International Research Journal of Engineering and Technology (IRJET) e-ISSN: 2395-0056
Volume: 06 Issue: 10 | Oct 2019 www.irjet.net p-ISSN: 2395-0072

Retinal Blood Vessel Tree Segmentation using Fast Marching Method

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Abstract - *In this work, Fast Marching Method (FMM) has been suggested for Retinal blood vessels segmentation. This method had been implemented using the M language in MATLAB R2016b. In this work start and end points had been determined so that we produce the basic information for the FMM algorithm to start exploring the retinal image. FMM performance had also been compared to other techniques used for retinal blood vessel detection like "Matched Filters". The results showed that the FMM performance overcame some of those techniques and close to other high resolution methods. The FMM algorithm had been validated using the well-known "DRIVE" data set and achieved a resolution of 93% with iteration number between 500 to 1000 (according to the optic disk position in the image) with an average time of 0.57 seconds for each iteration which means that the total running time is 5-10 minutes. FMM had also been validated using STARE data set and achieved a TPR of 90% for 700x605 STARE images in 15 minutes, and a TPR of 86% in 2.6 minutes when reducing image size to 350x303.*

Key Words: Fast marching method (FMM), Retinal blood vessel detection.

1.INTRODUCTION

The retina is a light-sensitive tissue that forms the inner layer of the eye. It contains neural tissues and blood vessels and considered as the only tissue of human body we can use to see blood vessel non-invasively which have great importance in diagnosis and treating many diseases such as diabetes, hypertension, cardiovascular diseases and cancers. segmenting retinal blood vessels is a challenging problem because of the variety of illumination conditions, low contrast small vessel detection, and the trade between accuracy and computational efficiency. Retina can be visualized as an image using the fundus camera. Those images are often noisy, poorly contrasted and non-uniformly illuminated in addition they suffer from brightness variations along the same image and likewise between different images.

2. Previous work

In order to segment retinal blood vessel tree, many methods have been reported including supervised methods [1] and unsupervised methods [2]. Many applications have been presented in the diagnosis of various eye and systemic diseases, such as diabetes, hypertension, and angiogenesis. Typical blood vessel detection methods apply an initial estimation of the vessel network, after that, tuning methods are used in order to improve the accuracy of the vessel detection [3]. Finally, post processing methods are applied to remove false detected vessels. Among the most important methods they mentioned mathematical morphology transformation [1], and vascular intersection detection [4].

In [3] a new multi-scale line-tracking procedure have been proposed. It starts from a small group of pixels, derived from a brightness selection rule, and terminates when a cross-sectional profile condition becomes invalid. The multi-scale image map is derived after combining the individual image maps along scales. This map contains pixels that certainly belong to a vessel. The initial vessel network is derived after map quantization of the multi-scale confidence matrix. After that median filtering is applied in the initial vessel network, and this restores disconnected vessel lines and eliminates noisy lines. At the end, erroneous areas are removed (during post-processing) using directional attributes of vessels and morphological reconstruction. Author in [3] declared "The experimental evaluation in the publicly available DRIVE database shows accurate extraction of vessels network. The average accuracy of 0.929 with 0.747 sensitivity and 0.955 specificity is very close to the manual segmentation rates obtained by the second observer".

In [5], a set of automated methods were proposed in order to analyze the retinal vessel network and to quantify its morphologic properties taking into consideration both arteries and veins, in two-dimensional color fundus images. The analytical methods included Formation of a well-connected vessel network, Structural mapping, Artery-venous classification and Blood vessel hemorrhage detection. On the other hand, quantification methods included vessel morphology analysis based on the measurement of tortuosity, width, branching angle, branching coefficient, and fractal dimension. Morphological parameters were measured with respect to arteries and veins separately in a vessel network. Then methods have been validated with the manually annotated retinal fundus images as a ground truth. The accuracy of the method was quantified using two metrics

1- misclassification rate: this metric gave a classification error rate of (17.07%) for single vessel trees (without AV crossing) and 4.96% for paired vessel trees (with AV crossing).

2- the histogram of pixel misclassification per image: The average misclassification rate was 8.56% which means that the accuracy of correct classification is 91.44%.

[5] declared that "The average running time per image starting at the readily available vessel segmentation to AV classification was 8 minutes including 7 minutes for structural mapping and 1 minute for subsequent AV classification, when processed in MatLab environment on a standard personal computer with Intel core 2 Duo processor, running at 3 GHz".

In [6] a novel blood vessel segmentation algorithm was proposed using fundus images. This algorithm extracts the major blood vessels by applying high-pass filtering and morphological transforms followed by addition of fine vessel pixels which had been classified by a Gaussian Mixture Model (GMM) classifier. This algorithm achieved more than 95% vessel segmentation accuracy on three publicly available data sets. After that, an iterative blood vessel segmentation algorithm was presented, it initially estimates the major blood vessels, followed by iterative addition of fine blood vessel segments till a novel stopping criterion terminates the iterative vessel addition process. This iterative algorithm is robust to thresholds since it achieves 95.35% vessel segmentation accuracy with 0.9638 area under ROC curve (AUC) on abnormal retinal images from the publicly available STARE data set.

For optic disk detection, a novel rule-based segmentation algorithm was proposed. This algorithm detects the OD boundary and the location of vessel origin (VO) pixel since it initially detects OD candidate regions at the intersection of the bright regions and the blood vessels in a fundus image as a first step, then it estimates a best fit ellipse around the convex hull that combines all the detected OD candidate regions. The centroid of the blood vessels within the segmented OD boundary is detected as the VO pixel location. The proposed algorithm achieved an average of 80% overlap score on images from five public data sets.

A novel computer-aided screening system (DREAM) was also suggested to analyzes fundus images and detect damaged regions affected by non-proliferative diabetic retinopathy (NPDR). The DREAM system achieved 100% sensitivity, 53.16% specificity and 0.904 AUC on a publicly available MESSIDOR data set with 1200 images.

In [7], an automatic unsupervised blood vessel segmentation method for retinal images was proposed. This method constructed a multidimensional feature vector using the green channel intensity and the vessel enhanced intensity feature by the morphological operation. Then, it exploited a self-organizing map (SOM) for pixel clustering, which is an unsupervised neural network. Finally, it classified each neuron in the output layer of SOM as retinal neuron or non-vessel neuron with Otsu's method, and got the final segmentation result.

In [8], an automated retinal blood vessel detection algorithm was investigated. Two algorithms were suggested in order to detect blood vessel maps in retina. The first algorithm used the integration of a Gaussian tracing scheme and a Gabor-variance filter. It traced the large blood vessel in retinal images using adaptive histogram equalization. On the other hand, small vessels were traced on further enhanced images by a Gabor-variance filter. The second algorithm is called a radial contrast transform (RCT) algorithm. It converts the intensity information in spatial domain to a high dimensional radial contrast domain. Different feature descriptors were designed to improve the speed, sensitivity, and expandability of the vessel detection system.

Performance results showed that this scheme can achieve similar or even better performance than human expert readers for detection of micro aneurysms on difficult images.

First algorithm achieved TPR of 84.75% and FPR of 0.15% (in Hoover's performance measure) on STARE data set. And to process one image with size 700x605, it takes 40 seconds. While the second algorithm achieved TRP/FPR reaches 78.19% / 4.4% (in Hoover's performance measure) and 30 seconds on a PC with 2GHz CPU.

3. THEORETICAL BASES

Fast marching method is an optimization process uses iterative exploration and exploitation procedures in order to find the minimum path between the starting points and the goal [9].

Assuming a closed curve (Γ) in the plane propagating normal to its self with speed (F). When (F>0) then the front will always move "outwards". The position of this front can be shown by computing the arrival time T(x,y) of this front when it crosses each point (x,y) as shown in figure (1) [10].

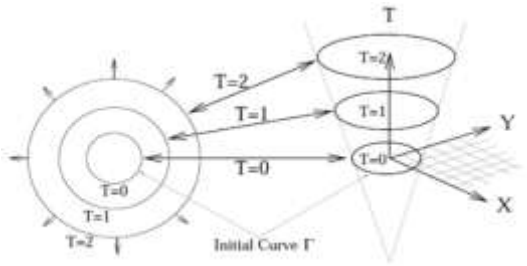

Fig -1: Transformation of front motion into boundary value problem [10].

The equation of the arrival time T(x,y) can be easily derived using "distance = rate * time" (figure 2) where:

$$dx = F\,(dT)$$

Hence:

$$1 = F\frac{dT}{dx} \qquad \dots (1)$$

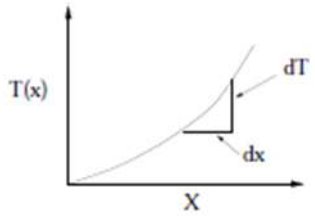

Fig -2: Setup of Boundary Value formulation [11].

In multi dimensions, the special derivative of the solution surface T becomes the gradient, which means:

$$|\nabla T|F = 1 \qquad T = 0 \text{ on } \Gamma \qquad \dots (2)$$

As a result, we can describe the front motion as the solution to a boundary value problem. And if the speed (F) depends only on position, then the equation can be reduced to the familiar Eikonal equation.

The Eikonal equation can be written as [11]:

$$\begin{aligned} |\nabla u| &= f \qquad in\Omega \\ u &= 0 \qquad on\Gamma \in \partial\Omega \end{aligned} \qquad \dots (3)$$

Finding the solution of this equation is a difficult task and it, in most cases, finding a global smooth solution of this equation is impossible. Thus, many methods have been explored in order to find the optimal solution of this equation. Among those methods we can find the fast marching method (FMM).

FMM uses First order numerical approximation to solve the Eikonal equation based on the following operators (assuming that a function u is given with the value ui,j = u(xi,j) on a Cartesian grid with grid spacing (h)) [9].

- Forward operator (direction x):

$$D_{i,j}^{+x}u = \frac{u_{i+1,j} - u_{i,j}}{h}$$

- Backward operator (direction x):

$$D_{i,j}^{-x}u = \frac{u_{i,j} - u_{i-1,j}}{h}$$

With similar Forward and backward operators in direction (y) (figure 3):

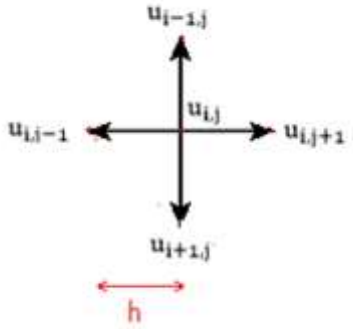

Fig -3: Forward and backward operators.

According to Godunov [12], the following upwind scheme is used to estimate the gradient ∇u in 2D:

$$\left\|\nabla u_{i,j}\right\|^2 = \begin{matrix} max\{D_{i,j}^{-x}u\,, D_{i,j}^{+x}u\,, 0\}^2 + \\ max\{D_{i,j}^{-y}u\,, D_{i,j}^{+y}u\,, 0\}^2 \end{matrix} = T_{i,j}^2 \qquad \dots (4)$$

Where:

$$T_{i,j} = T(x_{i,j})$$

$T_{i,j}$: is the cost function and it gives the (maximum) cost of moving from one point to its neighbouring point.

FMM solves this equation using the following algorithm [9]:

- **At the initial stage:**

The starting and the goal points are defined and divided into 3 groups:

- Accepted points: this group consists of the starting points (in the initial stage). And for later stages it will contain every point that we had computed its distance function (u) and considered it as fixed.
- Considered points: this group contains every point next to the points defined as "accepted". At these points the estimation (v) of the distance function (u) is calculated (this value won't be fixed).
- Far points: includes the rest of points in the image. The estimated distance values (v) of these points are not yet computed.

In addition, the distance function (u) would be defined as follows:

$$\begin{aligned} u(Accepted) &= 0 \\ u(Far) &= \infty \\ v(Considered) &= T(Considered) \end{aligned}$$

Where (T) is the cost function from one point to the neighbouring points.

- **The iterative stage:** this is done as follows

- As long as the goal points don't belong to the accepted group, we keep looking for the considered points that have minimum estimation value of the distance function.
- Points of minimum estimation values are called "trial", and once we get them we assign them as "accepted" and their distance function would be equals to their estimation values. i.e.

$$u(trial) = v\,(trial)$$

- After that we update all the points next to the "Trial" ones so that they become "Considered" and have an estimated distance value of:

$$v(x_k) = min_{y_k \in NeighAccepted(x_k)}\{u(y_k) + T(y_k)\} \quad \dots (6)$$

- The "Considered" points are then rearranged according to their priority.

Updating procedure [9]:

Updating procedure (demonstrated at figure 4) can be described as the following loop:

- For every point (x_k) in the "not accepted" neighboring of the trial points
- If (x_k) is "far", then move it to "Considered".
- if there is only one Accepted or one pair A of opposite Accepted configurations, then the estimation of the distance function at this point (x_k) is given by:

$$v_k = u_A + T_k \quad \dots (7)$$

- if there are at least two non-opposite Accepted configurations in the neighborhood of (x_k) then the estimation of the distance function at this point (x_k) is given by:
- Sort Considered according to the priority assignment.

Notice: T is calculated according to equation (4).

Back tracking stage:

In this stage the starting points (x_{start}) and the goal points (x_{goal}) are defined in addition to the forward path that we had in the exploration procedure. The goal points are assigned to be part of the back tracking path and then an iteration loop starts. During this loop the neighboring points of the goal points are investigated and the points with the least distance function value are chosen to become part of the back tracking path.

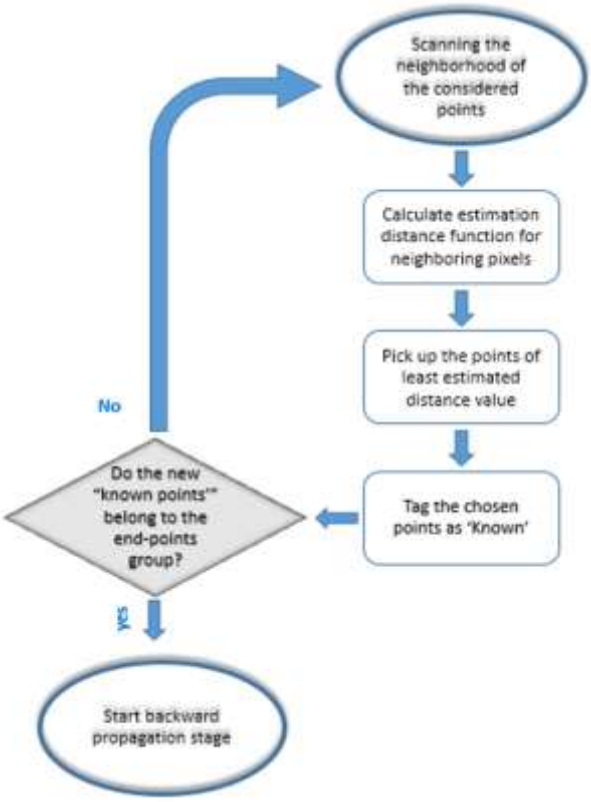

Fig -4: updating procedure flowchart.

4. THE PROPOSED METHODOLOGY

The goal of the FMM is finding the shortest path between two points without crossing constraints existing in between. The main advantage of the FMM is its ability to deal with branches and bifurcations without any additional computational cost. This advantage had been used in robotics to find the optimal path for the robot to move from the starting point to the goal with no collisions. Applying FMM on mazes is a good way to show the efficiency of this algorithm and its ability to achieve the goal it was designed for since it can be tested on a complex set of obstacles positioned between the starting and the goal points.

$$-if \quad T_k > |u_A - u_B|$$

$$v_k = \frac{1}{2}(u_A + u_B + \sqrt{2T_k^2 - (u_A - u_B)^2}) \quad \dots (8)$$

$$-else$$

$$v_k = u_A + T_k$$

After that, the FMM became widely used in image processing especially for medical images. And it is obvious that FMM would be completely efficient for tracking blood vessels in an image because of its ability to deal with bifurcations and thus it would be perfect for retinal blood vessel tree segmentation.

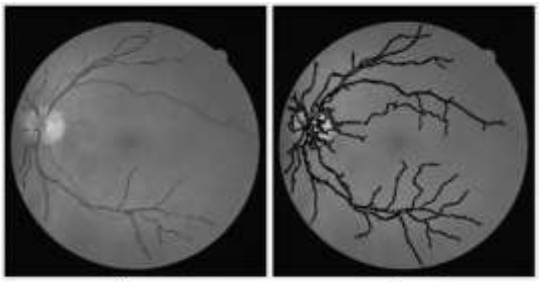

Fig -5: FMM (a) exploration stage (b) exploitation stage.

This algorithm was applied completely using the M language of MATLAB to extract the lines of blood vessels. We can say that FMM consists of the following main stages:

Initial stage: selecting the starting points of the FMM algorithm. Here we select points that belongs to the blood vessels of the optic disc since the optic disc is the origin of all vessels crossing the retina. After that we select the goal points of the forward propagation stage, those points are selected at the end of each blood vessel of the retina. FMM is then implemented so that it matches start points to the maximum available number of the goal points resulting in an approximated map of the retinal blood vessels. Then a back tracking procedure starts from the goal points towards start points drawing a single-pixel route from each end point to the start point. This route can be defined as the blood vessel tree of the retinal image.

The algorithm was applied on images taken from the familiar DRIVE and STARE data sets. Forward propagation and back tracking stages for a single DRIVE image with limited number of end points are shown in figure (5).

Pre-processing stage: here we try to have an initial approximation of the retinal blood vessel position. The importance of this stage comes from the huge amount of noise in fundus images and the convergence of the intensity values among adjacent pixel at the first place, and from the high sensitivity of the FMM against contrast values of the adjacent pixels. FMM efficiency increases obviously as contrast increase. On the other hand, FMM becomes blind when contrast decrease and tends to cross existing constrains which affects vessel tracing badly. To overcome these problems, the pre-processing stage included a median filtering procedure, followed by local numerical analysis of the retinal pixels in order to estimate most probable position of the blood vessel. This step is of great importance to magnify the FMM efficiency since it creates a kind of clear borders that can be considered during exploration process. This step can also reduce the number of iterations and time consumption required for exploration process. This initial estimation of the position of blood vessel is shown in figure (6).

Applying FMM on pre-processed fundus images:

In this stage, image enhancement is first performed to increase contrast between vessel pixels and non-vessel pixels, this enhances FMM performance since it enlarges variations between vessels pixels and background pixels. This stage consists of two main phases:

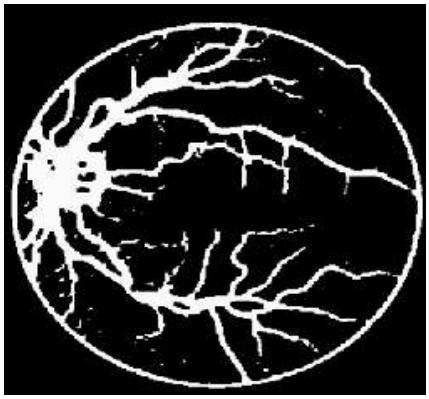

Fig -6: initial estimation of retinal blood vessel position in a fundus image.

In exploration phase, a forward propagation is implemented from stating points to the goal points. This phase gives every single point that have the probability of being among the vessel pixels.

In exploitation phase, the goal points of the exploration phase are considered as the starting points of exploitation phase, then a back tracking search is implemented in order to find pixels with least distance function values from goal points to start points. At this phase, we don't take all the pixels that may belong to vessel. Only a single pixel width tracking line is taken into consideration. This line connects the start and goal pixels and provide us the desired tree of the retinal vessels. Figure (7) shows FMM main phases.

4. RESULTS AND DISCUSSIONS

FMM has been validated on many different images taken from the familiar DRIVE data set. It achieved a TPR of 93% with an iteration number ranges between 100 to 500 according to the OD position (OD distance from retina's center). The average time of each iteration is about 0.57 sec this results in a running time of 5-10 minutes.

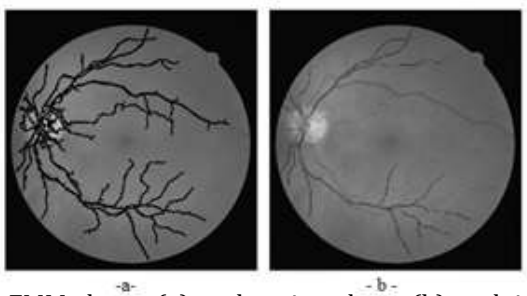

Fig -7: FMM phases (a) exploration phase, (b) exploitation phase.

FMM has also been validated using STARE data set that contain images with 700x605 pixels. For STARE data set, performance had been tested for images with different sizes using different performance measure like iteration number, time and TPR. Table 1, shows the FMM performance according to the mentioned measures where TPR-ah and TPR-vk are the TPR for two human supervisors in STARE data set while TPR-net is the TPR compared to the matched filter implemented in STARE data set.

Table -1: FMM performance in STARE data set.

Image size	iteration number	Single iteration time	Total time	TPR-ah	TPR-vk	TPR-net
700x605	1325	0.8 sec	17 min	0.88	0.9	0.84
350x303	700	0.22 sec	2.6 min	0.83	0.86	0.7
200x173	392	0.08 sec	31 sec	0.74	0.82	0.72
150x130	268	0.05 sec	12 sec	0.53	0.62	0.49

The results showed that this method has a priority comparing to matched filters proposed by Chaudhuri [13] and model based method proposed by Jiang & Mojon [14]. Its performance is also comparable to other high accuracy methods such as rule-based method proposed by Martinez [15] and vessel analysis using morphological and structural properties of the vessels which had an accuracy of 91.44% [5] in addition to multiscale line tracing method proposed in [3] which had an accuracy value of 92.9%.

Speaking of processing time, our method shows a relatively long run time, but it is still close to other researches that declared using MATLAB like the research mentioned in [5] that achieved a processing time of 8 minutes for DRIVE images. While we had a processing time of 6 minutes for DRIVE images.

3. CONCLUSIONS

In this article, we introduced a new method for automatic retinal blood vessel tree segmentation based on mathematical analysis of the retinal texture as a preprocessing stage then an FMM stage to trace vessels. We applied this method on images form DRIVE and STARE data sets using MATLAB. The proposed method achieved performance close to the other high accuracy algorithms used in this field.

At the end, it is good to refer to the ability of improving this algorithm by searching for more edge-enhancing techniques and taking the advantages of spectral domain to segment arteries and veins and to isolate crossing points of the vessel tree.

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