Automated pipeline for processing and analyzing MR Spectroscopic Imaging and segmentation data of human brain

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TARGET AUDIENCE

MR-researchers and MR-technicians using MR spectroscopic imaging (SI).

PURPOSE

There has been a long-standing interest in automated spectral processing for MRSI, which is driven by the need of standardized, easy-to-execute and rapid protocols. This goal, however, can be difficult because of the many artifacts that can arise and require individual judgment.

METHODS

Human brain SI (24×24 matrix dimensions) was performed at 3T and 7T (Siemens Magnetom). Data were acquired using a 32-channel head coil with body transmitter (3T), or an 8-channel transceiver array (7T). The 3T data (TE/TR 40 ms/2 s) were acquired in 19 min using a multi-band excitation (four 10-mm-thick 240-mm-FOV SI slices positioned over the fronto-parietal and temporal lobes spanning 48 mm; nominal voxel size was 1 cm^3) shimmed with *B0-l*oop *e*ncoded *r*eadout (*Bolero*). At 7T, the TE/TR were 40 ms/1.5 s. Spectral processing was performed using LCModel using 12-15-compound basis sets simulated using GAMMA. Spectral reconstruction, analysis and plotting were performed using MATLAB R2013b. The MPRAGE images were segmented to gray matter (GM), white matter, and cerebrospinal fluid and further parcellated into brain regions using FreeSurfer. The GM fraction from each MRSI voxel was calculated after including point-spread function and slice profile corresponding to the acquired MRSI data, as presented earlier [1].

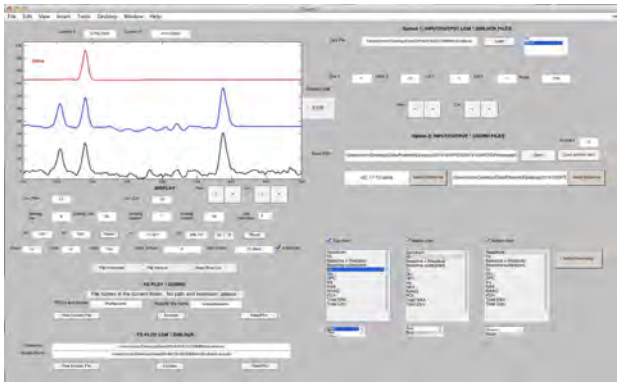

Fig. 1. An in-house written MATLAB application for manipulating and plotting the spectra, fits and individual metabolites (selected in the listboxes in the lower right corner) for the entire SI slice or for individual voxels with simultaneous retrieval and display of gray matter fraction (center, next to the plot window).

RESULTS

The MRSI protocol comprised the following steps: **1)** Reconstruction and channel recombination. **2)** Inverse FFT to create the time-domain data for LCModel input. **3)** Multivoxel SI analysis by LCModel and output of the spectra, fits and metabolite tables. LCModel output was validated against manually processed data. **4)** Automatic selection of voxels with acceptable fit quality and minimal baseline distortions and lipid+macromolecules contamination for further analysis. The typical filter parameters were: CV<6% for NAA+NAAG and Cr; CV<7% for GPC+PCh; (MM20+Lip20)/Cr≤2.5. This resulted typically in less than 3-6% of voxels misclassified as good/bad **5)** Calculation of metabolite ratios (total NAA/Cr and total NAA/total Ch). **6)** Manipulating and plotting the spectra, fits and individual metabolites for the entire SI slice or for individual voxels (Fig. 1). The entire MRSI protocol can be concluded in under an hour per patient, so the segmentation and parcellation is the longest part.

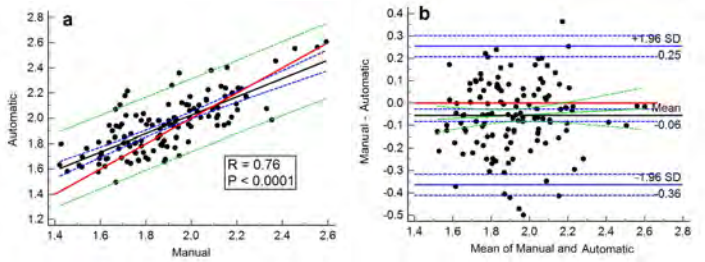

Fig. 2. An agreement between NAA/Cr values for a multi-voxel data set (3T, n=127) of an epilepsy patient processed automatically and manually (phase correction, spline baseline correction, Gaussian fit). (**a**) Regression analysis (red, line of equality; blue, 95% CI; green, 95% prediction), and (**b**) Bland-Altman analysis (red, line of equality; blue, limits of agreement and 95% CI for limits of agreement and mean of differences; green, regression of differences with 95% CI).

Figure 2 demonstrates good agreement between the metabolite ratios obtained using either the automated routine or traditionally (by an MR-spectroscopist processing and correcting spectra for each voxel). Bland-Altman plot [2] results in nearly zero mean bias (2.7% of average with 95% confidence interval (CI) of ±1.3%), limits of agreement of ~15% (95% CI of ±2.3 %) and no systemic variation over the range of measurement (Fig. 2b). The analysis of the tumor patient brain at 7T is shown in Fig. 3. The preliminary study of a small cohort (2 epilepsy subjects and 7 normal volunteers at 3T) shows the difference in the slope of the regression of Cr/NAA against GM fraction (Fig. 4): 0.30±0.05 in epilepsy vs. 0.20±0.05 in control, P<0.05, taking into account an age dependence of the slope (0.003/year of age, R^2=0.92, P=0.0007).

DISCUSSION AND CONCLUSIONS

Accurate and reliable automated protocols for MRSI of human brain with minimal operator intervention have been developed, refined and tested for multi-slice multivoxel SI data. Not surprisingly, the key limitation in the analysis is data quality, based on SNR and lipid suppression. This methodology allows the integration with estimation of significance of abnormality based on tissue content (gray matter fraction) as ascertained from tissue segmentation.

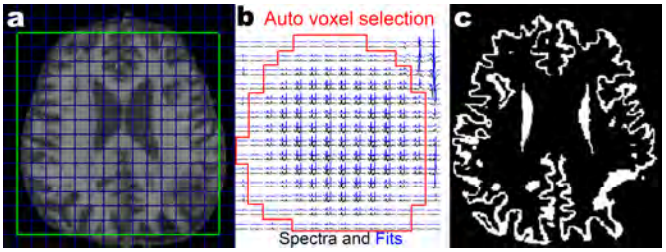

Fig. 3. (**a**) 7T MPRAGE image of a tumor patient brain corresponding to the MRSI slice. (**b**) Spectra (black) and fits (blue) in the green box in (**a**); those automatically classified as good are encircled by the red line. (**c**) A gray matter map. The tumor appears on the bottom right of the image.

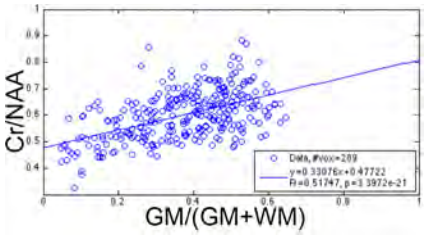

Fig. 4. Linear regression of Cr/NAA vs. GM fraction for the cortex of an epilepsy patient. 3T data, n = 289 voxels.

ACKNOWLEDGMENTS

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REFERENCES

1. Lee Y, Kim T, Zhao T, et al. *ISMRM-ESMRMB 2014*, 2888.
2. Bland JM, Altman DG. *Stat Methods Med Res* **8**, 135-60.