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An Algorithm for Step-wise Skeletonization of Blood Vessel Network

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Introduction

Clinical investigations of the cardiovascular system would be greatly facilitated if one could describe the network of blood vessels in a succinct way suitable for automatic image analysis. One common solution to this problem is extracting skeletons of blood vessels.

Skeletonization is an iterative process frequently used in image processing to reduce the pictorial content of an object to a graph representing only the general shape of the object. Among many other areas, skeletonization techniques are finding an increasing number of applications in automated medical analysis and diagnostics.

Generally, representations using skeletons are considered to provide better cues for human perception of the object's shape than other description forms [1]. Sometimes it is important to keep the principal object features such as its geometry or morphology. In other applications, such as reconstruction, a skeleton conveys complete geometrical information about the object, which can then be rebuilt with a minimal error using some algorithm.

Ability to have a concise description of the blood vessel network can be very useful for automated clinical diagnostics and localization of aneurysms in particular. An aneurysm is a blood-filled dilation of a blood vessel caused by a disease or weakening of the vessel wall. Being able to automatically locate an aneurysm, determine its size and shape, and then assign the aneurysm to a certain class would be an invaluable aid for clinicians in treating their patients.

Automatic detection of aneurysms is still an open issue requiring application of new mathematical methods [2, 3]. As an intermediate step towards the solution of this problem, we developed an algorithm for skeletonization of the blood vessel network. The algorithm scans the set of segmented blood vessels, extracts their skeleton and searches for shape abnormalities.

Since detection of aneurysms dramatically depends upon the quality of skeletons, the main requirements for a skeleton are its smoothness, continuity, centeredness, and thinness. These terms are briefly defined below.

Smoothness: The skeleton must adhere to the centerline, i.e. no scatter of the points is allowed.

Continuity: The skeleton cannot have any discontinuities, including intersections of blood vessels.

Centeredness: The centerline is not allowed to approach the vessel's wall.

Thinness: The skeleton should be a single path, one pixel wide.

Common Skeletonization Algorithms

There are half a dozen of basic methods used to extract skeletons. These include methods based on wavefront propagation, field of force, distance transform, iterative thinning, and Voronoi diagram [4]. Here, we will outline the last three methods that contributed most to the proposed technique.

In the distance-transform methods [5], each point represents a center of the maximum disc contained in the given component. These methods suffer from the major difficulty in specifying the connectivity criteria for objects with complex shapes.

Using the iterative thinning approach [6], the border points of a binary object satisfying the topological and geometrical constrains are deleted in iterative steps. The algorithm does not change the connectivity of the original data set, but the centeredness and smoothness of the curve are not always preserved. Also, parasitic branches may occur for complex objects.

The Voronoi-diagram methods [7] divide the image into cells, each containing one initial point and the loci of all the points closest to the initial point. When the density of the points goes to infinity, they converge on the skeleton. However, when the surface represents a complex structure, the Voronoi diagram becomes very complicated. This results in discontinuities and parasitic branches.

Therefore, when working with objects having complex shapes, some hybrid algorithm is used. In addition to some of the properties of the three groups

mentioned above, the algorithm usually includes other utility procedures such as smoothing, centering, etc.

Proposed Algorithm

Initialization. The input data to the algorithm are images of segmented blood vessels. The algorithm is initialized at a point P_i belonging to the vessel region. To find such a point in a segmented MRI is not difficult, because the widest blood-vessel regions are located at the head and neck intersection. Then, two vectors are obtained by drawing rays in all directions from the given point (Fig. 1).

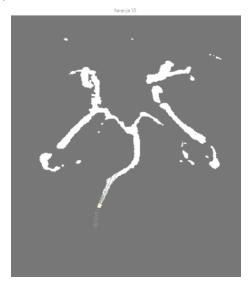


Fig. 1. Segmented blood vessels as input to the algorithm

After determining the direction vector V_i the Euclidean distance DR is calculated.

$$DR = \max \delta(P_i, B), \tag{1}$$

where B is a border point.

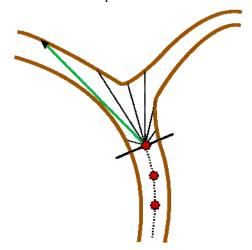


Fig. 2. Movement in the direction of the longest ray

Then, after finding the center of the vector VP_i perpendicular to the longest ray, rays are drawn again in all directions, and the direction vector V_i is updated (Fig. 2).

Moving. The next point P_{i+1} on the skeleton is found by moving along the longest ray. The distance S traveled from P_i to P_{i+1} is determined experimentally to meet the condition $S < DR_i$. This constraint assures the estimated skeleton's points never leave the boundaries of the vessel.

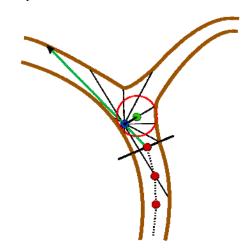


Fig. 3. Centering of skeleton points

Centering. The algorithm searches for the center PC_{i+1} of the circle passing through P_{i+1} that has the smallest diameter (Fig. 3). Then, multiple rays are drawn from PC_{i+1} in the directions spaced at 0.5° within the range $\pm 90^{\circ}$ relative to the direction of V_i . All the rays are checked against a collision with any of the skeleton's points already identified. If so, the associated direction is classified as wrong and removed from the list. This way the algorithm prevents reversions to the previous paths that are likely to occur for pronounced curvatures of a vessel.

Stop condition. Movement is performed until the longest ray distance becomes bigger than the stop parameter DRi > DS.

Branching. To determine a possible bifurcation of a blood vessel, additional analysis is performed. It consists of the following steps.

1. Local maxima are filtered out using the mean and Gaussian filters. At a branching point of vessels no more than two sharp maxima are allowed in the ray-distance graph. Each of them represents a separate branch of the blood vessel (Fig. 4).

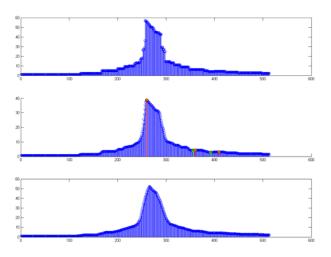


Fig. 4. Distribution of Euclidean ray distances after processing with the mean and Gaussian filters

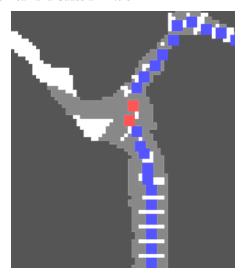


Fig. 5. Checking for branching of blood vessel

The upper histogram in Fig. 4 shows the distribution of the lengths (in pixels) of all the 512 rays. The middle histogram in Fig. 4 conveys the same information with the high frequencies removed using the mean filter. In the bottom histogram of Fig. 4, the high frequencies were removed using a Gaussian filter. Filtering of high frequencies is associated with removing local maxima from the plot, which in turn facilitates determining the number of global maxima. Two maxima clearly seen on the plot after the filtering indicate a branching. From the filtered histograms, the direction of the longest ray is determined, and this direction is used for moving further.

2. The circle within the three points is drawn. Two of the points are the end points of the longest rays and the third one is the start point P_{i+1} . The algorithm determines the number of times the circle crosses the blood-vessel region. For a single blood vessel, this number should be no more than two.

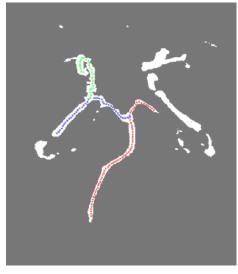


Fig. 6. Output of the algorithm showing color-coded skeleton of blood-vessel branches

3. After finishing movement along one branch, rays are drawn for all points of that branch in directions perpendicular to the direction vector. The points meeting the above conditions are determined, and movement in that direction is performed. This step is repeated for all the selected points. In Fig. 5, the two red squares denote the points containing a branching.

The output of the proposed algorithm is a skeleton shown on the original segmented images in various colors that are used to represent different branches of the blood vessel (Fig. 6).

Conclusions

- 1. Although several algorithms were proposed for performing skeletonization, they did not yield satisfactory results for the task of detecting the skeleton of blood vessels with further possibility of identifying regions containing an aneurysm. The main problems were related to deficient characteristics of the skeleton, such as its continuity, smoothness, and centeredness.
- 2. The key feature of the proposed algorithm is controlled movement in the direction of the longest ray followed by the procedure for centering the current skeleton's point. These measures insure the skeleton's points are kept inside the blood-vessel region.
- 3. At a bifurcation of blood vessels, two maxima can be seen on the ray-distance graph. This allows choosing the optimal direction for the longest ray.
- 4. Numerical experiments with simulated 2D and real data proved the efficiency of the algorithm in extracting the skeleton of blood vessels.
- 5. Currently, a 3D version of the algorithm is the stage of development. The algorithm will be based on the findings discussed in this paper. To accommodate the requirements of 3D space, the algorithm will use a plane to move along the skeleton of the chosen blood vessel (Fig. 7). The main challenge is anticipated to be in developing a branching mechanism suitable for 3D space.

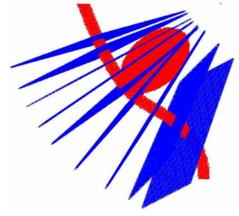


Fig. 7. Towards a 3D model: a plane moving along blood vessel

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Skeletonization is an iterative process frequently used in image processing to reduce the pictorial content of an object to a graph representing only the general shape of the object. We present an algorithm that extracts the skeleton from a set of segmented blood vessels. To accommodate the complexities of the blood vessels' shape, our solution combines some properties of the algorithms based on the distance-transform, iterative thinning, and Voronoi-diagram. In addition, the algorithm employs procedures for smoothing and centering of the estimated skeleton's points. These ensure the skeleton points are kept inside the region of interest. Numerical experiments with simulated 2D and real data proved the efficiency of the algorithm in extracting skeletons of blood vessels. Next we plan to extend the algorithm so that it is usable in 3D space as well. Ill. 7, bibl. 7 (in English; summaries in English, Russian and Lithuanian).

Я. Рокицки, Д. Миниотас, М. Мейлунас, А. Ушинскас. Шаговый алгоритм скелетирования для описания сети кровеносных сосудов // Электроника и электротехника. – Каунас: Технология, 2007. – No. 8(80). – С. 87–90.

Скелетирование — это итеративный процесс, часто изпользуемый в обработке образов для сужения объёма информации об объекте до графа, воспроизводящего только общую форму объекта. В настоящей работе предлагается алгоритм, предназначен для отыскания скелета в образах сегментированных кровеносных сосудов. В связи со сложностью формы кровеносных сосудов предлагаемое решение интегрирует самые полезные свойства других алгоритмов, базирующихся на трансформации расстояний, итеративном разведении и диаграмме Вороного. Кроме того, алгоритм использует процедуры для выравнивания и центрирования разыскиваемых точек скелета. Эти процедуры не позволяют разыскиваемым точкам выйти за пределы области данного кровеносного сосуда. Эффективность алгоритма проверено экспериментально так с реальными данными, так и с двухмерными моделями кровеносных сосудов. Планируется дальнейшее усовершенствование алгоритма с целью приспособления к трёхмерному пространству. Ил. 7, библ. 7 (на английском языке; рефераты на английском, русском и литовском яз.).

J. Rokicki, D. Miniotas, M. Meilūnas, A. Ušinskas. Žingsninis skeletavimo algoritmas kraujagyslių tinklui aprašyti // Elektronika ir elektrotechnika. – Kaunas: Technologija, 2007. – Nr. 8(80). – P. 87–90.

Skeletavimas – tai iteratyvus procesas, dažnai naudojamas apdorojant vaizdus informacijos apie objektą kiekiui sumažinti iki grafo, perteikiančio tik bendrą objekto pavidalą. Šiame darbe pristatomas algoritmas, skirtas skeletui rasti segmentuotų kraujagyslių vaizduose. Prisitaikant prie sudėtingos kraujagyslių formos, siūlomas sprendimas integruoja naudingiausias kitų algoritmų, kurių pagrindą sudaro atstumų transformacija, iteratyvusis ploninimas ir Voronojaus diagrama, savybes. Be to, algoritmas naudoja ieškomų skeleto taškų išlyginimo ir centravimo procedūras. Šios procedūros neleidžia ieškomiems taškams atsidurti už kraujagyslės srities ribų. Algoritmo efektyvumas patikrintas eksperimentiškai, naudojant tiek realius duomenis, tiek dvimačius kraujagyslių modelius. Kraujagyslių skeletavimo algoritmą numatoma tobulinti toliau, siekiant jį pritaikyti ir trimatei erdvei. Il. 7, bibl. 7 (anglų kalba; santraukos anglų, rusų ir lietuvių k.).