# Accelerating High-Resolution Semi-LASER <sup>1</sup>H-MRSI Using SPICE

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# Synopsis

Most of the current <sup>1</sup>H-MRSI techniques have several major practical limitations, including long data acquisition time, low spatial resolution and poor SNR. To overcome these limitations, we accelerate the semi-LASER technique by incorporating subspace modeling. With this improvement, semi-LASER is cable of achieving 1.9×1.6 mm<sup>2</sup> resolution in a 1.5 minutes scan, which is a significant improvement over the conventional semi-LASER. This imaging capability has been validated with *in vivo* experiments, and it may significantly enhance the practical utility of <sup>1</sup>H-MRSI.

#### Introduction

 $^1$ H-MRSI has long been recognized as a powerful tool for noninvasive metabolic imaging, but its applications are still quite limited due to several barriers, including long acquisition time, low resolution and poor SNR. To overcome these limitations, a novel data acquisition and processing method known as SPICE (SPectroscopic Imaging by exploiting spatiospectral CorrElation) has been recently proposed  $^{1-3}$ . SPICE exploits a unique property of spectroscopic signals known as partial separability (PS) $^4$ . This property reveals that high-dimensional spectroscopic signals reside in very low-dimensional subspaces and enables special data acquisition and image reconstruction strategies to be used to achieve rapid high-resolution MRSI. In this work, we integrate SPICE with semi-LASER (double spin echo sequence for Localized Adiabatic SElective Refocusing) $^5$  to accelerate  $^1$ H-MRSI. With this improvement, semi-LASER is cable of achieving  $1.9 \times 1.6 \text{ mm}^2$  resolution in 1.5 minutes, which is a significant improvement over the conventional semi-LASER MRSI. This imaging capability has been validated with *in vivo* experiments, and is expected to enhance the practical utility of  $^1$ H-MRSI.

## Theory and Method

# Data acquisition

The proposed acquisition scheme is illustrated in Fig. 1, which contains two key features: a) semi-LASER excitation, and b) large k-space coverage using extended EPSI trajectories  $^{6,7}$  and sparse sampling. Semi-LASER pulses are utilized to localize a restricted volume of interest, which helps to avoid signal contamination from subcutaneous lipid. The ADC is turned on for a short period (10 ms) during excitation to collect navigator signals for detection and correction of field drifts. Bipolar EPSI readouts are utilized to simultaneously encode spatial and spectral information. As shown in Fig. 2c, we use a much longer EPSI readout than conventional EPSI methods to achieve extended k-space coverage needed for high resolution. This sampling scheme will result in a violation of the temporal Nyquist sampling criterion, which is permissible by SPICE due to the use of the subspace model for reconstruction of the spatiospectral function. In addition, by taking advantage of parallel imaging, we sparsely sample outer k-space in the phase-encoding direction to further extend k-space coverage (Fig. 2b). These data acquisition strategies together enable the acquisition of a single-slice MRSI data set with  $1.9 \times 1.6 \text{ mm}^2$  nominal resolution in only 1.5 minutes.

#### Data processing

Our data acquisition scheme requires special methods for data processing, including: a) detection and correction of field drifts, b) removal of the residual water signal, c) reconstruction of the spatiospectral function.

First, resonance frequency drifts are corrected using field drift navigators<sup>8</sup>, and eddy current effects are corrected using two navigators with opposite polarities, acquired at the end of the scan. Then, the spatially under-sampled k-space data is interpolated using a hybrid GRAPPA/SENSE method<sup>9</sup>.

Second, the residual water signals are effectively removed using the union-of-subspaces model 10, where metabolite and water signals are assumed to reside in different low-dimensional subspaces.

Finally, the spatiospectral distribution of the desired molecules (metabolites and neurotransmitters) is reconstructed using the SPICE reconstruction method that incorporates both pre-learned spectral bases and spatial priors. Specifically, we express the desired spatiospectral function as

$$ho(x,f) = \sum_{l=1}^L c_l(x) arphi_l(f),$$

where  $\{\varphi_l(f)\}_{l=1}^L$  are pre-learned spectral basis functions, and  $\{c_l(x)\}_{l=1}^L$  are unknown spatial coefficients. The spatial coefficients are determined by solving the following regularized least-squares problem:

$$\hat{C} = rg \min_{C} \, \left\| d - \Omega \mathcal{F} B_0 \left( C \Phi 
ight) 
ight\|_2^2 + \lambda \left\| W D \left( C \Phi 
ight) 
ight\|_2^2,$$

where C and  $\Phi$  are matrix representations of the spatial coefficients and the spectral bases, respectively; d is the nuisance-removed (k,t)-space data;  $B_0, \mathcal{F}$ , and  $\Omega$  represent field inhomogeneity, Fourier encoding and sampling operators, respectively;  $\lambda$  is a regularization parameter; D is the finite difference operator and W is a weighting matrix for edge-preserving regularization. Once the spatial coefficients are determined,  $\rho = \hat{C}\Phi$  will give the desired metabolite distributions.

# **Results and Discussion**

In vivo data were acquired from healthy volunteers (with IRB approval) on a  $3~\mathrm{T}$  Siemens Prisma scanner. A single-slice semi-LASER  $^1\text{H}$ -MRSI sequence with weak water suppression was implemented with  $\mathrm{FOV} = 180 \times 180~\mathrm{mm}^2$ , slice thickness  $= 10~\mathrm{mm}$ , and  $\mathrm{VOI} = 90 \times 90 \times 10~\mathrm{mm}^3$ . Parallel imaging based sparse sampling (R = 1.45) was designed to cover extended k-space so as to achieve an in-plane resolution of  $1.9 \times 1.6~\mathrm{mm}^2$  (  $\mathrm{matrix\ size} = 96 \times 110$ ). Other parameters were:  $\mathrm{TE}/\mathrm{TR} = 40/1250~\mathrm{ms}$ , echospace  $= 1.76~\mathrm{ms}$ , total acquisition time  $= 1.5~\mathrm{minutes}$ .

Some representative results are shown in Figs. 3 and 4. In Fig. 3 we show the reconstructed high-resolution metabolite maps, overlaid on a  $T_1$ -weighted structural image. In Fig. 4 we show localized spectra within the selected region. As can be seen, the new improved semi-LASER method produced high-resolution metabolite maps and high-quality localized spectra with significantly reduced data acquisition time. We expect this capability to enhance the practical utility of  $^1$ H-MRSI.

#### Conclusion

We have successfully integrated SPICE into semi-LASER to significantly enhance its spatial resolution while reducing its data acquisition time. Experimental results show that high-quality 2D  $^1$ H-MRSI data from the brain with  $1.9 \times 1.6~\mathrm{mm}^2$  nominal resolution can be obtained in  $1.5~\mathrm{minutes}$ . We expect that this capability will enhance the practical utility of  $^1$ H-MRSI in various clinical and research applications.

## Acknowledgements

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#### **Figures**

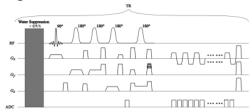


Figure 1. Pulse sequence diagram. Water and out-of-VOI signals are suppressed first, followed by the semi-LASER pulses. Navigator signals are collected between the third and fourth adiabatic pulses for detection and correction of resonance frequency drifts.

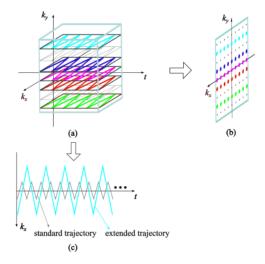


Figure 2. Illustration of (k-t) space trajectory. Note that  $k_y$  is under-sampled spatially and the echo spacing also violates temporal Nyquist criterion because of the extended EPSI trajectories used.

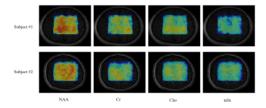


Figure 3. Representative peak integral metabolite maps reconstructed from *in vivo* data collected in 1.5 minutes with 1.9×1.6 mm<sup>2</sup> nominal resolution.

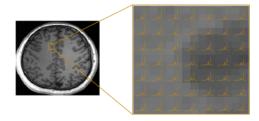


Figure 4. Localized spectra from the selected region. The spectra were obtained from an *in vivo* data set collected in 1.5 minutes with 1.9×1.6 mm<sup>2</sup> nominal resolution.

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