Improved Two-Dimensional *J*-Resolved Spectroscopy

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Introduction

One of the main limitations of proton spectroscopy is a heavy overlap of resonance lines due to a small chemical-shift dispersion and often complex multiplet patterns. A simple, but powerful sequence to alleviate the overlap and increase specificity is two-dimensional *J*-resolved spectroscopy (*J*PRESS) [1]. In this work, a modified *J*PRESS sequence to increase robustness and sensitivity is presented, which starts the echo sampling as soon as possible [2], henceforth called maximum-echo sampling. We investigate the eddy current behaviour in *J*PRESS and propose a 2D eddy current correction scheme derived from the 1D phase deconvolution method [3]. The advantages of *J*PRESS are shown by various measurements in the human brain and transplanted kidney.

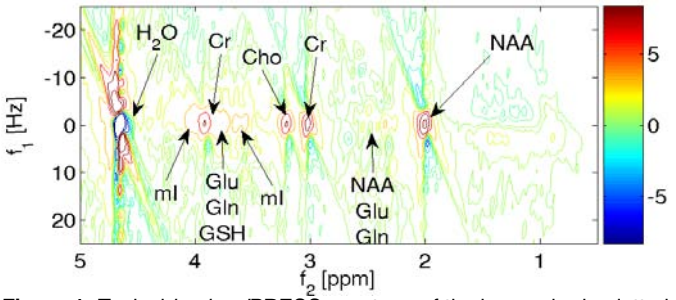

Figure 1: Typical *in-vivo* *J*PRESS spectrum of the human brain plotted with logarithmically scaled contour lines and in phased complex mode. The maximum-echo sampling leads to a tilt of the peak tails, which is particularly advantageous for poorly water-suppressed spectra. The data was zero-filled to 512 samples in the indirect dimension and apodised with a 2-Hz Gaussian filter in both t_1 and t_2. Directly visible are the predominant singlets from N-acetyl aspartate (NAA), total creatine (Cr) and choline-containing compounds (Cho), but also some of the *J*-coupled metabolites, namely *myo*-inositol (mI), glutamate (Glu), glutamine (Gln) and glutathione (GSH). More information can be extracted from the spectrum with advanced post-processing methods such as two-dimensional fitting [4].

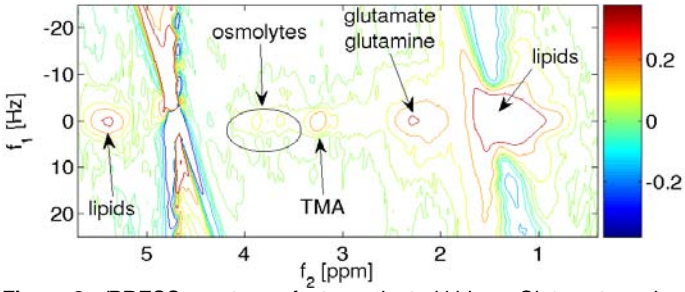

Figure 2: *J*PRESS spectrum of a transplanted kidney. Glutamate and glutamine are not as well resolved as in the brain due to the short T_2 relaxation time, visible by the broad line-widths in both f_1 and f_2. Other resonances stem from tri-methylammonium (TMA) and osmolytes [5]. Peak tails of lipids and the partially suppressed water are tilted away from the spectral region of interest, hence contamination is greatly reduced.

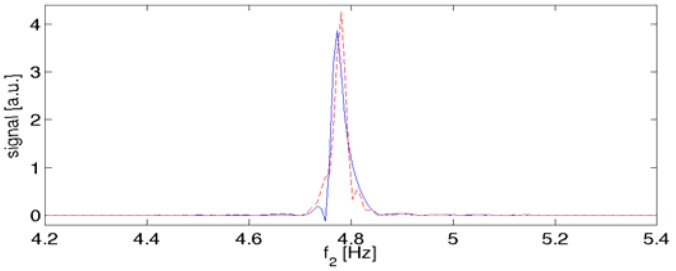

Figure 3: Zero-Hertz cross-section through *J*PRESS spectrum of water with (red dashed) and without (blue solid) eddy current correction. Symmetry and hence peak height is increased in the corrected data. The strength of the last pair of crusher gradients was increased from 12 to 20 mT/m in order to induce stronger eddy currents for illustrative purposes.

Theory and Methods

The *J*PRESS sequence is based on a standard PRESS sequence for single voxel volume localisation. The *J* coupling is encoded in the indirect dimension by shifting the last 180° refocusing pulse to different TEs. The acquisition starts directly after the final crusher gradient and the *J*PRESS experiment is reconstructed by time-shifting the different TEs to the same reference, the echo top. This sampling scheme increases sensitivity and tilts the peak tails away from the f_2 axis (Figs. 1 and 2). The latter is especially advantageous for a flat baseline, as the contamination of the partially suppressed water is greatly reduced. The indirect t_1 dimension is over-sampled in order to reduce contamination of the spectral region of interest through aliasing.

Eddy current correction requires the acquisition of a simple 1D water reference spectrum for the shortest echo time. The eddy currents are mainly induced by the last pair of crusher gradients. Acquisition always starts at the same relative time after the last crusher gradient. Therefore, the phase distortions in the time domain are approximately the same for all echo times, despite the shift of the echo top. The phase of the reference echo can simply be subtracted row by row from the phase of each water-suppressed echo. The real part of the phased spectrum is used for quantification as the eddy current distortions are low and the applied quantification is based on simulated model spectra with the same phase-twisted line shapes. The maximum information from these spectra was extracted through direct fitting in two dimensions [4].

All experiments were performed on a Philips Intera 3T scanner equipped with a transmit/receive head coil. The bandwidths in f_1 and f_2 were 0.5 kHz and 2 kHz with 100 and 2048 sampling points, respectively. Four-step phase cycling for each echo time and a repetition time of TR = 2.5 s lead to a total scan duration of 17 minutes. Twenty-seven healthy volunteers (age 35.4 ± 7.5) with written informed consent were scanned in the parietal lobe.

Results

*J*PRESS is comparably robust and easy to apply as the standard PRESS sequence. The eddy current correction generally leads to reduced line shape distortions (Fig. 3). The effects of eddy currents can be modelled by the same bi-exponential phase decay for all echo times. This physical model was used in the 2D fitting procedure [4]. The high robustness of JPRESS is exemplified by a brain spectrum (Fig. 1) and a kidney spectrum (Fig. 2).

The sensitivity was analytically compared to that of a standard short echo-time PRESS sequence by integration in the time domain. For typical values of T_2 = 200 ms and T_2^* = 50 ms and the chosen scan parameters, the maximum-echo sampled *J*PRESS experiment retains 95% of the sensitivity compared to PRSS. This means, that the loss due to T_2 relaxation is compensated by the maximum-echo sampling.

Discussion and Conclusion

The additional splitting from *J*-coupling leads to a greater information content of the spectra. The presented experimental improvements allowed an accurate extraction of this information through fitting [4]. The scan duration of 17 minutes is relatively long and was chosen mainly to increase sensitivity, the main limitation of spectroscopy. The scan time can be readily shortened by decreasing the amount of over-sampling in the indirect dimension or the number of phase cycles.

References

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