

# AUTOMATED QUALITY CONTROL OF PROSTATE CANCER MRSI USING INDEPENDENT COMPONENT ANALYSIS

A. J. Wright<sup>1</sup>, T. Kobus<sup>1</sup>, T. Hambrock<sup>1</sup>, T. W. Scheenen<sup>1</sup>, and A. Heerschap<sup>1</sup>  
<sup>1</sup>Radiology, Radboud University Nijmegen Medical Centre, Nijmegen, Netherlands

## Introduction.

The current diagnosis and localization of suspected prostate cancers requires TRUS-guided sextant (or more) biopsy with limited accuracy. MRI and MR Spectroscopic Imaging (MRSI) of prostate cancer patients can provide complimentary information to these techniques on the detection, localization and grading of prostate cancers with minimal risk to the patient [1]. However the spectra in MRSI data sets can contain artifacts, such as poor signal-to-noise, contaminating lipid signals and poor shim, which take expert knowledge to identify. If the analysis of MRSI data of prostate tumour is to be automated for clinical use then quality control (QC) will be a necessary step in that process. A previous method[2] of QC for prostate MRSI data at 1.5T used parameters of an applied quantification algorithm for quality control, such as the residual of the fit and the metabolite ratio that was also used for identifying tumour. We present a feature extraction method, using independent component analysis (ICA), that separates 3T MRSI data into acceptable and unacceptable quality groups using the raw spectra. We hypothesise that a feature extraction using independent components (ICs) generated from acceptable quality spectra will generate high scores for these spectra. Feature extraction of poor quality spectra will produce low scores for the same ICs as they will characterize these data less well giving a separation of spectra on the basis of quality.

## Methods

Informed consent was provided for the acquisition of MRSI data from 12 volunteers with proven prostate cancer. A total of 670 individual voxels were selected from these MRSI data sets (3T, 144ms TE, endorectal coil [3]) that represented healthy or tumour tissue. Each voxel was graded for spectral quality by two experts (with at least a years experience in prostate cancer MRSI). The experts were presented with the real spectrum of the voxel, simulated metabolite peaks that were fitted to the data using Metabolite Report (Siemens, Erlangen, Germany) and a residual of this quantification. They were asked to accept or reject each voxel on the quality (perceived accuracy) of the spectrum and the quantification algorithm. The same set of 670 individual spectra were imported into MATLAB (MathWorks, Natick, MA) phased, referenced to citrate at 2.6ppm and restricted to 4ppm-0.5ppm. Spectra that had both experts agree were of acceptable quality were used to generate two independent components. These two components were subsequently L2 normalised[4] and used for feature extraction of all 670 spectra in the data set [4]. Every spectrum ( $S$ ) is then represented by two coefficients ( $w_1, w_2$ ) of each of these ICs where:  $S=w_1IC_1+w_2IC_2$ . The two coefficients were plotted and a support vector machine (SVM) algorithm was used to train a classifier from the data set of spectra that both experts agreed were acceptable or unacceptable. Each of the 670 voxels were then re-classified by the SVM.

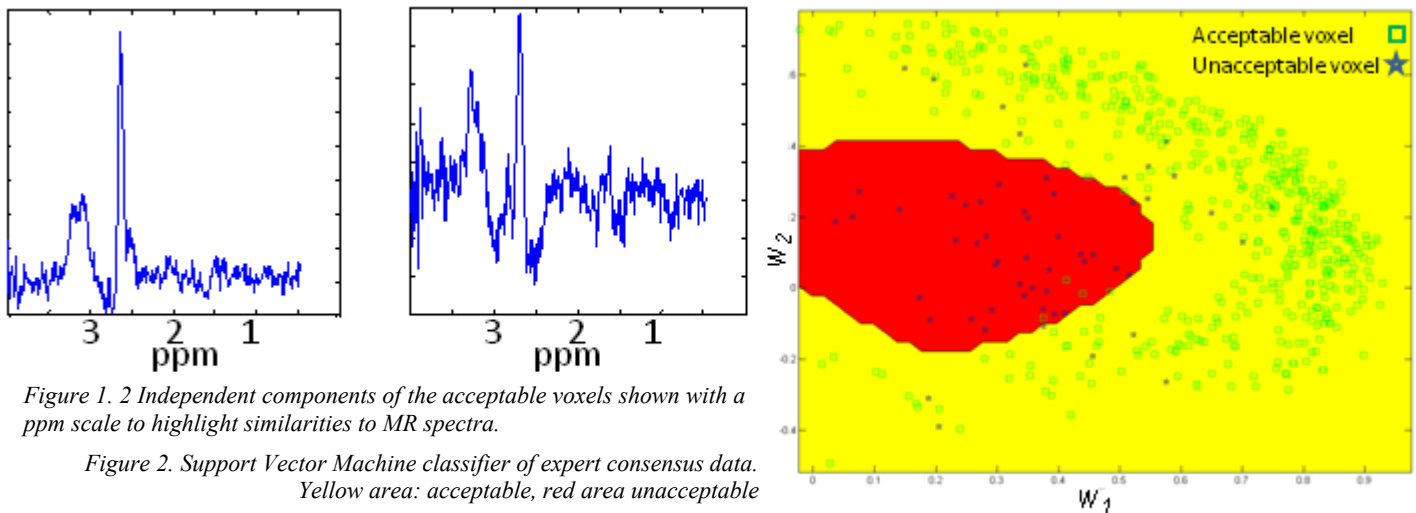


Figure 1. 2 Independent components of the acceptable voxels shown with a ppm scale to highlight similarities to MR spectra.

Figure 2. Support Vector Machine classifier of expert consensus data. Yellow area: acceptable, red area unacceptable

## Results and Discussion

Of the 670 voxels the experts agreed that 530 were of good quality and 57 were of unacceptable quality with 83 that had no consensus of opinion (88% agreement). ICA generated two components that have features similar to spectra from MRSI data sets of prostate spectra (Figure 1). There are peaks at the resonances of the expected metabolites (citrate, cholines and creatines) and they resemble spectra from normal or tumorous regions. Figure 2 shows a plot of the 587 voxels for which a consensus diagnosis was made and the SVM classifier that was trained on these data. The plot shows that, in general, unacceptable spectra have coefficients ( $w_1, w_2$ ) closer to 0 and are, therefore, less well characterized by the independent components than acceptable spectra. When all 670 voxels are classified by this algorithm, 624 were found to be of acceptable quality. When compared to each individual expert classification the agreement was 95% and 86% respectively; a comparable performance to the agreement between experts themselves. When compared to the 587 expert-consensus diagnoses there is a positive predictive value of 95% and a negative predictive value of 92%. This data suggests that feature extraction by ICA separates MRSI data, from prostate cancer patients, on the basis of spectral quality and can be used in an automated QC protocol.

References: [1]Nayyar *et al.* 2009 *BJU. Int.* 103, 1614. [2] Weiland *et al.* 2007. *Proc. ISMRM* 200. [3]Scheenen *et al.* 2007 *Rad.* 245, 507. [4]Wright *et al.* 2008 *MRM.* 59, 1274.