

## Two-Voxel Spectroscopy With Dynamic B0 Shimming and Flip Angles at Ultra High Field

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**Target Audience** - Scientists interested in functional spectroscopy.

**Purpose** - A recent advance in ultra high field MRI systems is dynamic B0 shimming which enables rapid switching between different B0 shim solutions for multiple locations to better optimize spectroscopy sequence performance. Analogous to dynamic B0 shimming, data can further be improved by dynamically applying different flip angles (OVS, VAPOR, excitation and refocusing) for multiple locations in a spectroscopy sequence. In this study, we will explore the potential of dynamic B0 shimming and dynamic flip angles for multiple voxels at ultra high field in order to acquire high spectral quality from multiple voxels within a single session.

**Methods** - Three volunteers were scanned using a 7T whole body MR system (Siemens, Erlangen) with a Nova Medical 32-channel receive array head-coil. The whole scan was conducted with barium titanate-based dielectric pads positioned on the top of the head to guarantee efficient B1 would be present in the volume of interest (VOI)<sup>1</sup>. Spectra were measured by semi-localization by adiabatic selective refocusing (semi-LASER)<sup>2</sup> pulse sequence (TE = 30 ms, TR = 7 s) with VAPOR<sup>3</sup> water suppression and outer volume suppression. Signal was acquired from 2 voxels located in the motor cortex (M1) of each hemisphere in an interleaving fashion alternating between each voxel (20 x 20 x 20 mm, 64 transients each). B0 Shimming was performed using GRESHIM<sup>4</sup> for the higher order shims and FAST(EST)MAP<sup>5</sup> for the first order shims. The higher order shims were optimized for both voxels and held constant for the duration of the experiment while first order shims, localization and VAPOR flip angles were dynamically changed between each acquisition. For comparison, single voxel spectroscopy was performed for the same two voxels using the same sequence and parameters except shimming (both first and higher orders) was optimized for each individual voxel with FAST(EST)MAP. Eddy current correction, reconstruction, and zero-order phasing of array coil spectra were carried out by using a reference water spectrum acquired from the same VOI. Metabolites were quantified with LCModel<sup>6</sup> using the unsuppressed water signal as reference. Only those measured reliably (Cramér-Rao lower bounds (CRLB) < 50%, cross correlation coefficients  $r > -0.5$ ) were reported.

**Results** - Spectra with good SNR and spectral resolution were consistently obtained from both regions with both interleaved and single voxel measurements (Fig. 1, data shown from each region). The spectral quality enabled the quantification of a neurochemical profile consisting of 14 metabolites in the motor cortex (Fig. 2).

**Discussion** - The same neurochemical profiles were obtained for both VOIs from both single voxel and two voxel interleaved methods. Identical water line-widths were achieved for both voxels with the B0 shimming procedure proposed in this study.

The water line-widths from both voxels were identical. The findings revealed that neurochemical differences between hemispheres might originate from different contributions from grey matter, white matter and/or CSF. In this study we have demonstrated that dynamically changing the first order shims and flip angles between interleaved measurements can be used to concurrently measure multiple accurate neurochemical profiles.

**References** - 1. Teeuwisse, WM. Et al. (2012). Magn. Reson. Med., **67**, 912-918. 2. Öz, G. et al. (2011). Magn. Reson. Med., **65**, 901-910. 3. Tkáč, I. et al. (1999). Magn. Reson. M., **41**, 649-656. 4. Shah et al. 17th ISMRM 2009; 565. 5. Gruetter, R. et al. (2000). Magn. Reson. Med., **43**, 319-323ed. 6. Provencher, S.W. (2001). NMR Biomed., **14**, 260-264.

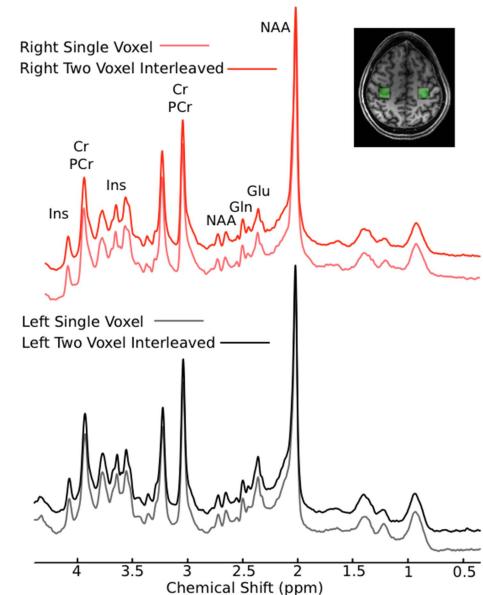


Figure 1:  $^1\text{H}$  MR spectra obtained using interleaved and single voxel semi-LASER (TR = 7, TE = 30 ms) from two VOIs.

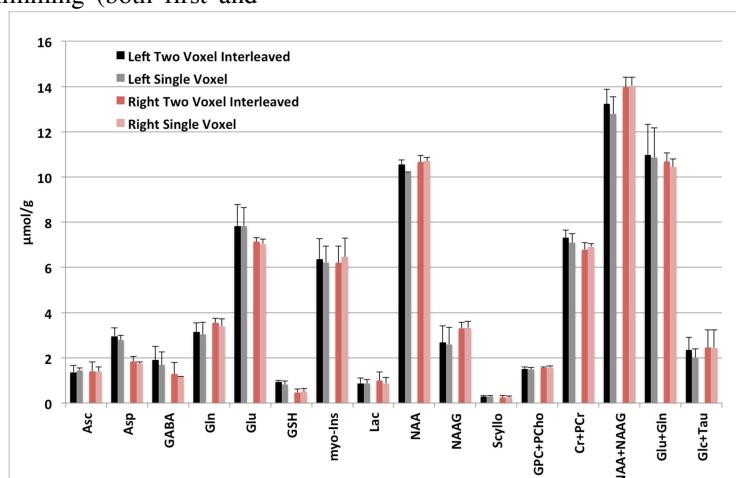


Figure 2: Metabolite concentrations determined by LCModel fitting. The error bars shown are standard deviation.