Minimizing Macro Vessel Signal in Hemodynamic Parameter Maps Using Independent Component Analysis

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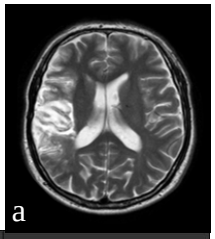
Introduction: High macro vessel signal intensity in cerebral parameter maps can complicate classification of stroke affected tissue and leads to over estimation of blood flow and blood volume. Thus a minimization of the influence of the macro vessel signal is important. Based on the assumption of statistical independence of tissue signal, arterial signal and venous signal, an ICA algorithm was applied to DCE-MRI data. It has been shown, that the independent components represent different signal components [1,2]. The purpose of this work was to use the identified independent components to correct the dynamic time series. Additionally rCBV, rCBF and rMTT maps were evaluated and compared to non corrected parameter maps.

Methods: DCE-MRI data were obtained using a clinical 1.5T MRI scanner (Philips Medical Systems, The Netherlands). A multi shot gradient echo EPI sequence was performed on brain tissue of 23 patients and analyzed retrospectively. The scan parameters were FOV/TR/TE/α = 23 cm/732 ms/8.5ms/45° with an image matrix of 128x128. 50 dynamic images in 12 slices were acquired. In a preprocessing step the image dimension was reduced by applying principle component analysis (PCA). On the reduced image set of principle components we applied a fast fixed point ICA algorithm [3] with a maximizing negentropy approximation. Maximum independent signals of arteries and veins can be clearly identified by a skilled operator with detailed knowledge about vascular territories and supplying vessels. Those independent components which only represent the macro vessel signal were eliminated. An inverse transformation was performed to restore the principle components which are now minimal influenced by the macro vessel signal. In a second back transformation step the dynamic time series was restored from the corrected principle components. The correction algorithm follows the scheme:

$$\mathbf{x} \xrightarrow{\text{PCA}} \tilde{\mathbf{x}} = \mathbf{E}\mathbf{x} \xrightarrow{\text{ICA}} \hat{\mathbf{x}} = \mathbf{A}\tilde{\mathbf{x}} \xrightarrow{\text{ICA}^{-1}} \tilde{\mathbf{x}}' = \mathbf{A}^{-1}\hat{\mathbf{x}}' \xrightarrow{\text{PCA}^{-1}} \mathbf{x}' = \mathbf{E}^{-1}\tilde{\mathbf{x}}',$$

where $\mathbf{x}$ denotes the dynamic images, $\tilde{\mathbf{x}}$ the principle components, $\hat{\mathbf{x}}$ the independent components, $\mathbf{E}$ the eigenvector matrix and $\mathbf{A}$ the mixing matrix. The primed variables denote the corrected independent components, corrected principle components and the corrected dynamic image series. Perfusion parameter maps showing rCBV , rCBF and rMTT were performed numerically for both, uncorrected and corrected time series.

Results: Figure 1 demonstrates the correction effect on tracer concentration time series at the time of bolus inflow for uncorrected (b) and corrected (c) series. The arrows mark the vascular regions where the influence of the vessel signal is minimized. Figure 2 shows tracer concentration as a function of time for uncorrected and corrected data. Curves were obtained from ROIs in vascular regions, gray matter and white matter. The comparison shows the decreased tracer concentration in macro vessels (sinus, artery) whereas gray matter tissue and white matter tissue is unaffected by this correction. Perfusion parameter maps obtained from the corrected dynamic series show a minimized influence of macro vessel signal. Due to the better tissue contrast, smaller changes in blood volume (a), blood flow (b) and mean transit time (c) could be observed (Figure 3).



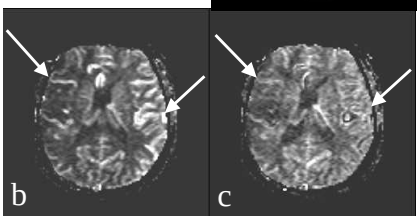
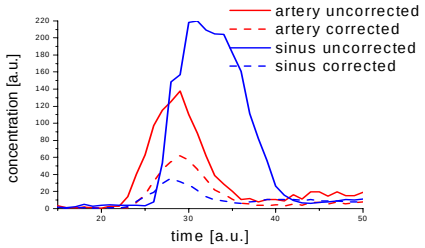


Figure 1: TSE image for morphological comparison (a). Tracer concentration at the time of bolus inflow for uncorrected (b) and corrected (c) DCE-MRI data.



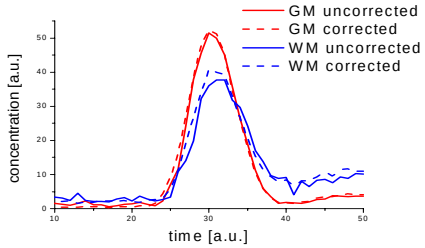


Figure 2: Tracer concentration time curves for different ROIs obtained from uncorrected data (solid line) and corrected data (dashed line).

Discussion: A fast and robust method for improving hemodynamic parameter maps was developed and evaluated in a set of double echo EPI scans obtained from stroke victims. The computing time is lower than one minute for a single slice. This short computing time is caused by PCA data compression. The number of principle components, which are the input signals for the ICA algorithm, are reduced from 50 to 8-12. These PCs contain the entire image information while the discarded PCs describe just pure noise. Using the first 8-12 corrected PCs for the back transformation, leads to a PCA filtered corrected dynamic time series with improved SNR. For the separation of the different independent signals the time resolution of the DCE-MRI data is crucial. A resolution lower than 1.4 seconds for separating venous, arterial, gray matter, and white matter signals, is recommended. However, the ICs have to be selected manually which requires a skilled operator. Automation of this process requires further developments.

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References:

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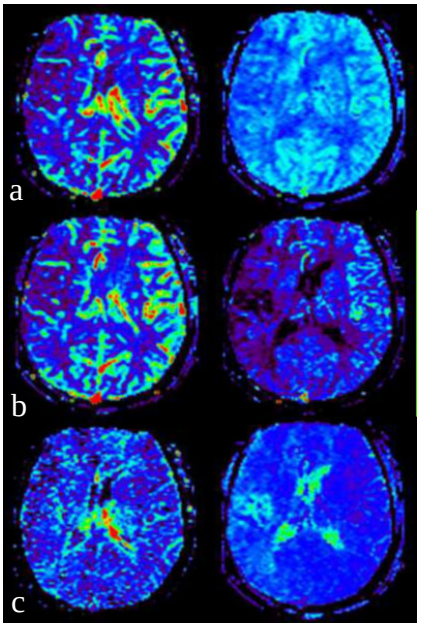

Figure 3: Parameter maps rCBV (a), rCBF (b) and rMTT (c) for uncorrected (left column) and corrected (right column) DCE-MRI data