

## Accelerated Multi-slice $^1\text{H}$ FID-MRSI in the human brain at 9.4 T

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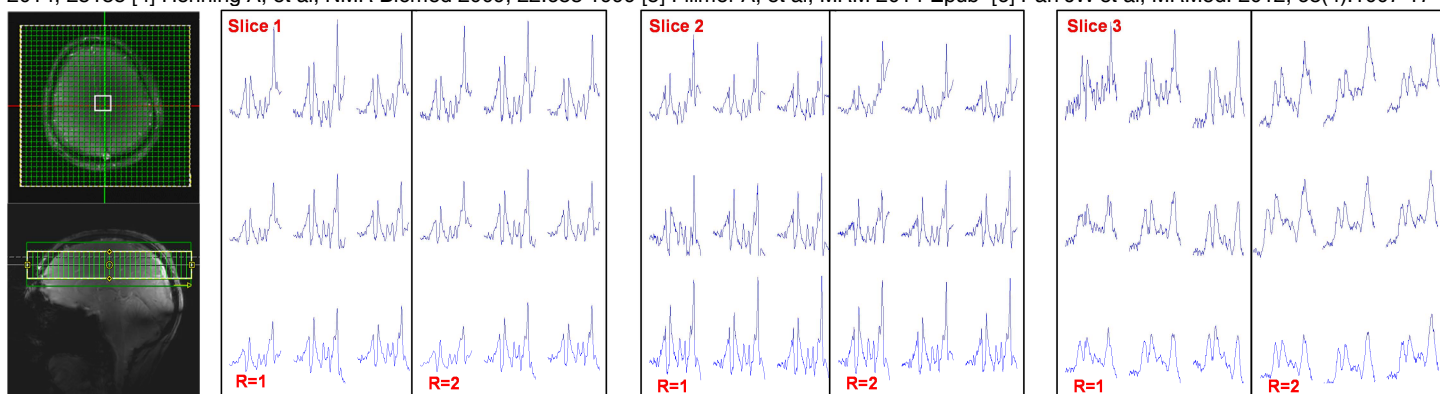
**Introduction:** Magnetic resonance spectroscopic imaging (MRSI) at ultra-high field strengths is a promising technique for mapping of the metabolites over the entire brain volume with a high signal to noise ratio. However, long acquisition time is a major limitation in MRSI. Along with short repetition times (TR) [1] parallel imaging strategies can help accelerate the scan by acquiring only a fraction of the data points in k-space, but an appropriate unfolding reconstruction algorithm is required. To that end, a target driven SENSE [2] reconstruction algorithm has been introduced [3], which minimizes the effects of voxel bleeding. **This study** represents the first demonstration of short TR twofold SENSE accelerated multi-slice FID MRSI of the human brain at 9.4T.

**Methods: Data Acquisition:** An in-vivo multi-slice  $^1\text{H}$  MRSI dataset was acquired from a healthy volunteer on a 9.4T whole body scanner (Siemens, Erlangen, Germany) with an in-house developed 8 channel transmit/receive coil using a customized FID MRSI sequence [4] incorporating an optimized 7-pulse water suppression scheme. The water suppression scheme was optimized to the shortest possible time duration (allowing enough time for spoiler gradients) so that the residual water signal was minimized over a range of T1 values (1–3 seconds) and a range of B1<sup>+</sup> values (assuming 50% inhomogeneity) using a constrained optimization algorithm performed by MATLAB's *fmincon* function (The Mathworks, Natick, MA, USA). The optimized 7-pulse water suppression scheme was 190ms long. No fat or outer volume suppression was applied in this experiment. Image-based second-order B<sub>0</sub> shimming was performed based on a rectangular shim volume (green frame, Fig 1). The following parameters were used in the scan: FOV: 200x200mm<sup>2</sup>, nominal voxel size: 6.25x6.25x10mm<sup>3</sup>, resolution: 32x32 voxels, number of slices: 3, acquisition delay (TE): 2.3ms, flip angle: 90 degrees, TR: 490ms, spectral bandwidth: 8kHz, 2048 complex data points, Total scan duration: 25 minutes. A retrospective twofold SENSE acceleration was performed on the data by down sampling the k-space by a factor of 2 in the anterior-posterior phase encoding direction which would reduce the scan time to 12.5 minutes. **Reconstruction:** A target driven SENSE reconstruction algorithm without overdiscretization was used to reconstruct the data [3]. This reconstruction algorithm reduces voxel bleeding by direct control of the spatial response function (SRF). Coil sensitivity maps were estimated using gradient echo scout images from all coils normalized by the sum of square image. A Gaussian function was used as the SRF target. The relative weight of noise regularization was adjusted empirically to yield optimal SNR and removal of fat artifacts. Spatial Hamming filtering was applied after reconstruction. **Spectral Processing:** All spectra were processed with a custom software written in MATLAB. The following post processing steps were performed on the spectra: 1- Removal of the residual water peak using the HSVD algorithm to avoid baseline distortion introduced by linear phase correction [4]. 2- First-order phase correction applied globally to all voxels. 3- Zero-order phase correction applied individually on each voxel. 4- Denoising with a 2-Hz exponential noise filter.

**Results/Discussion:** Figure 1 shows a selection of reconstructed spectra from a 3x3x3 voxel grid located in the center of FOV across all three slices. The water suppression scheme gives sufficient water suppression (>99%) while allowing for a low TR. The spectra are shown before and after twofold SENSE acceleration indicating high resemblance. As can be seen from this figure, in some of the voxels especially in the top slice (slice 3), the spectrum is contaminated by lipid signals and impaired by insufficient B<sub>0</sub> shim quality, which is partly due to the rather large size of the voxels. Also, the suboptimal B<sub>0</sub> shim quality in the subcutaneous lipids causes the lipid peaks to appear in different frequencies and deteriorate the quality of the spectrum, which can be largely improved by shim algorithms that weight the shim quality in the brain and skull regions against each other [5, Fig 6]. Applying a global or local fat saturation and reducing the voxel size by acquiring at a higher spatial resolution [1] can help to reduce this artifact further. Overall, as can be seen especially in slices 1 and 2, the twofold SENSE acceleration yields acceptable results, comparable to the fully sampled case.

**Conclusion:** In this study we show that short TR multi-slice  $^1\text{H}$  FID MRSI of the human brain is possible at 9.4T. Also, we show that SENSE acceleration in combination with a target driven reconstruction algorithm is a promising technique for reducing the rather long scan times of MRSI since it yields similar spectral quality as in the non-accelerated case. However, future work on advanced B<sub>0</sub> shimming methods [5, 6] is necessary to fully exploit the advantage of  $^1\text{H}$  MRSI in the human brain at 9.4T.

**References:** [1] Bogner W, et al, NMR Biomed, 2012; 25:873-882 [2] Pruessmann KP, et al, MRM [3] Kirchner T, et al, Magnetic Resonance in Medicine 2014; 25:185 [4] Henning A, et al, NMR Biomed 2009; 22:683 1999 [5] Fillmer A, et al, MRM 2014 Epub [6] Pan JW et al, MRMed. 2012; 68(4):1007-17



**Figure 1.** Representative spectra across all three slices from a 3x3x3 grid at the center of the FOV (shown on the transversal scout image in white). The slice positioning is shown in the gradient echo scout images (slice numbers increase from foot to head). The spectra are shown in the range of 1.8 to 4ppm. For each slice the left column shows the reconstructed spectra from the fully sampled dataset and the right column shows the same spectra reconstructed from a twofold accelerated dataset in the anterior-posterior direction (R=2).