Magnetic Resonance Spectroscopy data de-noising using Semi-Classical Signal Analysis approach: Application to in-vitro MRS data.

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Introduction: Localized Magnetic Resonance Spectroscopy (MRS) is a powerful technique used to study metabolism of tissue in vivo, to provide information that is useful in several diagnostics and treatment clinical applications [1]. However, the accuracy of the metabolite information is questionable due to the low Signal-to-Noise Ratio (SNR) of the acquired MRS data. Signal averaging is then required to preserve the SNR, which lengthens data acquisition time. To shorten acquisition time while accurately analyzing the collected data, we propose to use the Semi-Classical Signal Analysis (SCSA) method [2]. This method employs the Schrödinger operator to extract the most significant eigenfunctions and eigenvalues of the MRS signal, and uses them to reconstruct the de-noised MRS signal. The obtained results demonstrate the usefulness of the technique in precisely estimating the metabolite peaks information from low sensitivity in-vitro MRS data.

Material and methods: In vitro experiments are performed at 3 T (Tim Trio Siemens). Localized water suppressed spectra are acquired using the PRESS sequence (TE/TR=30/2000ms, voxel size=10*10*20 mm^3), from a phantom containing choline chloride (Ch) and N-acetyl-L-aspartic acid (NAA) with known concentrations, 10 mM each. Seven MR spectra with averaging values ranging from 2 to 32 are analyzed using the SCSA method where the signal, denoted y, is considered as potential of a semi-classical Schrödinger operator [2]. The discrete spectrum consisting of negative eigenvalues, is computed and used to reconstruct the signal as follows, $y_h(f) = 4h\sum_{n=1}^{N_h}\sqrt{-\lambda_{n,h}}\,\psi_{n,h}^2(f),\ f \in \mathbb{R}$ where $\lambda_{n,h}$and $\psi_{n,h}$ are the negative eigenvalues and the corresponding L^2- normalized eigenfunctions of the Schrödinger operator, respectively, such that: $-h^2\frac{d^2\psi(f)}{df^2} - y(f)\psi(f) = \lambda\,\psi(f)$.

The parameter h plays an important role in the SCSA. When h decreases, the approximation improves [2]. However in the de-noising process, it is recommended to retain the eigenfunctions belonging to the signal and discard those representing noise. This is achieved by an efficient choice of the parameter h, which is done by minimizing the following cost function $\| y(I) - y_h(I) \| + \frac{\propto}{|e|}$, where $e = \frac{\max(y)}{std(y(m_1:m_2))} - \frac{\max(y_h)}{std(y_h(m_1:m_2))}$, where $(m_1{:}\,m_2)$ and I are the noise and signal regions respectively. The quantity $\frac{\max(y)}{std(y(m_1:m_2))}$ is used to compute the SNR. $\propto$ is a weight function.

Results/Discussion: Figure 1 shows a noisy in-vitro spectrum (blue) and the reconstructed SCSA spectrum (red). A zoom on the choline and NAA region is shown on Figure 2, where the difference in spectra is shown in green.

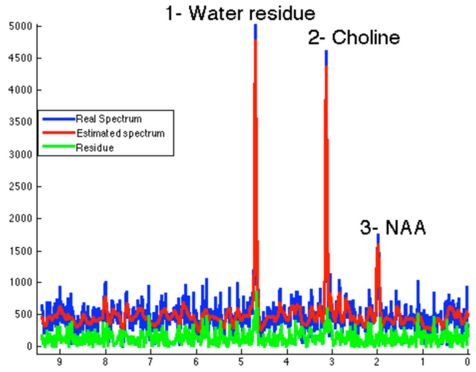

Figure 1: MR spectrum N°1 with avg. = 2, (see tables 1, 2)

A significant SNR increase on MRS data is obtained using the SCSA method (Figs. 1, 2). The quantification results of the metabolite peaks from the seven spectra (table 1), demonstrate that SCSA is able to accurately analyze the data with different sensitivity levels (table 2). The quantification is performed using an in-house Matlab program. Table 2 reports the amount of SNR increase for each spectrum and the corresponding h value used to separate between eigenfunctions of the signal and noise

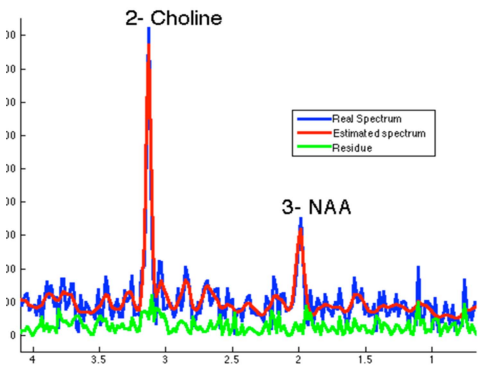

Figure 2: Zoom on the Choline and NAA peaks

The preliminary absolute quantification results (not shown) using water line as a reference [3] are better for both metabolites after the SCSA than before SCSA.

Spec. N / Peak area (a.u)	1	2	3	4	5	6	7	Avg ± std
Choline (a.u)	14.5	17.4	16.9	16.7	16.8	17.5	16.5	16.6 ± 1
	15.1	**17.5**	**17.7**	**17.7**	**19.0**	**19.4**	**18.5**	**17.8 ±1.4**
NAA (a.u)	5.67	5.46	5.42	5.65	4.88	5.09	5.48	5.38 ± 0.29
	6.45	**6.56**	**6.56**	**6.67**	**6.08**	**6.11**	**6.42**	**6.41 ± 0.23**

Table 1: Quantification results before and after SCSA (bold). The calculated Choline and NAA peak areas qre in arbitrary values (a.u).

Spectrum **N** (*average*)	h	before SCSA	after SCSA
1 (*2*)	67.58	23.57	50.64
2 (*4*)	68.24	49.77	105.6
3 (*8*)	70.95	60.55	124.73
4 (*12*)	55.79	67.64	150.03
5 (*16*)	44.56	91.85	234.2
6 (24)	45.31	93.31	219.76
7 (32)	46.89	128.21	445.61

Table 2: SNR values (a.u) before and after SCSA and the Corresponding h values.Spectrum **Number** and *average values*

Conclusion: These preliminary results have shown that the SCSA method is powerful in significantly reducing noise while preserving metabolite peak information. This will permit the use of the SCSA with low sensitivity MRS data, especially in studying tissue metabolism in-vivo. This will be validated by a complete study of in-vitro data with internal reference and in-vivo data.

References: 1) Martínez-Bisbal MC, et al. Q J Nucl Med Mol Imaging. 2009; 53(6):618-30. **2)** Laleg-Kirati TM, et al. Semi-classical signal analysis, Math. Cont. Sign. Syst. 2013; 25(1): 37-61. **3)** Serrai H. et al, J. Magn. Reson. 2001; 149(1):45-51.