Quantify renal ASL data with arterial input function (AIF) sampled from renal artery

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Target audience: Investigators that are interested in renal perfusion quantification with arterial spin labeling

Introduction: Due to the risk of nephrogenic systematic fibrosis (NSF), non-contrast imaging techniques are preferred for patients with renal function impairment. By manipulating the magnetization of inflowing arterial spins, arterial spin labeling (ASL) can create angiography with endogenous contrast and can be applied repeatedly within a few seconds (1). ASL can also be used to quantify renal tissue perfusion (2, 3), most commonly flow-sensitive alternating inversion recovery (FAIR), which collects two images for a given tissue slice: one with global inversion, and the other with a slice-selective inversion. Subtraction of the two images results in a "signal difference" image where only signals from inflowing arterial spins remain. In image acquisition, the imaging is done some time (termed inversion time, TI) after magnetization inversion. Similar to DCE MRI with exogenous contrast agent, ASL images can be acquired at different TI values and record dynamic transit of the arterial spins through the tissue of interest.

Current models for analyzing renal ASL data assume rectangular-shape function for tagged arterial input function (AIF). With imperfect magnetization inversion, this assumption can cause significant errors in the estimated perfusion. In this study using coronal FAIR labeling, we propose to sample AIF from renal segmental artery, and after some calibration with proton density, use the AIF to estimate renal tissue perfusion from ASL images.

Methods: *Data acquisition:* Following written informed consent, one healthy volunteer (male, 29 years) was scanned using a clinical 3T MRI scanner (TIM Trio, Siemens) with a combination of 8-channel spine array and 4-channel body array coils. 2D coronal FAIR-TrueFISP ASL was performed with parameters: matrix size 256×256, FOV 380 mm × 380 mm, flip angle 90°, slice thickness 10 mm, TE 1.84 ms, TR 10 sec, variable inversion times (TI) from 500 ms to 1600 ms with interval 100 ms. Acquisition at TI of 100 ms serves as a baseline before any labeled arterial spins reached kidney tissue. Each 20-sec acquisition at a single TI value was performed in a breath hold. The whole protocol was repeated 4 times to improve signal to noise ratio (SNR).

Fig. 1 Example of AIF sampling at renal segmental artery

Fig. 2 The sampled AIF after calibration, and the 'ideal' AIF

Data processing: Image registration was applied to eliminate any potential motion between images acquired in different breath holds. Four images of the same TI and of the same type, 'globally inverted' or 'slice-selectively inverted', were averaged respectively, and after subtraction, signal-difference image was obtained for each TI value.

AIF preparation: Region of interest (ROI) was manually defined at renal segmental artery in a 'signal difference' image (Fig 1) obtained at an early TI. Averaging all intra-ROI voxels at each TI, we obtained sampled AIF. To correct for partial volume effect, we calibrated the AIF using proton density (M0) measurement of aortic blood. Specifically, highest signal (S_{max}) in the sampled AIF and its TI value (TI_{max}) were recorded; at TI = 0, $S_{max}(0) = S_{max}/exp(-TI_{max}/T1)$; ideally signal from tagged blood at TI of zero should be $2 \cdot M_0$, so we propose a correction ratio of $2 \cdot M_0/S_{max}(0)$, and apply it for all data points in the sampled AIF. For comparison, we also generated an 'ideal' AIF with a rectangular function multiplied by blood T1 relaxation exponential; the same transit delay as in the sampled AIF was used for the 'ideal' AIF.

Perfusion estimation: Transit delay between renal artery and each renal tissue voxel was estimated with a linear regression technique applied on the initial upslopes of AIF and of tissue curves. Applying this delay and the corresponding blood T1 relaxation, we obtained localized AIF for each voxel. Using a convolution-based model that involves AIF, impulse retention function (IRF) and tissue T1 relaxation (4), we estimated perfusion for each voxel and thus the perfusion map. The model fitting was performed with both the sampled AIF and the 'ideal' AIF.

Results and discussion: Fig. 2 shows the sampled AIF after calibration and the 'ideal' AIF. The sampled AIF was lower than the ideal AIF in the starting part, probably because of imperfect inversion and transit dispersion. These factors are considered in the sampled AIF but not in the ideal AIF.

Fig. 3 shows the map for transit delay. Compared to renal artery, the tagged spins reach cortex region ~700 ms later, and medulla ~800 ms later. This implies that most of the contrast enhancement we found in renal cortex and medulla should be due to the inflow of labeled arterial spins that have travelled all the way from renal artery. This is quite possible as the image slice and selective inverted slice, which were positioned at the central coronal plane of the kidney, aligned with renal vasculature.

Fig. 4 shows the perfusion map estimated with the sampled AIF. From manually drawn ROIs, we obtained averaged perfusion values for renal cortex and medulla (Table 1).

Fig. 3 Map of transit delay (unit: sec), by robust linear regression
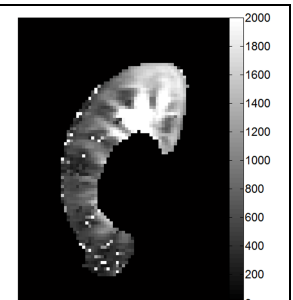
Fig. 4 Perfusion (ml/min/100g) estimated with the sampled AIF

Perfusion estimated with the 'ideal' AIF was lower than that from the sampled AIF, because without considering the various artifacts, the 'ideal' AIF is higher (Fig. 2).

For coronal kidney FAIR ASL, we proposed to sample AIF from renal segmental artery for improved quantification of total and local perfusion. To correct for partial volume effect in such AIF, we calibrated the sampled difference signals with measured proton density. Additional validation using a reference standard for perfusion will be the focus of future work.

Table 1	Perfusion (ml/min/100g)	
Tissue	Sampled AIF	Ideal AIF
Cortex	749 ± 64.7	467 ± 39.0
Medulla	384 ± 85.3	235 ± 48.3

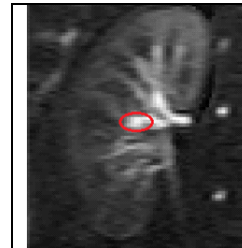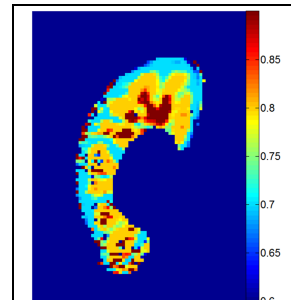**Reference**: [1] Kim et al. *MRM.***34**:293. [2] Martirosian et al. *MRM*. 51:353. [3] Tan et al *MRM*. EPub; 2013. [4] Buxton *et al. MRM.***40**:383.