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IMPLEMENTATION OF GRAPH THEORETICAL APPROACH IN RETINAL VESSEL SEGMENTATION

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ABSTRACT- The eye provides a window into the health of a person, from which one can actually see the exposed flesh of the subject without using invasive procedures. There are many diseases, like vascular disease that leave markers in the retina of the eye. The retina can be photographed more accurately with a fundus camera and now with direct digital imaging there is much interest in computer analysis of retinal images for identifying and quantifying the effects of diseases such as diabetes. A retinal image provides a snapshot of what happens inside the human body. In particular, the state of the retinal vessels shows the cardiovascular condition of the body. Necessary information on pathological changes will be provided by the retinal image. Hypertension, Arteriosclerosis, Cardiovascular disease and Stroke can be easily identified through our model. Analysis of retinal image plays major role in diagnostic procedures. The fact that retinal images are often noisy, poorly contrasted, and the vessel widths can vary from very large to very small, which makes the automatic retinal segmentation much complicated. So in this project, we can implement automated segmentation procedure based on graph theoretical approach in order to provide regional information using boundary measure. We represent the segmented vascular structure as a vessel segment graph and the problem of identifying the blood vessels in the graph using a given set of constraints such as CRAE and CRVE. These measurements are found to have good correlation with hypertension, coronary heart disease, and stroke.

Index Terms— Directed graph theory, neuronal tracing, retinal blood vessel tracing, tracing filamentary structures

I. INTRODUCTION

Diseases of the Central Nervous System (CNS) like Parkinsons and Alzheimers are caused by loss of neurons and their connections. To identify drugs to treat CNS diseases, it is important to conduct High Throughput Screens (HTS) of microscopic neuronal images, which naturally re-quests for automated neuronal tracers. However, most existing systems are semi-automatic, where human guidance is frequently required during the tracing process.

The widely used Image plugins such as Neurite Tracer, Simple Neurite Tracer, as well as the Vaa3D neuron module all fall under this category. Meanwhile, there are a few state-of-the-art systems that are able to trace neuronal structures automatically, including both academic efforts such as NeuroCyto and the commercial product—the neurite tracing module of Metamorph NX. Nevertheless, they often fail to reliably trace neurons in the presence of neurite crossovers, i.e. overlaps or touching neurites.

A very similar situation has also been observed in tracing retinal blood vessel trees from fundus images. There, topological and geometrical properties of retinal vessel trees provide valuable clinical information in diagnosing diseases such as proliferative diabetic retinopathy, glaucoma, and hypertensive retinopathy. Take as an example the disease of proliferative diabetic retinopathy, a leading cause of blindness in the working-age population of most developed countries. It is the result of progressive damage to the network of tiny blood vessels that supply blood to the retina, and is specifically characterized by the formation of newly formed vessels in the retina. This thus depends on the description of blood vessel tree structure in clinical diagnosis, and as a result, calls for proper tracing of the vessel trees from fundus images. Similar to what has happened to neuronal tracing, existing methods often fail to trace properly with the occurrence of crossover at the junctions, as it is challenging to predict whether the filaments contacting a junction belong to the same tree or different trees, and for the latter case, to which tree each filament belongs.

This work aims at automated tracing of filamentary structures in neuronal as well as fundus images. In particular, we focus on addressing the bottleneck crossover issue. One important observation is that local and global contextual information is crucial to resolve the crossover issue. For example, at a junction, it is very helpful to go beyond the current filament and examine the angular, morphological, and textural properties of all filaments of the junction. This information is unfortunately largely ignored by current tracers. Here we consider a two-step tracing approach that takes into account both local and global contextual information of the neuronal and the vessel network: The first step takes the raw image as input and produces a pixel-based segmentation map. After skeleton extraction, a novel graph representation is formed in the second step, where each filament in the skeleton map becomes a node, and a contact between two adjacent filaments could be translated to directed edges of these two nodes. Furthermore, the root nodes are naturally identified as either the DAPI tagged soma (aka cell body) in neuronal images, or the filaments touching the optic disk area in fundus images, and are further labeled with their unique IDs. The number of sub graphs to-be-found in the filamentary network thus equals to the number of root nodes. This naturally gives rise to a directed graph (or interchangeably, digraph) representation. The tracing problem is now formulated as label propagation on digraphs: The goal becomes that of propagating the sub graph labels from known root nodes to the rest of the digraph, such that the di-graph is partitioned into disjoint sub-graphs, which in turn delivers tracing result of the filamentary network. This allows us to consider and makes novel usage of the established matrix-forest theorem.

The main contributions of this paper are as follows. First, our approach, and in particular the second step, offers a principled way of addressing the tracing with crossover problem. By connecting to the well-established algebraic digraph theory, as well as the transductive inference in machine learning, local and global contextual information can be considered. We expect the graph representation, and the algebraic graph theory connection can open doors to more insightful understanding of the tracing problem at hand. Complexity analysis and generalization error analysis also provides useful characterization of the proposed approach. Second, our segmentation step is carried out with graph Laplacian based regularization, which facilitates the overall graph-theoretical framework considered in our tracing system. Third, we provide an in-house neuronal microscopic image dataset dedicated to the task of neuronal tracing. The dataset together with the gold-standard manual annotations have been made publicly available.

II. EXISTING SYSTEM

Ribbon of Twins (ROT) Model: The ROT model was proposed specifically for the vessel segmentation problem. Two twins of contours represent a ribbon along a vessel, with one twin on each edge of the vessel. Each twin consists of contours, one inside and one outside the vessel. The two outside contours are connected by pull forces to the inside contours, while the inside contours are connected by push forces to each other.

III. PROPOSED SYSTEM

A.GRAPH THEORICAL SYSTEM

This method aims to identify vessels and to present them in the form of binary trees for subsequent vessel measurements.
Two main steps:
1) Identifying crossovers,
2) Finding of the optimal forest (set of vessel trees).

1) Identification of Crossover Locations:

Vessels in a retinal image are frequently crossed over each other, at some point or over a shared segment. The former is called crossover points and the latter crossover segments.

2) Definition of Crossover Point:

In the set of white pixels P in a line image, a junction $J \in JP$ is a crossover point on the condition that the number of segments that are adjacent to J is greater than or equal to 4.

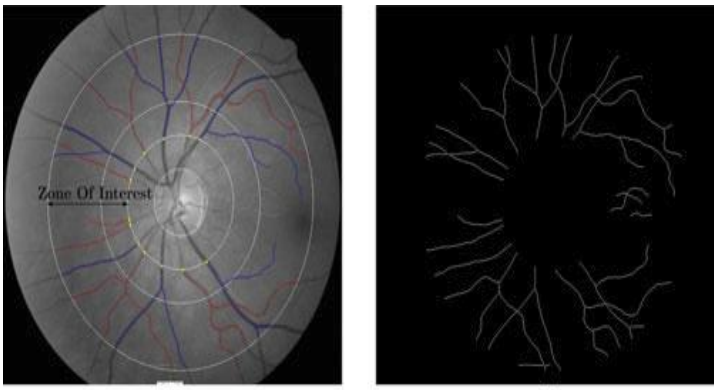

Fig.1

A crossover segment occurs when two different vessels share a segment. In the set of white pixels P of a line image, a segment $s \in SP$ is a *candidate* crossover segment while
$|s| < L$ and $\exists\, J1, J2 \in JP$ s.t. $adj(s, J1) \wedge adj(s, J2) \wedge \neg cross(J1) \wedge \neg cross(J2)$.
L is a parameter which limits candidates to short segments. Sometimes short segments between two junctions may not always true crossover segments. So, we tend to use the directional changes between adjacent segments and their pixel intensity values to differentiate crossover segments.

3) Definition of Directional Change Between Segments:

If two segments s_a and s_b that are adjacent to a common junction,
Let p_a and p_b be the end points of s_a and s_b that are nearest to each other. Let v_a be a vector that starts on s_a and ends at p_a, and v_b be a vector that starts from p_b and ends on s_b. Then, the directional change between s_a and s_b is given by

$\Delta D\ (s_a, s_b) = \cos{-}1(v_a \cdot v_b/|v_a\_v_b\ |)$
Where $\Delta D\ (s_a, s_b) \in [0\circ, 180\circ]$.
Intuitively, $\Delta D\ (s_a, s_b)$ measures the magnitude of a change in direction if we were to go from s_a to s_b.

4) Definition of Crossover Segment:

Given a candidate segment *seg* between two junctions *J*1 and *J*2, let $Si = \{s_a \in SP\ |adj\ (s_a, Ji) \wedge s_a = seg\}$ for $i \in \{1, 2\}$. Each *Si* contains two segments sharing the same junction as one end pixel of *seg*. Let
$A = \{seg\} \cup S1 \cup S2$ and $\Phi = \{\{s_a, seg, s_b\}|s_a \in S1, s_b \in S2\}$. Then *seg* is a crossover segment, i.e., *cross* (*seg*)
Is true, if all of the following conditions are true:

1. $\forall s, s\_ \in Si, i \in \{1, 2\}, \Delta D(s, s\_) > 30\circ$

2. $|seg| \leq L\theta \Rightarrow [\exists sa, sb \in S1, sc, sd \in S2$,s.t. $\Delta D(sa, sc) < 30\circ \wedge \Delta D(sb, sd) < 30\circ] \vee \min \varphi \in \Phi\ [sd(M(\varphi)) + sd(M(A - \varphi))] < sd(M(A))$

3. $|seg| > L\theta \Rightarrow [\forall s \in S1 \cup S2$,$\Delta D(seg, s) < \theta low] \vee [\forall s \in S1 \cup S2$,$\Delta D(seg, s) < \theta high \wedge \min \varphi \in \Phi\ [s_d(M(\varphi)) + s_d(M(A - \varphi))] < sd(M(A))]$

Condition 2 deals with the case when the length of *segment* is too short to determine the directional change. In this case, we do check whether a reasonable cross pattern is formed with adjacent segments such that their directional change is less than 30◦. Otherwise, we partition *it* into two Such that the sum of the s_d of both partitions is minimum. If this minimum is less than the s_d of all the segments in *it*, then *Segment* is a crossover segment.

Condition 3 states that if the length of *segment* is long enough and the directional change between *segment* and each of its adjacent segment is less than θ low, then *seg* is a Crossover segment. Otherwise, if directional change is less than Θ high, the s_ds of the segments' intensity values are compared as in Condition 2.

B. Find the Optimal Forest

Now, the segments are modelled as a segment graph and use constraint optimization to search for the best set of vessel trees (forest) from the graph.

Definition of Segment graph:

In a set of white pixels *W* in a line image, a segment graph *GW*= (*SW*, *EW*), where each vertex in *SW* is a segment and an edge $ei,j = (si, sj) \in EW$ exists if $adj(si, sj)$, $si, sj \in SW$, $i = j$.

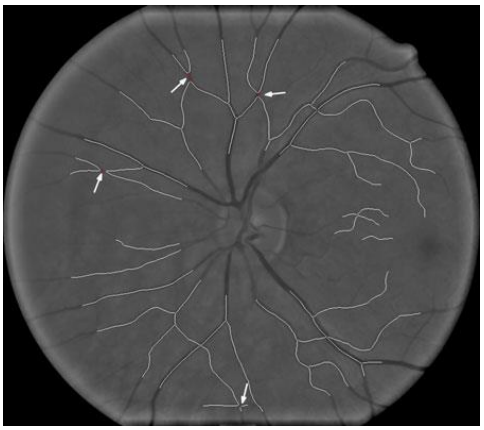

Fig.2. Identified crossover segments

Typically, G*W* consists of disconnected sub graphs that are independent and can be processed in parallel. Without loss of generality, we refer to each of these sub graphs as the segment graph *GW*. 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.

Definition of Vessel

Given a segment graph $GW = (SW, EW)$, vessel is a binary tree, $R = (sroot, VR, ER)$ such that sroot is the root node, $root(R) = sroot$, $VR \subseteq SW$, and $ER \subseteq EW$.

We call a set of such binary trees as *forest*. A binary tree is a natural representation of an actual blood vessel as it only bifurcates. End points of segment are 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

where a unique root pixel is contained. The optimal forest, $E^* \in EW$ that corresponds to vessels in GW is given by

$E^* = \arg\min cost(E)\ E \in EW$ Subject to the following constraints:

1) Roots are unique to each tree

$\forall R1 \in E,\ \forall R2 \in E - \{R1\},\ root$

$(R2) \in VR1$.

2) Directional change between parents and child segments are within the threshold $\forall R \in E,\ (sp, sc) \in ET$,

$[sp > L\theta \wedge sc > L\theta] \Rightarrow \Delta D\ (sp, sc) < 135^\circ$

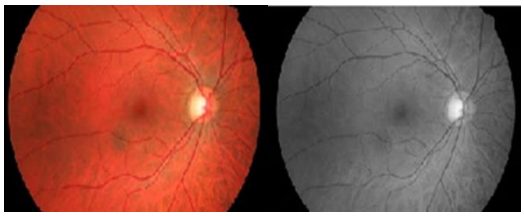

Fig.3 Input image and Gray scale image

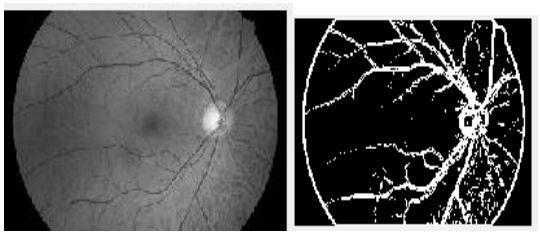

Fig.4 Sharpened image and vessel image

Fig.5 Graph theoretical model image

3) Any segment appearing in more than one tree must be a crossover segment

$\forall s \in SW,\ |\{R \in E | s \in VR\}| > 1 \Rightarrow cross(s)$.

4) A parent segment at crossover junction must connect to the child with minimum directional change

$\forall R \in E, (sp, sc) \in ET, \exists J \in JP$ s.t.$cross(J) \wedge \text{adj}(sp, J) \wedge \text{adj}(sc, J)$

$\Rightarrow child(R, sp) = 1 \wedge sc = \text{argmin } s \in A$

$\Delta D(sp, s)$ where$A = \{s \in SW - \{sp\} | \text{adj}(s, J)\}$.

5) Crossover segment is the only child and have only one child that has the minimum directional change

$\forall R \in E, (sp, sx), (sx, sc) \in ET, cross(sx) \Rightarrow child(R, sp) = 1 \wedge child(T, sx) = 1 \wedge sc = \text{argmin } s \in S\ \Delta D(sp, s)$

Where $S = \{s | (sx, s) \in EW \wedge s = sp \wedge \neg \text{adj}(s, ssp)\}$.

6) Leaf segment cannot be crossovers segments

$\forall R \in E, s \in VR, leaf(R, s) \Rightarrow \neg cross(s)$.

IV. 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 post processing step to vessel segmentation. The problem is modelled 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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