Local Arterial Input Function for Perfusion MRI Calculated Using Independent Component Analysis

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Introduction: Quantification of cerebral blood flow (CBF) using dynamic-susceptibility contrast (DSC) MRI relies on the deconvolution of the arterial input function (AIF) to calculate the impulse response function CBF·$R(t)$, where $R(t)$ is the tissue residue function [1]. The AIF represents the concentration of contrast entering the tissue of interest at time t, and it is commonly estimated from the signal changes in a major artery (e.g. the middle cerebral artery). However, it has been shown that the presence of bolus delay and dispersion between the artery and the tissue of interest can be a significant source of error in CBF quantification [2,3]. These effects could be minimized if a local AIF were used [4], although the measurement of a local AIF can be problematic due to, for example, partial volume effects. Independent component analysis (ICA) can be used to identify temporally independent patterns, and it has been previously used in DSC-MRI to remove the signal resulting from large vessels [5], and as a segmentation technique [6]. The present work describes the use of ICA as a tool to define a local AIF, with the aim of minimizing the effects of bolus delay/dispersion, and obtain a more accurate quantification of CBF.

Methods: The methodology to calculate the local AIF consists of the following steps: (*i*) the concentration time course $C(t)$ is calculated in each pixel [1]. (*ii*) The optimum number N of independent components is estimated according to the Bayesian Information Criterion [7]. (*iii*) $C(t)$ is decomposed into the N sources (and noise components, see Eq.(1a)). (*iv*) The data are denoised to create $C_{tissue}(t)$ by removing the noise components. (*v*) The arterial components are identified (in the present implementation, these were identified interactively by the user, based on their spatial distribution and temporal characteristics), and combined to create $C_{art}(t)$ (see Eq.(1b)). (*vi*) The $C_{art}(t)$ dataset is scaled to have the same area under the peak throughout the slice [8]. (*vii*) The pixels with an unrealistic shape on $C_{art}(t)$ (i.e. not resembling a peak) are removed. (*viii*) The AIF in these pixels is calculated from the surrounding pixels according to their distance to the pixel of interest using a gaussian-weighting factor. For the present study, a 10-pixel stdev for the gaussian was empirically chosen (based on the gap size typically found after removing the pixels in the previous step), and the gaussian-weighting was truncated to a box of 30×30 pixels to avoid non-local contributions. (*ix*) The resulting dataset is smoothed (with a 3x3 uniform kernel) to improve the SNR; this smoothed dataset represents the local AIF.

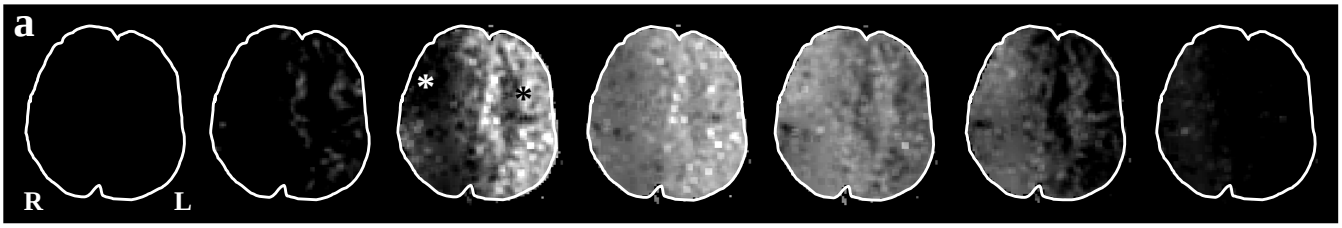
$$C(x,t)=\sum_{j=0}^{N} a_j(x)\cdot S_j(t)+noise=C_{tissue}(x,t)+noise \qquad (1a)$$

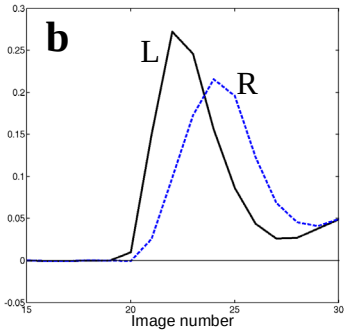
$$C_{tissue}(x,t)=\sum_{arterial} a_j(x)\cdot S_j(t)+\sum_{rest} a_k(x)\cdot S_k(t)=C_{art}(x,t)+\sum_{rest} a_k(x)\cdot S_k(t) \qquad (1b)$$

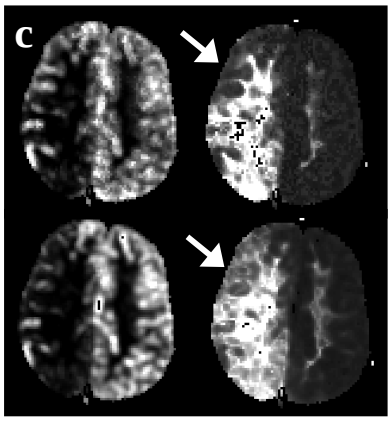
where x denotes the pixel position, and the N sources were divided into the arterial sources and the remaining sources.

The methodology was tested on data from patients with various vascular abnormalities. Data were acquired on a 1.5T Siemens Symphony scanner using a GE-EPI sequence (TE/TR=47/1250 ms) after the injection of a bolus of 0.15 mmol/kg of Gd-DTPA using an MR-compatible power injector (Medrad). To assess the effect of using a local AIF in quantification of DSC-MRI, the data were analyzed in two different ways. First, $C_{tissue}(t)$ was deconvolved using the local AIF generated in step (*ix*) above. Second, the same $C_{tissue}(t)$ dataset was deconvolved using a global AIF. The global AIF was calculated from pixels manually selected (with an early, large signal drop) in a major artery on the contralateral side. Deconvolution was performed using singular value decomposition (SVD) [9], but with a reduced threshold (5% [10]) for the truncation of the SVD expansion, due to the improved SNR after signal denoising using ICA (see step (*iv*) above). CBF maps were calculated from the maximum of the corresponding impulse response function [9], CBV maps were calculated from the area under $C_{tissue}(t)$ (normalized to the area under the corresponding AIF [1]), and MTT maps were calculated using the central volume theorem [1].

Results: The calculated local AIF was found to be heterogeneous in the patients studied, with some areas displaying delayed, wider peaks. This is illustrated in the figure, for the data from a patient with MRA turbulence in the right middle, posterior, and anterior cerebral arteries: (a) 7 images (during the passage of the bolus) of the calculated local AIF data set. A clear heterogeneity can be seen, with a delayed, wider, smaller AIF to the right side, particularly in the right frontal cortex (see figure (b) for the AIF in the two pixels indicated by the asterisks in (a)). (c) CBF (left) and MTT (right) maps calculated using the local (top) or the global (bottom) AIF. Various differences can be seen in the maps depending on the AIF used (e.g. CBF underestimation and MTT overestimation when the global AIF was used, see arrows).







Discussion: A new methodology to calculate the local AIF using ICA was described, and tested on data from patients with various cerebrovascular abnormalities. The methodology was compared to the conventional approach of using a global AIF (measured in a major artery). The new methodology produced higher CBF and shorter MTT (compared to the global AIF case) in areas with distorted AIFs, suggesting that the effect of delay/dispersion is minimized. The minimization of these effects using the calculated local AIF should lead to a more accurate quantification of perfusion, which can have important implications for diagnosis and management of patients with cerebral ischemia. A further advantage of the proposed methodology is the improved SNR due to the denoising capabilities of the ICA, which should further contribute to improve the accuracy of DSC-MRI quantification.

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