Definition of the macromolecular baseline based on T_1 as well as T_2 properties

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Introduction:
Inversion recovery (IR) [1] and saturation recovery methods [2] have been proposed for the determination of macromolecule (MM) contributions to ^{1}H MR spectra of the brain. IR can be combined with a specific delay time to obtain a metabolite-nulled spectrum. However, due to the difference in T_1 between metabolite peaks, there may still be residual metabolite signals in this spectrum. MM resonances are also known to consist of broad lines with short T_2, a property that has been used in post-processing to eliminate MM contributions from short TE spectra. Schemes, such as broad spline fitting or narrow width peak filtering of the metabolite-nulled spectrum [3], have been devised to accommodate this effect. An alternative method to determine the MM baseline (MMBl) is now proposed that directly makes use of the considerable T_1 and T_2 differences between MMBl and metabolites: combined fitting of multiple IR and multiple TE spectra (in the form of a 2DJ spectrum) enables the determination of the MMBl without contamination from metabolite contributions.

Methods:
Occipital grey matter IR and 2DJ PRESS spectra were obtained in twelve healthy volunteers on a 3T Siemens Trio system. Two of them were measured 5 times for repeatability. IR times (TI) of 30, 200, 450, 575, 700, 825, and 1200 ms were used with TE/TR of 20/2000 ms. The 2DJ spectrum was recorded with 24 equally spaced TE (20 - 307.5 ms; TR 2 s). Total scan time was 20 min. The MM model was defined as collections of Voigt lines with fixed spacing of 10 Hz and freedom to fit each area parameter. Two separate T_1 and T_2 times were accommodated, one set for the 0.9 ppm peak and one for the rest of the MMBl from 1.1 ppm to 4.5 ppm. Model fitting was performed with a tool allowing for 2D restrained linear combination model fitting including 2D prior knowledge adapted for the cases of IR and 2DJ spectra [4]. For MMBl determination, metabolite and MM parameters were adapted in an iterative process switching between 2DJ and IR spectral modeling. Separate fitting for IR only and for 2DJ only was also performed for comparison. Simulated spectra with varying noise realizations were used to test for systematic deviations from known true parameters.

Results and Discussion:
For each subject, a detailed spectral model was obtained with the iterative technique that allowed for T_1 and T_2 effects of both the metabolites and the MM to be accounted for. Fig. 1 compares the resulting MMBl obtained with the three techniques. It shows the mean ± 1 standard deviation range of the MMBl fitted for all subjects and for intra-individually repeated exams. Clearly the 2DJ PRESS technique shows most variance in the determined MMBl and the IR-only technique provides similar results as the currently tested version of the iterative technique. A further interesting observation is that - regardless of technique - the variance from repeated scans in the same subjects is clearly lower than for scans of different subjects. This suggests individual differences for the MMBl.

Conclusions:
A detailed MMBl model can be obtained with techniques based on T_1 only, T_2 only, or the proposed combined technique for individual subjects, though the latter presently at the expense of increased scan times. All three techniques can still be optimized in terms of ideal experimental conditions (number of different spectra, optimal TI, TE or their combination), which will lead to clearly reduced acquisition times. Inclusion of T_2 information for the determination of the MMBl is particularly promising for high fields where the difference in T_1 between metabolites and MM components is much reduced. Individual differences of MMBl composition may warrant its estimation in each subject to guarantee correct determination of metabolite contents.

References:
1. Behar et al MRM 32:294 (1994). **2**. Kreis et al *MRM* 54:4 (2005). **3**. Cudalbu et al *Meas. Sci. & Tech* 20:10 (2009). **4**. Chong et al *ISMRM 2009* #240.

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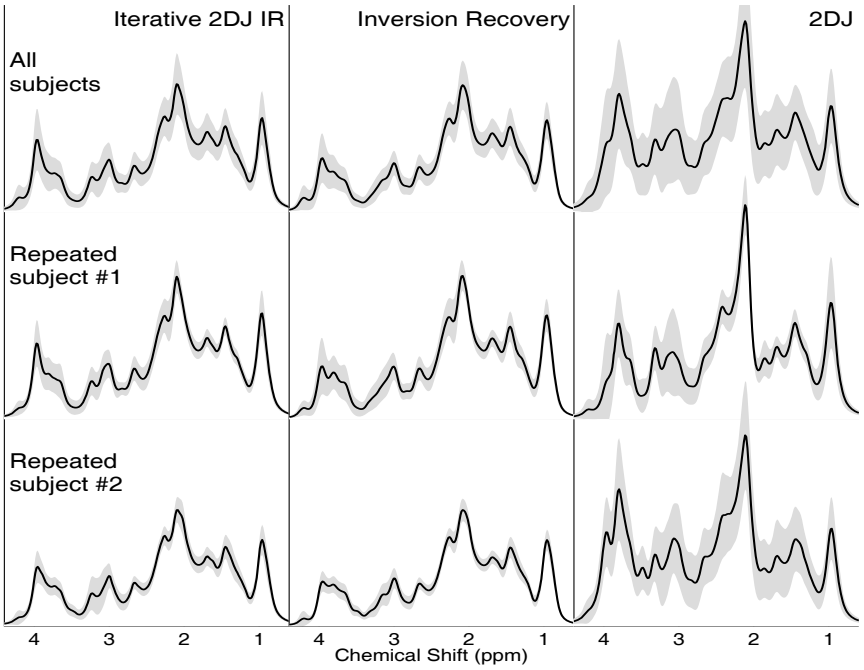

Fig 1. Fit results for the human in vivo data. Macromolecule baseline fits for the three methods, 2DJ-only, IR-only, and iterative 2DJ-IR. Three sets of data are plotted representing the cohort of 12 healthy subjects (top row), and 5 repeated examinations in two subjects. The black line represents the mean result enveloped by a light grey band of ±1 standard deviation over subjects (top) or repetitions.