Comparison of ASL kinetic curves between subjects and between brain areas

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Introduction: Arterial Spin Labelling (ASL) offers a non-invasive method to assess cerebral blood flow. A commonly used technique to reduce the scanning time is QUIPSS II [1]. This involves an additional saturation pulse at a fixed delay following the ASL tagging pulse, thus defining the trailing end of the tagged bolus. QUIPSS II allows a quantitative estimate of CBF from a single inversion time (TI), provided TI is long enough such that the descending portion of the signal kinetic curve is reached [2]. Typically TI=1.4s is used, but it is assumed *a priori* that this is long enough to satisfy the QUIPSS II assumption.
We measured the ASL kinetic curves (for multiple TIs) in resting normal volunteers to compare differences between brain regions and between subjects. We could then assess under what conditions the QUIPSS II assumption is valid.

Methods: 5 healthy volunteers (3 female, 2 male, age 22-27 years) were scanned using a Siemens 3T Trio system fitted with a single-channel T/R head coil. A single axial slice (4x4x6mm voxel size) was acquired, positioned to intersect the thalamus. Image read-out was GE-EPI with TR/TE = 3540/23ms following a perfusion preparation using the QUIPSS II variant known as Q2TIPS [3]. Bipolar flow-crushing gradients were used (b=5.3s/mm^2) to suppress the signal from large vessels. The ASL tag was achieved with an adiabatic FOCI pulse using a modified version of the sequence described in [4], with a tag-width of 100mm and an offset between the top of the tag and the imaging slice of 15mm. Alternating control and tag pairs were acquired with TI times of [300, 500, 750, 1000, 1250, 1500, 1750, 2100, 2500, 3000]ms in a randomised order. 30 control/tag pairs were acquired for each TI, giving a total scan time of ~36 mins. In order to minimise any bias between control and tag due to spin history effects, the tag inversion was immediately preceded by a series of 9 saturation pulses of the imaging slice, each followed by an axis-cycled dephasing gradient. For TI times greater than 750ms, the Q2TIPS saturation pulses were started at 700ms and stopped at least 50ms before the read-out, with an upper limit on the stop time of 1500ms.
Using Matlab (The Mathworks, Inc.) the mean perfusion-weighted image (PWI) across all TIs was calculated for each subject (see Figure 1). 8 ROIs were then hand-drawn on each PWI to mark corresponding anatomical areas. The shape of the ASL kinetic curves could then be compared across regions of the brain and between subjects.

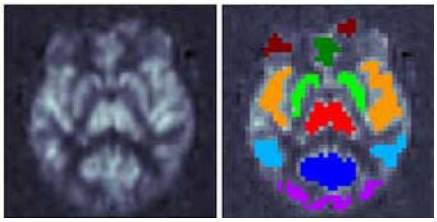

Figure 1: Perfusion-weighted image for a representative subject *(left)* and the hand-drawn anatomically-based ROIs *(right)*.

Results and Discussion: The kinetic curves for each of the ROIs for all subjects are shown in Figure 2. There is a striking variability in curve shape between brain regions which is markedly consistent between subjects. ROI 2, for example, rises early and peaks at TI = ~0.9s. ROI 5, however, rises much more slowly and peaks at TI = ~2s. This is consistent with the previous finding that the ASL transit time is longer in occipital than parietal areas [5].
The peak in the kinetic curves for 4 out of the 8 ROIs is ~1.5s or later. Given that 1.4s is often used as the single inversion time for QUIPSS II imaging, this would suggest that the assumption that the measurement is occurring on the downward slope of the curves is not always being met, and is brain region dependent. Such differences are likely to become even more evident in patient populations.

Conclusion: ASL kinetic curves show variations between brain regions which are consistent between healthy subjects. Large regions of healthy brains can have flow kinetics which, for commonly used parameters in QUIPSS II imaging, violate the assumption which allows use of a single inversion time. For study of brain areas where this assumption is questionable, an approach which measures several inversion times may be more appropriate.

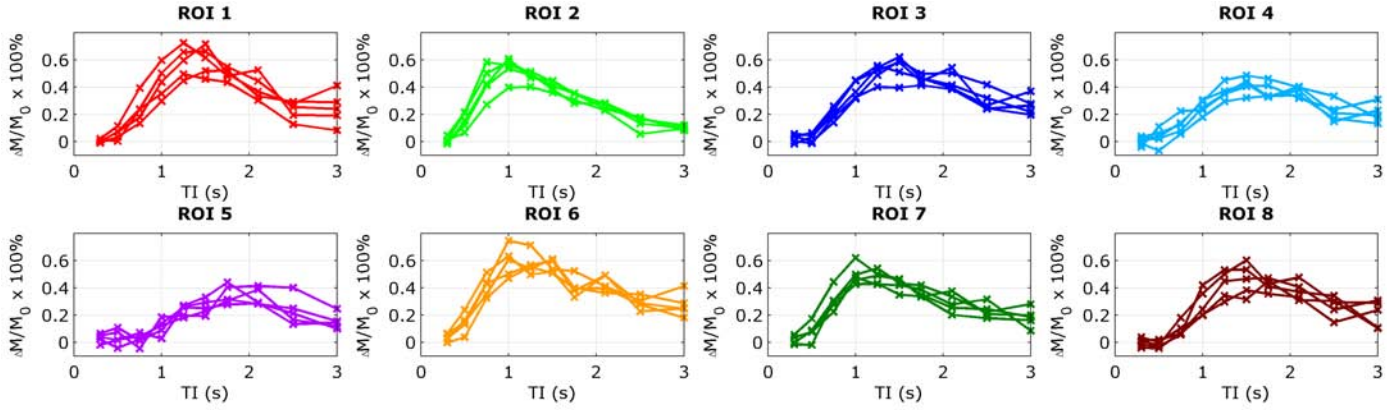

Figure 2: Kinetic curves for each ROI. Each subject is shown as a separate line in each plot.

References: [1] Wong *et al*, MRM 1998 39(5) 702-8; [2] Buxton *et al,* MRM 1998 40:383-96; [3] Luh *et al*, MRM 1999 41(6) 1246-54; [4] Kuijer *et al*, ISMRM 2003;664; [5] Wong *et al,* NMR Biomed. 1997 10(4-5) 237-49