

Multimodal Post-processing software for MRSI data evaluation

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Target audience: Scientists interested in advanced brain MRSI techniques and data quantification.

Purpose: Proton brain MRSI enables us to detect, quantify, and map several clinically valuable metabolites. To fully take an advantage of this information, the post-processing of the data should be standardized as well as automated to minimize the total processing time and to avoid any systematic error introduced by the investigator. Since advanced imaging and spectroscopic techniques, such as parallel imaging, spectral editing and different k-space trajectories are carried out at our institute, we aimed to develop a post-processing software tool tailored for our needs, however general enough to accommodate to various spectroscopic and imaging applications.

Methods: To facilitate multimodal post-processing and evaluation of acquired imaging and spectroscopic data, we have developed a software tool based on MATLAB (MathWorks, Natick, Mass, USA) and BASH programming languages while utilizing MINC (MINC tools; v2.0; McConnell Brain Imaging Center, Montreal, Canada) and FSL 5.0 (Analysis Group, FMRIB, Oxford, UK) packages. The software is operated via a MATLAB GUI, which allows the user to set the initial parameters and run the processing in a batch mode. The processing path is divided into MRI and MRSI parts. The information obtained from MRI serves as a prior knowledge for spectroscopic post-processing and might be used for multi-modal comparison.

MRSI pipeline: Firstly, GRAPPA, slice- or 2D-Caipirinha algorithms are implemented for reconstruction of undersampled MRSI data¹. An image-based coil combination² is applied for uncombined array coil data. Consequently LCmodel quantification is performed with dedicated prior knowledge basis sets. For display purposes, grids of spectra are plotted for sagittal, coronal and axial slices (fig.3). Metabolic maps are constructed together with maps of SNR (computed by home-written script based on the Pseudo-Replica method³), FWHM and CRLB for quality control (fig.2). Based on these quality maps, threshold criteria are set to exclude any voxel with values outside of the specified interval. Afterwards, all maps are co-registered to a common spatial reference frame (MNI 305, MNI 152 atlases) to enable an inter-subject or inter-session comparison.

MRI pipeline: T₁-weighted (or T₂-weighted) images are used to derive a brain mask (Brain Extraction Tool, FSL) and tissue-segmented masks (FAST, FSL) for partial volume correction. The segmented images of white matter, grey matter and cerebrospinal fluid are then convolved with the MRSI point spread function to achieve relative tissue volume contributions at each voxel.

Statistical analysis: All gathered data from a single subject are exported into a spreadsheet, where a voxel-wise analysis and basic statistical analysis are performed. The user can retrieve information on amplitude, SNR and CRLB values for each of the metabolites and voxel coordinates either from the whole volume or a specified ROI.

Discussion: The main advantage of our approach is its versatility – the post-processing pipeline can be effortlessly adjusted to any sequence or field strength and to various modalities due to its modularity. Thus it can serve as a test bench, where the user can process data acquired by specialized techniques as well as techniques used in clinical

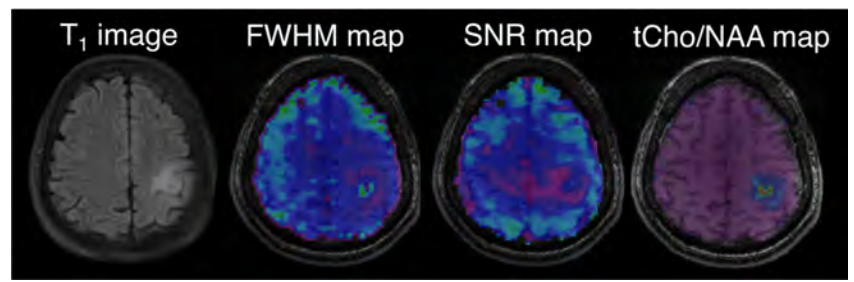


Figure 1 – T₁ MPRAGE image, FWHM, SNR maps (quality maps) and ratio map of total choline signal to total NAA of low-grade glioma patient. Maps were created using described post-processing software

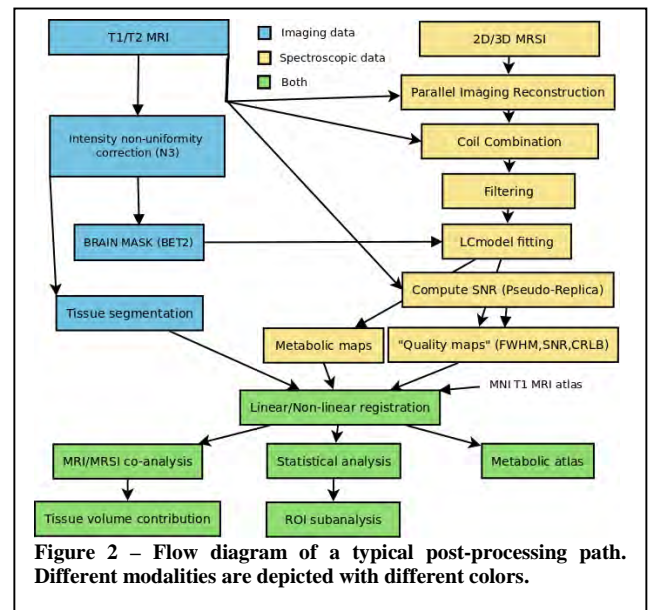


Figure 2 – Flow diagram of a typical post-processing path. Different modalities are depicted with different colors.

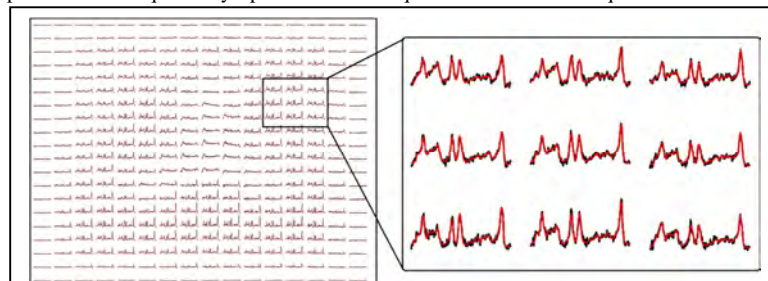


Figure 3 – Grid of spectra for transversal slice depicting the original (black) and fitted (red) spectra. The decreased signal in the central region corresponds to brain ventricle.

routine (PRESS, LASER, etc.). Another advantage is our open-source approach, allowing for easy adaptation to different needs.

Conclusion: The introduction of an automated processing pipeline without the need of any user-interference during the process into our routine led to a decrease of total post-processing time and minimization of user-induced bias. It enabled us to implement advanced spectroscopic techniques in short time maintaining quality control over data.

References: 1. Strasser et al., Proceedings ISMRM(22) 2014: 0651. 2. Strasser et al., NMR in Biomed, 2013; 26(12):1796–1805. 3. Robson et al., MRM, 2008; 60(4):895-907.