ACCOUNTING FOR DISPERSION IN ARTERIAL SPIN LABELING USING THE MASS TRANSPORT MODEL: VALIDATION USING THE ARTERIAL INPUT FUNCTION

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Introduction: Dispersion of labelled blood water is a recognised issue in the quantification of cerebral blood flow (CBF) using arterial spin labelling (ASL). The ASL signal measured in the tissue is the result of labelled blood water, described by an arterial input function (AIF), undergoing exchange with the extra-vascular space [1]. Dispersion occurs during the transit of the blood along the arteries and is thus seen in the AIF. The most widely used standard model [1] does not account for flow dispersion, assuming a uniform transport of the bolus. A number of models for dispersion have been proposed [2, 3], however they have each only included a relatively simple description of the dispersive process. Recently a mass transport model (MTM) of the dispersion of a bolus of labelled blood within an artery has been presented [4]. Results using the MTM to quantify CBF indicated that neglecting dispersion could lead to up to 60% underestimation. However, it was not possible to verify the accuracy of the MTM to describe the effects of dispersion using conventional ASL measurements, since the tissue signal is a result of both AIF and local exchange kinetics. Here we sought to validate the MTM description of the effects of dispersion by examining data in which measurements of the AIF itself were available.

Methods: Two multi-TI ASL datasets were examined: (1) Short bolus duration data of [5]: FAIR preparation, 3D-GRASE readout (26 slices, 5×5×4 mm^3) at 3T, 28 time steps starting at TI = 0.3 s with an increment of 0.1 s, constant bolus length of 0.5 s. The signal from the label at four different locations along the arterial tree was identified, at the internal carotid artery (ICA) just before entering the Circle of Willis and at three locations along the anterior cerebral artery (ACA). (2) Mixed ASL signal: containing both tissue and intravascular (IV) components: FAIR preparation, single-shot 3D-GRASE readout at 3T, (TR/TE 3110/23 ms, 3.44 × 3.44 × 5 mm^3, 22 slices, 64 by 64), 10 TIs (0.4, 0.62, 0.84, 1.06, 1.28, 1.5, 1.72, 1.94, 2.16, 2.38 s), each one repeated 5 times.
The MTM AIF was fitted to the short bolus dataset by minimizing the root-mean squared error (RMSE) using the Nelder-Mead simplex method. The MTM models dispersion by considering the passage of the bolus along a cylindrical vessel, hence the AIF had three free parameters: path length (L_a), the arterial average velocity (U_a) and signal magnitude (the product of the arterial blood volume and arterial magnetization (aBV×M_{0a})). For comparison a Gaussian shaped AIF similar to the model of [3] was also fitted using the same approach. For the mixed data two components were included in the model fit: The MTM AIF for the intra vascular (IV) component and a separate tissue concentration curve assuming rapid exchange [1]. The additional parameters were L_t, U_t and CBF×M_{0a} for the tissue curve. For comparison a tissue plus IV model assuming no dispersion was also fit as in [6] with free parameters of arrival time and bolus durations for each component plus CBF×M_{0a} (tissue) and aBV×M_{0a} (IV).

Results: Short bolus data: The MTM was found to give a good fit to the data at the four arterial locations as shown in Figure A, with low RMSE (Table 1), and appeared to capture the increasing dispersion of the bolus as it travels from one location to the next. The model predicted successive increases in vessel length and decreases in average velocity with the each of the four signals, Table 1, consistent with their locations in the arterial tree, with values in agreement with results reported in the literature [7-9]. For the ACA locations the MTM fit with lower RSME than the Gaussian AIF, only in the ICA was the Gaussian a better fit (RMSE = 33). However, in this case the Gaussian shape required the unrealistic arrival of labelled blood at negative inversion time (before label creation).

Table 1: Predictions of the physiological parameters

Vessel	L_a (cm)	U_a (cm/s)	aBV × M_{0a} $(a.u.)$	$\frac{L_a}{U_a}(s)$	RMSE $(a.u.)$	RMSE $Variance\ of\ \Delta M_a$
ICA	4.6	36	383	0.13	78	0.19 %
ACA_1	6.6	31	351	0.21	42	0.16 %
ACA_2	7.0	20	375	0.35	43	0.13 %
ACA_3	9.3	15	266	0.62	30	0.19 %

Mixed ASL data: Both the analysis with the MTM and the standard model produced similar spatial distributions of CBF as shown in Figure B. However, the MTM fit with a lower RMSE (4.62 for the MTM versus 6.39 for the standard) the reason for this can be seen in the example curves for a voxel proximal to the middle cerebral artery in Figure B, where the smoothing introduced by dispersion in the MTM appears to be a better representation of the real data. Particularly, as in this example, where both IV and tissue signals are present.

Discussion: It is clear that ignoring dispersion leads to underestimation of CBF and thus ASL analysis should employ a model that accounts for this. Here measurements containing predominantly arterial signal have been compared to the MTM predictions, providing support for this model of dispersion. Unlike alternative models, the MTM takes into account the effect of flow dispersion by using a physically realistic velocity distribution. Thus, for example, it does not lead to AIF that break causality as seen where a Gaussian form is employed [3] and allows the effects of dispersion to be characterised in meaningful physiological parameters, such as path length. A disadvantage of the MTM is its greater mathematical complexity leading to longer analysis times, something that may be addressed through the characterization of the MTM AIF curve shape.

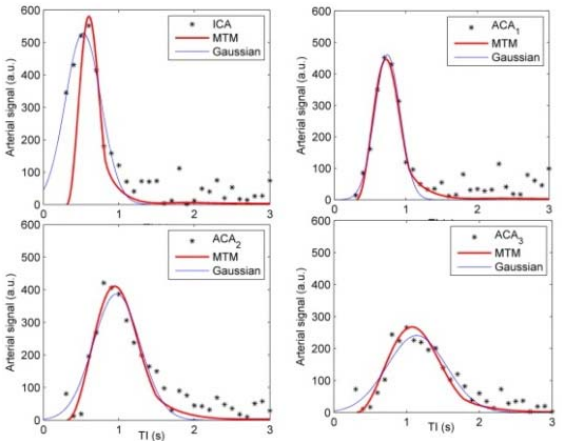

Figure A: AIF at four different locations: experimental data (black dot) and fitted model (dashed red line).

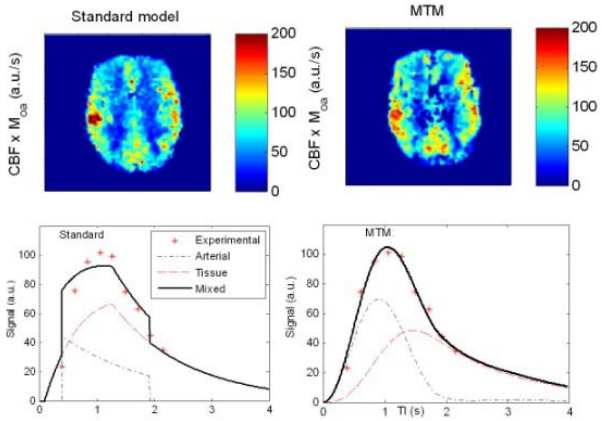

Figure B: CBF maps for the Standard and MTM models with curve fits from an example voxel (close to the MCA). The dashed black line corresponds to the fitted AIF, the dashed red line corresponds to the fitted tissue signal and the black solid line corresponds to the fitted mixed signal.

References

[1] Buxton *et al. MRM,* 1998.
[2] Gallichan and Jezzard, *MRM,* 2008.
[3] Hrabe and Lewis, *JMR,* 2004.
[4] Kazan *et al.*, *IEEE Trans Biomed Eng,* 2009.
[5] Günther, *ISMRM*, Hawaii, 2009.
[6] Chappell *et al.*, *MRM*, in press.
[7] Devault *et al.*, *MMS*, 2008.
[8] Moore *et al.*, *J Biomech,* 2006.
[9] Stergiopulos *et al.*, *J Biomech*, 1992.