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Shape “Break-and-Repair” Strategy and Its Application to Automated Medical Image Segmentation

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Abstract

In three-dimensional medical imaging, segmentation of specific anatomy structure is often a preprocessing step for computer-aided detection/diagnosis (CAD) purposes, and its performance has a significant impact on diagnosis of diseases as well as objective quantitative assessment of therapeutic efficacy. However, the existence of various diseases, image noise or artifacts, and individual anatomical variety generally impose a challenge for accurate segmentation of specific structures. To address these problems, a shape analysis strategy termed “break-and-repair” is presented in this study to facilitate automated medical image segmentation. Similar to surface approximation using a limited number of control points, the basic idea is to remove problematic regions and then estimate a smooth and complete surface shape by representing the remaining regions with high fidelity as an implicit function. The innovation of this shape analysis strategy is the capability of solving challenging medical image segmentation problems in a unified framework, regardless of the variability of anatomical structures in question. In our implementation, principal curvature analysis is used to identify and remove the problematic regions and radial basis function (RBF) based implicit surface fitting is used to achieve a closed (or complete) surface boundary. The feasibility and performance of this strategy are demonstrated by applying it to automated segmentation of two completely different anatomical structures depicted on CT examinations, namely human lungs and pulmonary nodules. Our quantitative experiments on a large number of clinical CT examinations collected from different sources demonstrate the accuracy, robustness, and generality of the shape “break-and-repair” strategy in medical image segmentation.

Index Terms

Shape analysis; surface interpolation; medical image segmentation; computer-aided detection/diagnosis

1 Introduction

Automated segmentation of anatomic structures depicted on three-dimensional medical images plays a crucial role in computer-aided detection/diagnosis (CAD) due to its capability of limiting disease detection and analysis in specific regions-of-interest (ROIs). However, the existence of image noise/artifacts and various diseases often makes it challenging to accurately delineate the boundary of the ROI. In this study, we introduce a “break-and-repair” shape analysis strategy and demonstrate its feasibility and generality by applying it to automated segmentation of two different anatomical structures depicted on computed tomography (CT) images:

Human lung segmentation

Automated lung volume segmentation is often used as a preprocessing step in computerized lung CT image analysis, and its accuracy has a direct impact on the performance of computerized noninvasive assessment of numerous lung diseases, including lung cancer, emphysema, pulmonary embolism, and interstitial lung disease (ILD) and other clinical practices (e.g., preoperative planning of lobectomies). Hence, the development of a robust automated lung segmentation scheme could be extremely beneficial for quantitative lung image analysis and routine clinical practices. Although threshold-based strategies [1], [2] can be used to extract lung parenchyma efficiently from CT images due to its obvious lower intensities in Hounsfield Unit (HU) as compared with the surrounding structures, the segmented lung volume is often inaccurate with irregular boundaries. Sluimer et al. [3] summarized the problems leading to inaccurate segmentation as

1. high density pathologies such as juxta-pleural nodules,
2. posterior and anterior attachments between left and right lungs,
3. false positive inclusion of other organs outside the lung (e.g., liver or spleen), and
4. nonsmooth exclusion of the trachea and vessels in the hilar regions.

Although a large number of approaches [4], [5], [6], [7], [8] have been developed to compensate the errors generated by a single thresholding, most of them were designed with consideration of specific applications, such as lung nodule detection [9], [10], lobe/fissure segmentation [11], [12], interstitial lung disease [13] and scleroderma disease [8] diagnosis, and airway detection and analysis [14]. Masutani [15] proposed to deal with irregular segmentation boundary using radial basis functions (RBFs), but users have to manually specify a set of points passing through the boundary of the anatomical structures. To the best of our knowledge, none of the available approaches are capable of generating a smooth and complete lung volume by handling all the above-mentioned issues in a unified framework instead of in a piecemeal manner without considering any specific characteristics of CAD applications.

Pulmonary nodule segmentation

Lung cancer is the leading cause of cancer-related deaths in the US and worldwide [16], and its existence is usually indicated by the identification of pulmonary nodules. In clinical practice, radiologists frequently measure nodule size in volume/diameter as well as changes of nodule size over time as depicted on sequential CT examinations for diagnostic and therapeutic purposes [17]. The primary purpose is to provide valuable information in regard to classification (e.g., benign versus cancer), possible prediction of cancer prognosis and the assessment of treatment efficacy [18]. However, it is an extremely difficult task to segment pulmonary nodules on CT images due to their wide range of sizes, intensities, and shapes [19], especially when the nodule is connected to or surrounded by other tissue structures with similar densities (e.g., vessels). The available nodule segmentation approaches can be

largely classified into two broad classes in methodology, including intensity-analysis-based method [20], [21], [22] and nodule shape-analysis-based method [23], [24], [25]. Despite the substantial investigational efforts, accurate nodule segmentation still remains a challenging task due to the diversity in appearances of nodules and their connection with surrounding tissues.

In this study, we present a shape “break-and-repair” strategy and use it to automatically segment human lungs and pulmonary nodules as two examples in a unified framework. Similar to the procedure of the surface approximation (e.g., spline surface interpolation) using a set of control points, the main idea is to automatically remove suspicious or problematic regions and then estimate a complete and smooth surface by fitting the remaining regions with high fidelity as an implicit surface. The innovation is the way of solving medical image segmentation problems in geometric space using techniques developed in computer graphics properly. A detailed description of this shape analysis strategy and its application to medical image segmentation as well as preliminary quantitative results is described in this study.

2 Method and Materials

2.1 Shape “Break-and-Repair” Strategy

The proposed shape “break-and-repair” strategy consists of three main stages, namely 1) modeling, 2) “break,” and 3) “repair.” The first stage extracts the raw ROI and represents it as a surface model. The second stage identifies and removes the problematic regions that are not parts of the anatomical structures in question or may potentially hinder a smooth or complete segmentation. The third stage fits the remaining incomplete regions with high fidelity as an implicit function, and the interpolation and extrapolation properties of an implicit function are capable of “repairing” (or estimating) the removed suspicious regions smoothly. Given a specific application, there may be somewhat differences in implementation details but the idea remains the same. In the following, we will explain our implementations of the above-mentioned procedures involved in this shape analysis strategy with consideration of medical image analysis.

2.1.1 Geometric Surface Modeling—Geometric surface is an intuitive way in the representation of the boundary of an anatomical structure. Since medical images can be regarded as scalar fields of voxels’ intensity levels, we use the Marching Cubes Algorithm (MCA) [26] to extract and represent anatomical structures depicted on images. MCA treats each voxel in the scalar field as a cube and determines the isosurface along each cube edge based on linear interpolation by considering the eight voxels at the corners of each cube (voxel). If a cube has one or more voxels with intensities larger and less than a predefined isovalue, this cube will contribute a set of triangles. After traversing all voxels, a triangular surface will be constructed. The detailed description of MCA can be found in [26]. When applying MCA to a scalar field, we need to specify an isovalue indicating the boundary of the anatomical structure in question. Due to the linear interpolation property of the MCA, CT examinations with different in-plane or through-plane resolutions can be processed directly without additional reconstruction. We note that the front faces of a surface model are consistently displayed in pink while the back faces in green in this study (e.g., Fig. 1).

2.1.2 Surface “Break”—Curvature is an intuitive way in mathematics of characterizing the geometric property of the surface of an object, by which it is easy to identify specific shape features of an object. Considering that the anatomical structures are usually in limited types of shapes (e.g., sphere, plane, or cylinder), we use principal curvatures in this study to identify and remove the potential problematic regions. However, it is difficult to derive an

analytical solution to the curvatures at points on a triangle mesh-based surface obtained by MCA because of its discrete presentation. In the field of computer graphics, there have been two broad classes of methods for calculating the curvatures at a point on a triangle mesh. The first one is based on discrete differential geometry analysis and estimates the surface curvatures using the relative position and direction information of neighboring vertices [27], [28]. The second one estimates the curvature at a point by fitting or parameterizing an analytic surface using the neighboring vertices of this point [29], [30]. In this study, we used the finite-differences approach proposed by Rusinkiewicz [28]. The main advantages of this technique are its efficiency in space and time (i.e., $O(n)$, where n is the number of vertices) and independence of its neighborhood size. The computation of the principal curvatures (i.e., the maximum and minimum values of the normal curvature at a point) and the principal directions (i.e., the directions along which the normal curvature reaches its maximum and minimum values) are performed by visiting the vertices of a triangle mesh once in a single pass. Most important, it offers a reasonable accuracy. At a given point on a surface, the surface near the origin can be represented by a quadratic $z = f(x, y) = Ax^2 + By^2 + Cxy$. Assuming that u and v form an orthonormal coordinate system at the given point, the normal curvature k_n in a direction for a smooth surface satisfies [31]:

$$k_n = \begin{pmatrix} u & v \end{pmatrix} \begin{pmatrix} 2A & B \\ B & 2C \end{pmatrix} \begin{pmatrix} u \\ v \end{pmatrix} = \begin{pmatrix} u' & v' \end{pmatrix} \begin{pmatrix} k_1 & 0 \\ 0 & k_2 \end{pmatrix} \begin{pmatrix} u' \\ v' \end{pmatrix}. \quad (1)$$

The principal curvatures k_1 and k_2 and the principal directions u' and v' can be determined by solving the eigenvalue system or diagonalizing the symmetric matrix in (1). To extend this definition from smooth surfaces to discretized triangle meshes, Rusinkiewicz used finite differences to approximate each triangle where three edges gave three directions. Thus, the second fundamental tensor is calculated by solving a linear system using least squares. After the curvature tensor of each triangle is computed, the curvature at each vertex is obtained by averaging the curvature tensors of its neighboring triangles according to their “Voronoi area” used in [27]. To assure accurate curvature estimation, a triangle mesh is smoothed using the Laplacian smoothing [32] before applying Rusinkiewicz’s method. The Laplacian smoothing iteratively adjusts the location of each mesh vertex to the geometric centroid of its neighboring triangles without modifying the topology of the mesh. The computational cost of Laplacian smoothing is linear in the number of vertices. Despite its simplicity, the Laplacian smoothing shrinks the size of an object. To avoid this undesirable effect, we only use the smoothed model for curvature estimation while keeping a copy of the original model for later surface fitting. The principal curvatures at each vertex of the smoothed triangle mesh are used to identify the problematic regions of the original model according to the specific application and remove them.

2.1.3 Surface “Repair”—The shape “break” operation results in a set of discrete and incomplete surface patches. Hence, we need to find a solution with interpolation and extrapolation capabilities so that the missing regions can be estimated in an accurate and smooth way. In this study, we propose to represent the remaining surface patches after removal operation as an implicit function, where the implicit function $F(x)$ passes through a given set of points $\{x_1, x_2, \dots, x_n\}$. To perform a smooth fitting of scattered points, we minimize the energy contained in the implicit function $F(x)$, which can be measured as a combination of the square of the second partial derivative along each dimension

$$E = \int_{\Omega} (F_{xx}^2 + F_{yy}^2 + F_{zz}^2 + 2F_{xy}^2 + 2F_{xz}^2 + 2F_{yz}^2) d\Omega, \quad (2)$$

where Ω denotes a surface region, and E is a measure of the “roughness” of $F(x)$. This energy minimization process can be solved through representation of a surface using RBFs [33]:

$$F(\mathbf{x}) = \sum_{i=1}^n \lambda_i \Phi(|\mathbf{x} - \mathbf{x}_i|) + P(\mathbf{x}), \quad (3)$$

where Φ is the RBF, λ_i are real number coefficients, P is a linear polynomial (i.e., $P(\mathbf{x}) = c\mathbf{x} = c_0 + c_1x + c_2y + c_3z$), and $\{\mathbf{x}_i\}$ are the scattered points. For three-dimensional applications, the biharmonic ($\Phi(x) = |x|$) and triharmonic splines ($\Phi(x) = |x|^3$) are often used [34]. In our implementation, the biharmonic splines were used as the radial basis function.

If F passes through all the scattered points $\{\mathbf{x}_i\}$, then, there is $F(\mathbf{x}_i) = 0$. To avoid trivial solution (i.e., the unknowns $\lambda = 0$ and $\mathbf{c} = 0$), we sampled additional points to make sure that $F(\mathbf{x})$ is nonzero. One simple approach is to sample off-surface points along the normal vectors of the scattered points. When an off-surface point is located on the positive/negative direction of a normal vector, it indicates the outside/inside of an object. Thus, we can assign a positive/negative value to this point, which can be the off-surface distance or simply set a small value. The off-surface distance should be small enough to ensure that it does not pass through other part of the same surface [34]. The above formulation is similar to the definition of the signed distance field of an object. Assuming that totally k off-surface points are sampled, (3) can be rewritten in a form of $A \cdot B = C$:

$$\begin{bmatrix} \Phi_{11} & \Phi_{12} & \cdots & \Phi_{1m} & 1 & x_1 & y_1 & z_1 \\ \Phi_{21} & \Phi_{22} & \cdots & \Phi_{2m} & 1 & x_2 & y_2 & z_2 \\ \vdots & \vdots & & \vdots & \vdots & \vdots & \vdots & \vdots \\ \Phi_{m1} & \Phi_{m2} & \cdots & \Phi_{mm} & 1 & x_m & y_m & z_m \\ 1 & 1 & \cdots & 1 & 0 & 0 & 0 & 0 \\ x_1 & x_2 & \cdots & x_m & 0 & 0 & 0 & 0 \\ y_1 & y_2 & \cdots & y_m & 0 & 0 & 0 & 0 \\ z_1 & z_2 & \cdots & z_m & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \lambda_1 \\ \lambda_2 \\ \vdots \\ \lambda_m \\ c_0 \\ c_1 \\ c_2 \\ c_3 \end{bmatrix} = \begin{bmatrix} v_1 \\ v_2 \\ \vdots \\ v_m \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \quad (4)$$

where $\Phi_{ij} = \Phi(|\mathbf{x}_i - \mathbf{x}_j|)$ with $i, j \in [1, m]$, $m = n + k$, $v_i = 0$ for all the points located on the surface, and $v_i = +1$ or -1 for the points located outside or inside the surface. As a symmetric linear system, a unique nontrivial solution is guaranteed for (4) [35].

The size of the linear system (i.e., (4)) used to compute the implicit function is proportional to the number of the sampled (scattered) points. Although as a symmetric matrix the storage requirement can be reduced to half by only storing the lower or upper triangle, the memory consumption remains very large with high computational cost. To approximate the surface of the anatomical structure in question at a predefined accuracy with a limited number of sampling points, we adopted an unbiased statistics-based sampling strategy proposed originally in [36], [37] where a set of vertices are selected from the broken and clustered lung surfaces as constraint points for (4). When mapping the implicit surface to medical images, we can check the sign of each voxel in the subvolume with regard to the implicit function, where the zero values indicate the boundary, and the negative/positive values indicate the inside/outside region.

2.2 Application I: Human Lung Segmentation

2.2.1 Thresholding and Geometric Modeling—Although a single thresholding operation, especially on noisy images as from low dose CT with severe pathologies, cannot result in a smooth lung boundary and often misses regions with specific diseases, it is the most practical and efficient way to extract the lung parenchyma depicted on CT images due to the obvious contrast of lung parenchyma and its surrounding tissues. Therefore, we use an established and computationally efficient threshold-based strategy [1] to segment the lung parenchyma depicted on CT images as the basis for further analysis, where the threshold is determined adaptively according to the intensity distribution. The isolated pockets of air between the patient and the CT bed as well as image noise or artifact are then filtered out by simply applying a size-based classification rule, i.e., only the largest connected volume is kept while other small regions are deleted. After that, we use MCA [26] to construct a triangle-based mesh from the three-dimensional scalar field (or voxels) formed by lung parenchyma. Defections caused by diseases, image noise/artifacts, or specific anatomy are depicted on this surface model (Fig. 1); hence, the lung segmentation problem now turns into how to fix these defections. The example in Fig. 1a is the modeled lung surface, where, undesirably, the surfaces of the vessels are modeled as well (Fig. 1b). Such a mesh model often contains a large number of triangles, e.g., the model in Fig. 1a consists of 13,890,394 triangles.

To reduce the computation cost incurred by such a large number of triangles, we apply an efficient mesh simplification algorithm, developed by Garland and Heckbert [38], to this model without substantial reduction in its shape precision. This mesh simplification algorithm reduces the number of triangles using iterative pair contractions and monitors the approximation accuracy using quadric error metrics, capable of producing high fidelity approximations of arbitrary triangle meshes efficiently with a substantially reduced number of triangles. A detailed description of this mesh simplification algorithm along with examples has been presented elsewhere [38]. The example in Fig. 1b is the simplified model with 100,850 triangles. Although some very tiny shape details in this model are missed, the simplified lung model (Fig. 1b) is not changed obviously in shape with an average error of 0.11 mm and a maximum error of 0.53 mm as compared with the original lung model (Fig. 1a). The average/maximum error is defined as the average/maximum of the smallest euclidean distances from each vertex in the simplified surface model to the original surface model. Also shown in Fig. 1 are several common issues related to lung segmentation, including the incomplete segmentation of the right and left lung junctions, vessel regions, and trachea. Since our approach only works on the three-dimensional triangle mesh representing the lung from now on, where the organs with high intensities such as liver and spleen under the lungs are removed by the thresholding operation, there will not be any false positive inclusion of these organs thereafter.

2.2.2 Problematic Region Removal Using Principal Curvature Analysis—By analyzing the regions that may potentially cause segmentation errors, we found that these regions are usually associated with high curvatures. Hence, we identify these regions with high curvatures and remove them. When applying this curvature estimation scheme to the smoothed model in Fig. 1, the larger principal curvature (i.e., the maximum normal curvature) is calculated and visualized with colors according to their absolute values in Fig. 2. Since the curvature at a point is equal to the inverse of its radius at this point, the vessel and the trachea regions have larger curvatures due to their relative smaller radii.

To remove these regions with high curvatures, we simply set up a threshold. When the curvature at a vertex is larger than this threshold, this vertex is deleted. In practice, it is very difficult to set an optimal curvature threshold that can remove all suspicious regions exactly

without any overremoval. With consideration of the size of lung vessels and trachea, this threshold is set empirically as 0.08 (1/mm) corresponding to a radius of 12.5 mm. It can be seen from the example in Fig. 3 that majority of the trachea and the vessel regions disappeared and the right and left lungs are separated due to this removal. Although this removal operation may result in some very small isolated regions due to local perturbations, they can be filtered out by simply checking their sizes. Obviously, this removal operation cannot assure a pure removal of the regions that cause segmentation “problems,” and some “good” regions (e.g., the ridges of each lung) may be deleted as well. Due to the approximation characteristics of the later surface fitting operation, those removed “good” regions as well as the “problematic” regions will be estimated.

2.2.3 Complete Lung Surface Estimation Using Implicit Lung Surface Fitting—

The surface removal procedure separates the right and left lungs by breaking the lung surfaces into pieces of patches. To identify the right and left lungs, we use a simple bounding box strategy considering that the outer convex region of the right or left lung usually has the largest surface area and encloses the inner concave regions. First, the two largest surface patches in area are identified and they correspond to the outer convex regions of the right and left lungs. Second, an axis-aligned bounding box (AABB) is built for each of the identified surface patches, respectively. Third, all of the remaining surface patches are classified into right or left lung regions by checking which bounding box they are located in. In case, there are vertices in the overlapping region between the two bounding boxes of left and right lungs, these vertices are simply discarded since misclassification of these points into either left or right lung will lead to an incorrect lung surface estimation. In Figs. 4a, 4b, 4c and 4d, 4e, 4f in the top row are the identified right and left lung regions viewed from different perspectives after applying this bounding box strategy to the example in Fig. 3. Given these clustered lung surfaces, the implicit surface fitting operation results in closed and smooth lung boundaries as shown in the bottom row of Fig. 4.

2.3 Application II: Pulmonary Nodule Segmentation

2.3.1 Thresholding and Geometric Modeling—When segmenting a nodule, a seed point is often needed. Once a seed point within a nodule is specified, this scheme first models the anatomic structure within a subvolume centered at this seed point. A subvolume is defined as a small cubic region aligned with axes of the coordinate system of a CT data set. For automated nodule segmentation purpose, the size of the subvolume is set in a way so that the largest nodule of clinical interest can be fully enclosed (e.g., $35 \times 35 \times 35 \text{ mm}^3$). Thereafter, MCA is applied to generate a triangle mesh surface from the scalar field within the subvolume (Fig. 5). Considering that majority of nodules have intensity values higher than -700 HU , we simply set the isovalue at -700 HU in this study.

2.3.2 Problematic Region Removal Using Principal Curvature Analysis—

Pulmonary nodules and other tissues with high intensity levels in the lung can be roughly classified into three types of shapes including spheres (e.g., nodules), cylinders (e.g., vessels), and lines or surfaces (e.g., fissures). In medical image analysis, Gaussian (K_G) and mean (K_H) curvatures are widely used for shape classification and are defined in terms of principal curvatures k_1 and k_2 :

$$\begin{cases} K_G = k_1 k_2, \\ K_H = \frac{k_1 + k_2}{2}. \end{cases} \quad (5)$$

By checking the sign combinations of the Gaussian and Mean curvatures, a point (or a voxel) is assigned (labeled) a specific type of shape [39]. However, it has been demonstrated

in [40] that the performance of the Gaussian/mean-curvature-based shape classification scheme was inferior to that proposed by Koenderink and van Doorn [41] where the shape index was defined as:

$$S = \frac{2}{\pi} * \arctan \left(\frac{k_1 + k_2}{k_1 - k_2} \right). \quad (6)$$

According to Koenderink's shape classification, five classes of shapes, including concave-ellipsoid, concave-cylinder, hyperboloid, convex-cylinder, and convex-ellipsoid (Fig. 6b), are defined by a continuous shape index value, namely, $[-1, -5/8]$, $[-5/8, -3/8]$, $[-3/8, 3/8]$, $[3/8, 5/8]$, and $[5/8, 1]$, respectively.

With consideration of the blob-like shape of pulmonary nodules and the shapes of other soft tissues such as vessels, we used the Koenderink's shape classification on the basis of a "visibility" testing procedure (Fig. 6a) to identify the points located on the surface of the very nodule defined by a specific seed point. First, a set of rays shoot out from the seed point s , and the intersecting points ($p_1, p_2 \dots p_m$) between these rays and the triangle mesh generated by the MCA are calculated. Second, a "visible" point is defined as the first intersecting point between a ray and a triangle mesh and all distant (or subsequent) intersecting points are defined as "invisible." "Invisible" points to the seed point are filtered out. Third, the shape indices as defined by (6) of the "visible" points are calculated, and the points that are classified as convex-cylinder type are removed. Finally, the remaining intermittent regions formed by all visible points are regarded as sections belonging to the nodule surface (the second column in Fig. 5b).

2.3.3 Complete Nodule Surface Estimation Using Implicit Lung Surface Fitting

—Given incomplete segmentation of lung nodule surfaces, applying the implicit surface fitting procedure explained in Section 2.1.3 to the identified partial surface (the second column in Fig. 5b) will result in a closed and smooth three-dimensional surface (the third column in Fig. 5b). Finally, a lung nodule is outlined automatically by mapping the reconstructed surface of a nodule onto the appropriate CT images (the fourth column in Fig. 5b).

2.4 Performance Assessment Method

To qualitatively assess the performance of the proposed shape analysis strategy in human lung and pulmonary nodule segmentation, we measured 1) the discrepancy errors by calculating the Root Mean Square (RMS)/maximum distances (or errors) and their standard deviations between the boundaries obtained by the computerized scheme and "reference standard" and 2) the overlapping ratios between the results delineated by the computerized scheme and radiologists (denoted as A and B, respectively), namely the overlapping ratio $(A \cap B / A \cup B)$. The discrepancy distance is calculated as the minimum distance from a vertex on the computerized surface to the surface of the anatomical structures in "reference standard." To demonstrate the performance of the proposed segmentation scheme in dealing with the problems summarized by Sluimer et al. [3] mentioned in Section 1, we also specifically measured 1) the sensitivity of juxtapleural nodule inclusion by replacing the lung segmentation module in our previously developed lung nodule detection scheme [42] with the one developed in this study and 2) the ratio of the successfully separated examinations when the right and left lungs are attached to each other by checking the existence of right and left lungs.

2.5 Testing CT Data Set

In this study, 230 chest CT examinations collected from three different sources were used for the performance assessment. The reason that we used multiple sources of CT examinations is due to the needs of different types of gold standards that are usually created by human experts, such as the “true” lung boundary, nodule boundary, and juxtaleural nodule positions in calculating the measures mentioned in Section 2.4. The first set of CT examinations contained 20 cases, where the lung boundaries have been manually segmented in a slice-by-slice manner under the guidance of a radiologist [43], these cases were used to measure the discrepancy errors and the overlapping ratios between the lung boundaries obtained by the computerized scheme and “reference standard.” These examinations were acquired from the lung apices through the upper abdomen by using a four-detector row CT scanner (Volume Zoom; Siemens Medical Systems, Erlangen, Germany). Please refer to [10] for a full description of these data sets and the creation procedure of the reference standard. It needs to point out that the trachea regions in these 20 examinations were regarded as part of lung regions in [43] but removed in this study by a radiologist. The second set of CT examinations contains 52 cases, where 58 juxtaleural nodules and their positions have been marked by radiologists, and these cases were used to measure the ratio of juxtaleural nodule inclusion. A detailed description of the CT data acquisition (including the x-ray dose and image reconstruction) protocols has been reported elsewhere [42]. The third set of CT examinations contains 158 annotated cases that were downloaded from the National Cancer Institute Website at <https://imaging.nci.nih.gov/ncia/login.jsf>. These examinations contained 1,842 marked nodules, 390 of which were identified as larger than 3 mm in size. The three-dimensional boundaries of these nodules larger than 3 mm had been outlined by anywhere from one to four radiologists in an unblinded reading manner (Table 1). In this study, these examinations were used to measure the discrepancy errors and the overlapping ratios between the nodule boundaries obtained by the computerized scheme and radiologists. There had been a detailed description of the CT acquisition protocols and nodule delineation procedures in [44].

Among these 230 CT examinations, we observed that there were 43 cases where the right and left lungs were attached to each other in a fraction of CT image slices. Considering that a single voxel may lead to the attachment of the right and left lungs, which may not be captured easily by a radiologist, a computerized tool was used to check the existence of the junctions between right and left lungs depicted. After a CT examination is thresholded, the scheme simply performs a two-dimensional “flooding” operation slice-by-slice and counts the number of connected regions in each slice. If there is only one large fused region, this case is classified as having junctions between right and left lungs. Meanwhile, this slice-by-slice fusing-check operation provided us with the knowledge of at which slices the right and left lungs are attached to each other. The seed points used for the above flooding operations are determined by randomly selecting a voxel forming the lung volume.

3 Results

For lung segmentation, the discrepancies in boundaries and volumes between the computerized scheme and the reference standards are summarized in Table 1. When the lung surface boundaries are considered, the RMS error is 0.15 ± 0.092 mm and the maximum error is 7.82 ± 3.37 mm. When the differences in lung volume are considered, the percentage of volume overlapping is $95.1 \pm 2.0\%$. Our preliminary study shows that all the 58 juxtaleural nodules identified by radiologists are properly included when applying this segmentation scheme to a nodule detection procedure to test the existence of these nodules (Fig. 7a). Also, for the 43 CT examinations, where the right and left lungs are attached to each other after thresholding, the right and left lungs are successfully separated after applying this scheme (Fig. 7b). In addition, all lung tracheas in these examinations were

removed successfully due to their relative high curvatures (Fig. 7). The computational cost of the lung segmentation process is around 7 minutes for a CT examination using a desktop PC computer (AMD Athlon 64 × 2 Dual 2.11 GHz and 2 GB of RAM).

For the pulmonary nodule segmentation, the distance discrepancies between the segmentation results by the computerized scheme and the radiologists are summarized in Table 1. On the whole, the maximum and mean discrepancies were 2.69 ± 1.28 and 1.08 ± 0.45 mm, respectively; the overlapping ratio between the computerized scheme and the readers was $69.91 \pm 9.43\%$. Given a seed point, the computational cost for segmentation of a lung nodule ranged from 0.6 to 7.4 seconds with an average 4.6 seconds on a desktop PC computer (AMD Athlon 64 × 2 Dual 2.11 GHz and 2 GB of RAM), depending on the size of the nodule. To visually demonstrate the performance of the pulmonary nodule segmentation schemes, several typical examples are presented in Fig. 8, including the segmentation of juxtapleural nodules with various shapes (Figs. 8a and 8b), the segmentation of nodules attached to other soft tissues, such as vessels and fissures (Figs. 8c and 8d), and the segmentation of nodules with spike shapes (Fig. 8e).

4 Discussion

In this study, we developed a shape “break-and-repair” strategy and used it to automatically segment anatomical structures depicted on CT images, such as lung volume and pulmonary nodules. Its performance was assessed qualitatively by testing against 230 clinical CT examinations collected from different sources, and the results demonstrated the feasibility, robustness, and generality of this proposed scheme. As compared with other previously developed schemes, this proposed shape analysis strategy works on a three-dimensional triangle mesh surface instead of CT images and its most distinct advantage is the capability of approaching medical image segmentations in a unified framework. For example, the problems involved in the lung volume segmentation, including the pathological regions such as juxtapleural nodules (Fig. 7a) and interstitial diseases (Fig. 1), right and left lung attachment (Fig. 7b), and potential false positive inclusions such as trachea or livers, are solved in a single pass; and the typical examples in Fig. 8 show that various pulmonary nodules are segmented successfully without dealing with each type of nodules separately. In addition, as the two segmentation examples presented in this study demonstrate, this strategy can be used potentially for other organ segmentations depicted on three-dimensional images as well as two-dimensional images and the implementation is easy and intuitive.

To evaluate the performance of this shape analysis scheme, we performed a qualitative assessment instead of a subjective rating because there are usually larger inter- and intrareader variabilities and objective qualitative assessment is more reliable given the availability of the reference standards provided by experts. As the experimental results in Table 1 show, the maximum error of the pulmonary nodule segmentation is smaller than that of the lung volume segmentation, while the RMS error of the pulmonary nodule segmentation is obviously larger than that of the lung volume segmentation. The primary reason for this phenomenon may be explained as follows: The lung boundaries in the reference standard were first marked by a computerized scheme and then modified by radiologists. Due to the large size of a lung volume, the “problematic” regions (e.g., juxtapleural nodule or other diseases) are relatively small in size as compared to the whole human lungs, leading to a small portion of modification from radiologists. In contrast, the size of a pulmonary nodule is relatively small with a size of 3.0–30.0 mm and the outlines of pulmonary nodules in the reference standard were completely marked by radiologists in a manual manner. Hence, small perturbations in the outlines of a lung nodule may result in an obvious difference in volume overlapping calculations as well as distance errors.

We recognize that the evaluation in this study is still preliminary, especially for clinical applications. For example, the assessment of this scheme in human lung segmentation primarily focuses on the most common problems as summarized by Sluimer et al. [3] and lacks a comprehensive validation using examinations with severe diseases (e.g., severe interstitial diseases, fibrosis, scarring, and atelectasis). In this study, our primary focus is on methodology and it is out of our capability at this stage to collect a large data set with various diseases and anatomical variability and test the performance of this scheme against this data set. In addition, due to the lack of using a common “reference standard,” it is very difficult to have a direct comparison with other approaches in this study. Indirect comparisons with other approaches indicated that our scheme had a relatively higher performance level. As for the human lung segmentation, the RMS error of Hu et al.’s scheme [2] when comparing with a reference standard in lung boundary was 0.54 mm, while the RMS error of our scheme was 0.15 ± 0.092 mm. As for the pulmonary nodule segmentation, the schemes developed by Way et al. [25] and Wang et al. [20] achieved an average overlapping ratio of 51 and 64 percent in volume, respectively, when comparing the nodule outlines marked, respectively, by the computer scheme and a radiologist, while our scheme has an average overlapping ratio of 70 percent. In efficiency, the average computational cost of Wang et al.’s segmentation method [20] was 13 seconds for a nodule, while it only took an average time of 4.6 seconds to segment a nodule.

Finally, we note that the proposed shape analysis method is not a fixed procedure for any segmentation applications but rather a strategy. As the two segmentation examples in this study demonstrate, specific analysis in each stage may change accordingly depending on the segmentation problem, but the basic steps involved in this strategy remain the same, following a “break-and-repair” procedure. Meanwhile, we recognize that proposed algorithm still needs further improvement. As the examples in Fig. 9 demonstrate, the shape interpolation based on implicit surface fitting will miss local sharp features of lung regions. If a small juxta-pleural nodule is coincidentally located at such “sharp” regions, it may be missed in the segmented lung volume. This limitation contributes to the maximum errors and majority of the undersegmentation in the evaluation of lung volume segmentation (Table 1). The reason behind this issue is that the regions with high curvatures are deleted and then estimated smoothly using shape interpolation in order to minimize the energy. It is difficult to overcome this limitation or dilemma because the smooth interpolation property of implicit surface function will definitely lead to the missing of very details with high curvatures. However, as the examples in Fig. 8 show, if the local important details of anatomical structures (e.g., the spike regions of a nodule) are preserved using a proper removal procedure, the segmentation errors caused by this dilemma will be alleviated largely. Hence, designing a flexible “break” procedure that identifies and removes the problematic regions plays an important role in the proposed segmentation strategy.

5 Conclusion

We presented a shape “break-and-repair” strategy for medical image segmentation and applied it to the segmentation of human lung and pulmonary nodules in this study. In this approach, the regions that may cause any problems in segmentation are removed and then estimated using implicit surface fitting based on RBFs. Its most important characteristic is the capability of segmenting anatomical structures depicted on medical images in a unified framework within a single pass. The preliminary assessment results are encouraging and demonstrate the feasibility, generality, and robustness of this strategy in segmentation.

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References

1. Armato SG III, Giger MI, Moran CJ, Blackburn JT, Doi K, MacMabon H. Computerized Detection of Pulmonary Nodules on CT Scans. *Radiographics*. 1999; 19:1303–1311. [PubMed: 10489181]
2. Hu S, Hoffman EA, Reinhardt JM. Automatic Lung Segmentation for Accurate Quantitation of Volumetric X-Ray CT Images. *IEEE Trans Medical Imaging*. June; 2001 20(6):490–498.
3. Sluimer I, Schilham A, Prokop M, van Ginneken B. Computer Analysis of Computed Tomography Scans of the Pulmonary: A Survey. *IEEE Trans Medical Imaging*. Apr; 2006 25(4):385–405.
4. Bartz D, Mayer D, Fischer J, Ley S, del Rio A, Thust S, Heussel C, Kauczor H, Straßer W. Hybrid Segmentation and Exploration of The Human Lungs. *Proc IEEE Visualization Conf*. 2003:177–184.
5. Garnavi R, Baraani-Dastjerdi A, Moghaddam HA, Giti M, Rad AA. A New Segmentation of Lung HRCT Images. *Proc Digital Image Computing on Techniques and Applications*. 2005:52–59.
6. Ali, AM.; Farag, AA. *Lecture Notes in Computer Science*. Vol. 5358. Springer; 2008. Automatic Lung Segmentation of Volumetric Low-Dose CT Scans Using Graph Cuts; p. 258–267.
7. Kim, HS.; Yoon, H.; Trung, KN.; Lee, GS. Automatic Lung Segmentation in CT Images Using Anisotropic Diffusion and Morphology Operation. *Proc. Seventh IEEE Int'l Conf. Computer and Information Technology*; 2007. p. 557–561.
8. Prasad MN, Brown MS, Ahmad S, Abtin F, Allen J, da Costa I, Kim HJ, McNitt-Gray MF, Goldin JG, Warfield SK. Automatic Segmentation of Lung Parenchyma in the Presence of Diseases Based on Curvature of Ribs. *Academic Radiology*. 2008; 15(9):1173–80. [PubMed: 18692759]
9. Lee Y, Hara T, Fujita H, Itoh S, Ishigaki T. Automated Detection of Pulmonary Nodules in Helical CT Images Based on an Improved Template-Matching Technique. *IEEE Trans Medical Imaging*. July; 2001 20(7):595–604.
10. Rubin GD, Lyo J, Paik DS, Sherbondy A, Chow L, Leung AN, Mindelzun R, Zinck SE, Naidich DP, Napel S. Pulmonary Nodules in MDCT Scans: Impact of Computer-Aided Detection. *Radiology*. 2005; 235:274–283. [PubMed: 15703314]
11. Zhang L, Hoffman EA, Reinhardt JM. Atlas-Driven Pulmonary Lobe Segmentation in Volumetric X-Ray CT Images. *IEEE Trans Medical Imaging*. Jan; 2006 25(1):1–16.
12. Wang J, Betke M, Ko JP. Pulmonary Fissure Segmentation on CT. *Medical Image Analysis*. 2006; 10:530–547. [PubMed: 16807062]
13. Wang J, Li F, Li Q. Automated Segmentation of Lungs with Severe Interstitial Lung Disease in CT. *Medical Physics*. 2009; 36(10):4952–4599.
14. Park W, Hoffman E, Sonka M. Segmentation of Intrathoracic Airway Trees: A Fuzzy Logic Approach. *IEEE Trans Medical Imaging*. Aug; 1998 17(4):489–497.
15. Masutani, Y. RBF-Based Representation of Volumetric Data: Application in Visualization and Segmentation. *Proc. Medical Image Computing and Computer-Assisted Intervention (MICCAI '02)*; 2002. p. 300–307.
16. Am Cancer Soc. 2009. Cancer Facts and Figures 2009.
17. Reeves A, Chan A, Yankelevitz D, Henschke C, Kressler B, Kostis W. On Measuring the Change in Size of Pulmonary Nodules. *IEEE Trans Medical Imaging*. Apr; 2006 25(4):435–450.
18. Petkovska I, Brown MS, Goldin JG, Kim HJ, McNitt-Gray MF, Abtin FG, Ghurabi RJ, Aberle DR. The Effect of Lung Volume on Nodule Size on CT. *Academic Radiology*. 2007; 14(4):476–485. [PubMed: 17368218]
19. Kawata Y, Niki N, Ohmatsu H, Eguchi K, Moriyama N. Shape Analysis of Pulmonary Nodules Based on Thin Section CT Images. *Proc SPIE*. 1997:964–974.

20. Wang J, Engelmann R, Li Q. Segmentation of Pulmonary Nodules in Three-Dimensional CT Images by Use of a Spiral-Scanning Technique. *Medical Physics*. 2007; 34(12):4678–4689. [PubMed: 18196795]
21. Diciotti S, Picozzi G, Falchini M, Mascalchi M, Villari N, Valli G. 3-D Segmentation Algorithm of Small Lung Nodules in Spiral CT Image. *IEEE Trans Information Technology in Biomedicine*. Jan; 2008 12(1):7–19.
22. Mullally W, Betke M, Wang J, Ko JP. Segmentation of Nodules on Chest Computed Tomography for Growth Assessment. *Medical Physics*. 2004; 31(4):839–848. [PubMed: 15125002]
23. Kostis WJ, Reeves AP, Yankelevitz DF, Henschke CI. Three-Dimensional Segmentation and Growth-Rate Estimation of Small Pulmonary Nodules in Helical CT Images. *IEEE Trans Medical Imaging*. Oct; 2003 22(10):1259–1274.
24. Kuhnigk JM, Dicken V, Bornemann L, Bakai A, Wormanns D, Krass S, Peitgen HO. Morphological Segmentation and Partial Volume Analysis for Volumetry of Solid Pulmonary Lesions in Thoracic CT Scans. *IEEE Trans Medical Imaging*. Apr; 2006 25(4):417–434.
25. Way TW, Hadjiiski LM, Sahiner B, Chan HP, Cascade PN, Kazerooni EA, Bogot N, Zhou C. Computer-Aided Diagnosis of Pulmonary Nodules on CT Scans: Segmentation and Classification Using 3D Active Contour. *Medical Physics*. 2006; 33(7):2323–2337. [PubMed: 16898434]
26. Lorensen WE, Cline HE. Marching Cubes: A High Resolution Three-Dimensional Surface Construction Algorithm. *Computer Graphics*. 1987; 21(4):163–169.
27. Meyer, M.; Desbrun, M.; Schroder, P.; Barr, AH. Discrete Differential Geometry Operators for Triangulated 2-Manifolds. In: Hege, HC.; Polthier, K., editors. *Visualization and Mathematics III*. Springer-Verlag; 2003. p. 35-57.
28. Rusinkiewicz, S. Estimating Curvatures and Their Derivatives on Triangle Meshes. *Proc. 3D Data Processing, Visualization, and Transmission (3DPVT)*; 2004. p. 486-493.
29. Goldfeather J, Interrante V. A Novel Cubic-Order Algorithm for Approximating Principal Direction Vectors. *ACM Trans Graphics*. 2004; 23(1):45–63.
30. Chen X, Schmitt F. Intrinsic Surface Properties from Surface Triangulation. *Proc European Conf Computer Vision*. 1992:739–743.
31. Cipolla, R.; Giblin, PJ. *Visual Motion of Curves and Surfaces*. Cambridge Univ. Press; 2000.
32. Field DA. Laplacian Smoothing and Delaunay Triangulations. *Comm in Applied Numerical Methods*. 1988; 4:709–712.
33. Dunchon, J. Splines Minimizing Rotation-Invariant Semi-Norms in Sobolev Spaces. In: Dolb, A.; Eckmann, B., editors. *Constructive Theory of Functions of Several Variables*. Springer-Verlag; 1977. p. 85-100.
34. Carr, JC.; Beatson, RK.; Cherrie, JB.; Mitchell, TJ.; Fright, WR.; McCallum, BC.; Evans, TR. Reconstruction and Representation of 3D Objects with Radial Basis Functions. *Proc. ACM SIGGRAPH '01*; 2001. p. 67-76.
35. Turk, G.; O'Brien, JF. Shape Transformation Using Variational Implicit Functions. *Proc. ACM SIGGRAPH '99*; 1999. p. 335-342.
36. Osada R, Funkhouser T, Chazelle B, Dobkin D. Shape Distribution. *ACM Trans Graphics*. 2002; 21(4):807–832.
37. Pu J, Ramani K. On Visual Similarity Based 2D Drawing Retrieval. *Computer Aided Design*. 2006; 38(3):249–259.
38. Garland, M.; Heckbert, PS. Surface Simplification Using Quadric Error Metrics. *Proc. ACM SIGGRAPH '97*; 1997. p. 209-216.
39. Magid E, Soldea O, Rivlin E. A Comparison of Gaussian and Mean Curvature Estimation Methods on Triangle Meshes of Range Image Data. *Computer Vision and Image Understanding*. 2007; 107(3):139–159.
40. Cantzler, H.; Fisher, RB. Comparison of HK and SC Curvature Description Methods. *Proc. Third Int'l Conf. 3-D Digital Imaging and Modeling (3DIM '01)*; 2001. p. 285-291.
41. Koenderink J, van Doorn A. Surface Shape and Curvature Scales. *Image and Vision Computing*. 1992; 10(8):557–565.

42. Pu J, Zheng B, Leader JK, Gur D. An Automated CT Based Lung Nodule Detection Scheme Using Geometric Analysis of Signed Distance Field. *Medical Physics*. 2008; 35(8):3451–3461.
43. Pu J, Roos J, Yi CA, Napel S, Rubin GD, Paik DS. Adaptive Border Marching Algorithm: Automatic Lung Segmentation on Chest CT Images. *Computerized Medical Imaging and Graphics*. 2008; 32(6):452–462. [PubMed: 18515044]
44. McNitt-Gray MF, et al. The Lung Image Database Consortium (LIDC) Data Collection Process for Nodule Detection and Annotation. *Academic Radiology*. 2007; 14(12):1464–1474. [PubMed: 18035276]

Biographies

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Fig. 1.

A lung model and its different versions: (a) The model obtained by the Marching Cube Algorithm. (b) The simplified version of (a). (c) The transparent version of (b) where the front faces of (b) are culled and the vessels are displayed. (d) and (e) The smoothed version viewed from different perspectives. The top row shows the local enlargement of the junction regions between the right and left lungs as indicated by the bounding boxes in the bottom row. The arrows indicate pathological regions.

Fig. 2.

Color-coded visualization of the maximum curvatures of the lung shape in Fig. 1: (a) and (b) Same lung model viewed from different perspectives without transparency, and (c) and (d) The transparent versions viewed from different perspectives. The bar on the top indicates the way of color coding.

Fig. 3.

The lung models after regions with high curvatures are removed: (a), (b), and (d) are the same model examined from different perspectives, and (c) the transparent version.

Fig. 4.

The top row shows the identified right lung ((a)–(c)) and left lung ((d)–(f)). The bottom row shows the lungs after implicit surface fitting operation.

Fig. 5.

Nodule segmentation using the shape “break-and-repair” strategy. The top and bottom rows in (b) correspond to the nodules A and B enclosed by the boxes in a CT examination (a). In (b), the first column shows the three-dimensional mesh models of the depicted nodules and their surrounding structures; the second column the identified partial surfaces of the nodules after principal curvature analysis; the third column the estimated surfaces of the indicated nodules; and the forth column the outlines of the estimated nodule surfaces.

Fig. 6. The “visibility” scheme (a) where intersection points p_1 , p_2 , and p_3 between the rays r_1 , r_2 , and r_3 and the object boundary are classified as “visible” while p_2 is “invisible,” and the associated Koenderink’s shape classifications (b).

Fig. 7.

Examples of human lung segmentation: (a) An example where there is a juxtapleural nodule, (b) An example where the right and left lungs are attached to each other, and (c) An example where the other organs (e.g., spleen and liver) are located in lung regions if examining the two-dimensional CT slices. The top row shows the original images, the middle row shows the thresholded images where the threshold was obtained adaptively (i.e., -587 HU), and the bottom row shows the segmentation results where the right and left lungs are coded in colors.

Fig. 8.

Examples of pulmonary nodule segmentation: (a) and (b) The segmentation results of two juxtapleural nodules. (c) The segmentation result of a nodule attached to vessels with similar intensity. (d) The segmentation result of a nodule attached to both vessels and fissures (the fissures appear in a linear shape). (e) and (f) The segmentation results of two nodules with relative complex shapes and connected with vessels. The top row indicates the original CT images, the mid row indicates the outlines of the nodule segmentation results in red, and the bottom row indicates the three-dimensional surfaces of the segmented nodules.

Fig. 9.

The local enlargement of the regions (a)–(c) indicated by the boxes in Figs. 7a, 7b, and 7c.

TABLE 1

The Discrepancies between the Results by the Computerized Scheme and the Reference Standard

	RMS Error (mm)	Maximum error (mm)	Overlapping (%)
lung segmentation	0.15±0.092	7.82±3.37	95.1±2.0
nodule segmentation	1.08±0.45	2.69±1.28	69.91±9.43