Scan Time Reduction in Spectroscopic Imaging Using HYPR

J. O. Perry[1], O. Wieben[1], C. Mistretta[1,2], S. Reeder[2], Y. Wu[1], Y. Wu[1]

[1]Medical Physics, University of Wisconsin - Madison, Madison, Wi, United States, [2]Radiology, University of Wisconsin - Madison, Madison, Wi, United States

Introduction: Magnetic Resonance Spectroscopic Imaging (MRSI) provides spatially resolved information on metabolites across an image. There are several methods to obtain relevant chemical shift information with MRSI. Many techniques use localization schemes to excite a larger volume (~cm^3) of tissue and then record an FID from that volume [1]. Other approaches such as EPSI [2] use images from multiple echo times with a subsequent Fourier transform to obtain spectroscopic information. In this case, the signal can be used to form images at selected or all represented off-resonance frequencies or to present the frequency spectrum in a voxel. We propose to use of a novel technique based on a HighlY constrained backPRojection (HYPR) reconstruction method [3] to obtain chemical shift information with high spatial resolution in a much shortened scan time.

Methods: A simulation of the HYPR method for spectroscopic imaging was implemented in Matlab (Mathworks, Natick, MA). The HYPR algorithm is a technique that works on azimuthally severely undersampled projection data representing time frames in a time series. In the context of spectroscopic imaging they represent different echo times as in EPSI-like imaging [2]. Individual echo time images are then reconstructed by backprojecting unfiltered projections of the current time frame with a more fully sampled composite image from all echo times and a normalization step derived from projections in the composite image. This processing combines the SNR characteristics and low streak artifact level of the composite images with the information in the heavily undersampled image representing a specific echo time. In this simulation, an input image were generated simulating three metabolites in the brain at 1.5 T: NAA(-127.7Hz), CHO(-204.4Hz) and CRE(-191.6Hz).100 time frames with only 15 projections per time frame were generated at echo time of 1.8 ms and incremented by 1 ms for each time frame. This is a reduction in total scan time by a factor 17 compared to Cartesian sampling with equal spatial resolution. The projection angles were interleaved for subsequent time frames so that no angle was acquired more then once. The readout was 256. Gaussian noise with zero mean and a variance of .001 was added. The simulations were performed in three steps: 1. Generate images with chemical shift information and added noise, 2. HYPR reconstruction, and 3. Calculate voxel spectrum or metabolite image with a zero filling factor of 2.

Results: The simulated acquisition provided a spectroscopic reconstruction with frequency resolution of 5Hz covering a bandwidth of ±500Hz. The Metabolite maps obtained with HYPR at the off-resonance frequencies of the three metabolites are displayed in Fig. 1. At -122 Hz, only the voxels containing NAA are apparent in the image (a). In the other two maps, CRE (b) and CHO (c) are visible in the image. These effects are also shown in the normalized spectrum obtained from a representative voxel containing the 3 metabolites in the input images and with HYPR spectroscopy are shown in Fig. 2.

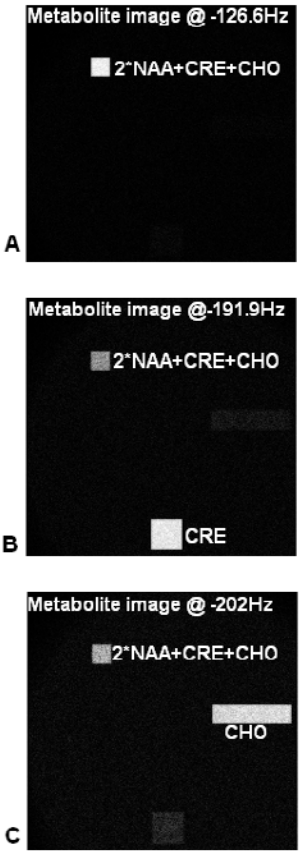

Figure 1: Metabolite images at three off resonance frequencies: -126Hz (a), -191Hz (b), -202Hz (c) reconstructed with HYPR.

Discussion: This simulation demonstrates that with HYPR reconstruction, spectra and metabolite images that closely resemble the input spectra and metabolite images can be obtained with speedup factors of 17 relative to Cartesian acquisition. Further studies are warranted to quantitatively investigate the ultimate tradeoffs between acceleration, SNR, and errors introduced and to validate the concept *in vitro* and *in vivo*.

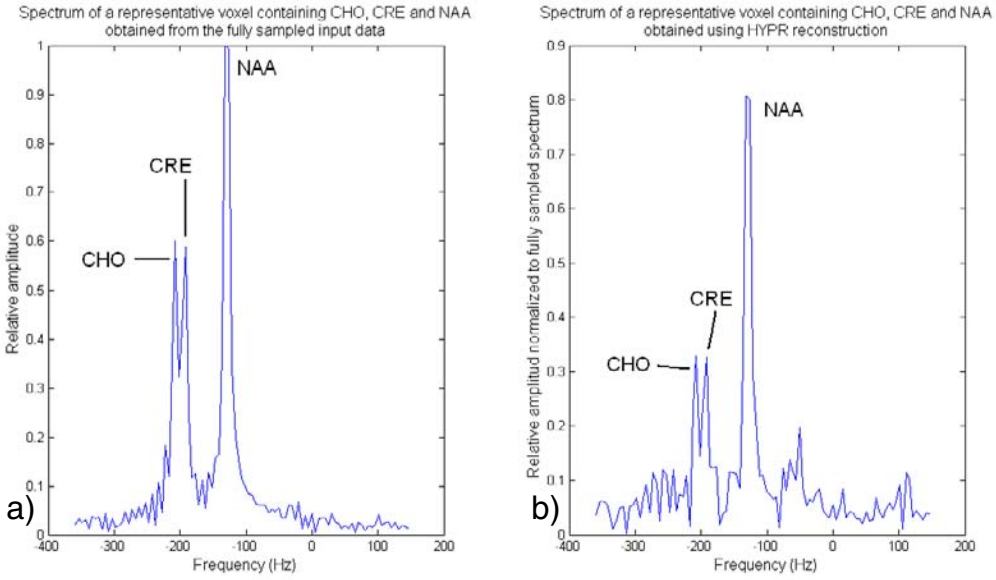

Figure 2: Spectra from a representative voxel containing three metabolites with (a) and without (b) HYPR reconstruction. While the noise level is increased from undersampling in (b), the peaks are readily identified.

References

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