Towards an Automatic Identification of Cancer Regions in *in vivo* MR Spectroscopy Data from the Prostate

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Introduction

In ^{1}H magnetic resonance spectroscopy of the prostate the metabolic ratio of (choline + creatine) / citrate ((Cho+Cr)/Ci) is interpreted as a marker for cancer tissue [1]. The analysis of prostate spectra correspondingly aims at identifying suspicious voxels inside the prostate, which spectra show high (Cho+Cr)/Ci ratios. However, *in vivo* spectra from prostate tissue can have broad line widths or contain lipid signal contaminations and arbitrary baseline components, which reduce the spectral quality and may hamper the fit. In addition, excited voxels close to the edges of the excited volume can originate from tissue surrounding the prostate gland (e.g. the seminal vesicles), of which the spectra exhibit similarly high (Cho+Cr)/Ci ratios. To ensure that a suspicious voxel represents true prostate cancer tissue it is typically visually checked for a descend fit quality and its proper location within the prostate gland – a time consuming procedure which is not applicable for the analysis of multi centre 3D-MRSI trials like the IMAPS trial. We therefore introduce an automatic quality control for prostate spectra and depict its outcome as an identification map.

Methods

As a first step 500 voxels of 38 patients from the IMAPS pool were analyzed, all measured with a standard MRSI pulse sequence for prostate spectroscopy [2] at 7 independent sites, using Siemens 1.5T MAGNETOM scanners. All voxels corresponded to cancer regions and their surrounding tissues. The spectral data was fitted in the time domain with model functions for the Ci, Cr and Cho signals with the PRISMA software package [3]. The spectra and fit results were visually inspected and classified as acceptable or unacceptable. Qualification rules were established for all selected voxels with a minimum (Cho+Cr)/Ci ratio of 0.7 and minimum signal to noise ratio of 5 based on the following criteria: coefficients of variation of the integral ratio (Cho+Cr)/Ci (CV) [4], mean frequency shift of fitted metabolites, residuum in the metabolic frequency range, residuum in the lipid frequency range.
In a further step these qualification rules were applied to the analysis of complete MRSI prostate data. Results were shown as identification maps of (Cho+Cr)/Ci, which depict regions of high (Cho+Cr)/Ci ratios with proven quality determined by the automated qualification rules on metabolite images.

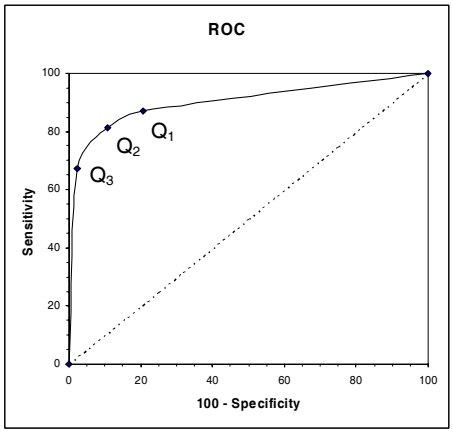

Fig. 1: ROC-curve for different qualification rules, which describes the match between the automated qualification and the visual inspection.

Results

Based on the tightness of the threshold values for the above quality criteria qualification rules with different sensitivity and specificity can be achieved as shown in the ROC-curve (fig. 1). Especially for the strictest qualification rule Q3, a good separation between acceptable and unacceptable voxel is realized, with a sensitivity of 67% for the acceptable voxels and almost no contamination with unacceptable results. CVs alone do not produce a good separation, which is probably due to partly insufficient model for strongly contaminated voxels in prostate MRSI.
First experience with the identification maps (fig. 2), based on qualification rule Q3, reveal their usefulness to localize regions with elevated (Cho+Cr)/Ci ratio in the prostate, that are highly suspicious for prostate cancer.

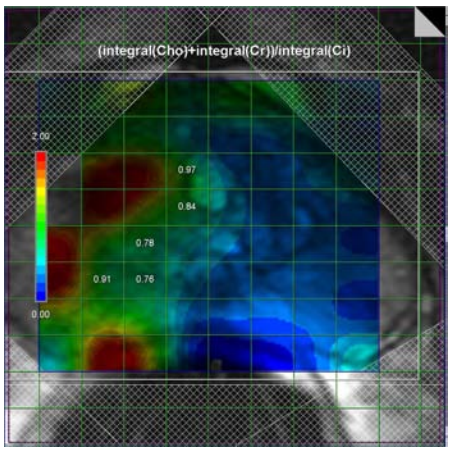

Fig. 2: Identification map for one IMAPS patient with prostate cancer: Suspicious voxels with high (Cho+Cr)/Ci ratios of proven quality, as specified by qualification rule Q_3, are highlighted by their ratio values on a metabolite image.

Discussion and conclusion

Automatic quality control of MRSI data can be achieved with the concept of quality rules. The optimal thresholds used for the identification maps need further investigation within the analysis of the IMAPS data pool. Nevertheless it is desirable to integrate those maps into the clinical post-processing workflow. In addition segmentation of prostate tissue will allow further automation in identifying suspicious prostate regions.

References: 1. Kurhanewicz J *et al.* Urology 1995;45:459-466. **2.** Scheenen T *et al.* Magn Reson Med 2004;52:80-88. **3.** Weiland E *et al.*, Proc. ISMRM 12, 2004; 2439. **4.** Jiru F *et al.* Magn Reson Mater Phy 2006;19:1-14. **website:** http://get.to/IMAPS