Robust Whole-Brain Blood Tracking from 4D Flow using Displacement Corrected Probabilistic Streamlines

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INTRODUCTION: 4D MR flow acquisitions provide both vascular morphology and hemodynamic information making them well suited to examine structure-fluid interactions. Typical angiographic evaluation currently utilizes only the velocity magnitude information, capturing both arteries and veins. In many applications, selective vessel visualization and analysis of feeding and draining vessels is desired, e.g. in the identification of filling patterns and draining vessels of arteriovenous malformations (AVMs). While this can be separately evaluated with intra-arterial X-ray fluoroscopy or with targeted arterial spin labeling (ASL) MRI, recent work has demonstrated the use of 4D MR Flow data to generate streamlines (or pathlines) [1] for similar purposes. Unfortunately, errors in the flow field accumulate over the path of streamlines leading to poor visualization of small and branching vessels. This work demonstrates a novel method combining probabilistic streamlines [2], displacement corrections [3], and fluid constraints to track blood movement throughout the brain using only 4D flow acquisitions.

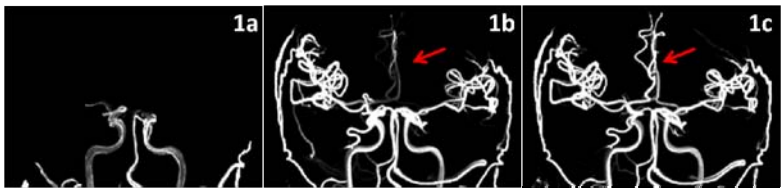

Figure 1: Coronal MIPs from a patient with a DAVF. Fig. 1a shows the algorithm without any corrections, 1b with stochastic corrections but without displacement corrections, and 1c the complete algorithm. Stochastic corrections are the most significant, but without displacement corrections some vessels are missed, such as the anterior communicating arteries pointed out with a red arrow.

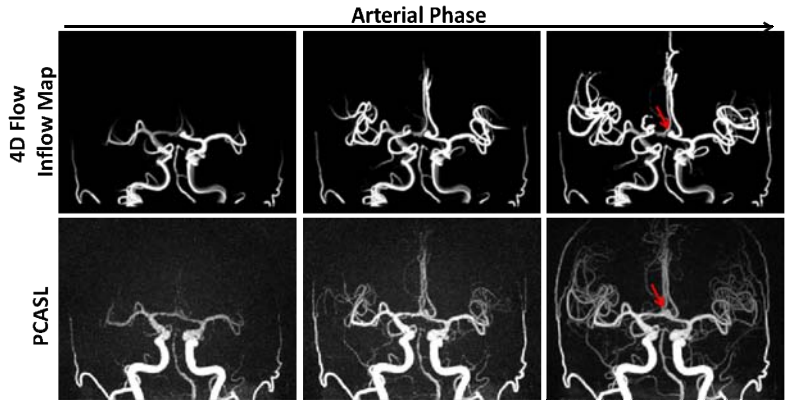

Figure 2: Comparison of coronal maximum intensity projections (MIPs) from a patient with an aneurysm in the anterior communicating arteries (red arrow). Good agreement is seen between the two sets of images, though the 4D flow method cannot follow vessels below a certain diameter.

METHODS: 4D MR flow data was acquired with a 3D radially undersampled phase contrast acquisition (PCVIPR) [4] on clinical 3T scanners (Discovery 750, GE Healthcare, Waukesha, WI) with a scan time of ~6 minutes and whole brain coverage. For comparison, dynamic ASL measurements were made using pseudo-continuous labeling (PCASL) and a 3D radial trajectory [5], with a scan time of ~7 min and whole brain coverage. The algorithm was tested on 4D MR flow datasets from 2 patients with AVMs, 2 patients with aneurysms, and a patient with a dural arteriovenous fistula (DAVF), all imaged with IRB approval and patient consent. PCASL datasets were available in all but 1 patient.

All streamline steps were calculated with the 4th order Runge-Kutta (RK4) method from time-averaged velocity maps of the brain. Streamline starting positions (seeds) were randomly placed within a masked plane in the neck for whole vascular images, or from a manually positioned sphere for isolating single vessels or AVM analysis. Every new point of a streamline was calculated with two RK4 steps, where the first step (t = 2.4-2.7 ms) was used to approximately compensate for velocity displacement artifacts, and the second (t=3 ms) was then the actual streamline step to calculate the new position. To account for stochastic noise, each streamline step is perturbed by a vector randomly sampled form a normal Gaussian distribution (σ=1cm/s). Additional constraints were imposed to select lines that minimize changes in kinetic energy, as well as preferring lines that stay within the vessel boundaries as determined from the PC MR angiogram.

RESULTS: Figure 1 shows inflow maps generated from the DAVF patient, demonstrating the improvements from adding stochastic modifications, as well as displacement correction. Figure 2 shows ASL data with different delay times and matching 4D MR flow processed data from an aneurysm patient. Good agreement is shown between the derived inflow map and the PCASL dataset, where the aneurysm filling can be isolated, though PCASL can visualize smaller arteries. Similar agreement was seen in all PCASL comparisons. Figure 3 demonstrates selective up and downstream streamline seeding in an AVM patient allowing visualization of the main feeding vessels and draining vein.

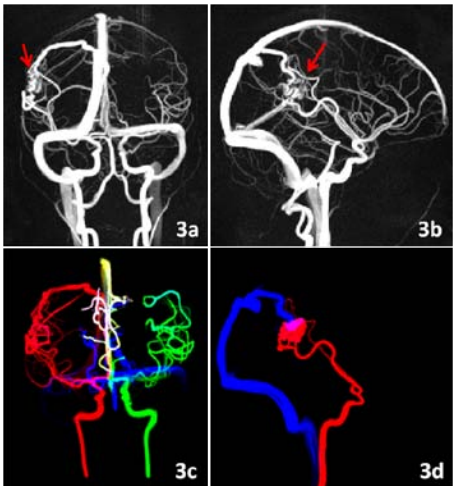

Figure 3: Coronal (3a, 3c) and Sagittal (3b, 3d) MIPs from an AVM patient, with the AVM pointed out with a red arrow. 3a and 3b show the standard complex difference angiogram from the 4D MR flow acquisition. 3c shows three inflow maps, each seeded at a different artery (red = left carotid, green = right carotid, blue = basilar), demonstrating the ability to measure vessel selective inflow. 3d shows the use of this algorithm seeded within the AVM, with blue lines integrating forwards depicting the draining veins, and red lines integrated backwards to depict the feeding arteries.

DISCUSSION: Whole brain 4D MR Flow with robust blood tracking allows for selective visualization of blood filling throughout neurovasculature with 'virtual contrast injections'. Unlike DSA and ASL, seed locations can be chosen retrospectively and placed in downstream vessel segments. This analysis is complementary to the quantitative flow analysis provided by 4D flow acquisitions, and is calculated solely with the MR data (i.e. no fluid modeling). In initial evaluations, good agreement was seen compared to PCASL, indicating accurate modeling of blood flow propagation. In future work, we plan to investigate resolution and SNR requirements to adequately characterize small vessels and prevent contamination of nearby vessels, and thoroughly compare the method across more subjects.

1) Edjlali, Myriam, et al. *Radiology* (2013). **2)** Friman, Ola, et al. *MICCAI (*2010) 416-423. **3)** Steinman, et al. *JMRI* (1997) *7*(2), 339-346. **4)** Johnson, Kevin M., et al. *MRM* (2008) 60(6), 1329-1336. **5)** Wu, Huimin, et al. *MRM* (2012).