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Purpose/Objective(s): MR spectroscopic imaging (MRSI) can characterize biochemical, metabolic and pathological changes in brain tissues before they are visible from conventional anatomical images. This makes MRSI a powerful tool to define biologically tailored target volumes for dose escalation in radiation therapy treatments. Although the numerous existing quantification techniques, it remains difficult to obtain accurate information from MRSI signals due to biological and experimental conditions decreasing the quality of the data. We present a comparison of metabolic maps generated from a conventional voxel-by-voxel quantification method and from a novel method incorporating spectral and spatial information of MRSI data into the quantification process.

Materials/Methods: A set of 20 synthetic brain MRSI grids of size 6x6 were generated based on values commonly reported in the literature. 400 in vivo 3D MRSI voxels from 3 boxes from a healthy volunteer and 2 patients with diagnosed GBM included in a prospective clinical trial were analyzed (1.5T, TE/TR = 135ms/1.5s). Metabolic maps were generated by using conventional quantification and our method. This method quantifies simultaneously all the signals within the MRSI box and exploits the sparsity of the MRSI data in the wavelet domain in order to increase the SNR of the signals during the quantification. With difference to previous methods, the prior information is exploited in both, the spectral and the spatial dimensions of the MRSI data and it is not imposed on the sought parameters but in the representation of the data the wavelet domain. A Monte Carlo study was performed to measure the performance of the methods with respect to the noise. To this aim five different levels of white Gaussian noise were added to the synthetic datasets. Estimated metabolite concentrations from in vivo MRSI data were also studied. The agreement between the derived maps and companion MRI images was analyzed.

Results: Experiments on synthetic data show that errors on the estimation of metabolite concentrations are reduced by a mean of 41% (range 24-54% depending on the level of noise) which leads to more accurate metabolite maps. For in vivo data, metabolite concentrations estimated from healthy voxels are more in accordance with values in literature. In addition, the spatial distributions of the metabolites are less noisy and in better accordance with the physiological structures visible from MRI images.

Conclusions: Incorporating spectral/spatial information within the quantification model improves significantly the robustness of the process and the accuracy of the metabolite estimates from MRSI data. This leads to more accurate an easy-to-interpret metabolite maps that can be used to define more targeted and more individualized radiation therapy treatments.

Towards Accurate and Robust MRSI Quantification to Improve the Radiation Therapy Treatment of GBM

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