MRSTANK - A user-friendly yet powerful alternative software package for spectral processing

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Introduction

There are many potential applications of Magnetic Resonance Spectroscopy in medicine as a biochemical diagnostic tool. Quantitative analysis of single-voxel *in-vivo* MRS spectra from infiltrating brain tumours provides a means for physical interpretation and classification, leading to improved diagnosis.

Various MR spectroscopy processing software packages are currently available [1-3], but are seen by many radiologists as complex and difficult to learn. The large number of different processing schemes may provide too much choice; often uncertainty about the optimum methods to apply and the lack of intuitiveness forces many to abandon spectral processing in favour of using simple peak fitting values or metabolic maps provided by manufacturers.

We have developed an intuitive GUI-driven application based upon a MatLab toolbox that is able to support clinicians with the ability to easily create unique spectral databases, and use these databases for any number of applications including: statistical analysis of patient data using different algorithms, direct comparisons with previous measurement data, mapping variations across different areas of the brain, classification using a multi-component linear classifier.

Methods

The software was developed using the MatLab platform; but has been compiled onto both Windows and Linux systems. As such it provides fast algorithms and advanced graphical functionality, while remaining compatible, transferable, and easy to install on most systems. The software works on data in the frequency domain which increases understanding and acceptance. The user interface was recognised as crucial to the clinical acceptance of the software, and was designed in conjunction with the radiology department. The GUI ensures all of the available functions are easily accessible, and provides a clear indication of the working mode.
Some of the features available are:

      Multiple database support for different acquisition modes.
      User defined peaks and database fields.
      Automated Voigt peak fitting with baseline correction.
      Batch processing using prior knowledge.
      Read data directly from clinical scanners (Siemens, GE).

Feature extraction based upon the following modes:
- User-defined peak fitted curves (optional auto tCr ratios)
- Principal Components Analysis (PCA)
- Independent Components Analysis (ICA)

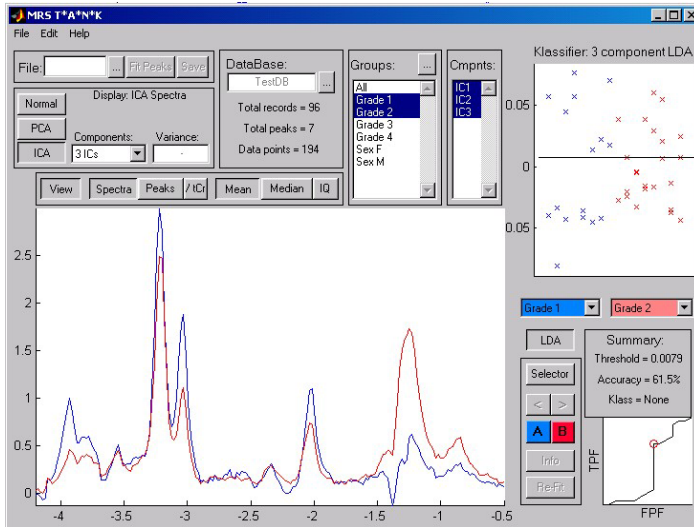Linear Discriminant Analysis (LDA) for classification.

Figure 1. The main interface dialogue. On the left is the data viewer which can be switched between spectra and peak-fit values. On the right the LDA classifier is shown applied to the first three Independent Components of Grade 1 / Grade 2 tumours, with the Receiver Operating Characteristic.
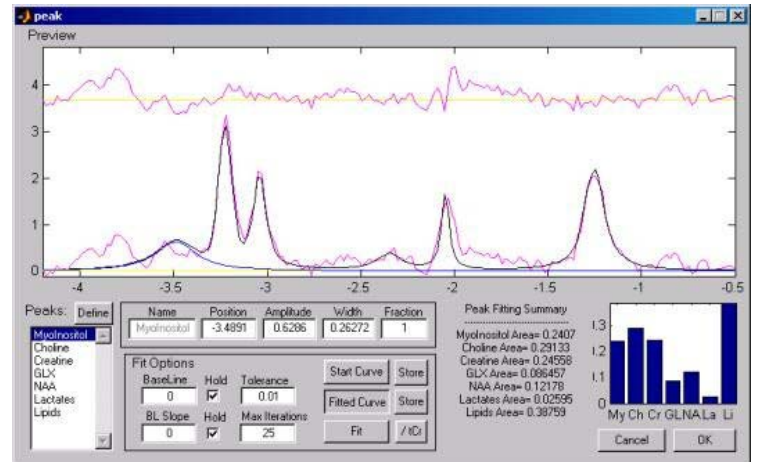

Figure 2. The peak fitting dialogue showing a fitted curve, residual noise, and peak properties. Any peak fitting can be manually reviewed and altered. The summary in the lower right displays the calculated peak areas and plots the results.

Results

Initial trials by radiologists have been favourable, with quick acceptance and good understanding of all of the functionality of the program. There is a large set of prior data that has been incorporated as a training dataset. Additional databases are planned at various echo times, on different machines and for different sequences. Pathological and histological tests are being used to train the datasets.

Discussion

We have presented a spectral processing application that trades on its easy-of-use and clear interface. The incorporation of ICA is also a novel feature that holds great possibilities in tissue recognition. Forthcoming adaptation of the program to incorporate CSI/multi-voxel images will provide an order of magnitude increase in the size of datasets, and improve the ability for tissue identification. In this area we have a particular interest in the correlation and registration of data with segmented MRI images and DTI. It is hoped that the compilation of diverse clinical datasets will provide a means not only for the statistical mapping of metabolic variation across the brain regions, but also for the direct comparison of the classification accuracy using multiple feature selectors. The configurable database structure also allows for the identification of environmental or patient factors that may have a bearing on measurements.

References

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