A Re-examination of the Impact of Dispersion on Quantitative Cerebral Blood Flow Measurements

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INTRODUCTION:

In magnetic resonance dynamic susceptibility contrast (DSC) perfusion studies, quantitative cerebral blood flow (CBF) estimates are determined from the peak of the residue function obtained through deconvolving the tissue concentration curve by the arterial input function (AIF) [1]. As pointed out by Calamante *et al.* [2], a basic assumption is that the measured AIF truly reflects the "exact" input to the tissue [2] despite being measured at some distance from the tissue. They attempted to determine the possible impact of delay and dispersion of the AIF on the CBF quantification and suggested the use of a number of different dispersion models. However it is now known that the standard singular value decomposition approach used in that analysis introduces an artificial CBF sensitivity to the arterial-tissue-delay (ATD) [3, 4]. We propose to re-examine the dispersion issue to determine if use of a delay-insensitive deconvolution algorithm [4] changes any of the fundamental conclusions made in [2].

METHOD:

Calamante *et al.* [2] showed that the changes in the tissue concentration signal caused by a dispersed AIF signal as it passed through a vascular bed (single, well-mixed compartment $R_{ANALYTIC}(t) = exp(-t / MTT);\ t \geq 0$ [1]) could be theoretically modeled as the convolution of an effective dispersed residue function $R_{EFFECTIVE}(t) = \beta * (exp(-\beta t) - exp(-t / MTT)) / ((1/MTT) - \beta);\ t \geq 0$ and a non-dispersed AIF signal. Two dispersion models discussed in [2] were used in this simulation study. The dispersion factor β was modeled as being fixed (in the range $0 \leq 1 / \beta < 6$ s) as per [2] and proportional to the arterial-tissue-delay ($1 / \beta = k$ ATD; k is a constant); an extension of the model suggested in [5] Tissue signal samples were generated using high temporal resolution numerical convolution ($TR_{CONVOLUTION}$ = 1 / 32s) of the effective residue function and an assumed gamma-variate AIF [1]; followed by decimation to produce the tissue signal $c_{VOI}(t)$ (TR = 1s). The ratio $CBF_{MEASURED}$ / CBF_{TRUE} was used to illustrate the impact of dispersion on the quantitative CBF estimate as per [4].

RESULTS:

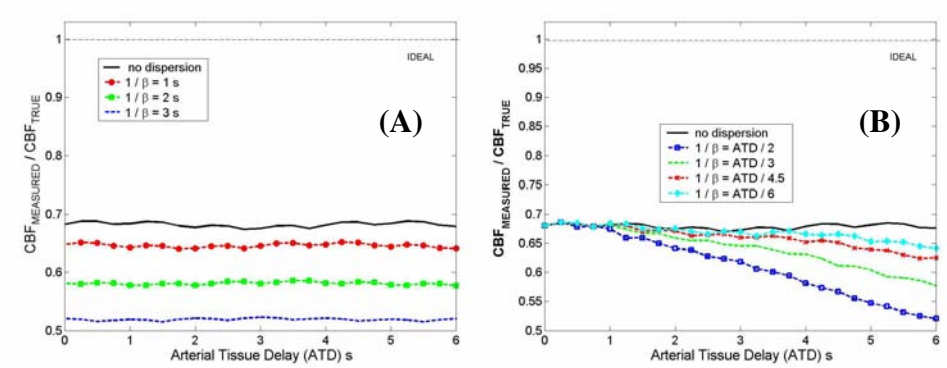

Fig. (A) Dispersion results are simulated for a well-mixed single compartment vascular bed with a tissue mean transit time of 6.2 s according to a fixed dispersion model [2]. (B) Using a model where the level of dispersion depends directly on ATD [5] leads to a smaller level of CBF under-estimation for small ATD than suggested with the fixed dispersion model, but greater under-estimation for longer ATD.

Calamante *et al.* [2] reported that using a fixed dispersion factor resulted in CBF estimates that varied with ATD for small ATD, became essentially ATD independent for large ATD (ATD > 1.5 s – 2.0 s). Estimates became more increasingly under-estimated, and less ATD sensitive, as $1 / \beta$ grew larger ($1 / \beta > 2$ s). It can be seen from (A) that use of a delay-insensitive deconvolution algorithm removes all of the dependence of dispersion on ATD for this fixed dispersion factor model. It requires a direct relationship between the dispersion level and ATD [5] to provide the more intuitive results where the level of CBF under-estimation increases with ATD (*i.e.* the dispersion is changed by the distance the bolus travels between being observed at the AIF location before becoming the "exact" input to the tissue site). With this model, the changes in CBF estimates due to dispersion are smaller than those reported in [2] for small ATD values but greater for larger ATD, with the equivalence point ($ATD_{EQUIVALENCE}$ = 1 / k s) depending on the dispersion model constant k.

CONCLUSION:

Use of a delay-insensitive deconvolution algorithm removes many of the effects of ATD-related dispersion effects reported when CBF estimates are calculated in the presence of a fixed dispersion factor as per [2]. Relating the dispersion directly to ATD as per [5] appears better describe the condition where dispersion causes the level of CBF under-estimation to increase the further the tissue site is from the location of measuring AIF. The simulation studies suggest that the changes caused by dispersion are less dramatic than originally suspected; at least for smaller ATD values.

However, when using any ATD-dependent dispersion model, how should the impact of dispersion be described in the presence of the negative ATD values observed with some patients? When ATD is negative, it must be assumed that the path taken by the bolus to the AIF location is now longer (rather than shorter) than the path taken by the bolus to the tissue location. Thus it will be the AIF signal that is the more dispersed, rather than the "exact" input function to the tissue area. This implies that, under these experimental conditions, dispersion will lead to a larger cerebral blood flow estimate rather than the more intuitive lower estimate! However, since the negative ATD ranges are reported as small (-2 s < ATD < 0 s), the enhancement can be expected to be minor (*c.f.* (B)).

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REFERENCES:

[1] Østergaard L *et al.*, *MRM* 1996; 36: 715-725.
[2] Calamante, F. *et al. MRM* 2000; 44: 466-473.
[3] Wu *et al.*, *MRM*, 2003;50(4):856-864.
[4] Smith MR *et al.,MRM,* 2004;51(4):631-634.
[5] Østergaard L *et al.*, *J Cereb Blood Flow Metab*, 1999; 19: 690-699.