

Spectro Image Registration And Metabolite-mapping Software (SIRAMAS), a new open source research tool

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Introduction

There are a variety of research and commercial software packages available for spectral analysis. Spectroscopy data is processed offline with any of these packages where routine analysis such as Lorentzian filtering, Fourier transformation, baseline correction and phase/frequency shifting is carried out. Unfortunately very little or no image-spectra registration is available with any of these packages. This work presents a research open source tool for image-spectra registration and metabolite map generation. This tool only utilizes peak tables generated by available spectra packages in combination with T2 image acquisitions and spectra headers for performing registration, metabolite maps generation and analysis.

Methods

SIRAMAS was mainly implemented in Matlab®. A main GUI (Graphical User Interface) was developed in order to combine all the necessary tools for spectro-image registration and metabolite-mapping analysis. Figure-1 shows a screenshot of SIRAMAS main GUI and functionality of the various push buttons and sub-windows. Crucial routines were developed in standard C and are called from main Matlab code. Three-dimensional (3D) Magnetic Resonance Spectroscopy Imaging (MRSI) data from four brain cases was used to assess this tool. The first two cases were scanned at GE-signa 1.5 T and the other two at GE- 3.T. Contiguous T2-weighted slices of 3mm thickness, were acquired for prescription of follow up 3D-MRSI acquisition. Brain optimised PROSE and PRESS acquisition pulses were used to obtain arrays of spectra at 1.5T and 3.T scanners respectively. Field of view (FOV) and phase encoding matrix choices varied from 8x8x8 to 12x12x8 resulting in a one cubic centimetre spectral resolution in each of the cases. Spectral volumetric definition and lipid contamination was improved with a combination of very selective saturation pulses (VSS) and added spatial selective saturation bands. Spectral data was processed off-line with Spectro Analysis GE™ (SAGE) package for base-line correction and off peak registration. Table peaks of Ch, Cr and NAA containing peaks heights and peak volumes were also generated with SAGE.

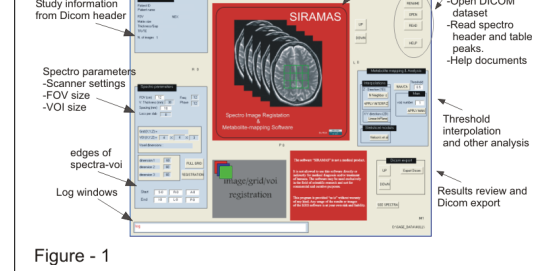


Figure - 1

Metabolite peak tables (*.stf), T2-weighted datasets and spectra header files (*.shf) of each case were processed with SIRAMAS for metabolite mapping generation. Automatic image-spectra registration was achieved in two steps. First of all, this tool performs a through plane registration where it finds the axial image with DICOM slice location tag (0020,1041) equal to location of the centre of the z-spectra FOV. Secondly it does the in-plane registration where distances from right-left and anterior-posterior to scanner isocentre of both image and spectra were used to compute the relative position of spectra FOV/VOI grid with respect to axial image. Interpolated and un-interpolated ratio metabolite maps of NAA to Ch were also generated for each of the cases. In order to assess the quality of the registration, centre slice and distances from axial slice to spectra-voi edges were noted off the console at the time of acquisition. This information was compared with results from SIRAMAS.

Results

Table 1 contains distances in mm from scanner iso-centre to spectra-voi edges. Values in blue were collected from console at the time of acquisition and values in green correspond to those calculated by SIRAMAS at the time of spectra-image registration. Values from both sources are almost identical. A Difference of about 0.1 mm was observed on case-1 posterior, case2 superior and left positions. Figure-2 shows screenshots of centre slice with superimposed spectra-voi and corresponding iso-centre to spectra-voi distances for both SIRAMAS on the left (figure-2a) and scanner console on the right (figure-2b). Straight axial centre slice locations were S28.12, S33.95, I30.0 and S17 for case1, 2, 3 and 4 respectively. Same slice locations were identified at automatic-registration process.

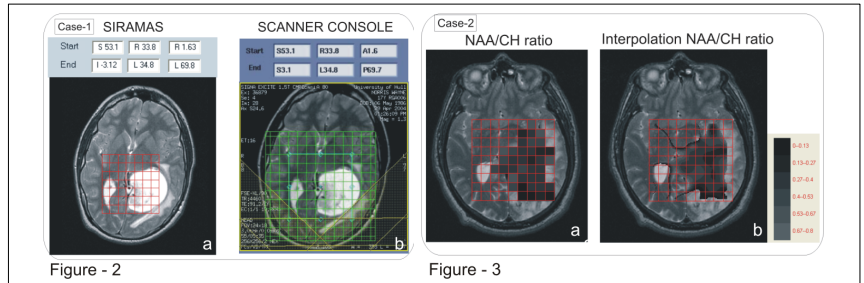


Figure - 2

Figure - 3

Figure-3 illustrates a typical example of un-interpolated (figure-3a) and interpolated (figure-3b) NAA to Ch ratio of six grey level maps. On figure-3 the darker the pixel the smaller the NAA to Ch ratio and the brighter the pixel the bigger the NAA to CH ratio. As an example, voxels with NAA to Ch ratio ranging from 0 to 1 were used as the criteria for depiction of malignancy, while voxels with ratios above one were left unfilled. Data from figure 3-b is the result of in plane cubic spline interpolation [1] of figure-3a.

Conclusions

Values on table 1 demonstrated the accuracy of the automatic registration, where only 0.1 mm deviation from console values was observed in two of the cases. This error can be considered insignificant when compared with in-plane 1mm and through-plane 3mm image resolution. Centre slices found at registration coincided with those used at prescription stage, which is an indication of the quality of the registration. Also it has been shown that this tool can be utilised for un-interpolated and interpolated metabolite mapping generation. Future work includes the spatial registration of selective saturation bands, use of non-axial images data set, three-dimensional rendering of spectra data and inclusion of various metabolite maps statically algorithms. One of the unmentioned features of this tool is its capability for exporting registered image-metabolite map as a new DICOM dataset for its potential use in either Radiotherapy or pre-surgical planning. We would like to make this tool and its code available to the scientific community with the hope of improving its potential research capabilities.

References

[1] De Boor et al, 'A Practical Guide to Splines.' Springer-Verlag, 1978

	Console			SIRAMAS		
Case-1 Start	S53.1	R33.8	A1.6	S 53.1	R33.8	A1.63
End	S53.1	L34.8	P69.7	S53.12	L34.8	P69.8
Case-2 Start	S58.9	R44.2	A27.0	S59	R44.2	A27
End	S8.9	L46.2	P61.7	S8.95	L46.3	P61.7
Case-3 Start	I4.9	L1.5	P2.5	I4.91	L1.56	P2.56
End	I54.9	L52.2	P52.1	I54.90	L52.20	P52.10
Case-4 Start	S42	R51.8	A51	S42	R51.80	A51
End	I8	R2	A1.4	I8.05	R2.04	A1.38

Table-1