

MISSA - A highly-developed clinical tool for MR Spectroscopy

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Introduction: It is still a debate in the community whether MR Spectroscopy (MRS) is a proven clinically valuable and helpful tool or not. Many different applications mainly in the brain, but also in the prostate and breast, show its impact on diagnosis and therapy. With MRS as a "metabolic window", the state of different metabolites such as NAA, choline and citrate can be investigated non-invasively in different regions of interest. Though, when measuring signals several possible disturbances can affect the quality and usability of the spectrum, e.g. low sensitivity of the observed nucleus (mostly ¹H) or improper acquisition parameters. Therefore, most of the existing devices lack performance in terms of speed or handling and are difficult to include into the clinical routine. Furthermore, there is no consistent and standardized MRS data format which often hampers data exchange and compatibility between MR scanner, PACS and clinical software assistant.

We present the novel software assistant MISSA (MEVIS Imaging and Spectroscopy Software Assistant) for the analysis of single- and multi-voxel 2D and 3D in-vivo-spectroscopy signals based on the rapid-prototyping platform MeVisLab [1]. As MRS is mostly used in addition to other imaging methods, the standalone software can also be integrated with other modalities such as DTI, fMRI, perfusion or PET-CT to a multimodality platform.

Methods and Implementation: MISSA has been developed on the basis of the research and development platform MeVisLab which is freely available [1]. For visualization and interactive graphics programming, several toolkits like OpenInventor, OpenGL, the Visualization ToolKit (VTK) and the Insight Segmentation and Registration Toolkit (ITK) with its standard segmentation and registration methods are included. As MeVisLab aims at seamless rapid prototyping of clinically applicable software assistants, it is very easy for researchers to integrate their own algorithms and workflows, also in MISSA.

Our goal is to support clinicians in a fast and robust interpretation of MRS signals and to allow them to interactively work with large volumetric data sets. Therefore, features for a stable and reliable standard analysis of MRS data in combination with sophisticated visualization techniques have been implemented: (1) Import of different data formats, (2) Post-Processing, (3) Quantification, (4) Visualization in 1D, 2D, 3D, (5) Diagnosis and Classification, (6) Reporting.

ad (1): We support all kinds of Siemens MRS data (ima, dcm, rda), but also from Bruker for preclinical and ex-vivo analysis. Furthermore, example data sets from GE have been imported successfully and a connection to the clinical PACS system is integrated.

ad (2): All standard methods are available, and can also easily be expanded by interested researchers: water suppression, baseline correction including different filters and removals, absolute and linear phase correction, apodization, zero-filling, Fourier-Transformation and frequency shift correction.

ad (3): Quantification can be done in a threefold manner: SELF-SVD [2] with a pre-selected frequency-bandwidth, Matrix Pencil Method [3], and area under the peak (Fig.1). The software offers the possibility to both quantify predefined metabolites as well as user-defined peaks or areas of interest.

ad (4): The visualization is based on the facilities of MeVisLab. Up to 4 different voxels of interest on a 2D-grid, overlaid on the morphologic MRI data, can be chosen easily and displayed enlarged in a single 1D-viewer to compare them in a comfortable way. Based on the quantification results, the data can also be visualized in a 3D-viewer (Fig.2)

ad (5): MISSA provides an option to grade single voxels with labels of different colors and shapes: The shape encodes the signal quality ("not evaluable" / "poor" / "good"), while the label color encodes the voxel class ("healthy" / "undecided" / "tumor"). Furthermore, labels may also be annotated by free-text strings. Additional or other label types may be incorporated. Afterwards, the labels can be exported as input to machine learning algorithms and classification tools for MRS data.

ad (6): A report including patient information, post-processing steps and annotations by the physician concerning the whole measurement can be added to a patient case.

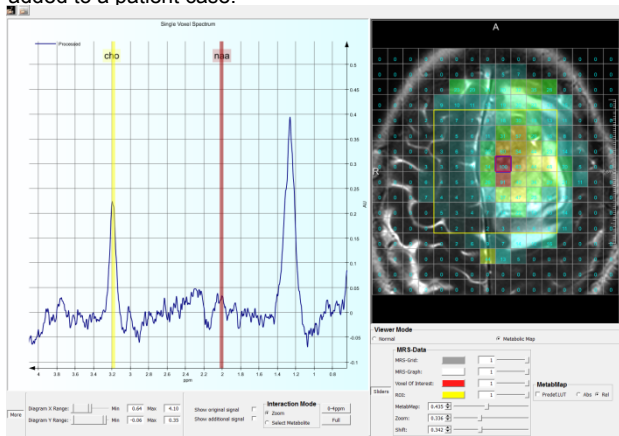


Fig.1: Screenshot of the quantification part of MISSA, showing the overlay of MRI, VOI-box and metabolic map (right) and the enlarged voxel-of-interest (left)

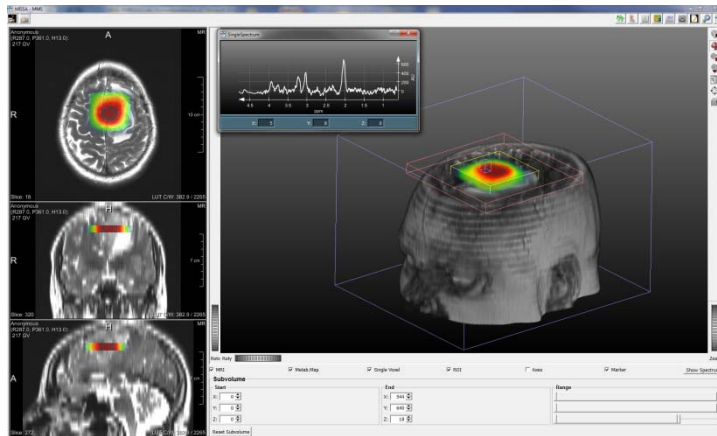


Fig.2: Calculated metabolic map with axial, sagittal and transversal plane (left) and a whole 3D-visualization of a brain with MRI data and the acquired 2D-MRS-grid including the metabolic map

Results, Discussion and Outlook: We successfully processed more than 50 different data sets (Siemens, Bruker, GE) of in-vivo brain, prostate and breast data as well as ex-vivo biopsate spectra from gliomas and preclinical research with the proposed software assistant. With MISSA, enhanced visualization methods and analysis of spectra can facilitate the use of MRS in the future clinical routine through synchronized viewing and optimized data handling and processing. A generalized import of Philips and GE data is topic of ongoing work as well as an integration of quantification results from LCModel and jMRUI. MR spectroscopy is still far from being a clinical routine tool, but MISSA is one important step forward to ease the handling of metabolic information in a clinical setup.

References: [1] MeVisLab 2.1, <http://www.mevislab.de>, [2] Stoica et al., J Magn Res, 165(1):80-88 (2003), [3] Lin et al., J Magn Res, 165(1):80-88 (2003). **We gratefully acknowledge: All the shown data by courtesy of MR-Center Bremen-Mitte, Bremen, Germany**