Iterative methods for fast reconstruction of undersampled dynamic contrast-enhanced MRI data

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Abstract. This paper introduces new variational formulation for reconstruction from subsampled dynamic contrast-enhanced DCE-MRI data, that combines a data-driven approach using estimated temporal basis and total variation regularization (PCA TV). We also experimentally compares the performance of such model with two other state-of-the-art formulations. One models the shape of perfusion curves in time as a sum of a curve belonging to a low-dimensional space and a function sparse in a suitable domain (L+S model). The other possibility is to regularize both spatial and time domains (ICTGV). We are dealing with the specific situation of the DCE-MRI acquisition with a 9.4T small animal scanner, working with noisier signals than human scanners and with a smaller number of coil elements that can be used for parallel acquisition and small voxels. Evaluation of the selected methods is done through subsampled reconstruction of radially-sampled DCE-MRI data. Our analysis shows that compressed sensed MRI in the form of regularization can be used to increase the temporal resolution of acquisition while keeping a sufficient signal-to-noise ratio.

Keywords: DCE-MRI, iterative reconstruction techniques, compressed sensing

1 Introduction

Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) is a method for quantification of parameters describing tissue perfusion. It is based on data

capturing spatiotemporal distribution of a contrast agent. Reconstruction of DCE-MRI data in general aims to reconstruct an image sequence from the raw k-space data. The result is subsequently used for pharmacokinetic modeling and perfusion-parameter estimation for each reconstructed-image voxel. In more recent years it is benefiting from both parallel imaging [2] and compressed sensing (CS) [3] due to their abilities to significantly reduce the number of acquired k-space data. The latter technique relies on adding sparsifying transformations to the acquired image sequence, such as the Fourier or the Wavelet transform [4], spatiotemporal finite differences [5], or combinations of these [6] and exploiting underlying temporal dynamics by employing principal component analysis (PCA) [8]. These data-driven sparsifying transforms assume that the image sequence can be represented by a matrix of low-rank or as a combination of low-rank and sparse components. Namely, this is the case of L+S model applied in [9], [10], however, these models presume global separability of the dynamic data and the background and such a separation is not generally applicable. A current improvement of this approach employs a patch-based decomposition [12] or applies PCA to obtain temporal basis functions from low-resolution data [8]. These are used as L1-penalized model-consistency constraints rather than imposing strict low-rank assumptions, while the model order needs to be determined heuristically. Generalizing CS approaches, variational models for image reconstruction allow to introduce different assumptions on an unknown object which weights regularization against data fidelity. A possible extension of the well-known total variation (TV) is the total generalized variation (TGV) functional [13], which balances between different orders of differentiation, enforcing linear or polynomial smoothness while still allowing sharp discontinuities [14]. Such a model was shown to be useful for still images [15] and highly parallelized CINE cardiac data [7]. This paper aims to assess selected approaches to reconstruct DCE-MRI image sequences from signal attained at small animal scanners, that have usually small parallelization (fewer elements of array coils) than clinical scanners and can have a smaller signal-to-noise ratio (SNR).

2 Models

2.1 TV regularization with pre-estimated temporal basis

Proposed variational formulation using total variation as a spatial image prior [1] combining temporal regularization using a PCA basis of the given data [8] (PCA TV) can be written as

$$\min_{u} \left\{ \sum_{t,i} \frac{1}{2} \| y_{t,i} - F_t S_i B_t u \|_2^2 + \lambda \| \nabla B_t u \|_1 \right\}, \tag{1}$$

where index t enumerates time frames, i receiver coils. In our study, non-Cartesian golden angle k-space sampling is assumed as one of the most popular compressed-sensing MRI acquisition method. Therefore, the Fourier transform for the time-frame t, denoted by F_t, is automatically assumed in its non-uniform variant [17].

All coil sensitivity maps S_i, i being a coil index, were estimated using the ESPIRiT algorithm proposed in [18]. Temporal basis functions at time frame t are denoted by B_t and are estimated using the PCA method from low-resolution data. Order of the basis is given to the model as an input parameter, $\|\cdot\|_1$ is the sparsity enforcing $L1$ norm and Frobenius norm $\|\cdot\|_2$ measured closeness to the measured k-space data y_i, t for time-frame t and coil i. Solution $x_t^* = B_t u$ for each time-frame t can be achieved using iterative technique Alternating Direction Method of Multipliers (ADMM) [16].

2.2 Low-rank plus sparse (L+S)

The L+S decomposition method [10] assumes that each time-frame x_t can be decomposed into a sum of two matrices, $x_t = l_t + s_t$, where matrix l_t represents the low-rank part of the signal and matrix s_t is assumed sparse in the sense of a linear transformation T (in this case temporal Fourier transformation). The overall formulation is

$$\min_{l,s} \left\{ \sum_{t,i} \frac{1}{2} \|y_{t,i} - F_t S_i (l_t + s_t)\|_2^2 + \lambda_l \|l\|_* + \lambda_s \|Ts\|_1 \right\}, \tag{2}$$

where $\|\cdot\|_*$ stands for the nuclear norm giving the sum of singular values and enforcing low rank. Contrasting with the previous model the temporal basis functions are estimated automatically.

2.3 ICTGV model

A possible extension of the TV regularization is employed in the ICTGV model proposed in [7]. This formulation regularizes data by weighting two TGV by infimal convolution

$$\min_{x} \left\{ \sum_{t,i} \frac{1}{2} \|y_{t,i} - F_t S_i x_t\|_2^2 + \lambda \mathrm{ICTGV}^2_{\beta_1,\beta_2,\gamma}(x) \right\}, \tag{3}$$

The ICTGV model itself was not implemented, but the reconstruction software AVIONIC written by its authors [7] was rather used for comparison with other methods.

3 Data acquistion and evaluation methods

Synthetic data were generated from a real DCE-MRI dataset (rat with brain tumor) [19]. 42 manually segmented regions of interests (ROIs) were assigned its reference perfusion parameters based on the values estimated from the real dataset as described in [19]. The concentration curves were constructed using the same pharmacokinetic model as the one used in [19]. 2D golden-angle radial-sampling k-space data were then constructed assuming a 2D SPGR acquisition

with TR = 15 ms, flip angle = 20 deg and acquisition time = 15 min, 128 samples per echo signal, a 4-element surface coil (sensitivities derived from the real recording), with additive corruption by Gaussian noise to average SNR = 26.7 dB (calculated as $SNR = 10 \log_{10}(P_{\text{signal}}/P_{\text{noise}})$, where P_{signal} is the mean power of the echo signals and P_{noise} the power of noise) to match the real data.

Real data originate from an in-vivo experiment with a normal Sprague-Dawley rat on a 9.4T Bruker BioSpin small animal scanner, 2D golden-angle SPGR acquisition with TR = 17 ms, flip angle = 25 deg, acquisition time = 14 min, 128 samples per echo signal, 4-element surface coil.

For both datasets, different levels of subsampling (skipping projections in the measured signal) were tested to explore the abilities of the models to reconstruct comparable intensity curves with higher temporal resolution. As a reference for evaluation of the algorithms, gridding [17] of fully-sampled data (i.e. 200 projections per time-frame) was used. In order to provide comparability between different models with various parameter settings, output curves were scaled to the $[0, 1]$ interval.

4 Results and discussion

Firstly, the selected models (L+S, PCA TV and ICTGV) were evaluated on a synthetic dataset. Image sequences were computed using various settings of parameters, levels of subsampling and ranks of temporal basis. Fidelity of reconstruction for a typical benchmark voxel (corresponding to a simulated tumour) can be found in Figure 1. It can be seen, that the nearest solution (in the sense of mean squared error) was achieved by the L+S model and the PCA TV reconstruction with a priori estimated basis functions of rank 3. The ICTGV method was not resulting in good fits to the reference curves, but it was the best at localising the position of the intensity peak.

Overall, it can be stated, that both L+S and PCA TV proved to be the best and the most robust (in terms of subsampling stability) models for synthetic data.

However, comparison on the real data showed a different situation. In order to avoid over-fitting of the models to the one specific experiment, rank 3 was assumed for both the PCA TV and the L+S model. Temporal basis functions were exploited from the regridded data and are shown in Figure 2.

The PCA TV model with estimation of the temporal basis of rank 3 led to a stable solution (in terms of mean squre error). It seems to allow to downsample (and thus increase the temporal resolution) up to the factor of 7 (see Figure 3). Surprisingly, the L+S model did not achieve as good results as for the synthetic data and the output intensity curves notably differed from the reference. The ICTGV model resulted in quite noisy, but with overall good fit to the reference. It is possible, that this behaviour can be improved by fine-tuning the reconstruction parameters. In selected regions, given the information about the temporal basis, the PCA TV model gave the best results for the measured data.

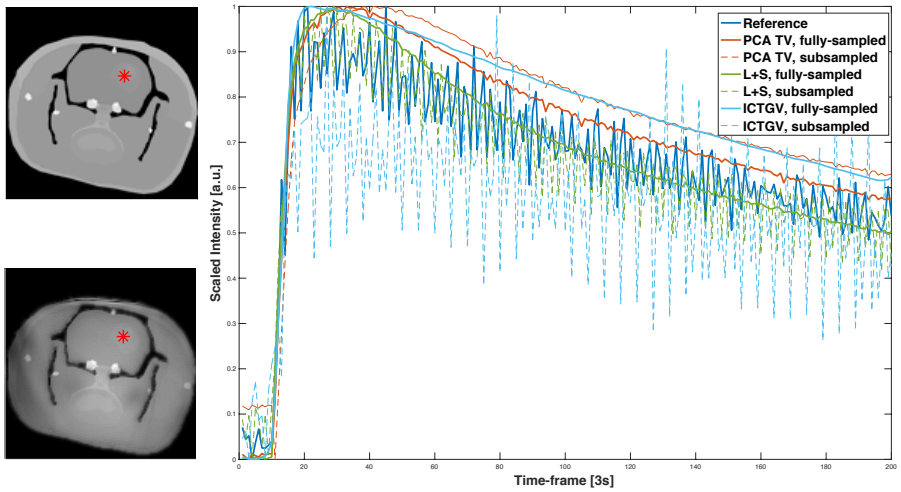

Fig. 1. One time-frame of the reference phantom image sequence(upper left) and the corresponding reconstructed time-frame (lower left) with output intensity curves for the marked pixel (tumour). Fully-sampled data use 200 radial projections per time-frame, subsampled reconstructions take 28 projections (i.e. 7x subsampling).

5 Conclusions

We have evaluated three different iterative methods for reconstruction of DCE-MRI data. The evaluation was done on both generated and real data, where it showed quite different results. It can be stated that models assuming a low-rank temporal basis (smaller than 3) were outperformed by those without this presumption or with the PCA-TV model working with a priori information about the character of the temporal dynamics. This can be due to the inability of a small basis to correctly describe the dynamics of the data or due to a lower SNR and fewer array-coil elements of a small-animal NMR scanner compared to clinical NMR scanners. In our experiments, PCA TV was the best reconstructoin method in terms of image quality and computational speed (enabling increasing time resolution up to the factor of 10). To draw stronger conclusions, the evaluation will be extended to a comparison of the reference and reconstructed data on the level of estimated perfusion parameters for various pharmacokinetic models.

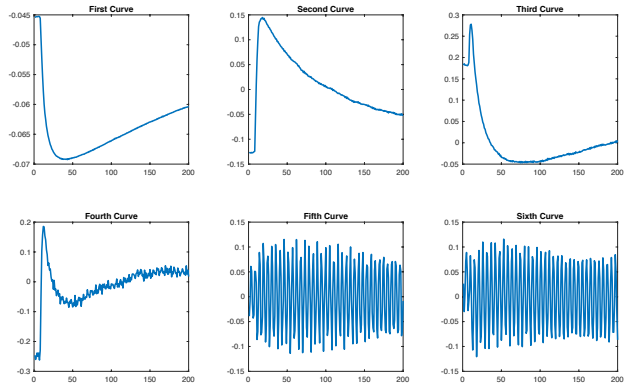

Fig. 2. Temporal basis functions of the real data ordered by significance

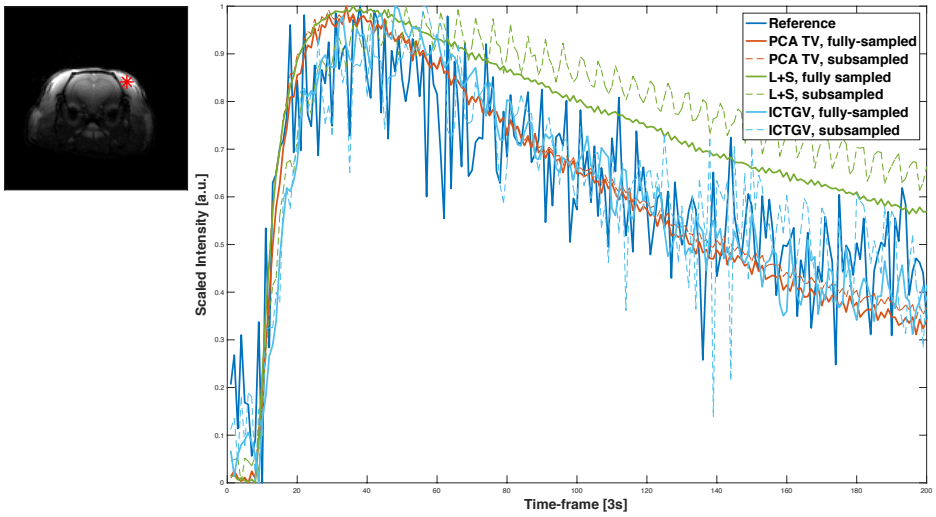

Fig. 3. Image reconstruction of real data with signal intensity curves of different methods in marked pixel (temporalis muscle).

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