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Separation of left and right lungs using 3D information of sequential CT images and a guided dynamic programming algorithm

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Abstract

Objective—this article presents a new computerized scheme that aims to accurately and robustly separate left and right lungs on CT examinations.

Methods—we developed and tested a method to separate the left and right lungs using sequential CT information and a guided dynamic programming algorithm using adaptively and automatically selected start point and end point with especially severe and multiple connections.

Results—the scheme successfully identified and separated all 827 connections on the total 4034 CT images in an independent testing dataset of CT examinations. The proposed scheme separated multiple connections regardless of their locations, and the guided dynamic programming algorithm reduced the computation time to approximately 4.6% in comparison with the traditional dynamic programming and avoided the permeation of the separation boundary into normal lung tissue.

Conclusions—The proposed method is able to robustly and accurately disconnect all connections between left and right lungs and the guided dynamic programming algorithm is able to remove redundant processing.

Keywords

Separation of left and right lungs; Lung segmentation; Dynamic programming algorithm; Computer Tomography

I. INTRODUCTION

Computed tomography (CT) produces 3-D volumetric image data and has demonstrated better sensitivity for early detection of lung diseases than other conventional imaging modalities (e.g., chest radiography). Advances in CT imaging technology has simultaneously reduced image acquisition time and increased spatial resolution, and, consequently thin-section CT examination has increased in popularity as an imaging tool to detect and quantify various lung diseases (e.g., lung cancer, pulmonary embolism, interstitial lung diseases, asthma, and chronic obstructive pulmonary disease). Although thin-section

CT has improved radiographic presentation of anatomic detail of lung structures and increased sensitivity in detecting pulmonary diseases at the early stage, the large amount of generated image data requires the radiologists to spend significant time and effort reading and interpreting thin-section CT examinations [1,2], which may not only affect the radiologists' performance, but also generate substantial inter-reader variability in detecting or diagnosing lung diseases [3]. Therefore, significant research effort has been invested in the development of Computer-Aided Detection and Diagnosis (CAD) schemes for variety of lung diseases during the last two decades in an attempt to assist the radiologists with rapid processing ability of large volumes of data and improve the diagnostic performance [4].

Among many of CAD schemes, lung segmentation is a precursor to quantitative analysis applications including lung parenchyma density analysis, airway analysis, lung and diaphragm mechanics analysis [5], visual information retrieval [6], detection of lung nodules [7], emphysema analysis [8], and in particular the local (lobe-based) lung function analysis [9]. Lung segmentation must be accurate because abnormalities such as lung nodules may exist at the extreme periphery of the lungs and quantitative assessment of lung volume for the evaluation of emphysema will be compromised by erroneous lung segmentation [4]. Although a number of papers regarding segmentation of lung areas depicted on CT images have been published [1,2,4,5,7,8,10–14], developing an accurate, robust, and computationally efficient scheme to segment lung areas remains a difficult and important challenge in light of the increasing resolution of CT examinations while manual segmentation is tedious and time consuming, lacking in precision, and impractical [15].

As a final step of the lung segmentation, separating left and right lungs is performed when the presence of a single, large lung segmentation region in any section (CT slice) is detected. In lung segmentation algorithms, applying any initial segmentation methods (e.g. single threshold method, watershed method, and expectation-maximization method) to segment lung areas depicted on one CT slice can generate distorted lung boundary in particular for diseased cases. To generate the smoothed lung segmentation boundary, one of the most popular reconstruction methods is applying a rolling ball algorithm [16] that uses morphological operations to detect and recover cavities on the lung boundaries [7,13]. Applying the gray-level threshold and a rolling ball algorithm to smooth lung boundaries may cause the two lung regions to fuse. Thus, detecting and separating the connection between two lungs is often needed in the lung area segmentation scheme and it is also important in the detection and assessment of many parenchyma diseases through the accurate global and local (i.e., lobe-based) lung function measurements without human intervention. Unfortunately, the step of separating two lungs was often omitted or not detailed reported in many of previous CAD studies.

Separation between the left and right lungs mainly composes three steps namely, (1) verifying if two lungs are connected, (2) identifying the suspicious area of the connection in CT images, and (3) searching for and identifying the accurate separating line or curve between two lungs. The errors in the first two steps and in the last step result in generating inaccurate classification of left and right lungs and separation line, respectively. The typical method to verify if lungs are connected is to check whether the processed CT slice depicts a single and larger segmented lung area than the pre-defined threshold on lung size depicted on a single CT slice [4,8,10]. Previous studies also reported several methods to identify the suspicious connecting areas including the detection of (1) the smallest vertical run length [8,10,17] and (2) the most anterior point along the cardiac aspect of the lung region [4]. To avoid using a straight line to separate two lungs, other researchers suggested and tested to detect suspicious connecting area based on the difference between the results of applying the iterative morphological operations such as dilation and erosion to the image [5,6,12,17]. After identifying the suspicious area, pre-defined ROI (region of interest) is set to reduce

computational complexity and separating left and right lungs is conducted in the ROI. Several separation methods have been proposed, which include the use of the maximum cost function based on dynamic programming [5,12], the morphological operators [17], vertically simple cut in the middle of ROI [6], the line fitting for pixels with the highest value in each horizontal line within a horizontal window [8,10], and searching for a series of rays to find local maximum in ROI [4]. One study tested and reported to use multiple active contour models to merge these three steps into one step [18].

There are several drawbacks (or limitations) among the previously reported schemes. The first limitation is the pre-assumption of the connecting area that may not be always accurate in the diverse clinical image data and result in the reduction of scheme robustness. For instance, only anterior areas [4,8,10,12,17] or anterior and posterior areas [5] were targeted in different schemes. Thus, a method has been proposed to separate connected lungs regardless of the connecting location [18]. The second limitation is that these schemes are unable to process the images in which two lungs are connected in multiple (i.e., more than two) locations. The last is that although the dynamic programming algorithm is widely considered a much more powerful and accurate tool to search for separating line along with the actual boundary between two lungs than other methods, it is not computationally effective because the algorithm tends to detect all possible “optimal” paths in entire ROI resulting in an inefficient search and still sometime generates the sub-optimal separation because of relatively high intensity of vessels and bones.

In this study, we proposed and tested a new scheme to resolve the weaknesses of the previous methods to separate the left and right lungs. By using consecutive 3D information contained in CT examination and a guided dynamic programming algorithm, the new scheme detects the suspicious connecting area depicted on individual CT image slices regardless of the positions (anterior, medio, posterior, or multiple) and the number of connections and assigns automatically and adaptively the start and end point of a guided dynamic programming so that the scheme can search more efficiently and accurately for the optimal separating line or curve between two “connected” lungs depicted on CT images. This paper is organized as follows. Section II gives a detailed description of the method. Section III provides experimental results, and Section IV and V contain a discussion and summary, respectively.

II. MATERIALS AND METHODS

A. Testing datasets

From a large lung CT image database involving more than 470 participants in a COPD (Chronic obstructive pulmonary disease) study project at University of Pittsburgh Medical Center [3], we selected 11 CT examinations in which the boundaries of two lungs are either originally connected [Fig. 1(a) and (b)] or merged by the boundary smoothing (i.e., rolling ball) algorithm [Fig. 1(c)]. When applying our previous computerized schemes [8,19] to these cases, the schemes failed to correctly separate the connections of two lungs primarily due to the multiple appearances and arbitrary location of the connections. In the 11 selected CT examinations, no patient underwent the examination had prior lung surgery and no severe abnormal lung patterns (e.g., ground glass and honeycombing) were identified along the two lung fusion areas in CT images. Among them, three examinations were used as training dataset for developing the proposed computerized scheme and eight examinations (Table 1) including 4034 CT image slices with 827 connections between two lungs were used for evaluating the scheme performance. These lung CT screening examinations were acquired using a LightSpeed CT scanner (GE Healthcare). The CT protocol varied depending on the subject size. Specifically, in the screening CT examinations the x-ray tube voltage was 120 kVp, the mean tube current ranged from 100.0 to 209.4 mAs. The scanning

CT acquisitions were contiguous and images were reconstructed at slice section thickness of 0.625 with 512×512 in plane pixel matrices using the high-spatial frequency “bone” kernel. The plane pixel dimensions in these CT examinations varied from 0.49 to 0.70 mm depending on body size of the patient being scanned.

B. Initial lung segmentation

A computerized scheme previously developed in our group [19] was applied to CT images of each examination to segment the 3-D lung volume depicted on the complete CT examination. In brief, our original lung segmentation algorithm includes two image processing steps. These are a 2-D based adaptive threshold (segmentation) step and a 3-D based region growing process step. In the first step the scheme determines a segmentation threshold value for each CT slice image. To automatically select this threshold, a histogram of the pixel values within each slice is computed. The scheme then searches the histogram for the minimum valley between two peaks representing the center of the foreground and background of lung regions to determine a threshold value for the image. In this segmentation step, the scheme typically generates multiple segmented and frequently isolated regions depicted on each CT image, which are named “2-D segments.” Some of the segments actually represent lung areas and others are related to non-lung areas and/or the CT table. To identify lung areas in each CT image and reconstruct a 3D lung volume by deleting all un-related segments, the second step of the scheme applies a 3-D region growing method based on grouping of 2-D segments. This step starts from a CT image that depicts the two largest 2-D segments representing the left and right lungs that are typically located in the middle section of the two lungs. The scheme then separately scans upward and downward to the top (apices) and bottom (diaphragm) of the segmented lung areas. During this scanning process the scheme gradually builds a 3-D lung volume by connecting 2-D lung areas segmented on all paired adjacent images and deleting all other isolated (unconnected) 2-D segments initially segmented on CT images.

C. The proposed lung separation method

1. Overview for classification of left and right lungs—To classify the 2D lung segments detected on each CT slice into the left or right lung, the scheme consists of three stages including detecting “connected” lung areas, separating the connected areas, and determining or classifying the separated areas into the left or right lung. Once the scheme reads sequentially each 2D CT image with lung segmentation results from apex to base, in the first stage, the scheme determines in heuristic way whether two lungs are connected namely, checking if there is a single and large segment (segmented area) depicted on one image. For example, if a segment locates on the center area and it covers half of the images in horizontal direction, lungs may be connected. In the second stage, the scheme searches for the suspicious region of the connection and separates left and right lungs in the suspicious region. This stage presents the main idea of this paper and is explained in the next two sub section, C.2 and C.3 in detail. At the end of the stage, the scheme repeats first and second stages until no more connection detected. Finally, the scheme classifies the two separated areas into the left or right lung. For example, if the center of one area is on the left side of the image, it is classified as the right lung. Otherwise, if the center of the area is on the right side of the image, it is assigned to be the left lung. When the scheme processes the final 2D CT image, the procedure of the lung classification is terminated (Fig. 2).

2. Search for the location of the connection—The location of the connection between two lungs should be detected before correctly separating the connection. To detect the connection, we use the fact that the lung areas depicted on two adjacent images are mutually similar in the size and shape because CT images are acquired sequentially with thin section. Therefore, during the sequential scan of CT images, if the scheme detects that

two lungs are connected in the “current” image, the center of the closest boundary points between the left and right lungs on the previous image can be mapped into the current image as the “separation seeds” to guide the scheme detecting the separation boundary of two connected lungs depicted on current image. Also, when the connection is detected in current image slice, the next image slice generally has the connection around the same location as the current image. Based on this observation and fact, the scheme is able to search fast and precisely for the suspicious region of the connection between two lungs using adjoining two CT images. Explanation of this section is described in detail through subsection C.2(a) to C.2(e) and the flow of the steps are visually shown in Fig. 3.

(a) Detection of first connection and facing lung boundary: During image scanning, the first connection of two lungs is detected by the scheme if the image contains only one segmented lung area that is larger than the predefined threshold on lung size (as described in subsection C.1). In this case, the scheme traces back to the previously scanned (adjacent) image and detects facing boundaries of two lungs. To detect facing boundary, the scheme steps along all pixels in x (horizontal) direction from a boundary pixel to the opposite lung. Once the scheme meets any pixel on opposite lung area without passing through own lung area, the boundary pixel is considered to be a facing boundary [Fig. 4(a)].

(b) Middle point and region of interest: After finding the facing lung boundary, for each pixel on the boundary the scheme searches for the closest pixel located on the facing boundary of the opposite lung. Then, the scheme computes the middle point, $P(x, y)$, between these two pixels (a pair). Each computed middle point P during the complete scanning is saved into the middle-point-list according to the distance between the two boundary points in ascending order. Then, P of the smallest distance among all pairs (or the first one in the list) is mapped to the current image and set a horizontal window (ranged 5 pixels in our experiments) to search for a point with the highest intensity. Then the retrieved point is used as the center of a region of interest (ROI). In our experiment, the border of the rectangle ROI is 70 pixels away from P in horizontal direction and 80 pixels away from P in y (vertical) direction [Fig. 4(b)].

(c) Separation using middle points: Finally, the scheme searches for the optimal path to separate the left and right lungs within this ROI using the proposed method that will be described in the next sub-section C.3. The scheme iteratively maps the next middle point to the current image and conducts above procedures until the two lungs are completely distinguished in the current image. After separating the connection between two lungs in this image, this image becomes the “previous” image and the next adjacent image to be scanned becomes the “current” image.

(d) Cut points as seed points for the next image: The optimal path distinguishing two lungs is the location of suspicious connection area in the next image, the optimal path, therefore, is used as seed points to separate two lungs in the next image. For this purpose, the scheme saves the optimal path and the middle point of the optimal path. The middle point was named “cut point”. There may be several cut points in one image according to the number of the connections. Each cut point is saved as “un-referred” value and once the cut points are referred in the next image, they are immediately set as “referred” to avoid being double-referred.

If un-referred cut points exist in the previous image, that means there were connections in the previous image, let one of them be P . At the moment, if P is not on the largest 2-D segment in the current image, the next closest point to P in the optimal path is set to be new P until new P is on the largest segment. A ROI is designated and centers at the P in the same manner as described in step (b). Then, the scheme separates the left and right lungs using the

proposed method to be described in the next sub-section, C.3. If no point in the optimal path is on the largest segment, it is considered that there is no connection around the optimal path. Then, the scheme searches for the suspicious regions using other cut points until all cut points are set as “referred”.

(e) New connection: Although all the cut points are referred, if two lungs are still connected, the new connection may appear somewhere in the image. In this case, the scheme finds the middle points between facing boundaries between two lungs in the previous image as if the first connection is detected, but excepting boundaries on the same location of the referred optimal paths in y axis to avoid double referring. Then the scheme follows step (b) and (c).

3. Separation of left and right lungs using a guided dynamic programming—

After detecting (or locating) the ROI that contains the connection of two lungs, the scheme should precisely and efficiently detect an optimal path to separate two lungs. For this purpose, we tested a guided dynamic programming algorithm in this study. Since dynamic programming attempts to overcome the limitations of either the greedy algorithms that are often trapped by the “best” local decisions without converging to the global optimization or exhaustive search algorithms that can produce the global optimality with the request of a prohibitive computational cost [20,21], it is a technique for efficiently implementing a recursive algorithm to search for all possibilities while storing partial results for sub-problems to avoid re-computing [22]. Storing the answer for each sub-problem in a look up table to replace the re-computation leads to a more efficient algorithm [20]. A well-known example of the dynamic programming is how to calculate Fibonacci numbers without recalculating sub-problems. When Fibonacci numbers are defined as $F_n = F_{n-1} + F_{n-2}$ where $F_0 = 0$ and $F_1 = 1$, a recursive function algorithm to calculate the numbers may be written in C style as below.

```
int fib_recursive(int n)
{
    If (n==0) return (0);
    If (n==1) return (1);
    return (fib_recursive(n-1) + fib_recursive(n-2));
}
```

It repeatedly computes the same sub-problems in a recursive algorithm. However, using a dynamic programming concept, the algorithm is revised to store all the results of the sub-problems and the results are referred to the answers of sub-problems. Revised new version of the function to calculate Fibonacci numbers using the dynamic programming is shown as below.

```
int fib_dynamicmic(int n)
{
    int i;
    int look_up[MAX_NUM];
    look_up[0] = 0;
    look_up [1] = 1;
    for(i==2; i<=n; i++) look_up[i] = look_up[i-1] + look_up[i-2];
    return (look_up[n]);
}
```


To increase the accuracy of the separation results and reduce the computational costs, we guided the dynamic programming algorithm to separate left and right lungs by selecting the start and end points in an adaptive and fully automatic way. The center of the scheme-identified ROI that contains the connection between two lungs becomes the start point of the guided dynamic programming. Note that the center of the ROI is a point on the optimal path of the current image or the middle of the narrowest boundary of the left and right lungs depicted on the previous image. The ROI is divided into the upper half ROI and the lower half ROI [Fig. 5(d)]. The scheme separately traces the optimal path within the two (upper and lower) ROI. The points on the top of the upper ROI and on the bottom of lower ROI are initially selected as the end points within two ROIs, respectively. While the optimal path is traced by dynamic programming algorithm from the start point to the initial end point, the algorithm stops when the point interfaces with the non-lung area. At this time, the point where the algorithm stops is the final end point and the optimal path traced by the guided dynamic programming is the boundary line between left and right lungs.

In the image processing, the optimal path using the traditional dynamic programming is defined as the path with the minimum cumulative cost that is the sum of the local costs on the path [15]. The cost matrix can be generated as a function of the image's properties such as pixel intensity, gradient magnitude, gradient orientation, etc [21]. In our experiments, we used the inverse CT attenuation value to compose a cost matrix to control the tracing process in our experiment, because the value is a good feature to distinguish between lung tissues and lung boundaries.

D. Performance evaluation

To test and evaluate the performance of the proposed lung separation scheme, we also designed and implemented an interactive image display screen or tool that allows the human observers to manually draw the boundary separation lines or curves between the left and right lungs using a mouse device after our automatic lung segmentation scheme has been applied to segment lung areas depicted on this CT slice. A research staff who has many year experience in conducting development and evaluation of CAD schemes for lung CT images in our imaging research center was asked to visually examine all CT image slices and manually separate two lungs if they are connected in these CT slices using this interactive tool. Then, we analyzed and compared the two-lung separation results generated using the automated scheme and the manual method. To compare two results, the separation lines (border pixels) of left and right lungs traced by manual method and the automated scheme were saved into two result files respectively.

In data analysis, three evaluation methods were used to compare and evaluate the scheme performance as well as the difference of lung separation between the manual and automated methods. First, we visually estimated whether the left and right lungs were completely distinguished at the connection areas. Second, we calculated the average distance between each newly defined boundary of the two lungs separated using the automated and the manual methods. For example, for each pixel on the new boundary defined using the automated scheme, the distance to the manually defined boundary was computed as

$$d_i = \min_j \left\{ \sqrt{(x_i^P - x_j^M)^2 + (y_i^P - y_j^M)^2} \right\} \text{ where } (x_i^P, y_i^P) \text{ is the pixel location of the proposed scheme-defined border and } (x_j^M, y_j^M) \text{ is a manually defined border pixel location. The}$$

average distance was computed using the following equation, $d_{avg} = \frac{\sum_{i=1}^l d_i}{l}$ where l is the number of points on the proposed scheme-defined new borders [5]. Third, we computed the

distributions of the pixel Hounsfield unit values (CT attenuation) on both boundary (separation) lines defined by the automated and manual methods. The difference of the two average Hounsfield unit values was computed and compared.

III. RESULTS

The experiment results showed that applying the guided dynamic programming algorithm to detect the optimal path (separation line) in the automated detected ROI successfully identified start point and end point between two adjacent images. The guided dynamic programming algorithm was more computational efficient by removing redundant processing from the previous dynamic programming [5,12]. For example, in the ROI on Fig. 5, the proposed algorithm discarded 15520 pixels (corresponding to 95% of total processing pixels) among 16261 pixels that need to be processed using the original dynamic programming methods. In general, the computation (image processing) time of using the guided dynamic programming algorithm was reduced to approximately 4.6% as compared to using the original dynamic programming. Also, the guided dynamic programming algorithm enables to avoid the incorrect optimal path tracing through the normal lung parenchyma, which could happen using the traditional dynamic programming algorithm (Fig. 6).

The experiment results showed that the automated scheme precisely and successfully detected and separate all 827 connections between left and right lungs depicted on total 4034 CT image slices in the eight testing examinations. The average and the standard deviation of difference between two boundary separation lines generated using the automated scheme and the manual method were 0.5 and 0.6 pixels, respectively (Table 2). The average pixel values of the separation boundary lines detected by the automated and manual method were -372.9 ± 167.0 HU and -501.5 ± 200.6 HU, respectively (Table 3). The performance of the scheme is independent to the locations (i.e., posterior, medio, and anterior) of lung connection and the scheme is able to distinguish and separate two lungs with multiple connections depicted on one CT image (Fig. 7).

IV. DISCUSSION

With advances in CT technology, voxels are more commonly reconstructed at smaller and approximately isotropic dimensions [19] allowing for non-invasive analysis of various lung diseases. However, the substantially increased number of CT images generated from one examination requires the radiologists to spend more and more time and effort in reading and interpreting CT data. Therefore, to reduce radiologists' workload and potentially improve their diagnostic performance, a large number of CAD systems for variety of lung diseases have been developed and tested. Lung segmentation is typically the initial stage of the CAD development, and this stage composes of several steps. Among them, initial lung segmentation step using pixel intensity based methods is applied to distinguish between lung and non-lung areas, while the boundary smoothing step helps generate the smooth segmented lung boundary or recover partial lost lung tissue near the lung boundary in the diseased cases. However, these two steps can also connect left and right lungs regardless of the positions around mediastinum such as at the anterior, medio, posterior, or multiple positions. Disjunction of the connection between two lungs is important in the detection of parenchyma disease and development of accurate local lung function measurements (i.e., within each lobe) without human intervention.

The new automated scheme tested in this study has several unique characteristics (or advantages). First, many of previously reported methods or algorithms assume that connection of two lungs was located only in certain range of lung area [4,8,10,12,17]. Consequently, the connection out of the assumed or targeted range could not be detected.

Our scheme has flexibility to detect and separate lung connections located in any positions of the CT images. Second, the previously reported methods based on the morphological operator iteratively conducted morphological opening and/or closing operations and used the difference of the results to check if there are connections between two segmented lungs and to detect the border (separation) line between two lungs (if they are connected) [17]. This iterative procedure is time consuming. Our scheme avoids such iterative morphological operations and is able to detect multiple connections in one image using the operation to find the narrowest boundaries between two lungs. The operation first identifies a seed point (the center point of the searching ROI) based on detecting and mapping two points that separately locate on the left and right lungs and have the smallest distance on the previous image in which two lungs are separated and then uses this seed to guide the scheme searches for and identifies the optimal separating line of two lung boundaries depicted on the current image. Therefore, our scheme is able to detect and separate multiple connections depicted on one image regardless of their locations.

In the previously reported studies, using morphological operator and line fitting methods often added artificial intervention to the disconnection procedure. Multiple active contours method was able to find the suspicious connection area regardless of the location but it was unable to draw the accurate border line between two lungs. Also, a traditional dynamic programming may create the unexpected optimal path along with the bright normal lung area formed by vessel and lung disease (Fig. 6). However, because the assigned seed or start searching point guarantees that it locates on the optimal path for separating the boundary between two lungs and the guided dynamic programming can automatically stop tracing the optimal path, our scheme can detect and separate connections between two lungs in a fully automated, adaptive, fast and more robust manner. For example, the traditional dynamic programming method detects the optimal path in whole ROI in Fig. 5(c), however, our guided dynamic programming search for the optimal path only in the lung area [Fig. 5(d)].

Normal lung tissue containing air is darker (with smaller Hounsfield value) than thoracic area outside of the normal lung tissue. Therefore, lung border between left and right lungs are brighter (with higher Hounsfield unit values) than normal lung tissue. From this fact, human observers separate left and right lungs by tracing the pixels that are visually brighter than surrounding pixels. However the manual method is tedious and time consuming and is not accurate because of the fatigue from long work and hand shaking (Fig. 8). Since the average Hounsfield unit value computed from the automated separation lines was higher than the one computed from the manual separation lines, it showed that using automated scheme preserved more pixels depicted lung tissue than using manual method. In addition, the smaller standard deviation indicated that using automated scheme (method) generated more consistent separation result than using manual method. Therefore, the proposed separation scheme can be used as an alternative tool for manual tool.

Although the testing results demonstrated the high performance of our scheme to automatically detect and separate the lung connection (or fusion) areas depicted on CT images acquired from a diverse patient database, we recognized that this was a very preliminary study including a number of limitations. For example, only a small number of cases with limited diseases were used to validate the performance of the scheme against differences in anatomy and pathology. In addition, the feasibility or performance of this automated scheme when applying to the CT examinations with prior lung surgery including pneumonectomy or severe lung abnormalities along the fusion area has not been investigated in this study. Therefore, the robustness of our scheme needs to be further tested using the large independent CT image databases that include the diverse cases with various lung diseases (i.e., interstitial lung disease, emphysema, lung cancer, etc) in future studies before it can be reliably integrated into the other CAD schemes of lung diseases.

V. CONCLUSION

After more than two decade intensive research effort in developing and evaluating CAD schemes and systems, using CAD has been proved helpful for radiologist to detect and diagnose many lung diseases. Separation of left and right lungs is the essential procedure as the last step of the lung segmentation because it is required for CAD schemes to conduct robust and accurate measurements of local lung functions. Previous methods conducting separation in only one 2D image produced inaccurate and un-stable results. To resolve the problem, we used and mapped the location where two lungs are disconnected in the previous image to define the searching seed in the current image in which two lungs are connected and developed a guided dynamic programming to fully automatically and adaptively trace the separation line between two lungs. To improve computational efficiency and separating accuracy, we also divided the initial searching ROI into two sub-ROIs and applied our guided dynamic programming algorithm to these two sub-ROIs separately. The algorithm is suspended once it reaches the adaptively and automatically selected end point. The experiment results showed that the proposed methods were able to robustly and accurately disconnect all connections between left and right lungs in our testing dataset and the guided dynamic programming was able to eliminate a large fraction of redundant processing using adaptive and automatic stopping condition.

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Figure 1. Examples of CT images from 3 examinations with various locations of connection. (a) A connection around medio area, (b) two connections in an image, (c) rolling ball makes two connections in an image.

Figure 2.
Flowchart illustrating the steps of the proposed scheme to classify left and right lungs

Figure 3. Flowchart illustrating the steps of the proposed method to separate left and right lungs. PI, CI, and OP indicate the “previous” image, the “current” image, and the optimal path, respectively.

Figure 4.

Example of searching for the first suspicious connection region. (a) Part of the previous image in which two lungs are unconnected. Red straight lines and yellow ovals indicate the lines that link two points located on two lung boundaries with the shortest distance and the middle point, $P(x, y)$, of the two points, respectively. Boundaries facing each other lung are drawn as orange. The middle points are saved into the middle-point-list in ascending order. (b) Part of the current image in which two lungs are connected. Bright green rectangle ROI is set to search for the optimal path separating two lungs. The center of the ROI is determined by mapping the smallest middle point (the first point in the middle-point-list) into the current image.

Figure 5.

Comparison between the guided dynamic programming and the traditional dynamic programming. (a) Original input image, red rectangle of ROI contains the connection, (b) lung segmentation result, (c) optimal path (yellow line) using traditional dynamic programming in ROI, (d) upper ROI and lower ROI with bright green rectangle defined using the proposed methods and optimal path (bright blue and yellow line) using the guided dynamic programming.

Figure 6. Comparison of the results using the traditional dynamic programming and the guided dynamic programming. (a) Examples showing that the traditional dynamic programming fails to correctly separate two lungs (b) Examples showing that the guided dynamic programming successfully separates the left and right lungs.

Figure 7.
Examples of successful separation results using the proposed methods

Figure 8.

An example of boundary difference between right lung and left lung separated by the manual and the proposed method. It includes (a) original input CT slice image with a connection between two lungs in red box, (b) scaled fusion area in the original CT slice image, and (c) scaled fusion area marked with two separation results produced by the manual and automated methods in which blue line indicates agreement between two methods, and the disagreement is shown in green (manual) and red (automated), respectively.

Table 1

Summary of eight testing CT examinations used in the study and the connections in the images

Examinations	Images	Total connections	One connection	Two connections
1	505	10	10	0
2	537	89	89	0
3	457	30	30	0
4	533	198	198	0
5	437	193	149	22
6	532	108	108	0
7	532	62	62	0
8	501	159	159	0
Total	4034	827	805	22

Table 2

The average and the standard deviation of difference in pixel between the borders defined by the proposed method and a manual method

Examinations	Average	Standard deviation	Maximum	Minimum
1	0.5	0.5	1.0	0
2	0.5	0.5	2.0	0
3	0.5	0.5	1.4	0
4	0.6	0.7	5.4	0
5	0.5	0.6	2.8	0
6	0.5	0.6	2.2	0
7	0.6	0.6	4.1	0
8	0.6	0.6	3.6	0
Total	0.5	0.6	5.4	0

Table 3

The average and the standard deviation of pixel values on the optimal path found using the proposed method and a manual method. HU means Hounsfield Unit

Examinations	Proposed method		Manual method	
	Average (HU)	Standard deviation	Average (HU)	Standard deviation
1	-544.6	279.9	-540.7	132.0
2	-386.1	130.1	-492.6	183.2
3	-241.6	208.7	-399.3	232.1
4	-369.3	189.5	-504.6	235.7
5	-416.1	143.0	-541.8	190.0
6	-275.4	152.9	-440.0	197.2
7	-492.3	100.3	-642.7	174.1
8	-250.9	134.7	-450.1	256.9
Total	-372.0	167.4	-501.5	200.6