ACCELERATING MR PARAMETER MAPPING USING MANIFOLD RECOVERY

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Introduction:

Magnetic resonance (MR) parameter mapping is a very useful quantitative analysis tool in disease diagnosis [1]. However the application of parameter mapping is limited by its long data acquisition time. To address this problem, several methods have been proposed to reduce data acquisition time [2-15]. In this paper, we model MR parameter mapping as a problem to recover a parametric manifold. A novel method is proposed to recover the manifold from undersampled data based on the parametric model. The method iteratively alternates between reconstructing the image series and recovering the parameters. The method is applicable to other quantitative imaging applications beyond MR parameter mapping.

Method:

In MR parameter mapping, the *m*th reconstructed image $\mathbf{I}_m$ is directly related to the *m*th data acquisition $\mathbf{d}_m$ that is formulated as: $\mathbf{d}_m = \mathbf{F}_m\mathbf{S}_m\mathbf{I}_m + \mathbf{n}_m$, where $\mathbf{F}_m$ is the Fourier operator with a specific undersampling pattern at *m*, $\mathbf{S}_m$ is a diagonal matrix representing the sensitivity map, and $\mathbf{n}_m$ denotes k-space noise. The image series $\mathbf{I}_m$ can be modeled with parameters ρ and θ as: $\mathbf{I}_m = \mathrm{P}_m(\theta)\rho$, where $\mathrm{P}_m(\theta)$ is a parametric function of θ, and also specifies scanning setting at the *m*th acquisition, and ρ is the parameter linearly related to the image. Both θ and ρ are the desired parameter that can be solved by the optimization problem: $\{\hat{\theta},\hat{\rho}\} = \arg\min_{\theta,\rho} \sum_{m=1}^{\mathrm{M}} \|\mathbf{d}_m - \mathbf{F}_m\mathbf{S}_m\mathrm{P}_m(\theta)\rho\|_2^2$. **Initialization: Image reconstruction (convex)**: We first reconstruct the image series by solving [16]: $\hat{I}_m = \arg\min_{I_m} \|\mathbf{d}_m - \mathbf{F}_m\mathbf{S}_m I_m\|_2^2 + \lambda \mathrm{R}(I_m)$, where $\hat{I}_m$ is the reconstructed image, λ controls the weight of regularization. Total variation is used as the regularization term. **Step 1: Projection onto manifold**: The initialized images are projected onto a closest manifold using $\mathrm{P}_\Omega(|\hat{\mathbf{I}}|) := \mathrm{argmin}_{\mathbf{I}}\left\{\left\||\hat{\mathbf{I}}| - \mathbf{I}\right\|_2^2 : \mathbf{I} \in \Omega\right\}$, where Ω is a manifold with parameter θ and ρ. $\mathbf{I}$ includes a series of images $\mathbf{I}_m$ at all *m*, $|\hat{\mathbf{I}}|$ denotes the operation of taking the magnitude of $\hat{\mathbf{I}}$. The projection is equivalent to finding the parameters: $\{\hat{\theta},\hat{\rho}\} = \arg\min_{\theta,\rho} \sum_{m=1}^{\mathrm{M}} \left\||\hat{\mathbf{I}}_\mathbf{m}| - |\mathrm{P}_m(\theta)\rho|\right\|_2^2$. **Step 2: Projection onto the subspace with data consistency**: The updated images series on the manifold are further transformed into k-space to enforce the data consistency constraint. Specifically, the image series are projected onto a subspace by maintaining the updated k-space data at the unacquired locations and replacing the k-space data at the acquired locations using a combination of the updated value and measurement [9]. The above two steps are then repeated iteratively until the result converges which is guaranteed.

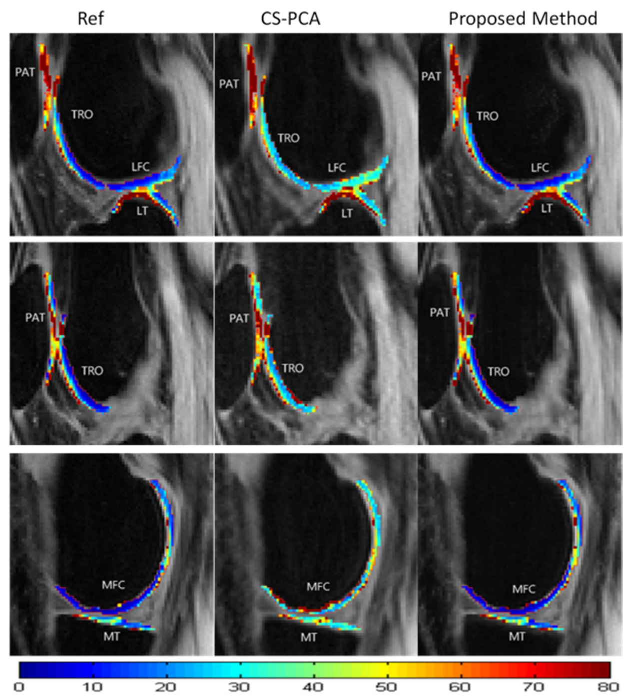

Fig. 1. Cartilage T1ρ map overlaid on the anatomic image.

Results:

The proposed method was evaluated using T1ρ mapping data from an in-vivo knee cartilage experiment. The T1ρ cartilage data was acquired from a GE Healthcare 3.0 T scanner with 8 coils using MAPS pulse sequence. The scanning parameters are: TSL = 0/2/4/8/12/20/40/80 ms, field of view = 140 mm, matrix size PE×FE×Echo×Slice = 128×192×8×28, slice thickness = 4mm, spin-lock frequency = 500Hz. Reduction factor of this experiment was 3. The proposed method was compared to compressed sensing based method which uses principal component analysis as a linearization measurement that represents the nonlinear signal model by linear combinations of training data (CS-PCA) [3]. Figure 1 is the experiment result of T1ρ knee cartilage between CS-PCA and proposed method. At ROI, T1ρ parameter map estimated from proposed method is more accurate than that from CS-PCA. Figure 2 provides quantitative analysis of T1ρ values at six regions of interest in knee cartilage. Compared to CS-PCA, the proposed method improves the T1ρ accuracy by approximately 9%.

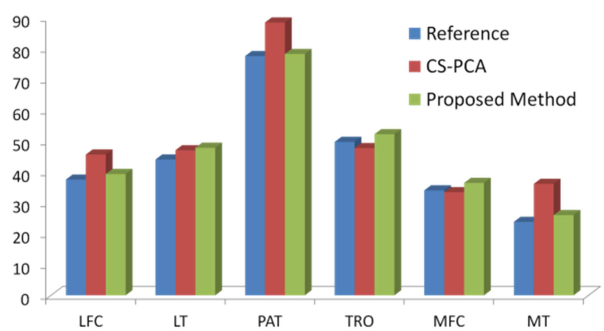

Fig. 2. Quantitative analysis of T1ρ knee cartilage

Conclusion:

In this paper, a novel manifold recovery method is proposed for MR quantitative imaging. Compared to the existing methods, the proposed method enforces the parametric model by projecting the reconstruction to its closest manifold and enforces data consistency at the same time. Both simulation and experimental results show the potential of highly accelerated quantitative imaging by the proposed method.

References: [1] L. M. Cheng, et al., JMRI, 36:805-824, 2012. [2] L. Feng, et al., MRM 65: 1661-1669, 2011. [3] J. V. Velikina, et al., MRM, 70: 1263-1273, 2013. [4] C. Huang, et al., MRM, 67: 1355-1366, 2012. [5] F. H. Petzschner, et al., MRM 66: 706-716, 2011. [6] Y. Zhou, et al., ISMRM: 1208, 2014. [7] M. Doneva, et al., MRM, 64: 1114-1120, 2010. [8] W. Li, et al., MR., 68:1127-1134, 2012. [9] Y. Zhu, et al., MRM, in press, 2014. [10] T. Zhang, et al., MRM, in press, 2014. [11] B. Zhao, et al., MRM, in press, 2014. [12] T. J. Sumpf, et al., JMRI, 34: 420-428, 2011. [13] J. P. Haldar, et al., ISBI: 266-269, 2009. [14] B. Zhao, et al., TMI, 33: 1832-1844, 2014. [15] X. Peng, et al., MEP, in press, 2014. [16] B. Liu, et al., ISMRM: 3154, 2008.