

## Volumetric Navigated MEGA-SPECIAL for real-time motion corrected GABA MRS

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**Target Audience:** This will be of interest to all applications that use J-edited single voxel spectroscopy (SVS) sequences to measure metabolite levels of GABA.

**Purpose:**  $\gamma$ -Aminobutyric acid (GABA) is the primary inhibitory neurotransmitter in the brain and accounts for almost half of the synaptic activity. Altered concentrations of GABA have been linked to several neurological conditions<sup>(1)</sup>. The ubiquitous sequence utilised to measure GABA in-vivo is MEGA-PRESS. Another sequence is MEGA-SPECIAL (MSpc), which comprises longer frequency selective editing pulses (26 ms) allowing the use of Henry's method to acquire GABA without macromolecule (MM) contamination at the echo time (TE) of 68 ms<sup>(2)</sup>. MSpc demonstrates reduced spatial variations within the volume of interest (VOI) and yields 10% improvement in editing efficiency of GABA-H4 at 3 ppm compared to MEGA-PRESS<sup>(2)</sup>. However, MSpc requires four acquisitions per edited spectrum rendering it more sensitive to subject motion than the two-acquisition MEGA-PRESS. Currently, motion and artefact corrections in GABA MRS data are based on retrospective frequency and phase corrections, and dedicated navigator echoes to remove data confounded by motion<sup>(3,4)</sup>. The aim of this work is to incorporate the echo planar imaging (EPI) volumetric navigator (vNav) into the MSpc sequence to correct in real-time for motion (MoCo).

**Methods:** The 3D multishot EPI vNav was added to the standard MSpc sequence (vNavMSpc) to measure head pose in real time prior to localization. The motion estimation was performed by coregistering subsequent vNavs to the first vNav after the preparation scans. The method for registration is based on a well-established algorithm for whole-brain EPI registration (PACE)<sup>(5)</sup>. The brain image reconstruction and registration was performed immediately after the navigator block in less than 80 ms. All scans were performed on a Siemens Allegra 3T scanner (Siemens Healthcare, Germany) using a single channel transmit and receive volumetric coil. The EPI vNav parameters were: isotropic resolution  $8 \times 8 \times 8 \text{ mm}^3$ , matrix size  $32 \times 32 \times 28$  and field of view (FOV)  $256 \times 256 \times 224 \text{ mm}^3$ , flip angle  $2^\circ$ , TR/TE 16/6.6 ms and bandwidth 3906 Hz/pixel. The MSpc parameters were:  $(3 \text{ cm})^3$  voxel positioned in a parieto-occipital region, 2048 points, bandwidth 2000 Hz, 192 averages and TR/TE 3000/68 ms. Prior to each excitation, outer volume suppression (OVS) and water suppression pulses were executed. GABA was acquired without MM contamination. Two healthy subjects were scanned with the standard MSpc sequence and with vNavMSpc. Data were acquired with MSpc in the absence of motion (A), vNavMSpc with no intentional motion (B), vNavMSpc with intentional motion and no correction (NoMoCo) (C), and vNavMSpc with intentional motion and MoCo (D). The duration of every scan was 9 minutes 36 seconds. The motion involved chin up-down and chin left-right rotations of about  $7^\circ$ . After every data acquisition involving motion, subjects were instructed to return to their original position. All subjects were trained and instructed on how to move before the experiments. All data were processed using the Gannet toolkit<sup>(6)</sup>, including frequency and phase correction of the individual spectra using Spectral Registration<sup>(4)</sup>. Residual fitting error (FitErr) and full-width half maximum (FWHM) of GABA at 3 ppm – measured by Gannet – were compared between data acquired using MSpc in the absence of motion and vNavMSpc in the presence of intentional motion and MoCo. FitErr and FWHM reflect fitting and spectral quality of the edited spectrum.

**Results:** Figures 1 and 2 show, respectively, typical motion profiles determined by vNav and GABA spectra for the four different acquisitions of one subject. Data for the other subject were similar. Fitting and spectral quality were similar between the data acquired using the standard and vNavMSpc sequences in the absence of intentional motion (Figs 2A and 2B). Motion caused extreme distortions of the GABA peak at 2.3 ppm (red arrow in Fig. 2C), the Glx peak (Glutamate + Glutamine) at 3.8 ppm (green arrow in Fig 2C) and the baseline between GABA at 3 ppm and Glx. Moreover, the GABA peak at 3 ppm had FitErr of 18% and FWHM of 7.74 Hz, which was similar to the FWHM of Creatine (Cr) 8.6 Hz in the edit-off spectrum. Figure 2D shows the spectrum acquired with MoCo, which resulted in a well edited GABA peak at 3ppm with FitErr and FWHM slightly lower than that obtained in the absence of intentional motion (Table 1).

**Discussion:** The addition of the vNav neither affected the edited spectrum (Figure 2A and 2B) nor increased the scan time, which was similar to previously reported studies<sup>(3,6)</sup>. Head pose was estimated in each TR using the vNav and if any motion was detected, the correction was applied in the following TR (Figure 1). Without motion correction, the edited spectrum suffered severe distortions affecting peaks over the whole spectrum, including baseline distortion (Figure 2C). Moreover, the FWHM of GABA at 3 ppm and Cr from the edit-off spectrum were similar, indicating almost no editing as previously reported<sup>(3)</sup>. The MoCo scan resulted in a well edited GABA spectrum at 3 ppm with FWHM and FitErr similar to previously reported values<sup>(3)</sup>. The standard sequence resulted in slightly higher FWHM and FitErr than the navigated sequence, probably due to the presence of involuntary motion such as swallowing.

**Conclusion:** Inclusion of the vNav did not affect the spectral and fitting quality. Furthermore, it corrected very well for motion in real-time without increasing the scan time and resulted in a well edited GABA spectrum. This technique can greatly benefit GABA MRS, which is challenging due to low signal often necessitating long acquisition times.

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**References:** (1)Levy L, Degnan A. GABA-based evaluation of neurologic conditions: MR spectroscopy. *AJNR*. 2013, 34:259-265. (2)Near J, Simpson R, Cowen P, et al. Efficient  $\gamma$ -aminobutyric acid editing at 3T without macromolecule contamination MEGA-SPECIAL. *NMR in Biomed*. 2011, 24(10):1277-1285. (3)Bhattacharyya P, Lowe M, Phillips M. Spectral quality control in motion-corrupted single-voxel J-difference editing scans: An interleaved navigator approach. *Magn Reson Med*. 2007, 58(4):808-812. (4)Near J, Edden R, Evans CJ, et al. Frequency and phase drift correction of magnetic resonance spectroscopy data by spectral registration in the time domain. *Magn Reson Med*. 2014. (5)Thesen S, Heid O, Mueller E, et al. Prospective acquisition correction for head motion with image-based tracking for real-time fMRI. *Magn Reson Med*. 2000, 44:457-465. (6)Edden RA, Puts NA, Harris AD, et al. Gannet: A batch-processing tool for the quantitative analysis of gamma-aminobutyric acid-edited MR spectroscopy spectra. *JMRI*. 2013.

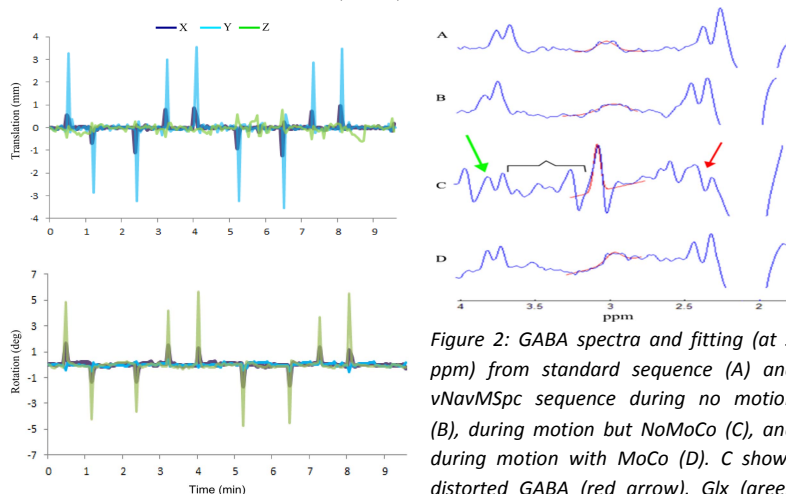


Figure 1: Changes in motion. Translation (A) and Rotation (B) in X, Y and Z directions.

Figure 2: GABA spectra and fitting (at 3 ppm) from standard sequence (A) and vNavMSpc sequence during no motion (B), during motion but NoMoCo (C), and during motion with MoCo (D). C shows distorted GABA (red arrow), Glx (green arrow) and baseline (bracket).

Table 1: Fitting and spectral quality comparisons expressed as mean  $\pm$  standard deviation (SD)

Parameters	Standard sequence	vNavMSpc with MoCo
FitErr (%)	15 $\pm$ 1	12 $\pm$ 2
FWHM (Hz)	15 $\pm$ 0	13 $\pm$ 1