

# Single-Shot MR Spectroscopic Imaging with Partial Parallel Imaging

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## Introduction

High-speed MR spectroscopic imaging (MRSI) is of considerable interest for hyperpolarized <sup>13</sup>C imaging, which requires temporal resolution on the order of seconds [1]. Recently, Mayer et al. described spiral-based fast metabolic imaging of systems with sparse spectra, using spatial reconstruction corrected for frequency offsets [2]. In previous work we have combined Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) [3] with partial parallel imaging and demonstrated up to 4-fold acceleration of 2D spatial mapping using 8-channel array coil to achieve acquisition times as short as 16 s.

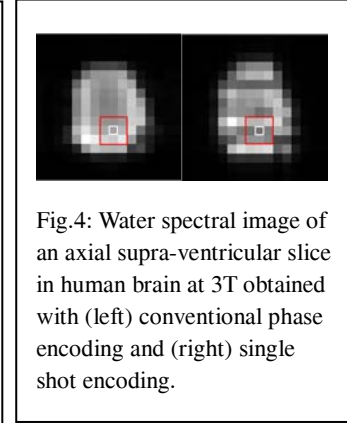
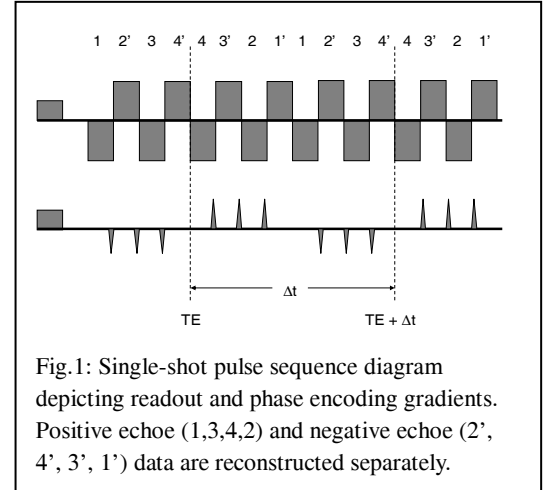
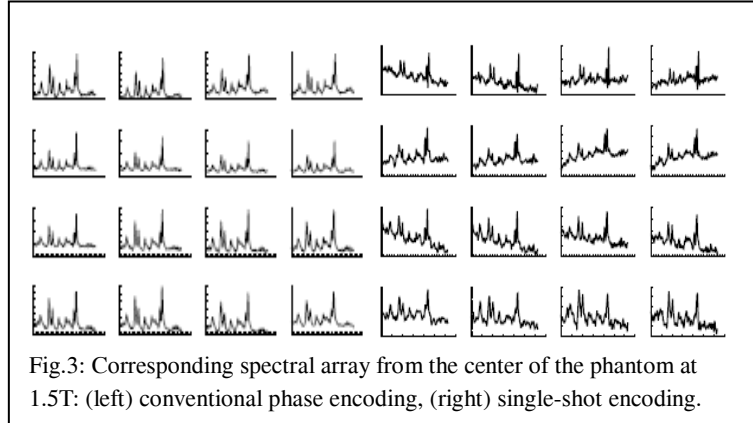
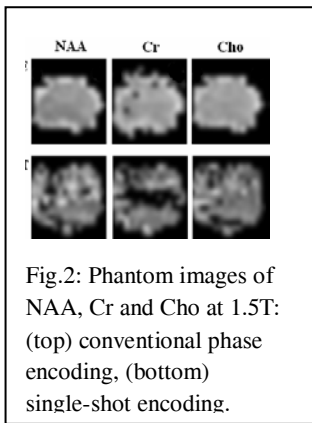
Here we extend this approach by integrating partial phase encoding into the PEPSI readout trajectory to enable single-shot MRSI. This approach enables increased spectral width as compared to fully phase encoded single-shot methods and reconstruction of absorption mode spectra.

## Methods

Spatial-spectral encoding of a zig-zag trajectory in  $k_x$ - $k_y$ - $t$ -space was performed by interleaving phase encoding gradient blips into the alternating readout gradient train (Fig.1). The phase encoding gradient moment steps through  $k_y$ -space by skipping R lines. The forward and backward  $k_y$ -trajectories were symmetric with respect to TE, minimizing first order phase errors in the reconstructed spectra. Even and odd-echo data were reconstructed separately using R-fold SENSE acceleration [3] and absorption mode spectra were combined after zero-order phase correction based on non-water suppressed data. Fully phase encoded data for coil sensitivity mapping and SNR comparison were obtained by adding a conventional phase encoding gradient to the sequence and by extracting the 2 echoes that correspond to the center of the  $k$ -space encoded by the phase encoding blips.

The pulse sequence was implemented on the Siemens Syngo platform with 2048 trapezoidal readout gradients (240  $\mu$ s duration), 100  $\mu$ s phase encoding blips, 4-fold uniform acceleration of phase encoding to encode a 16x16 spatial matrix with 192 mm minimum FOV. The reconstructed spectral width, which is determined by the time delay  $\Delta t$  (Fig.1), was 390 Hz. Data were acquired on a 1.5T Siemens Sonata equipped with 8-channel array coil and on a 3T Siemens Trio equipped with 32-channel array coil using short TE (15 – 35 ms), 3-pulse water suppression and 8-slice outer volume suppression. Spectra were quantified using LCMoDel. Fit quality was assessed using Cramer-Rao lower bounds.

## Results



The mean Cramer-Rao lower bounds of NAA, Cr and Cho (Figs.2&3) measured in a phantom with physiological metabolite solution at 1.5 T increased from 20 % with conventional phase encoding to 50 % with single-shot encoding. This is consistent with the expected 2-fold decrease in SNR due to 16-fold difference in measurement time and the 2-fold reduced sensitivity of the fully phase encoded scan due to the echo extraction; and additional g-factor (mean: 3.4) related noise amplification. Reduced noise amplification (mean g-factor: 1.6) was obtained at 3 T using the 32-channel coil array (Fig.4).

## Discussion

This study demonstrates feasibility of single-shot MRSI combining PEPSI with partial parallel imaging to increase spectral width. This methodology will not only be of interest for hyperpolarized MRSI, but also for MRSI in moving organs and for diffusion weighted MRSI [4]. Application at high field will benefit from the decrease in g-factor with field strength [5], enabling larger acceleration factor and spectral width.

## Acknowledgements

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