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Segmentation of target volume using MRS images

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Delivered by**:**
Institut Claudius Regaud

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Software for the Use of Multi-Modality images in External Radiotherapy

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1. Introduction

Magnetic resonance spectroscopic imaging (MRSI) is a powerful non-invasive tool for detecting markers of biological processes. In the radiotherapy context, this modality has the potential to define new target volumes due to its ability to characterize biochemical, metabolic and pathological changes in tissues [1, 2]. This offers the potential for more targeted therapies, improving treatment outcomes. However, there are several issues slowing the incorporation of this technique into the radiotherapy workflow. The lack of a standard format for storing the data which is vendor-dependent and not DICOM compatible is an example of these issues. Other issue is the inherent complexity and poor quality of the MRSI signals. This makes unavoidable to pre-process the data in order to extract reliable information. The lack of an established approach to pre-process and quantify MRSI data is also a main issue in the clinical use of this technique.
To overcome these limitations and to integrate the spectroscopy processing pipeline into the radiotherapy workflow is one of the goals of SUMMER and the subject of this report.

We present here a processing pipeline which applies advanced methods to segment radiotherapy target volumes in MRSI images.

2. Magnetic Resonance Spectroscopy Imaging (MRSI)

Several diagnostic questions such as the type and grade of the tumor are difficult to address using conventional MRI. MRSI is a non-invasive technique able to detect changes in tissues that are not visible from standard morphologic images. It relies in the same phenomenon as MRI (NMR) so data can be acquired in the same session and there are no known health risks associated to this technique. MRSI was initially developed for examination of human brain tumors, and its use has been extended for examination of prostate and breast cancers. Its complementary use with MRI provides useful information on tumor characteristics, progression and response to treatment. This technique is becoming a very useful modality in brain radiotherapy planning due to its ability to provide valuable information on possible sites of tumor relapse [1, 2]. This information can be used to determine potential target volumes for radiotherapy dose escalation according to the metabolic abnormalities [3].

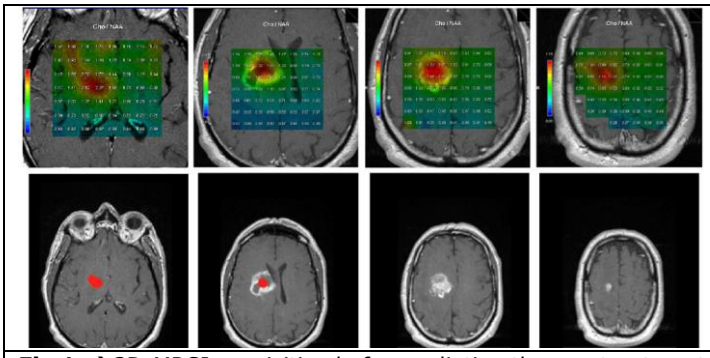


Fig.1 a) 3D-MRSI acquisition before radiation therapy treatment of a patient with confirmed glioblastoma located in the right capsulo-thalamic region. Extracted and edited from [3].

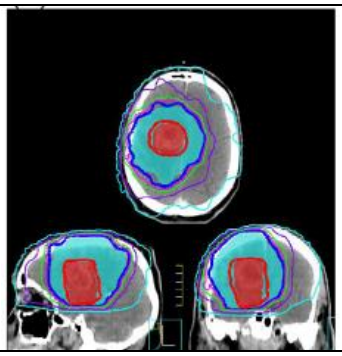


Fig.1 b) The integration of Cho/NAA abnormal volumes defines new target relative to MRSI, i.e. PTV2 color-washed in red. Extracted and edited from [3].

3. MRSI raw data handling

There is not a standard format for MRSI data. In fact, each vendor offers its own format. MRSI images are MRI spectroscopic maps overlaid on corresponding anatomical MR images and do not conform to DICOM standards. Therefore they are not compatible for automatic image fusion with the planning CT scans [3].

We have developed modules to read Siemens and Philips data. We are also able to place the spectroscopic VOI on a companion MRI image. The module to read Siemens raw data has been already integrated into de SUMMER plugin for MRSI data processing.

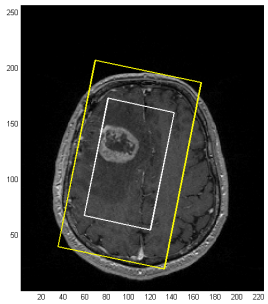


Fig.2 a) MRSI placed on companion MRI image

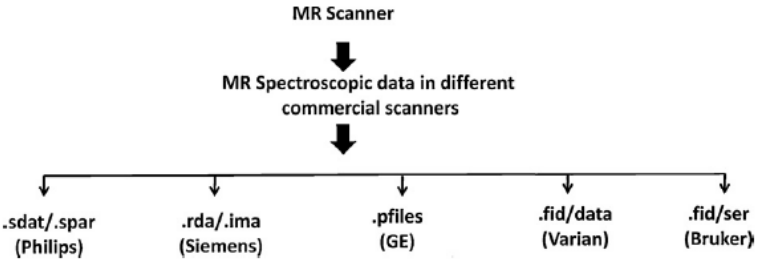


Fig.2 b) MRS file formats are verdor-dependent. Extracted from …

4. MRSI data pre-processing

Due to the complexity and poor quality of the MRSI signals, it is unavoidable to perform several pre-processing steps on the data in order to be able to extract reliable information [4]. We have focused our work in a denoising method to increase the SNR of MRSI data.

4.1. MRSI denoising

The low SNR of MRSI data comes from the combination of a weak MR signal, low metabolite concentrations and the presence of measurement noise. This makes accurate quantification of metabolite signals extremely challenging. Improving the SNR of MRSI signals is then a key factor in achieving more accurate quantitation results and, as a direct consequence, improving the clinical utility of this technique. We have developed a novel algorithm for noise reduction based on regularization techniques. This work has been presented at the EMBC 2013 [ref].

Signal denoising is to recover a true signal from an observed noisy signal, i.e., is to decompose the observed signal into two components, the true signal and the noise. In the ideal case, the noise has no any signal information. Let's then consider the following model:

$$z = s + n \tag{1}$$

where *s* and *z* are the true and observed MRSI signals respectively, and *n* is a Gaussian noise of diagonal covariance matrix Σ which has to be estimated. The aim is to recover *s* from the inverse ill posed problem (1). Several techniques to solve (1) have already been proposed. However, most of those techniques rely heavily on spectral constraints and thus are not able to describe the spatial variations exhibited by in vivo MRSI data. The method described here is able to overcome these limitations by removing the spurious irregularities while preserving spatial and spectral resolutions. This is achieved by considering a criterion able to capture the spatio-spectral nature of MRSI data to solve problem (1). Such criterion is defined as follows:

$$J(s) = D(z,s) + \lambda R^{spat}(Fs) + \beta R^{spect}(Ts) \tag{2}$$

where $D(z,s) = \|z-s\|^2_{\Sigma^{-1}}$ is the data fidelity term, R^{spat} (R^{spec}) describes the spatial (spectral) dimension of the data, *F* (*T*) is a 1D (2D) orthonormal wavelet decomposition operator and λ and β are regularization terms that balance the compromise between the spatial and the spectral dimensions.
The true signal *s* is then defined as the minimizer $\hat{s}$ of such criterion:

$$\hat{s} = \arg\min_s (J(s)) = \arg\min_s \left[D(z,s) + \lambda R^{spat}(Fs) + \beta R^{spect}(Ts) \right] \tag{3}$$

Since *J* is not necessarily differentiable, standard gradient-based algorithms for minimization cannot be

used. However, *J* is convex and so unicity of the target solution is guaranteed and (3) can be solved by a recently proposed fast optimization algorithm [5] able to deal with convex non-differentiable optimality criteria. Unlike other existing schemes, this algorithm is considerably efficient and it is not subject to local optima.
Fig. 4 shows an example of the denoising of a MRSI spectrum.

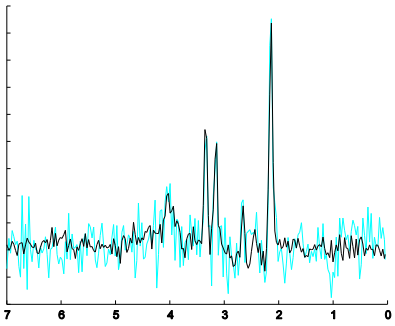


Fig. 3 Spectrum (cyan) denoising (black)

5. MRSI data quantification

To quantify MRSI signals we use a time-domain method that estimates metabolite concentrations by fitting a model to the observed data [ref]. The model used to fit the observed data in the time domain is the following:

$$S(t) = \sum_{k=1}^{K} a_k e^{i\phi_k} e^{(-d_k + if_k)t} v_k \tag{4}$$

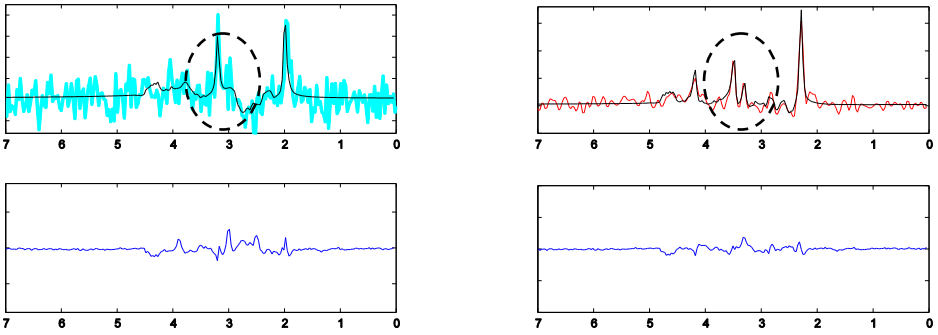
where *K* is the number of metabolites considered, $\{v_k$, for $k=1,\ldots, K\}$ is the set of metabolite profiles, a_k is the amplitude, ϕ_k the phase shift, d_k is the damping correction and f_k the frequency shift.
The basis set of metabolite profiles can be measured *in vitro* or simulated using quantum mechanics [7]. In this study, we used a simulated basis set containing metabolite signals typically present in healthy brain tissue, Choline (Cho), Creatine (Cr), N-acetyl-aspartate (NAA), Glutamate (Glu) and Glutamine (Gln) and Lactate (Lac).
In order to fit the model to the observed data, a non-linear least squares (NLLS) problem has to be tackled:

$$\min_{\{a_k,\phi_k,d_k,f_k,k=1\ldots K\}} \sum_{i=0}^{m-1} \left| z(t_i) - \sum_{k=1}^{K} a_k e^{i\phi_k} e^{(-d_k + if_k)t} v_k \right|^2 \tag{5}$$

Classical NLLS optimization methods, as the Levenberg-Marquardt algorithm [8], can be used to solve such problem.

6. SNR enhancement improves quantification

To measure the impact of denoising MRSI signals before quantitation, synthetic and in vivo MRSI data were quantified with and without previous denoising. The conclusion of the study was that the presence of noise in MRSI data hampers the correct fitting of MRSI signals by the quantitation model. As a consequence, the accuracy of the quantitation becomes poor and unreliable. Applying a denoising method, as the one described in this report, provides a significant improvement in the fitting of the quantitation model and the observed data (Fig. 3). As a consequence, the accuracy of the quantification results is significantly improved. The complete results of this study have been presented at the ESMRMB 2013 and can be seen at [ref].



(a) (b)

Fig. 4 a) Quantiation of a noisy signal. Top: noisy signal (blue) and fitted model (black). Bottom: Residual between the fitted model and the ground truth signal. **b)** Quantitation after denoising. Top: denoised signal (red) and fitted model (black). Bottom: Residual between the fitted model and the ground truth signal.

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7. References

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