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Research Article

HUMAN AUTHENTICATION USING RETINAL BLOOD VESSELS-A MODIFIED APPROACH

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ABSTRACT

Measurements of retinal blood vessel using morphology have been shown to be related to the risk of cardiovascular diseases. The improper identification of vessels may result in a large variation of these measurements, leading to a wrong clinical diagnosis. In this paper, we address the problem of automatically identifying true vessels as a post-processing step to vascular structure segmentation. We model the segmented vascular structure as a vessel segment patterns. We design a method to solve this optimization problem and evaluate it on a large real-world dataset of 50 retinal images. The patterns are stored in the database. We use the stored patterns to perform authentication process.

Keywords: Ophthalmology, Optimal Vessel Forest, Retinal Image Analysis, Simultaneous Vessel Identification, Vascular Structure.

INTRODUCTION

A Retinal image provides a snapshot of what is happening inside the human body. In particular, the state of the retinal vessels has been shown to reflect the cardiovascular condition of the body. Measurements to quantify retinal vascular structure and properties have shown to provide good diagnostic capabilities for the risk of cardiovascular diseases, arteries and veins in the retinal image, respectively.

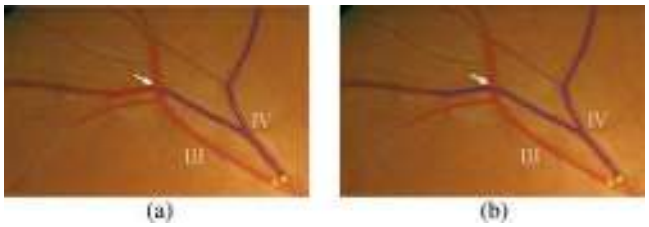


Figure 1: (a) Vessel III wrongly connected to a segment that should belong to IV. (b) Vessel correctly identified.

crossovers are often mistaken as vessel bifurcations, leading to I and II being regarded as a single vessel. Fig. 1(b) shows the correctly identified vessel structures for vessels I and II marked in blue and red, respectively. Note that the line segment at the second crossing (larger circle) is shared by vessels I and II.

In order to disambiguate between vessels at bifurcations and crossovers, we need to figure out if linking a vessel segment to one vessel will lead to an adjacent vessel being wrongly identified. For example, in Fig. 1(a), if we identify vessel III first without any knowledge of vessel IV, the junction indicate .Consequently, vessels III and IV will be incorrectly identified, leading to a large difference in vessel measurements. However, if both vessels were constructed and considered at the same time, it becomes obvious that one of the branches of vessel III should be an extension of vessel IV, as shown in Fig. 1(b). By considering multiple vessels simultaneously, information from other vessels can be used to better decide on the linking of vessel segments.

In this paper, we describe a novel technique that utilizes the global information of the segmented vascular structure to correctly identify true vessels in a retinal image. We model the segmented vascular structure as a vessel segment graph and transform the problem of identifying true vessels to that of finding an optimal forest in the graph. An objective function to score forests is designed based on directional information. Our proposed solution employs candidate generation and expert knowledge to prune the search space. We demonstrate the effectiveness of our approach on a large real-world dataset of 2446 retinal images. The proposed technique has been incorporated as part of the semi-automated Singapore Eye Vessel Assessment (SIVA) system that has been used in real-

world studies in both the community and hospital-based patient populations[1-4].

RELATED WORK

Retinal vessel extraction involves segmentation of vascular structure and identification of distinct vessels by linking up segments in the vascular structure to give complete vessels. One branch of works, termed vessel tracking, performs vessel segmentation and identification at the same time[5-8]. These methods require the start points of vessels to be predetermined. Each vessel is tracked individually by repeatedly finding the next vessel point with a scoring function that considers the pixel intensity and orientation in the vicinity of the current point in the image. Bifurcations and crossovers are detected using some intensity profile. Tracking for the same vessel then continues along the most likely path. This approach of tracking vessels one-at-a-time does not provide sufficient information for disambiguating vessels at bifurcations and crossovers.

Another branch of works treat vessel identification as a post-processing step to segmentation[9]. The work is required the user to resolve the connectivity of bifurcation and crossover points before vessels were individually identified. For a graph formulation was used with Dijkstra's shortest-path algorithm to identify the central vein. Similarly, Joshi *et al.* used Dijkstra's algorithm to identify vessels one-at-a-time and evaluated their method on a set of 15 images. However, these methods may lead to incorrect vessel identification because choosing the correct vessel segment to connect at a bifurcation or crossover requires information from other nearby vessels. Al-Diri *et al* used expert rules to resolve vessel crossovers and locally linked up segments at these crossovers to give a vascular network. However, they did not identify com-plete vessels.

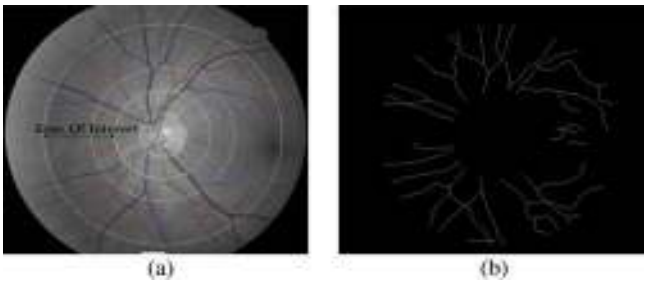


Figure 2: Example of junctions. Pixels belonging to a junction are shaded.

GRAPH TRACER

Our proposed method aims to identify vessels and represent them in the form of binary trees for subsequent vessel mea-surements. It has two main steps:

1) Identify crossovers, and

2) Search for the optimal forest (set of vessel trees). We describe the details in the following sections.

A. Identify Crossover Locations

Vessels in a retinal image frequently cross each other, at a point or over a shared segment. We call the former crossover points and the latter crossover segments.

Note that short segments between two junctions are not necessary true crossover segments, as shown in Fig. 6(b). Hence, we propose to use the directional change between adjacent segments and their pixel intensity values to differentiate crossover segments.

where $\mu(s)$ is the mean intensity of the pixels in

Condition 1 of Definition 7 handles the case when *seg* is at a bifurcation. For example, segment 4 in Fig. 8 is not a crossover segment due to the small directional change between segments 1 and 5.

Condition 2 in Definition 7 handles the case when the length of *seg* is too short to determine the directional change. In this case, we check if the adjacent segments of *seg* forms a rea-sonable cross pattern, i.e., if there exists some pairing of the segments in S_1 with those in S_2 such that their directional change are less than 30°. Otherwise, we partition A into two such that the sum of the *sd* of both partitions is minimum. If this minimum is less than the *sd* of all the segments in A, then *seg* is a crossover segment.

Find the Optimal Forest

Next, we model the segments as a segment graph and use constraint optimization to search for the best set of vessel.

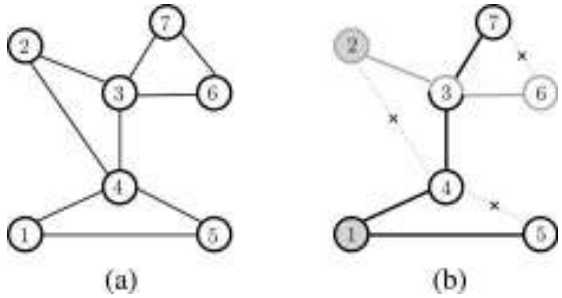


Fig. 3. (a) Segment graph corresponding to the segments in Fig. 3. (b) Ex-ample forest of two binary trees (gray and black) corresponding to two vessels rooted at segments 1 and 2 in Fig. 8.

The goal is to obtain a set of binary trees from the segment graph such that each binary tree corresponds to a vessel in the retinal image.

A binary tree is a natural representation of an actual blood vessel as it only bifurcates. Segment end points near the inner circle of the zone of interest are automatically identified as root pixels. The root of each tree corresponds to the root segment that contains a unique root pixel, i.e., the yellow dots in Figs. 1 and 2. Fig. 10 shows the segment graph and two binary trees corresponding to the two vessels in Fig. 8. We formulate the goal of simultaneous identification as a constraint optimization problem (COP).

To solve the COP, we use a candidate enumeration algorithm that utilizes the lower bound of the cost function to prune the search space.

EXPERIMENT RESULTS

We evaluate our proposed method on 2446 retinal images of patients from the Singapore Malay eye study [17]. For each image, the line image of the retinal vessels is obtained using the semi-automated retinal image analysis tool, SIVA. Trained human graders then follow a protocol to verify the correctness of the vascular structure obtained, e.g., arteries, veins, crossover locations, and branch points. We use these verified vascular structures as the *gold* standard and call the corresponding vessel center lines as *clean* line images.

We implement the *Graph* tracer and a *Solo* tracer that traces vessels individually without regard for other vessels. The Solo tracer works as follows: it starts from one root pixel and follows the adjacent pixels in the line image. When a split is encountered, a local look ahead is done to inspect the directional change of the segments. If they fit the crossover profile, the split is treated as a crossover; otherwise, it is a bifurcation and the tracer will follow both paths. It is greedy because unless a crossover is identified, it will add all the connected pixels to the same vessel.

All tracers are given the same OD, line image, artery/vein labeling, and use the same method to compute the vessel diam-eters. We evaluate their performance on both clean and *noisy* line images. Noisy line images are obtained using an existing vessel segmentation algorithm[9] and is representative of the real-world situation where segmentation is often imperfect. We use the following evaluation metrics based on the pixels in the entire vessels. Let *Big6* refer to the six largest arteries and veins ranked by the average width of the first segment of each vessel. Further, if a pixel of a traced vessel exists in the gold standard, it is called a *matched* pixel.

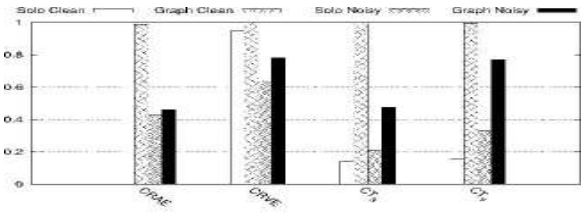
1) *Pixel precision*: Total number of matched pixels divided by total number of traced vessel pixels.
2) *Pixel recall:* Total number of matched pixels divided by total number of gold standard pixels.
3) *Big6 precision:* Total number of matched pixels divided by total number of traced pixels of Big6.
4) *Big6 recall:* Total number of matched pixels divided by total number of gold standard pixels of Big6.

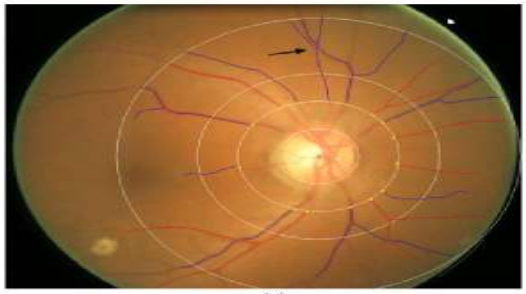
In our first set of experiments, we use both clean and noisy line images as inputs to the tracers. Fig. 12 shows the results. For the clean line images, both Solo and Graph tracers display good performance. In particular, the Graph tracer is able to achieve near perfect pixel precision (98.9%) and pixel recall (98.7%). The performance of both tracers decrease for noisy line images. We observe that the difference between the Solo tracer and Graph tracer is more pronounced, indicating that the Graph tracer is more robust. From these results, we conclude that tracing all vessels simultaneously is better than tracing vessels individually without current knowledge of other vessels.

For the second set of experiments, we analyze the impact of our methods on measurement quality by computing the *Pearson correlation coefficient (PCC)* between the measurements of the traced vessels and the gold standard. These measurements are automatically computed from the traced and gold standard vas-cular structures, respectively. The vessel measurements CRAE, CRVE, and average curvature tortuosity of arteries (CT_a) and veins (CT_v) have been found to be correlated with risks factors of cardiovascular diseases and are positive real numbers.

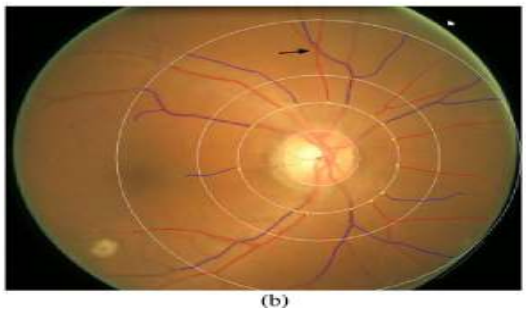
The PCC for noisy line images reaffirms that Graph tracer is more robust than the Solo tracer in the presence of noise. We observe that measurements of veins are consistently more correlated than those of arteries, indicating that arteries are more difficult to segment than veins.

Visual inspection on the results reveals that the Solo tracer often traces overlapping vessel segments or wrongly connected bifurcations that lead to poor measurements. An example mis-take made by the Solo tracer on a clean line image is shown in Fig. 14. The arrows indicate the location where two vessels cross near bifurcations that causes the Solo tracer to erroneously link segments belonging to other vessels. In contrast, the Graph tracer takes both overlapping vessels into account when jointly identifying the vessels resulting in better identification.





(a)



(b)

CONCLUSION

We have presented a novel technique to identify true vessels from retinal images. The accurate identification of vessels is key to obtaining reliable vascular morphology measurements for clinical studies. The proposed method is a postprocessing step to vessel segmentation. The problem is modeled as finding the optimal vessel forest from a graph with constraints

on the vessel trees. All vessel trees are taken into account when finding the optimal forest; therefore, this global approach is acutely aware of the mislinking of vessels. Experiment results on a large real-world population study show that the proposed approach leads to accurate identification of vessels and is scalable.

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