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Robust graph representation of images with underlying structural networks. Application to the classification of vascular networks of mice's colon☆

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ABSTRACT

In this letter, we consider scenes constituted by underlying structural networks. This is an important issue since such scenes appear in many domains of sciences with for instance images of road networks, vascular networks, root systems, etc. The extraction of information from such networks requires characterization methods specifically designed to preserve the topological structure of the network hidden in the image. We propose an entire image processing pipeline for this task with a robust joint segmentation and graph-based representation approach. The proposed method relates, in the closest literature, to the so-called Maximally Stable Extremal Region here extended to extremally stable graph. The method is successfully illustrated with a real world biomedical pattern recognition problem solved with our approach. The robustness of the most common graph parameters is discussed from Monte Carlo simulations on synthetic graphs.

1. Introduction

Networks are everywhere. They carry informations or matters at all scales and domains of sciences including neural networks, vascular networks, root systems for instances in life sciences or transportation networks, the internet and social networks for instances in human technologies. Analyzing the efficiency, robustness, evolution of networks is a domain of current huge interest. In human technologies, the topology and data produced by the networks are mostly directly accessible because they are manmade. In life sciences however, information concerning structural networks are to be extracted first before being accessible to the analysis. Bioimaging is a tool of choice for the nondestructive observation of such biological structural networks. One can think for instance to diffusion tensor magnetic resonance imaging for the observation of connected neural fibers, perfusion imaging or angiography for the analysis of vascular networks or X-rays for root systems.

In this letter, we consider the broad domain of imaging which produces images constituted by underlying structural networks from which one intend to extract topological informations. The extraction of information from such networks requires segmentation methods specifically designed to preserve the topological structure of the network hidden in the image. To the best of our knowledge, such tools do not currently exist and we give a first attempt in this direction with an original graph-based representation approach. The manuscript is organized in the following way. We start by describing the biomedical pattern recognition problem of vascular networks obtained from in vivo confocal endomicroscopy that we consider for illustration of our approach in this letter. Then, we give the principle of our graph-based representation and relate it to the closest works in the literature. We present the experimental results obtained on the considered pattern recognition problem. We finally confront these experimental results with a theoretical assessment of the sensitivity of network metrics before discussion and conclusion.

2. Biomedical classification problem

For illustration in this letter, we consider a pattern recognition problem dedicated to the classification of vascular networks in confocal endomicroscopy images of mice colon walls such as shown in Fig. 1. These images were acquired according to the protocol recently introduced in [1] and that we briefly recall. Mice were chemically treated during six months to induce colitis using a combination of azoxymethan (AOM, intraperitoneal injection,

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0167-8655/

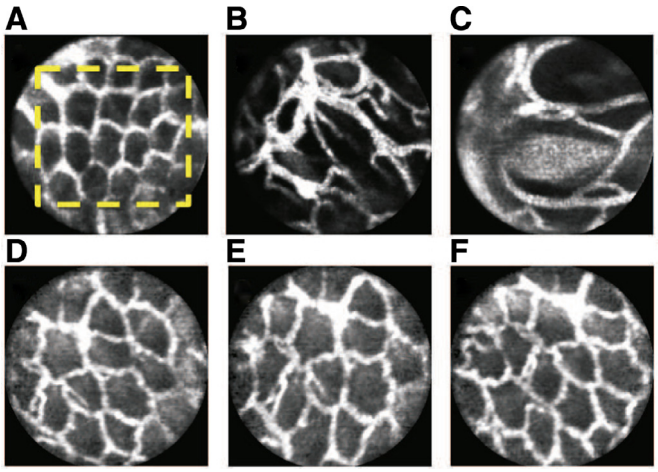

Fig. 1. A set of confocal endomicroscopy images of mouses's colon walls considered for segmentation. Panels A, B and C show three distinct stages of organization of the vascular networks, with various organization of the so-called vascular 'crypts', classified by physician experts as healthy tissue A, inflamated tissue B and tissue with dysplasia C. Panels D, E, F correspond to three consecutive frames on the same location in the colon. In the image processing pipeline of Fig. 2, a crop of 256 × 256 pixels corresponding to the yellow dotted square of panel A is realized. (For interpretation of the references to color in this figure, the reader is referred to the web version of this article).

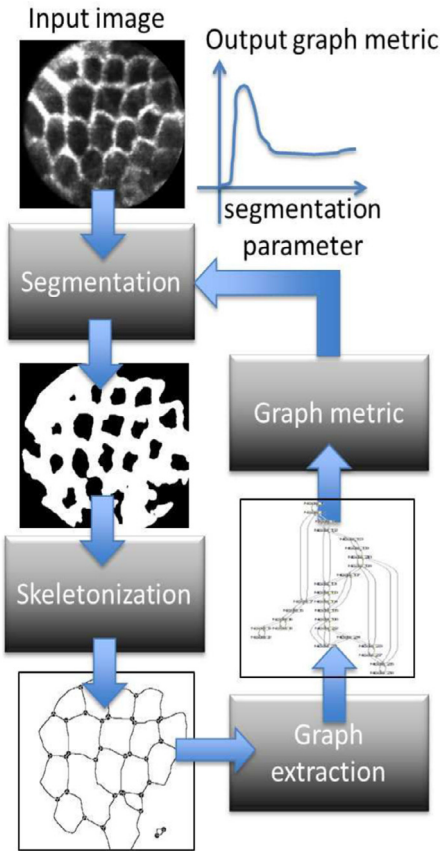

Fig. 2. General description of the image processing pipeline proposed for the graph representation of images with underlying networks. The feedback loop expresses that the segmentation parameters are tuned to satisfy a stability criterion of the graph metric.

10 mg/kg body weight) and dextran sulfate sodium (DSS, in drinking water, concentration of 2%). The experiments were led in accordance with the rules and regulations of the Université Lyon 1 Ethics Committee on animal experimentation. Prior to the experiment, mice were kept on a 12 h day/night rhythm in a 300 cm^2 plastic cages with straw bedding, pellet food and tap water. Mice were anesthetized using an isoflurane tabletop station (TEM Sega, Lormont, France). Animals respiratory index was monitored during the experiment by using a pressure sensor placed on the mouse's chest. Images analyzed in this article were chosen at the extrema of the respiratory cycle where the movements are the slowest so as to minimize artefact due to these movements. During the induction phase, mice were anesthetized with 3% of isoflurane and aspiration flow set up on 0.4 L/min. A 25 µL solution of Fluorescein Isothiocyanate FITC-Dextran 5% (Sigma Aldrich, Saint-Louis, USA), used as contrast agent, is injected in retro-orbital of the mouse's eye before the CEM investigation. During imaging, the anesthesia was maintained with 1.4 to 1.7% isoflurane vaporization and aspiration flow set up on 0.4 L/min. The endoscopic examination was performed using a mini multi-purpose rigid telescope dedicated to small animals (Karl Storz, Tuttlingen, Germany). Images were acquired using a 488nm confocal endomicroscope CEM (CellVizio©, Mauna Kea Technologies, Paris, France) combined with a 0.95 mm outer diameter Proflex MiniZ microprobe (PF-2173, Mauna Kea Technologies, Paris, France). The microprobe was inserted through the operating sheath of this endoscope and positioned on the mice colon walls. During the acquisitions, the depth assessed was approximately 58 µm for a lateral resolution of 3.5 µm and a frame rate of 12 fps. The output images size is 329 × 326 μm^2 corresponding to a matrix of 292 × 290 pixels.

In this experimental framework, our goal is here to propose the characterization of the vascular networks, appearing as connected 'crypts' in hypersignal in images in Fig. 1, and automatically classify the vascular network among the three possible classes given in Fig. 1 based on this characterization. This is an important translational biomedical issue since an early depiction of structural changes into the colon wall vascular network is mandatory to improve the patient's prognosis. In this biomedical context, the following report stands as a first attempt of image classification since the recent introduction of the image acquisition protocol for mice colon's wall in [1]. This also constitutes here an illustrative instance of scene where the object to be characterized corresponds to an underlying structural network. Here, the vascular network carries blood through the tissue. The topology of such networks is characteristic of the health state of the tissue as shown in Fig. 1A, B, C. Specifically, it is well-known from early work by Millikin [2] up to more recent studies [3] that the opening of the vascular crypt identified by confocal laser endomicroscopy is predictive of the progress of the inflammatory process. These images are however challenging for different reasons. They show non-uniform contrast due to the impossibility to ensure a perfect homogeneity of the concentration of the contrast agent in the vascular network during the acquisition of the image. Also, as depicted in Fig. 1D, E, F, due to the manual positioning of the probe during the acquisition, the same tissue can appear stitched depending on the pressure or the orientation of the probe on the tissue while the vascular network carrying the biological information on the health score of the tissue is unchanged. We propose to address this pattern recognition problem with the approach described in the next section where we specifically pay attention to extract a robust description of the underlying network in the image.

3. Proposed algorithm and related work

The global organization of the proposed image processing pipeline is depicted in Fig. 2. This pipeline takes as input images that can be seen as noisy images of a structural network over a background. Our goal is to produce a representation of this network so as to further allow to extract its topology. The first step

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