Bayesian Model-Based Correction for Macro Vascular Signal in Dynamic Susceptibility Contrast Perfusion MRI

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Introduction: In Dynamic Susceptibility Contrast (DSC) perfusion imaging the signal of interest arises from T_2 (or T_2*) changes brought about by Gadolinium contrast passing through the tissue's capillary bed. These time-dependent data, in combination with information regarding contrast delivery, permits cerebral blood flow to be calculated. The contrast agent will also be present within larger arteries, which is useful for defining the arterial input function (AIF) that describes its delivery to the tissue. However, this extra contribution to the signal will bias the CBF measurements in the vicinity of arteries. One proposed solution is to apply independent component analysis (ICA) to identify and subsequently remove signal components that are characteristic of this macro vascular (MV) signal [1,2]. This is done prior to CBF calculation, which is often performed using a Singular Value Decomposition (SVD) based deconvolution method [3,4]. More recently a model-based analysis has been proposed that employs a vascular model for the residue function [5]. This has shown to be less prone to underestimation of CBF at higher flow rates than the SVD variants. In this work we extend the vascular model-based analysis with the addition of a component based on the AIF to account for MV contamination, in a similar manner to a recent MV correction method for Arterial Spin Labelling (ASL) [6].

Methods: The method is illustrated on data from 2 patients. *Pat1*: left carotid stenosis (scanned post-carotid endarterectomy); *Pat2*: stroke patient with right middle cerebral artery (MCA) occlusion (scanned 9 hrs post-symptoms onset). DSC-MRI data were acquired at 3T (*Pat1*) or at 1.5T (*Pat2*), using a gradient-echo EPI, TE/TR= 20/1250ms (*Pat1*) or 60/1740ms (*Pat2*), and a single (*Pat1*) or double (*Pat2*) dose of contrast agent. The AIF was measured on a branch of the contralateral MCA using the semi-automatic method in Penguin (www.cfin.au.dk/software/penguin).

DSC-MRI data were fit using a variant of the vascular model proposed by [5]. As in that work, the signal time course was modelled including the conversion from concentration to signal magnitude, convolution of supplied AIF with the residue function multiplied by the relative CBF (rCBF), and a residue function based on a distribution of transit times through the tissue. This distribution was modelled as a gamma distribution with two parameters [5]: λ, describing the shape, and the mean transit time (MTT). In this work both were estimated during model fitting (rather than MTT being derived using the central volume theory from the data) using a log transformation to make the model more linear in these parameters and to aid convergence of the model-fitting algorithm. The data were fit both to this vascular model (VM) and with the addition of an arterial component based on the (normalised) AIF, this was scaled by the relative arterial blood volume (raBV) and subject to a delay that was also estimated during model-fitting. Fitting was performed using a Bayesian inference scheme [7] which was similar to that used in [5]. The combined VM+MV model was initialised using the estimates from the VM model, the aBV parameter was subject to a prior based on the cerebral blood volume estimated from the data and the prior information for MTT used the estimated MTT from the VM. For comparison, the data were also analysed using oSVD [4], and ICA was used in an attempt to remove MV contamination. ICA was performed using MELODIC [8] from the FMRIB software library (www.fmrib.ox.ac.ul/fsl), and the MV components were identified manually and removed from the data prior to oSVD analysis.

To examine the presence of MV contamination in the estimated rCBF images, the ratio of rCBF (CBFratio) to that in an ROI chosen within the deep white matter (without MV partial volume) was calculated. To quantify the changes in rCBF and parameters of the VM, two further ROIs were defined that represented areas of substantial and negligible MV contamination, respectively. These ROI were defined as voxels whose CBFratio reduced by more than 1 (high contamination) and less than 0.1 (low contamination) after the inclusion of the MV component within the VM. Within these ROIs the mean change in rCBF, λ and MTT were calculated.

Results: Fig. 1 shows the estimated rCBF and CBFratio images for *Pat1*, fig. 2 the aBV images for the two datasets and fig. 3 the rCBF and CBFratio for *Pat2*. Only in *Pat1* could distinct MV contamination components be identified from ICA. In the majority of voxels the CBFratio after correction with a MV component in the VM model was more consistent with those expected for white and grey matter in both datasets. Some residual contamination was visible in *Pat1*. Using ICA these residual areas of MV contamination were reduced, although lowering of rCBF in areas where MV contamination is not expected was also visible. Table 1 shows changes in rCBF, λ and MTT in regions where there were large (>1) and negligible (<0.1) changes in the CBFratio. As expected, in regions of large ratio change there were also substantial changes in all parameters, whereas in regions that were minimally affected by the inclusion of the MV component changes in the parameters were smaller.

Table 1: Percent Changes in parameters after MV correction in high and low MV contamination ROIs.

Contamination ROI		ΔCBFratio %	Δλ %	ΔMTT %
High	*Pat1*	-53.0	203.2	41.4
	Pat2	-70.1	158.3	22.1
Low	*Pat1*	5.0	-5.8	-0.7
	Pat2	28.8	1.9	-0.1

Discussion: Using a MV component based on the AIF within a Bayesian model-based analysis framework, it appears to be possible to substantially remove MV contamination from DSC CBF estimates. Due to the greater similarity between the AIF and tissue signals, this model-based approach appears to be more challenging that its equivalent in ASL [6], hence the careful use of initialization and prior information in this study. The comparison with an ICA based MV removal method is favourable. However, it was not possible to find distinct components to represent the MV contamination in one of the datasets used here. This illustrates the difficulty with ICA based methods of reliably identifying MV components in pathology. A model-based approach should be more robust to variations in contrast delivery, although in the current implementation it is reliant upon the correct identification of an appropriate AIF.

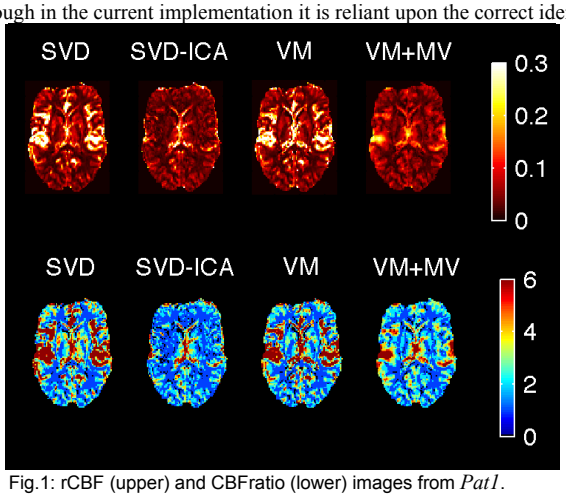

Fig.1: rCBF (upper) and CBFratio (lower) images from *Pat1*.

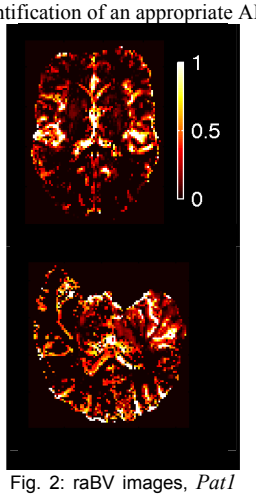

Fig. 2: raBV images, *Pat1* (upper), *Pat2* (lower).

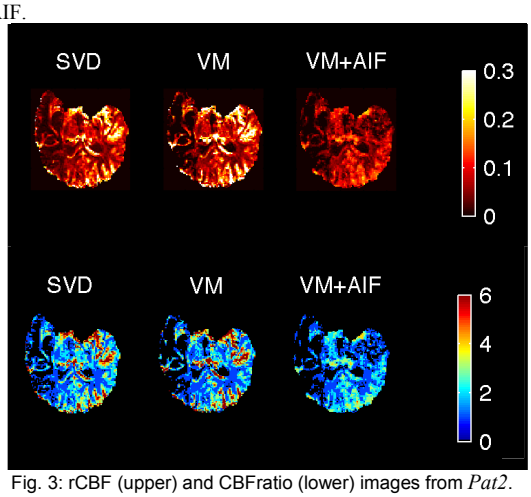

Fig. 3: rCBF (upper) and CBFratio (lower) images from *Pat2*.

References:

1. Caroll *et al.,* Am J Neuroradiol. 23(6):1007-1012, 2002.
2. Reishofer *et al.*, MRM, 65(3):848-857, 2011.
3. Ostergaard *et al.*, MRM, 36(5):715-725, 1996.
4. Wu *et al.*, MRM 50(1):164-174, 2003.
5. Mouridsen *et al.,* NeuroImage 33(2):570-579, 2006.
6. Chappell *et al.*, MRM 63(5):1357-1365, 2011.
7. Chappell *et al.*, IEEE Trans Sig Proc, 57(1):223-236, 2009.
8. Beckmann *et al.*, IEEE TMI 23(2):137-152, 2004.