

Improved Sensitivity in ^{19}F Cellular Imaging using Nonconvex Compressed Sensing

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Introduction

Great progress has been accomplished in the field of ^{19}F -marked stem cell tracking [1], nonetheless ^{19}F imaging suffers from low signal intensities and, thus, long data acquisition times due to averaging. The distribution of the ^{19}F signal is sparse in the image domain. To exploit the inherent sparsity of these datasets, one can use Compressed Sensing (CS) [3]. CS allows the reconstruction of sparse undersampled datasets and is becoming increasingly popular in the field of MRI since many MR applications exhibit sparsity (e.g. angiography). Classical Chemical Shift Imaging (CSI) offers the possibility to image multi-resonant ^{19}F compounds. Furthermore, classical CSI is a purely phase encoded technique; therefore, random sampling can be applied, being optimal for the CS reconstruction due to the incoherent undersampling artifacts. In this work we demonstrate the potential of Nonconvex CS [4] in cellular imaging using ^{19}F CSI. Although CS applied to CSI has been presented recently [5], this study is the first one where CS exploits solely the sparsity in image space and not in the spectral dimension. Initial results from retrospectively undersampled phantom and *in vivo* experiments are presented.

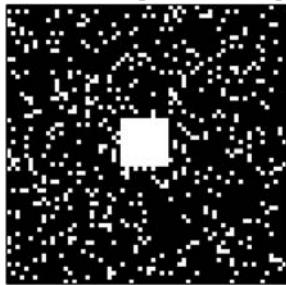


Figure 1: Sampling Pattern

Materials and methods

A phantom of six tubes filled with perfluoro-15-crown-5-ether (PF15C) emulsion (Celsense Inc., Pittsburgh, PA, USA) was imaged using a CSI sequence: Bruker BioSpec 7 T (Bruker Biospin GmbH, Rheinstetten, Germany), 64x64, FOV 40x40mm², TR=17 ms, 38.55 Hz/Px, 6 averages. For the *in vivo* experiments a PF15C emulsion was injected into the tail vein of a male C57/BL6 mouse with focal cerebral ischemia; measurement parameters of the CSI sequence: Bruker BioSpec 7 T, 48x48, FOV 30x30mm², TR=24 ms, 25 Hz/Px, 65 averages. To mimic accelerated imaging, the datasets (phantom and *in vivo*) were retrospectively undersampled using a random pattern with a dense sampling region in the center of k-space (see Figure 1). For the phantom experiments, 618 out of 4096 phase encoding steps were used for reconstruction, for the *in vivo* experiments 382 out of 2304 points were used. The data were CS reconstructed point-by-point along the spectral dimension according to [4,6].

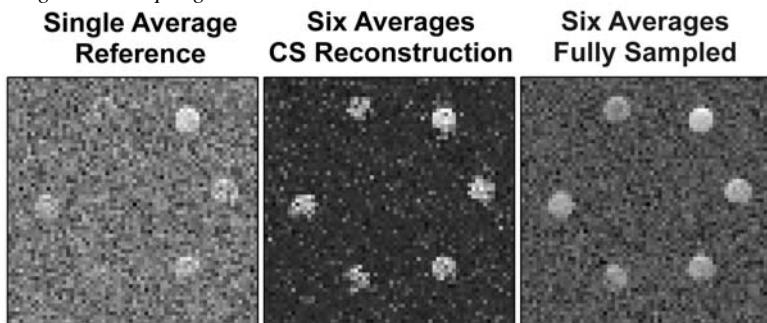


Figure 2: Results from the phantom experiments (single spectral point).

The acquisition time for the right image was six times longer than for the other images

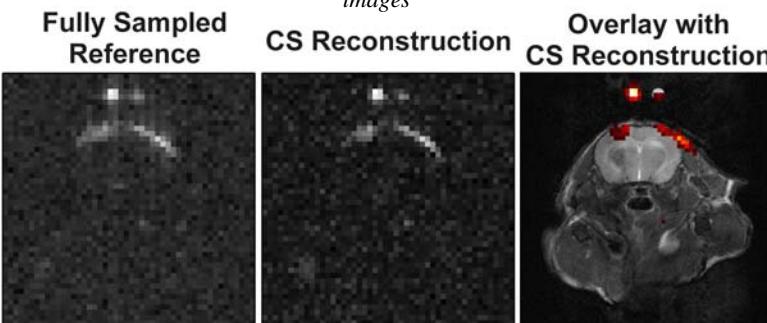


Figure 3: Results from the *in vivo* experiments. The CS reconstruction used approximately a sixth of the data of the reference; thus, the measurement time would have been reduced by a factor of approximately six

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