

Improving spatial localization in MR spectroscopic imaging with PSF-Choice

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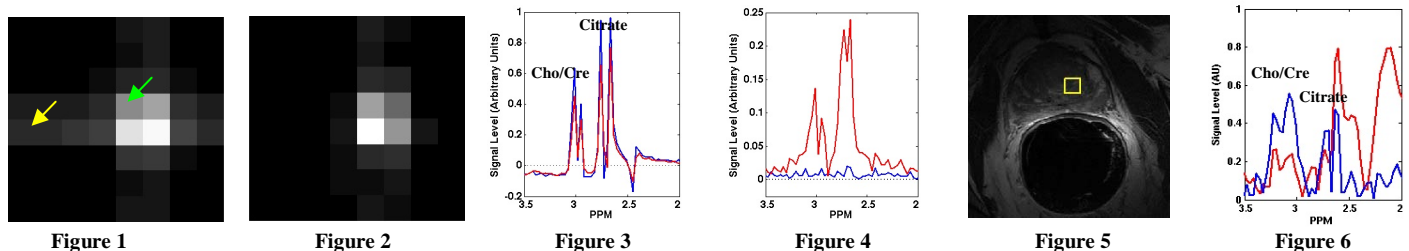
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Introduction

The purpose of this work is to improve the point-spread-function (PSF) of MR spectroscopic imaging (MRSI) to avoid corruption from neighboring voxels. Spatial resolution in MRSI is very low, thus spatial localization of spectra is difficult due to partial volume effects and truncation (or ringing) artifact. Poor localization is unavoidable if the voxel sizes are larger than the region-of-interest; however, it is degraded even further if the PSF extends beyond the voxel boundaries. Generally, the voxel size cannot be reduced due to SNR considerations; however, altering the PSF can improve localization by reducing or eliminating out-of-voxel contributions. Filtering can be used to alter the PSF, however, this either reduces spatial resolution or requires extending the acquisition in k-space at the cost of increased imaging time. Previously, a method called PSF-Choice was introduced that enables the shaping of the PSF in phase-encoding dimensions [1]. The method uses RF manipulation to improve spatial localization without increasing scan time or adversely affecting SNR. An implementation of this method is reported for MRSI of the prostate, where it is demonstrated that, in 13 of 16 pilot prostate MRSI scans, intra-voxel spectral contamination from lipid is significantly reduced.

Methods

PSF-Choice sequence: PSF-Choice (described in detail in [1]) replaces the standard 1D slice excitation with an additional pulse, creating a 2DRF pulse where excitation k-space is highly under-sampled (only 2 lines per excitation). With just 2 pulses in the RF train, we show that a Gaussian-shaped PSF can be created. Phase encoding remains unchanged but the amplitudes of the 2 sub-pulses in the train are varied for each phase-encoding step. The result is that overlapping (or aliased) Gaussian-shaped profiles are excited across the FOV due to the fact that excitation k-space is so sparsely sampled. On each phase encode, different sets of excitation k-space lines are excited resulting in different phase relationships between the aliased profiles. As in normal phase encoding, reconstruction is by Fourier transform, however, the resulting PSF is not the standard sinc-shaped profile but is instead determined by the weights applied to the sub-pulses. Virtually any PSF can be achieved with this method depending on the number of sub-pulses, the extent of the excitation k-space, and the weighting factors used.



MRSI Phantom Acquisitions: PROSE, a sequence modified from PRESS for MRSI of the prostate, was used to implement the PSF-Choice method along one dimension. Scans were conducted on GE Signa systems at both 1.5T and 3.0T. Figures 1 and 2 show MRS images obtained from a MRS phantom with a compartment containing prostate metabolites: choline, creatine and citrate. The images were obtained by integrating spectra under all metabolite peaks (from 2 to 3.5 ppm). The 8x8 image in Fig.1 is reconstructed from the normal PROSE phase-encoded acquisition. The 8x8 image in Fig.2 (shown with the same windowing as in Fig.1) is reconstructed from the acquisition with PSF-Choice encoding in the horizontal direction. Note the absence of truncation artifact in the PSF-Choice encoding direction in Fig.2 compared to the image in Fig.1 without PSF-Choice encoding. Figure 3 shows a comparison of the phased spectrum from a voxel in the metabolite compartment (see green arrow in Fig.1) obtained using PSF-Choice (plot in blue) and a spectrum from the same voxel obtained using the standard phase-encoding sequence (plot in red). Note the similarity in the quality of the spectra in the two approaches. Figure 4 shows magnitude spectra from a voxel at the edge of the FOV, well outside the selected region (see yellow arrow in Fig.1). There should be no signal outside the center 4 voxels; however, there is still significant signal in the spectrum obtained using the standard phase-encoding method (red plot in Fig.4) while the spectrum for PSF-Choice (blue plot in Fig.4) is at the noise level.

MRSI Prostate Acquisitions: The feasibility of PSF-Choice prostate MRSI has been evaluated in a study at 3T with 16 prostate patients. For the evaluation, a single 1.5cm slice was encoded using a 14x14 matrix in a 12cm FOV with TE/TR = 85/1000 ms. Data for both methods were acquired in an interleaved mode for a total scan time of 6.5 minutes after obtaining informed consent according to an approved IRB protocol. Figure 5 shows an axial reference image from one of the exams and spectra from one voxel (indicated by yellow box in Fig.5) are shown in Fig. 6. Metabolite peaks are clearly visible in the spectra obtained with PSF-Choice (blue plot). The spectrum obtained using standard phase encoding (red plot) is contaminated due to lipid signal from a neighboring voxel and is not diagnostically useful.

Evaluation of Prostate MRSI Results: The results for all 16 prostate scans were presented to an expert reader who was blinded as to which method was used. First, the reader was asked to determine which method showed the most out-of-voxel contamination due to fat by looking at the void outside the PRESS box. In 13 of the 16 cases, the standard phase-encoding method was selected as having the most contamination while, in the other 3 cases, neither method was selected. Next, the reader was asked to detect which method showed the most contamination of spectra within the prostate. In 10 of the 16 cases, the standard phase-encoding method was selected as having the most contamination of spectra in the prostate while, in the other 6 cases, neither method was selected. In not a single case was PSF-Choice selected as inferior according to these two evaluation criteria.

Discussion

PSF-Choice is being evaluated as to its ability to improve spatial localization for use in MRSI. The method is currently applied in-vivo in a single direction but has recently been implemented along two phase-encoding directions. As demonstrated in pilot prostate MRSI scans, PSF-Choice has the potential to improve data quality by significantly reducing contamination of spectra from fat signal in neighboring voxels.

References: [1] Magn. Reson. Med. 2005; 54(1):159-68.

Acknowledgement: This work is supported by NIH U41RR019703 and NIH R21CA110092.