

eXtended – Time Resolved Angiography using InfLow Subtraction (X-TRAILS)

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INTRODUCTION – Time-resolved Magnetic Resonance Angiography (tr-MRA) of the intracerebral vasculature is key to extract hemodynamic information and to assess vessel patency and stroke risks. This also includes imaging of intravascular abnormalities including carotid artery stenosis, aneurysms, and arteriovenous malformations. Recently, we introduced a novel 4D non-contrast enhanced tr-MRA technique called TRAILS (Time Resolved Angiography using Inflow Subtraction). It was used to acquire intracerebral hemodynamic information using pseudo-continuous arterial spin tagging as endogenous tracer in healthy volunteers and to acquire a static and tr-MRA with a high temporal and spatial resolution and low temporal footprint. Using TRAILS, dynamic and static whole-head angiographic data sets in healthy volunteers were acquired in a clinical feasible scan time with a maximum blood (label) transit time of up to 3 seconds on a 3T MRI system. TRAILS uses a spoiled gradient echo sequence and will therefore push the tracer into a steady state due to multiple RF exposures [1]. This is akin to a Look-Locker acquisition, which causes the subtraction based (label and control) angiographic signal to vanish. Here, eXtended-TRAILS (X-TRAILS) is introduced, a novel extension to TRAILS. X-TRAILS uses variable repetition times (vr-TR) to reduce RF exposure during the cine-like readout to accommodate patients that exhibit extremely slow blood flow patterns and consequently longer blood transit times.

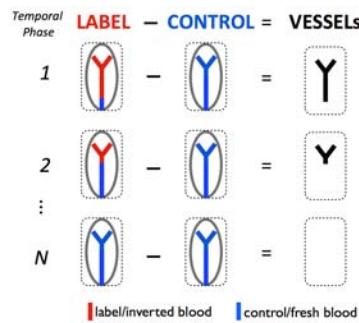


Figure 1: PCASL based X-TRAILS reconstruction is shown. The raw angiographic signal is computed by subtraction of the two tagging states, 'label' and 'control' from each other.

temporal footprint starting at 476ms (70 x TR1) for the first temporal phase and up to 1176ms (70 x TR3) for the last temporal phase. **Bloch Simulations:** Bloch simulations were performed with the sequence parameters to analyze potential saturation effects and signal loss, using $T1|2=1932|275$ ms for arterial blood and a magnitude based signal comparison between a fixed TR and vr-TR approach was performed. **Quantitative analysis:** The dynamic inflow of blood was visualized using a relative blood transit time map (rTT-map) for each volunteer. The rTT was defined as the transit time of blood from the tagging plane location when the normalized inflow signal curve reached half of its maximum signal. rTT was computed for each vessel segment/voxel and color mapped back to axial, sagittal and coronal MIPs.

RESULTS – Figure 2 shows that tracking of blood transit times of up to 6 seconds is possible (Bloch Simulations). **Figure 3** shows the rTT map of a subject with blood transit of up to 4 sec including a selection of temporal phases (Figure 4).

CONCLUSION & DISCUSSION – X-TRAILS allows – similar to

TRAILS - whole head coverage and the acquisition of both static and dynamic MRAs with a high spatial and temporal resolution within a single acquisition with the additional benefit of tracking blood transit times of up to 6 seconds according to Bloch simulations. References: [1] Kopeinigg D, et.al., MRM 2013; Oct 24. doi: 10.1002/mrm.24985. [2] Gurney PT, et al., MRM 2006; 55: 575-582. **Acknowledgements:** The authors would like to thank Ajit Shankaranarayanan, Julian McLaren, Rafael O'Halloran, Murat Aksay, Alexander Brost, Samantha Holdsworth, Ernesto Staroswiecki, Christian Langkammer, and Caroline Jordan for helpful discussions. This work was supported in part by the NIH (5R01EB011654, 5R01EB008706, 5R01EB002711, P41 RR009784), the Center of Advanced MR Technology at Stanford (P41 EB015891), Lucas Foundation.

MATERIALS & METHODS – **Data acquisition:** Imaging was performed on a high performance 3T MRI unit (Discovery 750; GE Healthcare, Waukesha, WI) with a gradient strength 50mT/m and a maximum slew rate of 300mT/m/ms with an 8-channel receive only head coil. Sequence parameters were: resolution 1x1x2mm, FA=6°, FOV: 200x200x150mm, TR1\2\3=6.8\11.8\16.8ms, 4.5 seconds tagging duration and 4.5s multi-phase SPGR readout. Using 3D Cones readout trajectories, the total scan time was under 6 minutes [2]. **Reconstruction:** Complex sensitive subtraction of label and control on a per-interleaf basis was used to form the angiographic data set. This subtraction between the label and the control data set is the essential step in to cancel the signal from the background tissue and to distinguish the label from the fresh inflowing blood. The reconstruction algorithm is visualized in Figure 1. Followed by gridding in conjunction with a sliding window reconstruction to reconstruct 210 temporal phases with a

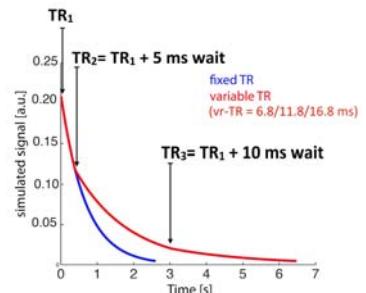


Figure 2: Bloch Simulations of the signal over time using the fixed TR (TRAILS) and the vr-TR readout. Clearly visible is the prolonged angiographic signal.

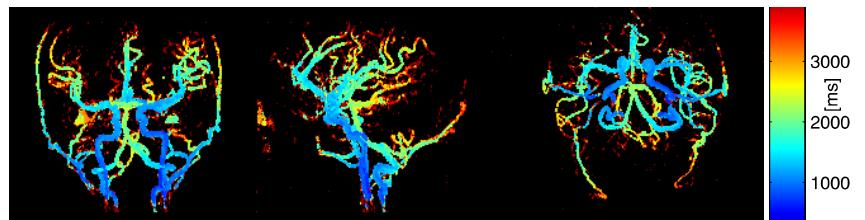


Figure 3: Relative transit time map of a subject undergoing X-TRAILS. Clearly visible are the varying blood arrival times in various cohorts, e.g. the tip of the basilar artery vs. the A1-MCA segment.

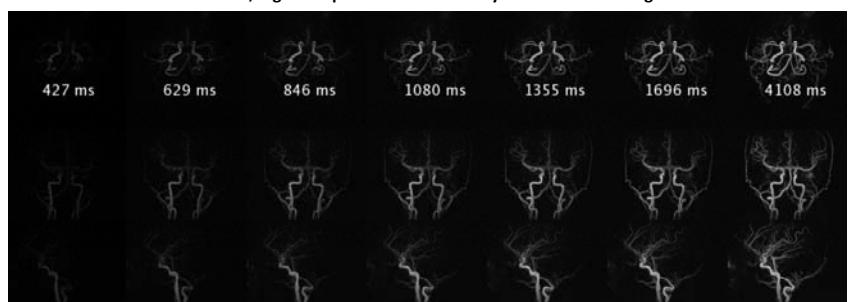


Figure 4: A selection of temporal phases as: axial, coronal, and sagittal MIPs from a X-TRAILS acquisition.