Automatic Macro-Vessel-Minimization using Independent Component Analysis and Local Scaling Functions

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INTRODUCTION: Strong signal changes in large vessels can be observed in dynamic susceptibility contrast MR images (DSC-MRI).This leads to an over estimation of hemodynamic parameters such as relative cerebral blood flow (rCBF), relative cerebral blood volume (rCBV) and relative mean transit time (rMTT). Previous studies demonstrated, that independent component analysis (ICA) has the potential to separate signals from different tissue types based on the assumption of statistical independence of parenchyma signal, arterial signal and venous signal [1]. Therefore independent components (ICs) can be used to correct the dynamic time series to minimize the influence of macro vessel signal [2]. However, two main problems still persist when using an ICA correction algorithm where the macro vessel ICs are removed prior to the back transformation step. First, the independent components representing macro vessel signal have to be selected manually by an experienced operator. Second, static signal fractions which are not influenced by the contrast media are removed and lead to a systematic bias. In this work we set out to eliminate user dependency by automating the selection of appropriate ICs using a local scaling function technique [3]. Furthermore we preserve the static tissue signal of the macro vessel representing IC by editing the time dependent mixing matrix in the ICA model before the back transformation is performed.

METHOD: In-vivo DSC-MRI data were obtained from patients with high-grade unilateral symptomatic stenosis of the internal carotid artery. Measurements were performed on a 3.0T MRI scanner (Siemens Tim Trio, Siemens Medical, Germany) with an 12 channel head coil (Siemens Medical, Germany). A Single Shot EPI sequence was used with the following parameters: FOV/TR/TE/α=230mm/1250ms/28ms/60° with an image matrix of 128x128, slice thickness of 5.4mm and a temporal resolution of 1.19s for 19 slices and 60 time points. A dose of 0.1 mmol/kg contrast agent (DOTAREM®, Guerbet, France) was injected intravenously via a power injector (Spectris; Medrad Inc., Indianola, PA, USA) at a rate of 5 ml/s, followed by 30 ml of NaCl 0.9% at the same speed.
ICA was applied on DSC-MRI data using the FastICA algorithm [4] to solve the linear problem x = As, where x is the measured dynamic time series, A the mixing matrix and s the set of independent components. To identify appropriate ICs, a similarity measurement between the arterial- and venous phase and the corresponding ICs was implemented. After clustering the source image (ICs) and the target image (arterial- or venous phase of the dynamic time series) into five cluster (K) using the k-means algorithm, we define a scaling function σ:

$$\sigma_{\text{target}}(i) = \frac{\sum_{x \in \{I_{\text{source}} = i\}} I_{\text{target}}(x)}{\sum_{x \in \{I_{\text{source}} = i\}} x}, \qquad \text{for } i \in K_{\text{n, source}} \text{ with n = 1,…,5}$$

The scaling factor σ links the pixel intensities of the ICs (I_{source}) with the pixel intensities of the macro vessel related tracer concentration images (I_{target}) for each cluster K_n in the source image. The best conformity of source and target is then given by

$$\left\| \sigma_{\text{target}}(I_{\text{source}}) - I_{\text{target}} \right\| = \min .$$

Target images were selected from the dynamic time series at the time point of the early arterial phase (t = 16) and at the time of the venous phase (t = 33) after the first pass. Once having identified the ICs representing arterial and venous signal we edit the corresponding columns of the mixing matrix A in the ICA model to eliminate time dependent intensity changes caused by the contrast media. The column values in the mixing matrix were set to a constant level, evaluated from the first twelve time points. In consideration of the new weighting matrix $\tilde{A}$, a vessel corrected dynamic time series was calculated using the back transformation $\tilde{x} = \tilde{A}s$. Hemodynamic parameter maps were evaluated using singular value decomposition (SVD). Software for post-processing was developed in house and programmed with Interactive Data Language (IDL 6.0, Research Systems Inc., USA) and Matlab (V 7.4, The MathWorks, Inc., MA, USA).

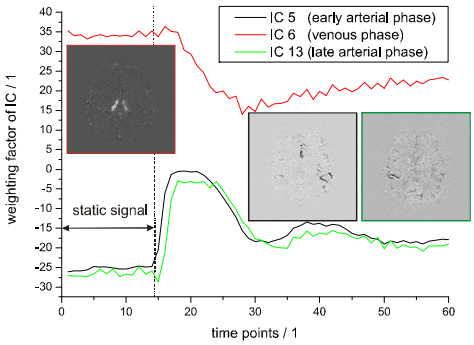

Figure 1: Columns of the mixing matrix A in the ICA model are temporal weightings of the independent components. Static signal fractions from the baseline are preserved. Note that the weightings can be positive or negative due to the sign of the IC.

RESULTS: DSC-MRI data of four patients were analyzed for three central slices using the automatic vessel-correction algorithm. The method of local scaling functions identified the arterial ICs and the venous ICs in all cases. Figure 1 shows the columns of the mixing matrix A for the identified ICs, which represent arteries in two different phases of tracer inflow, and the venous system of the choroid plexus. Hemodynamic parameter maps rCBF, rCBV and rMTT (Figure 2) evaluated from the corrected DSC-MRI data show a reduced influence of macro vessel signal (denoted by the white arrow)

CONCLUSION: The automatic identification of independent components is challenging due to the undefined sign and order of the ICs, which are model inherent properties. In this work we demonstrate that the method of local scaling functions is a robust similarity measurement to identify independent components which represent the arterial- and the venous phase of DSC-MRI time series. We further show that manipulating the mixing matrix in the ICA model enables the reconstruction of a dynamic time series with minimized macro-vessel signal while static tissue signal fractions are preserved. This algorithm is totally user independent and therefore applicable for clinical use.

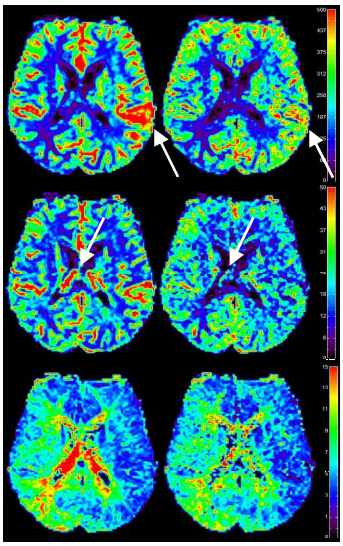

Figure 2: Hemodynamic parameter maps rCBF (first row), rCBV (second row) and rMTT (third row) for uncorrected (left column) and ICA corrected (right column) DSC-MRI data.

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