# Accelerated Phosphorus MR Spectroscopic Imaging of Human Brain Using Compressed Sensing

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**Introduction:** Phosphorus (31P) MR spectroscopic imaging can provide important information regarding the energetic and ischemic status of the tissue, as well as membrane degradation and synthesis, and pH for brain tumors. One of the major limitations of acquiring 31P MRSI in brain tumors is the long data acquisition time. Phosphorus is 15 times less MR sensitive than proton, and 31P MRSI requires larger voxels and averaging several acquisitions for adequate SNR. Compressed sensing has been proposed to accelerate MR data acquisition with less SNR penalty than other parallel imaging techniques [1], and has been successfully applied for acquiring faster 13C MR spectroscopic imaging [2,3]. In this study, we investigate the application of compressed sensing for accelerated 31P MR spectroscopic imaging.

**Methods:** A volunteer, who provided informed consent, was scanned on a 3T MR scanner (Philips Medical Systems) using a surface 31P coil. The coil had a disk at the center containing water and methylphosphonic acid, which was used as a localization reference. TFE survey images were acquired with the body coil (TR=75 ms, TE=5 ms, flip angle=30º). A 31P MR spectrum was acquired from the frontoparietal lobe with image selected in vivo spectroscopy (ISIS) [4] (TR=5s, 128 averages, 3000 Hz, dwell time = 0.333 ms, 1024 points, 27cc voxel size, scan time=11 min). The spectrum was processed using apodization with a 10 Hz Gaussian filter, phase correction and baseline removal and quantified using AMARES [5] within jMRUI. The amplitude (a) and frequency (f) factors calculated for each peak, k, with AMARES were used to reconstruct the time domain signal in MATLAB (The Mathworks Inc., Natick, MA) for creating a spectrum of a healthy voxel as,

$$y_n = \sum_k a_k e^{-(d_k + i2\pi f_k)t_n}$$ [1],

where $d_k$ was set to 30 Hz for all the peaks. Similarly, a spectrum of a tumor voxel was simulated. The peak amplitudes of the tumor spectrum were (0.49, 1.0, 1.0, 1.0, 2.16, 1.86, 1.47, 2.06, 2.63) times the peak amplitudes of the healthy spectrum for the PCr, γ- ATP, α- ATP, β- ATP, GPC, GPE, Pi, PC, and PE peaks, respectively. A 2D 8x8 31P MR spectroscopic imaging dataset that included a tumor region at the top left 4 by 4 voxels and a healthy region at the rest of the array was simulated using the healthy and tumor spectra. A random undersampling pattern that reduced the k-space data by a factor of 1.6 while preserving the central part of the k-space was implemented in MATLAB. The reduced dataset was 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 was inverse Fourier transformed along $k_x$, and for each x point, $k_y$-$k_f$ data were reconstructed. L1-norm and total variation weights were chosen empirically as 0.001. 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 signal to noise ratio (SNR) for PCr, Pi and β-ATP in original and compressed sensing reconstructed (CS) datasets. A p-value of less than 0.05 was considered as significant. A Bland Altman statistical test was used to detect a significant difference between the original and CS datasets.

**Results and Discussion:** Figure 1 shows 31P MR spectra of eight voxels from the original and compressed sensing reconstructed 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 both spectral datasets. Table 1 shows Pi/PCr, PCr/β-ATP, PCr/PE metabolite ratios and the SNR of PCr and Pi peaks in tumor and healthy regions for the original and compressed sensing datasets. Table 2 shows the results of Bland Altman statistical test that looked at the bias and the variation of the peak ratios for the original and compressed sensing datasets. Bland Altman test results showed that Pi/PCr, PCr/β-ATP in tumor regions, and PCr/PE in healthy regions were very similar (no outliers) between the original and CS datasets. However, there were only one outlier for PCr/PE in tumor, and Pi/PCr and PCr/β-ATP in healthy regions, but the bias was only significantly large for PCr/β-ATP in the healthy region. The denoising effect of compressed sensing reconstruction resulted in slightly higher SNR for the peaks especially in the tumor region. Tumor/healthy SNR ratios were higher for all the peaks in CS datasets than the original datasets. The ranksum test showed significantly lower PCr and higher Pi in tumor regions than healthy regions for both datasets ($p<0.05$). In conclusion, this study showed that compressed sensing reconstruction could be applied for faster 31P MR spectroscopic imaging. Future studies will measure the performance of compressed sensing reconstruction for 31P MRSI in patients diagnosed with brain tumors.

**Table 1.** Pi/PCr, PCr/β-ATP, PCr/PE metabolite ratios and the SNR values of PCr and Pi peaks in tumor and healthy regions of the original and compressed sensing datasets.

| | **Compressed Sensing (mean±std)** | | | | | **Original (mean±std)** | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Pi/PCr | PCr/β-ATP | PCr/PE | SNR(PCr) | SNR(Pi) | Pi/PCr | PCr/β-ATP | PCr/PE | SNR(PCr) | SNR(Pi) |
| Tumor | 0.82±0.2 | 1.83±0.36 | 0.86±0.3 | 31.73±11.7 | 23.87±3.47 | 0.92±0 | 1.60±0 | 0.65±0 | 22.8±0 | 20.87±0 |
| Healthy | 0.46±0.2 | 4.14±2.03 | 1.77±0.72 | 38.63±9.65 | 17.64±9.18 | 0.41±0 | 2.87±0 | 2.39±0 | 42.49±0 | 17.20±0 |
| Tumor/ Healthy | - | - | - | 0.82 | 1.35 | - | - | - | 0.54 | 1.21 |

**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 compressed sensing datasets.

| **Bland Altman test** | | **Pi/PCr** | **PCr/ β-ATP** | **PCr/PE** |
|---|---|---|---|---|
| **Tumor** | #outliers | 0 | 0 | 1 |
| | mean(difference) | 0.17 | 0.33 | 0.24 |
| | std(difference) | 0.14 | 0.28 | 0.25 |
| **Healthy** | #outliers | 1 | 1 | 0 |
| | mean(difference) | 0.09 | 1.41 | 0.70 |
| | std(difference) | 0.19 | 1.92 | 0.64 |

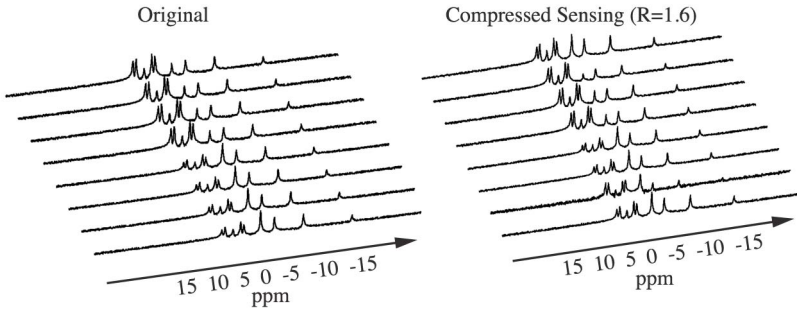


**Figure 1.** Eight voxels showing the transition between the healthy (bottom four) and tumor voxels (top four) for the original and compressed sensing datasets.

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