

David Robben¹, Engin Türetken², Stefan Sunaert³, Vincent Thijs⁴, Guy Wilms³, Pascal Fua², Frederik Maes¹, and Paul Suetens¹

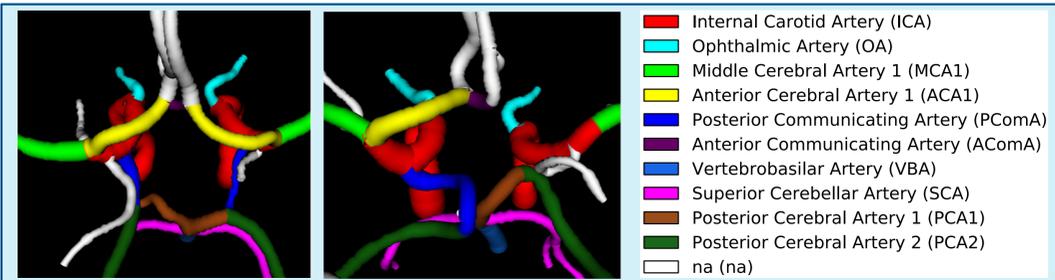
¹ iMinds - Medical Image Computing (ESAT/PSI), KU Leuven, Belgium

² CVLab, EPFL, Lausanne, Switzerland

³ Department of Radiology, University Hospitals Leuven, KU Leuven, Belgium

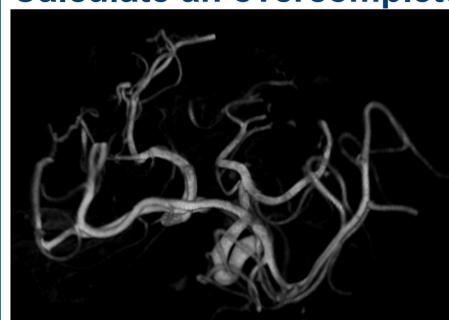
⁴ Department of Neurology, University Hospitals Leuven, KU Leuven, Belgium

Abstract. We present an 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 jointly optimize for both by simultaneously taking into account the image evidence and the prior knowledge about the geometry and connectivity of the vasculature. We show that our method compares favorably against state-of-the-art methods on a public dataset of 50 MRA.



Method

Calculate an overcomplete graph covering the full vasculature (and more)



Original image

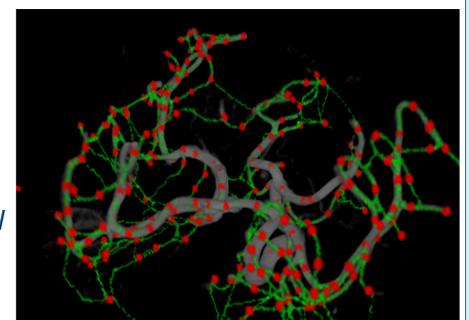
Calculate 4D tubularity image



Tubularity image (4D, position + scale)



Sample local maxima and connect them with minimal paths



Overcomplete graph $G = (V, E)$

Select a subgraph from G and anatomically label its edges such that it most likely represents the true vasculature

Edge pairs

The formulation uses consecutive edge pairs in the directed graph G as it:

- captures more global appearance and geometry information
- gives rise to a linear objective function and constraints.

$F = \{e_{ijk} = (e_{ij}, e_{jk})\}$: the set of pairs of consecutive edges

Labels

The vertices in our graphs do not need to lie on the vascular junctions. As a consequence, an edge can belong to multiple anatomical segments.

$S = \{s_j\}$: the anatomical labels for distinct segments of the vasculature e.g. ICA

$\hat{L} = \{(s_i, s_j, \dots) | s_i \in S, s_j \in S, \dots\}$: the edge pair labels

Variables

X_{ijk}^l Binary random variable representing whether the directed edge pair e_{ijk} belongs to the underlying vasculature and has the label $l \in \hat{L}$. Its realization is x_{ijk}^l .

Decomposed into

T_{ijk} Binary random variable representing whether the edge pair e_{ijk} belongs to the underlying vasculature.

L_{ijk} Random variable denoting the label $l \in \hat{L}$ of edge pair e_{ijk} .

Objective function

We look for the maximum likelihood solution, which can be written as:

$$\mathbf{x}^* = \arg \max_{\mathbf{x} \in \mathcal{X}} \sum_{e_{ijk} \in F} \sum_{l \in \hat{L}} \left[\log \frac{P(T_{ijk} = 1 | I, G)}{1 - P(T_{ijk} = 1 | I, G)} + \log \frac{P(L_{ijk} = l | I, G, T_{ijk} = 1)}{P(L_{ijk} = l | T_{ijk} = 1)} \right] x_{ijk}^l$$

Probability estimates are given by random forest classifiers.

Constraints

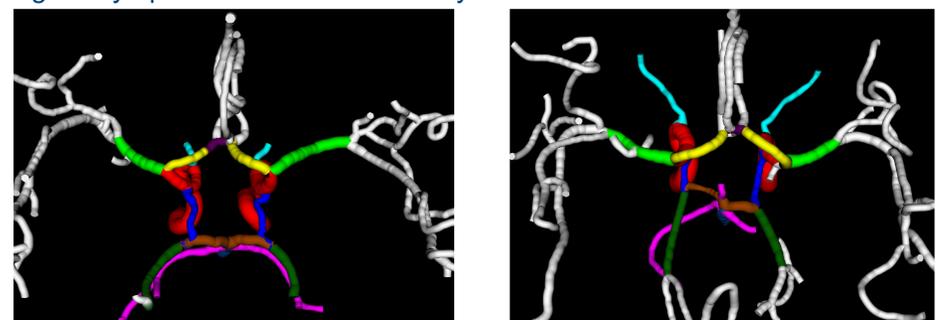
Our algorithm learns from the annotated training data which edge pair labels and configurations of labels are possible in the final solution, e.g.:

- labels of overlapping edge pairs should be compatible
- some labels can occur only in a furcation
- some labels cannot form loops

This is expressed as linear constraints on the binary x_{ijk}^l variables.

Optimization and result:

The globally optimal solution is found by an off-the-shelf branch-and-cut solver:



Evaluation

Labeling quality

We compare with a specialized algorithm for labeling ground truth centerlines (Bogunović et al., TMI2013). Hereto, we create graph G from the ground truth centerlines. By setting $P(T_{ijk} = 1 | I, G) = 1$, we can use our algorithm to only perform labeling. The positions of named bifurcations are compared with those in the ground truth annotation.

Bifurcation	Proposed			Bogunović et al.[1]		
	accuracy	precision	recall	accuracy	precision	recall
ICA-OA	99	100	99	-	-	-
ICA-M1	99	99	100	99	100	99
ICA-PCoMA	93	94	96	97	98	98
ACA1-AComA	92	93	97	98	97	100
M1-M2	89	89	100	82	82	100
VBA-SCA	95	98	97	-	-	-
VBA-PCA1	94	100	93	96	96	100
PCA1-PCoMA	96	100	94	98	97	100
PCA2-PCA3	89	92	93	-	-	-

Segmentation quality

To show the benefit of the simultaneous approach, we compare with Türetken et al. (CVPR2013), which has the same segmentation method but no simultaneous labeling. We sample paths with varying lengths from both our results and the ground truth centerlines. For every random path of either reconstruction, we look for a corresponding path (i.e. a Hausdorff distance less than 1.5 mm) in the other reconstruction.

