Automated lipid-removal for baseline correction of prostate-cancer MRSI data using prior knowledge.

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Introduction. MRSI is a promising technique for the detection and localization of tumours in patients with prostate cancer [1,2]. However, clinical use is far from routine due to the complexity, and lack of consensus on how to analyse, these data. One approach may be to use pattern-recognition techniques that have the potential to outperform quantification algorithms [3]. The performance of such algorithms is partly dependent on artifacts: variance in the data independent of the presence or absence of cancer. Artifacts include residua large lipid signals from the tissue surrounding the prostate; these signals are broad and can overlap with the citrate resonances at 2.6ppm that play a key role in cancer diagnosis by MRSI. We present an algorithm that uses prior knowledge to remove lipid signals from prostate MRSI data sets. This will allow the future development of pattern recognition techniques for tumour localisation, even in regions close to the edge of the prostate gland where cancer foci commonly occur.

Methods. MRI and MRSI data were acquired at 3T from 10 prostate-cancer patients. Complete prostatectomy was used for cancer tissue assignment and to characterize the origin of lipid resonances. The MRSI sequence has 145ms TE, water and fat suppression with MEGA pulses [4] to achieve as flat a baseline as possible. Voxels localized to the excitation box (10x10x10) in each MRSI data set were Fourier transformed and phased with an algorithm that maximizes correlation to the magnitude spectrum. Principal component analysis (PCA) was used to reference the centre of all citrate resonances in an MRSI dataset to 2.6ppm. The first principal components of the 10 MRSI data sets was used to determine common (lipid) resonances. A lipid removal algorithm was developed which models these lipids as a single Lorentzian, with a least squares fit to a region (2.41-2.34ppm) close to the citrate resonances. It allows variation in chemical shift (2.38-2.22ppm), line width and amplitude. Line width is limited so that overlap at the citrate position (2.6ppm) is never greater than half the maximum simulated-lipid height. The lipid-removal algorithm was tested on a set of 5 novel MRSI data sets. An automated HSVD algorithm, based on a previously published method often used for residual water removal [5,6], was also applied to this data. Each spectrum was modeled with 10 components, retaining the lipid components - for subtraction - with chemical shifts in the range 2.42-2.13ppm.

Results. PCA analysis of 10 prostate-cancer MRSI-data sets showed two broad resonances remain after MEGA lipid suppression in the 2.42-1.92ppm region (see Fig. A). These are assigned to allylic proton resonances of lipid molecules in tissue surrounding the prostate. One Lorentzian was found to be sufficient to model the components of these lipid signals, that overlap with the citrate resonances, if the fit was evaluated as close to these metabolite peaks as possible. The Lorentzian and HSVD lipid-removal algorithms were applied to 5 novel data sets and results were evaluated, over the region 2.87-2.39ppm that contains the citrate peaks, with two parameters: the percentage of the variance explained by the first principal component and the average cross-correlation between spectra in this region. These two measures evaluate the similarity in the citrate peak region before and after lipid removal. The HSVD algorithm showed improvement for four of the five datasets in each measurement. The Lorentzian algorithm showed improvement in all five sets over both HSVD and un-processed MRSI. Fig. B and C show an example of the Lorentzian lipid removal which fits all lipid signals whereas the HSVD method (Fig. D) fails to fit these signals in some spectra. Fig E. shows the 75% quartile at each data point in the spectrum for the whole dataset of 1000 spectra. HSVD decreases the lipid signals that overlap with the citrate region but these are reduced close to 0 with the Lorentzian algorithm.

Discussion. Remaining lipid peaks around 2.3ppm are commonly the reason why spectra in prostate cancer MRSI data sets are cumbersome to process and, in particular, those spectra from voxels close to the prostate capsule. A Lorentzian fitting algorithm with prior knowledge from experimental data on these lipid resonances, can restore a flat baseline by fitting and removing the section of these resonances close to the citrate peaks. This increases the similarity in the citrate signal region and thus provides a much better starting position for automatic spectral processing. We show that it performs better than an HSVD method that does not include prior information.

References. [1]Zakian *et al.* 2005 *Rad.* 234,804. [2] Nayyar *et al.* 2009 *BJU Int.* 103,1614. [3] Kelm *et al.* 2007 *MRM* 57,150 [4] Scheenen *et al.* 2007 *Rad.* 245, 507. [5] Van Huffel *et al.* 1994 *JMR(A)* 110,228. [6] Laudadio *et al*. 2002 *JMR* 157, 292. Acknowledgments: Support by the EU RTN project FAST

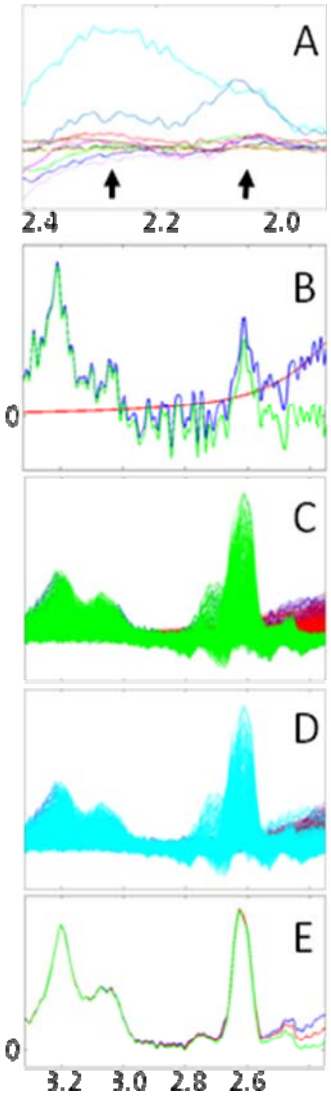

Figure: A) Principal components of 10 MRSI data sets showing two residual lipid signals (indicated with arrows). B) Example spectrum (blue) for the lipid removal algorithm with the lorentzian (red) subtracted to give corrected data (green). B) Overlay of 1000 spectra example-data set (blue) with lorentzian functions (red) and corrected spectra (green). C) As for (B) but with HSVD lipid functions (red) and the resulting corrections (cyan). D) The 75% quartile of 1000 spectra at each frequency point for: original data (blue), HSVD corrected (red) and Lorentzian corrected data (green). Chemical shift axes are given in ppm.