

A Segmentation and Abstraction of Blood Vessels from Volume Data for Surgical Simulation

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Abstract

In this paper, we present a robust segmentation method of blood vessels from medical volume data. It extracts the blood vessels with their important geometric features such as bifurcations, a location of centroid, diameter, and tangent vectors. It also generates an abstract model which has a tree structure in which the nodes store important features of the vessels. We use the extracted vessels data to simulate a variety of vascular and interventional radiology procedures.

Key words: Segmentation, Abstraction, Blood Vessels, Surgical Simulation

1. Introduction

Medical systems simulating a variety of surgical procedures require the geometric detail of human organs to visualize and analyze the procedures. Especially, in a vascular and interventional radiology simulation system, the blood vessels data is used for visualizing the fluoroscopic image, detecting collision between the catheter and the vessel wall, and dynamic simulation of the force feedback[5]. For visualizing the vessels, their voxel or polygonal surface model is efficient, but for collision detection or dynamic simulation, their implicit functional model is more efficient. Therefore it is difficult to generate one geometric model of the vessels so that it can efficiently serve all above operations. So we need an abstract or symbolic model from which we can obtain other appropriate structures which efficiently allow the operations[12].

It is common approach to visualize blood vessels and reconstruct their 3D structures using angiogram volume data which is imaged by CT angiography(CTA) and MR angiography(MRA)[1, 2, 13]. Angiography, a special X-ray procedure, is performed by the injection of radiographic contrast material (dye) into the blood vessels via catheter that is placed directly into the artery or vein. Thus the resulting images give us a good discrimination between blood vessels and other soft organs such as muscle, fat, and liver.

The reconstruction or extraction of blood vessels for the use of medical applications has been attempted in a variety of approaches[3]. The Marching cubes algorithm[9], as one of typical iso-surfacing methods[10, 4], can extract raw geometry of blood vessels from volume data.

It is very efficient for visualization of blood vessels, but not for simulation because a large number of triangles results in slow computation. Another attempt is to reconstruct 3D structure of blood vessels from biplane angiogram images[6, 14, 7, 8, 11]. It first segments or extracts contours or edges of blood vessels from biplane angiogram images, and reconstructs the 3D structure of blood vessels by fitting surfaces between the extracted contours or edges. Since this approach is mainly interested in estimating 2D features of the vessels such as medial axis and borders, it does not support quantitative 3D measures such as diameters, lengths and bifurcations.

Recently, a new method which can estimate quantitative measures of blood vessels was developed[16, 15]. Starting with a seed voxel, the method repeatedly finds its connected voxels that satisfy a constraint for classifying blood vessels. The method employs a concept called *wave propagation*, and propagates it by generating its next wave until no wave is generated. To detect bifurcations of vessels, the method examines whether each wave has one connected component or not. The merit of this method is to extract detail geometric features including bifurcations. However, since propagated waves are not parallel to cross section of the vessels, and also sometimes they are spreaded very long along an axis of the vessels, it requires a large number of activated images for processing and degenerates the accuracy in calculation of geometric features including diameters. And also, it is very sensitive to noises such as an appearance of small island inside the vessels. It will result in an infinite loop in wave propagation process inside vessels.

In our approach, to solve above problems, we introduce a *plane wave* concept in which wave propagation occurs on only the given plane so that a collection of generated waves can form a cross section of the vessels. Due to this technique, the estimation of geometric features is easily and exactly obtained and the number of activated images for processing is reduced. To generate an abstract model based on the curvature of blood vessels, we introduce another concept called *ray-shooting*. At the center of cross section of the vessels, a ray is shot with an axis direction of the vessels and stops if it hits a wall of the vessels. Since the distance the ray traveled is closely related to the curvature of the vessels, we used it to approximate the vessels by generalized cylinders.

In next section, we review the wave propagation concept and defined *plane wave* concept. In section 3, our segmentation method employing plane wave and ray-shooting is presented. The experimental results of our method and the conclusion of this paper will be discussed in section 4 and section 5, respectively.

2. Background

In this section, we review the concept of wave propagation proposed by Zahlton et al[16, 15] and define a new concept called *plane wave* for later use in this paper.

2.1 Wave Propagation and Plane Wave

For a given volume data V , let us assume that v is a voxel in V , i.e., $v \in V$, and Q is a set of voxels consisting blood vessels and $Q \subset V$. Then segmentation problem of blood vessel is represented by following function f .

$$f : V \rightarrow 0, 1, \quad f(v) = \begin{cases} 1 & \text{if } v \in Q \\ 0 & \text{if } v \notin Q \end{cases} \quad (1)$$

Basically, a *wave* is a wavefront spreading in all directions according to the Huygens' principle, with a constraint given by Equation 1. Thus its propagation sequence can be considered as repeated generation of wavefronts along blood vessels. The wave propagation sequence can be described by the equation 2.

$$W(v)_i^p = W(v)_{i-1} + W(v)_{i-1}^p \quad (2)$$

where $W(v)_i^p = \sum_{k=0}^{i-1} W(v)_k$ and $W(v)_{i-1}^p$ is the sum of all previous waves at i -th and $(i-1)$ -th step, respectively and $W(v)_{i-1}$ is the wave generated at $(i-1)$ -th step. If we assume that $v_{i-1} \in W(v)_{i-1}$ and denote the voxels 26-connected to v_{i-1} by $V_{v_{i-1}}^{26}$. Then i -th wave $W(v)_i$ can be represented by the following equation.

$$W(v)_i = \{v_i | v_i \in V_{v_{i-1}}^{26} \text{ and } v_i \notin W(v)_i^p \text{ and } v_i \in Q\} \quad (3)$$

Let us assume that $v \in V$, $v \in Q$, and denote a set of voxels on the plane P by R , where P is a given plane. Then we can define conditional waves constrained by the plane P as waves that are propagated from a seed voxel on P and consist of voxels on P . Equation 4 denotes the conditional waves.

$$W(v|P)_i = \{v_i | v_i \in V_{v_{i-1}}^{26}, v_i \notin W(v)_i^p, v_i \in Q, v_i \in R\} \quad (4)$$

Using the conditional wave concept, we define a *plane wave* as a set of conditional waves by the plane P and denote it by Equation 5.

$$P = \sum_{\text{for all } i} W(v|P)_i \quad (5)$$

The plane is described by two tuples, a normal vector N and the distance from origin D and also the wave is described by an initial seed point v_0 . Thus we can describe the plane wave by a normal vector N and an initial seed voxel v_0 . For example, Figure 1 shows a plane wave (shaded voxels bounded by circle) generated from both an initial point v_0 and the normal vector N .

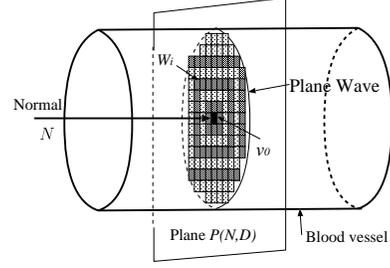


Fig. 1: The Plane Wave

Our plane wave concept has several characteristics as follows. Since the propagation direction of the plane waves is the axis vector of the blood vessels, we can easily estimate the axis vector by connecting between centers of adjacent successive plane waves. Using the axis vector, we can generate a plane wave so that it could be always perpendicular to an axis vector of the vessels. Using the plane wave, we can easily calculate the diameter and centroid of the vessels and also can detect bifurcations of the vessels by checking whether it has just one connected component or not.

3. Blood Vessel Segmentation

In this section, we describe our segmentation method which extracts blood vessels from volume data, and also simultaneously, abstracts them by a set of *generalized cylinders*. To do this, we use two concepts called *plane wave propagation* and *ray shooting*.

3.1 The Generalized Cylinder Approach

When abstracting blood vessels, we approximate them by a set of *generalized cylinders*. A new node as one end of a new generalized cylinder is generated at important points such as bifurcations, rapid change in the curvature or the diameter of vessels. As an abstract model of blood vessels, we generate a tree structure in which the nodes store important features of the vessels, such as the location of centroid, diameter, and tangent vectors. Figure 2 shows an approximation of blood vessels by generalized cylinders(b) and generation of a tree as abstract model of the vessels(c).

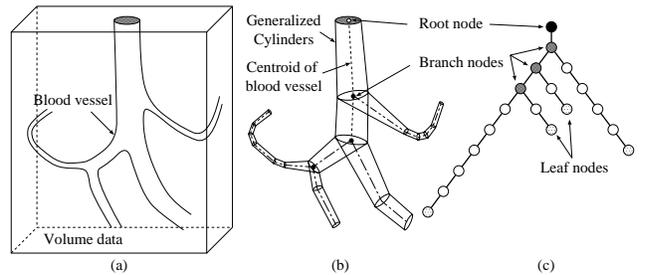


Fig. 2: Segmentation and approximation of blood vessels. (a) blood vessels within volume data, (b) the approximation by generalized cylinders, (c) a tree structure as an abstraction model.

3.2 The Basic Segmentation

Our segmentation method consists of three basic steps as shown in Figure 3. At first, it estimates a axis direction of blood vessels being approximated. After that, it estimates the curvature of blood vessels and determines a new position for creating a new node. To do this, we use plane wave and ray shooting. Finally, it generates a new node and cylinder and estimates important geometric features. These three steps are repeatedly applied until all the vessels are completely extracted from volume data and approximated by generalized cylinders.

For more detail description, let us consider Figure 4 and assume that the algorithm is working on i -th step. Then i -th node ($i > 1$) is already known, and also the cylinder \mathcal{C}_{i-1} , a center position c_i , a radius r_i and a plane wave \mathcal{P}_i , are already known.

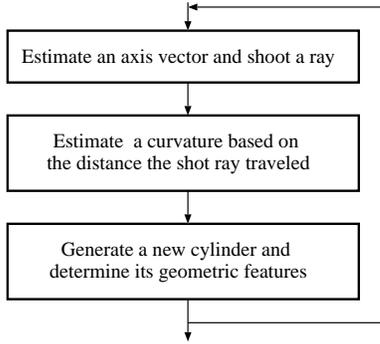


Fig. 3: Three basic operations in general step.

At first, it estimates a new axis vector L_i of blood vessels at the point c_i . This vector is used to estimate a curvature along the blood vessel. After generating a plane wave \mathcal{P}_i using both the plane normal and the point given initially, we propagate it towards its next wave \mathcal{P}_i^+ . Then a new axis vector L_i obtained by connecting centers of two successive plane waves (\mathcal{P}_i^+ and \mathcal{P}_i), i.e, $L_i = c_i^+ - c_i$.

After that, it determines the position p_{i+1}^0 to create a new node which is one end of a new cylinder. To do this, it shoots a ray at the center c_i of plane wave \mathcal{P}_i along with the axis direction L_i . Then, the shot ray travels until it hits a wall of the blood vessels. The distance d_i the ray traveled is proportional to a radius r_i of the blood vessel, and also is inversely proportional to its curvature. So we can represent the distance the ray traveled by Equation 6.

$$d_i = \rho \frac{r_i}{K_i} \quad (6)$$

where ρ is a proportional constant and K_i is a curvature of the blood vessel around i -th node. Then, we let the length of a new cylinder be proportional to the inverse of the curvature K_i .

$$d'_i = \sigma \frac{1}{K_i} = \sigma \frac{d_i}{\rho r_i} = \alpha d_i \quad (7)$$

where σ is a proportional constant and $\alpha = \frac{\sigma}{\rho r_i}$ is an *approximation parameter*, $0 \leq \alpha \leq 1$. Depending on this approximation parameter, the grain of approximation is

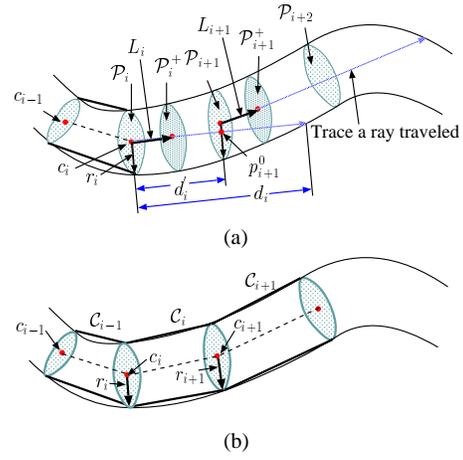


Fig. 4: Basic segmentation process. (a) approximation of blood vessels using plane wave and ray shooting, (b) resulting generalized cylinder models. Note: \mathcal{P}_i, c_i, L_i and r_i are a plane wave, a center position, a axis vector and a radius at i -th node, respectively. \mathcal{C}_{i-1} is a cylinder generated at i -th step and d_i is a distance that the ray shot at i -th node traveled.

determined. Then the new position p_{i+1}^0 based on curvature and radius is determined by Equation 8.

$$p_{i+1}^0 = c_i + d'_i L_i = c_i + \sigma d_i L_i. \quad (8)$$

Finally, our basic segmentation method generates a generalized cylinder \mathcal{C}_i and estimates geometric features ($c_{i+1}, L_{i+1}, r_{i+1}$) of blood vessels at the new node.

To obtain an abstracted representation of blood vessels, we should make a geometric relationship between generated cylinders, and also find important geometric features such as bifurcations. However, our basic segmentation method neither detects the bifurcation, nor makes a geometric relationship between cylinders. Thus, in the next section, we describe about the bifurcation detection method.

3.3 Detection of Bifurcations

Basically, bifurcations can be detected by performing connected component analysis for waves. If a wave has two connected components or more, there is at least one bifurcation. So, the relation between the number of connected components and the number of bifurcations is described as follows.

$$\mathcal{B} = \mathcal{C}_i - 1 \text{ for } \mathcal{C}_i \geq 2$$

where \mathcal{B} is the number of bifurcations, and \mathcal{C}_i is the number of connected components in the wave W_i .

In our basic segmentation method, the position of a new node depends on the *approximation parameter* α , which is predefined by a user before applying our basic segmentation method, and the distance the ray traveled. Therefore it can miss bifurcations if they occurs between i -th and $i+1$ -th node, as shown in Figure 5(a). In most cases, this missing occurs when the length d'_i of a new

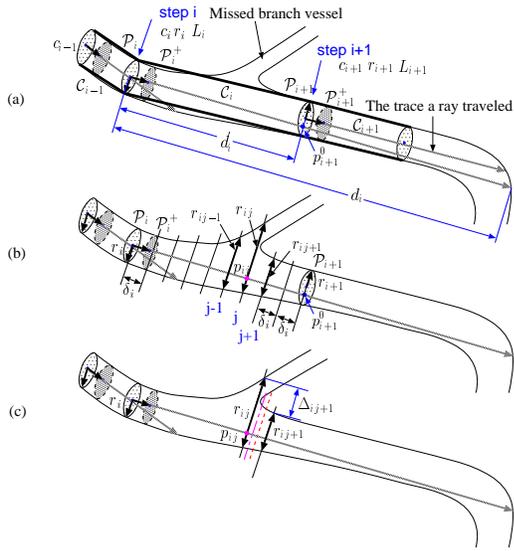


Fig. 5: Bifurcations of blood vessels. (a) A missing case of bifurcations when applying our basic segmentation method, (b) Detection of possible bifurcation intervals by inserting additional check points, (c) Find an exact bifurcation position by recursively bisecting the possible bifurcation interval.

generated cylinder is very much bigger than its radius r_i , i.e., $d'_i \gg r_i$.

To prevent our algorithm from missing the branches of blood vessels, we develop a bifurcation detection algorithm. In the algorithm, it first finds a possible bifurcation interval (in Figure 5(b), the interval between j and $j + 1$) by adding additional points with a constant interval δ_i between c_i and p_i^0 and checking the radius change between successive adjacent points. For the found possible bifurcation interval, it repeatedly and alternately applies two stages; the first stage bisects the interval into two sub-intervals and the second stage updates the interval by selecting a possible bifurcation interval among two sub-intervals. The bisection process continues until the interval is sufficiently small compared with the radius of blood vessels. To find an exact position of bifurcations, it generates a plane wave at one point of the selected interval, and propagates the wave towards the other point. During this wave propagation, it calculates the number of connected components for each plane wave. After finding bifurcation points, it calculates a center and a radius for each branch of the vessels, and again goes on the basic segmentation method.

In above bifurcation detection method, the size of blood vessels being detected depends on the constant interval δ_i between two adjacent check points. For a large δ_i , large branches of vessels will be missed, and inversely for small δ_i , small vessels will be missed. However, without the loss of generality, we used $\delta_i = r_i$ because the size of branch vessels is generally proportional to the size of their parent vessel.

In actual traversal, whenever detecting a bifurcation

of blood vessels, it generates a child node corresponding to each branch, and goes on its traversal in depth-first order. In other words, at a bifurcation point, it chooses just one branch to traverse and stores the remains into a stack. After finishing the traverse of the chosen branch, it returns to previous bifurcation point by popping stored branch up from the stack. Through these sequences, the blood vessels are segmented from volume data, and are simultaneously abstracted or reasoned by a set of generalized cylinders.

4. Experimental Results

For experiment, we implemented our algorithm in C++ and ran it on SGI Octane system. In order to prove a validity of the segmentation results, we also extracted the polygonal surface of blood vessels using the Marching Cubes algorithm. As test data, we used MR angiogram medical volume data about human abdomen. Its size is 512x512x128.

Figure 6(color plate) shows the segmentation results of both Marching cubes algorithm(a) and our segmentation method(b) for abdomen MRA volume data. In Figure 6(b)(color plate) which is the result of our segmentation method, the spheres correspond to the nodes of a tree, and also their size corresponds to the radius of vessels at that point. Comparing two results, we can see that they have the identical structure of vessels.

5. Conclusion

In this paper, we proposed a robust algorithm for segmenting blood vessels from volume data. Using wave propagation, plane wave and ray shooting, we extract blood vessels from volume data and simultaneously approximate them by a set of generalized cylinders. Finally, as an abstraction model of blood vessels, we generate a tree structure where the nodes store detail geometric features of vessels such as tangent vectors, location of centroid, and diameters at important points. Since the abstract model of vessels can be easily transformed into other computing model, it is useful for the medical applications such as catheterization surgical simulation in which various operations such as visualization and collision detection are required.

Acknowledgments

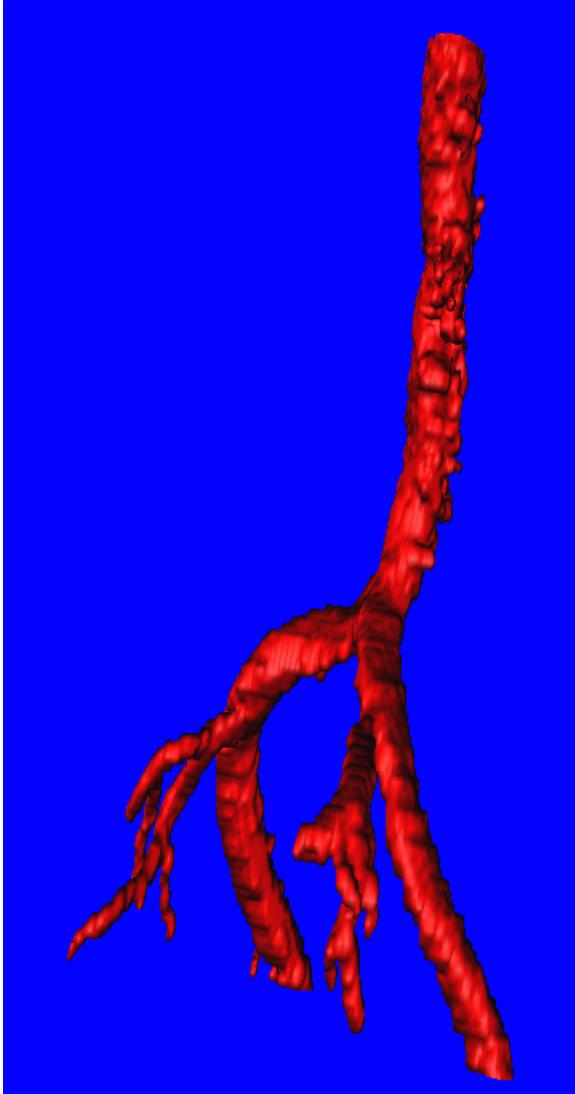
The authors wish to thank John L. Sibert at the George Washington University, who made valuable suggestions.

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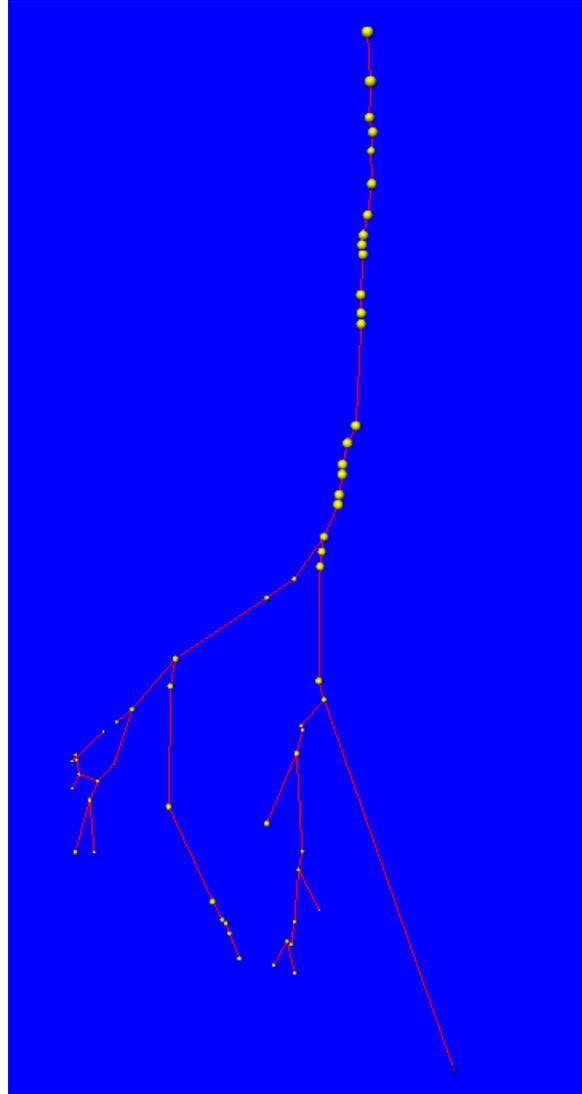
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2. Noninvasive 3d angiography-ct or mri. <http://www.netside.net/manomed/angio.htm>.

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[color plate]



(a)



(b)

Fig. 6: Abdomen MR angiogram volume data: (a) A polygonal surface extracted by Marching Cubes algorithm, (b) A tree structure of blood vessels generated by our segmentation algorithm.