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| Site (Name or Number) |  |  |  |
| 1. Hardware |  |  |  |
| a. Field strength [T] | 3 T  |  |  |
| b. Manufacturer  | Siemens |  |  |
| c. Model (software version if available) | Magnetom Skyra Software version VD13 |  |  |
| d. RF coils: nuclei (transmit/ receive), number of channels, type, body part | Body transmit, 32 channel head coil |  |  |
| e. Additional hardware |  |  |  |
| 2. Acquisition  |  |  |  |
| a. Pulse sequence  | MEGA-PRESS (provided by the CMRR at the University of Minnesota under a C2P agreement) |  |  |
| b. Volume of Interest (VOI) locations  | Dorsal ACC, Right DLPFC, Bilaterally in the occipital lobe.See figure 1 for mean voxel locations across all participants |  |  |
| c. Nominal VOI size [cm3, mm3] | dorsal ACC (30x30x20 mm)right dlPFC (30x20x20 mm)occipital lobe (20x30x25 mm) |  |  |
| d. Repetition Time (TR), Echo Time (TE) [ms, s] | TR = 1800 ms, TE = 68 ms |  |  |
| e. Total number of Excitations or acquisitions per spectrumIn time series for kinetic studies 1. Number of Averaged spectra (NA) per time-point
2. Averaging method (e.g. block-wise or moving average)
3. Total number of spectra (acquired / in time-series)
 | Number of averages = 200 On and Off spectra (400 total)ON and OFF sub-spectra were averaged on the scanner before export. |  |  |
| f. Additional sequence parameters(spectral width in Hz, number of spectral points, frequency offsets)If STEAM:, Mixing Time (TM)If MRSI: 2D or 3D, FOV in all directions, matrix size, acceleration factors, sampling method | Spectral Width = 1600 hzSpectral points = 1024Excitation frequency corresponds to a chemical shift of 3.00 ppm (referred to as offset frequency on scanner)Editing ON pulse frequency corresponds to 1.9 ppm, while edit off corresponds to 7.35 ppm. |  |  |
| g. Water Suppression Method | VAPOR |  |  |
| h. Shimming Method, reference peak, and thresholds for “acceptance of shim” chosen | Higher-order shimming was performed manually using iterative shimming after the system initial set shim using a 3D field map. We aimed for > 13 Hz with the shim, but to maximise data inclusion, went for as low as we could achieve. |  |  |
| i. Triggering or motion correction method(respiratory, peripheral, cardiac triggering, incl. device used and delays) | None |  |  |
| 3. Data analysis methods and outputs |  |  |  |
| a. Analysis software | GANNET 3.0 (Baltimore, MD, USA) in MATLAB |  |  |
| b. Processing steps deviating from quoted reference or product | standard processing steps, inbuilt models and assumptions for this software were used (details at http://www.gabamrs.com) |  |  |
| c. Output measure(e.g. absolute concentration, institutional units, ratio) Processing steps deviating from quoted reference or product | Ratio’s to Creatine. GABA is reported as GABA+  |  |  |
| d. Quantification references and assumptions, fitting model assumptions | The GANNET pipeline models GABA+, Glx and the creatine (Cr) reference as a single-Gaussian, doublet, and singlet, respectively. Data is reported as a raw ratio of area under the fitted curve (institutional units; i.u.) referenced to Cr (aligned with our previous report on this sample), for each metabolite, and does not account for differential proton densities, metabolite-specific relaxation properties, or tissue make up. While CSF correction is not necessary when using Cr as reference, grey matter (GM) contribution may however be of influence and is therefore controlled for in each analysis via partial Pearson correlations using GM as covariate. |  |  |
| 4. Data Quality  |  |  |  |
| a. Reported variables (SNR, Linewidth (with reference peaks)) | Data was included from 9 participants in GD and 13 in non-GD for the dACC voxel, leading to mean (and *SD*s)of thesignal-to-noise ratios (SNR) for Glx of 21.77 (14.99) and 29.10 (11.96) and for GABA+ of 15.54 (10.69) and 18.65 (8.30), respectively for GD and non-GD. For the right dlPFC voxel, 11 GD and 13 non-GD participants were included, with SNRs for Glx equalling 18.61 (8.47) and 22.13 (7.27) and for GABA+ of 12.77 (5.09) and 16.35 (5.24). For the occipital voxel, 8 GD and 10 (Glx) or 9 (GABA+) non-GD participants were included, leading to SNRs for Glx of 18.14 (6.23) and 19.12 (5.45) and SNRs for GABA+ of 19.44 (6.76) and 19.38 (5.90), respectively. |  |  |
| b. Data exclusion criteria | GANNET Model fit was assessed based on visual inspection and FWHM within 3 *SD*s from the group mean per metabolite. |  |  |
| c. Quality measures of postprocessing Model fitting (e.g. CRLB, goodness of fit, SD of residual) | The mean Gannet Fit Error (*SD*) for included dACC MRS data equalled 8.29 (9.66) and 5.36 (1.71) for Glx/Cr, and 9.42 (5.71) and 8.40 (3.75) for GABA+/Cr, respectively for GD and non-GD. The mean Gannet Fit Error (*SD*) for included dlPFC MRS data equalled 6.60 (3.09) and 5.96 (2.09) for Glx/Cr, and 8.93 (3.44) and 8.16 (3.69) for GABA+/Cr, respectively for GD and non-GD. The mean Gannet Fit Error (*SD*) for included occipital MRS data equalled 6.58 (2.99) and 6.02 (1.42) for Glx/Cr, and 6.47 (3.75) and 5.63 (1.60) for GABA+/Cr, respectively for GD and non-GD. |  |  |
| d. Sample Spectrum | See figure 2. |  |  |