Sampling strategy effects on *in vivo* 2D J-Resolved spectroscopy quantification

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Introduction

2D spectroscopy has great potential to unambiguously distinguish the metabolites [1,2] . This work investigates **irregular sampling strategies** of the indirect dimension. A statistical study employing a novel 2D quantification algorithm was carried out to compare optimized and regular sampling strategies, in terms of **reliability, bias and standard deviation**. *In vivo* and simulated 2D quantification results are presented for localized 2D MRS signals in mouse brain .

Method

A two-dimensional global fitting procedure has been developed, allowing quantification of J-resolved magnetic resonance spectroscopic data. Quantification stage uses **strong prior-knowledge**, consisting in a set of M 2D metabolite signals $x_{t,TE}$ calculated numerically using the GAMMA library [3,4] and a macromolecule signal modelled from *in vivo* acquisitions. A **non-linear optimization procedure** (MATLAB 7) fits a 2D time domain model function consisting in **a linear combination of metabolite signals**:

$$\hat{x}_{t,TE} = \exp\left[i\phi_0\right] \sum_{m=1}^{M} c_m \hat{x}^m_{t,TE} \exp\left[\left(-\frac{TE}{T_{2m}}\right) + \left(\triangle\alpha_m + i\triangle\omega_m\right)t\right]$$

where c_m, $T2_m$, $\Delta\alpha_m$, $\Delta\omega_m$ correspond respectively to concentration, transverse relaxation time, extra damping factor and frequency shift for the m^{th} metabolite and Φ_0 is a global zero-order phase.

Sampling optimization on simulated data

A 2D simulated 7T MRS signal was generated with typical ***in vivo* parameter values** and macromolecular contamination. The sampling in the indirect dimension (16 Echo Times from 20 to 140 ms) was optimized for each metabolite by minimizing the CRLB of the amplitude estimate and was compared to a regular TE sampling (**Fig. 1** & **2**).

A Monte Carlo study was carried out. It consisted of 200 repetitions of the quantification procedure for the above simulated data added to Gaussian noise. 4 sampling strategies were tested: 3 optimized samplings (Ala, Asp & GABA) and a regular sampling. Biases and standard deviations were computed for the amplitude estimates (**Fig. 3**).

In vivo study

The experiment was performed on a 7T Biospec BRUKER system. A volume transmit/receive coil was used to collect the signal from a 90 µL voxel within the brain of a 3 month old female swiss model mouse. Localized *in vivo* 2D spectroscopy was performed using a J-PRESS sequence (NA=128, TR=3s, VAPOR water suppression). The TE sampling was set up in order to cover the 4 previous tested strategies. Quantification results are shown in **Fig. 4** & **5**.

Results

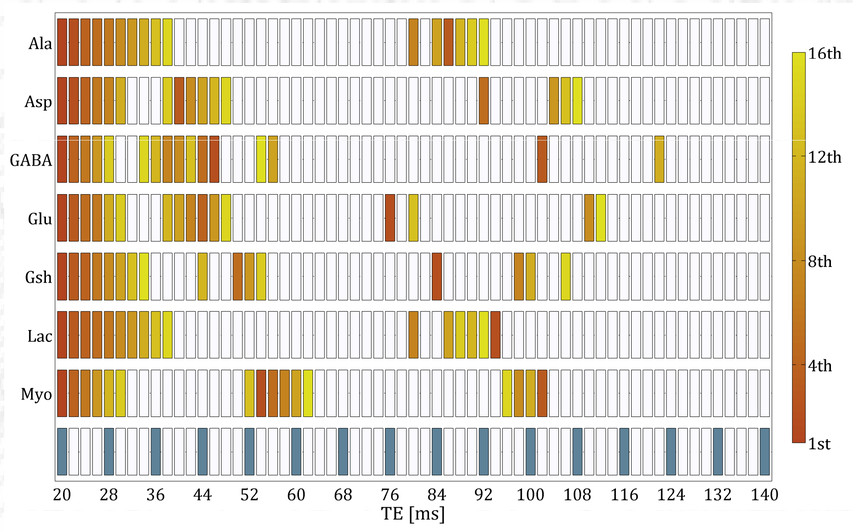

Fig. 1. Optimized TE sampling obtained for major coupled metabolites. The red-to-yellow color indicates the TE ranking computed by the algorithm .

	Optimized TE sampling	Regular TE sampling
Ala	51.6%	63.5%
Asp	38.9%	47.7%
GABA	47.5%	53.8%
NAA	5.4%	5.9%

Fig. 2. CRLB values computed for optimized and regular TE sampling.

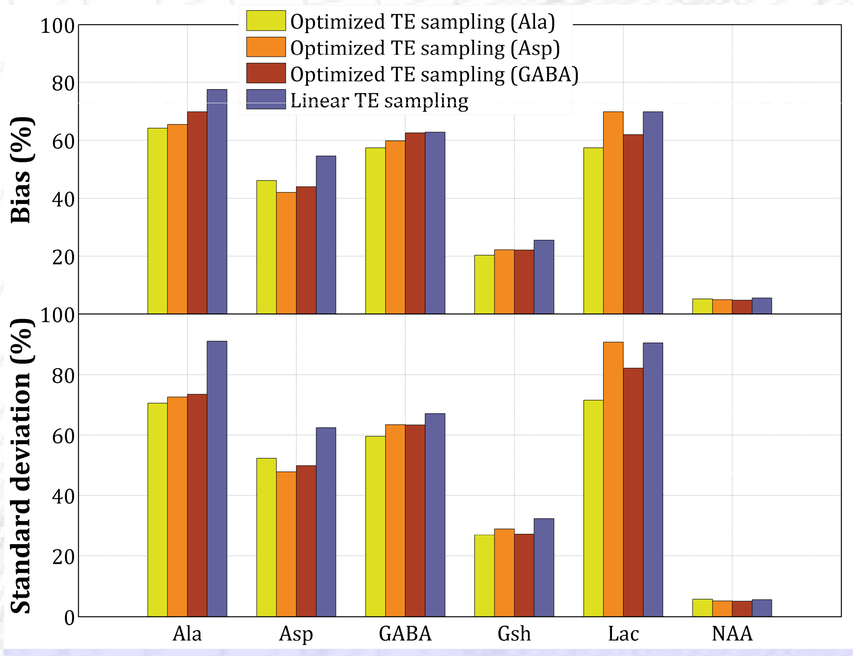

Fig. 3. Bias and standard deviations calculated of the amplitude estimates.

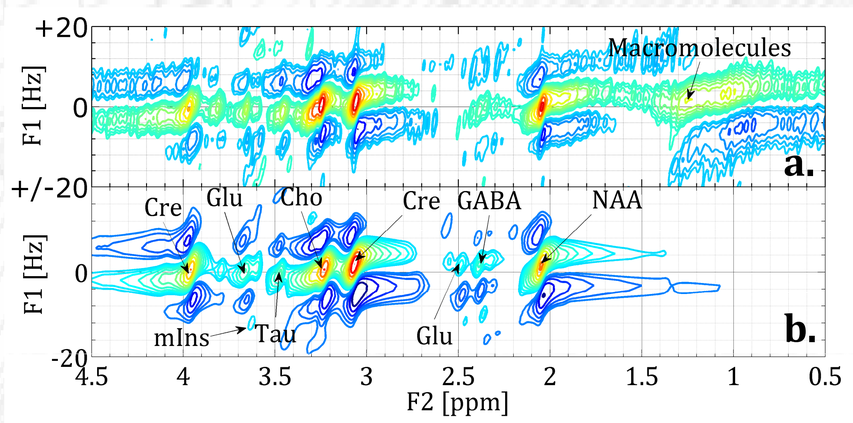

Fig. 4. A 7T *in vivo* 2D JPRESS spectrum (a) and its estimated spectrum (b).

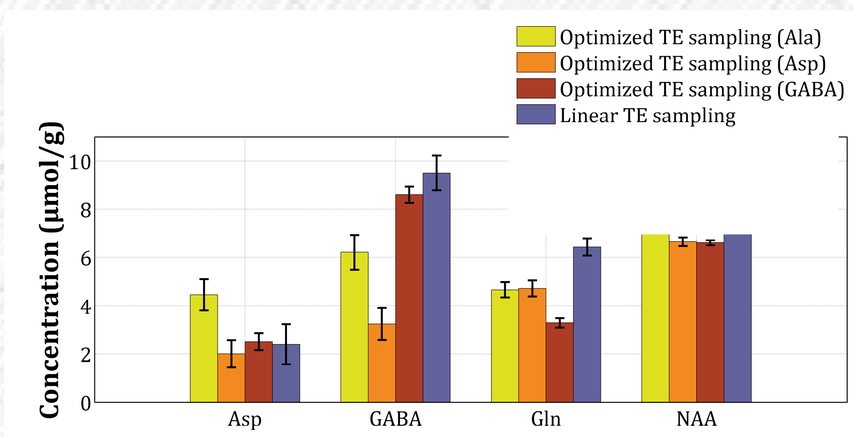

Fig. 5. *In vivo* quantification results: metabolite concentration estimates with CRLB error bars.

Discussions

As shown in **Fig. 2**, the reduction of CRLB of the metabolite amplitudes were obtained by optimizing the sampling following the t_1 direction (TE). **Some strongly coupled metabolites CRLB were greatly reduced** (~10%) in comparison with NAA or Creatine (<1%). Each metabolite had a dedicated TE sampling (**Fig. 1**) which can be close to other metabolites (Ala/Lac, Asp/Glu).

In agreement with the CRLB theory, the Monte Carlo study showed a **decrease of standard deviation** when using an optimized sampling strategy (**Fig. 3**). **Biases were also significantly reduced.**

The *in vivo* quantification results show a significant influence of the TE sampling schemes, especially for coupled metabolites (**Fig. 5**). In agreement with the theoretical results, the NAA concentration estimate is sampling scheme independent. The Asp sampling scheme resulted in concentration estimates close to literature values.

Conclusion

A new fitting algorithm **handling irregular TE sampling** has been developed, allowing the evaluation of *in vivo* 2D J-Resolved acquisition and quantification strategies. 2D MRS signals quantification in mouse brain remains a challenge regarding the handling of low SNR (<10), linewidth distortions, and macromolecular contamination (**Fig. 4**). This study demonstrates that TE irregular sampling schemes impacts quantification values offering new resources to improve accuracy and reliability.

References

[1] Thomas MA, et al, MAGMA. 2008;21(6):443-58
[2] Braakman N, et al, Magn. Reson. Med. 2008; 60:449–456
[3] Smith, SA et al., J Magn Reson. 1994; A106:75–105
[4] Govindaraju V, et al. NMR Biomed. 2000; 13(3):129-153

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