An Approach to Segment Lung Pleura from CT Data with High Precision

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An Approach to Segment Lung Pleura from CT Data with High Precision

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ABSTRACT

A new approach to segment pleurae from CT data with high precision is introduced. This approach is developed in the segmentation’s framework of an image analysis system to automatically detect pleural thickenings. The new technique to carry out the 3D segmentation of lung pleura is based on supervised range-constrained thresholding and a Gibbs-Markov random field model. An initial segmentation is done using the 3D histogram by supervised range-constrained thresholding. 3D connected component labelling is then applied to find the thorax. In order to detect and remove trachea and bronchi therein, the 3D histogram of connected pulmonary organs is modelled as a finite mixture of Gaussian distributions. Parameters are estimated using the Expectation-Maximization algorithm, which leads to the classification of that pulmonary region. As consequence left and right lungs are separated. Finally we apply a Gibbs-Markov random field model to our initial segmentation in order to achieve a high accuracy segmentation of lung pleura. The Gibbs-Markov random field is combined with maximum a posteriori estimation to estimate optimal pleural contours. With these procedures, a new segmentation strategy is developed in order to improve the reliability and accuracy of the detection of pleural contours and to achieve a better assessment performance of pleural thickenings.

Keywords: Malignant pleural mesothelioma, pleural thickening, segmentation, supervised range-constrained thresholding, Gaussian mixture model, expectation-maximization algorithm, Gibbs-Markov random field, maximum a posteriori estimation.

1. INTRODUCTION

Pleural mesothelioma is normally a rare malignant tumor of pleura. Pleurae are the smooth lubricated double membrane sacs containing the lungs. Pleural mesotheliomas are found 1000 times more often in asbestos exposed professionals than in the normal population [1]. It is statistically documented that most of them are related to asbestos exposure [2]. Pleural mesothelioma might develop from benign pleural thickening, and is known to grow rapidly after manifestation. A statutory prohibition of asbestos usage was introduced in the year 1993 in Germany. However, occurrence of malignant pleural mesothelioma morbidity in Germany is expected to peak during 2010s, due to a long latency period of - on the average - 35 years [3]. In Germany, an assessment program is applied to the asbestos exposed persons. This assessment program includes thoracic CT imaging for non-invasive diagnostic. A typical non-invasive diagnosis is based on thoracic axial CT images. Depending on the layers’ thickness, the number of images varies between 80 slices with a thickness of 5 mm to about 700 slices with a thickness of 0.5 mm. Physicians view each slice on a workstation in order to find pleural thickenings. The diagnostic findings are documented in a standardized form containing data such as their size, position, and growth rate. This visual diagnostic approach is a very time consuming procedure, taking about 20 to 30 minutes per data set, and this is considered as often being subjective [4].

To increase the accuracy of the localization and of the topological information of these quite small image regions within a subjective visual evaluation, an automatic diagnosis assisting computer system has been developed [4]. The computer system automatically detects and quantitatively assesses pleural thickenings in axial thoracic CT images.

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In the segmentation’s framework of the current system, an earlier segmentation used the technique of supervised range-constrained thresholding to detect lung pleura contours. Motion artifacts have a strong effect in thoracic CT images. Moreover in middle slices, some vessels and bronchi are included as pleural contour due to partial volume effects. Thresholding can not distinguish between voxels, with similar density values, affected by motion artifacts and partial volume effects. As consequence, lung pleura contour remains incorrect in the part of CT slice (Fig. 1), which is effected by artifacts.

To improve the reliability and accuracy of the detection of pleural contours, a 3D segmentation of lung pleura is developed and presented. The new approach is based on supervised range-constrained thresholding and a Gibbs-Markov random field model.

Fig. 1. A result of 2D CT image segmentation using solely thresholding technique. It can be perceived in the magnified figure that lung pleural contour still remains incorrect in certain areas.

2. METHODS

2.1 Segmentation of thorax and pulmonary organs

The first step is an initial 3D histogram-based segmentation. Thresholding, a widely used technique in image processing for preliminary segmentation, is applied with a novel technique, the supervised range-constrained Otsu thresholding [5][6]. The optimal threshold lies between two bounds of the histogram value where the frequency range of the object of interest is confined. First, the histogram of the region of interest (ROI) is built (Fig. 2). Then, from the histogram of the ROI, the range to which the threshold is confined is estimated using a priori knowledge. Finally, the threshold is determined by maximizing the interclass variance. Once supervised range-constrained thresholding was applied, 3D connected component labelling [7] is used to convert a stack of 2D binary images into a 3D symbolic data set where each connected component is assigned with a unique label. The 26-neighbourhood is applied to detect connected voxels. Then the thorax is identified as the component with the biggest volume.

Fig. 2. An example of a 3D histogram from a thoracic CT data set. The first peak corresponds to air, the second peak to lung tissue, while the third peak corresponds to other connective tissue such as muscles and vessels.
Now, the thorax region forms the operation mask (the current ROI) for the second step. Again, the 3D histogram is computed and supervised range-constrained thresholding with other suitable supervision parameters is applied to determine the threshold to segment the pulmonary organs, i.e. the lungs, trachea and bronchi. After thresholding, we use 3D connected component labelling to detect the largest region therein. Lungs, trachea and bronchi are labelled as one single region.

### 2.2 Segmentation of trachea and bronchi

As a result of initial segmentation, trachea and bronchi remain connected to lung tissue (Fig. 3). Thus, the aim of this step is to detect and remove the trachea and bronchi. For this purpose, lungs and trachea are used as a mask to build a new 3D histogram. The histogram can be modeled as a finite mixture of Gaussian distributions.

![Fig. 3. Results of the initial segmentation step. Trachea and main bronchi remain connected to lungs.](image)

In a finite mixture model, a data $x_i$ is assumed to be drawn from a mixture of a finite number $c$ of components $G_1, ..., G_c$ in some proportions $\omega_1, ..., \omega_c$ [8]. Given a normal component density function with $\theta_k$ the vector of mean and variance of the associated class (1), the mixture model is expressed by (2):

$$
p_k(x_i \mid \theta_k) = \frac{1}{\sigma_k \sqrt{2\pi}} e^{-\frac{1}{2\sigma_k^2}(x_i - \mu_k)^2},
$$

$$
p(x_i \mid \phi) = \sum_{k=1}^{c} \omega_k p_k(x_i \mid \theta_k),
$$

where $\phi$ is a vector of unknown parameters (mean, variance and proportion of each component), with $\sum_{k=1}^{c} \omega_k = 1$ and $\omega_k \geq 0$. In order to estimate the parameters of finite mixture of Gaussians, we seek the maximum of the likelihood function, or log-likelihood. For an independent samples $x_i$, the likelihood (3) and log-likelihood are expressed by (4)

$$
L(\phi) = \prod_{i=1}^{n} p(x_i \mid \phi)
$$

$$
\ln L(\phi) = \sum_{i=1}^{n} \ln \sum_{k=1}^{c} \omega_k p(x_i \mid \theta_k)
$$
To estimate the parameters of Gaussian densities, the expectation-maximization (EM) algorithm [8][9][10] is applied. It consists of two steps. Posterior probabilities (5) are estimated in the expectation step (E step), with given initial estimated parameters:

\[
\hat{h}_{ik} = \frac{\omega_k p(x_i|\theta_k)}{\sum_{i=1}^{n} \omega_i p(x_i|\theta_i)}.
\]  

(5)

Then in the maximization step (M step), new parameters are estimated (6) using posterior probabilities calculated in the E step:

\[
\omega_k = \frac{1}{n} \sum_{i=1}^{n} \hat{h}_{ik}, \quad \hat{\mu}_k = \frac{\sum_{i=1}^{n} \hat{h}_{ik} x_i}{\sum_{i=1}^{n} \hat{h}_{ik}}, \quad \text{and} \quad \hat{\sigma}^2_k = \frac{\sum_{i=1}^{n} \hat{h}_{ik} (x_i - \hat{\mu}_k)^2}{\sum_{i=1}^{n} \hat{h}_{ik}}.
\]  

(6)

Then the likelihood function is evaluated with these new parameters. The E-M steps are applied iteratively until the log-likelihood reaches the maximum.

As mentioned above, the histogram of lungs, trachea and bronchi were modeled as a mixture of Gaussians where parameters were estimated through the EM algorithm. After that, a labelling is done using the maximum a posteriori (MAP) to map all voxels of our data set to discrete labels \( L_k \) [11]:

\[
L_k = \arg \max_{\phi \in \Omega} p(\phi | x_k) \quad \forall x_k.
\]  

(7)

After region labelling with a suitable class number, we assume that lung tissue can not be distinguished from residual air inside the lungs, so lungs with air are together labelled with lower labels, corresponding to lower HU values. This assumption implies that voxels with the highest label can not be considered as belonging to lung tissue. Hence, these voxels represent soft tissue such as blood vessels, bronchi, and cartilage. Moreover, they represent also the occurrence of motion artifacts or partial volume effects within the CT data. Thus, they can be removed. After that, a threshold is applied in the remaining volume of connected lung tissue with air to extract air inside trachea and bronchi, followed by a morphological closing. Using connected component labelling, all connected voxels representing air are detected and can be removed. By finding the two largest regions and two biggest contours within the data, lungs are detected.

### 2.3 High precision segmentation using a Gibbs-Markov random field

Markov Random Field (MRF) modelling has been used widely in medical image processing [12][13][14][15]. This technique is particularly useful in a segmentation framework because it takes into account the labels of neighbouring elements to classify an element. In this step we apply a Gibbs-Markov random field (GMRF) to our initial segmented lung contours in order to improve the accuracy of pleural contours. A GMRF is applied in every 2D slice of the segmented CT data set. We denote CT image \( Y \) as the original observed field. \( \bar{X} \) is a Markov random field that contains the class \( \bar{X} \in \Omega \) for each pixel. Only two classes are considered, pixels belonging to lung and those which do not belong to lung.

The technique has been applied in this step as follows. Every pixel of our random field is initially estimated using the result of MAP estimator of the former step. Each pixel is labelled using information of the observed field and the relation with its neighbours. To estimate the optimal label of each pixel, the GMRF is combined with MAP. Using Bayes’ rule (8), the posterior probability is estimated (9). Since observed values do not change, \( P(Y) \) is constant, hence it can be omitted:

\[
P(X | Y) = \frac{P(Y | X)P(X)}{P(Y)}
\]  

(8)

\[
P(X | Y) \propto p(Y | X)P(X)
\]  

(9)
Next, the MAP rule is applied to estimate our optimal final labelling (10) [13]:

\[ \hat{X} = \arg \max_{X \in \Omega_x} p(Y | X)p(X), \] (10)

where \( p(X) \) is the prior probability. It depends on the relation of pixels to their neighbors. This relation is assessed via so-called cliques. A clique \( q \) is a group of a certain number of pixels, which are adjacent to each other [16]. In our approach we use second order cliques \( C \), consisting of diagonal, vertical and horizontal adjacency with two pixels. \( p(X) \) takes a Gibbs distribution where \( U(X) \) is called the energy function, a summation of potentials \( V_q \) of inhomogeneous cliques. \( n_A \) is the number of horizontal and vertical inhomogeneous cliques while \( n_B \) represents diagonal inhomogeneous cliques (11) [15]:

\[ P(X) = \frac{1}{Z} e^{-U(X)/T}, \quad U(X) = \sum_{q \in C} V_q(x_q) = n_A A + n_B B, \] (11)

where \( T \) and \( Z \) are constant. The diagonal potential \( B \) is set to \( 1/ \sqrt{2} \), the horizontal and vertical potential \( A \) to 1, due to the relation of the distance to the middle of the reference pixel.

We assume that \( p(Y | X) \) takes a Gaussian distribution, so that for all pixels \( i \) of every region \( j \in \Omega_x \), the optimal \( \hat{X} \) has to fulfill this condition (12):

\[ \hat{X} = \arg \max_{X \in \Omega_x} \left( \prod_{j=1}^{k} \prod_{i=1}^{N_j} p(y_i | x_j) \right) P(X) = \arg \max_{X \in \Omega_x} \left( \prod_{j=1}^{k} \frac{1}{\sqrt{2\pi \sigma_j^2}} e^{-\frac{1}{2} \sum_{i=1}^{N_j} (y_i - \mu_j)^2} \right) \frac{1}{Z} e^{-\left( n_A A + n_B B \right)/T}. \] (12)

Mean and variance are calculated according to (13):

\[ \hat{\mu}_j = \frac{1}{N_j} \sum_{i=1}^{N_j} y_i, \quad \hat{\sigma}_j^2 = \frac{1}{N_j} \sum_{i=1}^{N_j} (y_i - \hat{\mu}_j)^2. \] (13)

Then looking for minimum of the minus-log-likelihood function, the optimal solution of the binary segmentation is found (14) with \( T = 1 \):

\[ \hat{X} = \arg \min_{X \in \Omega_x} \left( \frac{1}{2} \sum_{j=1}^{k} N_j \ln \sigma_j^2 + n_A A + n_B B \right). \] (14)

A well known algorithm, iterated conditional modes (ICM) [17] is applied to find the solution. There is a difference between our approach and the original proposed by Besag. While Besag has applied the ICM algorithm to calculate the best value for every pixel in the image, we have applied this algorithm only to pixels lying on the lung contour \( C_i \subset R_i \), so that the current condition for the optimal \( \hat{X} \) is pixelwise (15) (16):

\[ \hat{X} = \arg \min_{X \in \Omega_x} \left( \frac{1}{2} \sum_{j=1}^{k} N_j \ln \sigma_j^2 + n_A A + n_B B \right), \quad \text{for } \forall i \in C_i, \] (15)

\[ \hat{X} = \arg \min_{X \in \Omega_x} \left( \frac{1}{2} (N_0 \ln \sigma_0^2 + N_i \ln \sigma_i^2) + n_A A + n_B B \right), \quad \text{for } \forall i \in C_i. \] (16)

Since the decision has to be done only between lung or not lung, while the lung tissue is the focus of our detection, the decision can be done according to (17):
The reason is our presumption that pixels whose label value may be changed are only in the border region to lungs. This method is called contour relaxation. After the first iteration, we obtain a new estimate of the lung contours, which is refined in the following iterations.

### 3. RESULTS

#### 3.1 Results from segmentation steps

In order to apply supervised range-constrained Otsu thresholding to separate pulmonary organs we need to estimate the proportion of volume of the thorax to the whole CT data set, and also the proportion of lungs to the thorax. To estimate these a priori parameters, CT data sets are manually investigated slice by slice to find the range of these proportions (Fig. 4) [18]. Volume integration over the CT stack leads to the value of the volume proportion for thorax to whole data and lungs to thorax (Table 1).

![Fig. 4. A priori data shows the range of the proportion of the lung area to thorax in every CT image [18].](image)

<table>
<thead>
<tr>
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<th>Lower bound</th>
<th>Upper bound</th>
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<tbody>
<tr>
<td>Thorax to whole data</td>
<td>0.62</td>
<td>0.68</td>
</tr>
<tr>
<td>Lung to thorax</td>
<td>0.22</td>
<td>0.38</td>
</tr>
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</table>

Table 1. The values of proportion of volume of interest, i.e thorax and lungs, to constrain the range of the threshold to separate the object of interest from the region of interest is confined.

After applying supervised range-constrained thresholding twice, pulmonary organs, i.e. lungs, trachea and bronchi are segmented and connected with each other. To model the histogram of lungs, trachea and bronchi, an optimal number of four Gaussians was proven to be useful (Fig. 5 left). Pixels labelled with the highest value are considered to be trachea, bronchi, motion artifacts and partial volume effects, and hence do not belong to lung tissue. Together, with the detected air inside trachea and bronchi using again thresholding, these pixels are removed (Fig. 5 middle). While three Gaussian classes remain supposedly to be part of the lung tissue, altogether they form the final mask for the detection of the initial lung contours (Fig. 5 right). Final lung pleural contours are obtained after applying the GMRF within the contour relaxation technique.
The lung contours after applying contour relaxation show that vessel branches, trachea and bronchi were automatically excluded from the lung region, which is the advantage of the new approach in comparison with the former one (Fig. 6). Moreover, the new approach delineated lung contours even without including the area of motion artifacts, while the former approach could not deal with this situation completely correctly (Fig. 7).

3.2 Evaluation

An evaluation was done with our medical partner, by measuring the performance of segmentation. Specificity, sensitivity, accuracy, precision and error were taken into account. The evaluation was done based on a CT data set consisting of 78 images. While a medical partner agreed thoroughly with the detected costal and most of mediastinal contours, only a small part of the endopulmonary vascular and bronchial indentations along the mediastinal boundary was noted to be anatomically incorrect and the posterior costophrenic angle of both inferior lobes of lung was not detected (Fig. 8). Therefore, the results yielded an overall performance of over 99% with an error of less than one percent (Table 2).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
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<td>Sensitivity</td>
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<tr>
<td>Accuracy</td>
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<td>Precision</td>
<td>99.60</td>
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<tr>
<td>Error</td>
<td>0.42</td>
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Table 2. Result of performance of our segmentation from one CT data set.

4. CONCLUSIONS

We have presented a new segmentation approach to segment lung pleurae with high precision in the segmentation’s framework of an automatic computer system to detect pleural thickening. With this new technique, trachea and bronchi can be automatically separated from the lung regions. An estimation of motion artifacts and partial volume effects is done using a mixture of Gaussians. Accuracy of lung pleura contour is improved using GMRF. The evaluation of results by our medical partner shows a good performance of the detection of the lung pleura contours. Future work will include a new 3D connected labeling algorithm to achieve a faster segmentation’s framework. Moreover, surface relaxation will be applied to integrate the 3D context of the pleural surface throughout the data set.
Fig. 6. Left: Lung contour after only one ICM iteration. Right: Result of pleural contours using old segmentation approach. While lung contours appear sharply delineated (Middle), the former approach was unable to separate trachea and bronchi (Top Right), or blood vessels (Down Right) from the detected lung contours.

Fig. 7. An example shows the result from an original CT image with motion artifacts (Left). While the new approach delineated lung contours without including the area of motion artifacts (Middle), the former approach was unable to exclude this area totally (Right).
Fig. 8. While a professional radiologist agreed with the detected costal and most of mediastinal contours, only a small part of the endopulmonary vascular and bronchial indentations along the mediastinal boundary (upper row) was marked (yellow line) as anatomically incorrect, and the posterior costophrenic angle of both inferior lobes of lung (lower row) was marked as not detected.

REFERENCES