

# Exploiting Known Resonance Structure of Lipids for Improved Nuisance Removal from $^1\text{H}$ -MRSI Data

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Running title: Exploiting Known Resonance Structure of Lipid for  $^1\text{H}$ -MRSI Nuisance Removal

Submission category: Note

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Approximate word count for the manuscript body: 26xx words.

## ABSTRACT

**Purpose:** To exploit the known resonance structures of lipid (and water) signals for improved nuisance removal from  $^1\text{H}$ -MRSI data.

**Methods:** The proposed method uses the resonance structures of water and lipid molecules to construct a parametric model for the nuisance signals and combines it with the union-of-subspaces (UoSS) nuisance removal framework. Specifically, this parametric model is used to estimate the water and lipid signals, which are used to estimate the subspaces for the water and lipid signals, respectively. The estimated subspaces are then incorporated in the UoSS framework for improved nuisance removal performance.

**Results:** The proposed method was validated using three-dimensional MRSI data collected from the brain using an FID sequence with short-TE and no suppression pulses from healthy subjects. Improvement in reducing the level of nuisance signals using the proposed method compared to the original UoSS method was observed without any noticeable distortion to the desired metabolite spectra. Moreover, a subspace-based spatio-spectral reconstruction was also performed to further demonstrate the effectiveness of the proposed nuisance removal method.

**Conclusion:** The known resonance structures of nuisance signals are useful prior knowledge that can be exploited for nuisance removal. Using this knowledge, the proposed method can effectively remove the overwhelming nuisance signals from  $^1\text{H}$ -MRSI data collected with neither water nor lipid suppression pulses, which is desirable for optimizing  $^1\text{H}$ -MRSI data acquisition.

## Keywords

spectroscopic imaging, resonance structure, nuisance removal, non-suppression pulses

## INTRODUCTION

$^1\text{H}$ -MRSI is a promising tool for early detection and diagnosis of various diseases by providing metabolic information non-invasively (1–3), but its practical use has long been limited by the challenges of effective removal of the overwhelming water and lipid signals (a.k.a. nuisance signals). Various methods have been proposed to tackle this problem, including nuisance suppression techniques during data acquisition (4–12) and post-processing methods (13–21), by exploiting the differences between nuisance and desirable metabolite signals in terms of resonance frequency, relaxation time, and spatial support.

In this work, we aim to further exploit the resonance structures of the nuisance components (especially of lipid) for improved  $^1\text{H}$ -MRSI nuisance removal. It has been shown that the major component of MR measurable subcutaneous lipid is triglyceride (22, 23), which has a well-defined resonance structure as shown in Table 1. By exploiting this resonance structure, one could expect: i) a better representation of the nuisance signals (and thus a cleaner removal) and ii) a better separation of the nuisance signals from the desired metabolite signals (and thus a better protection of metabolites). While the resonance structures of nuisance signals were used in various studies (24–27), explicitly using this readily available prior knowledge for nuisance removal has not yet been investigated to the best of our knowledge.

Our early attempt to use the resonance structures was reported in (28), where a generalized-series (GS) (29) is used to compensate any local line-shape distortions caused by field inhomogeneity, which results in a large, computationally expensive nonlinear optimization problem. In this work, we propose to use the resonance structures to construct a parametric model for the water and lipid signals; the nuisance subspace structures are then determined and incorporated into the union-of-subspaces (UoSS) nuisance removal framework for nuisance removal (21). The effectiveness of this proposed method has been demonstrated using experimental data acquired from healthy subjects on a 3 Tesla Siemens Trio MRI scanner. As we show later, incorporating known resonance structure allows the temporal sampling of MRSI signals to be below the Nyquist rate and as well as the elimination of the suppression pulses, both of which are desirable for MRSI data acquisition design. To further demonstrate the performance of the estimated subspace structure in protecting metabolite signals, a recent subspace-based reconstruction method (32, 33) was also performed to demonstrate the metabolic information obtained.

# THEORY

## UoSS Modeling

As described in the UoSS approach in (21), for practical applications of  $^1\text{H}$ -MRSI, there exist strong spatiotemporal or spatio-spectral correlations in the water and lipid components in the high-dimensional function  $\rho(\mathbf{x}, t)$ . Therefore,  $\rho(\mathbf{x}, t)$  can be represented by the following UoSS model.<sup>1</sup>

$$\rho(\mathbf{x}, t) = \sum_{l=1}^{L_F} u_l^F(\mathbf{x})v_l^F(t) + \sum_{l=1}^{L_W} u_l^W(\mathbf{x})v_l^W(t), \quad [1]$$

where  $\{v_l^I(t)\}_{l=1}^{L_I}$ ,  $I = \{\text{“F”}, \text{“W”}\}$  are the sets of temporal bases spanning the low-dimensional subspaces that the water and lipid signals reside in and  $\{u_l^I(\mathbf{x})\}_{l=1}^{L_I}$ ,  $I = \{\text{“F”}, \text{“W”}\}$  are the corresponding spatial coefficients. The letters “F” and “W” stand for lipid (fat) and water, respectively. We can see from Eq. [1] that the UoSS modeling can lead to low-rank matrix representations that reduce the degrees of freedom of nuisance signal significantly and thus, allows effective removal of nuisance from limited or sparsely sampled k-space data with the capability of incorporating other prior information (21).

## Resonance Structures of Nuisance Signals

The resonance structures of different molecules are known to significantly improve the spectral estimation of metabolites (34–37). Since nuisance removal can also be viewed as a spectral estimation problem (for nuisance components), the resonance structure of nuisance components may also help improve nuisance removal and can be incorporated besides the subspace constraints. The resonance structure of water is well-known to be a singlet at 4.7 ppm; the resonance structure of triglycerides (main component of MR measurable lipids (22, 23)) is a bit more complicated and shown in Table 1, where each of the resonance peak represents a structurally distinct proton moiety in a triglyceride molecule. As the level of saturation usually varies, ratios among different triglyceride peaks are usually not known a priori (25) (unlike the situation of metabolite quantification). In addition, no correlation has been observed between the line-widths of individual peaks of triglycerides (24). Therefore, the peaks shown in Table 1 should be treated individually. Specifically, we invoke the following

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<sup>1</sup>Here we have assumed that we can approximate  $\rho(\mathbf{x}, t)$  using water and lipid signals only, given the fact that the magnitude of metabolite signals is much lower than nuisance signals.

parametric model for the quantification of water and lipid spectroscopic signal:

$$\rho_W(\mathbf{x}_q, t_p; \Theta_q^W) = a_q^W e^{-\frac{t_p}{T_{2,q}^W} - j2\pi f_q^W}, \quad [2]$$

$$\rho_F(\mathbf{x}_q, t_p; \Theta_q^F) = \sum_{k=1}^K a_{q,k}^F e^{-\frac{t_p}{T_{2,q,k}^F} - j2\pi f_{q,k}^F}, \quad [3]$$

where water and lipid spectra are modeled by a sum of Lorentzian shapes with the chemical shifts of water and lipid shown in Table 1, and  $\Theta_q^I = \{\mathbf{a}_q^I, \mathbf{T}_{2,q}^I\}$ ,  $I = \{\text{"F"}, \text{"W"}\}$  are the sets of spectral parameters for voxel  $\mathbf{x}_q$ . In the next, we describe how to integrate the spectral constraints in Eqs. [2] and [3] into the subspace constraints proposed in UoSS for improved nuisance removal.

### *Exploitation of Resonance Structures in UoSS*

The UoSS model in Eq. [1] exploits the fact that each signal component lives in a low-dimensional subspace (21,31) and a key issue for nuisance removal using UoSS is to determine the temporal bases of the subspace. To this end, the model in Eqs. [2] and [3] allows us to quantify water and lipid and retrieve temporal bases from the estimated water and lipid signals. Assuming the discretized spatiotemporal signals  $d(\mathbf{x}, t)$ ,  $\mathbf{x} = \mathbf{x}_1, \dots, \mathbf{x}_Q$ ,  $t = t_1, \dots, t_P$ , have already been reconstructed from the (k,t)-space data, we propose to solve the following optimization problem:

$$\hat{\Theta}_q^W, \hat{\Theta}_q^F, \Delta \hat{f}_q = \arg \min_{\Theta_q^W, \Theta_q^F, \Delta f_q} \sum_{p=1}^P |d(\mathbf{x}_q, t_p) - [\rho_W(\mathbf{x}_q, t_p; \Theta_q^W) + \rho_F(\mathbf{x}_q, t_p; \Theta_q^F)] e^{j2\pi \Delta f_q t_p}|^2, \quad [4]$$

for  $q = 1, \dots, Q$ , where  $\Delta f_q$  is the field inhomogeneity at  $\mathbf{x}_q$ . The problem in Eq. [4] is a typical quantification problem with both nonlinear and linear parameters, which can be solved using the variable projection method (38,39). Using the estimated spectral parameters (i.e.,  $\hat{\Theta}_q^W$  and  $\hat{\Theta}_q^F$ ), we can synthesize water and lipid signals based on Eqs. [2] and [3] and get  $\hat{\rho}_W(\mathbf{x}_q, t_p)$  and  $\hat{\rho}_F(\mathbf{x}_q, t_p)$ . Then the temporal bases for water and fat,  $\{v_l^W(t)\}_{l=1}^{L_W}$  and  $\{v_l^F(t)\}_{l=1}^{L_F}$ , can be extracted as the dominant singular vectors of the Casorati matrices

$$\mathbf{C}^I(\boldsymbol{\rho}) = \begin{bmatrix} \hat{\rho}_I(\mathbf{x}_1, t_1) & \hat{\rho}_I(\mathbf{x}_2, t_1) & \cdots & \hat{\rho}_I(\mathbf{x}_Q, t_1) \\ \hat{\rho}_I(\mathbf{x}_1, t_2) & \hat{\rho}_I(\mathbf{x}_2, t_2) & \cdots & \hat{\rho}_I(\mathbf{x}_Q, t_2) \\ \vdots & \vdots & \ddots & \vdots \\ \hat{\rho}_I(\mathbf{x}_1, t_P) & \hat{\rho}_I(\mathbf{x}_2, t_P) & \cdots & \hat{\rho}_I(\mathbf{x}_Q, t_P) \end{bmatrix}, \quad I = \{\text{"W"}, \text{"F"}\}, \quad [5]$$

In addition, since field inhomogeneity can also be obtained from quantification, a separate acquisition for field map is not required.

## Estimation of Nuisance Signals

Once the temporal bases (denoted by  $\{\hat{v}_l^W(t)\}_{l=1}^{L_W}$  and  $\{\hat{v}_l^F(t)\}_{l=1}^{L_F}$ ) are determined, the nuisance removal problem is to determine their corresponding spatial coefficients from MRSI measurement in the  $(\mathbf{k}, t)$ -space, which can be modeled follows.

$$d(\mathbf{k}, t) = \int \rho(\mathbf{x}, t) e^{j2\pi\Delta f(\mathbf{x})t} e^{-j2\pi\mathbf{k}\mathbf{x}} d\mathbf{x} + n(\mathbf{k}, t), \quad [6]$$

where thermal noise  $n(\mathbf{k}, t)$  follows a white Gaussian distribution and  $\rho(\mathbf{x}, t)$  can be represented by

$$\rho(\mathbf{x}, t) = \sum_{q=1}^Q \rho(\mathbf{x}_q, t) \varphi_q(\mathbf{x}), \quad [7]$$

where  $\varphi_q(\mathbf{x})$  can be chosen as a 3D rectangular function for the  $q$ -th voxel. Then we have

$$d(\mathbf{k}, t) = w(\mathbf{k}) \sum_{q=1}^Q \rho(\mathbf{x}_q, t) e^{j2\pi\Delta f(\mathbf{x}_q)t} e^{-j2\pi\mathbf{k}\mathbf{x}_q} + n(\mathbf{k}, t), \quad [8]$$

where  $w(\mathbf{k}) = \int \varphi(\mathbf{x}) e^{-j2\pi\mathbf{k}\mathbf{x}} d\mathbf{x}$  and the sum over  $q$  can be computed efficiently by the fast Fourier transform (FFT) algorithm. Finally, by re-writing the UoSS model in Eq. [1] and the imaging model in Eq. [8] in a more compact matrix-form, we propose to estimate spatial coefficients by solving the optimization problem below.

$$\hat{\mathbf{U}} = \arg \min_{\mathbf{U}} \|\mathbf{d} - \mathbf{\Omega}_k \mathbf{W} \mathbf{F} \{\mathbf{\Omega}_x \mathbf{U} \hat{\mathbf{V}}^T \odot \hat{\mathbf{B}}\}\|_2^2 + \lambda \|\mathbf{U}\|_F^2, \quad [9]$$

where  $\mathbf{d}$  is to put  $d(\mathbf{k}, t)$  into a vector,  $\mathbf{\Omega}_k$  is the data sampling mask in  $\mathbf{k}$ -space,  $\mathbf{W}$  represents the weighting factor  $w(\mathbf{k})$ ,  $\mathbf{F}$  represents FFT from  $\mathbf{x}$ -space to  $\mathbf{k}$ -space,  $\mathbf{\Omega}_x = \text{diag}\{\mathbf{\Omega}_x^W, \mathbf{\Omega}_x^F\}$  is the spatial support for water and fat,  $\mathbf{U} = [\mathbf{U}_W, \mathbf{U}_F]$  contains the spatial coefficients to be estimated,  $\hat{\mathbf{V}} = [\hat{\mathbf{V}}_W, \hat{\mathbf{V}}_F]$  contains the estimated temporal bases by stacking  $\{\hat{v}_l^W(t)\}_{l=1}^{L_W}$  and  $\{\hat{v}_l^F(t)\}_{l=1}^{L_F}$  column-wisely, and  $\hat{\mathbf{B}}$  models the field inhomogeneity effects, i.e.,  $\hat{\mathbf{B}}(\mathbf{x}_q, t_p) = e^{j2\pi\Delta\hat{f}_q t_p}$ . The problem in Eq. [9] is a linear least squares problem with Tikhonov regularization and thus can be readily solved using the conjugate descent method, and the value of  $\lambda$  can be selected using the discrepancy principle (40). The estimated nuisance signals can then be represented by the UoSS model using  $\hat{\mathbf{U}}$  and  $\hat{\mathbf{V}}$  and removed from MRSI data.

## METHODS

### In Vivo Experiments

In vivo data were collected from healthy volunteers on a 3T Siemens Trio scanner (Siemens Healthcare) equipped with a 12-channel headcoil. The study was approved by the local Institutional Review Board. For

each subject, a high-resolution 3D  $^1\text{H}$ -MRSI dataset was acquired in a 7.6-minute scan using a gradient-echo based EPSI sequence with the following imaging parameters: FOV = 230 mm  $\times$  230 mm  $\times$  72 mm, excitation slab thickness = 60 mm, elliptically sampled spatial encoding matrix = 76  $\times$  76  $\times$  24 (i.e., 3 mm isotropic nominal resolution), TR/TE = 310/4 ms, flip angle = 43 $^\circ$ , echo spacing = 1.66 ms, number of echoes per TR = 128 (flyback acquisition), readout bandwidth = 125kHz. Two saturation bands were used to suppress signals outside the FOV along the slice selective direction. A five-minute 3D magnetization prepared rapid gradient echo (MP RAGE) (41) scan at 0.9 mm isotropic resolution was acquired for anatomical reference information. In addition, a two-minute low-resolution 3D  $^1\text{H}$ -MRSI dataset was acquired in order to retrieve metabolite basis for SPICE using the same sequence and imaging parameters, except that: spatial encoding matrix = 16  $\times$  16  $\times$  12, echo spacing = 0.66 ms, number of echoes per TR = 600 (bipolar acquisition), readout bandwidth = 68 kHz, signal average = 2, weak water suppression using WET pulses (7) and eight OVS bands surround the brain for fat suppression (8).

## Data Processing

For nuisance removal, the MP RAGE images were first aligned with the high-resolution 3D MRSI data and segmented using SPM8 (42) to obtain spatial supports of fat and water. The proposed quantification with water and lipid in Eq. [4] exploiting resonance structure was then performed to obtain field inhomogeneity  $\Delta\hat{f}(\mathbf{x})$  and temporal bases  $\hat{\mathbf{V}}$ , followed by the estimation of spatial coefficients  $\hat{\mathbf{U}}$  in Eq. [9]. An extra step is further used to locally handle the residual nuisance signals that cannot be predicted perfectly by the UoSS model due to practical issues such as large  $B_0$  inhomogeneity, partial volume effect, and subject head motion. To be precise, the extra step incorporates a convolution kernel in the frequency domain to the estimated water signals to account for peak distortions (as is done similarly in LCMoel (34)).

After nuisance signal removal, metabolite subspaces were estimated from the low-resolution 3D MRSI data, with which high-resolution metabolite signals were reconstructed from the nuisance removed data using SPICE described in (32, 33, 43). Both the nuisance signal removal and SPICE reconstruction were performed in a coil-by-coil fashion followed by SVD-based combination to form the final spatiotemporal reconstruction (44).

## RESULTS

Figure 1 compares the normalized projection errors of signals from the subcutaneous layer onto the subspaces estimated by the HSVD method used in original UoSS (21) (solid line) and by the proposed method exploiting resonance structures (dashed line). Both the two subspaces include the same set of water bases to account for water signals in the subcutaneous region so that Fig. 1 is focused on comparing the effects of different numbers of lipid bases. We can see as the number of lipid bases increases, both two curves decrease as expected. Moreover, the dashed line is consistently lower than the solid line, especially when the number of bases is less than 20, which indicates that the representation of lipid signals using the subspace estimated by exploiting resonance structures is more effective. Therefore, in practice, the proposed method allows the use of a lower model order for lipid in nuisance removal, which provides us more computational efficiency and potentially better metabolite protection.

Figure 2 shows the nuisance removal effect from one high-resolution 3D MRSI acquisition without suppression pulses, where the images of  $\ell_2$  spectral integral corresponding to only one of the phased-array coils are shown. Specifically, Fig. 2a is the unsuppressed MRSI signal; Fig. 2b is the residual after applying Papoulis-Gerchberg (PG) algorithm (45, 46) for removing signals lying in the subcutaneous layer and HSVD (13) for removing water components; Fig. 2c is the residual after applying the original UoSS method (21); and Fig. 2d and Fig. 2e are the residual signals after exploiting resonance structures of nuisance components in UoSS and the extra local removal step, respectively. We can see in Fig. 2b that the Gibbs ringing of lipid and residual water were still very large; the UoSS method significantly improved nuisance removal, but there were still noticeable residual signals, especially in the subcutaneous layer (Fig. 2c), which was further improved by the proposed subspace estimation method (Fig. 2d); finally, the proposed local removal step reduced any residual nuisance signals at voxels with strong spectral distortion to a negligible level (Fig. 2e). Note when performing the original UoSS method and the proposed removal method, same number of water and lipid bases were used. Therefore, the proposed physics-derived subspace estimation has the capability of better representing nuisance signals with a lower model order.

Figure 3 shows the  $\ell_2$  norm and some representative spectra of the nuisance removed data after a truncation in k-space for better SNR. Specifically, the residual after the proposed local removal step is truncated in the k-space from  $76 \times 76 \times 24$  to  $16 \times 16 \times 12$  with a hamming window applied. From the spatial distribution and representative spectra in Fig. 3, we can see that the desired metabolite signals are well-preserved without



significant contamination caused by residual nuisance signals.

Figure 4 summarizes the various information that can be retrieved from the high-resolution MRSI data collected without suppression pulses, including field inhomogeneity and  $T_2^*$  mapping. More importantly, with the help of the proposed nuisance removal method and an extra training dataset (required by SPICE), very rich spectral/metabolic information can be obtained at a high-resolution and high-SNR using SPICE, which is very appealing for various MRSI studies.

## CONCLUSION

This note investigates the use of known resonance structures of nuisance signals (especially of lipids) for improved nuisance removal. More specifically, the known resonance structures were used to derive the subspace representation for the water and lipid signals, which were then used in the union-of-subspaces framework for nuisance removal. The effectiveness of the proposed method has been demonstrated using in vivo short-TE  $^1\text{H}$ -MRSI data acquired without suppression pulses. The proposed method may provide new flexibility for  $^1\text{H}$ -MRSI acquisition.

## ACKNOWLEDGMENTS

This work was supported in part by the National Institutes of Health; Grant numbers: NIH-1RO1-EB013695 and NIH-R21EB021013-01.

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Table 1: MR Resonance Structure of Water and Triglycerides (25, 47)

Chemical Shift (ppm)	Assignment	Type
4.7	$\text{H}_2\text{O}$	Water
5.29	$-\text{CH}=\text{CH}-$	Olefinic
5.19	$-\text{CH}-\text{O}-\text{CO}-$	Glycerol
4.2	$-\text{CH}_2-\text{O}-\text{CO}-$	Glycerol
2.75	$-\text{CH}=\text{CH}-\text{CH}_2-\text{CH}=\text{CH}-$	Diacyl
2.20	$-\text{CO}-\text{CH}_2-\text{CH}_2-$	$\alpha$ -Carboxyl
2.02	$-\text{CH}_2-\text{CH}=\text{CH}-\text{CH}_2-$	$\alpha$ -Olefinic
1.6	$-\text{CO}-\text{CH}_2-\text{CH}_2-$	$\beta$ -Carboxyl
1.3	$-(\text{CH}_2)_n-$	Methylene
0.9	$-(\text{CH}_2)_n-\text{CH}_3-$	Methyl

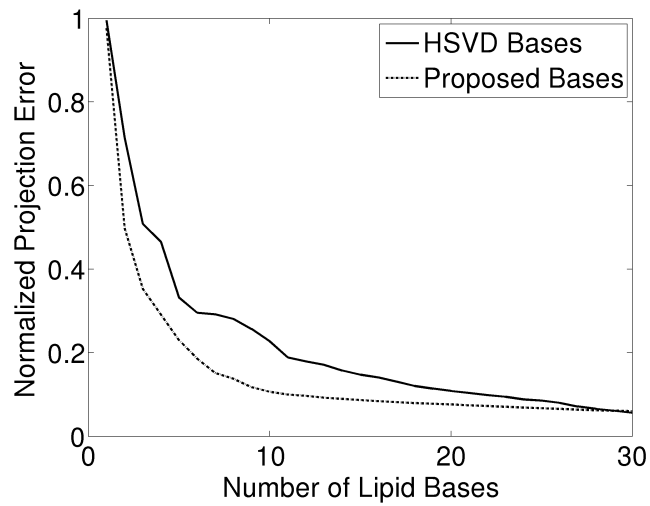


Figure 1: Comparison of the projection errors of lipid signals onto the subspaces obtained by HSVD in (21) (solid line) and the proposed method (dashed line), respectively. We can see that the dashed line is consistently lower than the solid line (i.e., more accurate representation), especially when the number of lipid bases is small.

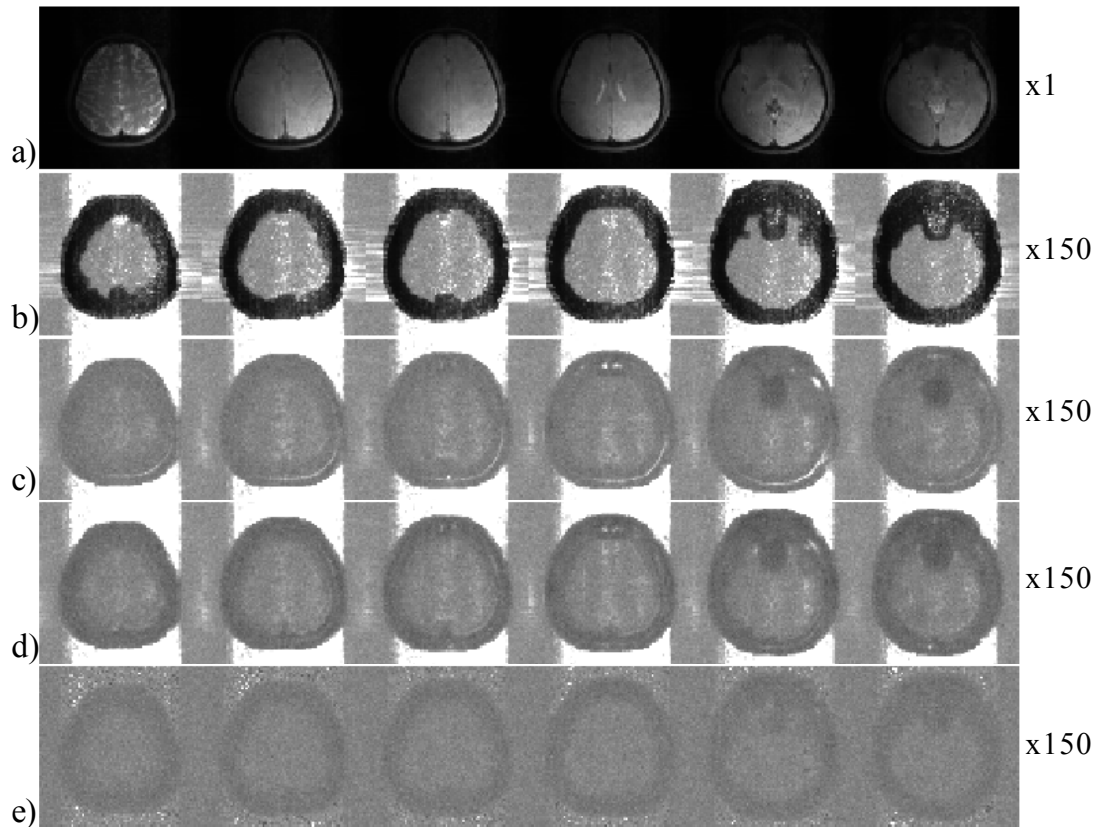


Figure 2: The spectral integral of a) the original unsuppressed MRSI signals from one coil and the corresponding residual signals after nuisance removal using b) PG and HSVD, c) the original UoSS method, d) and e) the proposed nuisance removal before and after the extra local removal step, respectively. Same number of water and lipid bases were used for both c) and d). Note the negligible level of nuisance signals in e) except for some isolated outer-brain regions.



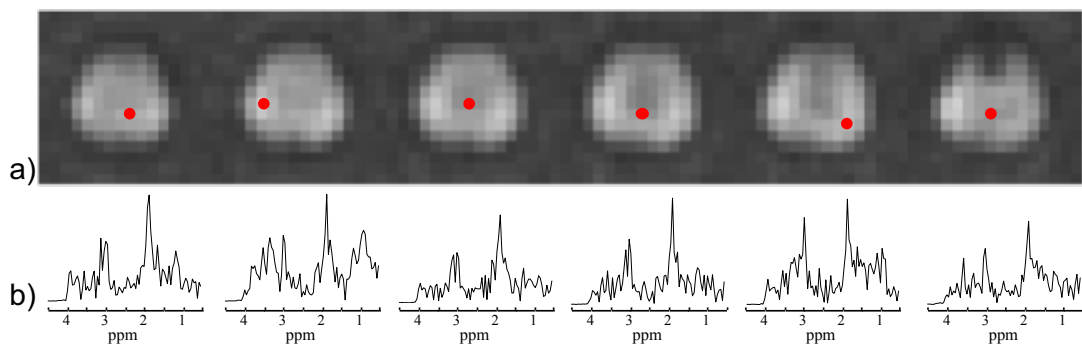


Figure 3: Illustration of the capability of the proposed method in protecting metabolite signals. a) The spectral integral of the nuisance removed data after truncation in k-space from  $76 \times 76 \times 24$  to  $16 \times 16 \times 12$ . b) Spectra from several representative locations, which are marked in red dots in a).

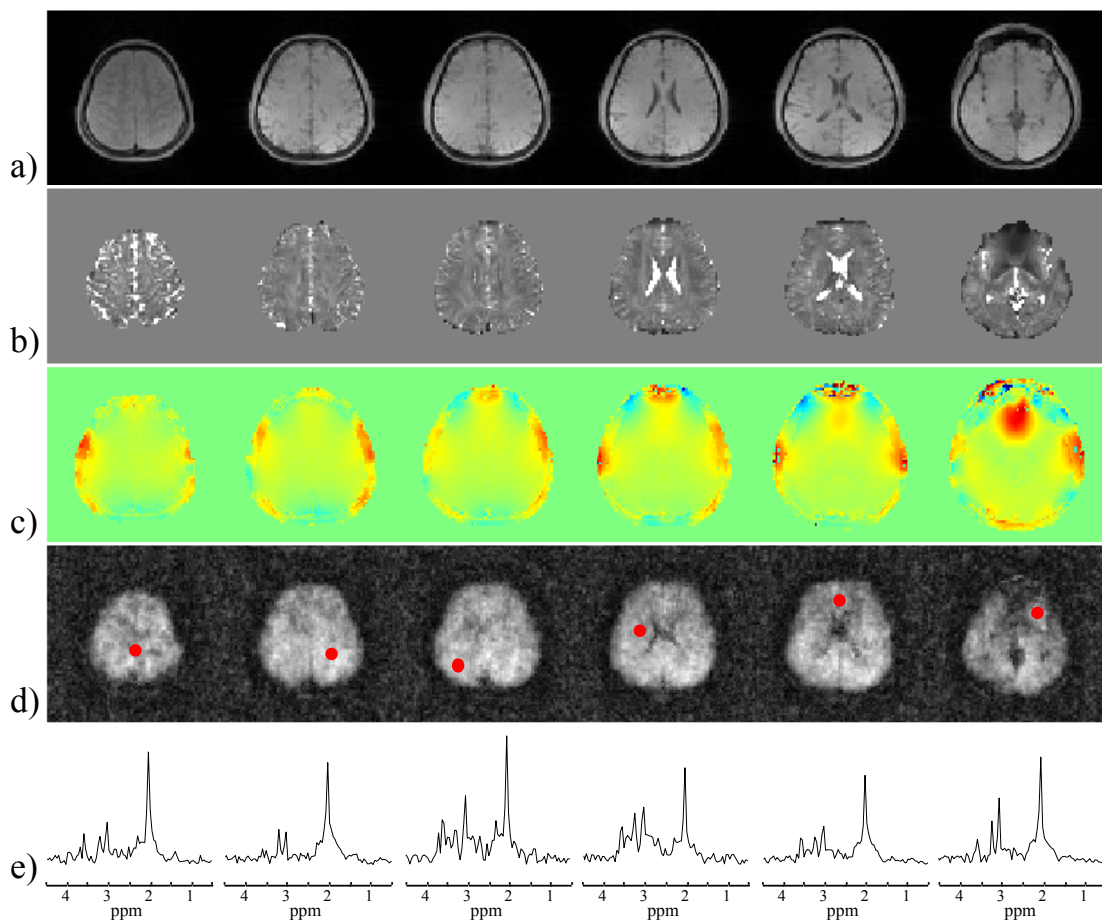


Figure 4: Various information that can be obtained within a ten-minute MRSI scan (one 7.6-minute high-resolution dataset and one two-minute low-resolution training dataset), enabled by the proposed nuisance removal method for unsuppressed MRSI data: a) water images, b)  $T_2^*$  maps, c) field inhomogeneity maps from the companion water signals, d) the NAA maps obtained from the nuisance removed data using SPICE, and e) representative spectra from the marked locations in d).