Fast CBF Estimation in Multi-Phase Pseudo-Continuous Arterial Spin Labeling (MP-PCASL) Using Signal Demodulation

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INTRODUCTION

The multi-phase pseudo-continuous arterial spin labeling (MP-PCASL) method [1] offers more robust cerebral blood flow (CBF) quantification than the conventional PCASL method [2] and higher SNR than Pulsed ASL. In addition, it provides phase tracking errors at the tagging locations, which gives additional opportunities for measuring and optimizing the tagging efficiency of conventional PCASL [3]. However, the MP-PCASL method requires a per-voxel fit to the nonlinear signal equation. This time required for this nonlinear fitting procedure (about 5 minutes) can be problematic for applications such as optimized PCASL for functional MRI studies [3]. Here we propose a signal demodulation processing method for MP-PCASL that reduces the required processing time by two orders of magnitude, while providing comparable estimates of CBF and phase errors.

THEORY

For MP-PCASL the phase increment between two successive RF pulses can be expressed by the equation: $\Delta\theta_n = \gamma Gtd + 2\pi n/N$, where γ is the gyromagnetic ratio, G is the average gradient strength, t is the interval between RF pulses, d is the distance from the gradient center to tagging location, n denotes the nth phase, and N is the number of phases. Here γGtd is the phase tracking term and $2\pi n/N$ is the phase offset which generates different amounts of inversion.

Fig. 1 shows a time series from a voxel obtained with 4-phase PCASL and its power spectrum (upper row). Because the power spectral density has a dominant component at the multi-phase frequency, the sinusoidal component at the multi-phase frequency (lower row of Fig 1) contains most of the information in the MP-PCASL signal. Under the assumption that the inversion response to the phase offset is sinusoidal, the per-voxel basis multi-phase modulated time course ($S_i(t)$) can be expressed as Eq. 1, where a_i is the magnetization of arterial blood at ith voxel that has been delivered to the voxel (or ASL signal), $\theta_{offset}(t)$ is the phase offset at tth phase, ε_i is the phase tracking error, and b_i is the baseline signal from static tissue. Because the modulated signal has the periodicity of the number of phases (m), a demodulation of the multi-phase frequency component (Eq. 2) can provide direct estimation of the multi-phase modulation: the magnitude and the phase of the demodulation can be interpreted as the ASL signal and the phase tracking errors, respectively, and the mean of the time course becomes the baseline signal from static tissues as shown in Eq. 3.

$$S_i(t) = a_i \cos(\theta_{offset}(t) - \varepsilon_i) + b_i \qquad \text{(Eq. 1)}$$

$$F_i(T/m) = \sum_{t=0}^{T-1} S_i(t) \cdot e^{-j2\pi \cdot t/m} \qquad \text{(Eq. 2)}$$

$$a_i = |F_i(T/m)|, \quad \varepsilon_i = \arg(F_i(T/m)), \quad b_i = \frac{1}{T}\sum_{t=0}^{T-1} S_i(t) \qquad \text{(Eq. 3)}$$

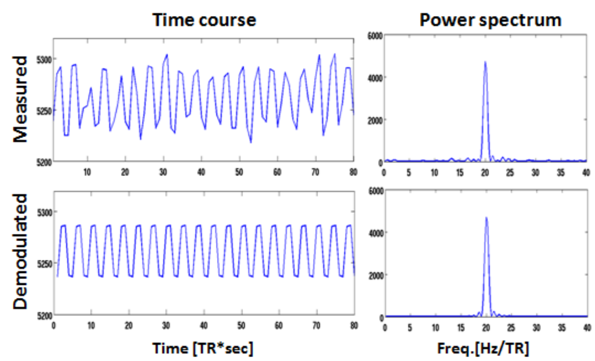

FIG.1. A time course and its power spectrum measured from a single voxel (upper row) and those from the sinusoidal component at the frequency of the multiphase modulation (lower row).

METHOD

We compared the mean gray matter CBF values obtained using 4-phase PCASL with the nonlinear fitting and the proposed demodulation methods over 5 subjects (3 men and 2 women). The experiment was executed on a 3T Signa HDx scanner with an 8-channel head coil (GE Healthcare, Waukesha, WI). PCASL scan parameters were 1600 msec tag duration, 1000ms post labeling delay, TR 3.6 sec, 80 reps. Imaging parameters included 24cm FOV, 20 slices (5 mm thick, skip 1mm), single-shot spiral acquisition (TE = 3ms), and 5 min. scan time. Mean gray matter CBF values and mean phase tracking errors were obtained from the gray matter mask, which was defined with a high resolution anatomical scan.

RESULTS AND DISCUSSION

The proposed demodulation is much faster (<3sec) than the conventional fitting method (~5min). As shown in Fig 2, the estimates of the ASL signal, the phase tracking error, and the baseline signal with the proposed demodulation method are comparable to that with the conventional fitting methods. Table 1 presents the mean gray matter CBF values and measured tracking errors with two estimation methods and the differences. The demodulation method provided slightly lower values (average of 1% decrease) of CBF estimates since the side lobe in the power spectrum in actual inversion response was not considered in the demodulation. Future work to include the sidelobe energy in the analysis may further reduce the difference. In summary, the proposed demodulation method can provide reliable CBF estimates while providing faster estimation time.

	Mean GM CBF (ml/100g tissue/min)			Δmean(ε)
	Fitting (A)	Demod. (B)	A-B (%)	
Subject 1	57.8	56.0	-3.11%	-4.7°
Subject 2	51.1	49.4	-3.33%	-3.3°
Subject 3	85.6	85.4	-0.23%	-1.3°
Subject 4	84.3	84.2	-0.12%	-7.5°
Subject 5	57.2	57.1	-0.17%	-6.5°
Mean	67.2	66.4	-1.16%	-4.7°

Table 1. Comparisons of mean gray matter CBF and the difference in mean phase tracking errors (Δmean(ε)).

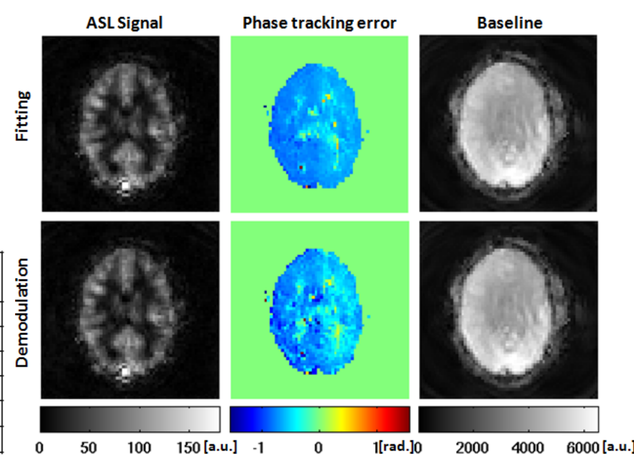

FIG. 2. An example of estimates of ASL signal, phase tracking error, and baseline signal with the two estimation methods.

REFERENCES

1. Jung et al., 17th ISMRM: 621, 2009.
2. Dai et al., MRM, v60, p 1488, 2008.
3. Jung et al, 17th ISMRM: 1578, 2009.