Accelerating T1-rho Cartilage Imaging Using k-t ISD with Locally-Adapted Thresholding and JSENSE

Yihang Zhou[1], Valentina Pedoia[2], Julien Rivoire[2], Yanhua Wang[1], Dong Liang[3], Xiaojuan Li[2], and Leslie Ying[1]

[1]*Department of Biomedical Engineering, Department of Electrical Engineering, The State University of New York at Buffalo, Buffalo, NY, United States,* [2]*Department of Radiology and Biomedical Imaging, University of California at San Francisco, San Francisco, CA, United States,* [3]*Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, Shenzhen, Guangdong, China*

INTRODUCTION:

T1-rho ($T_{1\rho}$) cartilage imaging provides information associated with cartilage matrix changes and enables the possibility of early stage cartilage degeneration detection [1]. However, acquisition of multiple echoes makes the $T_{1\rho}$ acquisition process time consuming. Compressed sensing (CS) is a promising technique that accelerates the acquisition speed through undersampling the k-space below the Nyquist rate [2]. When integrated with parallel imaging (pMRI) [3, 4], even higher accelerations can be achieved [5, 6]. The application of both CS and pMRI in $T_{1\rho}$ cartilage imaging could potentially reduce the acquisition time. In this study, we investigate the feasibility of an advanced CS-pMRI method in accelerating the $T_{1\rho}$ quantification in cartilage imaging without compromising the accuracy.

METHODS:

Imaging techniques: The $T_{1\rho}$ MR images of in-vivo human knee were acquired using a transmit - receive 8 channels knee coil on 3.0-T scanner (GE Healthcare) with a MAPS pulse sequence (time of spin-lock (TSL) = 0/2/4/8/12/20/40/80ms; spin-lock frequency: 500Hz; matrix size PE × FE × Echo × Slice = 128×192×8×28; field of view = 140mm; slice thickness = 4mm). To obtain the reduced acquisition retrospectively, the k-space data was randomly undersampled along the phase encoding direction at each echo time. Different sampling patterns are used at different TSLs. The central 32 lines of the k-space are fully sampled at all TSLs.

Reconstruction methods: We combine an advanced CS-based reconstruction technique, k-t ISD [7] with locally-adapted thresholding (named k-t LISD), and an advanced parallel imaging technique, JSENSE [8], to reconstruct the image sequence from the undersampled k-space data acquired at different TSLs. The fully sampled central 32 lines of the k-space at all times are used to estimate the initial coil sensitivity maps. The reconstruction process then alternates iteratively between k-t LISD for reconstruction of the image sequence and JSENSE for sensitivity estimation. The flowchart of the proposed method is shown in Fig. 1. Here, in k-t LISD, principle components analysis (PCA) is employed as the sparsifying transform along the temporal direction [9, 10]. In this sparse x-PCA space, the support (i.e., location of significant elements) is assumed to be $S = T \cup \Delta$, where T is the known part of the support S with a size $|T|$ and Δ is the unknown part with a size $|\Delta|$. With the known support T in CS reconstruction, we are able to restrict all the candidate sparse solutions to a smaller subspace which includes the support T by solving a truncated ℓ_1 minimization problem: $\min \|\boldsymbol{\rho}_{\Delta}\|_1$, s.t. $\|\mathbf{d} - \mathbf{F}_x \mathbf{P}\boldsymbol{\rho}\|_2 \le \varepsilon$, where $\mathbf{d}$ is the undersampled k-space data, $\mathbf{F}_x$ denotes the Fourier transform along frequency encoding direction, and $\mathbf{P}$ represents the PCA. Since the support information is not known a priori, we detect the support iteratively in the x-PCA domain from the current reconstruction. Instead of using a global threshold as in [7], we apply different thresholds to different pixels according to the maximum intensity at this pixel. Specifically, the support is updated by thresholding the reconstructed signals in the x-PCA domain using spatially adaptive thresholds $\mu\tau_i$, where $\tau_i = \max(|\tilde{\boldsymbol{\rho}}_i|)$ for pixel i and μ is a weighting parameter that decreases with iterations. Such locally-adapted thresholding can improve the quantification accuracy in compartments with low SNR such as MT and MFC.

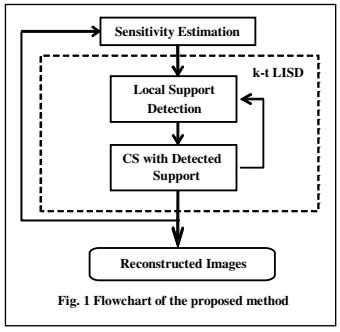
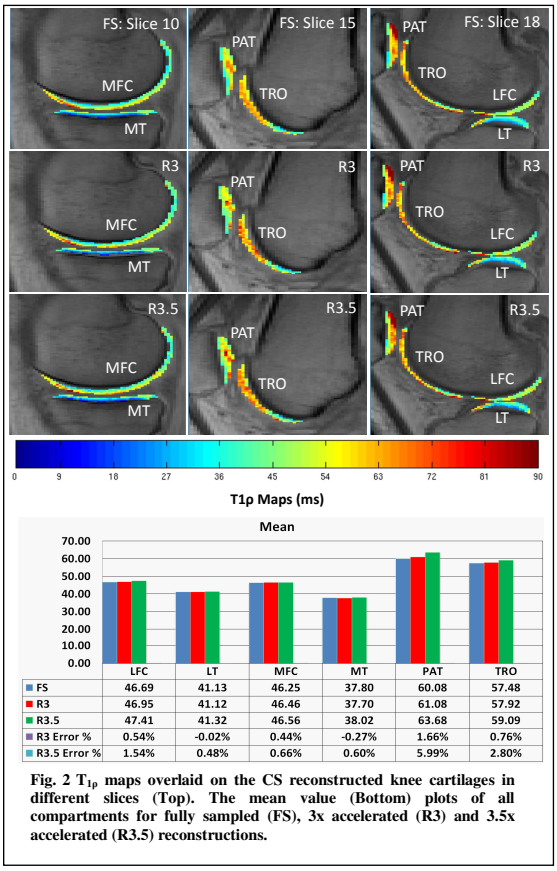


Fig. 1 Flowchart of the proposed method

Data analysis: The cartilage were segmented semi-automatically in six compartments (LFC: lateral femoral condyle; LT: lateral tibia; MFC: medial femoral condyle; MT: medial tibia; Pat: patella; T: trochlea) using a program developed in-house. The $T_{1\rho}$ map was reconstructed by fitting the $T_{1\rho}$-weighted images pixel by pixel. Quantification was compared between full sampled and under-sampled images using different acceleration factors.

RESULTS:

The reconstruction results from different slices with accelerations of 3 and 3.5 are shown in Fig. 2. The $T_{1\rho}$ maps are overlaid with the reconstructed cartilage images. It can be seen that the reconstructed $T_{1\rho}$ maps show good agreement with that from full acquisition in all compartments. The larger errors in TRO and PAT are primarily due to the fact that patella and trochlea compartments have a relatively low SNR. When applying k-t LISD, as the threshold is adapted pixel-by-pixel, some of these low contrast features are suppressed as noise while some noise is detected as low-contrast signals. However, as can be seen, these pixels are outliers. The overall $T_{1\rho}$ maps from acceleration 3 and 3.5 are consistent with that from full acquisition. This can be better appreciated in the statistical analysis. The mean values and the error percentage for all compartments of the accelerated reconstructions are calculated and plotted in Fig. 2 bottom. It can be seen that the overall error percentage is low (<2%) in all compartments for both accelerations of 3 and 3.5, except for PAT where the error is slightly higher with 1.66% for R3 and 5.99% for R3.5. The error in LT, MFC and MT are negligible (<1%). The mean error for all compartments is only 0.52% for 3x acceleration and 2.01% for 3.5x acceleration.



	LFC	LT	MFC	MT	PAT	TRO
FS	46.69	41.13	46.25	37.80	60.08	57.48
R3	46.95	41.12	46.46	37.70	61.08	57.92
R3.5	47.41	41.32	46.56	38.02	63.68	59.09
R3 Error %	0.54%	-0.02%	0.44%	-0.27%	1.66%	0.76%
R3.5 Error %	1.54%	0.48%	0.66%	0.60%	5.99%	2.80%

Fig. 2 $T_{1\rho}$ maps overlaid on the CS reconstructed knee cartilages in different slices (Top). The mean value (Bottom) plots of all compartments for fully sampled (FS), 3x accelerated (R3) and 3.5x accelerated (R3.5) reconstructions.

CONCLUSION:

Our preliminary results demonstrate the feasibility of accelerating $T_{1\rho}$ quantification by factors of 3 and 3.5 using CS combined with parallel imaging. The in vivo reproducibility of cartilage $T_{1\rho}$ quantification was reported to be approximately 5% [11]. The fitting error is significantly reduced by the proposed k-t LISD with JSENSE method compare with the earlier work reported [12] to combine CS with PI (ARC) without using correlation between images from different TSLs. The $T_{1\rho}$ quantification calculated from accelerated acquisition using proposed reconstruction shows good agreement with the one without acceleration in all compartments with a negligible error percentage. Further study will explore using prospective sampling in in vivo human studies and the clinical significance.

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