Non uniform sampling for sparse 2D correlated MRS: a quantitative point of view

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Target Audience: This paper could be of interest to the researchers doing methodological development in magnetic resonance spectroscopy (MRS) acquisition and quantitative analysis.

Introduction: 2D MR spectroscopy has the advantage to increase spectral resolution by unraveling the spectral information along a second dimension and results in a gain in quantification precision at the cost of increased acquisition time. To overcome this issue, non uniform sampling (NUS) allowing acquisition acceleration has recently been revisited as a solution in combination with the compressed sensing (CS) reconstruction or maximum entropy [1]. NUS scheme is generally designed with randomly chosen indirect dimension step (t1). Besides, by taking advantage of the prior knowledge on the spectral support of sparse spectra, one can optimize the indirect dimension NUS regarding the reconstructed spectral information in COSY (Correlation spectroscopy) type spectra [2]. The 2D time domain signal is a sum of separable terms resulting in separable spectrum with same spectral support in the two frequency domains. The sequential backward selection (SBS) algorithm can be used for choosing the indirect dimension step leading to decreasing noise and error in the reconstruction of the spectrum[2]. The aim of this work is to demonstrate and study the feasibility of time domain quantification for NUS applied on Localized COSY (L-COSY) spectra [3] by using this SBS approach.

Material and Methods: We used acquisition on subcutaneous fat performed *in vivo* on a 5 week ob/ob mouse on a 7T Bruker system. LCOSY (90°-180°-t1-90°-t2) acquisition was triggered on respiration (effective TR=3s, NA=1) and performed using a regular sampling scheme using 128 points in t1 dimension and bandwidth of 4000Hz. Time domain quantification procedure consisted in the parametric fit of the acquired signal, as a linear combination of weighted (including T2 relaxation) spin system signals. We used a quantum mechanically simulated basis set (obtained by the SPINACH package) of spin systems presents in the lipid spectrum. SBS was used to determine t1 line increments and for comparison randomly chosen. We tested two different NUS acceleration factors (defined as ratio of original and reduced number of step) for a signal to noise ratio of the reconstruction >11 dB (Reconstructed signal to noise ratio was calculated as $\mathbf{20\log_{10}}(\frac{\|x\|_{l2}}{\|x-\hat{x}\|_{l2}})$, where $\boldsymbol{x}$ is the fully sampled spectrum and $\hat{\boldsymbol{x}}$ the reconstructed one). Acceleration factors were 1.5 (128/85) and 2 (128/62). The quantification procedure was able to take into account this change in the time base.

Results: Figure 1 shows the result of quantification using original acquisition (Fully sampled). Figure 2 indicates results of quantification using different sampling schemes at different SBS acceleration factor and its equivalent using randomly chosen t1 steps.

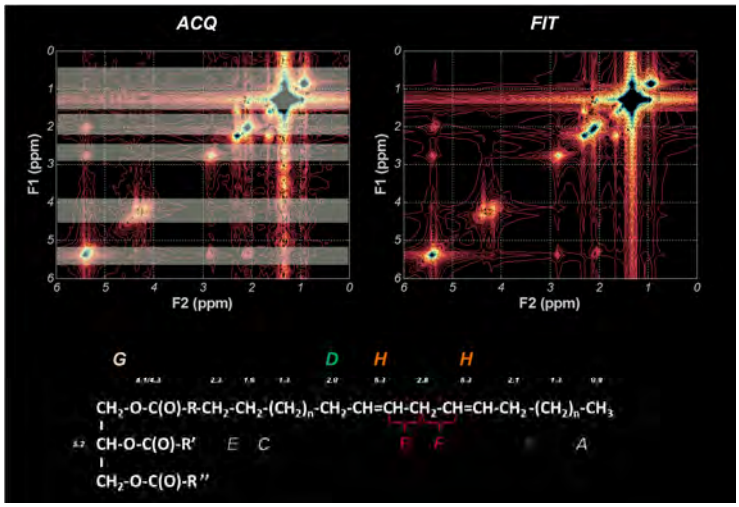

Figure 1: (up) Acquired LCOSY spectrum of subcutaneous fat (ACQ) in a 5 week old ob/ob mouse and its estimate results from its time domain quantification (FIT). Chosen spectral support for SBS is given in transparency. Resonance assignment of triglyceride compound is indicated on molecular drawing (down)

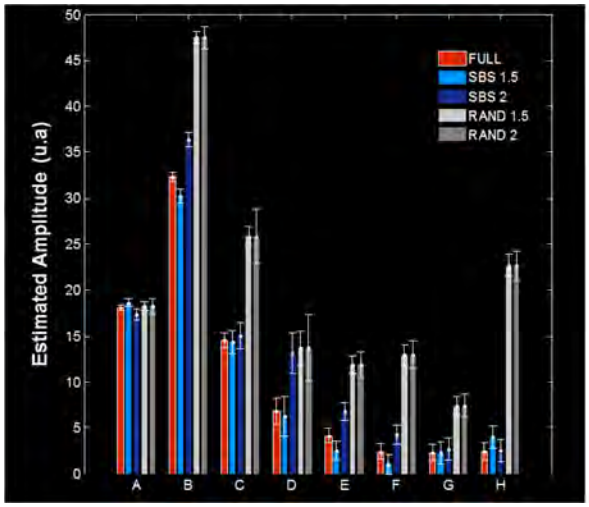

Figure 2: Amplitude estimation results using different sampling scheme. Cramér-Rao lower bounds (CRBs) are estimated using the parametric model and sampling scheme and indicated as relative theoretical error.

Discussion/ Conclusion: Quantification performed on fully sampled spectra show lipid compositions which appear to be in accordance with published results for this mouse model and acquired spectra [4,5]. Using SBS sampling scheme, estimation is close to fully sampled estimated spectra. Larger SBS Acceleration factor (R=2) resulted with some overestimation of amplitude and 1/T2 and lower estimation precision (higher Cramér Rao Lower Bounds). This acceleration factor is limited by the involved T2/T2* relaxations, directly related to the spectral support to consider and thus the assumed spectral parsimony. Randomly chosen t1 step merely converge to an inacurrate value which can be featured by a difficult T2 estimation. This could be overcome by emphasis the first t1 steps (or 'relaxation-matched' sampling) but then criteria for CS reconstruction are not fulfilled. The use of SBS allows having reliable quantification using less t1 steps and acceleration factor proportional to the parsimony of the spectrum. Next step of this study will be further in vivo experimentations to investigate quantification of fatty acids in subcutaneous fat using acquisition benefiting from SBS sampling scheme and L-COSY spectral resolution. Analysis of the SBS limits regarding spectral quantification and reconstruction are under investigation.

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