Accelerated DCE MRI using constrained reconstruction based on pharmaco-kinetic model dictionaries

Sajan Goud Lingala¹, Yi Guo¹, Yinghua Zhu¹, Samuel Barnes², R. Marc Lebel³, and Krishna S Nayak¹

¹Electrical Engineering, University of Southern California, Los Angeles, California, United States, ²Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, California, United States, ³GE Healthcare, Calgary, Canada

Target audience: Researchers and clinicians interested in DCE-MRI.

Purpose/Introduction: DCE-MRI of the brain is a powerful technique to assess the blood brain barrier permeability, and other neurovascular parameters. Applications include characterizing tumors and assessing degenerative conditions such as multiple sclerosis and Alzheimer's disease. Recently, sparse sampling and image based spatio-temporal constrained reconstruction schemes have been proposed to improve DCE-MRI [1]. DCE-MRI ultimately involves pharmaco-kinetic (PK) parameter modeling as a final step to derive important PK parameters such as the transfer constant (K^{trans}) between plasma and extravascular extracellular space, and fractional plasma volume (v_p) [2]. In this work, we utilize prior knowledge derived from PK models as a temporal constraint during the recovery of concentration time profiles from under-sampled k space acquisitions. Our approach is inspired from model based compressed sensing schemes originally developed for relaxation parameter mapping [3][4].

<u>Methods:</u> Step 1: Using the Patlak PK model [2], we simulate concentration time profiles for a broad range of PK parameters (K^{trans} =0-0.4 min⁻¹ in steps of 0.001 min⁻¹, v_p =0-40% in steps of 1%). We utilize a population based arterial input function [5].

Step 2: Using the k-SVD training algorithm [6], we determine an over-complete dictionary of temporal basis functions (denoted as V_{rxN}) that sparsely represent the concentration time profiles generated in step 1. Here r denotes the number of bases in the dictionary, and N denotes the total number of time instances. For over-completeness, the dictionary size r=55 was chosen to be larger than the number of time points in typical DCE data (N=50). The sparsity parameter in keVD (k) was chosen such that the error in estimating the PK parameters was negligible. As depicted in Fig.1, while the concentration profiles modeled with a dictionary estimated with k=1 introduced a considerable bias in PK estimation, the dictionary generated with k=2 modeled the concentration profiles with high accuracy; the average PK parameter deviation from the true values were of the order of 10^{-15} min⁻¹, $10^{-13}\%$ respectively for K^{trans} , and v_p .

<u>Step 3</u>: We solve for the concentration profiles X_{MxN} (M-number of pixels; N- number of time frames) from the under-sampled k-t space data (b) using the following minimization:

 $\min_{\mathbf{X},\mathbf{U}} \|\mathbf{X} - \mathbf{U}\mathbf{V}\|_{2}^{2}$; such that $\|\mathbf{u}_{i}\|_{0} < 2$; $\|A(\mathbf{X}) - \mathbf{b}\|_{2}^{2} < \varepsilon$ (1)

The operator A models for Fourier under-sampling, and transformation between signal time intensity and concentration time profiles using knowledge of T_1 , M_0 , and flip angle maps obtained from calibration data; ϵ denotes the noise level in k-t space. The product $U_{Mxr}V_{rxN}$ denotes the 2-sparse projection of X in the dictionary V; note the sparsity constraint is defined on each row of U. We solve the above optimization by iterating between (a) updating U using an orthogonal matching sparse projection step [6], and (b) updating X in the Fourier domain. We iterate until a stopping criterion of $\|x_i - x_{i-1}\|_2^2 < 10^{-6}$ is achieved. Once the concentration time profiles are obtained, we estimate the PK parameters (K^{trans} , V_p) by fitting to the Patlak model. Analysis: We performed retrospective under-sampling experiments on single slice data from fully sampled acquisitions of two brain tumor patients (3T GE HDxt scanner, Cartesian T_1 weighted spoiled gradient echo, FOV: 0.9x1.3x7 mm³; 5 sec temporal resolution). For undersampling, we utilized a randomized golden angle 3DFT sampling scheme [7]. We compared our approach with an image reconstruction scheme that uses temporal total variation (TV) as constraint on the signal intensity time curves. The TV regularization parameter was empirically optimized.

Results: The PK maps derived from fully sampled data after 2-sparse projection on the overcomplete dictionary (\mathbf{V}) were in excellent agreement with PK maps derived directly from fully sampled data (R=1). This is attributed to the high accuracy of dictionary in modeling typical DCE concentration profiles (Fig. 1). The differences in the K^{trans} maps amongst the different schemes were visually insignificant. Fig 2 compares the \mathbf{v}_p maps. At an acceleration of R=20, the proposed dictionary based approach depict the regions of tumor, and small vessels in the \mathbf{v}_p maps very well in comparison to the PK maps derived from temporal TV based reconstruction (see arrows in Fig 2). In particular, temporal TV based maps were noisy and resulted in smearing of tiny features (small vessels, tumor boundaries), while the proposed dictionary approach was more robust to these artifacts.

<u>Conclusion:</u> We propose a pharmaco-kinetic dictionary based approach to constrain the recovery of concentration profiles from under-sampled DCE -MRI acquisitions. This approach leverages the small basis set required to characterize all possible time-intensity curves. It is extremely tolerant of noise and incoherent under-sampling artifacts as these are poorly described in the dictionary. It can be further improved by leveraging complementary benefits from spatial-sparsity constraints, and parallel imaging. The approach is flexible to be generalized to incorporate more parameter PK models such as the Extended Tofts model, two-compartment exchange model, and a study in this regard remains a future work.

References [1] R.M.Lebel et al, 71(2): 635-644, MRM 2014, [2] S.Sourbron et al, 26(8): 1004-1027, NMR in Biomedicine 2013, [3] M.Doneva et al, 64(4): 1114-11120, MRM 2010, [4] W.Li et al, 68: 1127-1134, MRM 2012, [5] G.J.Parker et al, 56: 993-1000, MRM 2006, [6] M.Aharon et al, 54 (11): 4311-4322, IEEE-Trans.Sig.Processing, 2006, [7] Y.Zhu et al, p4365, ISMRM 2014.

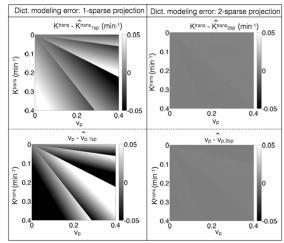


Fig.1: Bias in pharmaco-kinetic parameter estimation during dictionary modeling. Note the dictionary estimated using a sparsity level of 2 estimates the PK parameters with high accuracy resulting in extremely minimal biases in PK parameters.

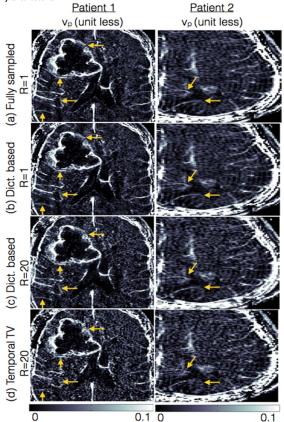


Fig.2: Comparisons of PK parameter (v_p) maps: Note in the accelerated regime, the subtle features such as small vessels, and tumor boundary regions to be depicted well with the dictionary based approach while considerably distorted in the temporal TV; see yellow arrows.