Automatic axis generation for virtual bronchoscopic assessment of major airway obstructions

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Abstract

Virtual bronchoscopy (VB) has emerged as a paradigm for more effective 3D CT image evaluation. Systematic evaluation of a 3D CT chest image using VB techniques, however, requires precomputed guidance data. This guidance data takes the form of central axes, or centerlines, through the major airways. We propose an axes-generation algorithm for VB assessment of 3D CT chest images. For a typical high-resolution 3D CT chest image, the algorithm produces a series of airway-tree axes, corresponding airway cross-sectional area measurements, and a segmented airway tree in a few minutes on a standard PC. Results for phantom and human airway-obstruction cases demonstrate the efficacy of the algorithm. Also, the algorithm is demonstrated in the context of VB-based 3D CT assessment. © 2001 Elsevier Science Ltd. All rights reserved.

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1. Introduction

Major airway obstruction is a common problem arising from lung cancer, benign processes, and other tumors that commonly metastasize the airways. Impending obstruction to the trachea is life threatening, while obstruction to the left or right main bronchi are associated with significant morbidity. These patients need adequate evaluation prior to an intervention such as laser resection, balloon broncho-plasty, stent insertion, cryotherapy or brachytherapy. Three-dimensional (3D) computed-tomography (CT) pulmonary images are commonly used for such evaluation [1]. The evaluation of these images is generally done manually with film records [2]. A film record shows a series of transverse-oriented two-dimensional (2D) slice images. The physician performs 3D mental reconstruction of anatomical structures depicted in the film to evaluate the case. While often suitable for the radiologist, this form of evaluation is typically inadequate for the bronchoscopist or surgeon, who need precise 3D ‘road maps’ to the surgical sites of interest [3].

Recently, virtual bronchoscopy (VB) has emerged as a paradigm for more effective 3D CT image evaluation [4–12]. VB is a sub-branch of the new field often referred to as virtual endoscopy [13,14]. When related to the chest, virtual endoscopy involves the use of computer-based image-processing and graphical techniques to observe structures inside the ‘virtual chest environment’, as defined by a 3D CT pulmonary image. Since all evaluation is computer-based, the user can navigate through the 3D chest environment with great flexibility.

3D CT images used in tandem with VB techniques can help the physician evaluate patients suffering from major airway obstruction. Systematic evaluation of a 3D CT chest image using VB techniques, however, requires precomputed guidance data [8]. This guidance data generally takes the form of central axes, or centerlines, through the major airways. Such axes not only give a means for evaluating a 3D CT chest image, but also potentially provide road maps for subsequent bronchoscopic procedures (the bronchoscope passes through the airways!).

We propose a semi-automatic axes-generation algorithm for VB assessment of 3D CT chest images. The proposed algorithm can generate a series of airway-tree axes for a typical high-resolution 3D CT chest scan in a few minutes on a standard PC. It is integrated into a PC-based system for VB CT assessment and follow-on bronchoscopic guidance.
2. Problem overview

Mathematical notation and problem constraints are defined within the context of finding the central axes of the major airways depicted in a 3D CT pulmonary image. We assume that V consists of a contiguous series of 16-bit slices spaced \( \Delta z \) apart. The transverse-plane sample spacings are \( \Delta x \) and \( \Delta y \). A voxel is denoted by \((x, y, z)\) and voxel \((x, y, z)\)'s intensity value is given by \(V(x, y, z)\). The airway tree consists of a complex, branching, connected set of dark airways surrounded by relatively bright airway walls. Limited spatial resolution, noise, partial volume effects, and image-reconstruction artifacts complicate the extraction of the airway-tree axial structure.

We assume that an algorithm devised for extracting the major airways and associated axes (also called paths) abides by the following requirements: (a) paths evolve slowly along their extent, thereby providing a smooth trajectory for navigation; (b) paths for a 'complete' tree are generated (i.e., smooth paths through multiple airways are generated in one pass); (c) the extracted airways conform to the measurable morphology and gray-scale characteristics of a typical 3D CT pulmonary image; (d) the algorithm preserves the homotopy of the original structure; (e) paths approximate the medial (central) axes of the branches in the structure; (f) airway cross-sections change little from one point along a path to the next.

Previously proposed axes-generation techniques have employed either manual image interaction or automatic processing. Manual approaches have a user either fully trace a path, do significant manual segmentation, or specify a priori sites (key frames) that are later interpolated into a complete path [4,13,17]. Unfortunately, a 3D image’s complexity and dimensionality make such procedures prohibitive for practical use, especially for images generated by new multidetector helical CT scanners [18]. Automated approaches have employed: (1) segmentation followed by 3D skeletonization [8,12,19–23]; (2) morphological operations [24–26]; (3) active contour modeling [27]; (4) tubular structure analysis, using differential geometry [23,28–33]. These techniques either lead to imprecise or missing axes (particularly when pathologies and noise may be present), require inordinate processing time, or are not well-suited to our specific problem of defining precise smooth central axes suitable for navigation through a complex branching-tree structure. For example, many techniques only give one path [21,22,27,29,31]. Many techniques do not give smooth navigation axes, but instead give coarser digitized axes [8,19,20,23–25,32]. A few proposed techniques for tracking vessels in coronary angiograms considered a problem similar to ours [26,28]. These methods used tree continuity assumptions and an adaptive tracking filter matched to the expected gray level profile of a vessel cross-section. These methods, while limited to 2D projection images of 3D structures, motivate our algorithm for true 3D airway analysis.

Our algorithm follows a two-stage approach. The first stage computes a Discrete Model that consists of a sparsely spaced set of data corresponding to the major airway axes. The second stage then uses the Discrete Model to define a smooth set of airway axes, a segmented airway tree, and other measurement data; these data constitute the Generalized Cylinder (GC) Model [34–37]. Fig. 1 schematically illustrates these two model components.

The basic flow of the two-stage algorithm is as follows. The user first specifies a starting point of interest for the airway tree, generally in the proximal end of the trachea. Then, to perform the Stage-1 calculation of the Discrete Model, an adaptive 3D searching technique steps through
the 3D image, building up a sparsely sampled set of central axes for the major airways. Stage 2 then applies a cubic-spline analysis and contour-finding procedure to the Discrete Model data to give a generalized cylinder representation for each airway central axis; this gives the GC Model. Section 3 gives a complete description of the two-stage algorithm and the model components.

3. Axes-definition algorithm

Section 3.1 defines many of the analytical quantities constituting the Discrete Model and GC Model. Section 3.2 summarizes the two-stage algorithm. Finally, Section 3.3 and Section 3.4 gives further details on key algorithm steps.

3.1. Two-stage model definition

The Discrete Model consists of a sparse set of viewing-sites, branch, and path data defining the central axes of the major airways. An individual point along an axis will be referred to as a viewing site. A set of contiguous viewing sites between an axis end point and branch point or between two branch points will be called a branch. A branch point is a viewing site where a single branch divides into two or more separate branches. One complete axis, or path, consists of a subset of connected branches, where the first and last path branches terminate the path with endpoints. More specifically, the Discrete Model consists of L viewing sites

\[ w_l, \quad l = 0, 1, \ldots, L - 1. \]  

(1)

M branches

\[ b_m = \{ w_{m,0}, w_{m,1}, \ldots, w_{m,\text{END}_m} \}, \quad m = 0, 1, \ldots, M - 1 \]  

(2)

and N paths

\[ p_n = \{ b_{n,0}, b_{n,1}, \ldots, b_{n,\text{END}_n} \}, \quad n = 0, 1, \ldots, N - 1, \]  

(3)

where \( L \geq 2, M \geq 1, \) and \( N \geq 1 \) (Technically, a tree can consist of only one branch and one path; i.e. \( M = N = 1 \). In this case, a branch can be terminated by two end points.). Each viewing site \( w_l \) belongs to only one branch unless it is a branch point. The special viewing site \( w_0 \) referred to as the root site, is picked manually, as discussed in Section 3.3. The root site \( w_0 \) starts the tree. Hence, it always starts the first branch \( b_0 \) and first path \( p_0 \). Per the definition (2), each branch \( b_m \) consists of a set of contiguous viewing sites from set (1). For the 3D chest problem, we assume that branch \( b_0 \) corresponds to the trachea and terminates at the main carina. Branch \( b_0 \) is a member of all paths. Per (3), a subset of connected branches starting from \( b_0 \) and terminating at a branch \( b_{n,\text{END}} \), that has an endpoint form a path \( p_n \), where the constituent branches are from branch set (2). In general, branches \( b_m \) can belong to many paths.

For Discrete Model shown in Fig. 1, the complete tree is represented as

\[ b_0 = \{ w_0, w_1, w_2 \}, \quad b_1 = \{ w_2, w_3 \}, \]  

\[ b_2 = \{ w_2, w_4, w_7 \}, \quad b_3 = \{ w_5, w_5 \}, \]  

\[ b_4 = \{ w_3, w_6 \}, \quad p_0 = \{ b_0, b_1, b_3 \}, \]  

\[ p_1 = \{ b_0, b_1, b_3 \}, \quad p_2 = \{ b_0, b_2 \}. \]  

The two viewing sites \( w_2 \) and \( w_3 \) are branch points.

A viewing site is more completely expressed as \( w_i = \{ s_i, d_i \} \), where

\[ s_i = [x, y, z]^T, \quad d_i = [d_{ix}, d_{iy}, d_{iz}]^T. \]  

(4)

\( s_i \) is the 3D location of \( w_i \); \( d_i \) is a 3D unit vector pointing in the viewing direction for \( w_i \) (\( ||d_i|| = 1 \)); \( x_i, y_i \), and \( z_i \) are the \( x \), \( y \), and \( z \) components of \( s_i \); and \( d_{ix}, d_{iy} \), and \( d_{iz} \) are the respective \( x \), \( y \), and \( z \) components of \( d_i \). At each viewing site \( w_i \) the viewing direction \( d_i \) defines a local coordinate frame such that the local \( z \)-axis is aligned with the axis of the tree at \( s_i \). As we will clarify in Section 3.3, adjacent contiguous viewing sites are not necessarily equally spaced.

The Discrete Model captures essential top-level topological structure of the airway tree in an efficient data structure. To limit redundancy, viewing sites are shared among branches and branches are shared among paths. But the Discrete Model does not contain detailed smooth paths and tree structure. For VB-based navigation through a 3D image, smooth paths are necessary. To meet this requirement, we propose the Generalized Cylinder Model, which builds upon the concept of a generalized cylinder (GC) [34–37].

A generalized cylinder is a generalization of a right cylinder. The axis of a GC is not confined to be a straight line. Instead, it can be an arbitrary open curved trajectory. Also, instead of a circular 2D cross-section, the cross-section of a GC can be an arbitrary closed contour subject to certain continuity constraints. GCs are particularly attractive, since their compact representation permit efficient computer implementation. The GC Model contains detailed structural information for each path. Each Discrete-Model path \( p_n \) is transformed into a GC that is composed of a spine (or primary axis) \( p_n(u) \) and a contour function \( c_n(u) \). With the spine and contour functions, the surface \( s_n(u) \) of the GC can be obtained. Fig. 1 depicts an example GC. Cubic B-splines are used to represent the spine and contour functions. For VB navigation, a spine corresponds to a desired smooth navigation path through an airway and the contour function defines the airway wall’s endoluminal surface about the spine.

Complete details on the B-spline functions representing the spines and contour functions are given in Section 3.4 and Ref. [38]. Below, we summarize the quantities defining these functions. The spine \( p_n(u) \) is a continuous, open,
parameterized curve in $\mathbb{R}^3$ given by

$$\mathbf{p}_n(u) = [x_n(u) \ y_n(u) \ z_n(u)], \quad 0 \leq u \leq u_n^{\max},$$

$$n = 0, 1, \ldots, N - 1,$$  \hspace{1cm} (5)

where $u$ is a distance parameter as one moves along the path from beginning to end, and $x_n(u), y_n(u),$ and $z_n(u)$ are B-spline functionals that determine $x, y,$ and $z$ position in 3D image space. Note that each point of the spine (5) also has a direction vector associated with it

$$\mathbf{d}_n(u) = [d_{x_n}(u) \ d_{y_n}(u) \ d_{z_n}(u)],$$

as in the case of the Discrete Model. The direction $\mathbf{d}_n(u)$ is not necessary for defining the spine per se, but it is necessary for virtual-endoscopic navigation and exploration as done for the examples of Section 4.3. As Section 3.3 describes, the viewing sites comprising Discrete-Model path $\mathbf{p}_n$ serve as interpolation points, or "knot points," for the B-spline $\mathbf{p}_n(u)$. The B-spline representation for the spine permits equispaced sampling (per $u$ or arc length) along the path. At each point $u$ along the spine $\mathbf{p}_n(u)$, the tangent to the spine, $\mathbf{dp}_n(u)/du$, defines the $z$-axis of a local coordinate frame. In this local coordinate frame, the contour function

$$\mathbf{c}_n(t, u) = [x_n(t, u) \ y_n(t, u) \ 0], \quad 0 \leq t \leq 1$$

represents the generalized cylinder's orthogonal cross-section, where $t$ is the distance parameter as one moves along the closed contour from beginning to end, $u$ is the position along the $n$th GC spine $\mathbf{p}_n(u)$, and $x_n(t, u)$ and $y_n(t, u)$ are the B-spline functionals that determine the $x$ and $y$ position in the 2D plane with respect to the distance parameter $t$. The contour function is a closed, parameterized B-Spline curve in the local coordinate frame constrained to the 2D plane orthogonal to the path tangent at $u$. Hence, the $z$ component of $\mathbf{c}_n(t, u) = 0$. Finally, a point on the surface of the $n$th GC is given by

$$\mathbf{s}_n(t, u) = \mathbf{p}_n(u) + \mathbf{c}_n(t, u)\mathbf{R}_n(u),$$

where $\mathbf{R}_n(u)$ is a $3 \times 3$ rotation matrix that rotates the global 3D image $z$-axis to the $z$-axis of the GC's local coordinate frame at point $\mathbf{p}_n(u)$; i.e. this rotation is given by the relationship between the global $z$-axis and $\mathbf{dp}_n(u)/du$.

3.2. Two-stage algorithm summary

The two-stage algorithm is summarized below. Complete details on the steps below are discussed fully in Sections 3.3 and 3.4 to follow.

Stage 1: discrete-model calculation

1. Starting with a given 3D 16-bit chest image $I$, the user specifies the root site $\mathbf{w}_0 = [s_0, \mathbf{d}_0]$, somewhere near the proximal end of the trachea.
2. Use $\mathbf{w}_0$ to begin a queue of pending viewing sites. Start branch $\mathbf{b}_0$ with $\mathbf{w}_0$ and start path $\mathbf{p}_0$ with branch $\mathbf{b}_0$.
3. Pick a viewing site $\mathbf{w}_i$ from the queue.
4. Perform a local 2D oblique-slice analysis at $\mathbf{w}_i$ to estimate the airway structure's cross-section. If the analysis passes a set of stopping criteria, then $\mathbf{w}_i$ corresponds to an endpoint; this terminates the current branch and path-go to step 6. Otherwise, use the centroid of the extracted cross-section as the refined viewing-site location $\mathbf{s}_i$ for $\mathbf{w}_i$.
5. Perform a 3D spherical search about the refined viewing site $\mathbf{w}_i$ to locate new viewing sites to analyze. If new viewing sites are found, then add them to the queue.
6. If either the cross-sectional analysis or spherical search reveals that $\mathbf{w}_i$ corresponds to an endpoint or branch point, then appropriately update the active branch and path information.
7. If the queue is not empty, return to step 3. Otherwise, the recorded viewing site, branch, and path information defines the final Discrete Model, per (1–3).

Stage 2: generalized-cylinder model calculation

1. For each path $\mathbf{p}_n$ in the Discrete Model data, $n = 0, 1, \ldots, N - 1$, compute the spine and contour functions of the associated generalized cylinder:
   (a) Perform a B-spline analysis to compute the spine $\mathbf{p}_n(u)$.
   (b) At equally spaced samples $\hat{u} = 0, u_1, u_2, \ldots, u_n^{\max}$ along the spine, compute the contour function $\mathbf{c}_n(t, \hat{u})$ using a B-spline analysis. Also, compute the GC's cross-sectional area at $\hat{u}$.
2. Construct a segmented airway-tree image by merging the surface functions (8) for all GCs in the GC Model. Also, compute endoluminal cross-sectional area measurements of the tree.

The final outputs are the smooth paths $\mathbf{p}_n(u)$, $n = 0, 1, \ldots, N - 1$, cross-sectional area measurements of the airway tree along the paths, the basic viewing-site/branch/path connectivity relationships per (1–3), and the segmented airway tree.

3.3. Stage-1 details

This section gives complete detail for the Stage-1 Discrete Model calculation. The step numbers below refer to the steps outlined in Section 3.2.

Step 1: specify root site
The root site $\mathbf{w}_0$ is specified manually by examining the 3D image data in an appropriate image viewer. We have used virtual-endoscopy systems built by our group for PCs and Sun workstations for this purpose [8,15]. This site is easily picked by locating any point near the proximal end ("top") of the trachea. This point need not be precisely located in the center of a tracheal cross-section, since the two-stage algorithm 'straightens out' the trajectory of travel.

Step 4: 2D oblique-slice analysis
First, a 2D slice of data that is centered about $\mathbf{s}_i$ and orthogonal to $\mathbf{d}_i$ is sampled from the given 3D image $I$. This is depicted in Fig. 2. Next, a set of equally spaced
rays perpendicular to $d_l$ are cast radially outward from $s_l$ on this slice. Points encountered by a ray are computed by using 3D nearest-neighbor interpolation on the original 3D image. In our results, we cast 16 rays. If a ray strikes an image point at distance $r_b$ having image value $f(r_b)$ that is greater than a prescribed threshold, then this marks a point on the airway lumen’s boundary; see Fig. 3. The complete set of boundary contour points provide an initial estimate of the airway lumen’s boundary at viewing site $w_l$. In a typical CT chest image ‘air’ values are near $-1000$ HU versus air + $100$ HU (or greater) for an airway wall. Hence, picking a threshold tends to be straightforward. We have also used a gradient-based technique and a local half-maximum approach to find where a ray strikes the airway lumen, but have not observed these methods to offer appreciable differences in the path calculation [17,38].

Fig. 3. Contour boundary finding. Rays are cast out from $s_l$ on the oblique slice. When a ray strikes a point $r_b$ that has a gray-level value $f(r_b)$ above a preset threshold, then this point specifies an endoluminal boundary point. For 3D CT data, the air appears black (near $-1000$ HU) and the brighter wall is generally above $100$ HU. (a) 2D oblique cross section sampled at $s_l$. (b) Gray-scale image profile $f(r)$ along a ray.
Two stopping criteria determine whether a particular viewing site is an endpoint: if the computed airway contour (a) has a radius below a prescribed minimum or (b) has a shape that is too far from circular (measured by computing the standard deviation of the ray lengths). We set the minimum radius to be 1/2 the coarsest spatial resolution dimension (usually the slice thickness $\Delta z$). We vary the standard deviation parameter depending on the operating conditions. The standard-deviation stopping criteria detects situations where a contour has a sudden break in it and leaks into the parenchyma; this happens when the airway wall becomes very thin or the airway becomes very small. If the viewing site $w_i$ passes either of these stopping criteria, it is deemed to be an endpoint—this terminates the currently active branch and path. Otherwise, the airway is sufficiently large and has a suitable shape. Thus, the analysis of this viewing site continues onto step 5. The centroid of the contour is used as a modified estimate of the viewing site’s location $s_i$. Also, the minimum radius $r_i$ of a circle that fully encloses the contour is calculated.

Step 5: 3D spherical operator search

The goal of this step is to perform a 3D search for airways emanating from the currently active viewing site. This is done by finding where air patches, which correspond to evolving airways, intersect the surface of an appropriately constructed tessellated 3D sphere situated about $s_i$. The intersecting spherical air patches indicate new regions to move to and help define new viewing sites to examine. The discussion below describes the construction and use of the sphere.

The modified viewing-site location $s_i$ and minimum radius $r_i$ from step 4 are used to define a 3D tessellated spherical search operator $S_i$. The radius of this sphere is given by $R_i = r_i + \delta r$, where $\delta r > 0$ is the minimum detectable airway wall thickness. We choose $\delta r$ so that it equals the minimum spatial resolution of the image (typically $\Delta x$ or $\Delta y$). By its construction, the spherical operator $S_i$ will be just large enough to completely contain the cross-sectional contour at $w_i$. At the same time, the sphere is small enough so that all airway branches emanating from $w_i$ can be detected. The resulting sphere is shown by the dashed lines in Fig. 4a. Note that the sphere is constructed to cover approximately a spherical volume in space. This gives isotropic search coverage to all directions. But the actual sampled form of the sphere is typically an ellipsoid, since the slice thickness $\Delta z$ tends to be larger than the transverse-plane sample spacings, $\Delta x$ and $\Delta y$.

In order to approximate a spherical shell, we use a tessellated spheroid generation technique developed by Paeth [39]. This results in a unit spheroid consisting of a list of vertices and normal vectors that form small triangles to approximate the surface of a sphere. Fig. 5a depicts the top view of a spheroid of depth 3 with vertices numbered counterclockwise out from the center. The depth corresponds to the factor of angular division within one octant of the sphere. The radius of the spheroid can be adjusted by scaling the vertex locations. Paeth gives complete detail on this structure [39, p. 179–90].

All airway branches emanating from the volume covered by the spherical operator $S_i$ will form closed ‘air’ patches $C_i$ at the intersections of airway walls and the sphere’s surface. See Fig. 5b. Detecting airway branches, and hence new viewing sites to search, then amounts to finding all connected spherical surface patches that intersect air regions $C_i$. If the 3D image point situated at a sphere vertex $P_i$ is below the acceptable threshold for air (as used for the 2D oblique-slice analysis), then this vertex is deemed to be contained by air patch $C_i$. All connected sphere vertices intersecting $C_i$ are deemed to constitute $C_i$. Rather than the traditional notions of 4- and 6-connectedness of a 2D pixel set, we perform connected-component analysis on the surface of a sphere. For our implemented case of a tessellated approximation to a sphere, we treat the vertices as a grid of points and the line segments connecting them (face...
edges) as the connectivity paths. See Fig. 5c; vertices $P_1$, $P_2$, $P_3$ and $P_4$ are found to be a connected cluster of sphere vertices passing through $C_s$. At least three connected vertices must be found to justify a valid cluster. Given the centroid $c_s$ of a cluster, $c_s$ specifies the location of a new viewing site to search and the vector $(w - c_s)$ specifies this new site’s direction. Note, that neither a viewing site’s location $s_l$ or direction $d_l$ is confined to integer coordinates.

The search is actually done over a hemisphere of directions situated about $s_l$ even though the entire tessellated sphere can be necessary for constructing the surface patches, with the orientation of the hemisphere determined by the current direction $d_l$. The spherical operator’s ‘snug’ construction about $w$ guarantees that all evolving airway branches are detected by the operator.

A new viewing site $w_{t+1}$ is always situated at a distance $R_s$ from $w_t$, as depicted in Fig. 4b; i.e. the search moves forward as far as possible and connected sites are not necessarily equidistant. Fig. 4c illustrates a 2D side view of how the 3D spherical search evolves during the Discrete Model’s construction.

The sphere’s depth is updated for each examined viewing site and is determined as follows. First, we assume that the smallest airway endoluminal structure that can be detected must have a radius $r_{min}$ of at least $1/2$ the slice thickness $\Delta z$. Since $\Delta z$ is generally greater than the in-plane resolutions, $\Delta x$ and $\Delta y$, the worst case is for a horizontally oriented airway in the $x-y$ plane of the scanned image that is visible on only a single slice.

We define $h$ as the distance from the sphere center to the midpoint of a chord connecting two neighboring vertices and $e$ as the maximal deviation of the chord from a true sphere of radius $R_s$ (Fig. 6a). Note that triangle facets tessellating the sphere vary in shape slightly across the sphere’s surface. The worst case is when a given facet is an equilateral triangle with sides of length $b$ (the maximal chord length) and when all three of its vertices are precisely on the inner wall of an airway’s cross-section. If the position of the triangle is translated at all or any of the triangle’s sides are shortened, then one or more vertices must fall outside the airway’s interior and hence result in a missed detection. The sphere’s depth must be large enough to prevent this occurrence. Fig. 6b depicts this situation. Combining the
relationships between $b$, $r_{\text{min}}$, and spheroid radius $R_s$ gives the required depth [38]:

$$\text{Sphere depth} = \frac{\pi}{4} \left( \sin^{-1} \left( \frac{\min(1+\sin \frac{\pi}{6})}{2R_s \cos \frac{\pi}{6}} \right) \right)^{-1}.$$  \hspace{1cm} (9)

This spheroid will then be guaranteed to have a tesselated surface with a fine enough resolution to detect any subsequent branching airway points subject to the minimum allowable size.

Step 6: update branch and path relationships
At the end of the analyses of Steps 4 and 5, the Discrete-Model requires updating. This requires some straightforward book-keeping, briefly highlighted below. Three cases arise as a result of the current viewing site’s analysis:

- If the current viewing site passes the stopping criteria (step 4) or if the spherical search finds no subsequent viewing sites, then $w_i$ is an endpoint: terminate the current branch and path.
- If one new viewing site is found, append it to the current branch.
- If two (or more) viewing sites are found, then $w_i$ corresponds to a branch point. Terminate the current branch and generate new branches for each new viewing site. The first viewing site of each new branch is the current viewing site $w_i$, and the second viewing site is the respective newly found viewing site. The connectivity between the current branch and the new branches is recorded in the Discrete Model.

Also, the currently active path is continued along one of the new branches, while a new path is initiated using the other new viewing site.

3.4. Stage-2 Details
This section gives more detail for the two steps of Stage 2. A generalized cylinder is computed for each Discrete-Model path $p_n$. As stated earlier, the GC requires a spine function $p_n(u)$ and a contour function $c_n(u,t,u)$. Both of these functions are computed using well-known cubic uniform B-splines [40]. Our GC-Model development adapts the efforts of Shani et al. to our 3D tree problem [35].

Step 1(a): spine calculation
The spine $p_n(u)$ of the $n$th GC is derived from $p_n$ and is represented as an open cubic uniform B-spline function. The basic steps of this calculation are as follows: (a) the viewing sites $w_i$ along $p_n$ serve as knot points $s_i$; (b) the knot points $s_i$ are used to compute control points $V_i$; (c) the path’s B-spline representation $p_n(u)$ is made up of a set of piecewise connected span functions $C_i(u)$, which are a function of the control points $V_i$. All essential detail for these calculations appears below.

Consider a Discrete-Model path $p_n$ made up of $P$ viewing sites

$$p_n = \{ w_0 \ w_1 \ w_2 \ w_3 \ w_4 \ w_5 \ w_6 \ w_7 \cdots w_{P-2} \ w_{P-1} \}.$$  \hspace{1cm} (10)

The viewing-site locations of the path, written as a $P$ element vector

$$\mathbf{S} = \{ s_0 \ s_1 \ s_2 \ s_3 \ s_4 \ s_5 \ s_6 \ s_7 \cdots s_{P-2} \ s_{P-1} \}.$$  \hspace{1cm} (11)

serve as knot points or interpolation points for the spine $p_n(u)$ (We drop the subscript $n$ for much of this discussion to simplify notation.). The spine $p_n(u)$ is guaranteed to pass through these points in 3D space. A set of $P+2$ control points $V_i$, $i = 0, 1, ..., P+1$, are derived from the $P$ knot points, where each $V_i$ is a point in 3D space. Each consecutive group of four control points

$$V_i = [V_{i-1} \ V_i \ V_{i+1} \ V_{i+2}]^T, \quad i = 1, 2, ..., P - 1$$  \hspace{1cm} (12)

are used to form a series of $P - 1$ third-order continuous $span$ polynomials $C_i(u)$, where

$$C_i(u) = [u^3 \ u^2 \ u \ 1] [C] V_i,$$  \hspace{1cm} (13)

and the $4 \times 4$ matrix $C$ is given by

$$C = \frac{1}{6} \begin{bmatrix} -1 & 3 & -3 & 1 \\ 3 & -6 & 3 & 0 \\ -3 & 0 & 3 & 0 \\ 1 & 4 & 1 & 0 \end{bmatrix}.$$  \hspace{1cm} (14)

So, for $0 \leq u < 1$

$$p_n(u) = C_i(u'),$$  \hspace{1cm} (15)

where

$$i = \text{int}[u(P - 1)] + 1, \quad i = 1, 2, ..., P - 1$$  \hspace{1cm} (16)

and

$$u' = (u(P - 1)) - i + 1,$$  \hspace{1cm} (17)

where $\text{int}(a)$ represents the integer part of $a$.

The only detail remaining is the computation of the control points. The knot points are related to the control points through the following matrix relationship:

$$\mathbf{S} = D \mathbf{V},$$  \hspace{1cm} (18)

where $\mathbf{V}$ is a $P$-element subset of the control points given by the vector

$$\mathbf{V} = [V_1 \ V_2 \ V_3 \ V_4 \ V_5 \cdots V_P]^T,$$  \hspace{1cm} (19)

and, for third-order B-splines, the $P \times P$ matrix $D$ is given by the well-known relation

$$D = \begin{bmatrix} 1 & 0 & 0 & \cdots & 0 \\ \frac{1}{2} & \frac{1}{2} & 0 & \cdots & 0 \\ \frac{1}{2} & 0 & \frac{1}{2} & \cdots & 0 \\ \frac{1}{6} & \frac{1}{2} & -\frac{1}{2} & \cdots & 0 \\ \frac{1}{6} & -\frac{1}{2} & \frac{1}{2} & \cdots & 0 \\ \frac{1}{6} & -1 & 1 & \cdots & 0 \\ \frac{1}{6} & 1 & -1 & \cdots & 0 \\ \frac{1}{6} & -\frac{1}{2} & \frac{1}{2} & \cdots & 0 \\ \frac{1}{2} & -\frac{1}{2} & \frac{1}{2} & \cdots & 0 \\ 1 & 0 & 0 & \cdots & 0 \end{bmatrix}.$$  \hspace{1cm} (20)
D = \frac{1}{6} \begin{bmatrix} 6 & 0 & 0 & \cdots & 0 \\ 1 & 4 & 1 & 0 & 0 \\ 0 & 1 & 4 & 1 & 0 \\ 0 & 0 & 1 & 4 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & 0 & 6 \end{bmatrix} \\
\frac{1}{6} \begin{bmatrix} a_{1,1} & a_{1,2} & 0 & 0 & \cdots & 0 \\ a_{2,1} & a_{2,2} & a_{2,3} & 0 & \cdots & 0 \\ 0 & a_{3,2} & a_{3,3} & a_{3,4} & \cdots & 0 \\ 0 & 0 & a_{4,3} & a_{4,4} & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \ddots & \vdots \\ a_{p-1,p-2} & a_{p-1,p-1} & a_{p-1,1} & \cdots & \cdots & a_{p-1,p} \end{bmatrix} (19)

w_i = a_{i+1,1}.

Given the values of \( y_i, w_i, \) and \( u_i, i = 1, 2, \ldots, P, \) we can now get the control points:

\[ V_p = \frac{y_p}{u_p}, \]

\[ V_i = \frac{y_i - w_i V_{i+1}}{u_i}, \quad i = P - 1, \ldots, 1. \] (28)

Finally, the terminating control points are given by the following and guarantee that the local curvature of the spine equals 0 at its ends:

\[ V_0 = 2V_1 - V_2, \quad V_{P+1} = 2V_P - V_{P-1}. \] (29)

Thus, overall, to compute \( p_i(u) \), the following procedure is followed: (a) use Eqs. (10) and (11) to set up the knot points; (b) use the starting condition (21) and relations (19), (20) and (22)–(26) to compute the intermediate quantities \( y_i, u_i, \) and \( w_i \), and Eqs. (27)–(29) to get the control points; (c) apply Eqs. (13)–(17). Finally, we point out that direction vectors \( d_i(u) \), Eq. (6), can be computed for each spine \( p_i(u) \), using the same procedure as above by using the \( d_i \), of Eq. (4) instead of the \( s_i \).

Step 1(b): contour-function calculation

The calculation of the contour functions again uses B-spline analysis as used for the spine calculations. For each value \( \hat{u} \) along the \( n \)th GC’s spine \( p_i(\hat{u}) \), the following steps give the contour function \( c_n(t, \hat{u}) \):

1. Find a set of \( P - 1 \) contour points defining the endoluminal surface at \( p_i(\hat{u}) \). This is done using the same ray-casting technique of Stage 1, step 4, with \( P - 1 = 16 \). This gives a set of points \( c_i, i = 0, 1, \ldots, P - 2 \), that serve as knot points in the spline calculations. These points, and other calculations, involve 2D calculations in the local coordinate frame for \( c_n(t, \hat{u}) \). To define a complete closed contour consistent with the needs of the spline calculations, we add the point \( C_{P-1} = C_0 \) to give the vector of knot points

\[ S_c = [c_0 \ c_1 \ c_2 \ c_3 \ c_4 \ \cdots \ c_{P-2} \ c_0]^\top. \]

2. To find the B-spline representation, we use the same
development as for the spine calculation, but make
the following substitutions:
(a) Vector \( \mathbf{S} \) takes the place of \( \mathbf{S} \) in Eq. (18).
(b) The \( P \times P \) matrix \( \mathbf{D} \) in Eq. (18) is replaced by
the \( (P - 2) \times (P - 2) \) matrix \( \mathbf{D}_c \), where
\[
\mathbf{D}_c = \frac{1}{6} \begin{bmatrix}
4 & 1 & 0 & \cdots & 1 \\
1 & 4 & 1 & \cdots & 0 \\
0 & 1 & 4 & 1 & \cdots & 0 \\
\vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\
0 & 0 & 1 & 4 & \cdots & 0 \\
1 & 0 & 0 & \cdots & 0 & 1 & 4
\end{bmatrix}
\]
This form accounts for the overlapping endpoints
at indices 0 and \( P - 1 \).
(c) The control-point end conditions (29) are replaced by
\[
V_p = V_0, \quad V_{p+1} = V_1.
\]
(d) \( P - 1 \) spans again are used to represent the
closed contour, but they are parameterized on \( t \)
instead of \( u \). Thus, for \( 0 \leq t < 1 \),
\[
c_c(t, \hat{u}) = C_i(t'),
\]
where
\[
i = \lfloor t(P - 1) \rfloor + 1, \quad i = 1, 2, \ldots, P - 1
\]
and
\[
t' = (t(P - 1)) - i + 1.
\]
The calculation of the contour functions is then
done as for the spine functions, with the obvious
substitutions (e.g. \( c_0 \) is substituted for \( s_0 \) in Eq.
(21), etc.).

Step 2: construct segmented tree
After the spine and contour functions are computed, a
segmented image is readily generated by applying Eq. (8).
The image is built up by combining the GCs for all
paths \( n = 0, 1, \ldots, N - 1 \), and sample values \( \hat{u} = u_1, u_2, \ldots, u_{n_{\text{max}}} \).
At each sampled value \( \hat{u} \), the contour function \( c_n(t, \hat{u}) \) is computed. The voxels covered by the
contour are included in the segmented image (nearest-
neighbor interpolation used). Also, endoluminal cross-
sectional area calculations are readily done using the
relation
\[
\text{area}(c_n(t, \hat{u})) = \frac{1}{2} \sum_{k=0}^{P-3} (c_k \times c_{k+1}) + (c_{P-2} \times c_0),
\]
where ‘\( \times \)’ is for vector cross-product [39]. The Eq. (30)
used for the area calculation for \( c_n(t, \hat{u}) \) is based on the
\((P - 1)\)-sided polygon defined by the points \( c_i, i = 0, \ldots, P - 2 \).
The polygon can be looked upon as enclosing
\((P - 1)\) triangles, each of which contributes an area term to
Eq. (30).

4. Results
The axes-generation algorithm has been tested on a wide
range of data. In this section we present phantom and human
results. We also give applications of the algorithm to
virtual-bronchoscopic assessment of human 3D CT pulmonary
images.

4.1. Phantom results
We created a computer-generated phantom consisting of
a single tube that branches into two tubes. Voxels located
inside the wall of either of two analytically defined curved
tubes are set to 127 (8-bit gray-scale) and background
voxels are set to zero. These mathematically generated
tubes have circular curvature (i.e. they each form one quad-
rant of a circle when viewed from the side) with a radius
of 64 voxels. Assuming that each voxel is an isotropic cube of
dimensions (1 mm)$^3$, then the radius is 64 mm and the
image dimensions are 128 \( \times \) 128 \( \times \) 128 mm. The inner radius of each tube’s cross-section (lumen) is
10 mm and the outer radius is 15 mm. To give a noisy image, we applied a window-average filter using a
3 \( \times \) 3 \( \times \) 3 kernel and then added Gaussian white noise (\( \sigma = 10 \) gray levels).

No operator intervention was required for finding an
appropriate seed point \( w_0 \) since the mathematical center is
voxel location (64,64,1) where the two tubes overlap. Fig. 7a
shows sagittal and coronal weighted-sum projections of the
phantom image along with automatically-generated paths.
Fig. 7b shows cross-sectional area measurements of each of
the two paths along with the true cross-sectional area of a
single tube. Note the fluctuation in cross-sectional area near
the bifurcation point at distance 32 mm. This is expected
because the cross-sectional area increases as the two tubes
begin to diverge until they no longer overlap. After the
bifurcation point is passed (distance \( = 45 \) mm), the cross-
section estimates are for the non-overlapping portions of
each tube, and the area measurement remains within a few
percent of the known 314.15 mm$^2$ (dashed line) for each of the
tubes (black and white lines).

To test the method for anisotropically sampled image
data, we down-sampled the same phantom in \( z \) by a factor of
5 resulting in voxel dimensions of 1 mm \( \times \) 1 mm \( \times \) 5
mm. This was accomplished by averaging the gray-scale
values at a given \( x-y \) coordinate over 5 slices to form a
single slice. Then, we added noise as before. Fig. 7c,d
shows the results of the algorithm using this image. Despite
the far lower resolution along the \( z \)-axis (note the stair-step
effect in the projection images), the path tracking performed
well. As expected, area estimation degraded due to the
coarse z-resolution. Exhaustive phantom results for tubes of other sampling factors and for cone phantoms, given in [38], confirm the efficacy of the algorithm.

4.2. Human studies

We next validated the methodology on a series of human cases. These cases had earlier undergone standard 3D EBCT (electron beam CT) scanning. They all involved upper-airway obstructions, such as a stenosed airway from an impinging cancer or a collapsed/compressed lung. All 3D CT images consisted of 512 $\times$ 512 transverse-plane slices, with a slice thickness $D_z \approx 3$ mm. The number of slices in the cases ranged from 24 to 80; scans were done to focus on the region of interest. The transverse-plane resolution ranged from $D_x = D_y = 0.410$ mm to 0.684 mm (One case involved 230 0.531 mm-thick slices, with $D_x = D_y = 0.531$ mm.).

We selected thirteen cases that had previously undergone prior manual path definition using the VIDA 3D analysis software [17,41]. The previous analyses done for these cases involved a skilled technician manually segmented one airway of interest. Axis measurements were next obtained using a package called TGA (Tube Geometry Analysis) contained in VIDA [41]. The basic steps performed in this analysis are as follows: (1) manually segment the airway of interest in all CT slices; (2) perform a shape-based interpolation of the segmented airway, to give a higher-resolution form of the segmented airway; (3) perform TGA analysis to semi-automatically find a central axis through the segmented airway. These steps required about 2 h of user intervention for a typical case.

To compare results, we applied our proposed algorithm using the starting point of the manual analysis as the root site $w_0$. Generation of the output results required roughly two minutes of computer processing per case (700 MHz Pentium-III PC used). Fig. 8 summarizes the results. These results focus on the differences between the central axes defined manually and automatically. Note the strong agreement between the results. We point out that the manually generated results, even though they were made painstakingly, are not ‘perfect’ ground truth. This is because manual segmentation, shape-based interpolation, and the semi-automatic path extraction method all introduce errors. If anything, the automated results are more reliable. Fig. 9 shows pictorial and numerical results for a typical human case in this study.
4.3. Application to virtual bronchoscopy

We have devised a PC-based system for virtual-bronchoscopic (VB) assessment of high-resolution 3D CT chest images. The system permits a user to build a multimedia HTML case report for a given 3D image. The basic steps in this evaluation are as follows:

1. Begin a case study by selecting a root site for the airway tree.
2. Run the automated axes-generation algorithm to extract the main airway axes, airway cross-sectional area values, and segmented airway tree.
3. Use the system’s many visual tools to peruse regions along the extracted axes. During this analysis, interesting snapshots and movies can be saved.

The details of this system are described elsewhere [15,16]. It is well-acknowledged that precomputed guidance data are

<table>
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<th>coordinate difference</th>
<th>normalized coordinate difference</th>
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<td>0.37</td>
</tr>
<tr>
<td>std. dev. 0.38</td>
<td>0.02</td>
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</table>

Fig. 8. Comparison of axis accuracy between manual and automatic methods. Thirteen 3D human CT cases, previously analyzed manually using VIDA are included in the study. “Coordinate Difference” refers to mean 3D image coordinate difference between a point on a manually defined axis and the corresponding automatically computed axis (1 unit = 1 voxel). “Normalized Coordinate Difference” is computed by normalizing the coordinate difference by the average diameter of the manually defined axis (1 unit = 1 diameter unit). The average airway diameters for the cases ranged from 3.42mm (5.0 voxels) to 12.31mm (9 voxels). The standard deviation (“std. dev.”) is computed for these two measures over the 13-case database.

Fig. 9. Manual versus automatic axis generation for a specific human case. The 3D EBCT image consisted of 40 512 x 512 3.0mm-thick slices with \( \Delta x = 0.684 \)mm. Average coordinate difference = 1.49; normalized coordinate difference = 0.138. Top: Coronal maximum-intensity projection showing automatically computed axis. The axis consists of 123 sites. An automated segmentation approach was used to remove the bones and mediastinal structures from the data before the projection was computed [8]. Bottom: 3D view of manual (solid line) and automatically-computed (+ line) axes.
The input 3D CT image was $512 \times 512 \times 133$ ($\Delta x = 0.586$ mm, $\Delta z = 1.5$ mm). The proposed axes-generation algorithm was used to extract a path through the region of the collapse. This axis is depicted as a line on the Coronal Projection tool (maximum-intensity projection computed, data between $200 \leq y \leq 300$ used to create view). The computed airway cross-sectional values along this axis are depicted on the Plot Tool. The large dot on the Plot Tool represents a site selected by the user. All other activated tools (Coronal Projection, Cube Tool, and STS Coronal Slab) depict renditions of the 3D CT data at this selected site. The Cube Tool shows a composite of the standard three MPR (transverse, sagittal, and coronal) slices at this site; the pointers on these views indicate the direction of travel along the axis for this site. The STS Coronal Slab shows a coronal front-to-back depth-weighted maximum thin slab (slab thickness = 20, depth of vision = 30) at the site [42]. These views clearly show the manifestation of the collapse in several different ways.

Example #1: A patient suffering from tracheomalacia (collapsed trachea) underwent an EBCT scan. Using a single 20-sec breath hold, a 3D EBCT image made up of 133 contiguous slices was reconstructed. Each slice consists of $512 \times 512$ voxels (slice thickness $\Delta z = 1.5$ mm, axial-plane resolution $\Delta x = \Delta y = 0.586$ mm). As discussed in Section 3.3 (step 1), we used the VB system to define a root site. An axis through the collapsed region was computed. This calculation required approximately 1 min of computation on a standard 700 MHz PC. This axis served as guidance data for interacting with the VB system.

Fig. 10 depicts a snapshot of the VB system. The solid line on the Coronal Projection image is the computed axis. Also, the Plot Tool shows a plot of cross-sectional area versus distance along the axis. One site near the 'bend' in the collapse was selected on the Plot Tool. This site is then highlighted on all other activated tools (Coronal Projection, Coronal Sliding Thin-Slab, and Cube Tools). The various views clearly show both visually and numerically the nature and extent of the collapse.

Example #2: A patient with a previously inserted stent, underwent an EBCT scan. As before, using a single 20-sec breath hold, a 3D EBCT scan was done. The reconstructed image consisted of 123 contiguous slices ($512 \times 512$ voxels per slice, slice thickness $\Delta z = 1.5$ mm, axial-plane resolution $\Delta x = \Delta y = 0.586$ mm). We used the VB system to define a root site. A complete set of axes through the major airways was extracted. This analysis again took on the order of 1 min on a 700 MHz PC.

Fig. 11 depicts part of the analysis of this case. The Coronal Projection shows the extracted airway tree axes. The 3D Surface Tool also depicts the airway tree axes in addition to the segmented airway tree. The STS Coronal Slab and Cube Tool clearly show manifestations of the stent. The small cross-section views give shots at a particular site. Again, the system composite view provides many renditions of the region of interest.

5. Discussion

For typical high-resolution 3D CT chest images, the proposed axes-generation algorithm requires less than a
few minutes of computation time on a standard PC. The algorithm uses the gray-scale data directly, and it does not require any interpolation or prior segmentation. With small modification, the algorithm could be applicable to other 3D tree-finding problems. Further work could be done in adapting the approach to find paths to preidentified suspect sites, such as airway narrowings and cancerous lymph nodes. Also, the method can have difficulty in cases where the airway wall becomes very thin, as a result of partial-voxel artifact. For such cases, the method can escape into the lungs and find many superfluous axes. Potential solutions to this problem are to incorporate iterative refinement and to have more robust wall-detection methods.

The method has been tested on phantom, animal, and human cases. This paper presented results for phantom and human cases. Refs. [38,43] give validation for animal cases. These results demonstrate the efficacy of the method. Further, the method has been integrated into Sun and PC-based software systems for virtual bronchoscopy [8,9,15,16,44]. Perhaps most significantly, we have successfully applied the method to live VB-based guidance of bronchoscopy for phantom and animal cases [15,16,44].

6. Summary

Major airway obstruction is a common problem arising from lung cancer, benign processes, and other tumors that commonly metastasize the airways. Three-dimensional (3D) computed tomography (CT) pulmonary images are often used for evaluating such cases. The physician typically evaluates a case by using 3D mental reconstruction of anatomical structures depicted in the images. While often suitable for the radiologist, this form of evaluation is typically inadequate for the bronchoscopist, who need precise 3D ‘road maps’ to the surgical sites of interest. Virtual bronchoscopy (VB) has emerged as a paradigm for more effective 3D CT image evaluation. Systematic evaluation of a 3D CT chest image using VB techniques, however, requires precomputed guidance data. This
guidance data takes the form of central axes, or centerlines, through the major airways. We propose an axes-generation algorithm for VB assessment of 3D CT chest images. For a typical high-resolution 3D CT chest image, the algorithm produces a series of airway-tree axes, corresponding airway cross-sectional area measurements, and a segmented airway tree in a few minutes on a standard PC.

Our algorithm follows a two-stage approach. The first stage computes a Discrete Model that consists of a sparsely spaced set of data corresponding to the major airways. The second stage then uses the Discrete Model to define a smooth set of airway axes, a segmented airway tree, and other measurement data; these data constitute the Generalized Cylinder (GC) Model. The basic flow of the two-stage algorithm is as follows. The user first specifies a starting point of interest for the airway tree, generally in the proximal end of the trachea. Then, to perform the Stage-1 calculation of the Discrete Model, an adaptive 3D searching technique steps through the 3D image, building up a sparsely sampled set of central axes for the major airways. Stage-2 then applies a cubic-spline analysis and contour-finding procedure to the Discrete Model data to give a generalized cylinder representation for each airway central axis; this gives the GC Model.

Quantitative results for phantom and human airway-obstruction cases demonstrate the efficacy of the algorithm. Also, the algorithm is used in conjunction with a PC-based system for virtual-bronchoscopic (VB) assessment of high-resolution 3D CT chest images. In this context, the algorithm is demonstrated for two cases involving major airway obstructions.

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