



Simultaneous segmentation and anatomical labeling of the cerebral vasculature



David Robben^{a,c,*}, Engin Türetken^{b,d}, Stefan Sunaert^{a,e,g}, Vincent Thijs^{a,f,h,i}, Guy Wilms^e, Pascal Fua^b, Frederik Maes^{a,c}, Paul Suetens^{a,c}

^a Medical Imaging Research Center (MIRC), KU Leuven, Leuven, Belgium

^b Computer Vision Laboratory, École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland

^c Medical Image Computing (MIC), ESAT-PSI, Department of Electrical Engineering, KU Leuven, Leuven, Belgium

^d Swiss Center for Electronic and Microtechnology (CSEM), Switzerland

^e Department of Radiology, UZ Leuven, Leuven, Belgium

^f Department of Neurology, University of Leuven, Leuven, Belgium

^g Translational MRI, Department of Imaging & Pathology, KU Leuven, Leuven, Belgium

^h Leuven Research Institute for Neuroscience & Disease (LIND), KU Leuven, Leuven, Belgium

ⁱ Laboratory of Neurobiology, Vesalius Research Center, Leuven, Belgium

ARTICLE INFO

Article history:

Received 20 August 2015

Revised 20 January 2016

Accepted 16 March 2016

Available online 1 April 2016

Keywords:

Cerebral vasculature

Segmentation

Centerline extraction

Anatomical labeling

Circle of Willis

Integer programming

ABSTRACT

We present a novel algorithm for the simultaneous segmentation and anatomical labeling of the cerebral vasculature. Unlike existing approaches that first attempt to obtain a good segmentation and then perform labeling, we optimize for both by simultaneously taking into account the image evidence and the prior knowledge about the geometry and connectivity of the vasculature. This is achieved by first constructing an overcomplete graph capturing the vasculature, and then selecting and labeling the subset of edges that most likely represents the true vasculature. We formulate the latter problem as an Integer Program (IP), which can be solved efficiently to provable optimality. We evaluate our approach on a publicly available dataset of 50 cerebral MRA images, and demonstrate that it compares favorably against state-of-the-art methods.

© 2016 Elsevier B.V. All rights reserved.

1. Introduction

Automated segmentation and anatomical labeling of blood vessels is an important problem with many practical applications. In clinical settings, it can give an interventional radiologist extra guidance when navigating through the vasculature of a patient or enable automatic quantification of specific vessel segments. In a research context, it can be used to detect patterns that may be correlated to the incidence of vascular pathologies.

In this work, we focus on the cerebral vasculature and more specifically on the Circle of Willis (CoW) and its adjacent vessels. The CoW is a circle of arteries at the base of the skull that connects the left and right side of the anterior cerebral circulation with the posterior cerebral circulation (Fig. 1). It is supplied with blood by three large arteries, namely the left and right internal carotid arteries (ICA) and the vertebrobasilar artery (VBA).

The CoW plays a crucial role in several vascular pathologies, notably hemorrhagic and ischemic stroke. Cerebral aneurysms are balloon-like bulges on the wall of cerebral vessels and their rupturing is the main cause of subarachnoid hemorrhagic stroke (van Gijn and Rinkel, 2001). About 90 % of all cerebral aneurysms are found on the CoW (Brisman et al., 2006). The specific topology of the CoW determines the redundancy in blood supply to the brain and is associated with the prevalence of border zone infarcts in patients with unilateral ICA stenosis (Hendrikse et al., 2001). Although the CoW has a very characteristic morphology, it is highly variable: less than half of the population has a complete circle because one or more arteries are usually missing (Krabbe-Hartkamp et al., 1998). This variability makes both segmentation and labeling challenging.

In the following section, we provide an overview of the state-of-the-art techniques for vascular segmentation and anatomical labeling. Subsequently, we propose a novel method that tackles both problems simultaneously. Finally, we evaluate our approach and demonstrate its advantage over current techniques.

* Corresponding author.

E-mail address: david.robben@esat.kuleuven.be (D. Robben).

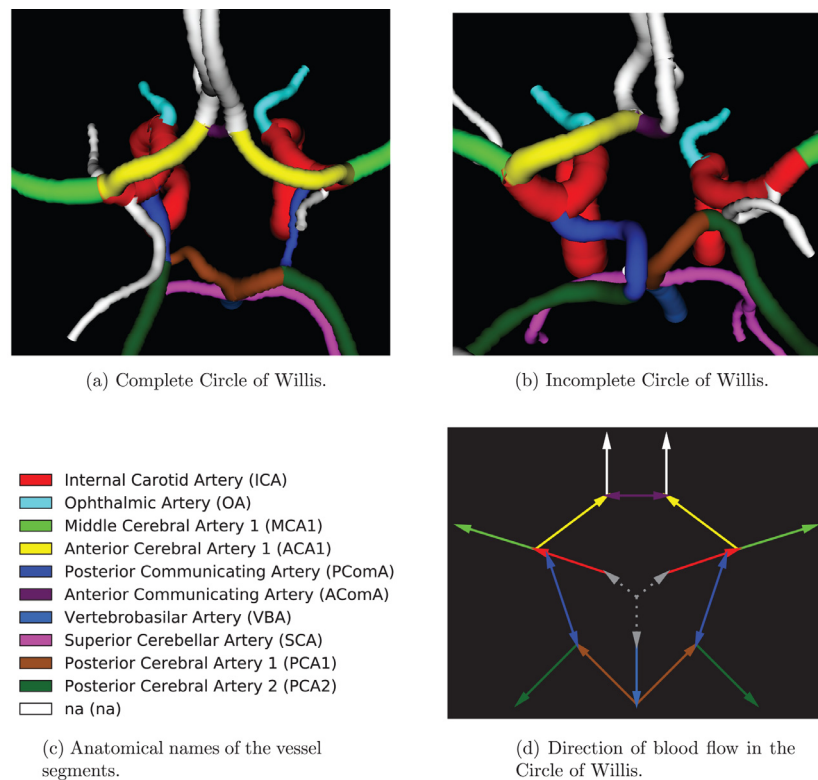


Fig. 1. (a,b) Anatomically labeled Circle of Willis in two healthy subjects. The colors refer to the anatomical names of the vessel segments as listed in (c). The CoW in (a) is complete, while the one in (b) misses several segments: right ACA1, right PCoMA and left PCA1. (d) Direction of blood flow in the Circle of Willis. The gray dotted arrows indicate the points where blood enters the CoW. Note that in the ACoMA and PCoMA the direction is unknown.

1.1. Related works on anatomical labeling of tubular structures

The problem of anatomical labeling of the vasculature can be posed more generally as labeling of a branched tubular structure. Most existing approaches formulate the problem in a graph-based setting, where the segmented object of interest is represented by a graph. In this graph, the vertices represent the branch and endpoints and the edges represent the branches. In the following, we present an overview of such methods.

A conventional approach to labeling is to anatomically match an unlabeled graph with one or more labeled graphs. This approach was successfully followed by [Graham \(2006\)](#), [Buelow et al. \(2006\)](#) and [Feragen et al. \(2012\)](#) to label the bronchi. However, as remarked by [Bogunović et al. \(2013\)](#), the reported results for approaches that learn a statistical labeling model are generally better.

[Tschirren et al. \(2005\)](#) label the bronchi of a patient by matching the graph edges with a labeled, probabilistic model containing for each label the mean and standard deviation of geometric properties. They take into account the length and direction of the edges and the angle and distance between pairs of edges. A learnt, fixed topology between the different labels is enforced. [van Ginneken et al. \(2008\)](#) label the bronchi with a probabilistic model that contains for each label the mean and standard deviation of the orientation, radius and angle with the parent edge. For all edges, label probabilities are calculated and the labels are assigned in a top-down fashion to the bronchial segments. [Mori et al.](#) published several works about bronchial labeling. Their latest approach ([Mori et al., 2009](#)) labels the bronchial branches in an edge matching approach. A trained classifier assigns a probability to each possible pair of edge and label. The algorithm then searches for the globally optimal assignment of edge labels taking into account several topological constraints. In another line of work, they label the abdominal arteries ([Mori et al., 2010](#); [Matsuzaki et al., 2015](#)), which

they consider more difficult than labeling bronchi due to the larger variability. They use an application-specific algorithm which they do not expect to work on vasculature of other organs. The method of [Bogunović et al. \(2011\)](#) aims at labeling five bifurcations in the anterior circulation of the CoW. This is done by explicitly enumerating all possible isomorphisms between a given graph and a pre-determined atlas, and then calculating a probabilistic cost function, which combines a data term based on bifurcation morphology with a prior term that imposes a certain ordering of the bifurcations. Although the performance of the method is very good, it is not computationally scalable: a preprocessing step is required to prune the graph to about 20 candidate vertices. [Robben et al. \(2013\)](#) label the full CoW by matching vertices to a probabilistic atlas. The approach relies on both unary potentials of the bifurcations and also pairwise potentials between them. [Bogunović et al. \(2013\)](#) also label the full CoW by matching bifurcations to an atlas. They use the bifurcation properties and have several reference graphs to model the topology of the bifurcations. The method is evaluated on ground truth segmentations as it requires topologically correct segmentations without loops, disconnected regions or spurious branches. [Bilgel et al. \(2013\)](#) label the anterior part of the cerebral vasculature using belief propagation on a Bayesian network. [Ghanavati et al. \(2014\)](#) label the complete vasculature of a mouse model. The labeling problem is formulated as a Markov Random Field and the optimal solution is sought through simulated annealing stochastic relaxation. It should be noted that these methods, except [Robben et al. \(2013\)](#), [Bogunović et al. \(2013\)](#) and [Ghanavati et al. \(2014\)](#), assume that the graph is a tree.

All these approaches rely on a pre-existing segmentation in the form of a graph of blood vessels or bronchi. When assigning the anatomical labels, they account for the fact that the vasculature and the airway system are not random sets of tubular structures but organs with specific connectivity patterns. However they do

Download English Version:

<https://daneshyari.com/en/article/6878178>

Download Persian Version:

<https://daneshyari.com/article/6878178>

[Daneshyari.com](https://daneshyari.com)