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# The use of multivariate MR imaging intensities versus metabolic data from MR spectroscopic imaging for brain tumour classification

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**Abstract**

This study investigated the value of information from both magnetic resonance imaging and magnetic resonance spectroscopic imaging (MRSI) to automated discrimination of brain tumours. The influence of imaging intensities and metabolic data was tested by comparing the use of MR spectra from MRSI, MR imaging intensities, peak integration values obtained from the MR spectra and a combination of the latter two. Three classification techniques were objectively compared: linear discriminant analysis, least squares support vector machines (LS-SVM) with a linear kernel as linear techniques and LS-SVM with radial basis function kernel as a nonlinear technique. Classifiers were evaluated over 100 stratified random splittings of the dataset into training and test sets. The area under the receiver operating characteristic (ROC) curve (AUC) was used as a global performance measure on test data. In general, all techniques obtained a high performance when using peak integration values with or without MR imaging intensities. For example for low- versus high-grade tumours, low- versus high-grade gliomas and gliomas versus meningiomas, the mean test AUC was higher than 0.91, 0.94, and 0.99, respectively, when both MR imaging intensities and peak integration values were used. The use of metabolic data from MRSI significantly improved automated classification of brain tumour types compared to the use of MR imaging intensities solely.


*Keywords:* Brain tumours; Classification; Magnetic resonance imaging; Magnetic resonance spectroscopic imaging; Linear discriminant analysis; Least squares support vector machines

## 1. Introduction

Magnetic resonance imaging (MRI) is an important noninvasive tool for identifying the location and size of brain tumours, because it yields morphological and anatomical information about the brain tissue. However, conventional MRI has a limited specificity is rather nonspecific in determining the underlying type of brain tumour and grade [1,2]. More recently developed MR techniques like diffusion-weighted MRI, perfusion-weighted MRI, and magnetic resonance spectroscopic imaging (MRSI) are promising new techniques in the characterization of brain tumours [3,4]. Diffusion-weighted MRI visualizes the tissue structure and is useful for assessing tumour cellularity, while perfusion-weighted MRI provides measurements that reflect changes in tumour vasculature and tumour grading. MRSI or multivoxel magnetic resonance spectroscopy (MRS) provides chemical information about metabolites present in normal and abnormal tissue [5–8]. Therefore, the differentiation of abnormal brain tissues, including brain tumours, from normal brain forms a potentially major clinical application of these new techniques. In general, diagnosis

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of brain tumours is based on the microscopic examination of tissue obtained by a biopsy, which includes risks associated with anesthesia and surgery. It would be very beneficial to the patient if the invasive biopsy could be guided or even avoided by the use of noninvasive techniques like diffusion-weighted MRI, perfusion-weighted MRI, and MRS(I). In this study, we combined the use of conventional MRI intensities and one of the new techniques, more specifically MRSI.

Several studies [9–18] have shown progress in automated pattern recognition for brain tumour classification using MRI or MRS(I). However, currently only few studies (e.g., [14,15]) have used a combination of MRI and MRSI features for classification of brain tumours. To enhance the diagnostic capabilities in clinical practice, we investigated whether the combined use of MR imaging intensities and metabolic data from MRSI could improve the discrimination between several brain tumour and normal brain tissue types. Although the radiologist also uses spatial and morphological information present in the MR images, these features were not taken into account in this study, as they are difficult to quantify. By comparing the results obtained, we evaluated the strength of both, MR imaging intensities and metabolic data from MRSI, in discriminating brain tissue types.

We considered linear as well as nonlinear classification techniques applied to several input features, such as short echo time magnitude spectra, imaging intensities, peak integration values obtained from the spectra and a combination of the latter two. The algorithms were designed to extract the most important features which were then used to classify each spectrum into the corresponding tumour type. As classification is required to be objective and user-friendly, all techniques were automated. The purpose of this paper was twofold:

- To investigate the discriminatory value of MRI intensities and metabolic data extracted from MRSI for automated brain tumour diagnosis. This analysis also provides the typical AUC values achievable for several relevant diagnostic problems of brain tumours.
- To apply and compare several classification techniques, including the investigation of the influence of the input features used.

## 2. Materials

### 2.1. Data

Data from 25 patients with a brain tumour and 4 volunteers were selected from the database developed in the framework of the EU funded INTERPRET project (IST-1999-10310) [19]. All data were provided by the acquisition center UMCN (University Medical Center Nijmegen), Nijmegen (The Netherlands). Each case was clinically validated. The patients' tumour type was determined by a central consensus histopathological validation. For one of the 25 patients no consensus was reached. Therefore, the data from the tumour region of this patient were not used.

The dataset contained MR images as well as MR spectra, acquired and preprocessed as described in [14]. For each subject, stacked MR images of cross-sections of the whole brain at four contrasts were acquired: $T_1$- and $T_2$-weighted images, a proton density weighted image and a gadolinium enhanced (Gd-DTPA) $T_1$-weighted image ($256 \times 256$, FOV = 200 mm, slice thickness = 5 mm). The image values will further be labeled as $T_1$, $T_2$, PD, and GD. No Gd-DTPA administration was applied to the healthy volunteers. Besides MR images, also $^1$H MRSI data were acquired for each subject, both with and without water suppression using a $16 \times 16$ 2D STEAM $^1$H MRSI sequence with acquisition parameters TR = 2000 or 2500 ms, TE = 20 ms, slice thickness 12.5 or 15 mm, FOV = 200 mm, SW = 1000 Hz, 1024 data points. The position of the MRSI slice was chosen according to the slice position of the GD image which showed the largest GD enhancement.

To ensure that image pixels from subsequent images originate from the same spatial location, the images were co-aligned [14]. All MRSI data were semi-automatically preprocessed (cf. [14]), which involved:

- Filtering of the k-space data by a Hanning filter of 50% using the LUISE software package (Siemens, Erlangen, Germany).
- Zero filling to $32 \times 32$, which involved an increase of the apparent spatial resolution with a factor of 2.
- Spatial 2D Fourier transformation to obtain time domain signals for each voxel.
- Correction for eddy current effects in the MR spectra using a method which prevents the occasional occurrence of eddy current correction induced artefacts [20]. This process resulted in a frequency alignment and zero order phasing of the MR spectra.
- Removal of the dominating residual water using HLSVD [21], with 12 singular values and 4.0–6.0 ppm as residual water region.
- Frequency alignment was performed semi-automatically. First, the position of the *NAA* peak (*N*-acetylaspartate, $^2CH_3$-group) in the mean spectrum of an MRSI dataset was set to 2.02 ppm. The obtained shift was used to reset each spectrum of the dataset in the time domain automatically.
- First order phase correction was also manually performed on the mean spectrum of a dataset. The obtained first order time instant was used to automatically correct each spectrum in the dataset.
- Fourier transformation was applied to the time domain data to obtain frequency spectra.