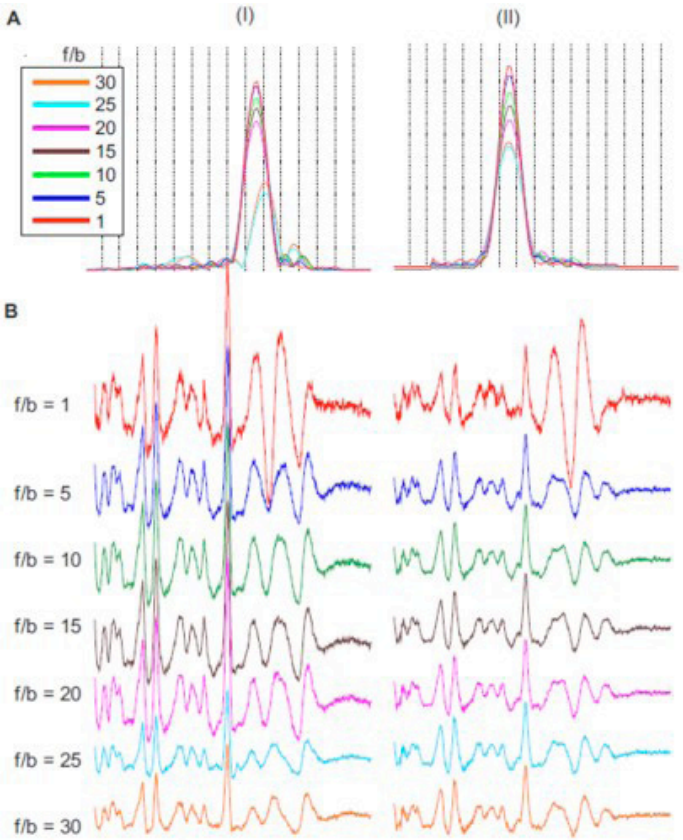


***Figure 2**: (A) Resulting SRF along the RL direction and (B) spectra from 0 to 4.0 ppm in the three voxels designated in Fig. 1 for different relative weightings of* fat (f) *tissue compared to* brain (b) *tissue in the two voxels I and II designated in Fig. 1*

f/b	(I)	(II)
1	1.37	1.35
5	1.44	1.42
10	1.48	1.49
15	1.50	1.54
20	1.54	1.64
25	(1.41)	1.75
30	(1.41)	1.75

***Table 1**: FWHM of the main lobe of the resulting SRF depending on* f/b *for the voxels I and II*

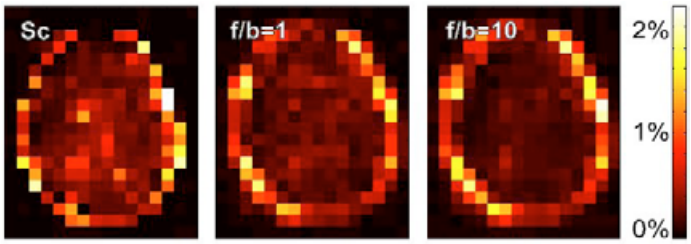


***Figure 3:** Maps of the integral over the modulus spectra between 0 and 1.8 ppm: Comparison of vendor pre-implemented reconstruction (Sc), the non-weighted overdiscretized reconstruction [2] (f/b=1) and with spatially selective weighting (f/b=10). Additional suppression of residual lipid artefacts at moderate levels of fat tissue prioritization during SRF optimization is observed. All maps are normalized to the total* fat *signal in the entire FOV.*

Discussion/Conclusion: Adapted target-driven, overdiscretized reconstruction largely reduces lipid artifacts in accelerated FIDLOVS MRSI through direct optimization of the SRF [2]. We demonstrate that a further suppression of any residual lipid artifacts in 1H brain spectra can be achieved by assigning a moderately elevated priority to SRF optimality in the region of subcranial lipids of 1H MRSI.

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Automatic Magnetic Resonance Spectroscopic Imaging segmentation using blind source separation techniques

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Purpose/Introduction: The procedures commonly used for prostate cancer diagnosis, one of the most common cancer among men, are invasive, unpleasant and often inaccurate. Metabolic profiling of the prostate using Magnetic Resonance Spectroscopic Imaging (MRSI) has shown to be a promising non-invasive diagnostic approach for prostate cancer. Viewing and analysing the multiple spectral patterns obtained by MRSI exam is very complex and time-consuming and needs specific spectroscopic expertise. To make this technique more practical in a clinical environment we propose an automatic MRSI data segmentation using a blind source separation technique (BSS) that provides, on individual patient level, easy-to-interpret images describing the prostate tissue types, their contribution (abundance) to the profile of the spectra, as well as the artifacts present in the data.

Subjects and Methods:

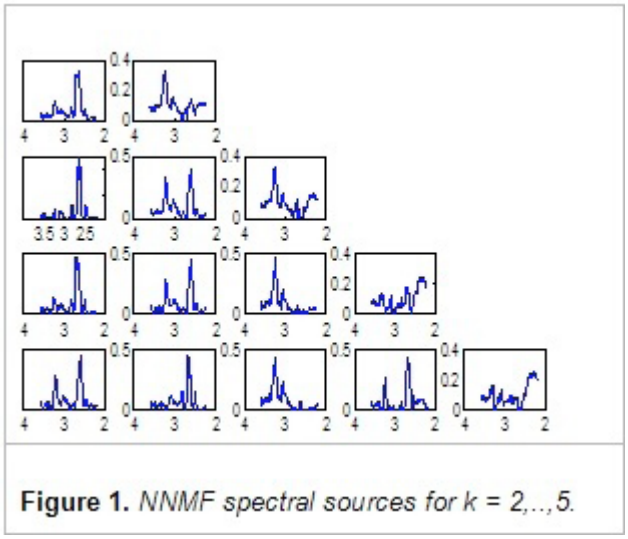


Figure 1. *NNMF spectral sources for k = 2,..,5.*

3D MRSI from 10 patients with prostate cancer were acquired with Siemens-Magnetom-Trio, 3T MRI (Erlangen, Germany), TE=145ms, TR=750ms, bandwidth=1250Hz, points=512, averages=6, matrix_size=16x16x16, voxel_size=6x6x6mm3, using an endorectal coil. The MRSI spectra were frequency aligned and a spectral quality control (QC) was performed as in [1]. Non-negative matrix factorization (NNMF) was applied to each MRSI grid separately in the region of interest [2.2-3.6] ppm and considering only the QC approved magnitude MRSI spectra. NNMF decomposes each matrix of MRSI spectra, X, into $X=AS$, where $S=(s_1,s_2,\ldots,s_k)^T$ contains the constituent spectral sources and A quantifies their abundance distribution. The method was tested for various k and the results were further exploited in order to construct easy-to-interpret images. K-means cluster analysis on the obtained A matrix was used for voxel tissues typing in two clusters. Performance accuracy was evaluated by comparison with histology results following radical prostatectomy.
Results: The results on a patient with prostate cancer, Gleasone Score 4+3=7, are presented in Figure 1 and 2. The NNMF extracted sources show metabolic features that resemble cancer and normal prostate tissue as described in [2], see Figure 1. Moreover, for higher k values, acquisition artifacts such as the contamination with Lipids are also captured as a source and therefore quantified, see Figure 2.A. Clustering analysis results are in agreement with histopathology, see Figure 2.B.

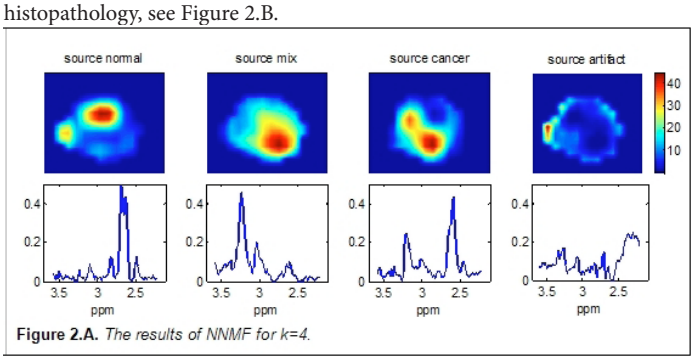


Figure 2.A. *The results of NNMF for k=4.*

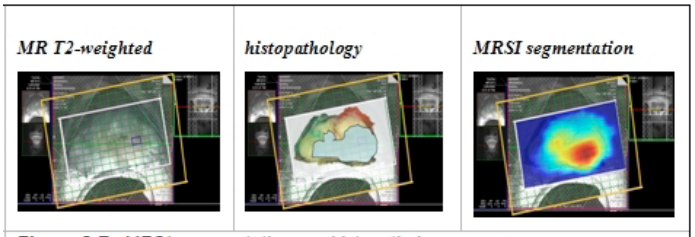


Figure 2.B. *MRSI segmentation vs. histopathology.*

Discussion/Conclusion: Automatic MRSI segmentation using BSS techniques can provide a fast, accurate and user friendly interpretation of MRSI. Therefore, it can increase MRSI contribution to prostate cancer diagnosis through MRSI guided biopsies and guiding appropriate treatment, thus preserving the patient's quality of life.

References:

[1]A.J.Wright et al., NMR in Biomedicine;2013,26:193-203.
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Metabolic whole brain 3D atlas derived from short TE fast MRSI (EPSI)

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Purpose/Introduction: To build a robust quantitative metabolite atlas at short echo time covering the whole brain using two EPSI dataset acquired in two orientations to minimize susceptibility artifacts and a fast whole brain quantitative proton density mapping to normalize metabolite maps by the absolute water signal.
Subjects and Methods: Data were acquired at 3T(Siemens, Verio system) using a 32-channel receiver head coil on six healthy volunteers. Water **T2* mapping** was performed by acquiring GE data sets with different echo times(TE). Water **T1 mapping** was based on a 3-D gradient echo(SPGR) with 2 different values of the nominal excitation angle α. The **$B1^+$-mapping** was calculated using the XEP sequence. The **$B1^-$-mapping** was calculated using the low-pass-filter method[1] applied on the lower nominal excitation angle α images acquired on the previous step[2]. Two **EPSI(Echo Planar Spectroscopic Imaging)**[3] sequences at short TE(20ms) were acquired along the AC-PC and AC-PC+15° lines. The proton density correction was applied on both SI acquisitions. Mean M and the normalized standard deviation nSTD= $\frac{\sqrt{Variance}}{mean}$, across subjects were generated to analyze global and regional distribution across slices. Then, a weighted mean wM defined as

$$wM = \tfrac{1}{2}[M_{ACPC}(1-\frac{nSTD_{ACPC}}{nSTD_{ACPC}+nSTD_{ACPC+15}})+M_{ACPC+15}(1-\frac{nSTD_{ACPC+15}}{nSTD_{ACPC}+nSTD_{ACPC+15}})]$$

was used to combine the both oriented EPSI to generate metabolite templates. N-Acetyl-Aspartate, choline, creatine and myo-inositol absolute quantifications were evaluated in global gray and white matters.
Results: Table.1 showed absolute metabolite values obtained in whole gray and white matters with acquisitions performed in AC-PC and AC-PC+15° planes. Similar global values between AC-PC (Figure.1.A) and AC-PC+15° (Figure.1.B) were obtained however statistical differences were noticed at regional scale showed significant metabolite signal variations in the cerebellum