An LCModel-based automatic software tool for the reconstuction of anatomically- and pathologically-matched voxels using high-resolution 3D-spectroscopic imaging: applications in tumour patients

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Introduction: Recently, it has been shown that satisfactory signal-to-noise ratio (SNR) can be achieved with high spatial resolution (e. g. 0.1- 0.5 cm^3) 3D spectroscopic imaging (SI) at 3 Tesla (1). Benefits of high spatial resolutions are decreased linewidths (meaning SNR does not decrease linearly with decreasing voxel size) and the possiblity to construct anatomically- and pathologically-matched voxels (AMV) without contamination from other tissues (1). The aim of this work was to develop a software strategy and tool to allow a user to select different regions, either anatomically-based (by a radiologist) or based on Cho/NAA metabolic maps, and then to automatically reconstruct and quantify AMV using LCModel (2) in a user-independent two-step procedure.

Materials and Methods: Spectra from seven tumour patients (Glioma WHO grade II and III) were measured using a standard 2D-CSI protocol with PRESS preselection (TE/TR=135/1600ms, 0.4 cm^3 voxel size) on a 1.5 Tesla Siemens Sonata scanner (Siemens Medical, Erlangen, Germany). AMV were reconstructed in the active tumours, based on Cho/NAA metabolic maps. Spectra of a healthy volunteer (male, 25 years) were acquired using 3D-SI with STEAM preselection (TE/TR=11/1600ms, 0.33 cm^3 voxel size) on a 3 Tesla Bruker system (Medspec S30/80, Bruker, Ettlingen, Germany).

Data Processing Procedure: The AMV was defined on a grid (see Fig. 2A) over all slices measured. The extracted voxels (4 to 33) were transferred to LCModel and processed. The LCM-estimated phase corrections were retrieved and applied to each extracted voxel. Additionally, all voxels were corrected for susceptibility shifts and summed to one AMV. Finally, the AMV was processed again with LCModel. To simulate an experiment with lower resolutions and to demonstrate the potential of this method, data were processed with and without susceptibility correction and compared for signal-to-noise ratio (SNR), linewidth and standard deviation estimated by LCModel.

Results: Fig. 2A shows a metabolic Cho/NAA map of a patient with an astrocytoma (WHO grade type III) measured at 1.5 Tesla. All voxels considered to be the active tumor region (red in Fig. 2A) were summed up to one spectrum (8 cm^3) and processed with susceptibility correction (Fig. 2B) and without (Fig. 2C). The spectral quality of Fig. 2B is superior to that of Fig. 2C. The linewidth was reduced by 43% and SNR improved by 21 %. Considering all seven 1.5 T data sets, there was a reduction in the linewidth ranging from 18 to 43 % (a mean value 28%) and improvement in SNR of between 12 to 28% (mean 18%). Metabolic ratios varied on average by 7%, with the standard deviation estimated by LCModel being reduced in all susceptibility-corrected data sets.

Discussion and Conclusion: These results demonstrate that 2D/3D-SI should be carried out with the highest possible resolution. SNR losses due to spatial averaging are partially compensated due to reduced inhomogenities in smaller voxels. The quality of spectra is improved drastically. These benefits may even be more significant at 3 Tesla (Fig. 1) using ultra-short echo-time 3D-SI. In conclusion, construction of AMV leads to superior spectral quality with high specifity for the matched anatomical or pathological structure.

Fig. 1: Summed voxel from the white brain matter at 3 T (AMV-volume 3.3 cm^3). Note the improved quality using susceptibility correction (A) compared to the spectrum without correction (B). Myo-inositol is recovered and artefacts and linewidth are reduced. SNR is clearly improved.

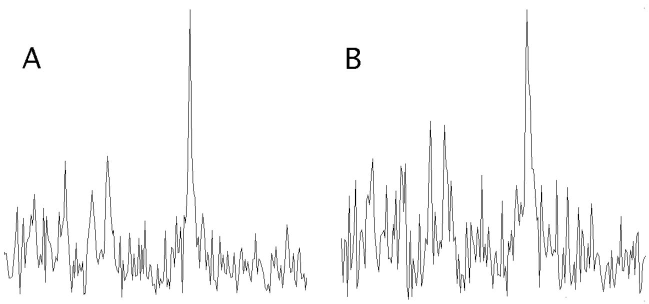
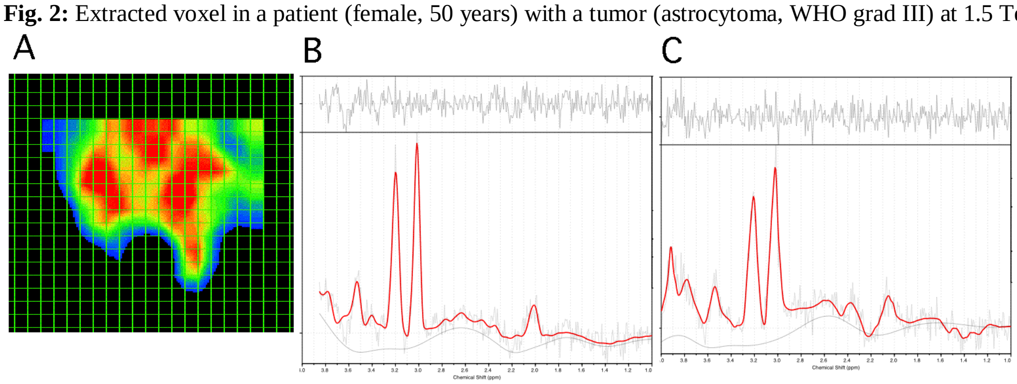


Fig. 2: Extracted voxel in a patient (female, 50 years) with a tumor (astrocytoma, WHO grad III) at 1.5 Tesla.



References:

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