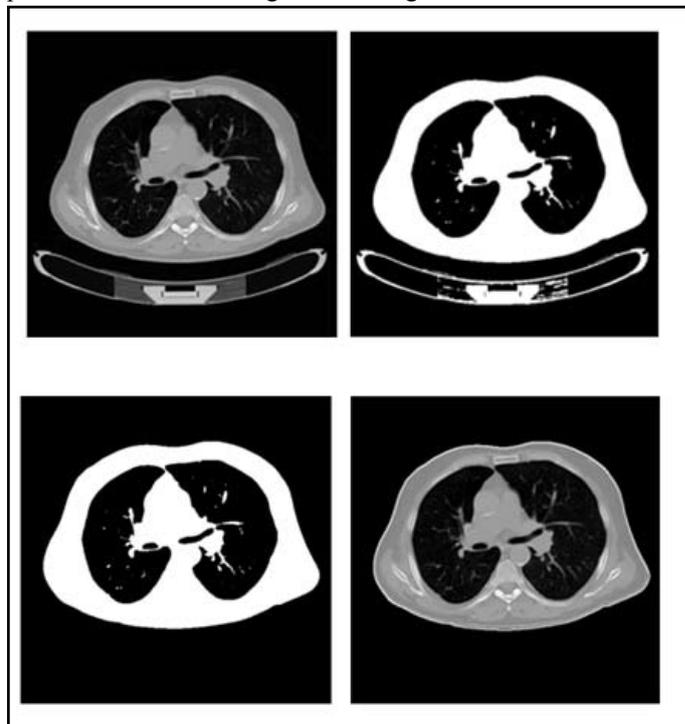

Fig. 1: From left to Right, Original DICOM Image, Image Thresholded With Fixed Threshold, Binary Image With Only Anatomical Pixels, Masked Image With Enhanced Image (for Better Visualisation).

After we have excluded all non-anatomical pixels, we can continue with segmentation process, in order to segment only lung areas. Histogram thresholding is used for determination of the actual binary masks for the lung area. Thresholding is the first step in segmenting the image because a lung CT contains two main groups of pixels: high intensity pixels located in the body and low intensity pixels that are in the lung and the surrounding air. Due to the intensity difference between these two groups, thresholding can be used to separate these pixels in two groups. This iterative procedure computes the value of a threshold so that the two groups of pixels are well separated. Binary masks are generated from input gray level CT data using the conventional thresholding algorithm, in which the threshold is simply chosen as the arithmetic mean between the two maxima of the gray level histogram, water and air.

A. Region Growing Algorithm

Region growing algorithm starts with a seed pixel, examines neighboring pixels that surrounds it, and, if it meets certain criteria, it is included in the region. This process is followed until no additional pixels can be added. The region is grown by examining all 4-neighboring pixels to the region. The difference between a pixels intensity value and the regions mean is used as a similarity measure, and the pixel with the smallest difference measured this way is allocated to the iteratively grown region, so the region growing process is completed when the intensity difference between region mean and new pixel is larger than a certain threshold.

For the region growing algorithm to be effectively finished, the crucial part is the position of the seed pixel, and it must be selected from which the region growing may start. The aim of our algorithm is the removal of the dark areas that does not belong to the lungs, a seed pixel must be selected from the dark region, and the approach used here finds the minimum pixel from the image on the boundary, that is on location (1,1), this is the first pixel on the left side of the image. In most cases, this is a dark pixel that represents background air, but in case of noise on the image, we added dark border 1 pixel thick around the image. After choosing the dark pixel region growing starts marking all the pixels that are in 4-connected neighborhood of the seed pixel, and this is done until all the dark pixels are not joined in. If the intensity value of checked pixel is close to the mean intensity of the region under consideration then it is assigned to the region, and the region grows until it collides with another region or it reaches a different intensity area. Finally this method stops when there are no more pixels to be classified, and the original gray scale image has been segmented into the lungs and trachea. The results are shown in fig. 2. However, with this approach we segmented all pixels that are outside of the lung parenchyma, so we created a negative of the image to get only inside structures of the lung tissue.
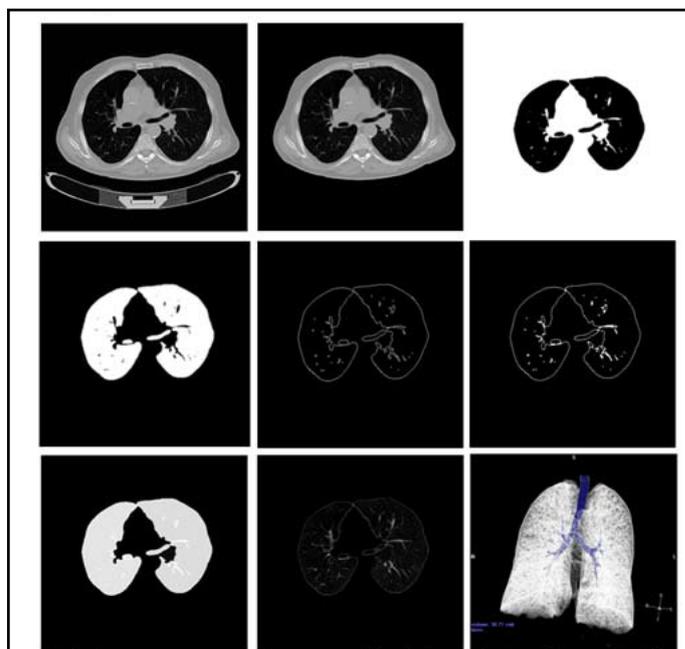

Fig. 2: Automatic segmentation process, from left to right. Top left - original image, top middle – non-anatomical pixels removed, top left - region growing of parenchyma nad airway mask, middle left – inverted mask of region growing of parenchyma nad airway mask, middle image - edge detection of the binary mask, middle left – morphological binary closing of the edges applied with element of radius 1, bottom left – morphological closing applied to include the blood vessels, bottom middle – segmented lungs with airway, bottom right – 3D visualisation of the segmented lungs.

After the region growing algorithm is finished, we applied the edge detector on the image, to create a mask for the extraction of the lungs. We didn't notice any difference in changing the edge detectors operators, so we used Sobel operator for this purpose. After edge detection, morphological binary closing is applied to each mask to close the borders of the edges. We conclude that the mask will not be created properly if this is not done; sometimes few pixels are missing, usually caused by noise, and we used disk as structuring element of pixel radius 1. Finally edges outside the lung region are filled, and morphological 3D closing procedure is applied to binary mask for the inclusion missing voxels corresponding to blood vessels and small bronchi that are excluded due to their high attenuation and the overall binary mask (OBM) is created, that contains entire lung, airway tree and bronchi. Extraction is done by combining the regions of binary map of the original DICOM image and from binary map of just its closed edges.

III. Results

The algorithm was performed by using open source software Mevislab version 2.2, and for evaluating the results, radiologists used Voxar 3D software on a standard radiological workstation. The thorax CT image data for this work was acquired on one 64-slice Siemens Sensation 64 and one 6-slice Siemens Sensation 6 CT scanners using a standard enhanced imaging protocol with slice thickness between 1-5 mm. The data are composed of 15 patients, representing a range of patients and pathology. All lungs were manually segmented by an experienced radiologist and confirmed by second radiologist, as reference for evaluation purposes. Segmentation program was performed using Intel Xeon 5140 2.33 GHz server with 4 GB RAM.

In order to compare the result of our method, the perfect way is to compare it with the gold standard, however, manual tracing of the extracted region would be very time consuming, and in the case of a high-resolution CT image that can include over 500 slices, it would last for more than 16 hours (approximately it takes 2 minutes per slice for manual annotation) to draw the tracings slice-by-slice and difficult to maintain high accuracy of the human tracings in 3-D space.

Two radiologists with over 20 years of experience helped to establish the segmentations gold standard. Radiologists first applied segmentation technique on the CT console, with the software that they are using for lung segmentation and is considered to be the gold standard, in this case Voxar 3D workstation. All thin-section CT images obtained with volumetric acquisition were imported into the workstation in DICOM format by using a local area network. The first step in this procedure was to perform automatic segmentation of the lungs on the basis of noise filtering. The software automatically reconstructed the lung binary volume from the voxels previously bi-thresholded. The binary volume was considered complete when all the connected voxels were included. With this fully automatic procedure, the reconstructed volume could not be completed if there was not a connection between voxels. After the automatic processing, the expert manually edited the results to in order to delete false detections and add missing regions. When the expert was satisfied with the edited results, the 3-D connected area was extracted and saved for use as the gold standard. This procedure was repeated for each of the images in the patients data set. After establishing this method as the gold standard, we apply our segmentation method with region growing method on the same set of CT data. We made a quantitative evaluation by comparing the segmentation result of the segmented volume with the gold standard.

As a quantity measure, the comparison of the segmented volume from both of the methods is used, measured in milliliters (ml), and we also find the difference between the two methods that can be seen in Table 1 and on fig. 3. To compare the volume extracted with the radiological automatic segmentation method with our proposed region growing method we used descriptor of overlap measure (OM). We confirmed that our method could recognize correctly the lung structure from 15 patient cases in which the lung structure could be almost identified visually on CT images. In the following section, a detailed performance evaluation is described for each processing step of our scheme. The overlap with the segmentation of the segmentation results, volume image was evaluated, using the Dice similarity coefficient (DSC) [15]:

$$DSC(X,Y) = \frac{2|X \cap Y|}{(X)+(Y)}$$

(1)

where X and Y represent the two segmentations volumes, and $| \cdot |$ denotes the number of voxels within the segmentation. An overlap measure DSC of 1 indicates perfect registration. A value of 0 means that the lungs had no overlap at all after segmentation. Pearson correlation coefficient used a measure of similarity and with the $P=0.996657$, we can conclude that there is a significant correlation between our method and the gold truth.

Table 1: Results of the Proposed Method

| Patient number	TLV*- Gold truth	TLV* - Our method	Overlap Measure (DSC)
1	5782.89	5723.12	0.990
2	5599.12	5463.90	0.976
3	5698.87	5609.00	0.984
4	5884.45	5752.46	0.978
5	5698.87	5617.03	0.986
6	4612.76	4510.68	0.978
7	4821.54	4759.87	0.987
8	5864.37	5661.87	0.965
9	4872.89	4766.71	0.978
10	5945.56	5873.44	0.988
11	4957.81	4852.46	0.979
12	5688.82	5616.29	0.987
13	5647.45	5571.66	0.987
14	5054.21	4981.73	0.986
15	5124.26	5045.14	0.985
TLV* Total lung volume			
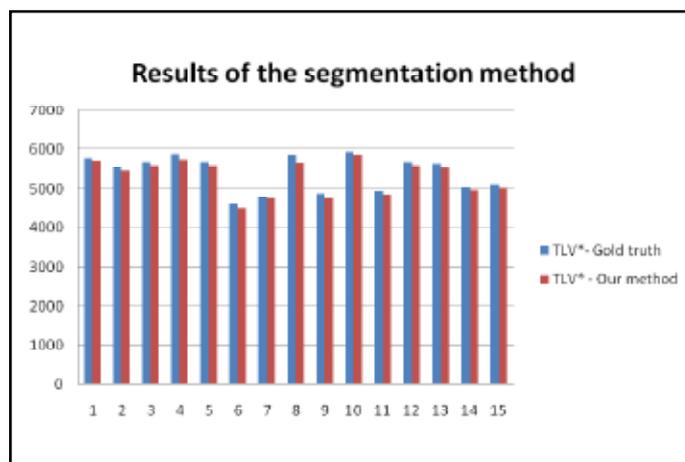
Fig. 3: Results of the Proposed Method

IV. Conclusion

We proposed a completely three-dimensional automated approach to the lung segmentation in chest CT scans with previous preprocessing of the images in order to remove all non anatomical pixels from patient scans. It provides a good basis for any CAD system for disease detection and lung segmentation algorithm. The main goal of our method is to propose a way for lung segmentation to allow radiologists to move away from the modality console working place as well as to avoid the need of expensive software applications provided by the modality vendors. The algorithm main features are the use of thresholding, region growing, and morphological operators. The algorithm, tested on 15 patients high-resolution CT scans, provides high performance and segmentation quality, showing high accuracy in the lung segmentation, as stated by comparison against ground truth and by visual inspection by radiologists.

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