Automated 4D Flow Whole Vessel Segmentation and Quantification using Centerline Extraction

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TARGET AUDIENCE: Physicists and clinicians interested in fast, automated whole vessel segmentation and quantification in 4D flow MRI.

PURPOSE: The recent emergence of 4D flow MRI allows for quantification of blood flow velocities with volumetric coverage. However, several clinical translational hurdles persist: 3D velocity acquisition through time results in large datasets and consequently long reconstruction and post-processing times. Additionally, quantification requires manual segmentation and careful placements of double-oblique 2D cut planes orthogonal to the direction of flow to localize measurements. In vessels with a tortuous path, such as in the siphon of the internal carotid artery (ICA), segmentations and measurements become increasingly user dependent. The purpose of this study is to develop and implement whole vessel automatic segmentation and flow quantification from time maximum intensity projection (tMIP) dynamic PC MRAs collected from 4D flow. This method is demonstrated for flow measurements in the ICA siphon.

METHODS: All processing is completed using an in-house tool developed in commercial software (Matlab, *Mathworks*, MA, USA). To separate foreground vessels from background noise, reconstructed tMIP is empirically thresholded at 18% its maximum signal. The binary volume is then skeletonized according to a thinning procedure suitable for elongated objects such as blood vessels[1], resulting in a one-voxel wide centerline vascular representation. Branch endpoints and junction points are identified and labeled within the vascular tree, producing a unique branch number for each vessel. Interactive 3D rotation of the tMIP (Figure 1A) allows for visualization and one-click selection of the vessel of interest, which is automatically segmented using its centerline (Fig. 1B). Points before and after the currently analyzed centerline location are used to calculate and extract orthogonal cross-sectional slices with respect to the propagation of the vessel. Within each cross-section, anatomical and blood flow parameters can be quantified from the time-resolved velocity data.

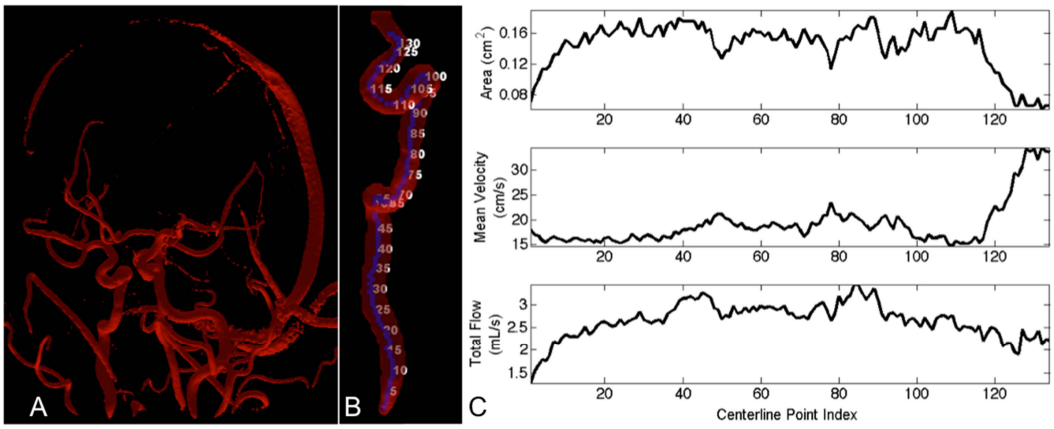

Figure 1. Cranial PC MRA from a 4D Flow scan of a healthy male, age 53 A: 3D tMIP vessel visualization. B: whole vessel segmentation in the right ICA including siphon with centerline (blue points). Numbers represent indexed points along centerline. C: Anatomical and physiological parameters at every centerline point with the same indexing.

Ten healthy adults (7M, age 37 ± 9 years) were imaged after informed consent with a 4D flow MRI technique[2] on a 3T system (Discovery MR750, *GE*, WI, USA). Scan parameters: 32 channel head coil, FOV = 22 x 22 x 22 cm^3, (0.7 mm)^3 isotropic spatial resolution, scan time = 9.5 min, Venc = 110 cm/s, 20 reconstructed cardiac time frames. Parameters measured within the ICA (20 total vessels) for this study were: cross-sectional area, mean velocity, and total flow over the cardiac cycle. To compare vessels across the group, parameters were calculated along the first 50 centerline points proximal to the ICA junction with the anterior and middle cerebral arteries.

RESULTS: Average post-processing time per vessel was 156 ± 21 seconds, including data loading, thinning and centerline extraction, vessel selection and segmentation, and quantification. Centerline computation and vessel segmentation were successful in all cases. Figure 1C displays calculation of parameters along the length of the vessel from Fig 1B. Averaging over all measured ICA siphons (Figure 2) demonstrates the ability to detect anatomical and flow differences within a healthy vessel, in this case lower cross-sectional area and higher mean velocity near the junction with the anterior and middle cerebral arteries.

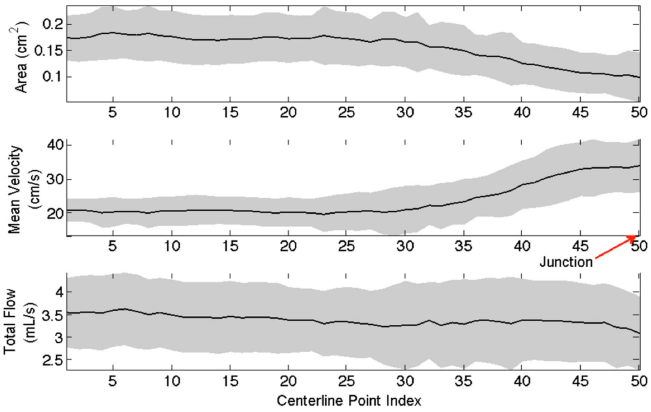

Figure 2. Mean (± stdev) within the siphon for all measured vessels indicates decreased area and increased velocity near the ICA junction (red arrow). Flow remains conserved as expected.

DISCUSSION and CONCLUSION: The ability to perform automated and user-independent vessel segmentation and flow parameter quantification allows for much faster analysis than is typically performed for 4D flow post-processing. By viewing vasculature as a tree of unique vessel branches, segmentation of any individual vessel (or concatenated vessels to follow blood along a certain route) provides comprehensive understanding of flow along the entire vessel. This study exhibits the implementation and initial testing of a fast, automated, and robust segmentation and quantification method for complete coverage vessels. Its functionality should lead to higher reproducibility in placement of planes orthogonal to vessel orientation, in contouring ROIs and subsequently flow measurements. This will be particularly important in multicenter trials where measurement consistency is paramount.

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REFERENCES: **1**. Palágyi K., et al. *IPMI 17th International Conference.* 2001. **2**. Gu T., et al. *AJNR*. 2005.