2D-SPIRiT accelerated MRSI of the brain using different calibration regions at 7T

Maryam Vareth[1,2], Yan Li[2], Janine M Lupo[2], and Sarah J Nelson[1,2]

[1]*UCSF/UC Berkeley Joint Group in Bioengineering, University of California, Berkeley, CA, United States,* [2]*Radiology and Biomedical Imaging, University of California, San Francisco, CA, United States*

Introduction: MR spectroscopic imaging (MRSI) is a powerful tool for diagnosis of brain tumors but long acquisition times cause patient discomfort and artifacts. The increasing availability of 7 Tesla MR scanners and multi-channel coil arrays allow for shorter acquisition times, higher spatial resolution, and larger spatial coverage for H-1 MRSI data, facilitating patient studies. Self-calibrating parallel imaging techniques such as GRAPPA[1], and SPIRiT[2], are particularly attractive for this application because coil sensitivity information is estimated from the data itself, but the dense sampling of the center of k-space required for accurate reconstruction is disadvantageous for MRSI where the typical 16x16 phase encodes allows for a 5x5 kernel. The purpose of this study was to develop a flexible platform on which to evaluate variable density sampling patterns and reconstruction strategies for accurate and robust metabolic imaging of the brain at 7T.

Methods:

Sampling and Reconstruction: The ability to acquire arbitrary, variable density sampling patterns was incorporated into our H-1 MRSI sequence to allow undersampling (US) of kspace along any phase encoding direction, with an option of including an interleaved flyback echo-planar trajectory. Sampling patterns were generated in MATLAB and played in the scanner. A modified SPIRiT reconstruction algorithm, a generalized form of GRAPPA with the ability to enforce an additional L_1 constraint in order to take advantage of compressed sensing[3] (L_1SPIRiT), was implemented in MATLAB such that the spectral dimension could be utilized in the estimation to improve the accuracy of weights from the restricted calibration region.

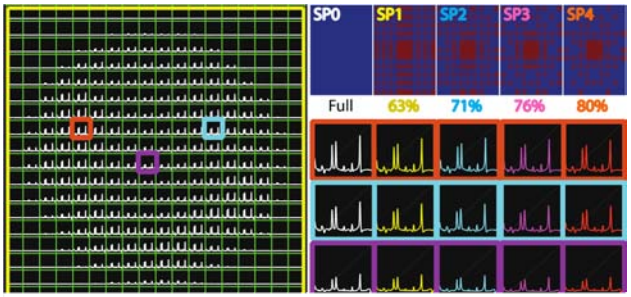


Figure 1: Phantom spectra for full kspace and SPIRiT with 4 sampling

Data Acquisition: Anatomic MR images and MRSI data were acquired on an MRS phantom and 2 human subjects using a 32-channel receive array with volume coil transmit on a GE 7 Tesla scanner. 2D H-1 MRSI was localized with CHESS water suppression, 8 VSS outer volume suppression, and spin echo slice selection, using a TE/TR=90/2000ms and spectra array=18x22. A B1-map was acquired to calculate the optimal transmit power for H-1 MRSI. Fully-sampled, water-suppressed (WS) and nonwater-suppressed (NWS) data were acquired in 13min and used as either a gold standard or to determine the optimal calibration for a 60% US scheme, respectively. The % US was then increased to 63,71,76, and 80%, corresponding to acquisition times of ~ 5, 4, 3 and 2min using the four variable density sampling patterns shown in Fig 1. The data from all 32 channels were combined and processed as described previously[4,5].

***Data Analyses*:** To evaluate the accuracy of each reduced k-space and calibration scheme, the fully sampled data was reconstructed as a gold standard and regression plots of all brain voxels were used to compare metabolite peak heights and ratios among different calibration regions and between each SPIRiT US scheme and full k-space data. The R^2 value from each linear regression was then utilized as a measure of accuracy.

Results: The reconstructions of fully-sampled spectra and SPIRiT for the 4 sampling patterns is shown in Fig 1 for 3 voxels at various locations in a phantom. The variable density pattern with more structure near the center and pseudo-random patterns outside performed best, tolerating a higher acceleration even in areas of lower SNR (Fig 1, bottom purple row). Although in the phantom, the difference between R^2 values obtained from fully-sampled NWS and 5x5 calibration region compared to the original data were not different (.99 for peak heights and .90 for ratios for both calibrations), the choice of calibration impacted the performance of SPIRiT in the volunteer data, as shown in Fig 2, where the SPIRiT recon with 18x22 NWS acquisition serving as auto-calibrating signal (in blue) more closely reflects the fully sampled spectra (in white) than the center 5x5 calibration region (in pink). Significantly higher R^2 values were obtained for all metabolic peak heights and ratios for the fully-sampled 18x22 NWS compared to the 5x5 SPIRiT calibration region. Utilizing the fully-sampled NWS calibration subsequently allowed for accelerations of up to 80% US without compromising reconstruction quality as shown by the R^2 values in Fig 3.

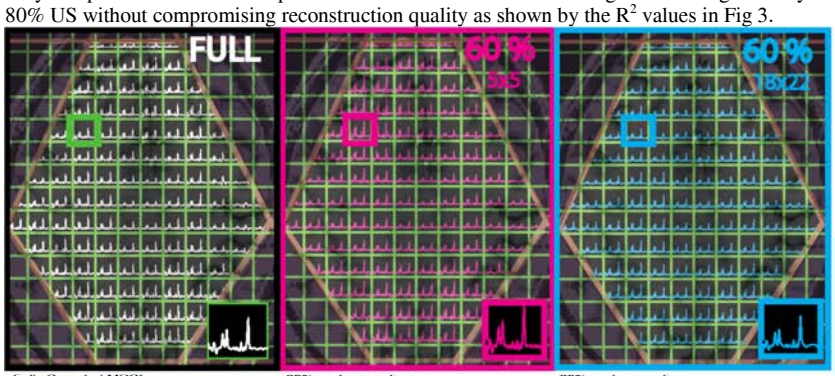
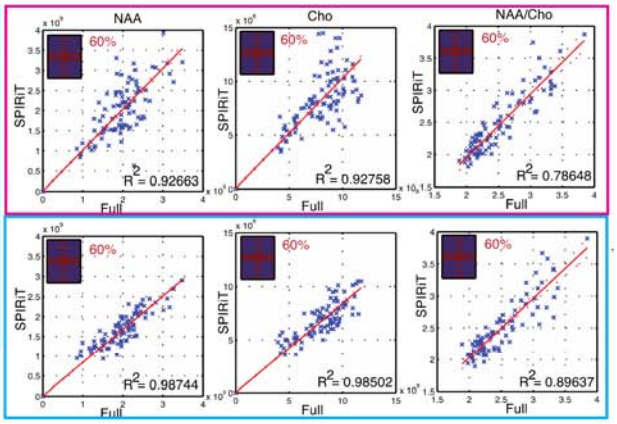


Figure 2: Volunteer data, full and SPIRiT, for 1 sampling pattern with a choice of two different calib. regions



Discussion: This work shows that MRSI at 7T can be accelerated 5-fold to provide high quality spectra in under 3 min if a NWS dataset is also acquired. Achieving a high acceleration factor with GRAPPA or SPIRiT is highly dependent on the calibration region, especially with small matrix size acquisitions like MRSI. We were able to improve the conditioning and quality of the calibration using a fully-sampled NWS acquisition which is often acquired for phase/frequency correction. This is because as the number of fits increases, the calibrated kernel more accurately represents actual frequency shifts rather than noise, improving the reconstruction. Implementation of Tikhonov regularization and truncated-SVD of the calibration region can further improve the conditioning to reduce the size of the calibration region. We are currently exploring faster options for fully-sampled calibration using a PD image of the MRSI region, which will allow for greater flexibility when a NWS acquisition is not feasible. These calibration improvements and will allow for ultra-fast whole brain MRSI suitable for routine patient studies at 7T.

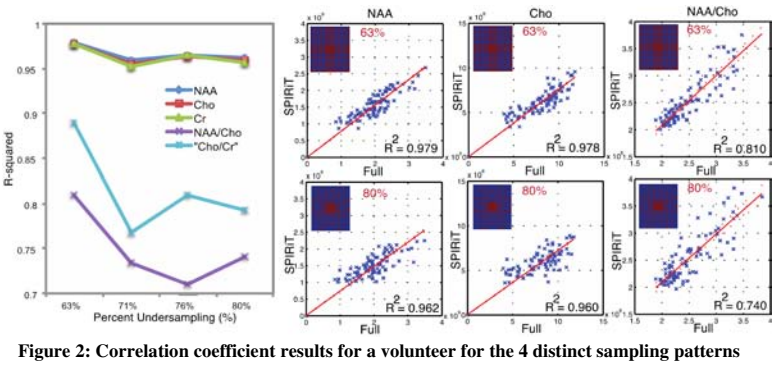


Figure 2: Correlation coefficient results for a volunteer for the 4 distinct sampling patterns

References [1] Griswold et al., Magn Reson Med. 2002. [2] Lustig et al., Magn Reson Med. 2010. [3] Lustig et al. Magn Reson Med. 2007 [3] Li, Y., et al. ISMRM 2012. [4] Nelson, SJ. Magn Reson Med, 2001.

Acknowledgements: P41 grant and UC Discovery Grant ITL-BIO04-10148