

Efficient Lung Air Volume Estimation Using Human Respiratory Image Sequences

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ABSTRACT

The proposed technique is capable of segmenting the lung's air and its soft tissues followed by estimating the lung's air volume and its variations throughout the image sequence. The work presents a methodology that consists of three steps. In the first step, CT image sequence are to be given as input where histograms of all images within the sequence are calculated and they are overlaid in order to form the sequence's combined histogram to extract lung air area. In the second step, segment the lung air area by using optimum threshold based method. In the third step, voxels in the rendered volume will be counted and the percentage of air consumption will be estimated. The result will indicate a very good ability of the proposed method for estimating the lung's air volume and its variations in a respiratory image sequence.

KEYWORDS

Air volume, Computed Tomography (CT) image, lung, segmentation, Volume Rendering Approach

I. INTRODUCTION

Statistics shows that lung disease death rate is still on the rise. According to the latest report by the American Lung Association, death rates due to lung disease are currently increasing, while death rates due to other leading causes, such as heart disease, cancer, and stroke are declining. High mortality rates of lung diseases have encouraged many researchers to focus their efforts on improving their diagnosis and treatment methods. Many lung disease diagnosis and treatment methods involve a procedure in which respiratory image sequences are analyzed. The image sequence may consist of several static breath-hold images or a respiratory-gated free-breathing image sequence. Estimation of lung air volume and its variations throughout a image sequence has been proposed by several groups in several applications. The disadvantage is the lack of reliable approach to get accurate upper and lower threshold values. The air volume variations in the sequence are then estimated by calculating the whole lung volume differences within the image sequence and the lung's air volume in each image needs to be estimated from the whole lung volume which usually results in higher errors in estimating both the lung's air volume and its variations throughout the sequence. A CT image would be very useful in tumor ablative procedures usually performed after the target lung is completely deflated before starting the surgery such as brachytherapy for treating lung cancer. Then for radiation pneumonitis is one of the conditions that can be assessed based on measuring the lung's air volume. This measurement

can be done noninvasively using Computed Tomography (CT) image-sequence segmentation in order to determine the extent of this disease and treat it properly to prevent radiation fibrosis. The proposed method analyzes a number of pre-operative breath-hold CT images at different lung volumes controlled by ventilator and a volume-meter transducer among them two successive CT images in the sequence are registered with each other to obtain the registration parameters. Each registration parameter corresponding to the totally deflated lung was then determined using extrapolation and then described as a function of the lung's air volume variation. Finally, the CT image of the totally deflated lung was reconstructed by registering the pre-operative image of the least inflated lung using the extrapolated parameters. Because of the highly complex geometry of the airways and alveoli segmentation techniques using deformable models or level set approach are not suitable for lung's air segmentation. As such, threshold-based segmentation is frequently the technique of choice for image-based lung's air volume estimation. However, finding the optimum segmentation threshold for a specific application is usually a challenging task. A priori information, such as physical density or statistical analysis, such as image's histogram is usually useful to select a more appropriate threshold. For example, the intensity value, which maximizes the separation between two peaks of a histogram, is typically used as a rough estimation for the threshold between the corresponding segmentation classes.

R. B. Reger estimated total lung capacity (TLC) using an accurate and rapid radiographic method. This uses a step-wise multiple regression model which allows total lung capacity to be derived as follows: posteroanterior and lateral films are divided into the standard sections as described in the text, the width, depth, and height of sections 1 and 4 are measured in centimetres.

G. Emmanuel followed a method is described for collecting and measuring the quantity of N₂ washed out of the lungs every half minute during oxygen breathing. The method described here requires considerably more time, skill in handling of equipment, and calculation than the conventional method, and it may therefore be unsuitable for routine use.

R J Pierce used the radiographic method described herein measures the displacement volumes of the lungs as geometric structures in space, using a digitiser and computer. It was developed from determinations of the cross-sectional shape of the chest and its contained structures in post-mortem anatomical sections and from computerised tomography (CT) scans in living subjects.

Alan E. Schlesinger followed a method in which, CT scan the lung margin was traced for each axial section (using soft-tissue window settings) by one observer using the cursor on the CT scanner display. The CT computer then calculated the cross-sectional area of the region of interest, multiplied the area by the slice thickness to calculate the lung volumes for each axial section, and summed the individual section volumes to obtain the total lung volume.

J. Clausen suggested the techniques available for estimating total lung capacities from standard chest radiographs in children and infants as well as adults are Computed tomography and magnetic resonance techniques are used to measure absolute lung volumes and offer the theoretical advantages that the results in individual subjects are less affected by variances of thoracic shape than are measurements made using conventional chest radiographs.

H. U. Kauczor designed a method to determine lung volumes using inspiratory and expiratory helical CT with two-dimensional (2D) and three-dimensional (3D) post processing and to compare the accuracy of those measurements with pulmonary function test results. However, the resulting rough segmentation sometimes requires additional fine tuning steps to make the segmentation contours more accurate. For estimating lung air volume and/or its variations, *Gamsu et al.* estimated total lung capacity (TLC) and forced expiratory volume using

posteroanterior and lateral X-ray images of the chest. Their estimation method consisted of manual segmentation of the lung's X-ray images followed by a set of distance measurements and volume calculations. Then Kauczor *et al.* used a threshold-based technique to segment the whole lung automatically from a static helical CT image sequence acquired at deep inspiration and deep expiration in order to estimate different lung volumes including the tidal volume. The concept proposed in this study was to be effective, but its implementation using static breath -hold CT images may not be practical in clinical settings. In contrast to the static breath-hold images, the free-breathing 4DCT is more suitable in the clinic as it is straightforward to implement and less time consuming and more convenient for patients. In a proposed method a technique for accurate image sequence segmentation is introduced based on a novel image sequence analysis.

The method is proposed to estimate the lung's air volume and its variations in CT image sequences using sequence combined histogram. Experiments were conducted on porcine left lungs to explain the validity of the proposed method. Using breath-hold CT image sequence with known lung's air volumes. At last the results indicate a very good ability of the proposed technique for estimating the lung's air volume and its variations in a CT image sequence.

II.METHODOLOGY

A.Initialization

Image segmentation is defined as the process of assigning each image pixel to their particular class. In segmentation methods, finding threshold, initial seed is a initial step. There is currently no segmentation method that yields acceptable results for any medical image usually results in significant errors during the segmentation process.

The proposed lung's air volume estimation method is based on a novel image-sequences segmentation technique that determines the threshold values systematically. The concept behind this technique takes advantage of the fact that the segmentation classes of background-air, lung's air, and soft-tissue appear in all images in the sequence, though with variable shape and size. The histogram threshold method is a good candidate for gray level image segmentation. It is based on the shape of the histogram properties, such as the peaks, valleys and curvatures of the smoothed histogram. It is formed by the Cartesian product of the original 1D gray level histogram and 1D local average gray level histogram generated by applying a local window to each pixel of the image and then calculating the average of the grey levels within the window. The change in the pixel value in the horizontal or vertical directions appears slow and the gradation change continuity appears strong compared to the change in the diagonal direction.

Thresholding is a simple segmentation technique that divides the image into specific classes by comparing each image pixel value with a number of intensity values called thresholds. The most important step in the thresholding method is fine tuning the threshold values because those values have important influence on the accuracy of the segmentation. During the thresholding process, individual pixels in an image are marked as "object" pixels if their value is greater than some threshold value and as "background" pixels otherwise. This convention is known as threshold above. Variants include threshold below, which is opposite of threshold above; threshold inside, where a pixel is labeled "object" if its value is between two thresholds; and threshold outside, which is the opposite of threshold inside.

In genetic algorithm a population of string which encode candidate solutions to an optimization problem, evolves toward better solutions. The fitness function is defined over the genetic representation and measures the quality of the represented solution. Once the genetic representation and the fitness function are defined, a GA proceeds to initialize a population of solutions and then to improve it through repetitive application of the mutation, crossover, inversion and selection operators. It is used to perform optimization in a proposed method. An Optimization problem consists of maximizing or minimizing a real function by systematically choosing input values from within an allowed set and computing the value of the function. More generally, optimization includes finding "best available" values of some objective function given a defined domain, including a variety of different types of objective functions and different types of domains.

For segmentation Active contour models, or "snakes," provide a novel method of delineating and linking edges in images when the gradient information is degraded by image noise or when the boundary of the object being imaged is naturally vague. A major task in applying an active contour model is the need to correctly set the contour regularization parameters that are responsible for controlling the smoothness of the result. Active contour model, also called snakes, is a framework for delineating an object outline from a possibly noisy 2D image. This framework attempts to minimize an energy associated to the current contour comparing to other techniques contour model can find edges, line ,and subjective contours efficiently. For finding contour, the active contour model minimizes the energy functional and exhibits dynamic behavior.



Figure 1: Results for Segmentation Using Contours.

B. Framework

Image segmentation plays a major role in many applications of biomedical imaging, such as diagnosis, localization of pathology treatment planning computer-aided surgery quantification of tissue volumes, and study of anatomical Structure. In a proposed method each image in the sequence consists of three segmentation classes including background, lung's air, and soft tissue. The method starts with the input as image sequence then histograms of all images within the sequence are calculated and are overlaid to form the sequence's combined histogram, then smoothing the histogram to remove noise-like variations, then the convergence points are identified when all the separate histograms converge together, for this standard deviation of all the histograms within the sequence is calculated for each intensity value, the converging areas are searched for the points with a minimum standard deviation, which are selected as the convergence points A and B.

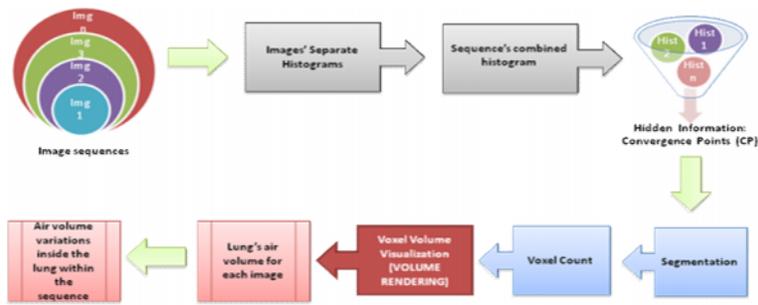


Figure 2: Block Diagram for Estimation of Lung's Air Volume and Its Variations.

The convergence point A, which corresponds to minimal number of voxels variation w.r.t. volume variation during respiration, is the best point that represents the interface regions. After point A, intensity values will correspond to air mixed with small amount of alveoli tissue. This continues until point B, where the lung tissue starts to be dominant with small amount of air. As such, each histogram curve between points A and B provides a good approximation to the lung's air volume. We argue that point B, the second convergence point in the combined histogram, is a good initial guess for the upper threshold. The convergence points are then used in the next block as initial guesses of the optimization algorithm. The points are used to obtain the optimized threshold values. Given that lower and upper segmentation thresholds have integer values in the image space, the optimization process can be simply performed by using genetic algorithm. The segmentation is performed using the optimized threshold values then counts the voxels segmented as the lung's air for each image individually. At last the lung's air volume is calculated for each image by multiplying the number of voxels counted as the air by the voxel size and calculates the air volume variations within the sequence by subtracting the lung's air volumes between successive images.

C.Result Analysis

The analysis includes a static breath-hold CT images from a respiratory sequence where the lung's air volume was known in each image. The lung was obtained from an adult 80 kg pig where the air volume inside the lung was controlled by the ventilator.

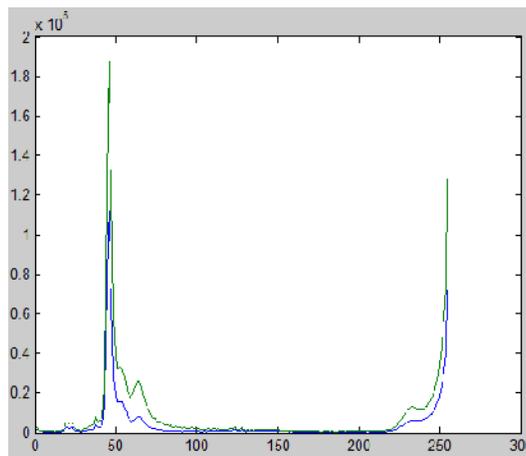


Figure 3: Shows The Combined Sequence Histogram Obtained For 3d Images.

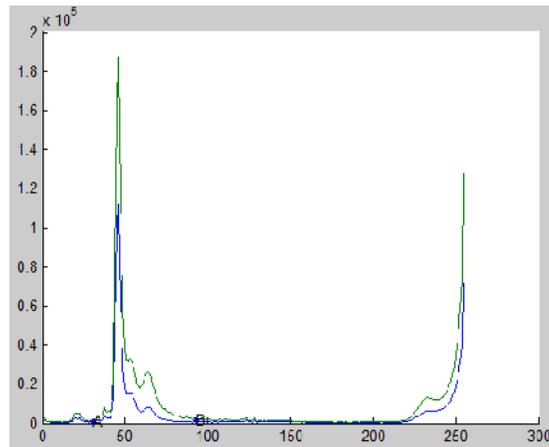


Figure 4: Shows The Convergence Points Of Combined Histogram.

In above Fig the convergence points are indicated by arrows at starting and ending in a graph denoted as A and B. The histogram regions before point A, between points A and B, and after point B correspond to the background-air volume, lung's air volume, and soft-tissue volume respectively. The convergence points are then analyzed to get the optimum points to be used as the upper and lower thresholds for segmenting the lung's air since those optimum points itself satisfy all the images' histograms. After extracting the convergence points they are used as initial guesses for finding optimized threshold values then that threshold values are used for lung's air estimation and for its variations. Tools used for Simulation is *MATLAB*. *MATLAB* is a high-performance language for technical computing. It integrates computation, visualization, and programming in an easy-to-use environment where problems and solutions are expressed in familiar mathematical notation.

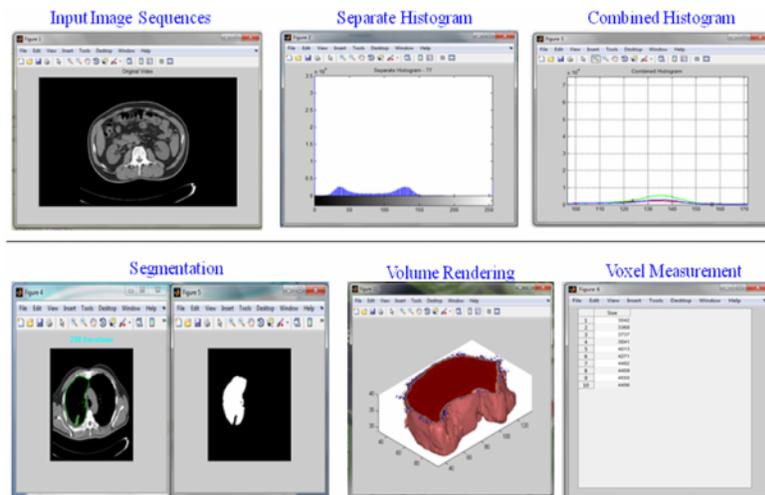


Figure 5: CT Images of Lung with Air Volume

Table I: Result Analysis of Lung with Known Air Volume

Image #	Lung's air volume	Convergence points		Maximum peak separation	
		Estimated lungs' air volume	Error	Estimated lungs' air volume	Error
1	700 ml	679 ml	3.0%	839 ml	19.8%
2	600 ml	576 ml	4.0%	740 ml	23.3%
3	320 ml	333ml	4.1%	540 ml	68.7%

Fig 5 demonstrates one middle slice of the CT images acquired at different volumes, where the air inside the lung is segmented using the obtained threshold values. The lung's air volumes calculated based on the performed segmentation using the thresholds obtained from the optimization algorithm. Table I includes the comparative results from the maximum separation method, where the threshold values were calculated based on maximum separation between two histogram peaks Based on the segmented threshold values the lung's air volumes are estimated.

Table II
Results of the Estimated Lung's Air Volume and Their Corresponding Tissue Volumes
In The 4-D-CT Respiratory Sequence

Phase	Whole lung volume	Estimated lung's air volume	Estimated Tissue volume	Maximum variation in Estimated tissue volume in comparison with all other phases
a	619 ml	234 ml	385 ml	3.6%
b	609 ml	222 ml	387 ml	3.1%
c	596 ml	207 ml	389 ml	2.6%
d	578 ml	185 ml	393 ml	1.5%
e	555 ml	159 ml	396 ml	2.8%
f	530 ml	132 ml	398 ml	3.3%
g	526 ml	127 ml	399 ml	3.5%
h	514 ml	116 ml	398 ml	3.3%

Each tissue volume was estimated by subtraction of the estimated lung's air volume from the whole lung volume. The maximum variation of estimated tissue volume in comparison with all other phases is also given for each phase.

III.CONCLUSIONS

In this research, the technique was used to estimate the lung's air volume and its variations in respiratory CT image sequences using a combined sequence histogram. In a proposed method a novel concept of image sequence analysis was introduced to obtain accurate lower and upper threshold values for segmentation. Then the proposed method was validated using a breath-hold CT image sequence with known lung air volumes. At last the obtained results shows very good ability of the method for estimating the lung's air volume and its variations throughout a respiratory image sequence. This technique can be used effectively in clinical applications, such as LDR lung brachytherapy, where the lung's air volume and/or its variations in a respiratory sequence are needed. The concept of finding the optimum segmentation threshold values from an image sequence's combined histogram introduced in this paper can also be used in other biomedical applications, where important physiological parameters need to be extracted. An example of such applications is estimation of the ventricle's ejection fraction from sequential cardiac images. Here, the proposed technique can be applied in order to find the optimum lower and upper thresholds for an effective segmentation of the ventricle's blood volume followed by a

calculation of the ventricle's blood volume variations throughout the end-diastole/end systole image sequence. This automatic method may improve or even substitute existing complex semiautomatic algorithms or empirical threshold-based methods currently used for ejection fraction estimation.

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