

Application of a respiratory CT sequence's combined histogram to estimate intra-sequence lung's air volume variations

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ABSTRACT

A technique is proposed to segment the lung's air voxels in an image sequence based on a novel image sequence analysis. The concept involves using the image sequence's combined histogram to estimate the lung's air volume and its variations throughout respiratory CT image sequences. Accurate estimation of these parameters is very important in many applications related to lung disease diagnosis and treatment systems (*e.g.* brachytherapy) where the air volume and its variations are either the variables of interest themselves or are dependent/independent variables. *Ex vivo* experiments were conducted on porcine left lungs in order to demonstrate the performance of the proposed technique. The proposed method was validated using a breath-hold CT image sequence with known air volumes inside the lung. The results 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, Segmentation, Respiratory, CT, Sequence, Lung, Brachytherapy

1 INTRODUCTION

Estimation of lung air volume and/or its variations throughout a respiratory sequence has been proposed by several groups in several applications [1, 2]. However, what seems to be a major shortcoming in most of these studies is the lack of a more reliable non-empirical approach to obtain customized upper and lower segmentation threshold values. Such systematic approach can replace existing empirical approaches that usually hamper segmentation accuracy. Since empirical approaches for finding upper and lower threshold values for accurate lung's air segmentation are usually unavailable, threshold values are often set to segment both lung tissue and air (whole lung). The air volume variations in the sequence are then estimated by calculating the whole lung volume differences within the image sequence. In this approach, however, the lung's air volume in each image needs to be estimated from the whole lung volume, or its corrected version using another empirical correction factor. This usually results in higher errors in estimating both the lung's air volume and its variations throughout the sequence.

There are other applications; *e.g.* lung brachytherapy systems, where the lung's air volume and/or its variations during a respiratory sequence could be used as either a dependent [3, 4] or independent [5] variable. However, in some cases, due to lack of a reliable method to track the lung's air volume variations, one might prefer to use other variables which are correlated with the volume changes while being easier to measure or track accurately [6]. In a recent study conducted in our laboratory, Sadeghi Naini *et al* proposed a novel method to reconstruct the CT image of a totally deflated lung based on its partially inflated images [5]. Such a CT image would be very useful in performing tumor ablative procedures such as brachytherapy [7] for treating lung cancer. These procedures are usually performed after the target lung is completely deflated before starting the surgery. This implies that the lung physical domain would be no longer represented accurately by the pre-operative CT images. The proposed method consisted of acquiring a number of pre-operative breath-hold CT images at different lung volumes controlled by a ventilator and/or a volume-meter transducer. Each two successive CT images in the sequence were, then, registered with each other to obtain the registration parameters. Subsequently, each registration parameter was described as a function of the lung's air volume variation. Registration parameters corresponding to the totally deflated lung were then determined using extrapolation. 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.

Although the concept proposed in this study was proven to be effective, its implementation using static breath-hold CT images may not be practical in clinical settings. In contrast to the static breath-hold imaging protocol, the free-breathing 4DCT is more suitable in the clinic as it is more straightforward to implement and less time consuming while being more convenient for patients. However, since there is no control mechanism over the lung's inhaled air volume while free-breathing 4DCT images are acquired, the lung's air volume corresponding to the image set is unknown. Hence, in order to apply the extrapolation technique in conjunction with the free-breathing 4DCT imaging protocol, an effective technique for estimating the lung's air volume and its variations is a paramount necessity.

In this paper, a technique for accurate image sequence segmentation is introduced based on a novel image sequence analysis. The concept is equally useful for segmenting image sequences, both static and dynamic. As described in Section 2, this concept is proposed to estimate the lung's air volume and its variations in respiratory CT image sequences using sequence combined histogram. *Ex vivo* experiments were conducted on porcine left lungs in order to demonstrate the validity of the proposed method. The proposed method was validated using a breath-hold CT image sequence with known lung's air volumes. The experiments conducted and the results obtained are presented in Section 3. As discussed and concluded in Section 4, the obtained results indicate a very favorable ability of the proposed technique for estimating the lung's air volume and its variations in a respiratory image sequence.

2 METHOD

2.1 Preliminaries

Image segmentation is defined as the process of assigning each image pixel/voxel to a specific class. Methods for performing image segmentation vary widely from simple techniques to complex algorithms. Typically, they depend on the specific application, imaging modality, and other factors. There is currently no general purpose segmentation method that yields acceptable results for any medical image. Although there are more general methods that can be applied for various types of images, methods that are specialized to particular applications can often achieve better performance by taking *a priori* knowledge into account. In many segmentation methods, finding proper algorithm parameters, *e.g.* threshold, initial seed, *etc.*, is a key step. However, these parameters are usually found empirically. This usually results in significant errors during the segmentation process.

Thresholding is a simple, yet often effective segmentation technique which divides the image into desired classes by comparing each image pixel/voxel value with a number of intensity values called thresholds. The most important step in the thresholding method is fine tuning the threshold values. These values have significant influence on the accuracy of the segmentation algorithm. As mentioned before, in many applications involving biomedical imaging procedure, this step is frequently implemented empirically. However, as suggested in the next section, a proper threshold value can be determined systematically for a given image sequence by simple analysis of the image sequence.

2.2 Air volume estimation algorithm

Fig. 1 shows a block diagram of the proposed method for estimating the lung's air volume and its variations in a respiratory CT image sequence. While simple, the main idea is quite effective. The concept takes advantage of the fact that the segmentation classes appear in all images in the sequence, though with variable shape and size. More specifically, each image in the sequence mainly consists of three segmentation classes including background, lung's air, and soft tissue. Considering mass conservation of the lung's air during respiration, a reduction in the volume of the background leads to equal increase in the volume of air in the lung and vice versa. In addition, taking into account the soft tissue incompressibility or near incompressibility, the volume of the soft tissue is (almost) constant throughout the image sequence. The proposed technique employs these constraints in order to find the best segmentation thresholds for a variable class throughout the sequence.

The algorithm starts with the input block where the whole image sequence is input. In the first step, histograms of all images within the sequence are calculated separately. These histograms are then passed to the second block where they are overlaid in order to form the sequence's combined histogram. After smoothing the histogram curves in order to remove high frequency noise-like variations, the convergence points in the sequence's combined histogram are extracted in the next block. The convergence points are defined as those intensity values within the combined histogram where all the separate histograms converge together, *i.e.* the distances between them tend to a minimum. These points are the optimum points to be used as the segmentation thresholds, since they best satisfy all the images' histograms besides satisfying the air mass conservation and tissue incompressibility constraints. After segmentation is performed using the determined threshold values in the fourth block, the fifth block counts the voxels segmented as the lung's air for each image separately. In the sixth block, the lung's air volume is calculated for each image by multiplying the number of voxels counted as the air by the voxel size. Finally, the

last block calculates the air volume variations within the sequence by subtracting the lung's air volumes between successive images. The experiments conducted to validate this approach are presented in the next section.

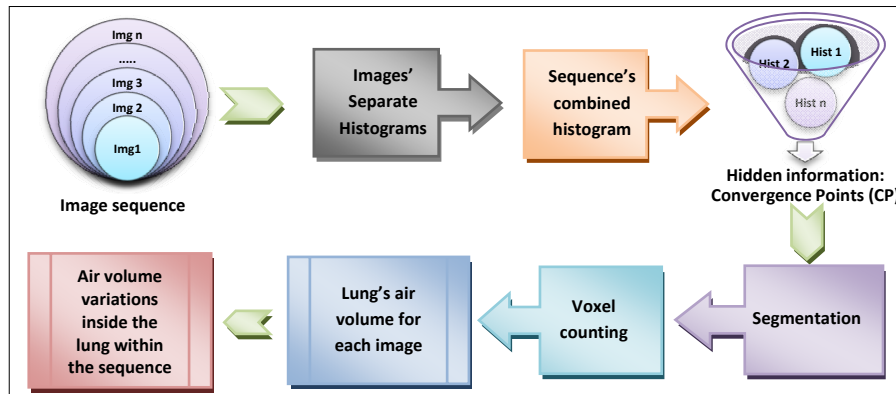


Figure 1. Block diagram of the algorithm proposed to estimate the lung's air volume and its variations in a respiratory CT image sequence.

3 Experiments and results

Ex vivo experiments were conducted on a porcine left lung in order to validate the proposed technique. The experiments were conducted using a number of static breath-hold CT images from a respiratory sequence acquired while the lung's air volume was controlled and known in each image. The lung obtained from an adult ~80 kg pig was inflated using an intra-trachea tube and a North American Drager Narkomed 2A ventilator machine. The air volume inside the lung was controlled by the ventilator. Micro-CT imaging was performed using a GE Locus Ultra scanner. The static breath-hold CT images of the lung were acquired at volumes of 700 ml, 600 ml, and 300 ml, respectively. The final images size was (228x186x324) voxels with a voxel size of (0.62³) mm³. These three 3D images were fed to the air volume estimation algorithm as the respiratory image sequence. Fig. 2 shows the combined sequence histogram obtained for these images. In this figure, the second hill belongs to the lung's air voxels in different images. The convergence points at the beginning and the end of this hill are indicated by arrows. As mentioned before, these points are the optimum points to be used as the upper and lower thresholds for segmenting the lung's air since they best satisfy all the images' histograms.

Fig. 3 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 are given in Table 1. The table indicates that the estimation errors range from 5% to 6.3%, which is reasonably low. In other words, the accuracy of the proposed method for estimating the lung's air volume in a respiratory sequence is sufficiently good.

1 Discussion and conclusions

In this paper, a novel concept of image sequence analysis was introduced in order to obtain appropriate lower and upper threshold bounds for threshold-based lung image segmentation. This concept is equally useful for segmenting both static and dynamic image sequences. In this research, the concept was utilized to estimate the lung's air volume and its variations in respiratory CT image sequences using a combined sequence histogram. *Ex vivo* experiments were conducted on porcine left lungs in order to prove the concept. The proposed method was validated using a breath-hold CT image sequence with known lung air volumes. The obtained results indicated a very good ability of the method for estimating the lung's air volume and its variations throughout a respiratory image sequence. Considering its favorable capabilities, this technique can be used effectively in clinical applications such as lung brachytherapy where the lung's air volume and/or its variations in a respiratory sequence are needed.

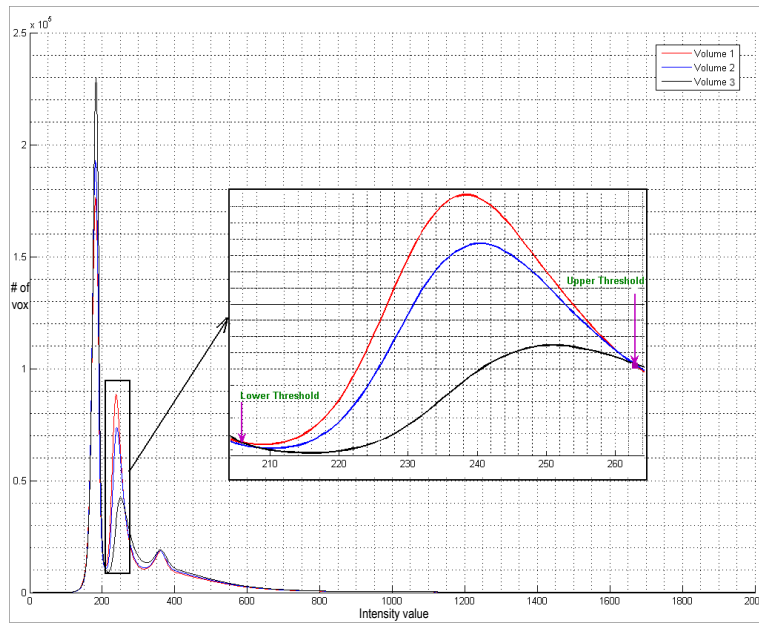


Figure 2. Combined sequence histogram for a respiratory sequence consisted of three static breath-hold CT images acquired at 700, 600, and 300 ml, respectively. The figure has been zoomed in to focus on the region of interest within the original combined histogram; lower and upper segmentation thresholds are indicated by arrows.

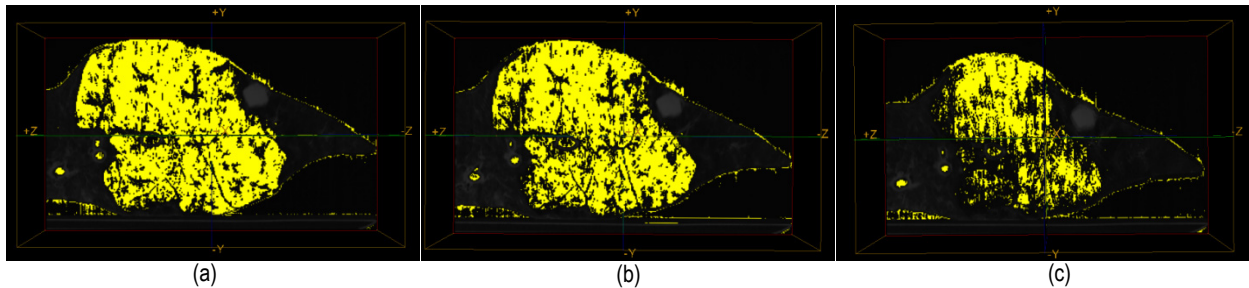


Figure 3. One middle slice of the static breath-hold CT images acquired at: (a) 700 ml, (b) 600 ml, (c) 300 ml; the air inside the lung is segmented using the lower and upper threshold values extracted from the sequence's combined histogram. The bright and dark regions show the air and soft tissue with the background, respectively.

Table 1. Summary results of estimated lung's air volumes in the respiratory CT sequence.

Image #	Air volume inside the lung	Estimated air volume inside the lung	Error
1	700 ml	665 ml	5%
2	600 ml	562 ml	6.3%
3	300 ml	319 ml	6.3%

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