In-vivo Hadamard Encoded Continuous Arterial Spin Labelling (H-CASL)

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Introduction

Continuous arterial spin labelling (CASL) [1] MRI can generate images of cerebral blood flow (CBF) non-invasively with good spatial and temporal resolution. A confounding factor for quantifying CBF with CASL is the transit time of blood water: the time it takes to travel from where it is labelled to where it enters the cerebral tissue. In order to eliminate this problem, ASL measurements with a range of post labelling delays (PLDs) between the end of the labelling pulse and image acquisition can be performed at the cost of a significantly increased total scan time [2]. Recently, Hadamard encoding techniques have been applied to the CASL labelling pulse to increase the efficiency of this approach [3]. However to our knowledge this work has not yet been extended beyond basic phantom validation. In this study we demonstrate that this method can be successfully applied *in-vivo* to measure CBF and arterial transit time (δa) in the rat brain. . Reconstructed Hadamard encoded perfusion weighted images (H-CASL) are combined with CASL data acquired at a single PLD (H-CASL + CASL) and compared to the standard multi-time-point CASL approach at equivalent PLDs, acquired in the same imaging time. We have modified the ASL quantification model to take account of the new encoding approach and demonstrate an improvement in the precision of the δa estimates compared to the standard method.

Method

MRI studies were performed on an anaesthetised male Sprague Dawley (182g) rat using a 2.35T horizontal bore magnet interfaced to a SMIS console, with a volume coil transmitter and a passively decoupled surface coil for signal reception. The Hadamard encoded CASL scheme was implemented as in [3] where the long continuous labelling pulse is encoded into several individual boli, each of relatively brief duration. The individual bolus duration (τ) was 0.3s to produce 7 effective PLD times (0.02 0.32 0.62 0.92 1.22 1.52 1.82s). These 8 H-CASL acquisitions were interleaved with 14 standard CASL acquisitions at 7 equivalent PLD times with a 3 second labelling duration. Six standard CASL acquisitions at fixed PLD of 0.5 seconds were additionally captured and combined with the 8 H-CASL acquisitions for equivalent imaging times between the two methods (14 acquisitions in total). Coronal images were acquired of a slice 0.3 mm caudal to the bregma using an EPI readout. Tagging pulses were applied to a plane 2mm caudal to the cerebellum. The protocol was repeated 15 times. Other acquisition parameters were: slice thickness = 2mm; image matrix size = 128×64; field of view = 40×20mm^2; TE = 36ms; inter-experiment delay = 4s. For each method, all the data were averaged across the 15 repeats to produce a high SNR data set for which CBF and δa maps were generated. In addition the data were split into 5 groups of 3 repeats and averaged across the 3 repeats. A Gaussian filter with kernel size of [3 x 3] and a standard deviation of = 1 was applied to the "Gold Standard" and "low SNR" perfusion weighted images to increase the SNR of the data before CBF and δa quantification. CBF and δa estimates were calculated for pixels within a cortical ROI for each of the 5 groups. The standard deviations of the CBF and δa estimates across the 5 groups for each of the pixels within the cortical ROI were calculated to assess the precision of the estimates. For the standard CASL measurements, CBF and δa were quantified according to [4]. Buxton's general kinetic CASL model [2] was used to quantify CBF and δa from the H-CASL perfusion weighted images since this model accounts for the brief tagging duration (τ = 0.3s).

Results

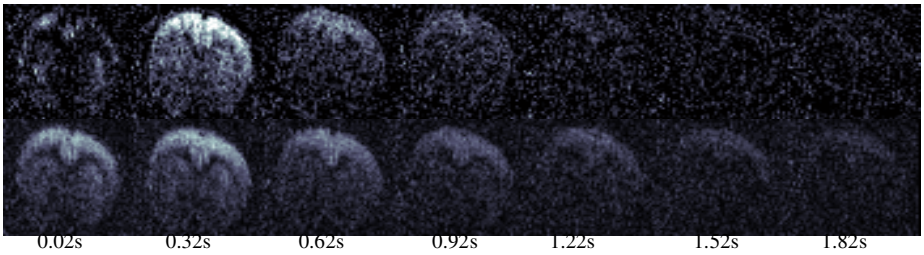

Figure 1 The *in-vivo* perfusion weighted images derived from the delivery of the H-CASL (top row, τ = 0.3s) and standard CASL (bottom row, τ = 3s) bolus at the $PLD_{(eff)}$ times below the respective images. The patches of high intensity in the H-CASL images at the earliest PLD_{eff} are likely represent the first inflow of labelled blood into the tissue and seem to be broadly concordant with the regions of short transit time in the standard CASL δa map (see Figure 3).

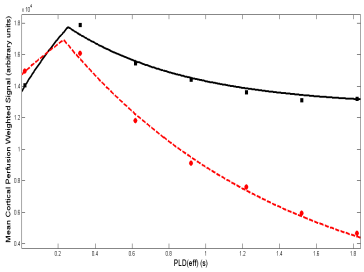

Figure 2 The mean i*n-vivo* cortical perfusion weighted signal in the high SNR data against PLD for the CASL (red) and H-CASL (+ CASL) sequences (black). Also plotted are the model fits to the data.

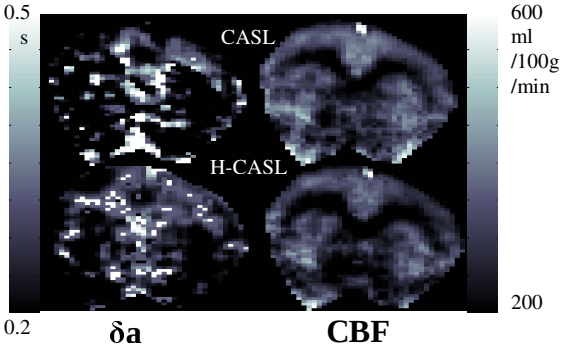

Figure 3 The *in-vivo* CBF (right column) and δa (left column) maps generated from the CASL (top row) and H-CASL (+CASL) (bottom row) schemes

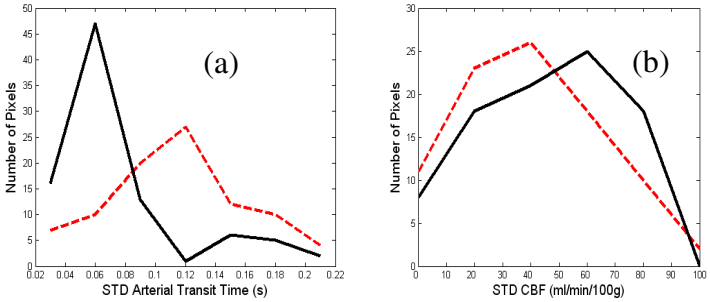

Figure 4 Histogram of the standard deviation of each of the pixels across the 5 cortical ROIs of the δa (a) and CBF (b) estimates for the CASL (red dashed line) and H-CASL (+ CASL) (black solid line) *in-vivo* data. The H-CASL (+ CASL) δa estimates display a marked reduction in SD in comparison to standard CASL, denoting increased precision. However, visual assessment of (b) suggests that the precision of the CBF estimates is slightly reduced in H-CASL (+ CASL) when compared to the standard approach.

Conclusion

This study demonstrates the potential utility of the H-CASL sequence in CBF and δa estimation. Several factors provide evidence that this novel approach is viable for accurate cerebral haemodynamic parameter quantification: (i) the good model fit to the data (Figure 2) (ii) the noticeable lack of artefacts in the H-CASL perfusion weighted images (Figure 1) (iii) the similarity of contrast within each of the cerebral parameter maps between the H-CASL(+CASL) and CASL methods (Figure 3). H-CASL can result in a marked improvement in the precision in δa estimation (Figure 4) since it is able to sample the first inflow of labelled blood into the tissue (Figure 1). Work is underway to better optimise the H-CASL sequence for improved CBF estimation.

References: [1]Detre, et al. Magn Reson Med 1992; 23:37-45. [2] Buxton *et al.,* Magn Reson Med 1998; 40:383-396 [3] Guenther. 2007. Proc. Intl. Soc. Mag. Reson. Med. 15, abstract 380. [4] Alsop, Detre. J Cereb Blood Flow Metab 1996; 16:1236-49.