Comparison of 2D Iterative Frame Based and 3D Direct Compressed Sensing Reconstruction for Accelerated Phosphorus MR Spectroscopic Imaging of Human Brain

Gokce Hale Hatay[1], Emre Okeer[2], Bahattin Hakyemez[2], and Esin Ozturk-Isik[3]

[1]*Department of Electrical and Electronics Engineering, Yeditepe University, Istanbul, Turkey,* [2]*Department of Radiology, Uludag University, Bursa, Turkey,* [3]*Department of Biomedical Engineering, Yeditepe University, Istanbul, Turkey*

Introduction: Two main limitations of using ^{31}P-MRSI for imaging brain tumor patients are inherent low signal to noise ratio (SNR) and long data acquisition times. Compressed sensing reconstruction [1] has been successfully applied for accelerating ^{31}P MR spectroscopic imaging with less SNR penalty [2]. However, the reconstruction of the compressed sensing accelerated 3D ^{31}P-MRSI data was conducted as an iterative 2D frame based reconstruction for a total reduction factor (R) of 1.6. This study investigated the feasibility of an improved 3D direct compressed sensing reconstruction for a faster (R=4) ^{31}P-MRSI, and studied its relative performance with respect to the 2D iterative frame based reconstruction.

Methods: A ^{31}P MR spectrum was acquired from the frontoparietal lobe of a volunteer, who provided informed consent, with image selected in vivo spectroscopy (ISIS) [3] on a 3T MR scanner (Philips Medical Systems) using a surface ^{31}P coil (TR=5s, 128 averages, 3000 Hz, dwell time = 0.333 ms, 1024 points, 27cc voxel size, scan time=11 min). Time domain signal parameters quantified using AMARES within jMRUI program [4] were used to create a healthy and a tumor spectrum in MATLAB (The Mathworks Inc., Natick, MA) [2]. Two dimensional 16x16 and 32x32 ^{31}P MR spectroscopic imaging datasets that included a tumor region at the top left voxels and a healthy region at the rest of the array were simulated. Two random undersampling patterns that reduced the k-space data by a factor of 4.26 for 16x16 and by 3.71 for 32x32 arrays while preserving the central part of the k-space were employed. The effective spatial resolution of the undersampling patterns was estimated using a simulation of the 3D point-spread function (PSF) in MATLAB [5]. For 2D iterative frame based reconstruction, reduced datasets were first inverse Fourier transformed along k_y, and for each y point, k_x-k_f data were reconstructed using the SparseMRI software package [1]. Then, the resultant data were inverse Fourier transformed along k_x, and for each x point, k_y-k_f data were reconstructed. For 3D direct reconstruction, routines in SparseMRI software package were modified to directly reconstruct 3D k_x-k_y-k_f compressed sensing accelerated ^{31}P-MRSI data. L1-norm and total variation weights were chosen empirically as 0.01 and 0.001, respectively. A 2D length-4 Daubechies Wavelet transform was used as the sparsifying transform. A ranksum test was used to see if tumor and original voxels had significantly different Pi/PCr, PCr/β-ATP, and PCr/PE metabolite ratios in original and 2D and 3D compressed sensing reconstructed (CS) datasets. Bonferoni multiple comparison correction was applied, and a p-value of less than 0.005 was considered as significant. A Bland Altman statistical test was used to detect a significant difference between the original and 2D iterative frame based and 3D direct reconstructed compressed sensing datasets.

Results and Discussion: Figure 1 shows ^{31}P MR spectra of eight voxels from the 32x32 original and 2D iterative frame based and 3D direct reconstructed compressed sensing datasets. The top four voxels had tumor spectra, and the other four voxels had healthy spectra. Tumor and healthy spectral regions were clearly separable in 3D reconstructed CS dataset. However, spectra of the 2D iterative reconstructed CS dataset was distorted in several voxels and the peaks were not visible for R=3.7. Effective spatial resolution factor was calculated as 1.213 for 32x32, and 1.821 for 16x16 CS undersampling pattern. Table 1 shows Pi/PCr, PCr/β-ATP, and PCr/PE metabolite ratios in tumor and healthy regions for the original and CS datasets. The ranksum test showed statistically significantly different peak ratios between healthy and tumor voxels for the original and 3D direct reconstructed CS datasets ($p<0.005$), but not for the 2D iterative frame based reconstructed CS dataset. Table 2 shows the results of Bland Altman statistical test that looked at the bias and the variation of the peak ratios between the original and CS datasets. Pi/PCr, PCr/β-ATP, and PCr/PE were very similar with small bias between the original and 3D direct reconstructed compressed sensing dataset. However, there were only a few outliers due to the small standard deviation. For the 2D iterative reconstructed dataset, the bias and standard deviation were large for all the peak ratios. In conclusion, this study showed that 3D direct compressed sensing reconstruction works better than a 2D iterative frame based reconstruction.

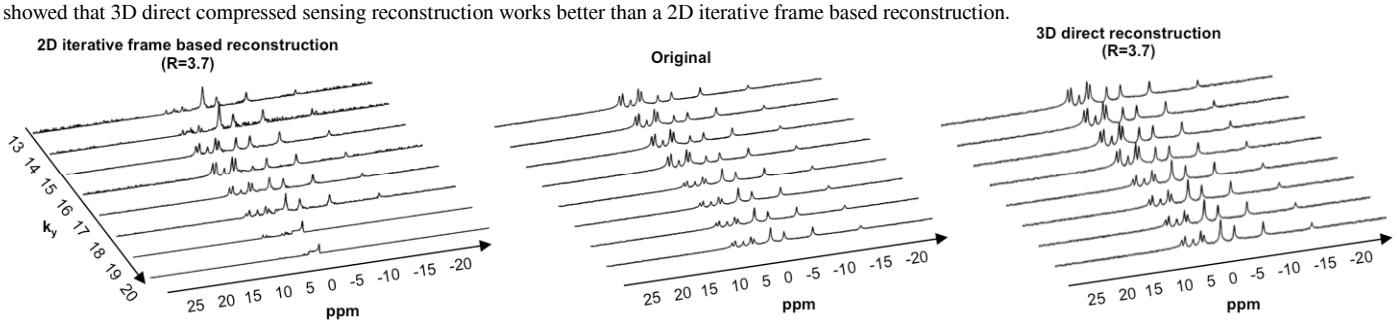

Figure 1. Eight voxels showing the transition between the healthy (bottom four) and tumor (top four) voxels for the original and 2D and 3D reconstructed CS datasets.

Table 1. Pi/PCr, PCr/β-ATP, PCr/PE metabolite ratios and in tumor (T) and healthy (H) regions of the original and 2D and 3D reconstructed compressed sensing (CS) datasets.

			Pi/PCr	PCr/β-ATP	PCr/PE
T	Original		0.9±0.0	1.6±0.0	0.7±0.0
	16x16	2D CS	29.3±113	13.6±54	33.8±120
		3D CS	0.72±0.04	1.9±0.1	0.9±0.1
	32x32	2D CS	52.8±154	4.7±6.2	43.6±167
		3D CS	0.36±0.03	2.9±0.2	2.7±0.5
H	Original		0.3±0.0	3.04±0.0	2.7±0.0
	16x16	2D CS	0.45±0.5	26.9±85.9	58.3±205
		3D CS	0.86±0.09	1.7±0.2	0.7±0.1
	32x32	2D CS	0.86±0.09	1.7±0.2	0.7±0.1
		3D CS	0.34±0.0	2.7±0.05	2.4±0.1

Table 2. Bland Altman test results for the number of outliers, bias and std(bias) between the peak ratios of the similarity of the original and 2D and 3D reconstructed compressed sensing datasets.

Bland Altman Test Results (16x16)		2D Iterative Frame Based Reconstruction			3D Direct Reconstruction		
		Pi/PCr	PCr/β-ATP	PCr/PE	Pi/PCr	PCr/β-ATP	PCr/PE
T	#outliers	4	2	3	0	1	2
	mean(diff)	29.3	12.6	33.4	0.1	0.3	0.2
	std(diff)	112.7	54.1	120.3	0.04	0.1	0.09
H	#outliers	4	3	3	0	4	4
	mean(diff)	52.6	3.7	43.6	0.02	0.1	0.4
	std(diff)	154.7	5.3	166.7	0.02	0.1	0.3

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