Perfusion quantification by bolus-tracking: an alternative solution to the problem of tracer arrival timing

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INTRODUCTION

CBF quantification with DSC-MRI using the algebraic approach set out in [1] is sensitive to (positive or negative) delays between the Arterial Input Function (AIF) and the tissue concentrations [2,4]. In this work we show that the solution proposed in [4] is restricted by the requirement that the tissue concentrations vanish at the end of the measurement. It further doubles the size of the numerical problem, which can lead to significant increases in calculation time for regularization approaches with higher computational complexity. We propose an alternative approach which does not suffer from these shortcomings by generalizing the tracer kinetic model to the case where causality is violated. In a practical implementation this generalization leads to a minor alteration in the procedure outlined in [1], and is equivalent to a method which enforces positive delays by artificially shifting the measured AIF towards earlier times. We motivate our approach by theoretical considerations and verify it using simulated data.

METHODS

We place $t_0 = 0$ at some time before the arrival of the contrast anywhere in the image volume and measure a total of n data points at regular intervals TR, starting at $t = t_0$. Setting $f(t_i) = f_i$ for all functions involved, the procedure given in [1] leads to Eq.[1]. C(t) are the concentrations in the tissue, the kernel K(t) is proportional to the impulse response and the numbers A_i are defined by $6A_i = AIF(t_{i-1}) + 4\,AIF(t_i) + AIF(t_{i+1})$.

Our modification leads to Eq. [2] , with the number k chosen so that k TR > maximal |delay| (throughout we define 'delay' as the difference in bolus arrival time between the tissue and arterial region). Note that the C_i at $i < 0$ do not need to be measured as they are exactly zero. Using Eq.[2] the kernel is calculated at k negative times, and in the presence of negative delays the values at these times will be strictly positive. We note that in order to absorb positive delays it is essential to include at least k precontrast data in the AIF.

$$\begin{bmatrix} C_0 \\ C_1 \\ \vdots \\ C_{n-1} \end{bmatrix} = \mathrm{TR} \begin{bmatrix} A_0 & 0 & \dots & 0 \\ A_1 & A_0 & \ddots & \vdots \\ \vdots & \ddots & \ddots & 0 \\ A_{n-1} & \dots & A_1 & A_0 \end{bmatrix} \begin{bmatrix} K_0 \\ K_1 \\ \vdots \\ K_{n-1} \end{bmatrix} \quad (1)$$

$$\begin{bmatrix} C_{-k} \\ C_{1-k} \\ \vdots \\ C_{n-1-k} \end{bmatrix} = \mathrm{TR} \begin{bmatrix} A_0 & 0 & \dots & 0 \\ A_1 & A_0 & \ddots & \vdots \\ \vdots & \ddots & \ddots & 0 \\ A_{n-1} & \dots & A_1 & A_0 \end{bmatrix} \begin{bmatrix} K_{-k} \\ K_{1-k} \\ \vdots \\ K_{n-1-k} \end{bmatrix} \quad (2)$$

We simulated the tracer kinetic model following the procedure described in [1,2,4]. Linear inversion of Eqs.[1,2] was regularized with standard-form Tikhonov regularization, using the L-Curve Criterion for selection of the regularization parameter [3]. As a point of reference we compared Eq.[2] to Eq.[1] and to the method outlined in [5]. The latter is identical in form to Eq.[1], but uses a more accurate formula for A_i. In [5] it was shown that this improved matrix naturally leads to more accurate rCBF estimates in the absence of delay.

RESULTS

We show the results for a dispersed triangular kernel, with SNR = 5 at maximum concentration and time resolution TR = 1.0 sec. These data are representative of the fundamental behaviour in general. Figures 1,2 compare the results calculated with Eq.[1] (thick solid line), Eq.[2] (dashed line) and the correction from Ref.[5] (dotted line).

All simulated results agree entirely with theoretical expectations. First, the solutions obtained with Eq.[2] compensate for delays which are integer multiples of TR by a corresponding shift in the kernel. As a consequence, such delays do not affect the maximum (rCBF) and integral (rCBV) of the solution. Second, at positive delays smaller than TR the method from Ref.[5] is superior. Third, at positive delays larger than TR all methods are essentially equivalent.

Figure 1 shows more clearly how Eq.[1] leads to overestimations in the presence of negative delays: the values at positive times are increased to compensate for the missing data at negative times. Eq.[2] solves this problem by calculating the values at negative times as well. This is equivalent to the circulant approach [4] where those values 'wrap around' and appear at the end of the measurement window.

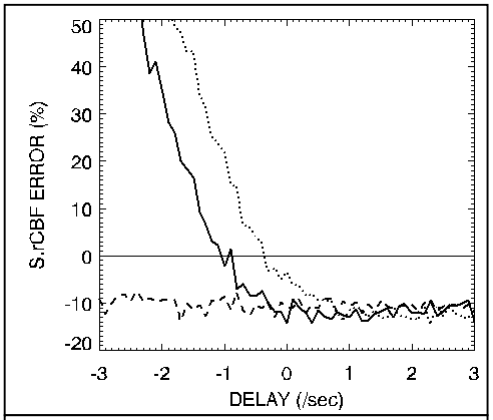

Fig. 2: Systematic error in rCBF estimate as a function of the delay in the AIF. The error is expressed as a percentage of the correct rCBF.

CONCLUSION

We conclude that in a measurement context where negative delays can not be avoided, Eq.[2] must be used to discretise the problem. In case the tissue concentrations are measured until they vanish (or when they are forced to do so, eg. by gamma-variate fitting), the circulant embedding proposed in Ref. [4] is equivalent to Eq.[2] in terms of outcome, but computationally more expensive. When delays are definitely positive, the method described in Ref.[5] must be used.

REFERENCES

[1] Østergaard et al. (1996) MRM 36:715-725.
[2] Calamante et al. (2000) MRM 44 :466-473.
[3] Sourbron et al. (2003) Proc ISMRM 11:2207.
[4] Wu et al. (2003) MRM 50:164-174.
[5] Sourbron et al. (2003) MAGMA 16, suppl 1:134.

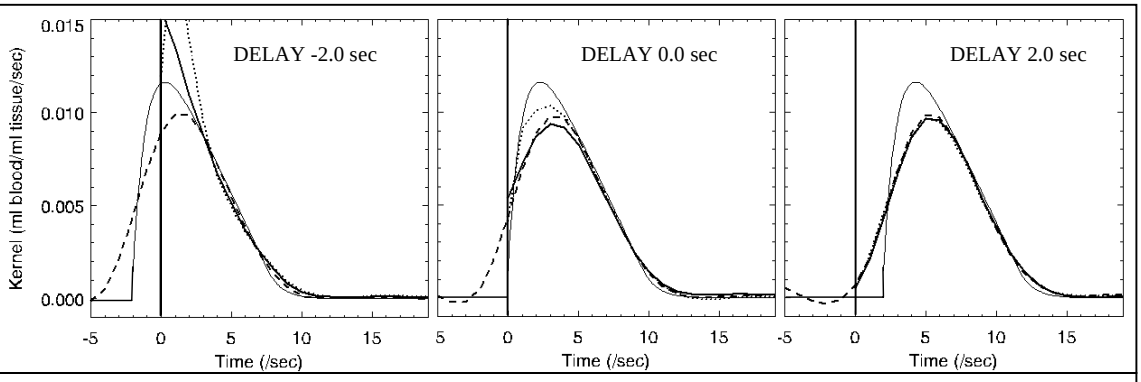

Fig. 1: Plot of the fitted kernel for the three regimes of delay. The thin continuous line represents the exact kernel.