A tool for MRS Visualization & Tumour Classification

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Abstract

Our objective is to develop a decision support system that improves the accuracy of non-invasive brain tumour diagnosis and grading by using data from Magnetic Resonance Spectroscopy (MRS).

The system, which uses pattern recognition techniques, is trained on validated database spectra. An innovative user-interface presents on one hand the pre-process spectrum and on the other hand the classification results as a two-dimensional overview plot.

This work has been developed within the framework of EU- funded research project e-Tumour (an integrated Project in the field of health composed by 22 European partners in the health, university and industry fields) .

Our effort has been focused on the discrimination of the four most prevalent types of brain tumours: meningiomas, glioblastomas, astrocytoma grade II and metastases.

The results obtained have been around 95% accuracy and a easy-to-use interface, so for this reason this tool will help clinicians in the diagnosis of brain tumours.

1. Introduction

When planning treatment for a patient with a suspect of a brain tumour the clinician needs to know exactly what he or she is dealing with. Currently the gold standard for brain tumour diagnosis is the histopathologic study. This requires surgical extraction of tissue from the area of the tumour and is needless to say, unpleasant and even hazardous for the patient. Also, this kind of surgery cannot be constantly repeated to follow tumour evolution or response to treatment. Our objective is to improve the accuracy of non-invasive tumour diagnosis and grading and consequently reducing the biopsy.

An MR spectrum consists on a series of peaks, where the position of the peak along the x-axis (measured in ppm) determines the particular biochemistral, and the size of the peak is a measure of its concentration.

Although MRS gives significantly improved brain tumour categorization, radiologists have problems in interpreting spectral data [2]. Projects like INTERPRET [2] and e-Tumour [1] have as one of the main objectives the automation of pattern recognition for the diagnosis, the interpretation of the tumour spectrum making possible to solve this problem.

Brain tumour MRS provides information non-invasively on tumour biochemistry [3]. We want radiologists to analyze the spectrum through our DSS

as well as to verify their diagnose and decision on brain tumour using and comparing the results of the classifiers based on the application of pattern recognition techniques.

In the next sections we will speak about the development of the DSS, how the pattern recognition techniques have been applied to generate the classifiers and how to apply these classifiers to the spectra offering results and being interpreted by the clinican.

2. Material and Methods

2.1. Spectra

MRS studies showed clear differences between one spectrum obtained from one healthy person and one with a brain tumour [3]. The differences are represented with ratios between metabolites and studied by the clinicians to know what kind of tumour the patient has.

Our DSS allows separately working with two kinds of spectrum: short (20ms-30ms) and long echo (135ms-136ms) time. The echo time affects the information obtained with MRS. Spectra represented with TE short are richer in metabolites but noisier; however with TE long only the main metabolites like N-acetyl-aspartate, Creatine and Choline are expressed [4]. In the figure 1 a representation of the different visual features in a spectrum with short and long echo time is showed.

These spectra are obtained automatically after some pre-processing steps implemented as independent modules. Moreover the Fourier transform and the corresponding zero filling necessary to reach certain spectral resolution, a phase correction using the water signal and a Lorentzian apodization are carried out.

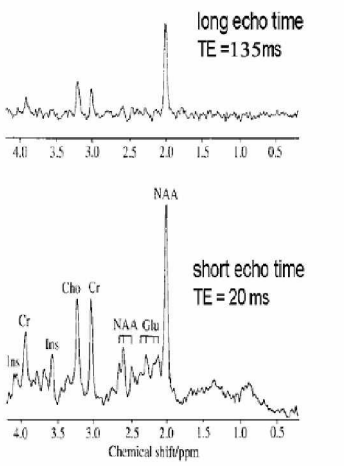

Figure 1. Example of a MR spectra

The biochemical study can be carried out by the clinicians through our DSS once the spectrum has been pre-processed. In table 1 are represented some metabolites in the biochemical structure and the figure 2 represents one example of one MRS spectrum with the characteristic peaks of these metabolites.

Table 1. Proton Metabolite

Metabolite	Abbreviators	Ppm
Lipids	Lip	0.9-1.4
Lactose	Lac	1,35
Alanine	Ala	1,47
Acetate	Ac	1,92
N-acetyl aspartate	NAA	2,02
Glutamate	Glx	2,10
Creatine	Cr	3,03
Choline	Co	3,20
Myo-inositol	MI	3,55

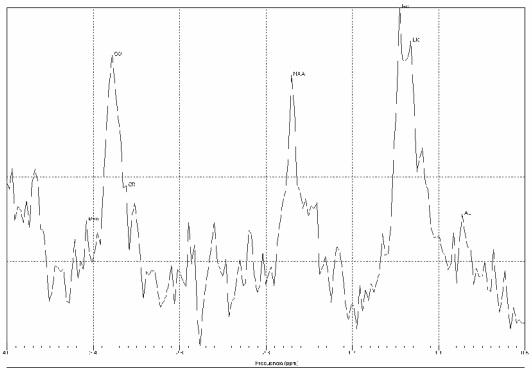

Figure 2. Example of MR Spectrum with the peaks of metabolites showed in Table 1.

2.2. Classifiers

The spectra that we have used as samples to train the classifiers come from the first version of eTumour database called eTDB0. It containts 64 cases of meningioma, 84 cases of gliobastomas, 39 cases of metastases and 22 cases of astrocytoma grade II. These spectra have been adquiered from Philips, General Electric and Siemens machines, however and by the moment, the DSS only reads spectra manufactured by General Electric.

The pattern recognition techniques applied have been LDA and K-nearest neighbours. We consider both techniques between two different extremes. K-nearest neighbours is based on the distance of the closest samples to the test case to classify it (local boundaries); LDA draws decision boundaries based on data projection to separate the different classes [5, 6].

We must consider the dynamic character of these classifiers. This is due to the architecture provided by the DSS, which allow the incorporation of new classifiers by means of XML documents without recompiling the tool. Once the program is restarted, the new introduced classifiers are automatically available.

2.3. Interface

Because of the fact that there are several classifiers based on different PR techniques trying to solve different brain tumour discrimination, an interface which allows communication between the DSS and the available classifiers is needed.

This communication is done in the following way: in first place the DSS reads all available classifiers taking into account their description, in other words, what kind of brain tumours classify among, what accuracy this classifier has and what kind of signal (echo time) does it need as input.

Once this information is obtained, the interface shows a list of the available classifiers that can cope with the given spectrum input.

At this moment the clinician can decide which of the classifiers wants to use among the offered by the interface.

Finally, once the classifier is selected, the interface launches the execution. When it has been performed, the results obtained are sent again to the interface which connects with the GUI for showing the results in a graphical mode to the clinicians. The figure 3 represents a schema of the interface communication between the GUI and the classifiers

In case the clinician does not decide to apply one concrete classifier, then the DSS takes a decision based on the result of the classifier with more accuracy.

It has to be taken into account that the output of this classifier might not be the solution of the question the clinician would like to be answered, but the answer of the best classifier obtained up to the moment.

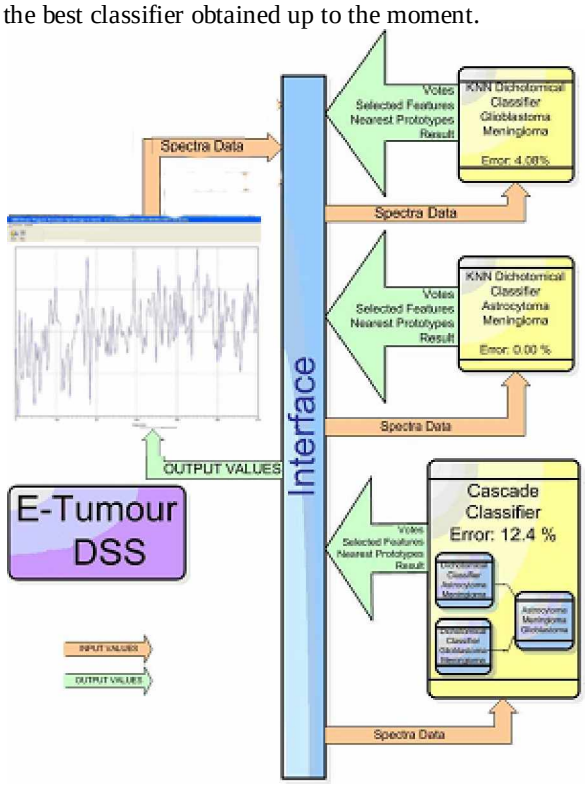

Figure 3. Scheme of the communication protocol between the DSS and the classifiers

3. Results

The results that this tool can offer are useful in different aspects. In a first step the clinician obtains the signal of a spectrum pre-processed with the modules described in section 2. This pre-processed spectrum is showed with the values of the peaks of metabolites and his relative ratios. Furthermore, the points of the pre-processed signal are exported in a

text format with the possibility of being used with any other program e.g. Excel, Matlab, etc.

The classifiers integrated until now are based on K-Nearest Neighbors and Linear Discriminant Analysis, obtaining both of them around 95% of accuracy.

In case a classification based on k nearest neighbors is performed, the class closer to the tested case and the number of votes obtained for each class will be showed as output.

On the other hand, if the classifier is based on LDA, the DSS will offer as output a 2D LDA projection of the cases used for training the classifier as well as the case being tested. It is also which is the closest class to the tested case. In Figure 4 an output of a LDA classifier is showed, each color representing a group of tumours.

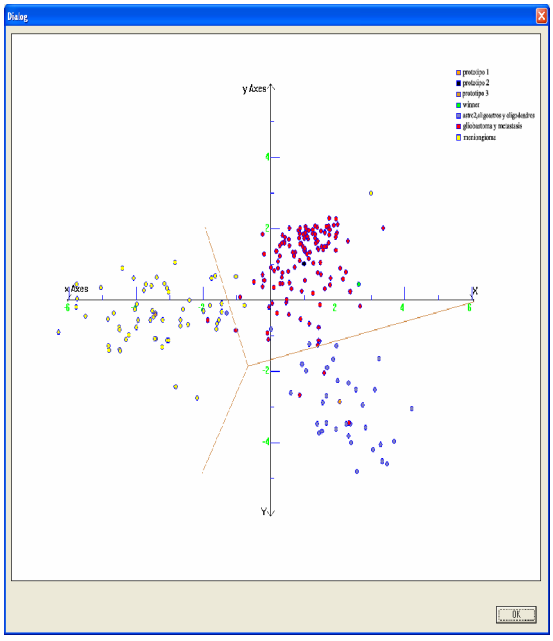

Figure 4. An example the classification obtained by LDA, the tested case being a meningioma.

4. Future Work

In the next versions we will introduce new classifiers as well as apply combination of some of them in a decision tree fashion. We also want also to develop a way to visualize all the combined classifiers graphically, and incorporate statistical functionalities for increasing the usefulness of the DSS for the clinicians.

5. Acknowledgements

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6. References

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