Optimal processing in the automatic detection and localization of brain tumors using MRSI

B. H. Menze[1], B. M. Kelm[1], M. P. Lichy[2,3], P. Bachert[3], H-P. Schlemmer[2], F. A. Hamprecht[1]

[1]Interdisciplinary Center for Scientific Computing, University of Heidelberg, Heidelberg, Germany, [2]Radiological Diagnostics, University of Tuebingen, Tuebingen, Germany, [3]German Cancer Research Center, Heidelberg, Germany

Introduction:

In comparison to single voxel H1-MRS, the higher spatial resolution of MRS images comes at the cost of an increased number of spectra that need to be scrutinized. A user friendly representation of the relevant spectral information requires an automated processing of these data volumes. Standard approaches based on resonance line fits present the diagnostic information in terms of metabolic maps or relative ratios thereof.

Unfortunately, in clinical practice spectra from MRSI are of varying quality. Results from line fits on this data can only be trusted after manual inspection and confirmation that the fitting procedure has worked successfully. This need for checking the line fit for every single spectrum hinders a routine access to the full information of big data sets, especially from high resolution MRSI with hundreds to thousands of single spectra for each recorded volume.

Objective:

While sophisticated processing and display of nosologic images has been proposed, we restrict ourselves to a classification task as simple as the differentiation between tumorous and non-tumorous spectra by means of pattern recognition. We compare the reliability of this method against standard resonance line fits. Results have the potential to be used as accessory information in tumor localisation, e.g. in routine radiation therapy planning.

A robust and automated "push-button" algorithm is proposed, that can:

1. separate spectra with insufficient signal-to-noise ratio or corrupted by artefacts
2. map the metabolic information linearly within a predefined range between the extremes "definitely normal state brain tissue" (white/grey) and "definitely tumor" (average pattern from astrocytoma grade I-IV, meningioma, metastases)

Methods:

A first data set comprising N_tumor = 30 and N_normal = 32 high quality single voxel spectra (TE/TR 135/1500, 1.5T Siemens Magnetom Vision, see [Schlemmer 01]) with labels from follow up examinations was used to train the classifier. Following the results of [Menze 04, 05], a linear regression model (partial least squares) was favored. It was applied to a spectral region including Cho, Cr and NAA resonances after smoothing and subsampling of the spectral pattern. Another nonlinear classifier (randomForests) was trained to assess categorically the diagnostic value of a spectrum.

These algorithms were applied to a second data set of 31 MRS images (PRESS, TE/TR 135/1500, 1.5T Siemens Magnetom Vision, resolution FoV 24x24, interpolated 32x32, voxel size 8.75x8.75x1.5mm³, see [Lichy 05]) according to the following scheme: If the first level classifier determined a sufficient data quality, the diagnostic prediction was derived from the spectrum by the second layer classifier and displayed (cf. Fig.1).

Within the data set the diagnosis (tumor center/tumor border/normal) from 369 spectra (104/68/197) was confirmed during follow-up. These spectra were quantified (Luise, Siemens) including manual check and adjustment of the line fit. Diagnostic ratios of these quantities were calculated as proposed by [Schlemmer 01]. These traditional values were compared in sensitivity and specifity with the regression values from the proposed pattern recognition algorithm.

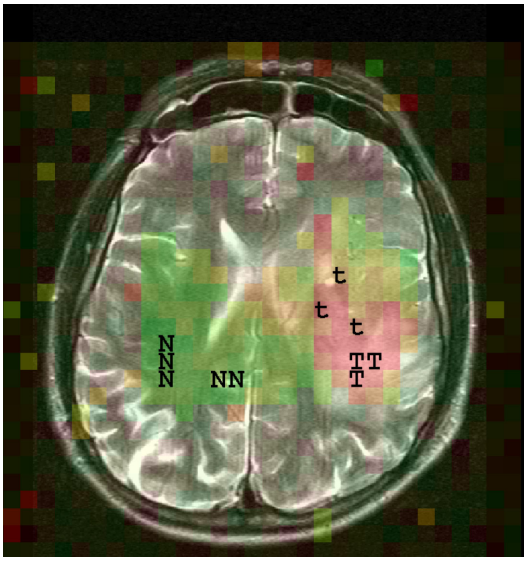

Fig.1: Diagnostic map. Labels from clinical follow-up: 'T' - tumor center, 't' - tumor border, 'N' - normal state. Coloring shows the diagnostic prediction by our method, where low opacity indicates non-evaluable spectra. Colorbar see Fig.2.

Results:

The first level classification provided a robust separation between evaluable and non-evaluable spectra (cf. Fig.1). Second level regression of the diagnostic prediction reached a sensitivity of 95% at a specifity of 98% in a fully automated operation mode compared to 93/98% (sens./spec.) by the best processing after semi-manual resonance line quantification (cf. Fig.2).

Discussion:

The proposed algorithm is able to automatically evaluate the quality of a spectral pattern. It performs (at least) as well as an analysis based on operator controlled resonance line integration.

This facilitates a potential application in departments with high throughput of patients and for high-resolution MRSI.

The linear regression model is an ideal basis to infer the percentage of tumorous infiltration [Stadlhuber 04] once increasing spatial resolution of the CSI grids will have overcome the major partial volume effects.

Current work is on the probabilistic interpretation of the spectral quality assessment.

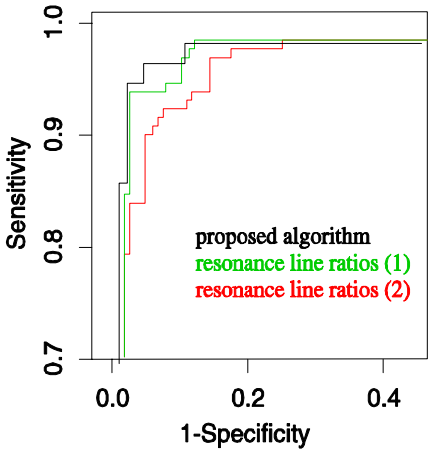

Fig.2: Partial ROC for the discrimination of spectra from tumor (center) and normal state tissue. Automated selection and regression (black) outperforms manual selection and resonance line based analysis (green, red).

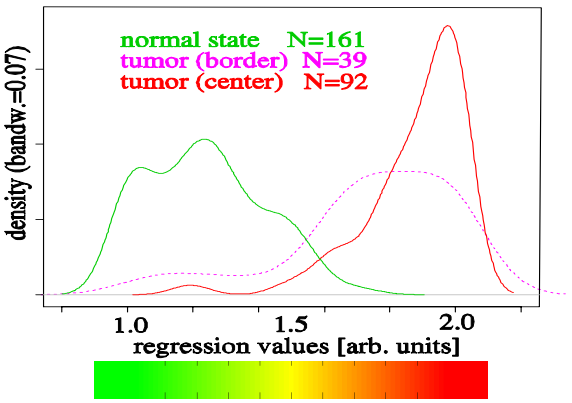

Fig.3: Top: Distribution of diagnoses from a human expert over diagnostic predictions from the regression (after decision of first level classifier). Bottom: Colorbar used for the mapping of the linear regression values (cf. Fig.1).

Literature:

Lichy et al., Radiologe, submitted
Menze et al.,,p. 2261, ISMRM04
Menze et al., LNCS, 2005
Schlemmer et al., 1316ff, AJNR, 2001
Stadlhuber et al., p. 2053, ISMRM04