

Bridging Disconnected Curvilinear Structures via Numerical Evolutions of Completion Process in Ophthalmologic Images

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1 Abstract

Geometric changes of curvilinear structures in ophthalmologic images have been widely considered as the early signs for the diagnosis of eye-related and systemic diseases. For instance, retinal vascular tortuosity is an important biomarkers for indicating retinopathy of prematurity [1], and the density of corneal nerve fibers is used to predict type-II diabetes [2]. As such, detecting the curvilinear structures and analyzing the variation of their geometric properties in an automatic way are important in the computer-aided diagnosis.

Many methods have been proposed for the extraction of the curvilinear structures in ophthalmologic images [3, 4]. In general, most of these methods focus on picking up the elongated segments as many as possible, without considering the connectivity of structures. In particular, these methods can be easily affected by classical issues like contrast changes, non-uniform illumination and low signal to noise ratio in the images. Thus, disconnected curvilinear segments may often occur in the segmentation results. Moreover, many tracking based approaches highly rely on a pre-determined skeleton from a binary segmentation, so they will not be able to trace a complete curvilinear network based on an imperfect skeleton map. In clinical analysis, interrupted curvilinear networks may lead to unreliable quantitative measurements of biomarkers, e.g. incorrect statistics of vessel tortuosity, fiber length or density. There is also a shortcoming of methods [5, 6] with insufficient quantitative evaluations for dealing with the gap filling problem in the literature. Therefore, an automatic method for the reconnection of gaps is essentially important for improving the accuracy in the assessment of health biomarkers.

In this work, we propose an automatic method for solving the gap filling problem in the skeleton of curvilinear structures. This method employs the completion process, i.e. mathematical modeling of the direction process [7] to achieve line and contour propagation/completion. The completion process is inspired by the geometry of the visual cortex [8], and it can be used to reconstruct interrupted curves by considering their consistency. Different numerical approximations [9] have been used to model the completion process on the roto-translation group $SE(2) \equiv \mathbb{R}^2 \rtimes S^1$, i.e. the coupled space of positions and orientations. Here

we rely on our previous finite difference explicit implementation [9] to construct the 3D completion kernel. To process curvilinear structures in $\mathbb{R}^2 \times S^1$, the framework of orientation scores [10] are exploited to lift 2D curvilinear structures into the 3D coupled space, where the crossing elongated structures are disentangled into different layers according to their local orientations.

The propagations and reconnection of interrupted curvilinear structures are achieved by convolving the completion kernel with orientation scores via iterative group convolutions. After each group convolution step, the curvilinear skeleton map needs to be updated for the next iteration. To overcome the incorrect skeletonization of 2D thinning approach at junctions, a 3D segment-wise thinning technique is proposed to process each binary segment separately after thresholding the 3D convolved orientation scores. By taking the maximum responses over all orientations per position in orientation scores, a 2D skeleton map with propagated curvilinear structures is obtained. The broken structures are reconnected after several iterations (1 to 3 in our experiments). Experiments are performed on the manual annotations of curvilinear structures in four datasets with different image modalities, i.e. retinal images and corneal nerve fiber images, where artificial gaps with different sizes are created on segments and junctions. The validation results show that the proposed method works robustly for curvilinear skeleton reconnection.

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