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

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Abstract

Purpose 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.

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. The spatial response function and hence the exact voxel size and shape are calculated in parallel including the same processing parameters. Using this mechanism sequentially along with AMARES time-domain modeling, we also implemented automated quantitative and 

31P-3D-CSI of the heart of a healthy volunteer is also shown.

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.

Keywords Chemical shift imaging · Voxel-shift · Processing · Magnetic resonance spectroscopy · Metabolite mapping

Introduction

NMR chemical shift imaging (CSI) provides spatially encoded metabolic information. As opposed to single voxel spectroscopy, the entire imaging volume is encoded in data sets from one to three spatial dimensions and a spectral dimension. The high dimensionality of the available data raises the question of how the contained information can be (a) visualized in the most user-friendly way and (b) quantified appropriately.

(a) One requirement for CSI visualization is the dimensional reduction of the spectral-spatial space containing the data. This is generally achieved by extracting data either along a temporal line of that space for spectral visualization, or from a spatial plane to obtain metabolite maps. Today’s CSI analysis tools (commercial CSI software by Siemens, Philips, GE and Bruker, as well as [1–6]), however, clearly separate their interactive analysis procedures into a spectral and a spatial thread. For instance, the user interaction is limited to two spatial dimensions requiring the extraction of a single spatial slice prior to further analysis. The main reason for this separation is that the data set is spatially interpolated...
prior to analysis, and an interpolation in three spatial dimensions would require unacceptably high computer memory resources and data transfer times (e.g. 64 GB for a complex data set interpolated to $256^3 \times 1024$ points).

(b) Ideally, the software should output a map containing all quantified metabolic information. It should also depict the spatial response function (SRF), which represents the weighted contribution of every point in space to the spectrum, and which defines the true spatial resolution of the data. In order to accurately adjust the position of a region of interest, the grid spacing of the map should be comparable to that of the underlying morphologic reference image and not be related to the CSI spatial resolution.

For pure visualization, the user can either be interested in the interactive selection of voxels (“multi-voxel” aspect) or in metabolite maps. Both aspects should be accessible rapidly and with a minimum of computational resources. In this work, we propose a post-processing strategy and software that closes the gap between these two aspects. The concept is based on the voxel-shift technique, which in the past has mainly been used for grid shifts with CSI techniques or for slice shifts (re-slicing) in 3D imaging. However, the grid shift in the cited software is done as a whole in a separate step. In this work, it is employed to fulfill the aforementioned requirements without need for significant computer resources.

**Materials and methods**

**Algorithms**

**Interactive processing**

The processing algorithm is depicted in Fig. 1. The first step of the interactive analysis typically consists of selecting a voxel position on a 2D or 3D proton reference image. A slider allows navigation through the data set in a third spatial dimension if necessary. A spectrum from the selected position is then calculated for visualization and quantification. The voxel position space is virtually continuous in three dimensions; it does not have to lie on a specific grid because voxel-shift by spatial first-order phase manipulation [1,7,8] is used to extract the spectrum from any given position. The spectrum can be used as reference for manual or automatic phase correction of the entire data set. It further allows the interactive selection of a frequency offset range for which the spatial distribution (metabolite map) is calculated. At each new spectral range selection, only the extracted data is summed, zero-filled, Fourier transformed in the remaining spatial dimensions and displayed at the selected “slice” position. The voxel shape is displayed as a contour of the spatial response function (SRF) at a level of 64% of its maximum representing the true spatial resolution. The SRF is systematically calculated by Fourier transform of the $k$-space sampling scheme taking into account all spatial processing parameters at each time the data set is processed in spatial dimension.

The novelty in this processing strategy is that only the original data set before Fourier transform is kept in working memory allowing efficient use of computer resource on the one hand and grid-free spatial and spectral navigation through the data set on the other hand. All processing operations are carried out at each new selection of locations or parameters including phase correction or filtering. All dimensions of the data set are accessible through simple interactive navigation. An interactive AMARES a priori information selector and an interface to the original AMARES routines (MRUI 99, http://sermn02.uab.cat/mrui/mrui_Overview.shtml) allows fitting of the currently displayed spectrum. Figure 2 illustrates the