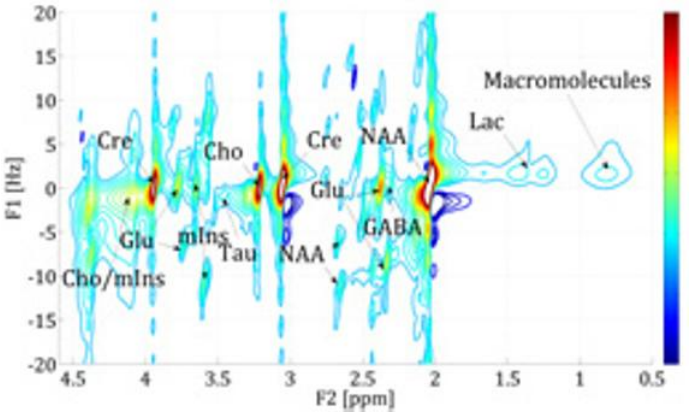

Fig.2. a 4.7T simulated 2D J-PRESS spectrum

Results: Biases and standard deviations were lower for 2D quantification, especially for coupled metabolites. Accurate and reliable amplitude quantifications were reached for Glu, mI (SD<10%) and Gln (SD<20%). In spite of the great decrease of the GABA bias estimate, its quantification remains inaccurate in this 4.7T simulation.

Discussion/Conclusion: A new fitting algorithm has been set-up for the quantification of 2D in vivo acquisitions starting at short echo times. Macromolecular contribution has been taken into account with a time truncation strategy. For a given acquisition time, 2D quantification is more efficient in term of biases and standard deviations. On these grounds, improved quantification handling macromolecular contamination will be set up.

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Quantification of *in vitro* MRS signals with lineshape correction

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Purpose/Introduction: Accurate quantification of *in vivo* Magnetic Resonance Spectroscopy (MRS) signals relies on the acquisition and processing procedure. Distorted signals normally due to eddy currents, inhomogeneities in the magnetic field or heterogeneities of the tissue need to be corrected before performing quantification. Different approaches have been developed to deal with this problem [1]; however, results are not always satisfactory. Here, we present results of quantification applying a modification of the method described in [2] and also investigated in [3]. The advantage of this method is the reduced number of parameters involved in the correction of the lineshape.

Subjects and Methods: As described in [3] the assumption that all spectral components in the signal have the same damping is the foremost characteristic taken into account to obtain a common lineshape of a MRS signal. When the same lineshape is assumed for all components, the exponential damping function $\exp(-d_k t)$ in the model is replaced by the common factor g(t), resulting in:

$$y(t) = g(t)\sum_{k=1}^{K} a_k exp(j\phi_k) exp(2\pi j f_k t) v_k(t)$$

where K is the number of metabolites, $v_k(t)$ the profile of metabolite k in the basis set, a_k the amplitude, ϕ_k the phase shift correction, f_k the frequency shift.

To evaluate the performance of the algorithm, 1H NMR spectra were acquired placing the VOI close to an air bubble and changing the shimming settings. Quantification was performed using the method AQSES [4] with integration of the lineshape method that corrects distortions [3].

Results: Quantification of distorted signals with lineshape correction showed satisfactory results. The good performance of the method is evaluated with the residual of the quantification before and after applying the lineshape correction. The method is able to correct for all distortions as shown in figures 1 and 2 where quantification was improved when using the lineshape estimation.

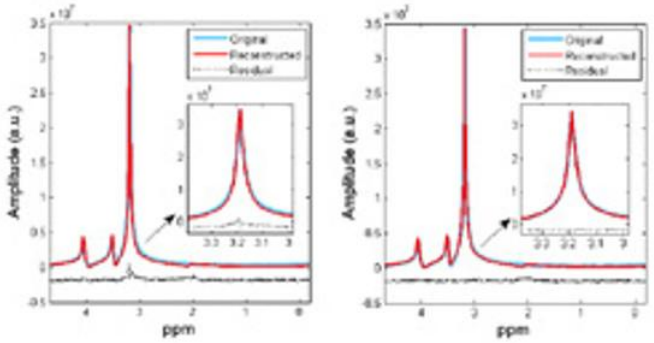

Figure 1. Choline signal acquired at 9.4T with a Bruker biospec system using a PRESS sequence with TE=20ms. Measurement was obtained from a VOI placed close to an air bubbel having first performed exclusively global shim. Left: results using standard quantification method AQSES. Right: results using AQSES included the method of Lineshape estimation. The norm of the residual was 2.9364×10^7 and 2.2455×10^5 respectively.

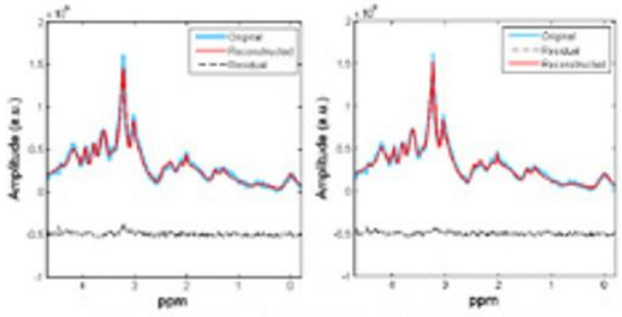

Figure 2: Mixture of metabolites containing Alanine, Creatine, DDG, GABA, Glutamine, Glutamate, Lactate, myo-Inositol, NAA, Phosphorylcholine and Taurine, acquired at 9.4T with a Bruker biospec system using a PRESS sequence of TE=20ms. Measurement was done near an air bubbel with global shim and the VOI was off center. Left: AQSES results. Right: AQSES with Lineshape estimation results. The norm of the residual was 4.3476×10^7 and 4.1242×10^6 respectively.

Discussion/Conclusion: We found lineshape estimation by self-deconvolution a good method to correct MRS signals that must be accurately quantified. This method was able to correct for distortions and further improve the required quantification. Improvement of MRS signals quality and their quantification is essential when clinical data need to be analyzed, therefore we consider this approach as an important step for further applications in *in vivo* signals.

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Computer Aid Decision System (CADS) of eTUMOUR. Initial results of clinical evaluation for brain tumour classification

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Introduction: In vivo 1H MRS can provide significant metabolic information for supporting the diagnosis of different types of cancers, like brain, breast, prostate, colon and ovarian tumours among others. However the added value of MRS strongly depends on a minimum expertise in processing and analyzing MRS spectra. Although this condition can be easily achieved in medical centres with multidisciplinary teams, it is not universally available for many radiological services. Therefore, a CADS system as automated as possible will be desirable for increasing the use of 1H MRS and for improving the diagnosis and prognosis of different types on cancers. In this communication, we will show the results of the clinical evaluation of the CADS developed in FP-VI eTUMOUR project used in a fully automated and objective manner for supporting brain tumour classification by exclusively using SV 1H MRS data.

Subjects and Methods: eTUMOUR CADS was installed in 7 different centres (Hospital La Ribera-Alzira, Hospital Clínico Universitario-Valencia, Hospital Quirón, Hospital Universitario Peset, Hospital Josep Trueta-Tarragona, IDI-Badalona, IRCCS - Fondazione Instituto Neurologico Mondino-Pavia). An on-line methodology was developed for CADS installation and training. CADS evaluation includes two different questionnaires and a minimum set of fully anonymized data for ten patients, enclosing: i) pathology results; ii) MRI diagnosis; iii) directly and automatic CADS classification and; iv) results of classification of brain tumours by using comparative analysis of average spectra and the spectrum under consideration. The CADS version 1.0.1 used in this evaluation was designed for solving one of the significant questions, as proposed in the user's requirements: the differences in the aggressiveness in the most common brain tumours, glial, and the difference with meningiomas.

The percentage of positive results between CADS, average spectra, radiology and pathology results will be presented for the first set of data used in the evaluation.

Results: An agreement of 79.1%was obtained between fully automatic CADS results from SV (mainly using TE short and long) and radiology diagnosis. This result increases up to 88.4% when average spectra from CADS were used in brain tumour classification. A 76.7, 79.1 and 81.4 % of agreement were obtained when CADS, average spectra and radiology results were compared to pathology diagnosis, respectively.

Discussion/Conclusion: The results obtained are indicative that the CADS developed in eTUMOUR, as fully automated and objective tool for processing SV spectra and supporting brain tumours classification, could be, in principle, useful for a large set of radiological services.

