Spline Temporal Basis for Improved Pharmacokinetic Parameter Estimation in SENSE DCE-MRI

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Purpose: Dynamic Contrast Enhanced (DCE)-MRI exhibits stronger sparsity than the static MRI problem due to temporal correlation. The dynamic object's underlying spatio-temporal subspace can be estimated via low-rank methods [1]. However, these methods do not explicitly leverage the temporally smooth characteristics of concentration agent time series in DCE-MRI. This work uses a predefined low-rank spline temporal basis for reconstructing a DCE-MRI image, followed by pharmacokinetic parameter estimation. With Compressed Sensing pseudo-random undersampling, we can design short frames to retain fine temporal information and reconstruct more accurate voxel and contrast agent concentration time series. We combine this low-rank model with parallel imaging and spatiotemporal regularization to achieve aggressive undersampling yet accurate pharmacokinetic parameter estimation.

Methods: Let N_f denote the number of frames for the desired temporal resolution and experiment duration and N_p the number of voxels. We parameterize the object with only N_t temporal basis frames, s.t. $N_f / N_t \in \mathbb{N}$. The proposed model has only $N_p N_t$, rather than $N_p N_f$, degrees of freedom for x, which can be estimated: $\hat{x} = \underset{x}{\operatorname{argmin}} \frac{1}{2}||y - \mathbf{PTFS}x||_2^2 + \lambda_s R_s(x) + \lambda_t R_t(x)$. The image coefficients, x, describe spatial values at each temporal basis frame time index. **S** is a stack of sensitivity encoding matrices for each temporal basis frame, **F** executes the DFT for each coil and temporal basis frame, **P** is the k-space sampling matrix, and **T** interpolates the temporal basis coefficients to achieve N_f frames. $R_s(x)$ is an edge-preserving spatial regularizer and $R_t(x)$ provides additional temporal smoothing as a quadratic temporal regularizer. We selected quadratic B-splines for their shift invariance so that **T** can be efficiently implemented with convolution. B-splines have been investigated [2-4] for characterization of perfusion functions in DCE MRI and SPECT. The proposed model is distinct from the conventional dynamic reconstruction approach in which inter-frame correlation is induced solely by the temporal regularizer, equivalent to choosing a rectangular temporal basis, whose functions have non-overlapping support. This model also differs from other methods with temporal splines [5] in that Fourier encoding is performed on the image coefficients rather than the full dynamic object, for a factor of N_f / N_t fewer FFTs in each application of the system matrix.

Results: The spline temporal basis model was tested on a simulated breast tumor with rapid contrast agent enhancement (K^{trans} = 2 min^{-1}, k_{ep} = 6 min^{-1}) over 4 min. Perfusion functions were based on population-based averages and pharmacokinetic parameters were estimated with variable projection [6]. $R_s(x)$ was chosen to be a Fair potential of finite-differences. We used a spline temporal basis function of width 7.5 s, for an undersampling factor of 20 given a TR of 4.6 ms, image size of 156x212, and a variable density Poisson disk sampling pattern. The model was compared to a "wide" rectangular basis function with 7.5 s long frames and a "skinny" rectangular basis function with 2.5 s frames and 60x undersampling. The cost function for all models was minimized using conjugate gradient initialized with datasharing. Table 1 lists the resulting k_{ep} and K^{trans} estimates and computation times. The computation times indicate seconds until k_{ep} and K^{trans} variation remained within 1% of the final estimated value.

The proposed spline model was also applied to free-breathing abdominal DCE MRI data from a 6.5 year old male patient with an abdominal mass. The data was acquired on GE 3T MR750 scanner with a 3D modified SPGR sequence with Butterfly motion navigation [7] and a VD Rad sampling pattern [8] with TR of 3.7 ms, flip angle 15°, voxel size of 1.1x1.1x0.9 mm. The 2D slice size was 156x 100 with 18 frames of 7.6 seconds each, resulting in an undersampling factor of 7.6. Sensitivity maps were estimated with [9] and motion compensation was added to the proposed spline basis model via soft respiratory gating [10], using Butterfly navigators. Fig. 3 shows a representative frame from the spline basis estimate. Fig. 2 compares a voxels' time series estimated from different temporal basis models.

Table 1.

	datasharing	spline basis	wide rects	skinny rects
k_{ep} % error (computation time)	9.0	0.67 (915 s)	12.7 (599 s)	1.5 (1125 s)
K^{trans} % error (computation time)	9.4	0.52 (256 s)	10.8 (801 s)	0.01 (1664 s)

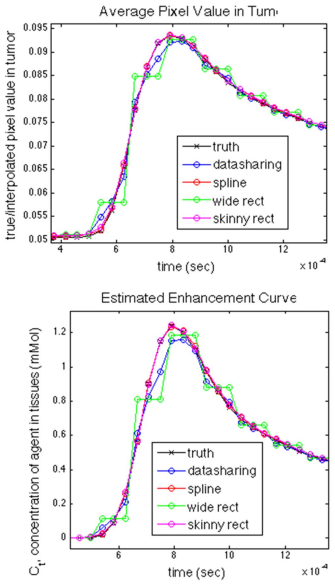

Figure 1. (top) Estimated voxel value during bolus arrival for datasharing, and CG solutions of temporal spline and rectangle models, (bottom) Estimated concentration agent time series during bolus arrival .

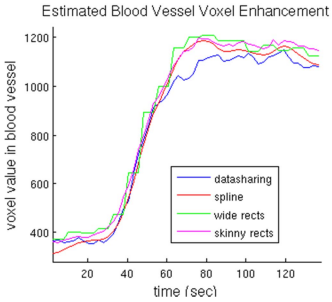

Figure 2. Dynamic voxel value for small abdominal blood vessel, estimated using different temporal basis models.

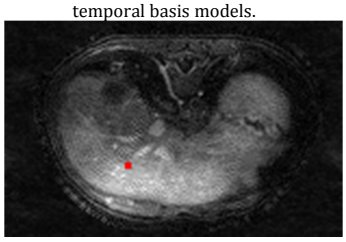

Figure 3. Final frame of spline basis estimate for experimental data. The red pixel marks the small blood vessel whose time series is shown in Fig. 2.

Discussion: The spline basis and skinny rectangular basis yielded lower errors for k_{ep} and K^{trans} than wide rectangles and datasharing by using finer temporal information. However, the spline basis model implementation arrives at its final solution much quicker than the skinny rectangle basis because it does not rely on temporal regularization alone to share information across frames. The proposed method was verified for experimental data, producing qualitatively improved voxel time series compared to datasharing and rectangular temporal bases.

Conclusion: The proposed spline temporal basis model permits faster and more accurate pharmacokinetic parameter estimation than datasharing and the conventional rectangular temporal basis. Supported in part by NIH grants P01 CA87634 and P01 CA059827.

References: [1] JP Halder et al. ISBI 2010; pp 1052-1055. [2] G Adluru et al. MRM 2007; 57:1027-36. [3] M Jerosch-Herold et al. Med Phys 2002; 29:886-97. [4] TE Nichols et al. IEEE TMI 2002. 21:395-404. [5] M. Filipovic et al. MRM 2011; 65:812-22. [6] C. Yang et al. MRM 2007; 58:1266-75. [7] JY Cheng et al. MRM 2012; 68:1785-97. [8] JY Cheng et al. ISMRM WDSIR 2013. [9] MJ Allison et al. IEEE TMI 2012; 32: 556-64. [10] T Zhang et al. JMRI 2013. [11] ZP Liang. ISBI 2007; pp 988-991.