Combining parallel detection of proton spectroscopic imaging (PEPSI) measurements with a data-consistency constraint improves SNR

Shang-Yueh Tsai[1], Ying-Hua Chu[2], Yi-Cheng Hsu[3], Wen-Jui Kuo[4], and Fa-Hsuan Lin[2]

[1]*Graduate Institute of Applied Physics, National Cheng-Chi University, Taipei, Taiwan,* [2]*Institute of Biomedical Engineering, National Taiwan University, Taipei, Taiwan,*

[3]*Department of Mathematics, Nnational Taiwan University, Taipei, Taiwan,* [4]*Institute of Neuroscience, National Yang-Ming University, Taipei, Taiwan*

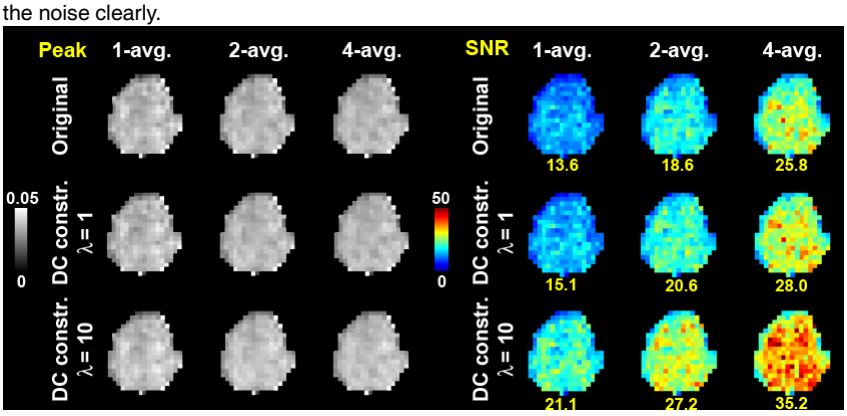
TARGET AUDIENCE Scientists interested in reducing noise in spectroscopic imaging data acquired from a coil array.

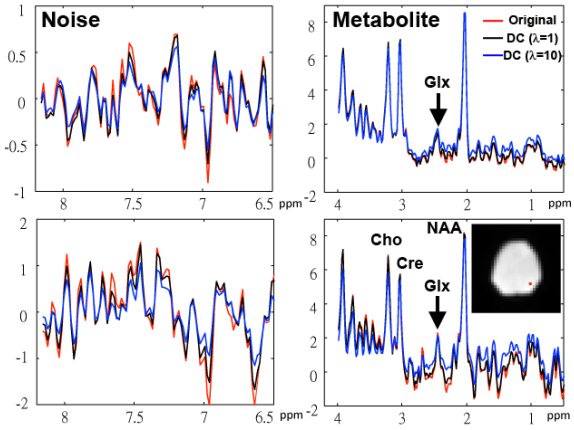
PURPOSE Fast MR spectroscopic imaging (MRSI) can be achieved using EPI[1] or spiral readouts[2]. Yet one major challenge of MRSI is its relative low signal-to-noise ratio (SNR), which can be improved by using a surface coil array. Instead of utilizing the spatial sensitivity of different channels of a coil array to accelerate image encoding at the cost of the reduced SNR[3,4], here we propose to exploit this sensitivity information to enforce the *k*-space data-consistency (DC) in order to suppress noise and consequently to improve MRSI SNR. With *in vivo* experimental data at 3T using a 32-channel coil array, we found that the DC constraint can improve the SNR of PEPSI by approximately 40%.

METHODS Assuming the coil sensitivity profiles of a MRI detection array are distinct and spatially smooth, each chosen *k*-space data point of a coil can be expressed as the linear combination of the k-space data points from all coils at the vicinity of the chosen *k*-space data point. Mathematically, such DC relationship is $\mathbf{x} = \mathbf{G}\,\mathbf{x}$, where $\mathbf{x}$ denotes the concatenation of *k*-space data from all coils and $\mathbf{G}$ is a convolution kernel[5]. Practically, we first estimated the convolution kernel $\mathbf{G}$ and then reconstructed images at each channel $\mathbf{x}$ by minimizing the cost function $|\mathbf{Sx}-\mathbf{y}|^2+\lambda|\mathbf{Gx}-\mathbf{x}|^2$, where $\mathbf{S}$ is an index matrix indicating the *k*-space coordinates of the acquired data, $\mathbf{y}$ is the acquired *k*-space data across all channels, and λ is a regularization parameter.

PEPSI[1] was performed on healthy volunteers using a 3 T scanner (Tim Trio, SIEMENS Medical Solutions, Erlangen, Germany) and a 32-channel array. PEPSI data were acquired from a para-axial slice at the upper edge of the ventricles with TR 2 s and short TE (15 ms), using a 32x32 image matrix. Complete 8-slice outer volume suppression was applied along the perimeter of the brain to suppress lipid signal. Even- and odd-echo data were reconstructed separately using a non-water suppressed reference scan for automatic phasing and frequency shift correction. The total scan time for 1-, 2-, 4-average data were 64, 128, and 256 s. We used non-water suppressed image to estimate $\mathbf{G}$ because it has a higher SNR. Then an iterative reconstruction method based on the conjugated gradient algorithm was used to minimize the cost for each time point of the water-suppressed scan. We chose $\lambda = 0$ (no DC constraint), 1, and 10 in this study. Finally, all images were reconstructed by sum-of-squares.

RESULTS Figure 1 shows the peak value and SNR maps of N-Acetyl-Acetate (NAA) using the standard deviation between 6.5 and 8 ppm as the noise estimate. The SNR in the brain parenchyma was slightly and significantly improved with DC constraint λ =1 and 10 respectively. Comparing to the metabolite peak with λ =0, the metabolite peaks were similar with λ =1 and slightly decreased with λ =10. However, the noise level was clearly suppressed in λ =1 and further suppressed with λ =10. Thus overall SNR (yellow numbers) is improved with λ =1 and λ =10. Similar improvement was observed for 1-, 2-, and 4-average data. Using the DC constraint with λ = 10, the SNR for 1- and 2-average data approximated the SNR for 2- and 4-average data without using the DC constraint. Figure 2 shows the spectra in metabolic range between 0.5 and 4 ppm as well as in noise range between 6.5 to 8 ppm. NAA, creatine (Cre), and choline (Cho) metabolite peaks were clearly identified in all spectra. Noise level was reduced by the DC constraint for both 1- and 4-average data. Interestingly, around 2.2 ppm, spectra show similar peaks, potentially from the glutamine/glutamate (Glx). Yet the DC constraint suppressed the noise clearly.





DISCUSSION We proposed a MRSI reconstruction algorithm enforcing the *k*-space data consistency among channels of a coil array such that the noise disturbing such a consistency is suppressed. Different from the optimal reconstruction of coil array images[6], our method does not require explicit estimate of coil sensitivity maps, which in practice can be tedious. The results of using a DC constraint to significantly suppress the noise at the cost of marginally reducing the signal (metabolite peak) is similar to the advantage of using a prior to regularize parallel functional MRI reconstruction[7]. Yet our method does ot need to explicitly specify the prior either. Choosing a larger regularization parameter (λ =1000) can bias the reconstruction into the null space of $\mathbf{G}$ (not shown). The proposed reconstruction algorithm can also incorporate image sparsity feature in order to further suppress noise. Our results suggest that the carefully optimized combination of MRSI data from a coil array can save around 50% of scanning time to obtain a similar image and spectra SNR.

REFERENCES

1 Posse S., Tedeschi G., Risinger R. et al. High speed 1H spectroscopic imaging in human brain by echo planar spatial-spectral encoding. Magn Reson Med.1995; 33:34-40.

2. Adalsteinsson E., Irarrazabal P., Topp S. et al. Volumetric spectroscopic imaging with spiral-based k-space trajectories. Magn Reson Med.1998; 39:889-898.

3. Sodickson D. K. & Manning W. J. Simultaneous acquisition of spatial harmonics (SMASH): fast imaging with radiofrequency coil arrays. Magn Reson Med.1997; 38:591-603.

4. Pruessmann K. P., Weiger M., Scheidegger M. B. et al. SENSE: sensitivity encoding for fast MRI. Magn Reson Med.1999; 42:952-962.

5. Lustig M. & Pauly J. M. SPIRiT: Iterative self-consistent parallel imaging reconstruction from arbitrary k-space. Magn Reson Med.2010; 64:457-471.

6. Roemer P. B., Edelstein W. A., Hayes C. E. et al. The NMR phased array. Magn Reson Med.1990; 16:192-225.

7. Lin F., Huang T., Chen N. et al. Functional MRI using regularized parallel imaging acquisition. Magn Reson Med.2005; 54:343-353.