

## Gannet: GABA Analysis Toolkit for edited MRS

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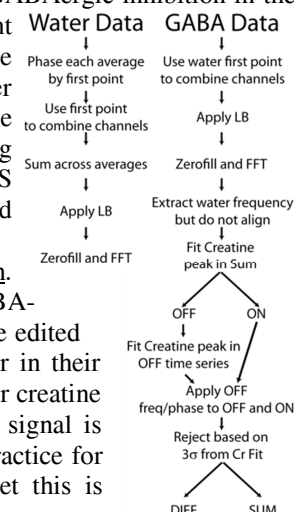
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**TARGET AUDIENCE** Researchers interested in applying J-difference editing for detecting the neurotransmitter GABA in the brain.

**PURPOSE** Substantial recent interest in using edited magnetic resonance spectroscopy (MRS) to study GABAergic inhibition in the brain has generated increasing demand for robust analysis methods. The most widely used experiment currently applied to detect GABA is MEGA-PRESS, a J-difference editing experiment. Some groups have used pre-existing tools, such as LCModel and jMRUI, to analyse GABA-edited MRS data, but these differ in the degree of pre-processing and batch automation that they offer. Other groups have written in-house scripts to perform the same analysis, which are sometimes incompletely described in the literature making site-to-site or study-to-study comparisons difficult. In this abstract, we present the Gannet GABA-MRS Analysis Toolkit, which is designed for the user-independent batch analysis of edited MRS spectra acquired on GE, Philips and Siemens scanners, to make analyses transparent and the pipeline more widely available.

**METHODS** Gannet is implemented within matlab, with code available through [gabamrs.blogspot.com](http://gabamrs.blogspot.com). Analysis proceeds in two stages: GannetLoad processes raw time-domain data from the scanner into GABA-edited frequency-domain difference (DIFF) spectra; and GannetFit fits the spectra in order to quantify the edited GABA signals. J-difference editing of GABA involves the acquisition of two experiments which differ in their manipulation of the GABA spin system; subtracting the two reveals GABA signals from under the stronger creatine (Cr) signal at 3 ppm. Difference editing involving subtracting large (Cr) signals to reveal a smaller signal is inherently sensitive to experimental instabilities such as scanner drift and subject movement, and best practice for the analysis of such data includes frequency and phase correction before time averaging<sup>1</sup>. In Gannet this is

performed by frequency-domain fitting of the Cr signal, in the editing-OFF spectra. Other processing steps performed by GannetLoad are summarised in Figure 1. GannetFit quantifies spectra by modelling the GABA signals in DIFF spectra (using a simple Gaussian model with a linear baseline) across a frequency range from 2.8 to 3.6 ppm, the Cr signals in OFF spectra (using an equivalent Lorentzian model) between 2.7 and 3.1 ppm and, where available, the unsuppressed water spectrum (using a Gaussian-Lorentzian model) between 3.8 and 5.6 ppm. GannetFit reports GABA values as an integral ratio relative to Cr, and as a concentration in institutional units (i.u.) relative to water.



**Figure 1:** GannetLoad Processing Flow diagram

20 healthy subjects gave informed consent under local IRB approval and GABA-edited MRS data were acquired twice in up to three regions: occipital (OCC), sensorimotor (SM) and dorsolateral prefrontal (DLPF) on a GE Signa HDx 3T MR scanner, using standard methods described in [4].

**RESULTS** The output summaries from GannetLoad and Gannet Fit are saved in pdf format.

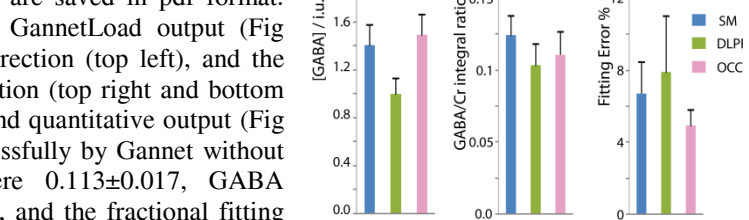
**Figure 2:** GannetLoad and GannetFit output pdf files.

GannetLoad output (Fig 2a) shows the edited spectrum before and after frequency correction (top left), and the shot-by-shot frequency of water and Cr signals used for correction (top right and bottom left). GannetFit shows the data, best-fit models and residuals, and quantitative output (Fig 2b). Of the acquired data, all 106 spectra were processed successfully by Gannet without need for user intervention. GABA:Cr integral ratios were  $0.113 \pm 0.017$ , GABA concentration relative to water was quantified as  $1.33 \pm 0.26$  i.u., and the fractional fitting error was  $6.4\% \pm 2.4\%$ ; these data are displayed by region in Figure 3.

**DISCUSSION** 106 GABA-edited spectra (up to 3 regions in 20 subjects; 2 repeats) were successfully processed in Gannet. Other options are available for analyzing GABA-edited MRS data, including LCModel<sup>2</sup> and jMRUI<sup>3</sup>, although neither is specifically targeted for this purpose.

**CONCLUSION** The use of J-difference edited spectroscopy of GABA for clinical applications or psychology has lead to an increasing need for analysis methods that are robust but do not require complex setup or user-intensive pre-processing. Gannet allows batch processing of datasets, with no user intervention, and provides a summary of data quality to allow rigorous quality control.

**REFERENCES** 1. K Waddell et al. MRI 2007; 25(7):1032-8. 2. S Provencher. NMR Biomed. 2001 Jun;14(4):260-4. 3. A Naressi et al. MAGMA 2001;12:141-152.



**Figure 3:** Quantitative output from Gannet analysis of 120 spectra.