

An Integrated Analysis Platform for Magnetic Resonance Spectroscopy

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Introduction

In vivo magnetic resonance spectroscopic imaging (MRSI) provides information that can be a boon for the non-invasive diagnosis of disease; however, the sheer quantity of information involved can lead to difficulties. To understand the scale of this problem, consider first a relatively small data set, consisting of 8 phase encodes in each dimension, or a total of 512 unique spectra. Quantitation of a single spectrum often results in 10 to 15 metabolite concentrations and measures of uncertainty, meaning that the single data set results in $O(10^4)$ data points. In practice, clinical studies may involve multiple acquisitions from several subjects and require comparison to a healthy population, implying the collection of hundreds of MRSI data sets. In these situations, one obtains $O(10^6)$ data points and the need for a system capable of automating the analysis and organization of this information becomes obvious.

To address this problem, we have created an integrated analysis platform for MRS data. The goals in its design are threefold. First, it must be a complete representation of the data collected; the system will be used for analysis of all information generated at the various stages of processing, and one should never need to refer back to earlier steps. Second, it should automate as much of the data entry and final analysis as possible, removing the likelihood of operator error and making it easy to deal with large volumes of data from multi-centre studies. Finally, the system needs to be sufficiently flexible to incorporate multiple modalities and varying analyses.

Methods

The system itself consists of two parts: a database to store the data and a client application for processing, uploading and analysing the data. This server-based storage allows many researchers to work with the same data, while providing controlled access for each user. As the client application is responsible for uploading, remote submission of data in multi-centre studies is possible simply by distributing the client program.

The data are stored in a MySQL¹ database designed to model the real-world organization of information in that any one subject may have had a number of exams, such as MR, or CT. Each of these exam types is represented by a table within the relational database, and foreign key constraints maintain the referential integrity back to the subject from whom they were derived. A similar table structure holds for the variety of tests which are performed in the course of any single exam. This makes the database very flexible and able to include multiple modalities.

The client software for accessing the database is built on the same data model as the database and is written in the programming language Python. This makes it very easy for individual users to develop add-in modules that tailor the system to their own needs.

Results and Discussion

This analysis system is currently in use in a number of studies. The client is capable of automatically entering results from each processing step into the database. With all relevant information in a single accessible location, one is ready to perform final analyses of the data, including population studies. This final analysis can be performed in one of two ways: interactively through the client's graphical user interface, or via a flexible analysis and reporting system.

There are a number of interactive displays that allow visualization of the data. Figure 1 shows a simple example, the results of an LCMoDel² quantitation of MRSI data overlaid on an anatomical image. At the far right, the quantitation results are displayed and updated automatically as the mouse is moved over individual spectra. Being in constant contact with all information in the database means the client is also capable of displaying the data in more clinically-relevant ways. For example, by internally performing classifications of the individual spectra, then highlighting potentially diseased regions on an anatomical image.

A second possibility for analysing the data is through an automated reporting system. The desired analyses and the method of displaying the data are specified by the user as an add-in module. When this module is activated, the analyses are performed and a final processing report is created in a platform-independent format³ suitable for presentation. The results of such an automated analysis are also shown in Figure 1. These particular data were taken from a study collecting spectra from a healthy population organized according to brain region and age. The average over each of the individual brain regions, subject to a number of conditions ensuring data quality, is calculated and compared to the entire population in a given age range. The generated report displays these results and a summary of a number of diagnostic tests which allow one to judge the quality of the data.

In summary, we have presented a new system for individual and population analyses of magnetic resonance spectroscopy data. The system consists of two parts: a database for storage, and a client application for accessing the information and performing analyses. Combined, these two parts give an analysis platform capable of managing the large volumes of information generated and sufficiently flexible to accommodate several sources of clinically-relevant data.

References

1. MySQL, MySQL AB, Uppsala, Sweden
2. Provencher, S.W. Magn. Reson. Med. **30** (1993) 672-679
3. Portable Document Format (PDF), Adobe Systems, San Jose, CA, USA

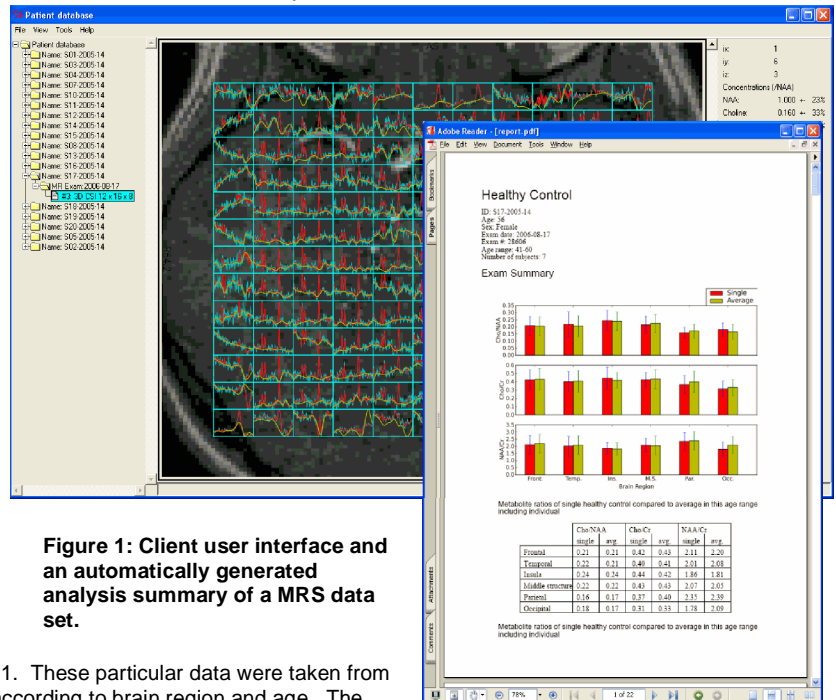


Figure 1: Client user interface and an automatically generated analysis summary of a MRS data set.