rect for this [1-3]: natural logarithm, square root, inverse, natural logarithm of the inverse, and square root of the inverse. Repeatability (2 × 1.96 × within subjects standard deviation [4]) was calculated on a transformed scale, where measurement error was not proportional to the mean, then transformed back onto the non-transformed scale [2].

Results: Thresholding excluded 152 (12%) of spectra leaving 1,108 voxels; all with varying proportions of grey and white matter, and cerebrospinal fluid. Measurement error (absolute difference between datum one and datum two) for NAA:choline was proportional to the mean; see Figure 1A. Only the square-root of the inverse transformation removed this dependence; see Figure 1B.

Constant repeatability limits were calculated on the transformed scale, see Figure 2A, then transformed back to the natural scale (where the repeatability limits were now non-constant); see Figure 2B. The proportion of data lying between the repeatability limits in figures 2A and 2B are 95.1% and 94.4% respectively, proving that they act as the desired 95% confidence limits.

Discussion/Conclusion: Measurement error for MRSI metabolite ratios in the healthy human brain can be proportional to the mean meaning that mathematical transformation of the data would be necessary in order to calculate meaningful estimates of repeatability which will, in turn, permit robust clinical application of MRSI (e.g. defining the minimum significant difference for longitudinal studies).

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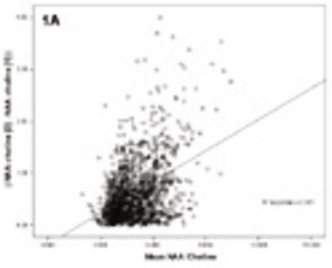

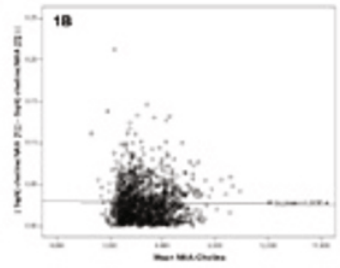

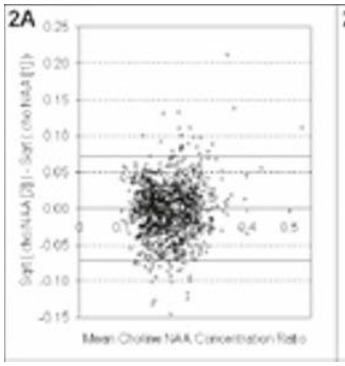

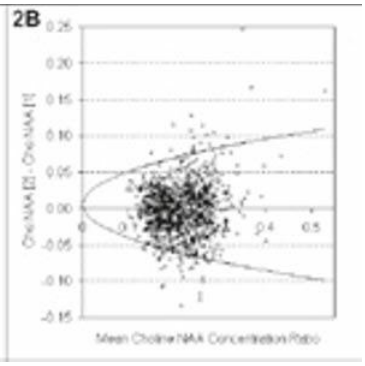

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In vivo and ex vivo investigation of fat deposits in mice of different ages

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Introduction: High resolution ^{1}H-NMR spectra of lipid extracts provide quantitative information about the chemical composition of the fat, namely average chain length (L), medium unsaturation (MU) and polyunsaturation (PI) indexes [1]. This information can also be obtained by in-vivo localized ^{1}H MRS [2-3] on live animals, opening the way to longitudinal studies over the same subject. Such studies are relevant for investigating effects of specific dietetic regimens or specific therapies. Compared to ex-vivo ^{1}H-NMR, in-vivo data are characterized by broader line-width and partially overlapping peaks and requires computer-aided analysis. This study compares quantitative results obtained by analysing in-vivo ^{1}H-MRS signals to ^{1}H-NMR spectra of lipid extracts. Analysis was performed by LCModel and HSVD methods [4].

Subjects and Methods: In-vivo experiments were carried out using a 4.7T Bruker Biospec System, a double configuration coil and a PRESS sequence without water suppression. Spectra were acquired in inguinal fat deposits in 4 groups of FVB mice with ages ranging from 1 to 12 months. Animals were then sacrificed, the inguinal deposits removed and processed according to [1]; finally, the lipid phase was dissolved in deuterated chloroform. High resolution spectra of lipid extracts were acquired using a Bruker DRX 500 spectrometer operating at 500.13 MHz. Mean lipid acyl chain unsaturation (MU) and polyunsaturation (PI) indexes and average chain length (L) were calculated from ^{1}H spectra according to the methods reported in literature [1] exploiting the areas of the peaks of different chemical groups.

Results: Fig1 shows representative spectra of in-vivo and ex-vivo inguinal fat. In the inguinal fat deposits of 1-month old mice L, PI and MU amounted to 17.26 ± 0.21, 0.34 ± 0.02, and 0.99 ± 0.01, respectively, as determined by ex-vivo ^{1}H-NMR with no relevant alterations with age. Analysis of in-vivo spectra, performed either with LCModel or SVD based methods, provided results in good agreement with ex-vivo data.

Conclusion: A new method for in-vivo quantitative evaluation of lipids constituting fat deposits, based on **^{1}H-MRS** and quantitative analysis, has been proposed and validated through comparison with the high-resolution results of ex-vivo techniques. Experiments in diabetic rats are currently in progress.

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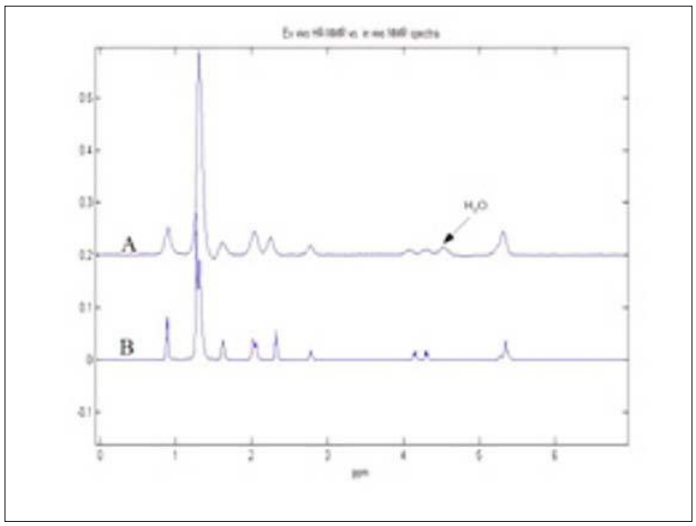
Fig 1: In-vivo 1H-NMR (A) and ex-vivo 1H NMR (B) spectra of mouse inguinal lipid tissue.



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Quantification in magnetic resonance spectroscopy with SELF-SVD

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Purpose/Introduction: In MR Spectroscopy, quantification plays a key role in the evaluation of the different metabolites and helps physicians reveal the presence of pathologies. Quantification remains however a major challenge in MRS.

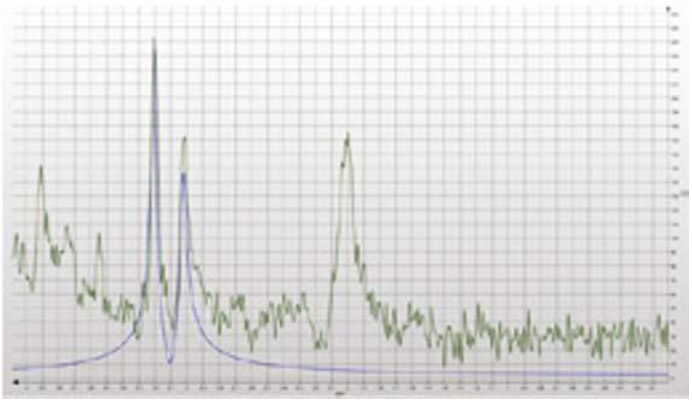
Selective-frequency singular value decomposition (SELF-SVD) has been presented in [1,2] as a promising quantification tool. In this work we propose a systematic analysis of the algorithm using both simulated and real 1H MRS in-vivo data.

Subjects and Methods: SELF-SVD is used to estimate the modes of the MRS signal lying in a predefined frequency range. The algorithm was implemented in an MRS software assistant, based on MeVisLab's development platform [3].

Multiple automated tests were performed in order to measure the influence of the parameters of SELF-SVD and the characteristics of the input data on the estimation quality.

In the in-vivo tests, data was acquired in a PRESS sequence with TE=135ms on a 3T Siemens Verio. The quantification results were compared to those obtained from the Siemens Syngo MRSI software.

Results: The simulated tests bring insight on some of the complex dependencies existing between the characteristics of the various components of the data (peak separation, damping of modes, etc.), the setting of SELF-SVD parameters, and the estimation results.



The figure above presents the spectrum of a voxel from an in-vivo brain dataset. The original signal is in green and the resulting estimation by SELF-SVD is given in blue, where choline (3.18 ppm) and creatine (3.03 ppm) are modeled.

SELF-SVD was successfully applied on the in-vivo data. The algorithm is nevertheless sensible to the correct setting of its parameters, in particular the length of the FIR filter for amplitude estimation. Time-wise, the method is efficient when performed on restricted frequency regions. The modeling of the choline and NAA peaks for 8x8 voxels takes less than two minutes.

Discussion/Conclusion: SELF-SVD provides rapid quantification of metabolites in MRS data, but requires good parameter setting. Estimating the noise in the data would enable a better adjustment of the amplitude precision parameter.

A robust estimation of the number of modes in the frequency ranges where the method is launched could further improve and automate the assigning of the parameters. This would be possible through the calculation of the effective rank of a noise-affected data matrix internally constructed in SELF-SVD.

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Matlab tool for segmentation and re-creation of MRS volumes of interest in MRI image stacks

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Purpose/Introduction: In brain Magnetic Resonance Spectroscopy (MRS) the volume of interest (VOI) is limited to finite minimum dimensions. Hence, spectra often include contributions from unwanted structures. It is therefore desirable to determine the ratios of gray and white matter and CSF in VOI, especially for absolute quantification of data. However, some MR systems only display the VOI boundaries in the anatomical images during planning; afterwards this information is lost, making it difficult to assess the tissue ratios retrospectively.