Stand-alone GUI of analyzing and displaying proton 2D/3D MRSI data sets with LCModel

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Introduction

LCModel [1] has been widely used for analyzing Magnetic Resonance Spectroscopy (MRS) and provides reliable relative and absolute quantification of metabolite concentrations. As the increasing interest of applying MR spectroscopic imaging (MRSI) to clinical studies, LCModel also enhanced the ability to analyze MRSI data set. However, the possibility to browse all analyzed results combining anatomy information is not given in the original software package, especially for 3D MRSI due to numerous output files. McLean et al. [2] set up a system within the General Electric (GE) Sage/Idl processing package dedicated to process GE MRSI data only. In the meanwhile, Ko et al. [3] developed a GUI tool in Matlab to facilitate analyzing and displaying Siemens SI data.

Based on the latter the aim of our work was to implement a stand-alone and user-friendly tool to browse the resultant spectra both for 2D and 3D MRSI data set with excellent processing efficiency and compatibility. Compared with the previous work [3], C-based environment benefits a better efficiency and compatibility for various kind of information. Therefore, the user-friendly 3D MRSI visualization and analyzing GUI will be particularly useful for clinical diagnosis and further statistical analysis.

Materials and Methods

The software was programmed with Borland C++ Builder 6.0 (BCB, Borland, Inc.) on Windows XP (Microsoft, Inc.) system. The whole package was compiled as a stand-alone file and can be executed without the installation of BCB 6.0. For 3D display, we used OpenGL embedded in our C-program. The software was tested with phantom and volunteer data sets.

Results and Discussion

The GUI framework of our program is shown in figure 1. The "Coord" files generated by LCModel can be automatically loaded as input of our software. The main window (Fig.2) includes the display of all information obtained from LCModel for the whole MRSI data sets, and of the corresponding anatomical MRI data sets, calculation of arbitrary metabolite maps, ROI functionality on metabolite maps and an export function of the ROI results as an ASCII file for further statistical processing, which is consistent with the previous work by Ko et al. [3]. Basic functionality to save or print the images, spectra, and metabolite maps are provided. Anatomical reference MR images can be loaded and the VOI in MRS and MR images of DICOM format will be registered and displayed automatically. As there is increasing interest of 3D MRSI in clinical studies, the tool was extended to handle 3D MRSI data sets as well. Existing 3D-visulization of MR images and spectra from OpenGL were integrated into our C-based program. The whole software was finally compiled as one executable file, which means users don't have to install any additional software. Additional functions such as export for statistical analysis as well as an output module for general image formats (jpeg, bmp, etc.) have been implemented. The characteristic of flexibility and powerful library support for C-language leaves us an ample room for more functionalities of this program in the future.

A user-friendly tool for analyzing, integrating, and displaying of 2D/3D MRSI data sets is developed. It provides users not only the essential functionalities for MRSI data but also information combining anatomy with spectra, which benefits the diagnosis in clinics and studies. The software can easily be modified in order to fit the original format of MRSI data from scanners of various manufactures. The previous work performed in Matlab [3] has provided the principal functionalities for 2D MRSI, yet the adaptability of Matlab for 3D visualization of MRI and MRSI is still limited. The tool programmed in C serves for both 2D and 3D MRSI data and will be very valuable for clinical research studies.

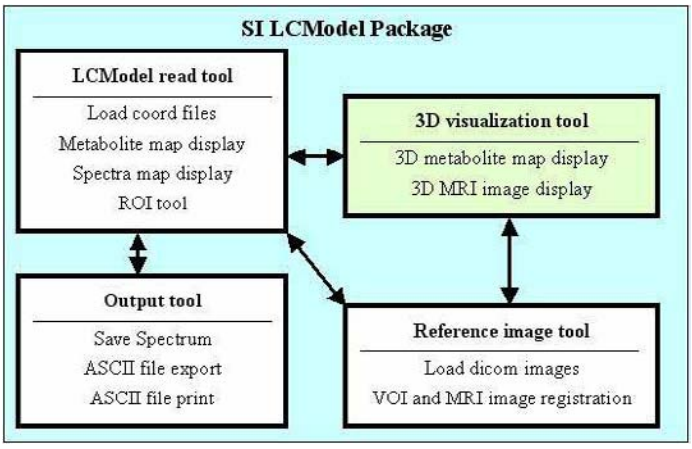

Figure 1. The framework of the 2D/3D MRSI Package.

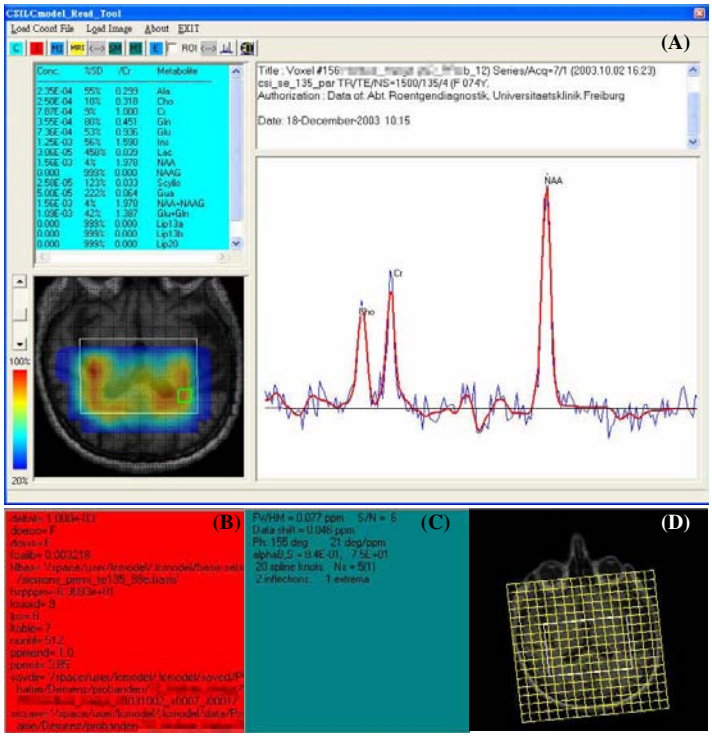

Figure 2. The main GUI (A) of the display including a reference image, the calculated metabolite map for selected voxels , original and fitted spectrum, and the concentration table. The sub-window of concentration table can be switched to display control parameters of LCModel (B), analysis parameters (C) as well as full reference image (D).

References

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