Optimized Filtering of ICA Corrected DCE-MRI Perfusion Images Using Tikhonov Regularization

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INTRODUCTION: Dynamic susceptibility contrast (DCE-MRI) is a widely used technique for studying hemodynamic changes in brain tissue. Hence, an important objective for the quantitative assessment of cerebral perfusion using DCE imaging is the estimation of a convolution integral, which can be achieved by the process of deconvolution. Various Methods, such as "Singular Value Decomposition" (1) have been developed for this purpose in the last decade. A serious drawback of these methods is a systematic overestimation of CBF and CBV in areas that contain many macro-vessels. To avoid this pitfall, multivariate statistical methods such as "Principle Component Analysis" (PCA) and "Independent Component Analysis" (ICA) have been applied as a pre-processing step to reduce the influence of macro-vessel signal in parameter maps (2, 3). ICA has the potential to separate signal assigned to macro vessels from tissue signal. The clearly identified independent components, representing vessel signal, are removed from the data set. Inverting the ICA transformation with the remaining images restores a set of corrected PCs with a minimized influence of macro-vessel signal. In a second back transformation step, the PCA transformation is reversed to restore the corrected DCE-MRI data. However, the back transformation of a linear system in the presence of noise is inherently an ill-posed problem, and the direct matrix inversion may not yield useful results. Therefore "Tikhonov Regularisation" has been applied to both, PCA- and ICA-back-transformation step to reduce noise amplification and stabilize results.

METHOD: In-vivo DCE-MRI data were obtained from routine examinations 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 (MAGNEVIST®, Schering AG, Germany) 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.

In a pre-processing step PCA was applied for whitening and for reducing the dimension of the ICA input data from 60 to 15. ICA was performed using a fast fixed point algorithm with a negentropy approximation for the cost function in the optimization problem (4). The inverse ICA transformation $x_{PC} = A^{-1}x_{IC}$, where $\mathbf{x}_{PC}$ are the principle components, $\mathbf{x}_{IC}$ are the independent components and **A** is the mixing matrix, restores the set of principle components. The second back transformation, $x_{DCE\text{-}MRI} = W^{-1}x_{PC}$ where $\mathbf{x}_{DCE\text{-}MRI}$ are the images of the restored dynamic time series and **W** is the whitening matrix inverts the PCA transformation step. The inverse solutions of both ill-posed linear equations were found by solving the following penalized least squares problem:

$$x_{PC,\alpha} = \arg\min \left\| A^{-1}x_{IC} - x_{PC} \right\|_2^2 + \alpha^2 \left\| Lx_{IC} \right\|_2^2 \qquad \text{and} \qquad x_{DCE-MRI,\alpha} = \arg\min \left\| W^{-1}x_{PC} - x_{DCE-MRI} \right\|_2^2 + \alpha^2 \left\| Lx_{PC} \right\|_2^2$$

Choosing the matrix operator **L = I**, the identity matrix, yields the well known Tikhonov regularization (5). The regularization parameter α was estimated by the L-curve method. Hemodynamic parameter maps rCBF, rCBV and rMTT were calculated from the original and ICA corrected concentration time series, using singular value decomposition (SVD). All post processing was performed offline on a 2 GHz dual core PC. 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).

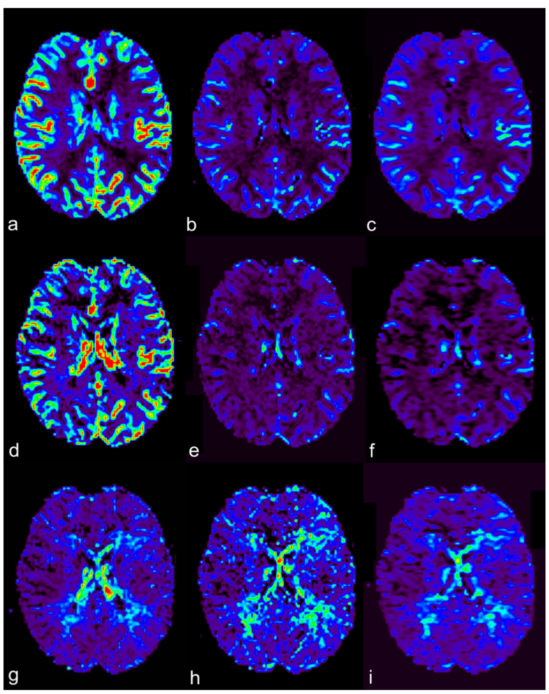

Figure 1: Hemodynamic parameter maps rCBF, rCBV and rMTT for unprocessed DCE-MRI data, ICA processed data and regularized ICA processed data.

RESULTS: Figure 1 shows the hemodynamic parameter maps rCBF (first row), rCBV (second row) and rMTT (third row) for uncorrected data (first column), ICA processed data (second column) and ICA processed data with regularized back transformation (third column). The window levels were set equally for related parameter images and no additional filter was applied. The amplified noise due to the solution of the ill-posed back transformation leads to higher noise level in macro-vessel corrected hemodynamic parameter maps (b,c,e). Regularization of the back transformation steps has an filtering effect on the reconstructed dynamic time series from which smoother parameter maps can be calculated (c,f,i). Regions of Interest (ROI) were obtained from not regularized and Tikhonov regularized reconstructed dynamic time series in veins, arteries, gray matter and white matter. The mean difference was lower than 1% for all regions.

Conclusion: Minimizing macro-vessel signal using independent component analysis involves the solution of ill-posed linear systems. Direct back transformation leads to noise amplification in the reconstructed dynamic time series which results in noisy parameter maps. We found that Tikhonov regularization improves the visualization of hemodynamic parameter changes without affecting the quality of macro-vessel minimization through ICA. Contrary to a simple filter process regularization finds the optimum between underregularization, which is dominated by amplified noise and overregularization where data are oversmoothed. However, other regularizations and methods for evaluating the optimal regularization parameter are currently investigated for further improvement.

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