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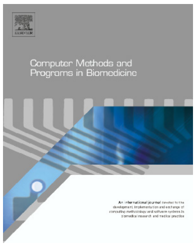

jSIPRO – Analysis tool for magnetic resonance spectroscopic imaging

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ABSTRACT

Magnetic resonance spectroscopic imaging (MRSI) involves a huge number of spectra to be processed and analyzed. Several tools enabling MRSI data processing have been developed and widely used. However, the processing programs primarily focus on sophisticated spectra processing and offer limited support for the analysis of the calculated spectroscopic maps. In this paper the jSIPRO (java Spectroscopic Imaging PROcessing) program is presented, which is a java-based graphical interface enabling post-processing, viewing, analysis and result reporting of MRSI data. Interactive graphical processing as well as protocol controlled batch processing are available in jSIPRO. jSIPRO does not contain a built-in fitting program. Instead, it makes use of fitting programs from third parties and manages the data flows. Currently, automatic spectra processing using LCModel, TARQUIN and jMRUI programs are supported. Concentration and error values, fitted spectra, metabolite images and various parametric maps can be viewed for each calculated dataset. Metabolite images can be exported in the DICOM format either for archiving purposes or for the use in neurosurgery navigation systems.

1. Introduction

An accurate determination of the metabolite signals in the spectrum is a crucial step in in vivo magnetic resonance (MR) spectra analysis. Magnetic resonance spectroscopic imaging (MRSI) typically involves a huge number of spectra to be processed, analyzed and interpreted in relatively short time. Therefore, a tool allowing for the reliable and automatic processing of MRSI data is of great importance for the clinical application of MRSI. Scanner vendors address this problem by installing various MRSI processing packages on scanners. However, these packages are primarily intended for online data processing in the clinical environment and offer limited functionality. This situation provided the impulse for the development of tools for MRSI data processing from third parties.

In principle, any program enabling single voxel spectra processing can be adopted for MRSI data evaluation. However, specific requirements for MRSI processing programs exist. Firstly, such a program should allow specific MRSI data pre-processing and post-processing. Secondly, it has to allow data processing in a batch mode, i.e. the repeated processing of several spectra without any user intervention. Thirdly, the

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program has to allow the display of the spectroscopic grid and calculated metabolic maps overlaying the anatomical images of the measured sample. The last requirement in particular disqualifies many sophisticated programs available for MR spectroscopy data processing.

Numerous home-made MRSI processing tools have been reported [1–11], however, mainly due to their unavailability and/or missing detailed documentation, they have not attracted much attention. In contrast, two programs for the processing of in vivo MR spectroscopy data and also enabling MRSI data fitting are currently widely accepted within the in vivo MR spectroscopy community: LCModel (Linear Combination of MODEL spectra [7]) and jMRUI (Java based Magnetic Resonance User Interface [8]). LCModel provides for the sophisticated fitting of MRSI data; however, it does not implement by itself either any data pre/post processing or the graphical display of MRSI on the anatomic images. The recently released new jMRUI version (ver. 5) enables the processing of MRSI data using several fitting routines (AMARES – Advanced Method for Accurate, Robust, and Efficient Spectral Fitting, AQSES – Automated Quantitation of Short Echo time MRS Spectra, and QUEST – quantitation based on QUantum ESTimation). MR spectra as well as calculated metabolite images can be viewed overlaid on the anatomical base images in jMRUI.

Our many years of experience with clinical MR spectroscopy have shown that a high quality MRSI processing program should meet the following requirements:

1. Possibility of selecting a suitable fitting program;
2. Automatic selection of base (anatomical) images;
3. Availability of post-processing routines;
4. User friendliness and simplicity;
5. Availability of tools for result analysis; and
6. Multi user access to data.

Despite the high complexity of available MRSI processing programs none of them has met all the requirements. Following the above criteria the jSIPRO (java Spectroscopic Imaging PROcessing) program has been developed. jSIPRO is a platform independent graphical interface enabling preprocessing, post-processing, viewing, analysis and result reporting of MRSI data. jSIPRO does not contain a built-in fitting program. Instead, it makes use of fitting programs from third parties and manages the data flows. In other words, external programs offer only the fitting routines themselves, while the remaining MRSI functionality is provided by jSIPRO. This approach enables the decoupling of the requirements for sophisticated data fitting and for the remaining MRSI data processing functionalities. In our experience, different processing programs may be suitable for processing particular MR spectra types (e.g. LCModel or TARQUIN for 1H brain spectrum, AMARES for 31P muscle spectrum). Therefore, the possibility to select different fitting programs in jSIPRO turned out to be of great importance for universal and flexible MRSI spectra processing. Several post-processing routines as well as tools for result analysis have been implemented in jSIPRO in a user friendly way making it a convenient MRSI data processing tool.

jSIPRO is freely available upon registration at [12] along with detailed documentation and a discussion board.

2. jSIPRO: architecture and features

2.1. *General description of the jSIPRO program*

jSIPRO has been written in the Java programming language and has the extended functionalities of the program CULICH [13]. The basic schematic diagram of jSIPRO is depicted in Fig. 1, where three main functional blocks can be recognized: (1) the automatic import of the spectra along with anatomic high resolution images, (2) MRSI data preprocessing and initialization of spectra fitting, and (3) the automatic download of the results of the spectra fitting, their viewing and analysis. The main functionality of each block is described below.

2.1.1. *Data import and data management in jSIPRO*

The required data (spectra and base images) are imported to jSIPRO using dedicated import facilities. Currently, import from the selected data folder and import from the relational database are supported. If the spectra headers contain information about associated base images, such as in SIEMENS DICOM (Digital Imaging and Communications in Medicine) [14] VB15, VB17 files, the base images are automatically found and downloaded by the jSIPRO importer; alternatively, the user has possibility to select the series with the base images manually or let jSIPRO find the base images with the orientation most parallel to the orientation of the given MRSI dataset. The same applies for reference (water unsuppressed) spectra that can be automatically identified based on the header entries.

jSIPRO also supports importing data from the external (relational) database. Given the rigid structure of the database tables jSIPRO queries the database and downloads required spectral and anatomical datasets. The required structure of the database tables is given in the jSIPRO manual.

To avoid the need for the repeated loading of all required datasets when the same dataset is to be re-processed, the imported data are stored in the disk. Each saved dataset is identified by an identification based on the subject name,

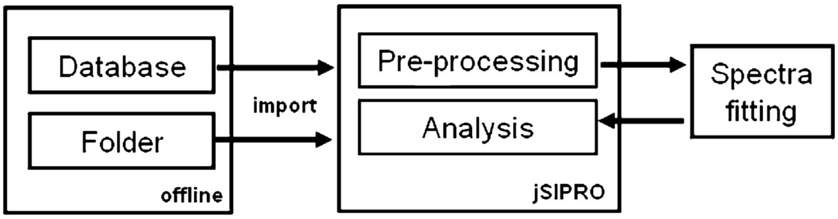

Fig. 1 – The basic schematic diagram of jSIPRO.