Classification of the quality of in vivo 1H spectra from human brain tumours using ICA

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INTRODUCTION:

The current eTUMOUR project (http://www.etumour.net/) aims to develop a Decision Support System to aid brain tumour diagnosis by ^{1}H MRS. Hence a central eTUMOUR database is being created by acquiring ^{1}H spectra from several clinical centres in Europe for development of diagnostic classifiers by automated pattern recognition methods (1,2). The issue of spectral quality is important, as it is essential that ^{1}H spectra in the database are representative of their associated tumour diagnoses and not distorted by artefacts, low signal to noise ratio or broad lines. However, poor spectral quality is not always obvious and there is no consensus on what defines a 'good' spectrum (3). Currently in eTUMOUR, a panel of expert spectroscopists grade each spectrum as acceptable or unacceptable for inclusion in the database. As the number of acquired spectra increases, and with the inclusion of MRSI data in the project, it becomes more desirable that an automated quality control system (4) is used instead. Independent component analysis (ICA) is a method (5) that has been shown to automatically decompose a set of ^{1}H brain tumour spectra into metabolite-like components (6). We present here the results of using ICA as a method to automatically classify human brain tumour ^{1}H spectra according to quality.

METHODS:

A test data set of brain tumour ^{1}H spectra graded by a panel of MRS experts as either good (n=30) or unacceptable (n=45) was obtained from the INTERPRET project database (4). The spectra had been acquired with a mixture of short and long echo times, and with both PRESS and STEAM pulse sequences. The histopathological diagnoses of the lesions associated with these spectra included glioblastomas, astrocytomas, metastases, meningiomas, oligodendrogliomas, haemangioblastomas and abscesses. First, the data of the 30 good spectra were reduced to the two most significant principal components from which two independent components were extracted using the FastICA algorithm (5). Next, a least squares decomposition was used to generate coefficients of the two independent components (ICs) for each 'good' or 'unacceptable' spectrum. A scatter plot of these coefficients was made, each point corresponding to a good or an unacceptable spectrum in the data set.

RESULTS:

Fig. 1

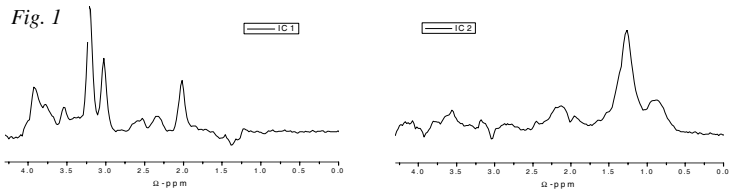

Figure 1 *Two independent components (shown inverted above) generated from the 30 good spectra have spectral features found in brain tumour spectra.*

Fig. 2

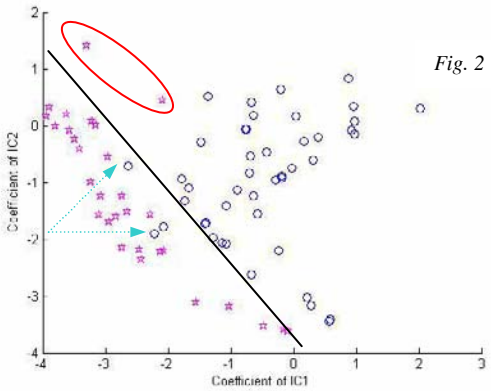

Figure 2 *A scatter plot (right) of coefficients of IC1 against IC2 for each spectrum in the test data set: good - magenta stars; unacceptable -blue circles.*

Independent component analysis (ICA) generated the two ICs from the set of good spectra as shown in Figure 1. IC1 has features corresponding to metabolite components: Glx (3.78 ppm), mI (3.6 ppm); cholines (3.2 ppm), creatines (3.0 ppm), NAA (2.05ppm); lactate (1.3 ppm). IC2 is dominated by components similar to the lipid and macromolecule peaks seen in the higher-grade brain tumours at 2-2.5 ppm, 1.3 ppm and 0.9 ppm. The scatter plot shown in Figure 2 shows a clear tendency for good and unacceptable spectra to cluster in different regions, and a dividing line has been drawn to highlight the separation of good and unacceptable spectra. Two good spectra (circled in red) that fall above the line were long TE spectra, and three 3 'unacceptable' spectra fall below the line (turquoise arrows).

DISCUSSION:

ICA was used to generate just two independent components that separate the 'metabolite' and 'macromolecule' features common to a variety of brain tumour ^{1}H spectra. Despite a mix of PRESS and STEAM data, as well as long and short TE spectra, an analysis of spectrum IC coefficients gave a good separation based on spectral quality. It has also previously been shown that accurate tumour classification with mixed STEAM and PRESS data is possible (1). Our data suggest it may be possible to create a generic tool to assess the quality of spectra independent of precise acquisition parameters or the MR system used. There were two 'good' long TE spectra that fell above the arbitrary dividing line, but they are clearly separate from the unacceptable data, and non-linear methods such as support vector machines to determine classification boundaries may prove more reliable (2). Future work must use separate test and training sets of good and bad spectra to confirm these results. It is also likely that with a larger set of spectra there will be a continuous distribution rather than a clear division between acceptable and unacceptable data. An ultimate goal would then be to develop an algorithm to provide a spectrum quality score that will be useful in selecting spectra for the development of diagnostic classifiers, and for automatically assessing the diagnostic quality of ^{1}H spectra in a clinical setting.

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ACKNOWLEDGEMENTS: This work was funded by EU Grant LSHC–CT–2004–503094 (eTUMOUR project), Cancer Research UK Grant C12A/A1209 (FAH & JRG). All spectra were originally acquired by partners of the INTERPRET project (http://azizu.uab.es/INTERPRET/).