

CBF Quantification in Infants Using Look-Locker ASL and a Single Blood Compartment Model

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Background

For accurate quantification of cerebral blood flow (CBF) using Arterial Spin Labelling (ASL), multiple time point measurements are required, allowing model fitting for arrival time (tA) and CBF. A standard sequence such as EPISTAR [1] is time-inefficient as no signal is collected during the delay period which typically ranges from 800 to 2000 ms. A more efficient approach is to use a Look-Locker (LL) readout [2], where multiple readouts follow each labelling pulse, collecting data at a full range of delay times. This greatly shortens the acquisition time, while maintaining high SNR which is so important for high quality ASL images. This is particularly important in the neonatal and infant brain where time is paramount. In addition, the LL sequence allows dynamic changes in both CBF and tA to be measured. Despite these clear advantages of a LL-readout, the sequence is not widely used as the train of readout pulses affects the apparent T_1 , leading to complex quantification models [2,3]. The aim of this work is to develop a simplified quantification model for the LL using a single blood compartment model [4]. The model is tested from data on a healthy volunteer at a range of flip angles. The technique is applied to infants in routine clinical practice.

Methods

Modelling

It is assumed that labelled water remains in the blood and that no labelled water leaves the voxel, an approach that has been shown to be reasonably accurate [4]. Considering the difference image (control – label), the magnetisation ΔM in the voxel can be described by:

$$\frac{d\Delta M(t)}{dt} = -R_1 \Delta M(t) + f m_a \quad \text{For STAR labelling, } m_a = 2M_a^0 \alpha \exp(-tR_{1b}) \quad \text{for } t > t_a \text{ and } t < \tau$$

where R_1 is the apparent R_1 of blood during LL readout, f is CBF and m_a is the magnetisation of arterial blood. t_a is the arrival time and τ is the bolus width. M_a^0 is the equilibrium magnetisation of arterial blood, α is the inversion efficiency and R_{1b} is the R_1 of blood. According to [2] $R_1 = R_{1b} - \ln(\cos\theta)/T_{I2}$ where θ is the flip angle and T_{I2} the spacing of the LL readout. We find solutions for ΔM .

Data acquisition

To test the model we acquired data in a healthy volunteer (age 60) at 4 flip angles (10, 20, 30 and 40 degrees) on a 3 T Philips scanner. STAR labelling was used and LL-EPI readout with the following parameters: 3.5 x 3.5 x 6 mm voxels, 10 slices, 8 readout pulses between 300 and 2050 ms with step size of 250 ms, TR 4 s, TE 12 ms, 30 pairs of label and control images; total acquisition time 4 minutes. To calculate M_a^0 a separate set of images were acquired (for each flip angle) with TR = 10s and 25 read-out pulses. Mean subtraction signal over a whole brain region was determined for each delay time and each flip angle and the data was fit to the single blood compartment model.

The same ASL-LL protocol with flip angle of 40 degrees was applied in general clinical practice at Alder Hey Children's hospital in 9 infants with an age range from (10 – 17 months), while under general anaesthesia.

Results

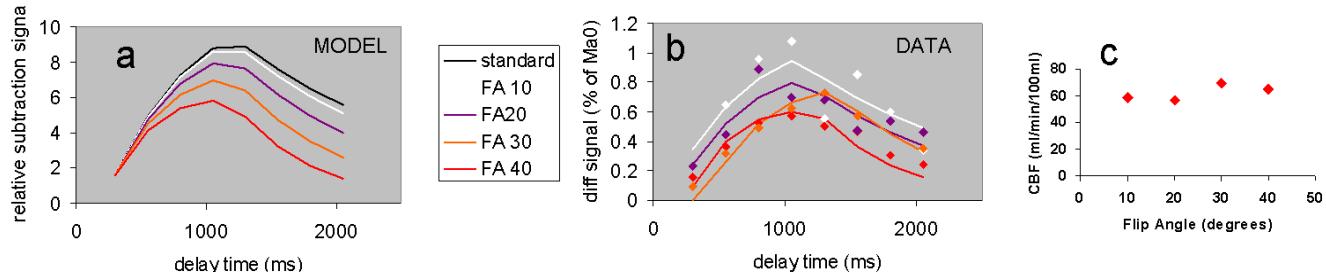
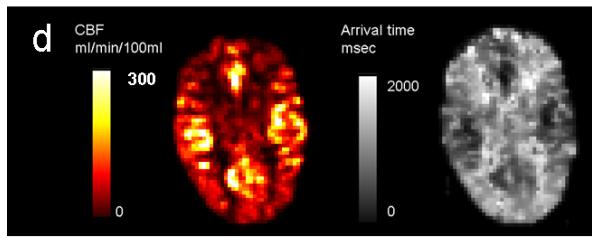


Figure a) shows the model results at various flip angles (colors) compared to the standard single blood compartment model (black). The model predicts that, for low flip angles, the LL subtraction signal departs only minimally from the standard acquisition approach. The signal is predicted to decline more markedly for flip angles above 10 degrees. Figure b) shows the % signal in the difference image across the whole brain normalised to the equilibrium magnetisation for arterial blood, and the fitted model curve. It can be seen that the model fits the data well at all flip angles. The noise in the data is seen to decline markedly at higher flip angles. Figure c) shows mean perfusion from the model fit, which is reasonably constant across flip angles, suggesting that the model is compensating adequately for the reduced signal due to the LL read-out.



The figure on the left (d) shows typical CBF and arrival time maps for one of the infants. Image quality appears high. Mean CBF over the 9 infants is 106 ± 27 ml/min/100ml which is higher than the adult values (above), and in agreement with literature [5]. Mean arrival time was 880 ± 130 ms.

This protocol with 8 time-points allows a maximum of 10 slices which is sufficient for whole brain coverage of the infant brain. However we have since developed a new LL protocol with 15 slices and 4 time-points allowing whole brain CBF and tA mapping in the adult brain within 5 minutes.

References

1. Edelman et al, Radiology 192:513-520 [1994];
2. Gunther et al, MRM 46:974-984 [2001];
3. Francis et al, MRM 59:316-325 [2008];
4. Parkes and Tofts MRM 48:27-42 [2002];
5. Biagi et al, JMRI 25: 696-702 [2007].