Retinal vessel segmentation using a probabilistic tracking method

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ABSTRACT

Vessel structures such as retinal vasculature are important features for computer-aided diagnosis. In this paper, a probabilistic tracking method is proposed to detect blood vessels in retinal images. During the tracking process, vessel edge points are detected iteratively using local grey level statistics and vessel's continuity properties. At a given step, a statistic sampling scheme is adopted to select a number of vessel edge points candidates in a local studying area. Local vessel's sectional intensity profiles are estimated by a Gaussian shaped curve. A Bayesian method with the Maximum *a posteriori* (MAP) probability criterion is then used to identify local vessel's structure and find out the edge points from these candidates. Evaluation is performed on both simulated vascular and real retinal images. Different geometric shapes and noise levels are used for computer simulated images, whereas real retinal images from the REVIEW database are tested. Evaluation performance is done using the Segmentation Matching Factor (SMF) as a quality parameter. Our approach performed better when comparing it with Sun's and Chaudhuri's methods. ROC curves are also plotted, showing effective detection of retinal blood vessels (true positive rate) with less false detection (false positive rate) than Sun's method.

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1. Introduction

The automatic analysis of blood vessels is a very important task in many clinical investigations and scientific research related to vascular features. The early diagnosis of several pathologies, such as arterial hypertension, arteriosclerosis or diabetic retinopathy could be achieved by analyzing the vascular structures. Moreover for many clinical investigations, vessel segmentation is becoming a prerequisite for the analysis of vessel parameters such as tortuosity and variation of the vessel width along the vessel and the ratio between the venous and arterial vessel width. Many vessel extraction methods, using different approaches, have been reported in the literature. A major review of these methods can be found in [1]. The techniques published in the research literature in response to the importance of retinal vessel extraction may be roughly categorized into methods based on matched filters [2–8], adaptive thresholds [3,9], intensity edges [10,11], region growing [12], statistical inferencing [13], mathematical morphology [12,14,15], and Hessian measures [16–19].

Most of the work on vessel segmentation techniques can be divided into two main groups: pixel-based methods and tracking methods. An advantage of tracking based methods is the guaranteed connectedness of vessel segments whereas in pixel processing based methods, connectedness is not guaranteed. A number of features are computed for every pixel in an image in the case of pixel processing based methods. Based on these features, each pixel is assigned a label that indicates the probability that the pixel is inside a vessel. Various supervised [18,20,21] and unsupervised [22–25] pixel labeling frameworks have been proposed. Since each pixel is classified independently, a disadvantage of such methods is that gaps can appear in the segmented vessels resulting in an unconnected vessel network [26].

Vessel trackers choose seed points on the edges and the centerlines of vessels, either automatically or manually, and follow vessels from these points [4,10,27,28]. Given the location and direction of a vessel, they take a small step in the direction of the vessel and look for the vessel edges or the centerlines or both nearby [29]. When new edges are found, an estimate of vessel direction is made, and a new step is made in this direction. As vessels are connected in the retina, tracking methods can follow a whole tree without examining the vast majority of the image that does not contain vessel. Vessel tracking can thus give information on vessel structure such as branching and connectivity. Vessel trackers must however include some logic to respond to vessel endpoints and to branch points.

Techniques used for identifying vessels are based on matched filters [10], morphological filters [15], optimization of Gaussian profiles [30] or fuzzy c-mean classifiers [31], Bayesian inference [27,24]. Other techniques combining the two approaches described above have been also used to improve performance [20,22,23]. Among tracking methods, few probabilistic approaches have been reported in the literature of vessel segmentation [32].

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The main ideas of a probabilistic tracking method have been presented in our previous article [33], which needed some improvements like modeling the blood vessel more accurately and handling different vessel configurations.

Two stages are needed for a tracking method to detect the whole vascular tree. The first one is the selection of seed points all over the retinal image. The second one is based on tracking from these seed points and combining the results of local vessel segmentation to get the final detected vascular tree. Local vessel segmentation [34–36] is the foundation to segment the whole vascular tree. Our study focuses on this second stage, which takes into account local vessel detection, including the vessel edges and centerline detection. In this paper, a novel improved tracking-based method using a probabilistic formulation is introduced. The new approach uses a Gaussian model to approximate the vessel's sectional intensity profile, identifies bifurcation and crossing configurations, and improves the detection results as shown in the experiments and discussion section. A probabilistic segmentation scheme is associated with the Maximum a posteriori (MAP) as criterion to estimate local vessel edges. In the following, Section 2 gives a general description of our method and explains the concept of statistical sampling model. Bayesian segmentation is described in Section 3. Finally results and discussion are given in Section 4.

2. Method description

2.1. General description

The proposed method is based on an iterative tracking algorithm. The tracking process starts from an initial point which is selected manually by the user. Vessel edge points are then detected iteratively using local grey levels statistics and the information obtained from the previous iterations. This process stops when current blood vessel ends or the vessel branches are found. All found branches are considered as new blood vessels and are processed by the same iterative algorithm. Many methods have been used to find branching in a vascular tree and endpoints when tracking blood vessels [10,27,37]. The logic to detect these important features is based on center line extraction [10], filter response [27], or diameter computation [37] for branching and branch detection [27] or poor contrast [37] for endpoint localization. None of them uses probabilistic consideration as the case in our approach.

For clarity, the tracking process is described as follows:

- **Initialization**: In practice, two initial edge points are chosen manually diametrically opposed on the interested blood vessel. Center point is chosen and initial tracking direction is set along local vessel's direction.
- **Iteration**: At current iteration, local blood vessel parameters including vessel edge points, center point, direction and diameter are supposed to be obtained in the previous iteration. A search window with a statistical sampling method is then used to select the most probable vessel configuration (normal, bifurcation or crossing) using Bayesian theory with MAP as a criterion. This selection is done when testing all the possible configurations with 2 edge points (normal), 4 edge points (bifurcation), or 6 edge points (crossing). Blood vessel parameters including edge points, direction, and diameter are then obtained for the next iteration. The configuration models will be described in detail below.
- **End**: When the blood vessel diameter is less than one pixel, the current vessel's end is found and the tracking of the current vessel stops. Besides, when the vessel branches are found, all

initial information of the branches are obtained by the algorithm. In this situation, the current tracking process stops, and the tracking of these branches, which are considered as new blood vessels, starts.

2.2. Dynamic search window

At a given step, a semi-ellipse drawn in the current studying area is regarded as a search window (see Fig. 1). In order to deal with the complex geometrical features of the retinal blood vessels, the semi-ellipse should be dynamic and self-adapting during the tracking process. When vessel's diameter increases, the semi-ellipse should be enlarged in order to cover the potential position of the new edge points. When vessel's diameter decreases, we should reduce it to avoid inaccurate detection, such as detecting another vessel near the current one. Besides, the minor axis of the ellipse, which is parallel to local vessel's direction, could denote the look-ahead distance. To make the algorithm robust to highly curved blood vessel, the minor axis is set adaptive to local vessel's curvature. A smaller minor axis is chosen when vessel's curvature increases, so that the tracking direction could catch up with vessel's change more easily.
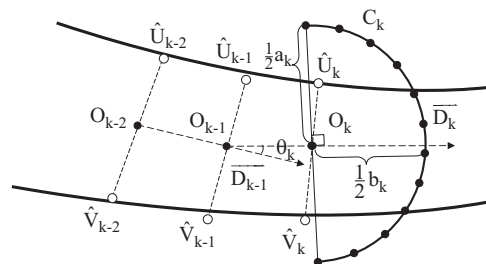
At iteration k, vessel edge points $\hat{U}_k$, $\hat{V}_k$, center point O_k, direction $\overrightarrow{D_k}$ and diameter d_k are known parameters. O_k is the middle point of $[\hat{U}_k, \hat{V}_k]$. $\overrightarrow{D_k}$ heads towards $\overrightarrow{O_{k-1}O_k}$ and is defined as a unit vector. Local diameter is $d_k = |\hat{U}_k\hat{V}_k|$. A semi-ellipse C_k is defined to be centered on O_k and heading towards $\overrightarrow{D_k}$. As shown in Fig. 1, its major axis a_k is perpendicular to $\overrightarrow{D_k}$ while the minor axis b_k is parallel to it. a_k and b_k are fixed as follows:

$$\begin{cases} a_k = \alpha d_k \\ b_k = \beta(\pi - \theta_k)\, d_k \end{cases} \tag{1}$$

where θ_k is the angle between the current and previous vessel directions: $\theta_k = \arccos(\overrightarrow{D_{k-1}} \cdot \overrightarrow{D_k})$. θ_k provides the information of local vessel's curvature. α, β are constant factors whose values have been set based on the simulated results. In this study, α was fixed to 2, and β was set to $1/\pi$ so that the magnitude of the minor axis is less than local vessel's diameter.

2.3. Configuration model

A number of edge points candidates are selected on the semi-ellipse search window. In order to choose new edge points among these candidates, we define configuration models which combine the points candidates with vessel's structures. In this study, we categorize vessel's structures into three types of configurations: normal, bifurcation and crossing. The normal case is regarded as the situation in which only a single vessel exists in current search

Fig. 1. Statistical sampling scheme: $\hat{U}$ and $\hat{V}$ are the vessel edge points, O is the center point, $\overrightarrow{D}$ is the vessel direction, and k is the index of the iteration. C_k is the semi-ellipse at iteration k. a_k and b_k are the major and minor axes of C_k, respectively. Black points on C_k show the possible locations of new edge points.