Optimized 3D Dictionary-Learning Compressed-Sensing Reconstruction for Quantitative Sodium Imaging in the Skeletal Muscle

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Synopsis

Quantitative sodium MRI could be a sensitive tool for therapy monitoring in muscular diseases. However, sodium MRI suffers a low signal-to-noise ratio (SNR). 3D dictionary-learning compressed-sensing (3D-DLCS) enables SNR improvement and acceleration of sodium MRI, but it is dependent on parameterization. In this work a simulation based optimization method for 3D-DLCS is presented, which finds the most suitable parameters for 3D-DLCS in the context of sodium quantification. The method is applied in an in vivo study to quantify sodium in the skeletal muscle. The optimized 3D-DLCS yields a lower quantification error than the reference reconstruction method (Nonuniform FFT).

Introduction

Tissue sodium concentration (TSC) is potentially a useful measure for muscle tissue constitution and could be an impactful tool for therapy monitoring in muscular diseases[1,2]. Sodium MRI (^{23}Na-MRI) is a non-invasive method to quantify TSC[2]. However, ^{23}Na-MRI suffers from low signal-to-noise ratio (SNR) due to the low gyromagnetic ratio, low in vivo concentration and fast relaxation times of sodium. Compressed sensing[3] (CS) based approaches[4,5] have been shown to be very effective to improve SNR for ^{23}Na-MRI. Although these iterative methods are dependent on parameterization. In particular sparsity weighting is still a frequently discussed topic and there is no gold standard for assessment. In this work, a simulation based assessment method of CS reconstructions for the application of TSC quantification is proposed. The method is applied in an to vivo study to optimize parameters for reconstruction with 3D dictionary-learning compressed-sensing[6] (3D-DLCS). Quantitative in vivo TSC maps are reconstructed, which are undersampled to decrease measurement time and facilitate clinical applicability.

Methods

The assessment approach is based on simulation of an analytical phantom of the human calf (see Fig. 1). Different tissue types are simulated with assigned concentrations and T2* relaxation times corresponding to literature[6,7] (fat tissue: 10 mMol/L, blood vessels: 80 mMol/L, muscle tissue: 12-25 mMol/L, see Figure 1). Four reference tubes (10, 20, 30, 40 mMol/L) are simulated for normalization and complex white Gaussian noise is added to match the SNR of the in vivo measurements. The assessment method refers to the phantom as ground truth (GT) and uses a region-of-interest (ROI) based determination of the TSC. The normalized maximum (mxE_{norm}) and mean error (mE_{norm}) w.r.t. the GT and the normalized mean standard deviation (mSD_{norm}) are evaluated inside each ROI. An error metric (em) is applied to assess reconstructions:

$$em = \sqrt{(mxE_{norm})^2 + (mE_{norm})^2 + (mSD_{norm})^2} = \sqrt{\max\left(\frac{\overline{X}_i - \overline{X}_{i,ref}}{\overline{X}_{i,ref}}\right)^2 + \mathrm{mean}\left(\frac{\overline{X}_i - \overline{X}_{i,ref}}{\overline{X}_{i,ref}}\right)^2 + \left(\frac{\sigma_i}{\overline{X}_{i,ref}}\right)^2}, i \,\epsilon\, [1, \#ROI],$$

where X_i, σ_i, are the mean intensity and SD of a chosen ROI in the reconstructed TSC map and $X_{i,ref}$ the mean intensity in the same ROI of the GT. em weights the SD against the quantification errors to find the result with lowest uncertainty (low mSD_{norm}) without over smoothing (low mE_{norm}, mxE_{norm}). The assessment method uses em to find an optimized sparsity weighting factor λ_{em}. To emulate multiple acquisitions, N acquisitions with different white Gaussian noise distributions are simulated and reconstructed for every λ. The reconstruction with the lowest em score determines λ_{em} for the dataset. Simulations: The analytical calf phantom (see Fig. 1) was simulated with different undersampling factors (USF: 1, 3.2, 4.4, 6.7) and reconstructed with 3D-DLCS and nonuniform FFT with a Hamming filter (hNUFFT) for reference. Values for λ_{em} were determined for each USF (see Fig. 2) by the proposed method for optimized 3D-DLCS (optDLCS). Parameters: block-size: 3x3x2, dictionary size: 300. In vivo study: ^{23}Na-MRI was conducted on a 3-T whole body system (MAGNETOM Skyra, Siemens Healthcare GmbH, Erlangen, Germany). TSC maps were acquired from the right calf muscle of four healthy volunteers (2 female, 2 male, 28 +/- 4.7 years old) with four reference tubes containing NaCl (10, 20, 30, 40 mMol/L) for normalization. A density-adapted 3D radial acquisition sequence with an anisotropic field of view[8] was used to acquire images with a nominal spatial resolution of 3x3x15mm^3. Acquisition Parameters: TE/ TR = 0.30/150 ms; α = 90°; readout duration TRO = 10 ms. TSC maps with the same USFs as used in the simulations were acquired and the same reconstruction parameters were applied (Acquistion times (TA): USF=1: 22:42 min, USF=3: 6:53 min, USF=5: 4:40 min, USF=7: 3:05 min). The most suitable sparsity weighting factor λ_{em} determined in the simulations for each USF was chosen for the optDLCS reconstructions (see Fig. 2).

Results

For simulations, the mE_{norm} stays below 5% for TSC maps reconstructed with optDLCS. The SD and mE_{norm} is lower than using hNUFFT (see Fig. 3). In the in vivo study the mean quantification error (mE_{ref}, USF = 1 as reference) stays within 3% using optDLCS for USF = 3, 4.4 (USF 6.7: 6%, see Fig. 4). hNUFFT reconstructions with USF > 1 yield a mE_{ref} of more than 5% and a higher SD than optDLCS. The increases of mE_{ref} and SD with increasing USF are more pronounced for hNUFFT compared to optDLCS (see Fig. 4).

Conclusion

In this work, we demonstrated that it is possible to accurately quantify TSC from undersampled ^{23}Na-MRI data using 3D-DLCS with priorly optimized parameters. Application of the method for undersampled in vivo TSC maps show promising results, which might enhance clinical applicability of sodium quantification using ^{23}Na-MRI.

Acknowledgements

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References

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Figures

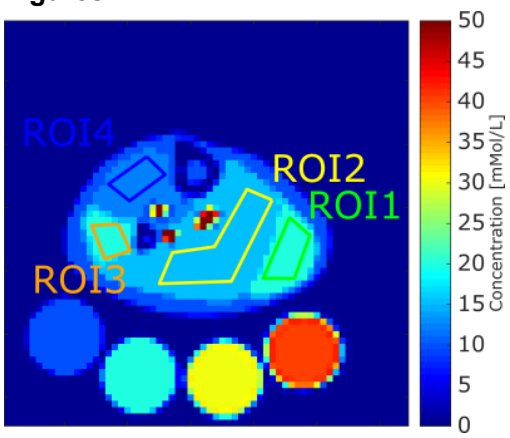

Figure 1: Simulated phantom based on a high-resolution ^{1}H-image of a human calf with assigned ^{23}Na-concentrations: fat tissue: 10 mMol/L, blood vessels: 80 mMol/L, muscle tissue: 12-25 mMol/L; natural fluctuations in muscle tissue are simulated by using three different regions (ROI1: 20 mMol/L, ROI2: 15 mMol/L, ROI3: 17 mMol/L, ROI4: 12 mMol/L). Four reference tubes (10, 20, 30, 40 mMol/L) are simulated below the calf for normalization.

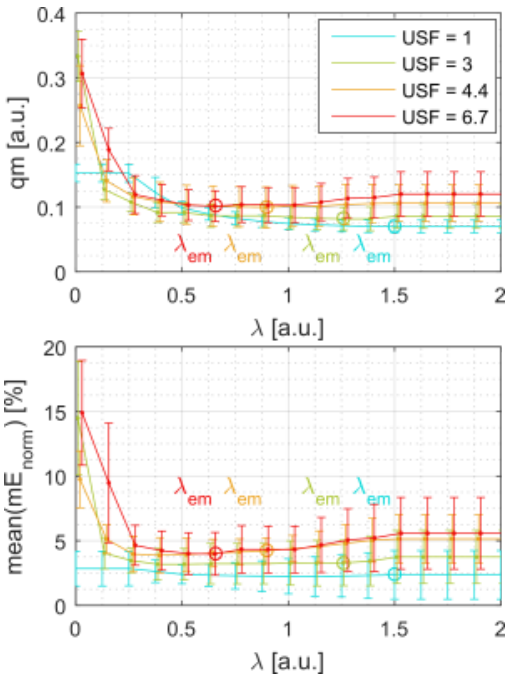

Figure 2: (a) Determination of λ_{em} for the considered USFs (1, 3, 4.4, 6.7) by evaluating em for N repetitive, simulated measurements with random noise distributions (N = 50 for USF = 2, 5, 7 and N = 20 for USF = 1). (b) Reconstructions with λ_{em} yield a low mE_{norm} of below 5% for all USFs and a low SD over all repetitions.

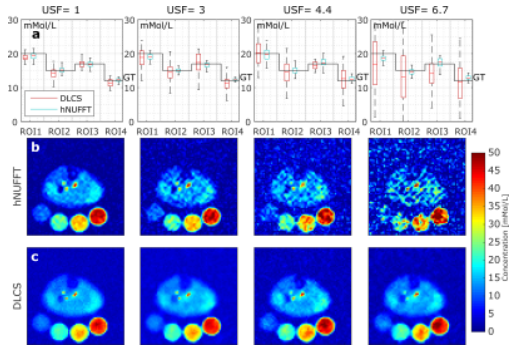

Figure 3: (a) TSC values for the simulated TSC maps in four different ROIs (see Fig. 1) using the hNufft and optDLCS reconstruction. Black lines correspond to the GT. The concentration error as well as the SD are lower for optDLCS. Qualitative comparison of reconstruction results are shown for hNUFFT (b) and optDLCS (c). TSC maps appear less noisy for optDLCS compared to hNUFFT.

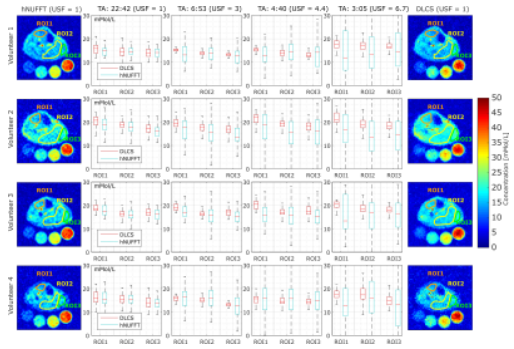

Figure 4: Quantification results for four healthy volunteers (two female, two male, 23-35 yrs. old). hNUFFT and optDLCS reconstructions with ROIs for quantification are shown in the first and last column (USF = 1). TSC values for three ROIs are depicted in the boxplots in columns two to five. The USF is increased from left to right decreasing the acquisition time (TA). optDLCS reconstructions yield a low difference between fully sampled and undersampled TSC quantification results, while maintaining a low SD in comparison to hNUFFT reconstructions.