

RETINAL VASCULAR NETWORK MODEL

An Automatic Approach

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Abstract: In this paper, we propose a retinal vascular network model, which is an automatic process of generating a graph representation (i.e., a tree) of the retinal blood vessels and includes vessel geometrical features. It maps the retinal blood vessels and can facilitate vascular features such as the vessel width, bifurcation angle, among others to predict or earlier diagnose cardiovascular and related diseases. The proposed tree-model is based on vessel's centerline, cross-sectional width, and bifurcation, branching and crossover points. The optic disc center is computed using the *Hough transformation* and vessel centerlines are tracked from out side its radius. Blood vessels are fragmented as vessel-segments based on the bifurcation, branching and crossover points. For each blood vessel we construct a binary tree which is linked in the root of the tree-model. Our automated method achieves an accuracy of 91.23% in extracting the vessel-segments.

1 INTRODUCTION

Recent research suggests that retinal imaging can play an important role in prediction or earlier diagnosis of diseases. For example, research shows that retinal vessel caliber changes are associated with hypertension, diabetes and cardiovascular diseases (CVDs). Usually, the retina is analyzed by direct viewing or a semi-automatic method. However, direct viewing of the eye or the manual analysis of the retinal photographs is time-consuming and expensive as it requires human effort. Semi-automatic method also requires an expert intervention and significant amount of time. Thus an automated image analysis should play a central role in analyzing large volume of images.

An automatic method of mapping the retinal vasculature and corresponding features, with high accuracy, will greatly enhance the speed and significantly reduce the costs involved in diagnosing diseases. This paper presents a retinal vascular network model (i.e., tree-model) to achieve these goals. Although a number of schemes (Pinz et al., 1998),(Chow et al., 2006),(Li and Qu, 1998),(Mattes et al., 1999) has been proposed to represent image features in a tree structure, none of these methods is concerned with retinal vascular imaging. The tree-model is an automated method for mapping the blood vessels and cor-

responding features in a color retinal image. It represents the vascular features in a graph form shown in Figure 1b. The features are incorporated in consideration of their importance in the diagnosis of diabetes, hypertension or cardiovascular diseases.

Several research articles (Lin et al., 2009), (Zhou et al., 2005), (Martinez-Perez et al., 2002), (Taarnhoj et al., 2008), (Stanton et al., 1995), (Hart et al., 1999) have appeared on retinal vascular feature analysis for disease diagnosis. Most of these techniques are manual or semi-automatic, require expert intervention and none of these techniques is based on a graphical representation of the vascular features. In (Martinez-Perez et al., 2002), the authors have presented a method which can trace an individual vessel and summarize its features. Another method for vessel tracing is presented in (Lin et al., 2009). None of the methods obtain vascular features with maintaining actual vessel-segments' hierarchy. None of these techniques is able to match the vascular features from two images based on vessel-segments' hierarchical position, which is important for patient's longitudinal studies.

Previous methods of tree representations (Mattes et al., 1999),(Li and Qu, 1998),(Mosorov, 2005),(Chow et al., 2006) mainly consider the global higher level features (i.e., histogram) and segmented regions as corresponding features of the images. For

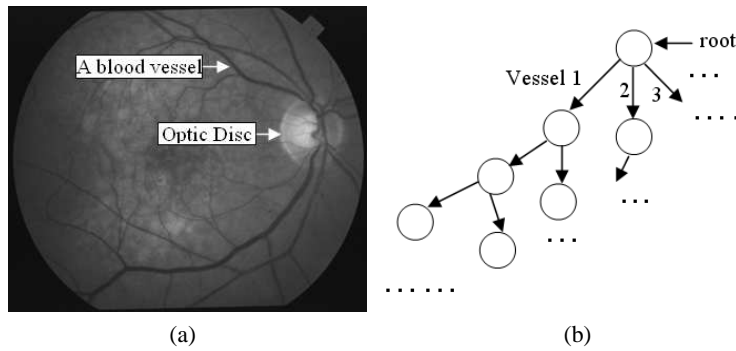


Figure 1: A retinal image showing the blood vessels (a) and proposed graph model of the retinal vascular network (b).

instance, an image is represented with its histogram on the root and the local region based features on the children nodes of a tree, which is used for image classification. None of these schemes consider a retinal vascular network and its feature(s) representation which is the main focus in our work.

The rest of the paper is organized as follows. Section 2 provides the method of tree-model construction, and section 3 provides evaluation of the tree-model. Conclusions are drawn in section 4.

2 TREE-MODEL CONSTRUCTION

The tree-model is constructed by traversing through the vessel centerline image. The details of the tree-model construction procedure are described in the following subsections.

2.1 Vessel Centerline Detection

In (Bhuiyan et al., 2007a) a method is presented for blood vessel segmentation based on the texture property analysis of vessel and non vessel parts in the color retinal image. Following this a morphological skeletonisation operation is applied on the segmented image to extract the vessel centerlines.

2.2 Vessel Landmarks Classification

A method for blood vessel bifurcation, branching and crossover point (landmark points) detection using the vessel geometrical features is proposed in (Bhuiyan et al., 2007b). Vessel centerline image and a width measurement method (Bhuiyan et al., 2008) are used for landmark points classification process.

2.3 Fragmenting Vessel Centerlines

We fragment the vessel centerlines into different vessel-segments based on the landmark points and use this fragmented centerline image to construct the tree-model. This is for searching and traversing the vessel centerlines as well as constructing the tree-model conveniently. For fragmenting the vessel centerlines, we use the landmark points along with the corresponding vessel-segments' start or end points. The landmark points and their corresponding vessel-segments' start or end points are obtained from landmark points classification method (Bhuiyan et al., 2007b). We compute the connectivity (i.e., the path) between each landmark point and its corresponding vessel-segment's start or end points, and delete the connectivity for fragmenting the centerlines. Figure 2 shows a cropped vessel centerline image (left) and its fragmented output image (right).



Figure 2: A cropped vessel centerline image (left) and its fragmented output image (right).

2.4 Optic Disc Center Computation

Optic disc center is computed by applying *Hough transformation* on the optic disc region in the image. To detect the optical disc, we find a rough estimation of pixel positions by thresholding the retinal image on intensity value. Then we determine a square region on which we search for a circular object. Hence, we can apply Hough transformation in a smaller region which provides more efficiency in optic disc center computation. We apply *Hough transformation* in the edge image which we obtained earlier.

2.5 Binary Tree Construction

After computing the optic disc center and radius, we find the vessel centerline pixels by searching in a circular region outside this radius. Once a vessel centerline pixel is found, it is inserted into the root of the tree-model and a binary tree construction starts for this vessel. This starting pixel is considered for initiating the traversal process in the fragmented vessel centerline image.

The traversal process uses the 3×3 connectivity mask to find the neighboring pixels in the vessel-segment. The mask is applied by considering the starting pixel of any vessel-segment as its center. Once a neighboring pixel is found it replaces the previous one. Each time a pixel position is considered a flag value is assigned so that this pixel is not considered for the next time. Once the traversal process reaches the vessel-segment's end point, it stops if it belongs to a bifurcation or a branch. The features of this vessel-segment are computed and inserted into the corresponding node in the tree-model. Using this vessel-segment's end point we determine the starting point of the daughter vessels and the landmark point. After receiving the starting points, we classify their corresponding vessel-segments as the left and right children in the tree-model for the current parent. We discuss this in the next section. The vessel-segment, which is classified as a left child, is considered for continuing the process. The right vessel-segment's information is inserted into a stack and considered latter for constructing the tree-model.

For crossover points we use flag values for the end points. We determine the landmark point for the current vessel-segment's end point and find the other vessel-segments' start or end points. Then we measure the slopes considering the line segments between the landmark and vessel segments' start or end points. The traversal process selects the vessel-segment, which has the closest slope value to the current vessel-segment.

Determination of Left Child and Right Child in the Tree-model

A vessel-segment is classified as the left or right child in the tree-model, based on its starting point location around the parent vessel. Let us consider Figure 3. Assume that the end point returned by the traversal process is (x_1, y_1) . Using this end point, we determine other two vessel-segments' starting points (x_2, y_2) and (x_3, y_3) along with the landmark point (x_L, y_L) . From these points, we can obtain the centerline equation as follows

$$(x - x_1)/(x_1 - x_L) - (y - y_1)/(y_1 - y_L) = 0 \quad (1)$$

We compute the slope of the line (i.e., vessel-segment) as $m = (y_1 - y_L)/(x_1 - x_L)$. We fit (x_2, y_2) and (x_3, y_3) to the above line equation. If the slope $m > 0$ (as in Figure 3(a)) and (x_2, y_2) returns a value less than the value returned by (x_3, y_3) for the left hand side in line equation (2), we assign (x_2, y_2) (i.e., its vessel-segment) as a left child in the tree-model, otherwise it is a right child. If the slope $m < 0$ (as in Figure 3(b)), the rules are opposite.

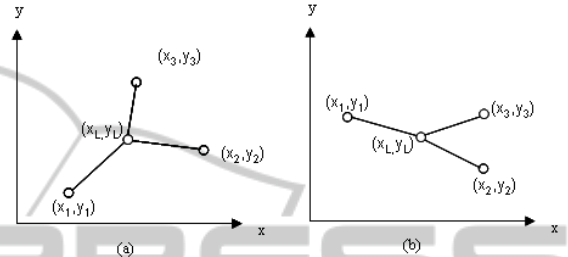


Figure 3: Vessel-segment appears with positive slope (a) and negative slope (b).

If the centerline segment is parallel to x-axis or y-axis (Figure 4) we find the positions (as left or right) of these points as follows. If the vessel-segment is parallel to y-axis (i.e., $x_L - x_1 = 0$), at first we consider if $y_L - y_1 > 0$ (as in Figure 4(a)). In this case, if $x_2 > x_3$, (x_2, y_2) is on the left side. Otherwise it is on the right side. If we invert the vessel direction in Figure 4(a), i.e., $y_L - y_1 < 0$, the rules are opposite. Similar rules are applied for the vessel-segments which are parallel to x-axis (Figure 4(b)).

Once we classify these vessel-segments starting points as left and right children, we consider the left child (i.e., vessel-segment) to be inserted into the tree-model. The right child (i.e., starting point) is inserted into a stack along with the address of its parent node (to be considered latter). We implement the stack using a linked list so that it can handle essentially any number of elements dynamically.

Each time the traversal algorithm returns a vessel-segment's end point, using this we search for the landmark point and starting points of the daughter vessel-segments. If there is no start point, the traversal pro-

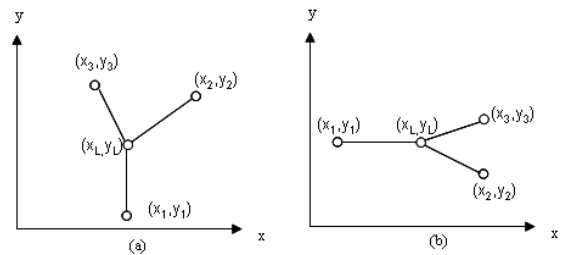


Figure 4: Vessel-segment appears as parallel to y-axis (a) and x-axis (b).

cess is terminated. Then we compute the vascular features for the current vessel-segment and insert them into the corresponding node in the tree-model. Following that we access the stack for a vessel-segment's start point along with its parent address in the tree-model. Then consider this vessel-segment for inserting into the tree-model. If there is a start point of a vessel-segment, we trace this vessel-segment and insert its features into the corresponding node in the tree-model. This process continues until the end of the entire vessel or the stack is empty. Once a vessel is considered for the tree-model, the binary tree construction is started for the next vessel and so on.

2.6 Appending Vascular Features

The vascular features are added to each node, which represents a vessel-segment. Each time a node is inserted, it also includes the corresponding vascular features. Some vascular features require daughter vessel-segments information. These are: ratio of trunk width and branch width, acute angle between parent and smaller daughter vessel, and bifurcation angle. For these we need to consider the related vascular features for parent and daughter vessel-segments. Therefore, a node includes only the features of the same vessel-segment if it does not have any daughter vessel-segments.

3 EVALUATION OF THE TREE-MODEL CONSTRUCTION

We evaluate our technique using two publicly available data sets with images of diseased retinas; the STARE database (Hoover et al., 2000), (STARE-project, 2006) and the DRIVE (Staal and Abramoff, 2004). We demonstrate the feature analysis using the STARE database which has labeled images of diabetic and normal retinas. It took approximately 1.69 minutes using MATLAB version 7.5 to produce each output tree-model on a 2.66 GHz Pentium 4 Duo CPU with 3.25 GB of RAM. For evaluating our method, we considered the vessel-segments' hierarchy and positional information (i.e., daughter vessel as left or right to the parent vessel) and observe if they are represented similarly in the tree-model.

For each image, we selected the starting point coordinates of a vessel, i.e., actual starting position of a vessel-segment (Figure 5). We observed the tree-model to see if this point was assigned in the root. Then we tracked the end point of that vessel-segment

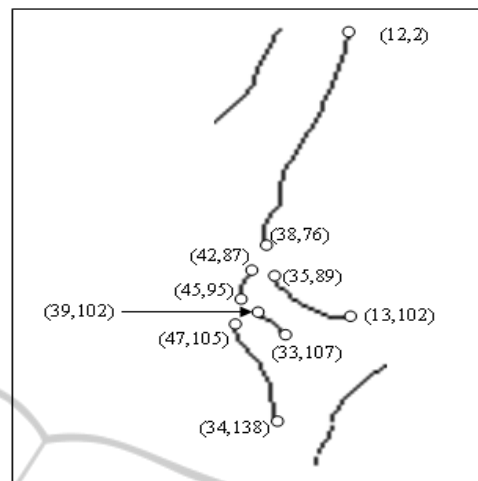


Figure 5: A cropped vessel-segments with marked end points.

and checked whether it is assigned to corresponding binary tree of the tree-model or not (Table 1). Following that we considered the daughter vessels on the labeled image and then checked the tree-model if they are correctly assigned as left and right children nodes in the corresponding binary tree. We continued this process until the end of each vessel and stopped after considering all the vessels in an image.

Table 2 shows the number of calculated vessel-segments in a manually labeled image and the number of vessel-segments that were represented by the corresponding binary tree in the tree-model. When the number of vessel-segments were correctly inserted into the corresponding binary tree in the tree-model, it is true positive or agreed (column 4). The number of vessel-segments that were missed in the corresponding binary tree of the tree-model, shown as missed (column 5). When a vessel-segment was inserted in the binary tree of the tree-model but is not a part of the binary tree (i.e., belong to another vessel) it is spurious (column 6). After finding these segments for all vessels we used the following formula to compute error in constructing the tree-model for an image.

Error = (Segments missed + Spurious segments)/(Total number of vessel-segments).

For each vessel the accuracy $(1 - error) \times 100$ is obtained in percentile. Then we measure the accuracy of constructing the tree-model for an image by averaging the accuracy of all the vessels. We considered forty images (twenty from DRIVE and twenty from STARE database) for evaluation process and achieved an overall accuracy of 91.23%. Table 3 shows the process on five different images. We note that the construction accuracy of the tree-model depends on the segmentation of the blood vessel. If the segmentation

Table 1: A binary tree representation of a blood vessel with node values.

Index	End Point Coordinate		nodes			Values			
	x	y	parent	left child	right child	Tortuosity	$\frac{w_2^2+w_3^2}{w_1^2}$	Bi Angle	L/W
1	38	76	0	2	3	0.112	1.223	0.893	21.25
2	45	95	1	4	5	0.112	1.032	0.793	6.12
3	13	102	1	0	0	0.08	0	0	14.12
4	34	138	2	0	0	0.15	0	0	14.89
5	33	107	2	0	0	0.112	0	0	5.23

Table 2: The evaluation of tree-model for an image.

Vessel Number	Tree-Model Construction		Post Analysis			Accuracy (%)
	Total Vessel-Segment	Number in Tree	Agreed	Missed	Spurious	
1	12	10	10	2	0	83.33
2	7	7	7	0	0	100
3	14	12	10	2	2	71.43
4	9	9	8	0	1	88.89
5	11	11	11	0	0	100
6	11	11	11	0	0	100
7	6	6	6	0	0	100
8	12	12	11	1	1	83.33
9	5	5	5	0	0	100
Average Accuracy						91.89

Table 3: Overall Accuracy on Tree-Model Construction.

Image Number	Total Vessel-Segment	Accuracy (%)	Average Accuracy(%)
1	80	91.89	91.44
2	67	92.98	
3	79	90.05	
4	82	89.29	
5	73	93.01	

method fails to obtain a minor vessel, the next process fails to obtain the landmark point. Consequently, we missed a node in the tree-model.

Among the vascular features, we evaluated the width measurement accuracy against five different graders and the results are reported in (Bhuiyan et al., 2008). Further, the accuracy of bifurcation and branching angle measurement along with landmark classification are reported in (Bhuiyan et al., 2007b). Blood vessel tortuosity is reported in (Bhuiyan et al., 2010).

4 CONCLUSIONS

In this paper we proposed and evaluated a new method for constructing a vascular network model (the tree-model). We used the vessel centerline and edge image and classified landmark points to con-

struct this tree-model. We computed vascular features which are significant for disease diagnosis and provided an example of using the tree-model in disease diagnosis.

The primary goal of our research is to facilitate and access the vascular features efficiently by representing these in a graphical form. The medical practitioners can access and analyze these vascular features according to their requirements.

Our experimental results establish that the method can be readily used in medical applications with high accuracy. Further, we envisage that the tree-model will be very efficient in finding the corresponding vessels for matching two images. In this tree structure, each vessel segment can be searched with $O(\log n)$ operations where n is the number of vessel-segments.

The proposed tree-model is based on the blood vessel segmentation accuracy, and the tree-model is achieving 91.23% construction accuracy. We are cur-

rently investigating various approaches to improve our segmentation method based on texture, edge information and Markov random field. This should further enhance the accuracy of the tree-model construction.

Our contributions in this paper are summarized below:

- We proposed a new and efficient method to construct a tree-model, which includes a number of significant vascular invariant features.
- The tree-model is an automatic process to represent the vascular features and can readily be used in feature analysis for earlier diagnosis of different diseases.

REFERENCES

- Bhuiyan, A., Nath, B., Chua, J., and Ramamohanarao, K. (2008). Vessel cross-sectional diameter measurement on color retinal image. *Communications in Computer and Information Science*, 25:214–227.
- Bhuiyan, A., Nath, B., Chua, J., and Kotagiri, R. (2007a). Blood vessel segmentation from color retinal images using unsupervised classification. *In the proceedings of the IEEE International Conference of Image Processing*, pages 521–524.
- Bhuiyan, A., Nath, B., Chua, J., and Ramamohanarao, K. (2007b). Automatic detection of vascular bifurcations and crossovers from color retinal fundus images. *Proceedings of Third International IEEE Conference on Signal-Image Technologies and Internet-Based System (SITIS)*, pages 711–718.
- Bhuiyan, A., Nath, B., Ramamohanarao, K., Kawasaki, R., and Wong, T. Y. (2010). Automated analysis of retinal vascular tortuosity on color retinal images. *Journal of Medical Systems*, pages 1–15.
- Chow, T. W. S., rahman, M. K. M., and Wu, S. (2006). Content-based image retrieval by using tree-structured features and multi-layer self-organizing map. *Pattern Analysis and Applications*, 9:1–20.
- Hart, W. E., Goldbaum, M., Cote, B., paul Kube, and nelson, M. (1999). Measurement and classification of retinal vascular tortuosity. *International Journal of Medical Informatics*, 53:239–252.
- Hoover, A., Kouznetsova, V., and Goldbaum, M. (2000). Locating blood vessels in retinal images by piece-wise threshold probing of a matched filter response. *IEEE Transactions on Medical Imaging*, 19(3):203–210.
- Li, X. and Qu, X. (1998). Matching spatial relations using db-tree for image retrieval. *Proceedings of the International Conference on Pattern Recognition (ICPR'98)*, 2:1230–1234.
- Lin, K.-S., Tsai, C.-L., and Sofka, M. (2009). Vascular tree construction with anatomical realism for retinal images. *In the Proceedings of Ninth IEEE International Conference on Bioinformatics and Bioengineering*, pages 313–318.
- Martinez-Perez, M. E., Hughes, A. D., Stanton, V., Simon A Thom, N. C., Bharath, A. A., and Parker, K. H. (2002). Retinal vascular tree morphology: A semi-automatic quantification. *IEEE Transactions on Biomedical Engineering*, 49(8):912–917.
- Mattes, J., Richard, M., and Demongeot, J. (1999). Tree representation for image matching and object recognition. *Proceedings of the 8th International Conference on Discrete Geometry for Computer Imagery*, LNCS 1568:298–309.
- Mosorov, V. (2005). A main stem concept for image matching. *Pattern Recognition Letters*, 26:1105–1117.
- Pinz, A., Bernogger, S., Datlinger, P., and Kruger, A. (1998). Mapping the human retina. *IEEE Transactions on Medical Imaging*, 17:606–619.
- Staal, J. and Abramoff, M. D. (2004). Ridge-based vessel segmentation in color images of the retina. *IEEE Transactions on Medical Imaging*, 23(4):501–509.
- Stanton, A. V., Wasan, B., Cerutti, A., Ford, S., Marsh, R., Sever, P. P., Thom, S. A., and Hughes, A. D. (1995). Vascular network changes in the retina with age and hypertension. *Journal of Hypertension*, 13:1724–1728.
- STARE-project (2006). <http://www.ces.clemson.edu/~ahoover/stare/>. last accessed on 21 November.
- Taarnhoj, N. C. B. B., Munch, I. C., Sander, B., Kessel, L., Hougaard, J. L., and Kyvik, K. (2008). Straight versus tortuous retinal arteries in relation to blood pressure and genetics. *British Journal of Ophthalmology*, 92:1055–1060.
- Zhou, P., Wang, M., and Cao, H. (2005). Research on features of retinal images associated with hypertension and diabetes. *Proceedings of the 2005 IEEE Engineering in Medicine and Biology 27th Annual Conference*, pages 6415–6417.