Superresolution Parallel Spectroscopic Imaging

R. Otazo[1], F-H. Lin[2], G. Wiggins[2], R. Jordan[1], and S. Posse[1,3]

[1]Electrical and Computer Engineering, University of New Mexico, Albuquerque, NM, United States, [2]Massachusetts General Hospital, Boston, MA, United States, [3]Psychiatry, University of New Mexico, Albuquerque, NM, United States

INTRODUCTION.

Parallel magnetic resonance imaging methods can be used to accelerate the spatial-encoding process in MR spectroscopic imaging (MRSI) [1-2]. However, residual aliasing artifacts may be produced due to coil sensitivity variation within the low spatial resolution MRSI voxels [3-4]. This effect leads to increased lipid contamination and it is amplified for array coils with a large number of small elements, i.e. large-N array, which present stronger sensitivity variation. In this work, a novel parallel MRI method known as superresolution SENSE (SURE-SENSE) is proposed as an alternative to standard SENSE using large-N arrays for MRSI. Acceleration is performed by acquiring the central region of k-space instead of increasing the k-space sampling distance. Intra-voxel reconstruction is performed using coil sensitivities acquired with higher target spatial resolution. The increase in spatial resolution will be determined by the degree of coil sensitivity variation within the low resolution voxel.

METHODS.

DATA ACQUISITION: Human brain MRSI data with two spatial dimensions were acquired with Proton Echo Planar Spectroscopic Imaging (PEPSI) [5] in axial orientation using a 64×64×512 spatial-spectral matrix (x,y,v). Data acquisition was performed on a 3 Tesla MR scanner (Tim Trio, Siemens Medical Solutions, Erlangen, Germany) using a 32-channel array coil with soccer-ball geometry [6]. The FOV was 256×256 mm^2 and the slice thickness was 20 mm resulting in a voxel size of 0.32 cc. The spectral width was set to 1087 Hz. Data acquisition included water-suppressed (WS) and non-water-suppressed (NWS) scans. The NWS scan was used as a reference to estimate the coil sensitivity maps, spectral phase correction, Eddy current correction and absolute metabolite concentration. Low spatial resolution WS data was obtained from the central 32×32 k-space matrix.

SURE-SENSE RECONSTRUCTION: The spatial encoding equation $\mathbf{y}=\mathbf{E}\mathbf{s}$ for SURE-SENSE was constructed for each spectral point assuming that $\mathbf{y}$ is the multi-coil low spatial resolution representation of $\mathbf{s}$. A conjugate gradient algorithm [7] was used to solve the computationally intensive inverse problem. Pre-conditioning of the encoding equation was employed to regularize the conjugate gradient solution by solving the transformed system $\mathbf{M}^{-1}\mathbf{E}^{H}\mathbf{E}\mathbf{s}=\mathbf{M}^{-1}\mathbf{E}^{H}\mathbf{y}$, where $\mathbf{M}$ is a matrix that approximates $\mathbf{E}^{H}\mathbf{E}$, but it is easier to invert. For $\mathbf{M}$ we used the matrix $\mathbf{E}^{H}\mathbf{E}$ for the case of fully-encoding where we have a diagonal matrix with entries given by the sum of coil sensitivity squares. The transformation resulted in inverting a well-conditioned encoding matrix, i.e. low g-factor, at the expense of limiting the maximum spatial resolution in the reconstructed image. The spatial resolution in the reconstructed image was quantified using the full width at half maximum (FWHM) of the point spread function (PSF).

DATA PROCESSING: Reconstruction of the spatial dimensions was performed by separating positive and negative echoes in the PEPSI data. Coil sensitivity maps were computed using spectral water images and refined with a 3rd order polynomial fitting. Low resolution data is reconstructed using SURE-SENSE and conventional DFT with sensitivity-weighting combination and zero-filling (DFT-SW-ZF). For error quantification purposes, the fully-encoded data is reconstructed using DFT with sensitivity-weighting combination (DFT-SW). Positive and negative echo data are combined after spectral phase correction. Metabolite images were obtained by spectral fitting using LCModel [8] with analytically modeled basis sets [5]. A threshold of 20% was imposed on the Cramer-Rao lower bound (CRLB) to accept voxels.

RESULTS.

Superresolution SENSE reconstruction reduced the strong effect of k-space truncation in the simulated low resolution (32x32) PEPSI data set, resulting in metabolite maps with enhanced spatial resolution and spectra with reduced lipid contamination as compared to DFT reconstruction with k-space zero-filling (Fig. 1). The average FWHM of the PSF was 4.2 voxels for DFT-SW-ZF and only 1.4 voxels for SURE-SENSE, while lipid contamination was reduced 3.1-fold on average. SURE-SENSE metabolite concentration maps were similar to the fully-encoded reconstruction: average errors of 2.1%, 1.7% and 3.4% for NAA, Creatine and Choline respectively.

DISCUSSION.

Superresolution SENSE provides a powerful approach for accelerating MRSI data using large-N array coils. While stronger coil sensitivity variation produces artifacts for standard SENSE, it improves the performance of SURE-SENSE. The technique can be also used to improve the spatial resolution of metabolite maps and reduce lipid contamination from conventional Fourier reconstruction of MRSI data acquired with low spatial resolution. SURE-SENSE is particularly suitable for MRSI at high magnetic field strength where the coil sensitivity maps present stronger spatial modulations and overall sensitivity is higher. In future work, SURE-SENSE-PEPSI will be implemented at 7 Tesla using a similar array coil.

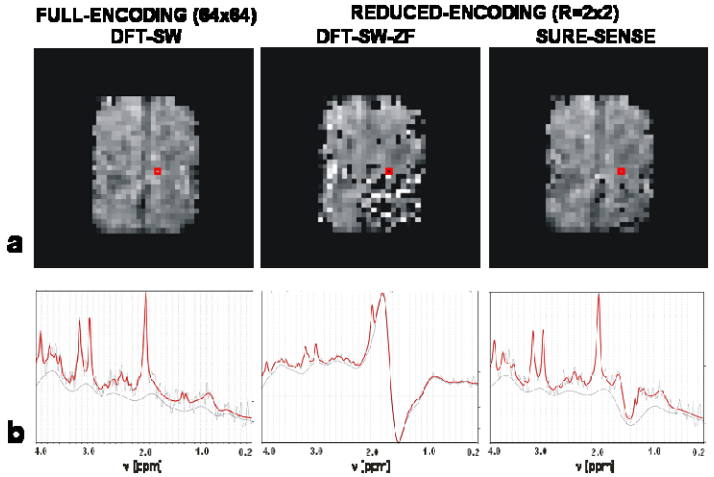

Fig. 1: a) Creatine concentration maps and b) spectrum from the voxel indicated in part a. Conventional DFT with sensitivity-weighting (DFT-SW) reconstruction of the fully-encoded data (spatial-encoding matrix size: 64x64), DFT-SW with zero-filling (DFT-SW-ZF) and SURE-SENSE reconstruction of the data with reduced spatial encoding (spatial-encoding matrix size: 32x32, R=2x2).

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