Grid-free interactive and automated data processing for MR chemical shift imaging data

Y. Le Fur[1], M. Guye[1], S. Confort-Gouny[1], P. J. Cozzone[1], and F. Kober[1]
[1]Centre de Résonance Magnétique Biologique et Médicale (CRMBM) UMR CNRS 6612, Université de la Méditérranée, Marseille, France

Introduction

Today's available chemical shift imaging (CSI) analysis tools are based on Fourier transform of the entire data set prior to interactive display. This strategy is associated with limitations particularly when arbitrary voxel positions within a 3D spatial volume are needed by the user. In this work, we propose and demonstrate a processing-resource-efficient alternative strategy for both interactive and automated CSI data processing up to three spatial dimensions.

Materials and Methods

This approach uses real-time voxel-shift by first-order phase manipulation as a basis and therefore allows grid-free voxel positioning within the 3D volume. The corresponding spectrum is extracted from the 4D data (3D spatial/1D spectral) at each time a voxel position is selected by the user. The spatial response function and hence the exact voxel size and shape is calculated in parallel including the same processing parameters. This strategy permits visualization of the true voxel size and precise positioning at the location of interest as shown in figure 1 in comparison with traditional CSI post-processing tools.

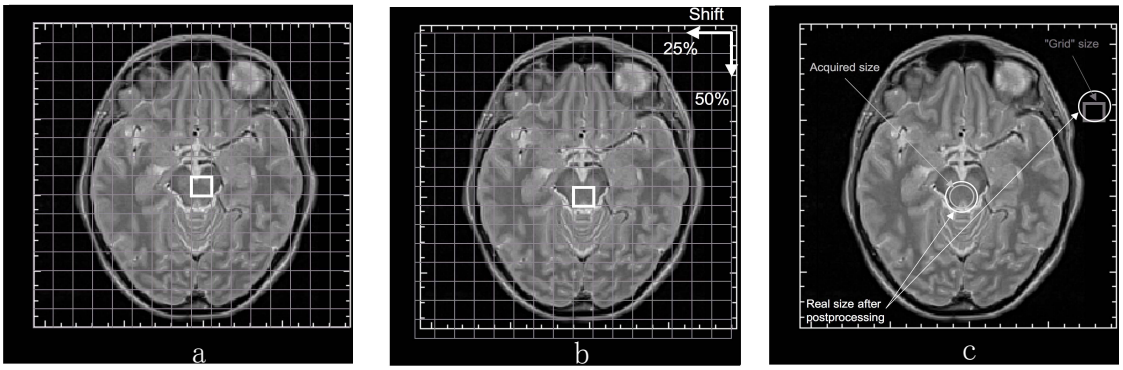
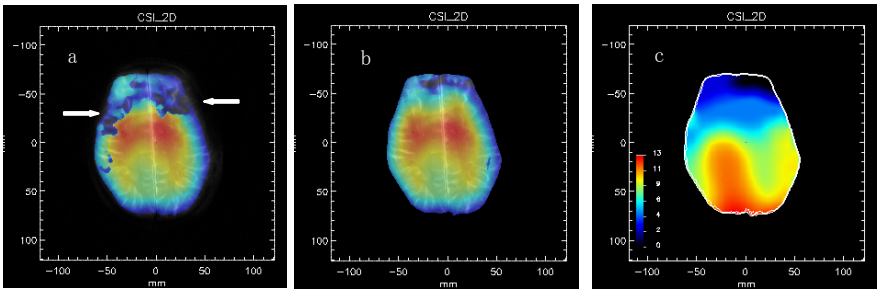


Figure 1: *(a) 13 x 13 phase-encoded CSI data set as shown by the 16 x 16 voxel and grid representation of traditional CSI analysis tools. (b) shifting the voxel on off-grid locations requires the recalculation of entire array in spatial dimensions. (c) Grid-free voxel selection by real-time voxel-shift and voxel display based on the final SRF. The white circle represents the contour of the SRF at 64 % of its maximum. The gray square shows the voxel shape corresponding to the 16 x 16 grid usually shown for these data sets.*

Using this algorithm sequentially along with AMARES time-domain modeling, we also implemented a new approach for automated quantitative and B_0-insensitive metabolite mapping. In a two-step procedure, AMARES fits restricted on fitting the NAA resonance are first obtained from every location within the brain lying on a low-resolution grid of 64 x 64 pixels, the spectral information being extracted by voxel-shift at each step. The frequency of NAA fitted with this algorithm is used to obtain a B_0 map, which enters a second time-domain fitting sequence as input information. The second fitting sequence is carried out on all brain metabolites and on a high-resolution grid of locations, again using voxel-shift.

Results

The real-time voxel shift approach along with the proposed B_0-correction helped obtaining reliable and operator-independent metabolite maps as shown in Figure 2. The frequency tolerance of the AMARES algorithm could be set as low as 12 Hz when the B_0 correction algorithm was used. When the B_0 correction was omitted, mis-attribution of signal in regions with poor homogeneity required user interaction despite large frequency tolerances in AMARES. The metabolite maps are unbiased by B_0 and baseline variations and show good homogeneity across large territories. Metabolite maps of (Naa, Cho, Cr...) were obtained reliably in various clinical research studies including volunteers and patients. The realtime voxel shift method also allowed selection of arbitrarily shaped compartments by sequential calculation as shown in figure 2 (d).



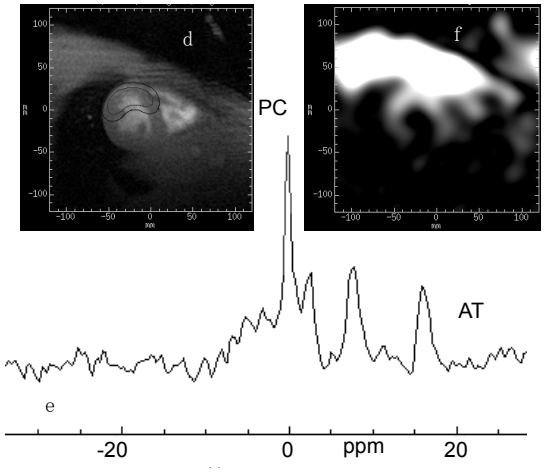


Figure 2: *(a) NAA map calculated without frequency correction. The arrows show misfitted regions due to B1 inhomogeneity. (b) NAA map calculated using the frequency correction map shown in (c). The frequencies observed in this plane were in the range of 13 Hz. (d) voxel shape obtained by sequential voxel shifts adapting to the heart's morphology shown on a proton short-axis image. (e) spectrum obtained from the volume shown in (d). (f) phosphocreatine map obtained by integrating the PCr spectral region.*

Conclusion

The calculated metabolite maps demonstrate good stability and accuracy of the algorithm in all situations tested. The suggested algorithm constitutes therefore an attractive alternative to existing CSI processing strategies. Accurate display of voxel size and shape helps reducing errors made through misinterpretation.