Retinal Vessel Classification In Fundus Imaging Using Vampire For Biomarker Identification.

D. Relan [a], T. MacGillivray [a,c], C. Gray [a,c], L. Ballerini [b], E. Trucco [b]

[a] Clinical Research Imaging Centre, University of Edinburgh, [b] School of Computing, University of Dundee, [c] Wellcome Trust Clinical Research Facility, University of Edinburgh

INTRODUCTION

Retinal blood vessels observed with fundus imaging provide important indicators not only for clinical diagnosis and treatment of eye diseases but also for systemic diseases such as diabetes, hypertension etc. which manifest themselves in the retina. Quantitative structural analysis of the retinal vasculature not only helps in the diagnosis of retinopathies but also provides potential biomarkers of systemic diseases. Crucially, the vasculature change that appears during the onset of disease can affect arterioles and venules differently.

AIM

An essential part of a system such as VAMPIRE (Vasculature Assessment and Measurement Platform for Images of the REtina) for retinal image analysis is a computational method for automatically classifying vessels into arterioles and venules. The lack of automated techniques restricts the possibility of large scale studies investigating retinal biomarker of diseases. Thus, to this end we present our vessel classification algorithm.

Material and Method

70 colour fundus images with resolution of 2048×3072 pixels and captured with Canon CR-DGi non-mydriatic retinal camera with 45 degree field of view were analysed in this study. The images were selected at random from a large database of non-mydriatic fundus images which were obtained from the Orkney Complex Disease Study (ORCADES).

We automatically classify retinal vessels in digital colour fundus images as arterioles and venules using 4 fixed colour features using a Gaussian Mixture Model, an Expectation-Maximization (GMM-EM) classifier and a quadrant-pairwise approach. Classification is performed on illumination-corrected images in Zone B (Fig (1)) of retinal image.

The image was divided into four quadrants by locating the OD and its approximate diameter. Then the centreline pixels were found (Fig. 2) in each quadrant and four colour features (Mean of Red (MR), Mean of Green (MG), Mean of Hue (MH) and Variance of Red (VR)) were extracted from the corrected colour channels and from a circular neighbourhood around each centreline pixel, with diameter 60% of the mean vessel diameter. Finally, each set of colour features of pixels were classified using GMM-EM classifier. The classification was performed by working separately on two quadrants at a time in a clockwise direction which gives two labels/pixel. Then the quadrant was rotated by 45 degree clockwise (dashed lines in Fig. 1) and the pixels belonging to each of the rotated pair of quadrants were classified again, generating two more labels to each pixel. The vessels were assigned a status of an artery, vein or not labelled based on the maximum number of labels of each kind to pixels belonging to a vessel (Table 1).

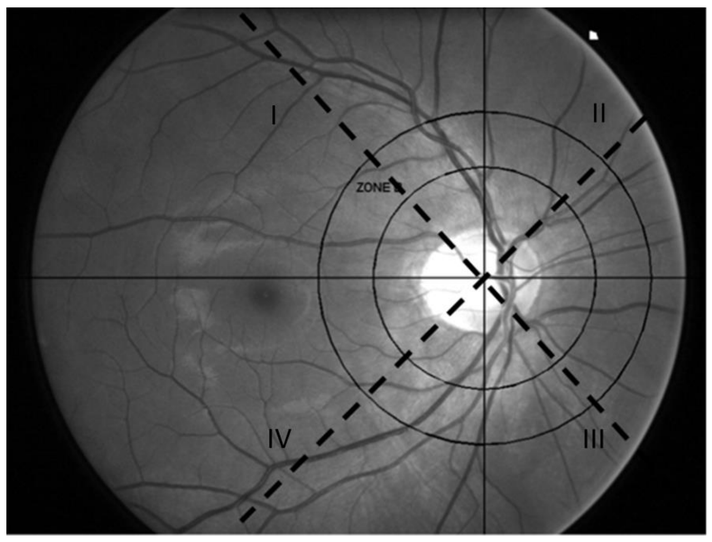

Figure 1: : Rotated quadrant by 45 degree (marked as black dashed line in the image) and measurement zone: Zone B ((0.5 to 1 disc diameter from the optic disc margin surrounding the OD)

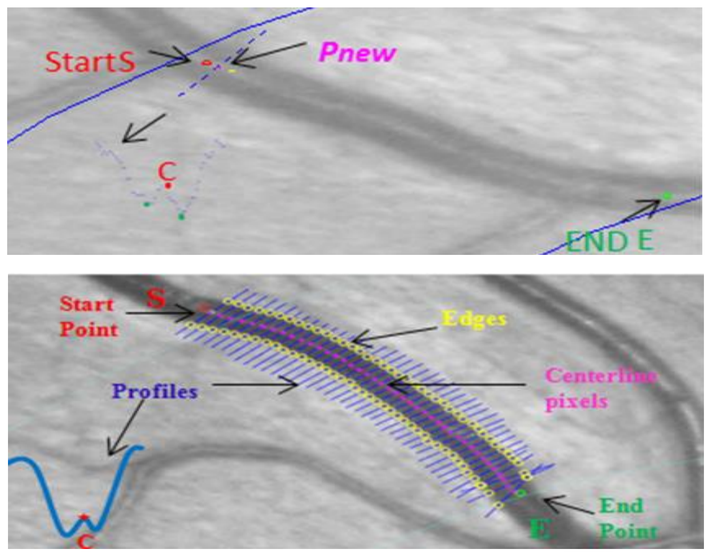

Figure 2: : Centreline pixel extraction

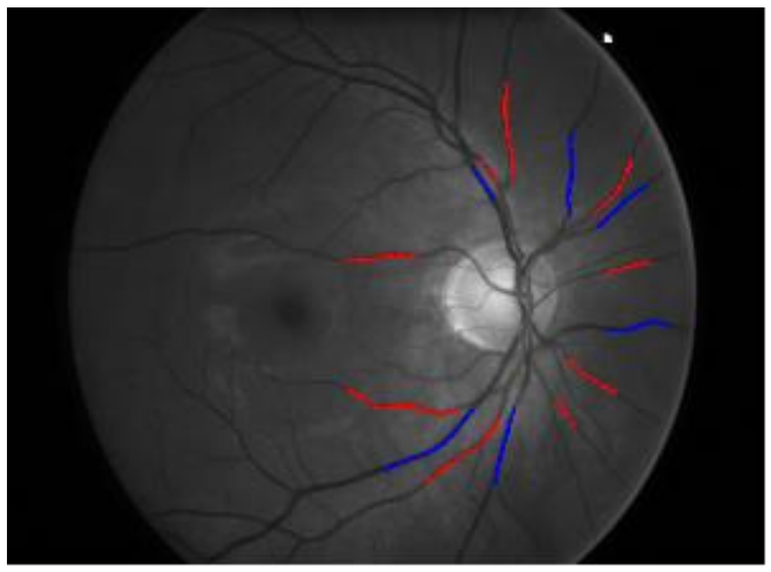

Figure 3: Vessel in red and blue are classified arteries and veins respectively

Pixels belonging to a vessel (I)	Four labels per pixel (II)				Final label to each pixel (artery) (III)
1.	*a*	a	a	a	*a*
2.	*a*	a	v	a	*a*
3.	*a*	a	v	a	*a*
4.	*a*	a	a	a	*a*
5.	*a*	v	v	v	*v*
6.	*a*	n	n	a	*n*
7.	*a*	n	a	a	*a*

Table 1: Example of assigning Final Label to a vessel from centerline-pixel labels

RESULTS

802 vessels from 70 colour fundus images were processed resulting in 90.45% correct classification with 13.8% unclassified. These images were from the Orkney Complex Disease Study (ORCADES). The Orkney Complex Disease Study (ORCADES) is family-based, cross-sectional and genetic epidemiology study based on an isolated population in the north of Scotland that aims to discover the genes and their variants which influence the risk of common, complex diseases .

CONCLUSION

Our approach has high classification accuracy and low classification error rate for both arterioles and venules in our test image dataset. This vessel classification will enable us to measure parameters such as AVR for the entire ORCADES data set (~2,000 participants) in an efficient manner and with the aim of providing accurate retinal biomarkers of cardiovascular disease and future disease risk.

Acknowledgments
Research work is supported by Leverhume trust grant RPG-419