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# Geometric connectivity analysis based on edge co-occurrences in retinal images

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## Abstract

The network of tiny blood vessels in retinal images might be affected by several diseases such as diabetic retinopathy or hypertension. Analysis of the properties of this network is a classical source of rich diagnostic information. Several vessel segmentation and tracking techniques to automatically extract retinal vasculature biomarkers from retinal fundus images have been proposed in the literature. Tracking methods (such as graph-based techniques) to detect fully connected networks of blood vessels are often dependent on a proper initial vessel segmentation and skeleton extraction step. However, errors can easily propagate in the full tracking pipeline starting from segmentation, because of the presence of noise, low contrast regions, loss of information and interrupted vessel segments.

Junction points are key decision points during construction of the full vasculature network consisting of several tree-like structures. At these points, each tree either bifurcates to new branches or crosses other trees. The human brain is capable of grouping local edges into global contours remarkably easily. Inspired by this capability, a new method was proposed by [3] to distinguish the correct connections among the blood vessels at junction points. Contextual information is deployed in a similarity measurement approach based on the geometry of the primary visual cortex (V1) and further processed in a spectral clustering step for retrieving the individual perceptual units (blood vessels) from segmentations. By creating a 3D representation of a 2D image in a coupled space of positions and orientations using the orientation score transformation [2], crossing elongated structures in retinal images were disentangled from each other. The cortical connectivity in this lifted domain was modelled stochastically (using the Markov Chain Monte-Carlo method [5]) by the fundamental solution of the time-independent Fokker-Planck equation for Mumford's direction process [4]. There exist various numerical approximations, and exact solutions for this equation. For a recent and complete comparison see [8] and the references therein.

In [6] it is shown that there is a close relation between the statistics of edge co-occurrence in natural images and the contour perception problem. In this work, we propose to learn the kernel from retinal images and use this statistical kernel directly in connectivity analysis. In order to obtain the edge co-occurrence (considered as the statistical kernel), the retinal images are lifted to the coupled

space of positions and ( $\pi$ -periodic) orientations in  $\mathbb{R}^2 \times P^1$ . Using this information and by the assumption of translation invariance, a 4D histogram in  $\mathbb{R}^2 \times P^2$  is obtained by finding the cross-correlation histogram of relative positions and orientations of vessel centerline points. Then by assuming the rotation-invariance property, the relative positions are rotated using the relative orientations and the 4D histogram is converted to a 3D kernel of rotated positions and relative orientations. This so-called data-driven kernel has been created for two different public datasets having different pixel sizes and resolutions. The vessel centerlines are created by thinning the vessel segmentations.

These data-driven kernels are compared with each other and the  $l_2$ -norms of their differences are obtained. The obtained results show that the kernels have very similar characteristics and their mutual differences are less than 2%. Therefore, they can be used interchangeably. In another step, each statistical kernel is compared against a set of solutions of the Fokker-Planck equation obtained using a Fourier-based technique [1] varying its parameters. Then we obtain the parameters of the best numerical approximations of the data-driven kernels which result in the least squared errors (less than 1% for both datasets). These parameters are very close to the ones used for creation of the stochastic kernel in [3], which were found heuristically. Furthermore, we could make the vessel connectivity analysis technique fully automatic by using not only the data-driven kernel as the cortical connectivity model, but also by exploiting a self-tuning spectral clustering technique [7] for detecting individual blood vessels based on the affinity matrix. This connectivity analysis can be further used in the creation of a model of the entire retinal vasculature and analysis of its properties. Moreover, the same approach can be used in parameter tuning of perceptual completion tasks.

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