ACCELERATED ECHO PLANAR J-RESOLVED SPECTROSCOPIC IMAGING IN PROSTATE CANCER: NONLINEAR RECONSTRUCTION USING TOTAL VARIATION AND MAXIMUM ENTROPY

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Target audience: MR pulse sequence developers, scientists/clinicians interested in accelerated imaging and non-linear reconstruction in prostate imaging

Introduction: Prostate cancer is the second leading cause of cancer death in men next to lung cancer. The American Cancer Society's estimates 238,590 new cases and 29,720 deaths from prostate cancer in 2013 (1). One in 6 men will get prostate cancer during his lifetime and one in 36 will die of this disease. Current limitations of single voxel and multivoxel prostate spectroscopic imaging are due to the overlap of metabolite resonances, quantifying few metabolites only (citrate (Cit), choline (Ch), creatine (Cr) and spermine (Spm)) and long echo times. A single-voxel based two-dimensional (2D) J resolved spectroscopic sequence (JPRESS) has been implemented and demonstrated in prostate cancer, and showed improved spectral dispersion due to the added spectral dimension (2,3). Compressed sensing was recently introduced as a powerful method to accelerate MRI by exploiting the sparsity of the images in a known transform domain to reconstruct non-uniformly undersampled (NUS) k-space data (4). By combining EPSI with JPRESS, 2D spectra can be recorded in multiple locations in prostate using four dimensional (4D) Echo-Planar J-Resolved Spectroscopic Imaging (EP-JRESI) combining 2 spectral with 2 spatial dimensions. A pilot feasibility was demonstrated recently to map metabolites in the human prostate (5). Maximum entropy (MaxEnt) and total variation (TV) image reconstruction have been used to reconstruct NUS indirect spectral and spatial dimensions (6). The goal of the present work was to compare and correlate the significant metabolites of the accelerated 4D EP-JRESI data acquired in prostate cancer and reconstructed with MaxEnt and TV.

Materials and Methods: Twenty two prostate cancer patients with a mean age of 63.8 years (range: 46–79 years) were investigated in this study. Prostate-specific antigen (PSA) varied from 0.7 to 22.8 ng/mL (mean of 6.23 ng/mL) and the mean delay between biopsy and MR investigation was 8 weeks. This study was approved by the Institutional Review Board, and informed consent was obtained from each patient. A Siemens 3T MRI Scanner with high-performance gradients (Trio-Tim, Siemens Medical Solutions, Erlangen, Germany) was used in this investigation. A 4D NUS EP-JRESI sequence was implemented on the 3T MRI scanner and the volume of interest (VOI) was localized using three slice-selective radio-frequency (RF) pulses (90^0-180^0-180^0). The total time for obtaining a fully sampled 4D EP-JRESI data (TR of 1.5s, 16ky*16kx, 64-100t_1, 512t_2) can be more than 25 minutes. The MaxEnt and TV reconstructions enable a stable and accurate reconstruction from the NUS based EP-JRESI data (25% of t_1 and k_y increments) with a reduced total time. The parameters for the EP-JRESI were: TR/TE/Avg = 1.5s/30ms/1-2, 16 phase encoding steps, 512 complex points with an F_2 bandwidth of 1190Hz. For the second dimension (F_1), 64 increments with bandwidths of 1000Hz were used. A 4X NUS was imposed along the plane containing incremented spectral and spatial dimensions (t_1 and k_y). The individual voxel volume in human prostate was 1ml. Two sets of data were collected, one with water suppression (WS) with a total scan time of 6-12 minutes and second with non-water suppression (NWS) using 1 average only. The NUS data was reconstructed by MaxEnt and TV separately. A modified Split-Bregman algorithm (6) solves the unconstrained TV optimization problem as shown in Eqn.(1) below:

$$\min_{m} \|\nabla_m\|_1 + \lambda \| F_u m - y\|_2 \qquad (1)$$

where ∇ is the gradient operator, m is the reconstructed data, $\|x\|_1$ is the l_1-norm, λ is a regularization parameter, F_u is the under sampled Fourier transform, and y is the under-sampled data. The above equation removes the incoherent artifacts due to NUS by minimizing the total variation (TV) while maintaining consistency with the sampled measurements. MaxEnt is a constrained convex optimization algorithm that uses a variant of the conjugate gradient method to iteratively solve the inverse problem (6-8):

$$\text{maximize } S_{1/2}(f) \text{ s.t. } \|F^{-1} Kf - D\|_2 \leq \sigma \qquad (2)$$

where f is the estimated fully-sampled spectrum at each iteration, F^{-1} is the inverse Fourier transform, K is the NUS matrix, D is the measured time-domain data, σ is the noise standard deviation, and $S_{1/2}(f)$ is the spin-½ entropy of the estimated spectrum (6-8).

Results and Discussion: All NUS based 4D EP-JRESI data were processed using TV and MaxEnt reconstruction with custom processing software. We observed decreased levels of Cit, Spm and mI with respect (Ch+Cr) in cancer locations compared to non-cancer locations in both TV and MaxEnt reconstruction. Also we have compared and correlated the TV with MaxEnt reconstruction methods of a few metabolites which showed significant decrease as well as decreasing trend in the cancer locations compared to non-cancer locations. Figure 1 shows the correlation of maxEnt and TV of Cit/(Ch+Cr) and Spm/(Ch+Cr) in cancer and non-cancer location. Similarly a positive correlation was found in the following metabolites in cancer locations: Cit/(Ch+Cr) (R^2=0.8708), mI/(Ch+Cr) (R^2=0.972) and Spm/(Ch+Cr) (R^2=0.7348). Also we observed positive correlation of Spm and mI in non-cancer location. Table.1 shows the metabolites ratio of maxEnt and TV in cancer and non-cancer locations. There was an overlap between cancer and non-cancer locations, possibly due to the low signal-to-noise ratio of the Cr peak. In addition, Ch and Cr were not always well resolved especially in cancer locations, adding to the uncertainty. The advantage of NUS based 4D EP-JRESI sequence will record short TE-based spectra from multiple regions of a prostate and will show more metabolites, such as glutamate (Glu), glutamine (Gln), myo-inositol (mI), taurine (Tau), lactate (Lac), and choline groups, in addition to the normally detected Cit, Cr, Ch and Spm.

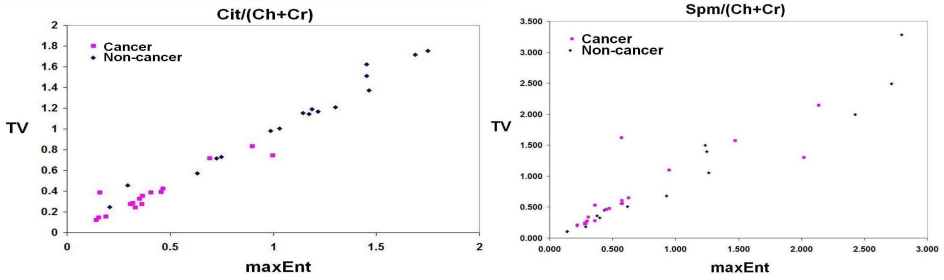

Figure 1. Correlation of MaxEnt-processed data with TV of Cit and Spm ratios

Metabolites wrt (Ch+Cr)	Cancer (Mean ± SD)	Non-Cancer (Mean ± SD)
maxEnt		
Cit	0.378±0.213	1.115±0.442
Spm	0.498±0.323	0.633±0.560
mI	0.189±0.119	0.232±0.146
TV		
Cit	0.413±0.252	1.108±0.449
Spm	0.505±0.319	0.918±0.817
mI	0.214±0.154	0.276±0.215

Table.1. Metabolites ratio of maxEnt and TV

Conclusion: We were able to detect and quantity metabolites using NUS based 4D EP-JRESI data acquired in clinically acceptable time (<12 minutes). We have shown that it possible to undersample the 4D EP-JRESI sequence with an acceleration factor of 4X and the data can be reliably reconstructed using TV and MaxEnt methods. Both non-linear reconstruction methods provide comparable results.

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