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journal homepage: www.elsevier.com/locate/patrecFast vascular skeleton extraction algorithm[☆]Kristína Lidayová^{a,*}, Hans Frimmel^b, Chunliang Wang^{c,d,e}, Ewert Bengtsson^a, Örjan Smedby^{c,d,e}^a Centre for Image Analysis (CBA), Division of Visual Information and Interaction, Department of Information Technology, Uppsala University, Sweden^b Division of Scientific Computing, Department of Information Technology, Uppsala University, Sweden^c Department of Radiology and Department of Medical and Health Sciences, Linköping University, Linköping, Sweden^d Center for Medical Image Science and Visualization (CMIV), Linköping University, Linköping, Sweden^e School of Technology and Health, KTH Royal Institute of Technology, Stockholm, Sweden

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ABSTRACT

Vascular diseases are a common cause of death, particularly in developed countries. Computerized image analysis tools play a potentially important role in diagnosing and quantifying vascular pathologies. Given the size and complexity of modern angiographic data acquisition, fast, automatic and accurate vascular segmentation is a challenging task.

In this paper we introduce a fully automatic high-speed vascular skeleton extraction algorithm that is intended as a first step in a complete vascular tree segmentation program. The method takes a 3D unprocessed Computed Tomography Angiography (CTA) scan as input and produces a graph in which the nodes are centrally located artery voxels and the edges represent connections between them. The algorithm works in two passes where the first pass is designed to extract the skeleton of large arteries and the second pass focuses on smaller vascular structures. Each pass consists of three main steps. The first step sets proper parameters automatically using Gaussian curve fitting. In the second step different filters are applied to detect voxels – nodes – that are part of arteries. In the last step the nodes are connected in order to obtain a continuous centerline tree for the entire vasculature. Structures found, that do not belong to the arteries, are removed in a final anatomy-based analysis. The proposed method is computationally efficient with an average execution time of 29 s and has been tested on a set of CTA scans of the lower limbs achieving an average overlap rate of 97% and an average detection rate of 71%.

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1. Introduction

Due to the immense impact of arterial disease on public health, a large proportion of clinical medical imaging procedures are devoted to the imaging of blood vessels. The trend with minimally invasive therapeutic procedures supplanting open surgery has greatly increased the demand for non-invasive vascular imaging for treatment planning. Currently, Computed Tomography Angiography and Magnetic Resonance Angiography (MRA) are the most popular non-invasive techniques for accurate morphological imaging of arteries. With the introduction of new Computed Tomography (CT) hardware with up to 320 detector rings, the spatial resolution has increased, and modern CTA technique has shown good agreement with invasive methods even in the coronaries, which offer special challenges due to

their motion [1]. Increased resolution, on the other hand, puts higher demands on the performance of the software processing continually increasing volumes of image data.

The increasing proportion of endovascular treatment for various arterial diseases – aneurysms and dissections as well as atherosclerotic stenoses [18] – has led to a growing need for accurate methods to identify and measure the centerline of arteries, as this is used for selecting suitable stents and placing them appropriately. In addition, the centerline is useful for visualizing stenoses with curved planar reformatting (CPR) [21]. Segmentation of tubular structures, which is a specific segmentation challenge, can be facilitated and accelerated by first identifying the centerlines. Therefore, there is a need for fast vascular centerline tree extraction algorithms. In this paper, we present such an algorithm. The proposed algorithm is intended as part of a complete arterial tree segmentation, where the vascular centerline is used as seed. The overall goal is to obtain a precise segmentation with enough coverage and with a computation time short enough to permit interactive clinical use.

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Finding the centerlines of vessels can be seen as a special case of image skeleton extraction algorithms. An image skeleton should fulfil the criteria of being a subset of the original object, thin - one voxel wide, being topologically equivalent to the object and allowing reconstruction of the object [13].

Our proposed skeleton extraction method is based on the concept of reducing the dimensionality of the problem before performing the actual analysis [8,9]. Although the input data is a 3D volume, the problem is simplified into a set of 1D processes. The resulting centerline tree is thin, roughly centrally located and has the same topology as the vascular tree. It is a subset of the original object and it is possible to reconstruct the vascular tree from it. It thus fulfils the general criteria of being a skeleton as described above. The reconstruction method, however, has to be more advanced than a simple distance-based expansion in order to reproduce an accurate segmentation of the vascular tree. For this purpose, we are using a reconstruction method that combines level sets with an implicit 3D model of the vessels [22]. That method takes an approximate centerline tree as input, generates a 3D vessel model from it and uses it to guide the level set propagation. The result is a segmented vasculature with subpixel precision.

The whole concept of vascular segmentation based on vascular skeleton extraction and level set propagation was experimentally proven in [22]. However, in that paper the vascular skeleton extraction was based on a semi-automatic, relatively time consuming approach. In this paper, we focus on the vascular skeleton extraction part, showing how it can be made fully automatic and run at speeds compatible with interactive exploration of the volume images.

2. Previous work

Numerous methods have been proposed for vascular segmentation. Since no general purpose segmentation method is suitable for all applications, this problem still attracts interest of many researchers. Roughly, the approaches can be classified [20] as either skeleton-based (extracting vessel skeleton) or non-skeleton-based (extracting vessel walls). For vascular skeleton extraction, there are, in principle, two approaches. The first approach assumes pre-extracted vascular surface representation as an input, the second one finds centerlines directly from the MRI or CT intensity images.

This section focuses on various methods for skeleton extraction directly from CTA images with more attention to algorithms that are able to extract the whole vascular centerline tree or give information about the execution time. Detailed surveys on different vessel segmentation algorithms can be found in [12,14].

Most centerline extraction algorithms are semi-automatic, based on one or more user-defined seed-points and their propagation. Particularly popular are minimal-path approaches identifying the minimum-cost path as the vessel centerline. The cost function can be efficiently calculated by using various operators such as medialness filters [2,5,10], vesselness filters [7], or optimally oriented flux [4].

In a coarse-to-fine approach presented by [6], Dijkstra's shortest path algorithm creates an initial coarse centerline, which is thereafter refined by an active contour model combined with polyhedra placed along the model. Experimental results for a real CT dataset with $512 \times 512 \times 386$ voxels show that, depending on the number of polyhedra surface points, the centerline extraction can take 2.3–31.4 s for 12–272 surface points respectively. However, the length of the extracted centerline is less than 100 voxels.

Work presented by [15] extends the shortest path computation using one additional dimension – the vessel radius. The resulting paths are better centered and the vessel surface can be directly extracted without any post-processing, nevertheless the computation time is a drawback. For a 3-D CT image of the size $110 \times 90 \times 80$ voxels, the aorta centerline extraction “takes less than 2 min”.

Another work is based on intensity ridge traversal [2] and states an execution time of 15 min to process an intracranial MRA dataset.

In contrast to techniques that can only detect a single centerline, some algorithms can propagate outward from only one seed point and detect multi-branch centerlines simultaneously [10,16]. Gülsün and collaborators have tested their method on coronary artery CTA data where the full coronary artery trees were extracted in 21 s in average.

Wang and Smedby [23] proposed a coronary artery segmentation and skeletonization algorithm based on a fuzzy connectedness tree. The algorithm also works well outside the coronary region, and with very limited user interaction it is possible to extract the full body vascular skeleton. This algorithm is used to evaluate our proposed method.

This brief review of previous work done in vascular skeleton extraction shows the need for a method able to extract a whole-body centerline tree that is fast enough to permit interactive clinical use.

3. Proposed method

The proposed method for fast extraction of the vessel centerline tree takes a 3D unprocessed CTA scan as input. The output is a graph where the nodes are centrally located artery voxels found by a set of criteria and the edges represent the connections between them. The algorithm consists of three main parts that are repeated in two passes. An outline of the proposed algorithm is presented in Fig. 1.

During the first pass, the algorithm focuses on extracting the centerline of large arteries, and therefore only reliable parts of the artery structure are detected. The output of the first pass is refined by an anatomy-based analysis which removes structures that do not belong to the arteries. During the second pass, additional finer structures are added to the graph.

Each one of these two passes consists of the same three main steps. The first step automatically selects parameters from the intensity histogram of the data. The second step detects centrally located voxels that are part of the arteries. Finally, these centrally located voxels are connected as nodes into a graph structure, corresponding to the vascular tree.

3.1. Parameter selection

Parameters used in the proposed method can be divided into two groups. The fixed parameter group contains parameters that need to be determined once and are based on vascular morphology. The second group are changeable parameters, consisting of intensity ranges for relevant tissues such as fat $[\theta_{low}^f, \theta_{high}^f]$, muscles $[\theta_{low}^m, \theta_{high}^m]$ and blood $[\theta_{low}^b, \theta_{high}^b]$. These intensities depend on various factors and have to be adapted for each patient separately. We propose a way to set them automatically.

3.1.1. Fixed parameters

The group of fixed parameters consists of $[min_radius, max_radius]$, $cutting_thresh$, $short_graph_thresh$ and $gradient_thresh$. By changing $[min_radius, max_radius]$, we select the size of the arteries we aim to detect at each level. At the rough level, we focus on arteries having a radius smaller than 25 mm and larger than 2 mm, as arterial diameters above 50 mm are only found in aneurysms. At the fine level, we aim to detect arteries with a radius smaller than 2.5 mm. The lower radius limit in this case is limited by the size of the voxel in the database. However, these values can be modified depending on the requested artery size. With the $cutting_thresh$ parameter, we influence the threshold for cutting off very short branches. In this paper, we are using $cutting_thresh$ equal to 5 times the radius of the artery at a bifurcation point. This threshold permits the removal of most of the non-arterial branches which originate from noise or from nodes detected very close to

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