

Towards very high net acceleration factors in hyperpolarized ^3He human lung Parallel Imaging using SPIRiT

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Introduction: Parallel Imaging [1,2] is a promising approach for reducing acquisition and breath-hold times in hyperpolarised noble gas lung MRI [3]. Due to limited reproducibility of breath-hold positions, auto-calibrating methods such as GRAPPA [2] are preferred for this application. The additional auto-calibration lines result in an overhead in scan time, reducing the net acceleration factor R_n , defined as the total number of image voxels divided by the number of acquired samples. Here, we demonstrate improved image quality for highly under-sampled ^3He ventilation 3D volume data by using the recently introduced SPIRiT reconstruction algorithm [4] when compared to conventional GRAPPA.

Methods: ^3He ventilation data was acquired with a 3D SPGR sequence on a 1.5T HDx scanner (GE, Milwaukee, USA) using a 32-channel receive array coil combined with an asymmetric transmit birdcage [5]. Pulse sequence parameters were: (64 \times 64 \times 32) matrix, (6 \times 6 \times 6) mm 3 voxel, TE/TR 1.1/3.1 ms, receiver bandwidth \pm 31.25 kHz. Raw data were retrospectively under-sampled using the patterns in Fig. 1, maintaining a fully sampled centre of 11 \times 11 points for auto-calibration. The under-sampled data were then reconstructed with the GRAPPA implementation from the SPIRiT package [4,6] and a non-linear conjugate gradient version of k -space SPIRiT, written in-house in Matlab, using parts of code from the SPIRiT [4,6] and SparseMRI [6,7] packages. Quality of the reconstructed images was assessed visually and by the mean absolute error (MAE) relative to the fully sampled images [7].

Results and Discussion: Resulting images are shown in Fig. 2 for a representative slice. It can be seen that for high R_n , image quality is better maintained in the images resulting from the SPIRiT reconstruction. A $R_n > 10$ still yields acceptable image quality for SPIRiT, while resulting GRAPPA images are not satisfactory. This is also reflected in the MAE values shown in Fig. 3, which rise faster for the GRAPPA reconstruction as a function of R_n . Hence, the SPIRiT method is well suited for reconstruction of highly under-sampled ^3He human lung ventilation images. It offers inherent auto-calibration like GRAPPA, but preserves image quality better for high net acceleration factors. As it is an iterative method, extending it to an L1-penalised method with random under-sampling patterns (Compressed Sensing) is straightforward [4]. Poisson-disk random under-sampling patterns (not shown in Fig. 1) and L1 penalisation were evaluated but did not result in any further improvement, because the in-plane resolution was kept fairly low in favour of isotropic voxels, resulting in limited image compressibility. Different R_n were evaluated for the same data set to enable comparison with fully sampled data. In prospectively under-sampled data the flip angle could be increased with R_n , improving SNR of the resulting under-sampled images [3]. Hence, SPIRiT potentially offers an opportunity for ^3He human lung imaging with very high SNR per unit time.

References: [1] Pruessmann et al., MRM 42:952-962 (1999), [2] Griswold et al., MRM 47:1202-1210 (2002), [3] Lee et al., MRM 55:1132-1141 (2006), [4] Lustig et al., MRM 64:457-471 (2010), [5] Deppe et al., ISMRM 18, 3838 (2010), [6] <http://www.eecs.berkeley.edu/~mlustig/Software.html>, [7] Lustig et al., MRM 58:1182-1195 (2007).

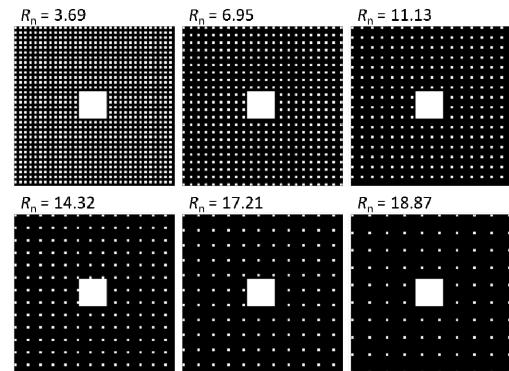


Figure 1: Under-sampling patterns and their net acceleration factors R_n .

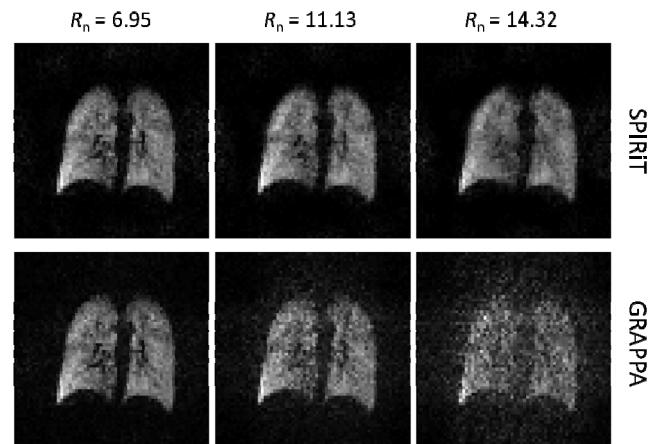


Figure 2: Representative images for SPIRiT and GRAPPA for different R_n . Image quality deteriorates for higher R_n , but SPIRiT preserves it better.

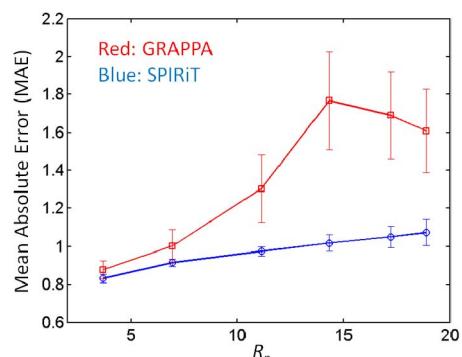


Figure 3: Average MAE as a function of R_n for GRAPPA and SPIRiT, averaged over all 32 coronal slices; error bars are respective