Improved estimation of renal perfusion with multiple inversion-time acquisitions in arterial spin labeling

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Target audience: Investigators interested in measuring renal perfusion with arterial spin labeling

Purpose: Arterial spin labeling (ASL) is a promising MRI technique for measuring tissue perfusion without contrast injection. It typically involves the acquisition of two images per tissue slice; one with global inversion, and the other with a slice-selective inversion. The difference between the two images results from inflowing arterial blood, which is inverted only in the globally-inverted image. This flow-weighting enables estimation of perfusion from ASL images. Inversion time (TI), the time delay between inversion and imaging, is another important factor affecting the signal difference. At very short TI, for instance, when tagged spins have not reached the imaging slice, the signal difference is zero. A simple and robust model has been widely used to quantify perfusion (*f*) from ASL data acquired at a single TI [1, 2, 3]:

$$\Delta M(TI) = 2M_0 \cdot \alpha \cdot TI \cdot \frac{f}{\lambda} \cdot \exp(-TI/T_1) \quad (1)$$

where ΔM(TI) is the signal difference obtained at TI, M_0 is the equilibrium magnetization of tissue, λ is the blood tissue-water partition coefficient, α is the efficiency of the inversion pulse, *f* is perfusion, and T_1 is the longitudinal relaxation time (assumed to be identical between tissue and blood). A major assumption in Eq. (1) is that the transit delay (termed TD in this study) between tagging site and tissue voxel of interest is small enough to be ignored. This could cause substantial error in perfusion estimates when it does not match the underlying physiology. In this study, we compared a convolution-based model incorporating transit delay to the conventional approach using both simulated and human kidney ASL data.

Methods: A convolution-based model for analyzing renal ASL data expresses the ASL difference signal ΔM(t) with three components: the concentration of tagged spins in the artery (AIF), the impulse retention function (IRF), and the T1 relaxation of the tagged spins (R(t)):

$$\Delta M(t) = 2M_0 \cdot f \cdot \int_0^t AIF(\tau) \cdot IRF(t-\tau) \cdot R(t-\tau) d\tau \quad (2)$$

Following convention, we characterize the AIF as rectangular function of width *w* and transit delay TD, during which T1 relaxation occurs [4]. The IRF is modeled as delayed exponential decay [5]. R(t) is a mono-exponential decay with T1 of renal tissue. Note, unlike the conventional Eq. (1) where only perfusion f is unknown, with Eq. (2) both *f* and transit delay TD must be fitted, requiring signals acquired at two or more different TI values.With a simulation, we aimed to evaluate the error in perfusion estimates obtained using the conventional method (Eq. (1)), and its sensitivity to selected TI. We simulated an ideal ASL difference signal for renal tissue using the above convolution formula (2) and the following parameter values: f = 300 mL/100mL/min, M_0 = 1, TD = 0.6s, *w* = 0.75s, *α* = 1, minimal transit time (minTT) = 1s, washout rate constant (*k*) = 0.5s^{-1}, and TI from 0 to 3.0s. Different from conventional formula (Eq. 1), Eq. (2) allows for different T_1 values for tissue and blood, $T1_{blood}$ = 1.5s, $T1_{tissue}$ = 1.1s. We applied the conventional method to the simulated signal difference at each TI value to estimate perfusion and compared the results to the true value. To investigate the effect of transit delay on estimated perfusion error, we simulated tissue ASL signals over a range of TD from 0s to 1s at an interval of 100ms and estimated perfusion using Eq. (1) from the simulated signal at a fixed TI (1.35s).

Renal ASL data were acquired from a healthy subject (male, 29 years) in a breath-hold using a FAIR TrueFISP sequence [6] with the following parameters: FOCI inversion pulses with 320° flip angle and 0.3 gradient scale, TR 3s, TE 1.84ms, TI [0.1, 0.5:0.1:1.6]s, matrix size 256 x 256, FOV 380mm x 380mm, and 10mm slice thickness. The imaging plane was placed coronally covering both kidneys. The whole protocol was repeated 4 times along with registration and averaging of corresponding images to boost SNR. Difference signal images were obtained by subtracting nonselectively inverted images from their slice-selective counterparts. In the signal difference image with strong cortex and medulla contrast, cortical and medullary ROIs were manually drawn. To compare the precision of estimated perfusion, we applied the conventional method and the convolution based method to the acquired human data. As the convolution based method requires data of at least two different TI values, we tested the TI-value dependence of perfusion estimates by running the model with all non-zero signal pairs that were acquired with at least 200 ms interval between two TI values.

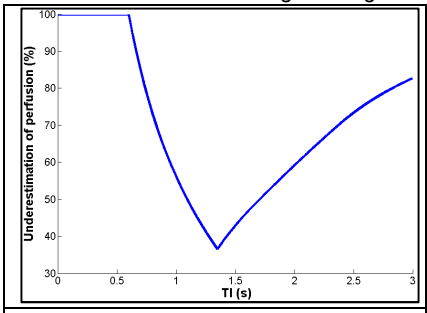

Fig.1: Perfusion estimation error with the conventional model as a function of TI value

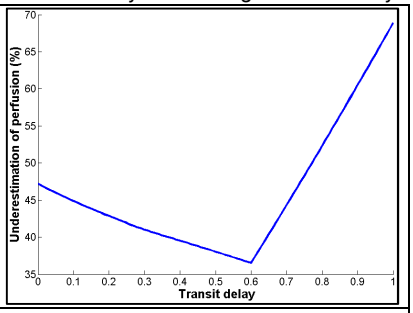

Fig. 2: Perfusion estimation error with the conventional model for simulated data of varied transit delay (TI of 1.35s)

Results and Discussion: Simulation results showed that the conventional model significantly underestimated perfusion at all tested TI values (Fig. 1), with the minimal error at a TI of 1.35s. This underestimation arises because the conventional model ignores the transit delay present in simulated data. The TI of 1.35s corresponds to the instant when all tagged spins have entered the tissue voxel, producing the maximal tissue-signal level. Fig. 2 shows the dependence of estimated perfusion on transit delay when calculated using the conventional method. For TI of 1.35s, the minimal perfusion error is found at a TD of 0.6s. This result implies that if the conventional model has to be used, data should be acquired at the TI value when all tagged spins enter tissue voxel. Table 1 compares the variability of perfusion estimates obtained from the human subject data using the conventional method (on data acquired at single TI) and the convolution-based method (on data acquired at two TI values). Similar to the simulation, with human data, the conventional method provided lower perfusion values than convolution based method. Additionally, perfusion estimates obtained with the convolution-based method demonstrated substantially less variability in both the cortex and medulla. We also found that, compared to perfusion estimated from all data points, estimates from data pair sampled around 1.0-1.5s gave relatively low error.

Table 1	Estimated perfusion (mL/100mL/min)	
Tissue	Conventional	Convolution-based
Cortex	516 ± 347 (67.2%)	674± 83 (12.3%)
Medulla	170 ± 141 (82.9%)	379± 51 (13.5%)

Conclusion: The conventional method to estimate renal perfusion from ASL data is sensitive to the selection of inversion time. By sampling the difference signal at multiple TIs and analyzing them with a convolution-based model, we can estimate renal perfusion with much lower variability.

References: [1] Kim et al. *MRM.***34**:293. [2] Martirosian et al. *MRM*. 51:353. [3] Tan et al *MRM*. EPub; 2013. [4] Buxton *et al. MRM.***40**:383. [5] Zhang *et al. MRM* **59**:278.