

## Whole-brain CBF measurements using DCE-MRI and 3D k-t PCA

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**INTRODUCTION:** T1-weighted dynamic contrast enhanced (DCE) MRI has emerged as a promising technique for quantifying cerebral blood flow (CBF) and other vascular properties [1,2]. However, the clinical feasibility of DCE-MRI perfusion imaging is currently limited by low SNR and poor spatial coverage. To overcome these problems the data acquisition needs to be extended from current 2D techniques to a true 3D volumetric approach. This in turn requires a dramatic acceleration of the data acquisition in order to maintain sufficient temporal resolution to quantify CBF. The recently proposed k-t PCA technique [3] allows a considerable data reduction in dynamic MRI by jointly exploiting the separation of the aliased signals in  $x$ - $f$  space [4] and the sparsity of dynamic data when subjected to principal component analysis (PCA). In this study we investigated the quality of whole-brain CBF measurements using 3D k-t PCA.

**METHODS:** Five patients with optic neuritis underwent 3D DCE-MRI as part of their clinical routine examination. Imaging was performed on a 3.0 Tesla MR system (Achieva, Philips Healthcare) equipped with a sixteen-element head receive coil. DCE-MRI was performed in an axial stack using a matrix size of  $96 \times 60 \times 20$  ( $k_x$ ,  $k_y$ ,  $k_z$ ) and 96 time frames. We used a saturation recovery (SR) prepared spoiled gradient echo readout,  $FOV = 230 \times 180 \times 160 \text{ mm}^3$ ,  $\alpha = 15^\circ$ ,  $T_R = 3.9 \text{ ms}$ , and  $T_E = 1.9 \text{ ms}$ . Both phase encoding dimensions ( $k_y$  and  $k_z$ ) were undersampled by a factor of six. However, the central part of  $k_y$ - $k_z$  space was fully sampled in order to generate low-resolution images used for training the PCA model [3]. The matrix size of the training data was  $96 \times 11 \times 11$  ( $k_x$ ,  $k_y$ ,  $k_z$ ). For both the training data and the undersampled data, an elliptical k-space shutter was applied in  $k_y$ - $k_z$  space, reducing the number of points to be sampled by approximately 25% [5]. Hence, the net acceleration factor was 4.7, resulting in a temporal resolution of 1.2 seconds per frame. Perfusion was calculated using model-independent deconvolution based on singular value decomposition (SVD) [6]. The arterial input function (AIF) was derived from the left ICA. To correct for partial volume effects, the AIF was rescaled by normalizing the area under the curve to that of a venous outflow curve (sagittal sinus) [7].

To simulate the behaviour of 3D k-t PCA over a broader range of acceleration factors, a fully sampled 2D DCE-MRI examination was performed in one patient in the coronal plane. This strategy was chosen because 1) only with 2D imaging can we obtain fully sampled data at high temporal resolution (here 0.8 seconds per frame), and 2) the  $k_y$ - $k_x$  data of the coronal plane correspond to the  $k_y$ - $k_z$  space of the 3D axial stack at a single frequency encoding position,  $x$ . The  $x$  position was chosen to include both ICAs and of course GM and WM, and undersampling was simulated along both  $k_y$  and  $k_x$  of the coronal plane.

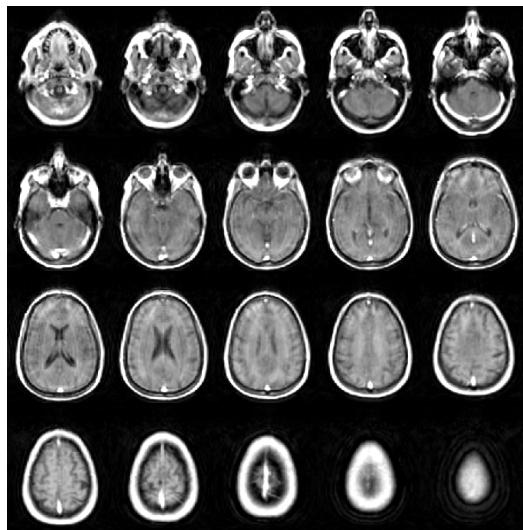


Fig. 1. Typical whole-brain 3D DCE-MRI images.

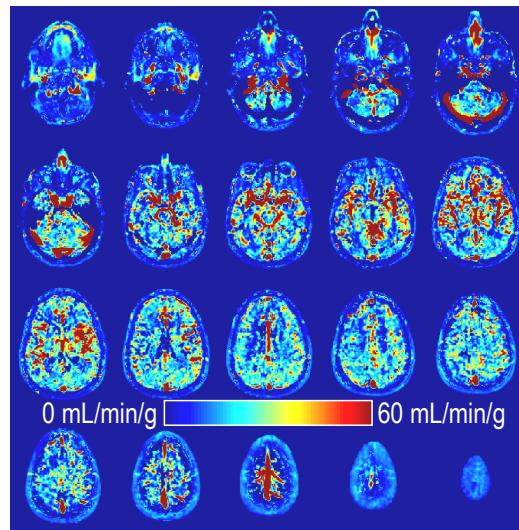


Fig. 2. Whole-brain CBF map (same patient as in Fig. 1).

**RESULTS:** Figure 1 shows representative 3D DCE-MRI images covering the whole brain, and Fig. 2 shows the corresponding CBF maps. Overall, the CBF estimates were higher in grey matter (GM) than in white matter (WM). In a previous study using DCE-MRI, average CBF values were found to be 70 mL/min/g in GM and 20 mL/min/g in WM [2]. The average CBF values obtained in this study were slightly lower: 8 mL/min/g in WM and 30 mL/min/g in GM. To investigate if CBF underestimation could be related to the use of k-t PCA, we calculated the reconstruction error for signal intensity vs. time curves derived from the ICA, GM, and WM in the fully sampled 2D DCE-MRI data. As illustrated in Fig. 3, the reconstruction error should be relatively small at six-fold acceleration used in this study.

**DISCUSSION:** We have presented experimental verification that whole-brain CBF maps can be obtained from 3D DCE-MRI when accelerated with k-t PCA. Although the CBF values were underestimated by approximately a factor of two, they remained within the physiological range and, in agreement with the literature, CBF values were 3-4 times higher in GM than in WM. The simulations suggest that the CBF underestimation is not related to the k-t PCA reconstruction; the signal in the ICA is very accurately reproduced over the entire range of acceleration factors, implying that the reconstructed AIF is essentially error-free. Also the tissue curves (GM and WM) are also fairly well reconstructed, though the error tends to be higher for WM than for GM. We expect that the reconstruction error for GM and WM can be further decreased by using the recently proposed compartment-based k-t PCA technique [9]. However, we are still investigating automatic strategies for robustly identifying the different anatomical compartments.

The temporal resolution of 1.2 seconds per frame used in the current setup should be sufficiently high to allow CBF quantification. While some underestimation of CBF should be expected when using SVD-based deconvolution, it is more likely that the underestimation seen in this study is due to the effect of water exchange. For our 3D DCE-MRI sequence, the time delay between the SR preparation pulse and the center of k-space is approximately 600 ms, which is approximately five times longer than for conventional 2D DCE-MRI perfusion techniques [1,2]. In this case, CBF will be systematically underestimated [8]. This calls for use of a model-based deconvolution technique that incorporates the water residence time in the vascular space, or alternatively the k-space ordering needs to be changed such that the central part of  $k_y$ - $k_z$  space is sampled first. For the time being, we are dealing with the underestimation by globally scaling CBF according to the CBF of a reference tissue.

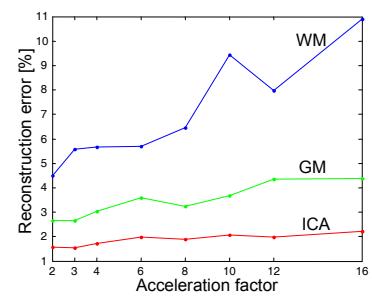


Fig. 3. Reconstruction error in WM, GM, and the internal carotid artery (ICA) as a function of the acceleration factor. The error is given by the mean deviation of the reconstructed signal intensity curve (over time) relative to the reference curve (i.e., fully sampled), normalized by the peak signal intensity of the reference curve. The arterial input function (AIF) was derived from the ICA.