UNSUPERVISED QUALITY CONTROL OF PROSTATE MRSI USING NON NEGATIVE MATRIX FACTORIZATION

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Target Audience: MR spectroscopists interested in Quality Control of prostate MRSI data

Introduction: MR Spectroscopic Imaging (MRSI) is a promising tool in prostate cancer diagnosis and treatment planning [1], but the variable data quality is still a major limitation. Prostate *in vivo* MRSI spectra can be affected by broad resonances, low signal-to-noise and contaminating lipid signals from adipose tissue. As some spectra may be of insufficient quality for further analysis, expertise is needed to discriminate bad from good quality spectra. Nevertheless it is essential to remove the subjectivity of an expert's decision. Thus far, several automated spectral QC methods have been introduced based on supervised learning [2,3]. However, since these methods require the availability of a training set formed of *a priori* labeled MRSI measurements, the performance of such methods is reliable only when applied to data measured using identical MRSI acquisition protocols. (e.g. echo times). The objective of this study is to develop an automated, unsupervised QC method for 3D ^{1}H-MRSI data based on non-negative matrix factorization (NNMF). The main advantage of NNMF is that it requires no prior information so the method can be applied to any MRSI prostate measurement, regardless of the MRSI acquisition parameters or the type of the NMR scan used.

Methods: Fifteen patients who underwent multi-parametric MR including MRSI MEGA-PRESS as a part of the routine radiological examination on a Siemens Magnetom Tim Trio at 3T (Siemens, Erlangen Germany) using surface array coils in combination with an endo-rectal coil for signal reception. All MRSI measurements were achieved with TE=145ms, TR=750ms, vector size=512 points and receiver bandwidth=1250 Hz. The MRSI data sets were restricted to the voxels within the excitation volume and not overlapped by the outer-volume suppression (OVS) bands and also restricted to the chemical shift range: (2.2-3.6) ppm for subsequent analyses. NNMF, a matrix decomposition method, is applied to each matrix of MRSI spectra, X, to decompose it into $X=AS$, where $S=(s_1,s_2,\ldots,s_k)^T$ are the constituent spectral sources and A quantifies their abundance distribution. For this decomposition, the parameter k (the number of spectral sources) needs to be known *a priori.* In this work k is automatically estimated using an iterative method called the Bayesian Information Criterion [4]. The algorithm proceeds with classification to provide a straightforward segmentation for the MRSI grid. The aim is to cluster the MRSI data sets in subsets *(C1,C2,..Cn)* based on the similarities in the abundance patterns of the voxels computed by NNMF in the matrix *A*. so similar voxels will be grouped together. The Set of vectors containing the abundance values for each voxel were clustered using a replicated k-means clustering.

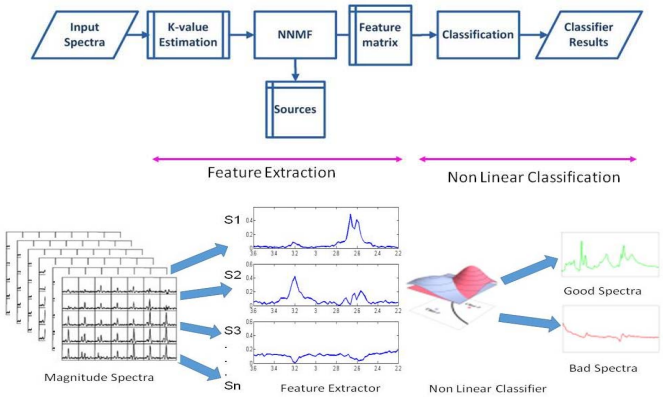

Fig 1. Schematic of the algorithm. Feature extraction including dimension estimation leading to number of possible "*S spectral sources*" within the spectra followed by classification of the features *"A abundance distribution matrix"*

Results: The performance of the algorithm is validated against expert labeling. A quality assessment panel formed by four experts labeled the spectra as good or bad [3]. The NNMF extracts sources that show metabolic features that resemble cancer or normal prostate and sources that capture acquisition artifacts such as the contamination with Lipids (see Fig 1)**.** The proposed automated QC agreed with each expert in 88% ± 2 (Average ± std) of cases. For further performance assessment the decision of the algorithm versus three of the experts were compared against the decision of one of the individual experts versus the other three experts. The algorithm results from all spectra agreed with three other experts in 88%±2 which was not significantly different from the one expert versus other three experts 88%±3. The spectra were separated for quality by the algorithm with 90% Sensitivity, 90% Specificity and an AUC of 0.93 for the gold standard data where experts agreed. The quality control results of the proposed algorithm versus the labeling of the quality assessment panel for four consecutive slides of one patient is illustrated in Fig 2.

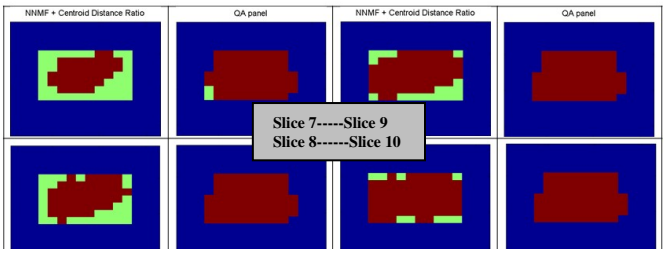

Fig 2. The automatic QC algorithm results using NNMF vs. Quality assessment (QA) panel for four consecutive slides. The red voxels are labeled as good quality while the green ones are bad labeled by the QC algorithm and QA panel.

Discussion: Automatic quality control of spectra is a crucial step towards rapid processing of prostate cancer data to transform MRSI into a routine clinical tool in diagnosis and prognosis of prostate cancer patients. The visual inspection of the spectra for the purpose of Quality Control QC is subjective and prone to human errors. Alternatively, some experts perform QC by observing the quality of fitting performed by a quantification algorithm which can be also inaccurate due to incorrect quantification algorithm. In this study we have shown that NNMF method is able to capture the artifacts present in the data which will be described by one or more of the extracted spectral sources. Thus, NNMF being an unsupervised method, eliminates the need to generate training data sets, allows an automatic QC, can facilitate determining spectral quality by replacing tedious, time consuming visual inspection of prostate cancer MRSI data, and avoids the experts' inevitable subjective decisions. The proposed QC had comparable performance to a panel of expert spectroscopists, who were presented with the same spectra. This has high accuracy (sensitivity and specificity = 90%) for the gold standard data where experts agreed.

References: [1] Scheenen et al., Invest Radiol. 2011;46(1); [2] Wright et al., NMR Biomed 2013;26 (2); [3] Menze et al., NMR Biomed 2006;19(5) [4]Schwarz. Ann Stat 1978, 6(2);

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