Accelerating fat fraction measurements in muscular dystrophy using compressed sensing and parallel imaging

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Target audience : Physicists and clinicians interested in the practical use of compressed sensing to accelerate skeletal muscle examinations.

Introduction : Undersampled acquisition of MR data with constrained non-linear reconstruction[1] can potentially save scanner time and improve patient compliance, and would be useful for the measurement of fat fractions derived from chemical shift imaging to assess longitudinal change in muscular dystrophy. A number of abstracts have shown qualitatively promising reconstructions combining compressed sensing and parallel imaging[2,3], but there have been no prospective quantitative analyses. This study optimizes and assesses the quality of reconstruction of chemical shift separated images from prospectively undersampled 3D data using a custom pulse sequence compared to fully sampled data in muscular dystrophy patients to determine any systematic or random error in the fat fraction introduced by the undersampling.

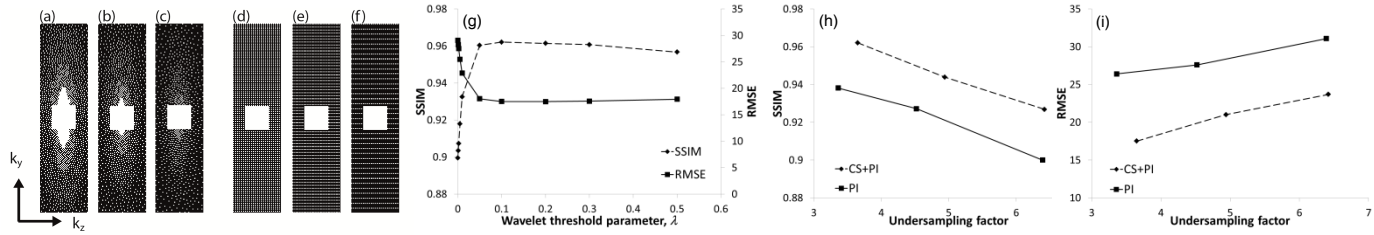

Figure 1 : (a) 3.65×, (b) 4.94× and (c) 6.42× phase-slice undersampling schemes. (d-f) coherent equivalent undersamplings for PI alone. (g) finding optimal λ for a 3.65× undersampling by optimizing SSIM and RMSE. (h),(i) Comparison of SSIM and RMSE for reconstructions with CS+PI and PI alone.

Methods : Fully-sampled and prospectively undersampled data were acquired on a 3T Philips Achieva using a custom 3D gradient echo pulse program with variable density Poisson disk undersampling[4] with a central fully-sampled region of 24 x 24 for coil calibration: three prospective undersamplings were acquired, with data reductions of 3.65×, 4.94× and 6.42× (Figure 1a-c). A 6 channel cardiac coil (Philips, Best) was used for signal reception and raw data was acquired separately for each coil element. A 256×190×48 matrix (resn: 1.25×1.0×5mm), and three gradient echoes were acquired, TR/TE/FA = 10ms/4.40,5.18,5.96ms/3°. The fully sampled acquisition time was 273s and the undersampled acquisition times were 75s, 55s and 43s. 8 ambulant patients with a genetic diagnosis of Becker muscular dystrophy were recruited under local ethical approval and informed consent. Separate imaging blocks were acquired for calf and thigh muscles with the read direction left-right. The data were reconstructed taking advantage of both parallel imaging and compressed sensing (CS+PI) using the ESPIRiT approach as advocated in ref. 5, where we minimize,

$$\sum_{i=1}^{N}\left\|y_i - DFS_i m\right\|_2^2 + \lambda\left\|\Psi m\right\|_1^2$$

where y_i is the acquired data for coil i (of N coils), m is the image space, S_i are the coil sensitivities, F is a Fourier transform operator, D is an operator that selects only those locations where data has been acquired (to match y_i), and Ψ is the sparsifying transform, here a Daubechie 4 wavelet. Note that this formulation only uses the first eigenvalue map. Equivalent coherent undersamplings were acquired for PI reconstruction alone (GRAPPA), 3.36× for all subjects and 4.52× and 6.39× for 3 subjects (Figure 1d-f).

Table 1 : Mean fat fractions for 8 patients on per ROI basis (%)

Region of interest	Full	3.65x	4.94x	6.42x
Tibial bone marrow	98.8	98.7	98.7	98.8
Biceps femoris long head	76.5	76.8	76.9	76.8
Semimembranosus	68.5	68.6	68.9	68.9
Semitendinosus	60.1	60.2	60.1	60.0
Vastus lateralis	50.2	49.8	50.5	51.0
Vastus intermedius	48.4	48.6	49.3	49.3
Medial gastrocnemius	47.8	48.0	47.9	48.0
Rectus femoris	34.2	33.8	33.2	33.7
Lateral gastrocnemius	29.8	29.4	29.6	29.9
Soleus	16.0	15.7	15.5	15.8
Sartorius	11.7	11.6	12.2	11.4
Tibialis anterior	6.6	6.6	6.4	6.6

The optimal wavelet thresholding coefficient, λ, was determined by minimizing the RMSE and maximizing the structural similarity index (SSIM)[6] subject to an intensity threshold mask on the fully-sampled image to exclude areas of noise. The chemical shift separation was performed using the graphcut algorithm of Hernando with a 6-component fat model[7]. Using ImageJ (NIH), regions of interest were drawn on 10 axial sections on the fully sampled left leg on the areas listed in Table 1. The mean fat fraction was evaluated and averaged for each anatomical area on the fully and undersampled reconstructions. 920 pairs of data were evaluated for each undersampling to derive Bland-Altman parameters of bias and reproducibility.

Results and Discussion : From Figure 1g, the optimal λ was found to be 0.1 and this was found to be consistently true across all measurements and undersamplings. The SSIM was consistently found to be higher, and RMSE found to be lower with CS+PI than with PI alone (Figure 1h and 1i), indicating more faithful reconstruction. Figure 2 shows that image quality of the fat fraction map and total signal (needed for ROI marking) is very good for all CS+PI undersampled data, whereas that of PI alone is subject to noise breakthrough and artifact, hindering ROI delineation. The Bland-Altman analysis of ROIs (Figure 3) shows no net bias between the two fat measurements: -0.02%, 0.07% and 0.14% for the 3.65×, 4.94× and 6.42× undersampling respectively which are not clinically significant and a reproducibility of 1.57%, 2.17% and 2.42% between the undersampled and fully sampled reconstructions. For 3.36× PI only reconstruction the bias was 0.15% and the reproducibility 2.79%, 1.8 times worse than the equivalent CS+PI reconstruction. Paired t-testing for ROIs shows no systematic differences in fat fraction (Table 1).

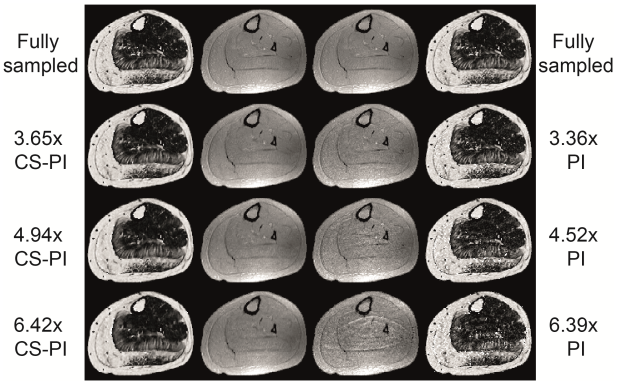

Figure 2: Comparison of CS-PI and PI reconstructions for fat fraction maps and total (fat+water) maps used for ROI delineation

Conclusion : The fidelity of quantitative chemical shift separation accelerated using Poisson Disk undersampling and reconstruction combining parallel imaging and compressed sensing is very good, better than PI alone and acceptable for clinical studies.

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References : [1] Lustig *Magn. Res. Med.* 2007; 58: 1182, [2] Sharma *Magn. Res. Med.* 2012 epub, [3] Wiens *Magn Res Med* 2013 epub, [4] Cook *ACM Trans Graph* 1986;5:51, [5] Uecker *Magn. Res. Med.* 2013 epub; [6] Wang IEEE *Trans Image Process* 13:600, [7] Hernando *Magn. Res. Med.* 2010; 63: 79.

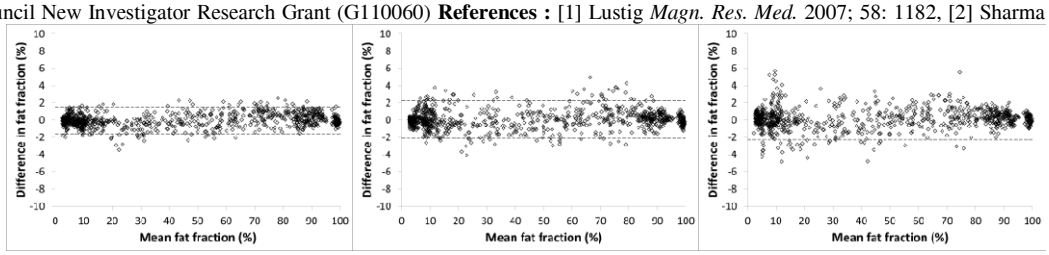

Figure 3: Bland-Altman plots comparing the fat fractions reconstructed by CS-PI from the (left) 3.65×, (middle) 4.94× and (right) 6.42× undersamplings respectively.