Rapid Multi-Echo Measurement of Brain Metabolites T2 values at 7T Using a Single-Shot Spectroscopic CPMG Sequence and Priors

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Introduction: Transverse relaxation rates of brain metabolites are tightly connected with the physicochemical nature of their surroundings and thus are sensitive to alterations in tissue microscopic structure and macromolecular content in specific diseases and additionally are of importance for MRS quantification in general [1, 2]. Here we present a rapid method for the robust and accurate estimation of brain metabolite relaxation rates based on a single-shot CPMG sequence with 8 echoes. Each echo consists of a small number of acquired time-domain points. These truncated data sets are subsequently extended with additional data points calculated via solving a set of linear equations for the peak amplitudes using previously estimated frequencies and linewidths as priors. These priors are obtained from a short single volume MRS experiment with subsequent linear prediction using singular value decomposition (LPSVD) processing (e.g. [3])

Methods: 5 healthy volunteers were scanned for this study. *Scanner*: Philips 7T Achieva (Philips, Best, The Netherlands) equipped with a quadrature transmit head coil and a 32 channel receive coil array. The sequence used was based on a multiecho PRESS sequence with phase cycling of the multiecho part set to a CPMG sequence (90_x-[180_y-180_{-y}]$_n$-acq). Two volumes of interest (VOIs) of 2x2x2 cm^3 were selected – one with predominantly parietal white matter and one that consisted mostly of gray matter. For each tissue type three experiments were performed – two PRESS experiments with two different echo times – 40 and 180ms (BW=5000Hz, #points=2048, #averages=64, TR=4s), followed by an 8-echo CPMG experiment on the same volumes (TE=40ms, echo spacing=69ms, #points=128, TR=4s, #averages=64). LPSVD (typically 14-20 spectral components) was used to generate priors from the short-TE PRESS data. For the multiecho data, the priors were used to generate the components amplitudes within each echo data, and FIDs were then extended to 2048 points. Zero-mean Gaussian noise was added to the extended FID portion with a value equal to the RMS of the noise in the PRESS experiment. MRS data were subsequently processed with LCModel [4]

Results and conclusions: in figure 1, panel (a) shows the quality of the LPSVD fit to the short TE data. Spectral residuals are small and stochastic. Panel (b) shows the results obtained from the first of 8 echoes (TE=40ms) in the CPMG experiment, where the FID consisted of 128 points, and was then extended to 2048 points using the LPSVD results. Here, no priors are used, and the residuals show strong deviations near the NAA and the 3.0ppm tCr peak when the resulting spectrum is compared with the native spectrum from panel (a). In panel (c) the same data are used, only this time the extension of the FID is calculated based on solving the system of equations for the peak amplitudes, using the priors calculated for the spectrum in (a). The fit is markedly better, and remains so for all echoes. Figure 2 is a zoomed-in stacked plot of the spectra obtained from the CPMG data with the procedure described before. Figure 3 shows the amplitudes of the main singlets estimated with LCmodel for all CPMG echoes. Only white matter data are shown, but gray matter data are obtained similarly. A summary of the data for all subjects and the three main metabolites is shown in figure 4. The results are robust and reproducible, and provide higher T_2 values than those obtained from a variable TE experiment (data not shown). This is expected as CPMG, in addition to efficiently compensating for imperfections of the refocusing pulses, also helps refocus additional dephasing effects such as diffusion in non-homogeneous B_0 [5]. Thus, T_2 values of the main brain metabolites can be accurately and robustly estimated with a multiecho data acquired in a short acquisition time (less than 5 minutes).

Figure 1

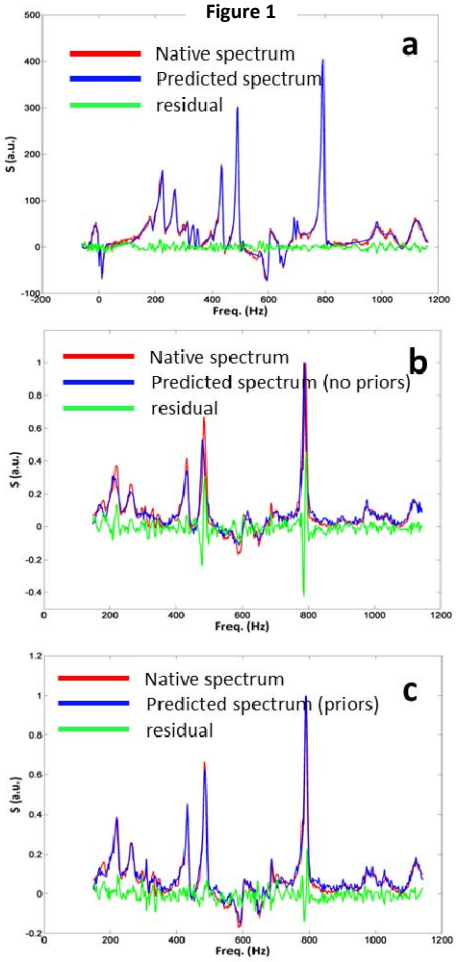


Figure 2

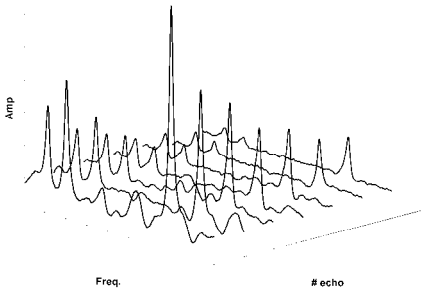


Figure 3

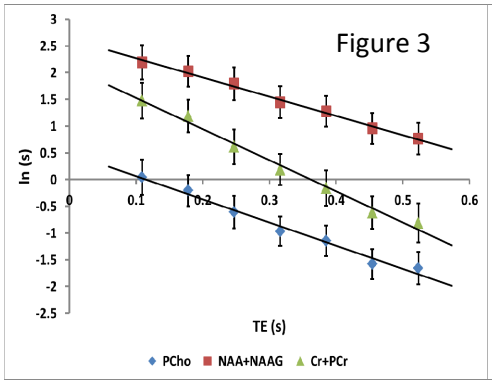
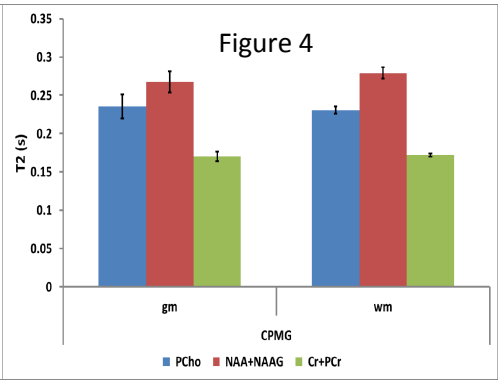


Figure 4



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