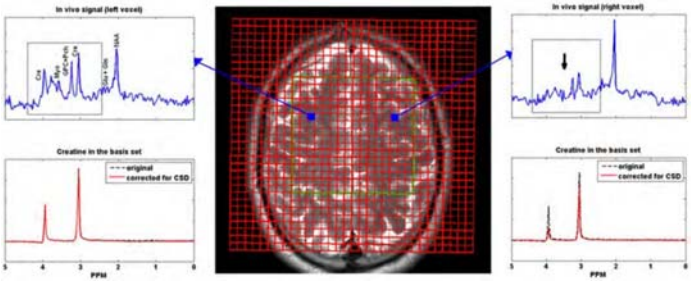
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### Metabolite quantification of MRSI data with an automatic correction for the chemical shift displacement artifact

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**Purpose/Introduction:** Chemical shift displacement (CSD) is an artifact of volume localization techniques stemming from the phenomenon that signals from protons with different chemical shifts arise from spatially shifted excitation volumes. Metabolite quantification of MR spectroscopic imaging (MRSI) might misleadingly indicate low concentrations at the borders of the localization volume for metabolites resonating further away from the carrier frequency. We propose an MRSI metabolite quantification method based on basis sets of metabolites that are spatially corrected, e.g., the creatine signal for a voxel affected by CSD is a modified version of the original creatine signal that is used for non-affected voxels.



**Subjects and Methods:** 2D PRESS 1H MRSI brain data from healthy volunteers were acquired with TE=35ms on a 3T MR scanner (Achieva, Philips, Best, The Netherlands). Nine metabolites (NAA, Glu, Gln, Cre, Myo, Pch, GPC measured in vitro and simulated lipids at 1.3 and 0.9 ppm, respectively) are used as basis set for time-domain quantification with AQSES-MRSI [1].
Spatial displacement of the excitation profile corresponding to two protons with different chemical shifts is proportional to the chemical shift difference [3]. We compute the expected spatial offset at all frequency shift values spanning the spectral range of interest and apply all these offsets to a simulated high-resolution image of the PRESS excitation profile. Then, each obtained image is discretized at MRSI resolution, leading to specific suppression factors per voxel location. For each voxel, a location-dependent metabolite basis set is computed by dividing each spectral point of the original basis set to the corresponding suppression factor.
**Results:** Our acquisition protocol implies about 1cm displacement per 1ppm frequency shift. Without CSD correction, the concentration maps of Cre, Myo, Pch, GPC are affected by significant underestimations at the top&right borders of the PRESS matrix, and Lips at the bottom&left borders. The correction method reduces the underestimation region, though the Cramer-Rao lower bounds are still much higher at the borders compared to the center of the PRESS matrix.
**Discussion/Conclusion:** We use a PRESS excitation profile to correct for underestimation of metabolites at the border of the MRSI volume. Post-processing of metabolic maps was previously proposed [2], but assumed only one resonance frequency per metabolite. Our method uses whole metabolite profiles incorporating simulated CSD effects within metabolite quantification.
**References:**
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### B0 field Mapping to improve prior knowledge in quantitative 2D-MR Spectroscopy

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**Purpose/Introduction:** Recent studies (1,2) have demonstrated that quantitative 2D-MR-Spectroscopy (Q-2DMRS) provides an enhancement of the accuracy of metabolite concentration estimation. This is especially interesting when the spectral dispersion is limited by the magnetic field strength (≤7T). However, from the quantitative point of view, the information gain with the unraveling of the F1 dimension is limited by the increased number of parameters to estimate. In this work, to lower the number of parameters, we validate on phantom measurements the incorporation into our 2D spectroscopic signal model of a prior knowledge on $T_2$ inhomogeneity ($T_{2inhom}$), obtained from a B0 field map, and demonstrate via the Cramér-Rao Theory how Q-2DMRS performances are improved.
**Subjects and Methods:** **Acquisition:** Two 2D-MRS sequences involving different relaxation time weightings along the two spectroscopic dimensions were implemented on a 4.7T-Bruker-Biospin magnet: Localized CT-COSY (3) and JPRESS (4) (Figure 1).

$$\hat{s}_{2D\text{-}MRS} = \sum_{m}^{M} c_m \hat{x}_m(t_1,t_2)\, f_1(t_1,t_2,T_{2inhom},T_{2m})\, f_2(t_1,t_2,\Delta\omega,\phi_0)$$

$$f_1 = \begin{cases} \exp(-\frac{t_1}{T_{2inhom}})\exp(-\frac{t_2}{T_{2m}^*})\ \exp(-\frac{t_C}{T_{2m}}), & \text{for L-CT-COSY with a constant time tc=70ms} \\ \exp(-\frac{t_1}{T_{2m}})\exp(-\frac{t_2}{T_{2m}^*}), & \text{for JPRESS} \end{cases}$$

$$\text{and using } \frac{1}{T_2^*} = \frac{1}{T_{2m}} + \frac{1}{T_{2inhom}},$$

$$\textbf{Model 1}: \frac{1}{T_{2inhom}} \text{ is estimated, } \textbf{Model 2}: \frac{1}{T_{2inhom}} \text{ is a priori known from measured } \int_{voxel} \gamma\Delta B_0$$

**Figure 1 :** model functions for Localized CT-COSY and JPRESS: where M is the number of metabolites, $\hat{x}_m$ the simulated metabolite 2D signals, with concentration $c_m$ (parameters of interest). $f_2$ accounts for frequency shifts and zero-order phase.

The phantom consisted in an admixture of 9 metabolites in low melting 2% agarose gel. The B0 field map is constructed from a 3D-double gradient echo dataset with phase difference calculation, and subsequent phase unwrapping (FieldMAP). $1/T_{2inhom}$ estimation was obtained by integrating the B0 map over the MRS voxel. The measurements were performed three-times. Relaxation times were fitted for the main singlets (Figure 2). **Simulation:** Cramér Rao lower Bounds (CRBs) were calculated using the two JPRESS models described in Figure1, using typical in vivo concentrations, and simulated 2D metabolite signals.

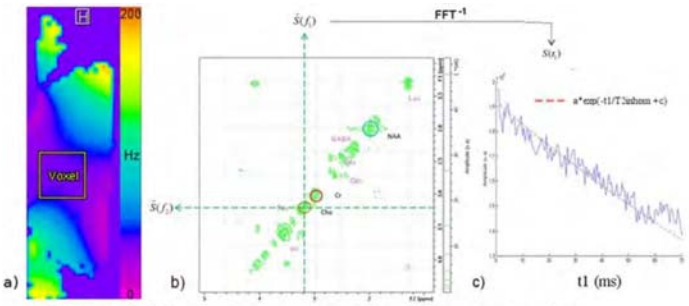



**Figure 2:** a) B0 field Map and MRS voxel localization b) L CT-COSY Map for a phantom of 9 metabolites (50mM concentration for NAA, Creatine, myo Inositol, Glutamate, Glutamine, Lactate, Taurine, GABA and 15mM for Choline), acquired with VAPOR water suppression, Tacq=15min, tc=70ms, TR=3500ms, SW1=3500Hz, SW2=2000Hz. c) fit of the $T_{2inhom}$ along the indirect dimension, on the Choline singlet extraction