Classification of MR Spectra by Means of Pattern Recognition

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Summary
This work presents the results of a systematic and quantitative comparison of methods from pattern recognition for the analysis of magnetic resonance spectra. The medical question addressed in this study is the classification of cerebral neoplasm after radiotherapy.

Introduction
Compared to tomographic images, magnetic resonance spectra offer complementary diagnostic information, but are not as intuitively accessible. Considerable effort has been undertaken to make it available for medical diagnostics. In current medical practice, spectral peaks are quantitated by fitting functions, the parameters of which provide the basis for further statistical analysis. Alternatively, pattern recognition or machine learning approaches have been proposed for MRS classification. These methods require a large number of spectra for training, but can be fully automated. Provided their reliability can be demonstrated, they have the potential to ease the usage of adjunct MRS information in medical decisions.
Pattern recognition involves two major steps: Since the dimensionality of the data (in our case ~100) often exceeds the number of samples per class a large number of algorithms is available. To the best of our knowledge, comparisons of different methods are only published for either of them. In contrast, no comprehensive quantitative evaluation of combinations of preprocessing and classification methods is available to date.

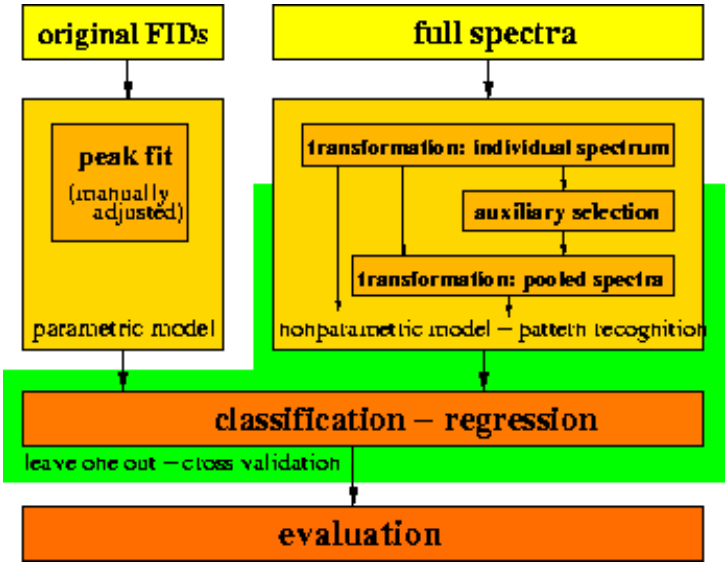

Figure - *different ways of spectral information retrieval*:
a) fit of model functions as performed in the traditional analysis
b) pattern recognition approach as evaluated by us

Methods used
Data
The data stems from a retrospective study on the usage of MRS in the evaluation of brain lesions after radiotherapy [Schlemmer 01] and comprises 90 single voxel spectra, acquired with long echo time (TE 135 ms) on a 1.5 T scanner. The spectra were labelled in accordance with the final diagnosis as 'normal state', 'progressive disease', or 'non-progressive disease'.
The conventional spectral analysis was performed with commercial software (Luise, Siemens) and included baseline removal and quantitation of the Choline (Cho), Chreatine (Cr), and N-Acetyl Aspartate (NAA) peaks [Schlemmer 01].
When used as input for our pattern recognition methods, we removed the water peak with help of the Mrui software [Boogaart 96], and cut out a spectral region including the Cho, Cr and NAA peaks.

Pattern Recognition Algorithms
We evaluate the combination of dimension reduction methods such as subsampling, binning, selection of wavelet coefficients, principal component analysis, independent component analysis, with classification methods such as partial least squares, neural networks, random trees ensemble methods and support vector machines.
Generalization performance was estimated using leave-one-out cross validation and evaluated in terms of the area under curve in the receiver-operator-characteristic.

Results
- On average, the combination of shrinkage regression methods operating on smoothed subsampled spectra works best for our data.
- Classification results are around 22% better than a standard approach, i.e. linear discriminant analysis on quantitated peak ratios.
- Compared to support vector machines and neural networks, shrinkage methods perform better by roughly 17% and 14%, respectively.

Discussion
We have identified the optimal combination of preprocessing and classification methods for in vivo, long echo time spectra of cerebral neoplasms. The procedure proposed requires no manual interaction whatsoever and yields classification results which are 22% better than the procedure used in current clinical practice. Since several classifiers hit the same upper bound on performance, we are able to assess the limits of MR spectral information for the distinction between the different types of tissue.

References:
Schlemmer, HP et al. (2001): Proton MR Spectroscopic Evaluation of Suspicious Brain Lesions After Stereotactic Radiotherapy. *Am J Neuroradiol, 22, 1316-1324*
van den Boogaart, A et al. (1996): MRUI: a graphical user interface for accurate routine MRS data analysis. *In: Proceedings of the ESMRMB 13th Annual Meeting, Prague, p.318, 1996*