Arterial Transit Delay Measurement Using Pseudo-Continuous ASL with Variable TR and Interleaved Post-Labeling Delays

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Introduction: Transit delays in an ASL experiment refer to the time required for the labeled blood to arrive in the imaging slice. Knowledge of the transit delays is very important for conducting ASL experiments. Conventionally, transit delay measurements consist of a series of separate ASL experiments acquired at several different post-labeling delays (PLD). The data is then fitted to a mathematical model to obtain estimates of the transit delays. Additional scans are usually needed to map T1 and blood magnetization (M_0) for CBF quantification. Such measurements are usually time-consuming [1,2] and can be formidable overheads for ASL studies. The time requirement also makes the measurements highly sensitive to motion. A few studies have suggested the use of Look-Locker sampling [3] or 3D imaging [4] technique to improve the time efficiency. However, there are more direct ways to address the issue by simple modifications of the conventional method. This study presents a modified method for measuring transit delay with shorter scan time and less motion sensitivity.

Theory: The proposed method relies on the pre-saturation pulse that is typically applied in ASL experiments to saturate the imaging slice immediately before the labeling pulse (Figure 1). The pre-saturation pulse causes the tissue signal to recover from zero at the beginning of each TR, which has the following results: 1) the tissue signal intensity is independent of TR, which means that we can use shorter TR for scans with short PLDs and increase TR as PLD increases; 2). the tissue signal intensity at each PLD follows a saturation recovery curve determined by the tissue T1 (Figure 2), allowing T1 and M_0 estimation without the need for additional scans. Both these features can enable a reduction in scan time. Additionally, ASL experiments require many averages to gain signal to noise ratio (SNR). Conventional transit delay methods acquire all the averages at one PLD before moving to the next PLD. Our method acquires one tag/control pair for every PLD point and then moves to the next pair (Figure 2). Such an acquisition scheme reduces the sensitivity to motion since head movement will be less likely to cause complete loss of one or more of the PLD points.

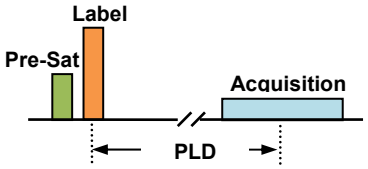

Figure 1. An ASL pulse sequence including pre-saturation and labeling pulses. The time between labeling pulse and data acquisition is the post labeling delay (PLD).

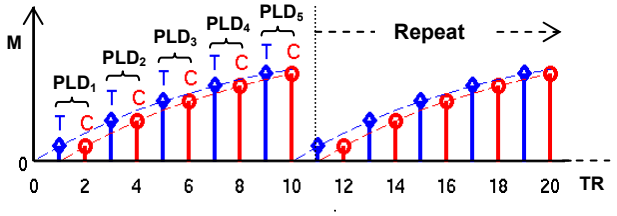

Figure 2. Acquisition scheme for measuring transit delay. T denotes tag (or label) and C denotes control. The tag and control image intensities follow a saturation recovery curve at different PLDs.

Methods: The acquisition scheme was implemented with an in-house ASL pulse sequence with variable PLD, variable TR capability and single shot spiral acquisition. Data was acquired on a healthy human subject on a General Electric (GE) Signa HDx 3.0 Tesla research scanner with a standard 8 channel head coil (GE, Milwaukee, Wisconsin). An optimized pseudo-continuous ASL (PCASL) [5] method was used with following parameters: labeling duration 1.0 sec, TE 3 ms, Variable TR (1.8 - 4.2 sec), 20 slices, 5mm thick with no gap, FOV 22cm, 64x64 matrix, 7 PLD points {0.2 0.6, 1.0, 1.4, 1.8, 2.2, 2.6 sec}, 10 pairs of Tag and control images at each PLD, total scan time 7min. Tissue T1 and M_0 were fitted using the averaged tag and control data at each PLD point. Perfusion signals were calculated by pair-wise subtraction of the tag-control series at every PLD. The perfusion data and T1 maps were then passed to a single compartment model [6] for estimating transit delay and CBF.

Results: Figure 3 shows the estimated transit delay and CBF map for 6 slices. The estimated mean transit delay is 0.95±0.36 sec in whole brain gray matter and 1.19±0.45 sec in white matter. The mean gray matter CBF is 79.8 ± 35.2 ml/100g/min and the mean white matter CBF is 49.2 ± 25.0 ml/100g/min, all within the typical range reported for healthy humans.

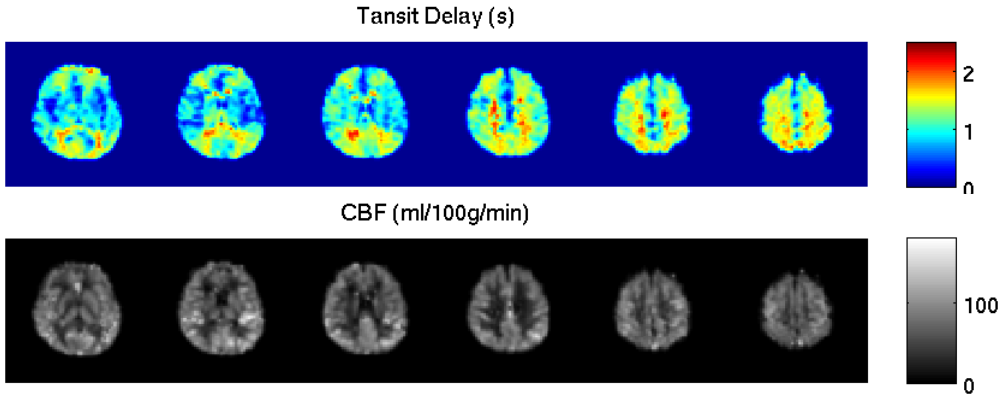

Figure 3.Estimated transit delay (s) and CBF (ml/100g/min) maps.

Discussion: Due to inflow effects, the tissue signal at each PLD does not strictly follow a saturation recovery curve. However the error is within 1% assuming the arterial content of tissue is 1% [6]. This error is tolerable for T1 and M_0 mapping. The proposed method can also be implemented using pulsed ASL methods, such as FAIR and PICORE. The shorter labeling durations in pulsed ASL allows for a wider range of PLD values to be sampled, which should improve the accuracy of T1 estimation. However, the inferior SNR of pulsed ASL compared to PCASL mandates more averages (thus longer scan time) for reliable perfusion measurements. Our preliminary test data collected using FAIR with similar parameters produced noisier estimates than the PCASL data and is not shown. Finally, the proposed method also relies on near complete saturation of imaging slice by the pre-saturation pulse. Partial saturation will cause the magnetization to vary from TR to TR and thus induce errors in the data. Nevertheless, the proposed method is a simple yet effective modification of the conventional transit delay measurements. It requires shorter scan time and is less sensitive to motion. Such a method could be beneficial to all ASL studies.

References: [1] Mildner T et al, NMR Biomed 18, p19, 2005. [2] Wu WC et al, IEEE Tran Med Imag 26, p84, 2007 [3] Brookes MJ et al, Magn Reson Med 58, p41, 2007. [4] Gunther M et al, Magn Reson Med 54, p491, 2005. [5] Jung Y et al, 17th ISMRM, p1578, 2009. [6] Buxton RB et al, Magn Reson Med 40, p383, 1998.