Denoising of Arterial Spin Labelling perfusion data using Independent Component Analysis

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Introduction: Arterial spin labelling (ASL) techniques have advantages over alternative approaches in the measurement of cerebral perfusion, particularly since they are totally non-invasive, and suitable for serial measurements [1]. However, their clinical application has been fairly limited due to several drawbacks. One of the main issues is the poor signal-to-noise ratio (SNR) of the perfusion-weighted images acquired. In particular, perfusion measurement in white matter tissue has proven very challenging, and typically only global (rather than regional) white matter values are reported.

ASL techniques involve the acquisition of pairs of images, in one of which the incoming blood is labelled (to form the label image), whereas in the other the blood is not labelled (the control image). Subtraction of the control from the label image ($\Delta M=M_{label}-M_{control}$) yields a perfusion-weighted image. Ideally, multiple images at many inversion times (TI) are acquired, allowing characterization of the entire $\Delta M(TI)$ curve, which can then be fitted for perfusion, taking arterial transit times and coil inflow times into account [1, 2]. The maximum ΔM signal that can be expected in grey matter regions is only ~1% of the equilibrium tissue signal, M_0, at typical clinical field strength [1], and significantly lower than this (~0.3%) in white matter due to the lower perfusion values. Building up sufficient SNR in the ΔM image through signal averaging therefore remains problematic in white matter.

Independent component analysis (ICA) can be used to identify temporally independent patterns, and has previously been used in functional MRI and bolus tracking perfusion MRI (see, for example, [3, 4]). Furthermore, it is able to identify noise and artefact components in the acquired data. In this study, we describe the use of ICA as a pre-processing step for the denoising of ASL data, particularly with the aim of investigating the possibility of making robust regional white matter perfusion measurements.

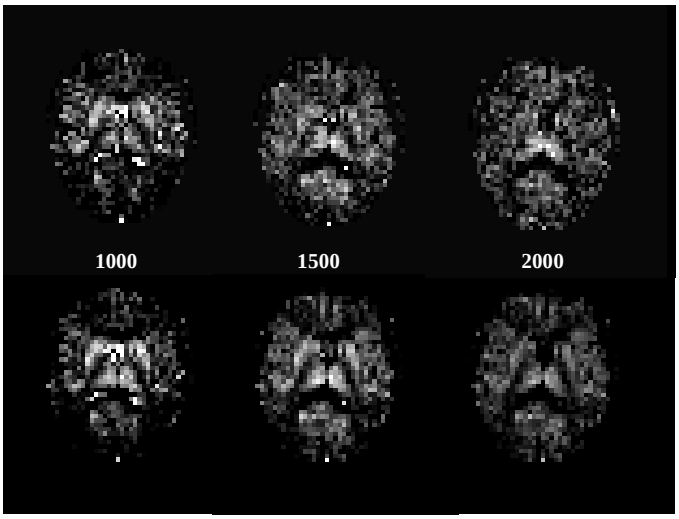
Methods: Multiple TI FAIR [5] data were collected on a 1.5T Siemens Vision system, from 4 healthy volunteers. Single-slice data were acquired using a gradient-echo echo-planar imaging sequence, from a slice positioned axially through the basal ganglia. The sequence parameters were: 13 TI times (150-3500ms), 10 averages per TI, labelling:imaging slice ratio of 3:1, 10mm slice thickness, 64×64 matrix, 250mm^2, 4s delay time, TE 25ms. Bipolar gradients were included (b=2s/mm^2) to minimise vascular signal contribution. Scanning took approximately 35min per dataset.

The set of 130 difference images were visually inspected for movement artefacts, and any artefacted images were excluded. ICA was then used to identify and remove the noise components from the set of ΔM images. The optimum number of independent components used in the ICA was determined according to the Bayesian Information Criterion [6]. For both the original and denoised datasets, the images were averaged at each TI time to produce a single ΔM image per TI.

Small regions (4-10 pixels) were drawn within the grey and white matter in both the original and denoised datasets. Small regions were used since transit times and perfusion values are known to be heterogeneous, and this has been shown to introduce errors into perfusion quantification [7]. The $\Delta M(TI)$ data for each region were then fitted to the standard FAIR equation for perfusion, including arterial transit time and coil inflow time [2].

Results: In all cases, the use of ICA to identify and remove the noise components from the FAIR ΔM data significantly improved the SNR in the averaged ΔM images at each TI. This is illustrated in Fig. 1, which shows some example ΔM images from one of the volunteers, at various TI times. Both the original FAIR images (top) and the denoised image (bottom) are shown for comparison. The delineation of the tissue structures, in particular the sub-cortical grey matter, is significantly improved in the denoised images.

The $\Delta M(TI)$ timecourses were improved for both the grey and white matter regions. In particular, while the white matter regions could not, in general, be used to obtain a perfusion value in the original dataset (the fitting typically failed), a reliable fitting could be obtained using the denoised dataset. Figure 2 shows two examples of $\Delta M(TI)$ data for small white matter regions drawn in one of the volunteers. In general, the fittings gave white matter values in agreement with the literature [1].



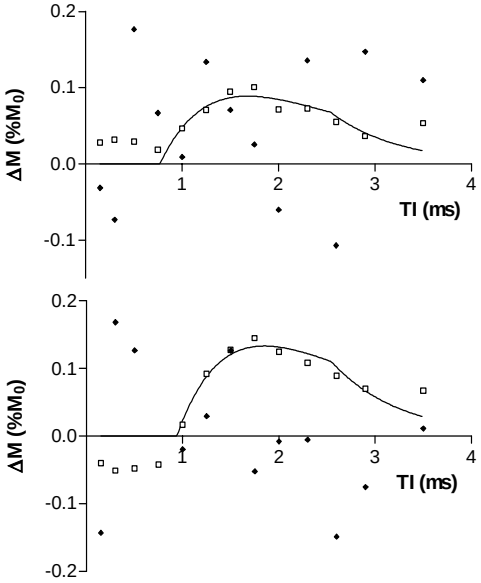


Fig. 1 (left). ΔM data at several TIs (as marked, in msec). Top row; original FAIR data. Bottom row; denoised FAIR data (noise components removed using ICA).

Fig. 2 (right). $\Delta M(TI)$ data for two occipital white matter regions. Diamonds: original dataset. Open squares: denoised dataset. Fitted curves are shown for the denoised data (the fittings for the original data failed). Fitted perfusion values, in ml/100g/min, (± 1 standard error of the fit), are 14±3 (top), and 25±4 (bottom).

Discussion: The application of ICA to FAIR ΔM datasets served to improve the visual quality of the $\Delta M(TI)$ images significantly (e.g. see Fig. 1) in all 4 volunteer datasets. It also allowed a reliable fitting of the data in white matter regions, with the fitted perfusion values in agreement with reported values. It should be noted that the original FAIR data typically proved too noisy for reliable curve fitting. The improved SNR in the white matter has made apparent a small offset at low TI values that we also observed in cortical regions in the original FAIR data, and further work is required to investigate the source of this effect.

Although this study concerns FAIR data, the approach is also applicable to other ASL techniques. In this preliminary study, ICA was used only to remove the noise components within the ASL data; it may also be possible to identify and remove movement artefacted components, thus improving the quality of the ASL data further.

References: [1] Calamante F *et al*, JCBFM 1999;19:701. [2] Pell GS *et al*, *MRM* 1999;41:829. [3] McKeown MJ *et al*, *HBM* 1998;6:160. [4] Carroll TJ *et al*, *AJNR* 2002;23:1007. [5] Kwong KK *et al*, *MRM* 1995;34:878. [6] Kolenda T *et al*, *Proc ICA 2001*, 540. [7] Figueiredo P *et al*, *ISMRM* 2002;623.