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Biomedical Image Processing II

Alan C. Bovik
Vyvyan Howard
Chairs/Editors

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BIOMEDICAL IMAGE PROCESSING II

Volume 1450

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Session 1—Filtering and Reconstruction of Biomedical Images
Barry J. Sullivan, Northwestern University

Session 2—Segmentation and Feature Detection in Biomedical Image Processing
Dmitry B. Goldgof, University of South Florida

Session 3—Analysis, Classification, and Recognition of Biomedical Images
Raj S. Archarya, SUNY/Buffalo

Session 4—Special Session on Motion Analysis in Biomedical Image Processing
Alan C. Bovik, University of Texas/Austin

Session 5—Special Session on 3-D Microscopy
Mark A. Browne, University of Manchester Institute of Science and Technology (UK)

Conference 1450, *Biomedical Image Processing II,* was part of a three-conference program on Image Processing, held at the SPIE/IS&T Symposium on Electronic Imaging Science and Technology, 24 February–1 March, 1991, in San Jose, California. The other conferences were:

Conference 1451, *Nonlinear Image Processing II*
Conference 1452, *Image Processing Algorithms and Techniques II*

Program Chair: **Terrance Lund,** Eastman Kodak Co.

INTRODUCTION

This year's proceedings on Biomedical Image Processing II contains thirty-one papers directed toward the development of new image processing theory and techniques for the acquisition, processing, and analysis of two-, three-, and four-dimensional biomedical image data. The types of images acquired in the various biomedical disciplines, well exemplified by this collection of papers, is as varied as the sensing apparatuses used. Optical (both passive and active), thermal, ultrasonic, radiographic, and physical scanning techniques are all represented, over scales of imaging ranging from the macroscopic imaging of internal organs to the submicron measurement of cellular structure. The dimensionality of the image data includes simple two-dimensional projections, sequences of projections that sample three-dimensional space, and time sequences of three-dimensional data.

The first session, Filtering and Reconstruction of Biomedical Images, addressed the generation and reconstruction of images derived from sources such as tomography, x-ray data, and the newly developed scanning electrochemical microscope. These and other imaging modalities invariably suffer from degradations related to the physical limitations of the sensing apparatus. Several of the papers detail techniques for reducing or ameliorating the effects of these degradations, for the purpose of improved visual interpretation or to enhance the efficacy of later automated processing.

Session 2, Segmentation and Feature Detection in Biomedical Image Processing, represented attempts to apply low-level digital image processing and machine vision algorithms for the purpose of emphasizing significant image structures, for automatically separating these structures from the ambient image data, and for quantifying the properties of these structures. Typical goals of the segmentation and feature detection processes, as represented by these papers, is either to allow for the direct measurement of physical object parameters or to enable the detection and classification of the objects in the images by type.

Session 3, on Analysis, Classification, and Recognition of Biomedical Images, dealt directly with the higher level problems of object classification and/or recognition. These techniques typically operate on images that have already been segmented or preprocessed to enhance certain relevant features. Meaning is

subsequently affixed to the quantitative measurements made on the image data. This distilling of information may be regarded as a process of image-to-symbol conversion, where the symbols derived enhance the ability of a human interpreter or technician to understand the intrinsic properties of the image data.

The final two special sessions of these proceedings detail topics of emerging and special interest for researchers in biomedical image processing. Session 4, devoted to Motion Analysis in Biomedical Image Processing, contained papers that study the evolution of images of objects that change over time. It is being increasingly recognized that a complete understanding of many biological processes will require that time-dependent phenomena be quantified, particularly in the morphometric analysis of tissue or organ deformation. This is particularly true in instances where the local shape change properties of tissue are to be studied, where statistical characterizations over large samples of subjects may not yield the required information. Most of the papers presented are involved with cardiac image data, which is a natural application since the motion of the heart is of acute interest to cardiologists. However, it is expected that analogous techniques will soon be developed for analyzing other spatially varying biomedical image data.

The fifth session, Three-Dimensional Microscopy, focused on the imaging, visualization, and analysis of microscopic data in three space dimensions. The problem of observing the geometric properties of very small objects has historically been made difficult by the optical resolution limitations of conventional microscopes. New microscope technologies, in particular the confocal microscope, offer increased resolution with less noise. All six of the papers presented in this section are devoted to imaging using confocal instruments. The focus of the papers included attempts to elicit images of unprecedented resolution from living tissue structures, to reduce imaging artifacts, to quantify three-dimensional structure, and to present the three-dimensional information in a format that is easily visualized by a human observer.

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SESSION 1

Filtering and Reconstruction of Biomedical Images

Chair
Barry J. Sullivan
Northwestern University

3-Dimensional Reconstruction of Pulmonary Blood Vessels by Using Anatomical Knowledge Base

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ABSTRACT

This paper presents a knowledge-based method for automatic reconstruction and recognition of pulmonary blood vessels from chest X-ray CT images with 10-mm thickness.

The system has four main stages: (1) automatic extraction and segmentation of blood vessel components from each 2-D images, (2) analysis of these components, (3) a search for points connecting blood vessel segments in different CT slices, using a knowledge base for 3-D reconstruction, and (4) object manipulation and display. We also describe a method of representing 3-D anatomical knowledge of the pulmonary blood vessel structure.

The edges of blood vessels in chest X-ray images are unclear, in contrast to those in angiograms. Each CT slices has thickness and blood vessels are slender, so a simple graphical display, which can be used for bone tissues from CT images, is not sufficient for pulmonary blood vessels. It is therefore necessary to use anatomical knowledge to track the blood vessel lines in 3-D spaces.

Experimental results using actual images of a normal adult male has shown that utilizing anatomical information enables to improve the efficiency and precision in the processing such as blood vessel extraction and searching for points connecting.

1. INTRODUCTION

Much works has been done in recent years in the field of medical image understanding. Some systems that combine image processing technologies with artificial intelligence approaches are already being studied for medical images produced by cephalograms and coronary angiograms [1,2].

3-D reconstruction using computer graphics manipulation is widely studied as a means of understanding the three-dimensional (3-D) structure of organs. Some studies demonstrate the technique's potential as a clinical tool in planning surgical treatments [3]. It can also be used to reconstruct the 3-D structure of vascular configurations from biplane X-ray recordings, and to explore 3-D reconstructions of vessels of interest, such as coronary vessels and cerebral arteries [4,5].

The ability to recognize pulmonary blood vessels in necessary for diagnosing lung diseases, such as lung cancer [6]. Physicians normally trace pulmonary blood vessels from a set of chest X-ray CT images

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of a patient in order to learn the 3-D structure of arteries and veins. This suggests an approach to developing a system for automatic recognition of pulmonary blood vessels from CT images.

The edges of blood vessels in chest X-ray images are unclear, in contrast to those in angiograms. Each CT slice has thickness and blood vessels are slender, so a simple graphical display, which can be used for bone tissues from CT images, is not sufficient for pulmonary blood vessels. It is therefore necessary to use anatomical information to track the blood vessel lines in 3-D space.

This study investigates the reconstruction of pulmonary blood vessels from chest X-ray CT images with 10-mm thickness. The system first extracts blood vessel segments from each CT image. A search for points connecting these segments in different CT slices is then carried out, using a knowledge base for reconstruction. We also describe a method of representing anatomical knowledge of the pulmonary structure, for accurate reconstruction and future interpretation of the branch names of blood vessels.

2. KNOWLEDGE REPRESENTATION FOR ANATOMICAL INFORMATION

2.1 Pulmonary Blood Vessel Structure

The lungs are divided into a number of extended regions by pulmonary structures. Each lung lobe is divided into segments. The segmental vein is located at the boundary of each segment. The segmental artery is generally above the bronchus. Veins and arteries extend from hilar points, and there is an underlying principle in the way that pulmonary blood vessels diverge [7]. This information enables physicians to infer the location of any part of the lungs. Figure 1 shows the structure of the pulmonary artery. we can see that primary arteries are addressed by notations such as A^3a. The capital A stands for artery, the suffix number indicates the segment number, and the lowercase letter indicates the sub-segment symbol.

To reconstruct 3-D pulmonary blood vessels from CT images with 10-mm thickness, information is necessary about the way in which the pulmonary blood vessels extend and about the anatomical principle.

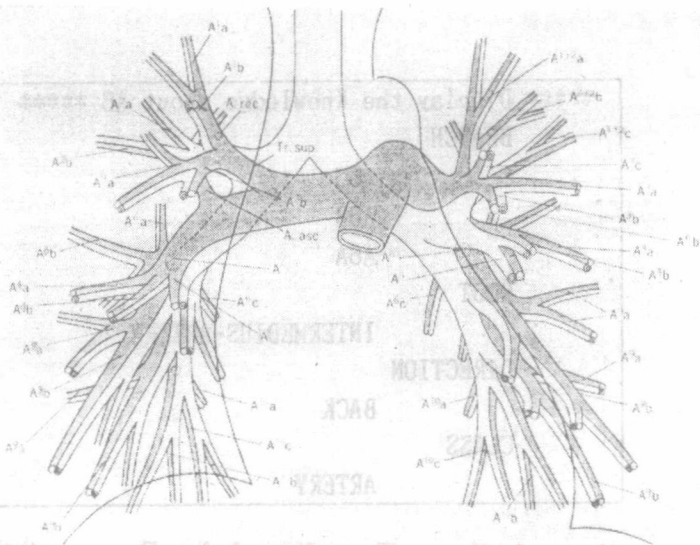

Figure 1. Structure of the Pulmonary Artery

2.2 Anatomical Knowledge Representation

In regard to the pulmonary blood vessel anatomy, we propose a tree-like representation. One branch was defined as a section of a blood vessel from its inner divergence point to its outer one. In the knowledge representation, the direction of each branch is expressed by 26 combinations of three pairs of opposites: (1) up, down, (2) fore, back, and (3) right, left. we described each branch by a fragmentary vector-like representation (Figure 2). This description is converted into a frame-type knowledge representation in the knowledge representation in the knowledge base (Figure 3).

Vector-like representation enables us to reconstruct the 3-D structure easily. Figure 4 shows a 3-D model of pulmonary veins derived from the information in the knowledge base. Figure 5-1 shows a 3-D model of right pulmonary arteries and Figure 5-2 shows the actual 3-D structure that was reconstructed from CT images by an expert physician. These figures show that simple qualitative descriptions such as direction and length are very useful.

We also describe in Section 3 a part of the knowledge base containing general rules on the way blood vessels extend.

```
(BRANCH RMPA TR-SUP LEFT)
(BRANCH RMPA INTERMEDIUS-ARTERY LEFT DOWN)
(BRANCH TR-SUP A1 UP BACK)
(BRANCH A1 A1A UP)
(BRANCH A1 A1B FORE)
(BRANCH TR-SUP A3 FORE)
(BRANCH A1 RECURRENT-ARTERY LEFT UP BACK)
                :
```

Figure 2. Example of Fragmentary Representation of the Right Pulmonary Artery Structure

```
***** Display the Knowledge about A6 *****  World: Model
    BRANCH
                A6C
                A6B
                A6A
    ROOT
                INTERMEDIUS-ARTERY
    DIRECTION
                BACK
    CLASS
                ARTERY
```

Figure 3. Frame-Type Knowledge Representation of Pulmonary Artery A^6

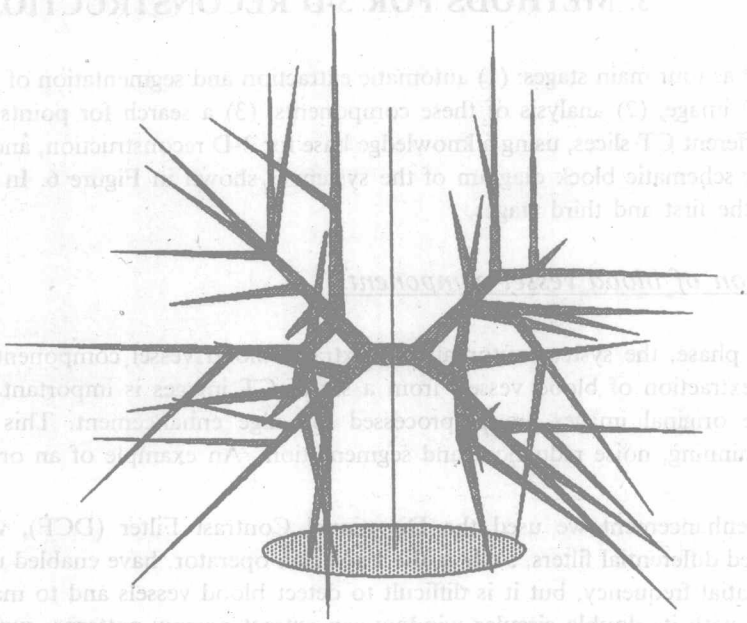

Figure 4. 3-D Model of Pulmonary Veins Derived from the Information in the Knowledge Base

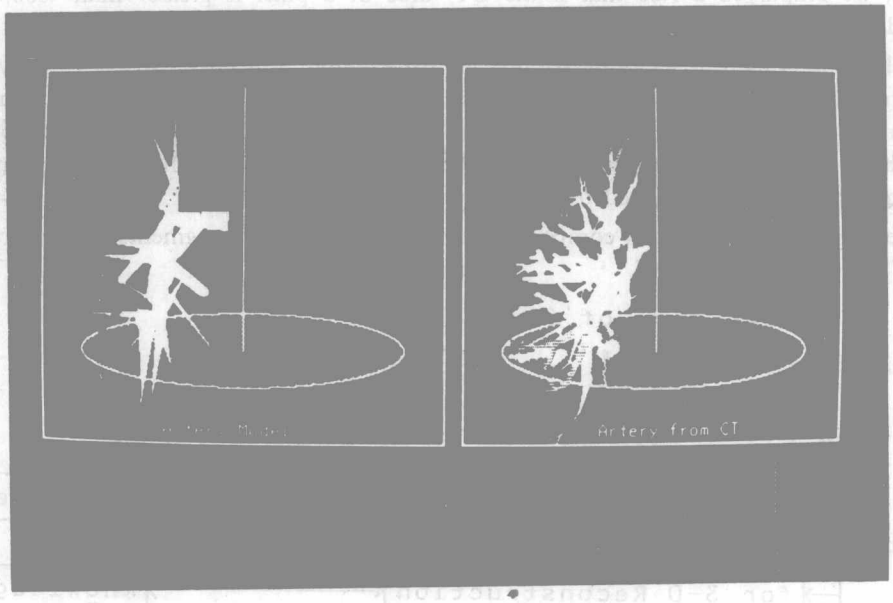

Figure 5-1. 3-D Model of Pulmonary Arteries in the Right Lung

Figure 5-2. Actual 3-D Structure of Pulmonary Arteries in the Right Lung

3. METHODS FOR 3-D RECONSTRUCTION

Our system has four main stages: (1) automatic extraction and segmentation of blood vessel components from each 2-D image, (2) analysis of these components, (3) a search for points connecting blood vessel segments in different CT slices, using a knowledge base for 3-D reconstruction, and (4) object manipulation and display. A schematic block diagram of the system is shown in Figure 6. In this section, we describe the details of the first and third stages.

3.1 Extraction of blood vessel components

In the first phase, the system automatically extracts blood vessel components from 2-D CT images. The accurate extraction of blood vessels from a set of CT images is important in reconstruction a 3-D structure. The original images are preprocessed for edge enhancement. This process is followed by binarization, thinning, noise reduction, and segmentation. An example of an original image is shown in Figure 7.

For edge enhancement we used the Directional Contrast Filter (DCF), which we developed [8]. Commonly used differential filters, such as the Laplacian operator, have enabled us to extract components with a high spatial frequency, but it is difficult to detect blood vessels and to maintain their connectivity [9]. The DCF with its double circular window can extract narrow patterns, such as blood vessels, from noisy medical images and maintain their connectivity. The DCF responds to patterns with long, narrow shapes, thereby excluding other patterns such as small, circular shapes. However, some blood vessels extend vertically upwards or downwards across more than one CT slice. In such cases, the shape of each blood vessel is a small, circular pattern, and the DCF often excludes this kind of pattern. To cover this problem, we employed a rule that if the CT-value of a pixel is greater than -600, then the pixel is extracted as a part of a blood vessel.

Thresholding is used to make binary images. An example of a binary image is shown in Figure 8. To extract blood vessel components, this process is followed by thinning and noise reduction. Results are shown in Figure 9 and 10 respectively. Our noise reduction process eliminates short, isolated skeletons, except those with high CT values, as high frequency noises, checking the measurement of run-length on the binary line drawings obtained by the process of thinning.

These extracted blood vessel components must be divided into segments, which are represented as a series of axis data.

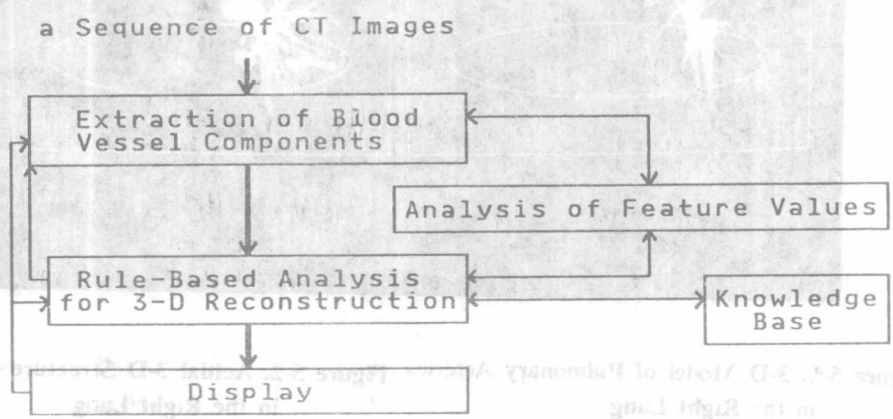

Figure 6. Reconstruction of Pulmonary Blood Vessel Structure from CT images

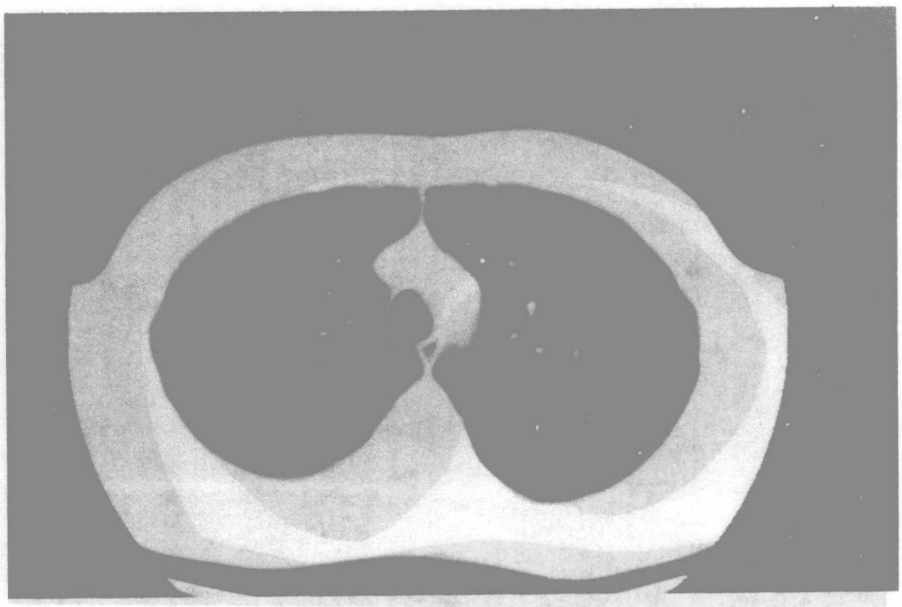

Figure 7. Example of Original CT Image

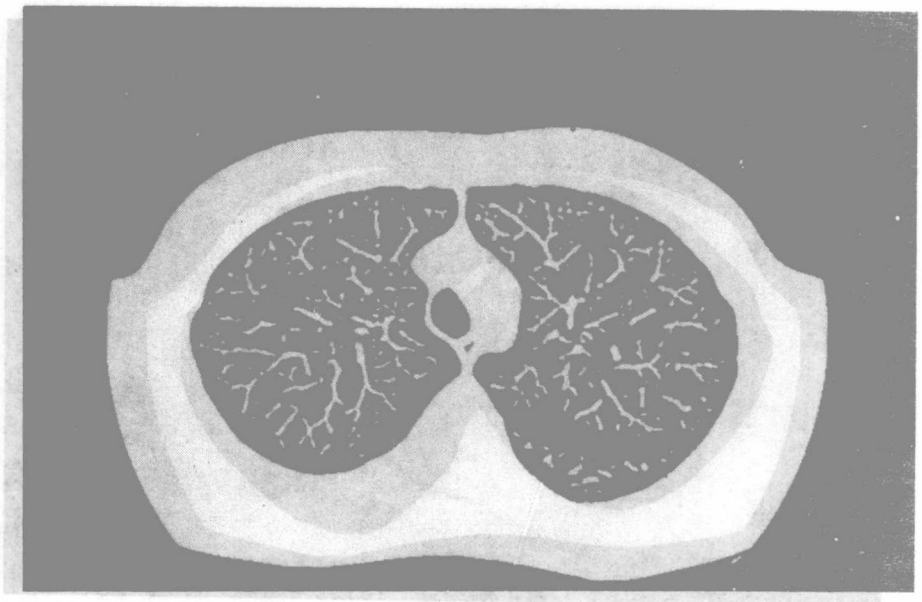

Figure 8. Blood Vessel Enhanced Image

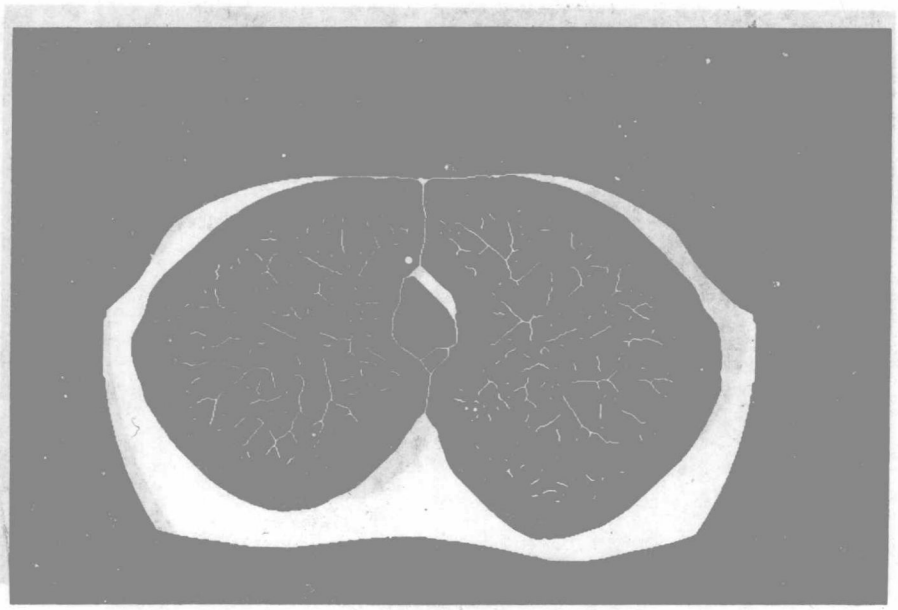

Figure 9. Thinning Image

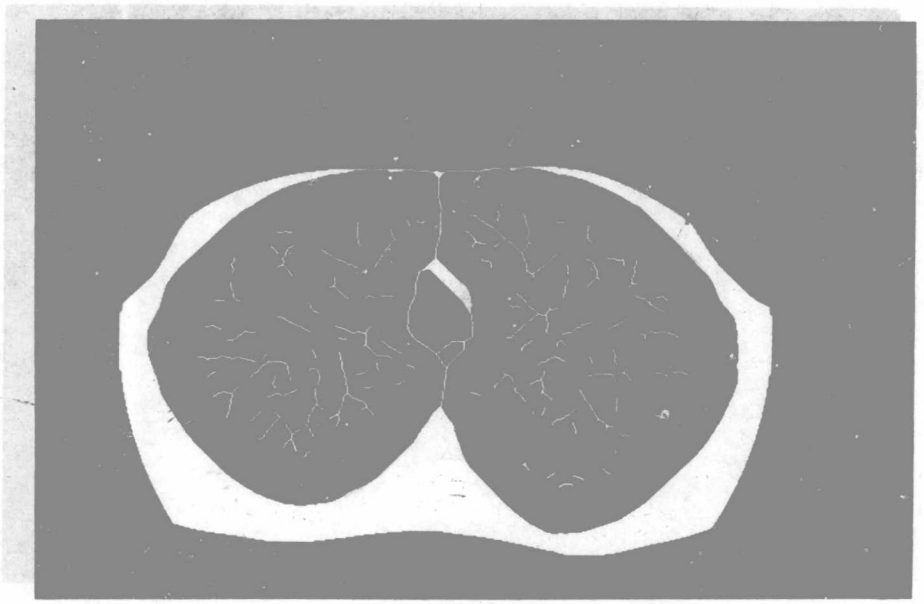

Figure 10. Blood Vessel Segments after Noise Reduction