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Visual Analysis of Magnetic Resonance Spectroscopy Imaging Data for the Study of Human Brain Tumors

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Abstract

Magnetic Resonance Spectroscopy Imaging (MRSI) is an in-vivo method for measuring metabolite concentration in various tissues. Typically, individual metabolites are examined in detail. We provide an interactive visualization tool that allows for the simultaneous analysis of all metabolite concentrations. The multi-dimensional data visualization is based on star coordinates interaction in a projected view. We derive a segmentation of the accompanying magnetic resonance image (MRI) to investigate the metabolite distribution within tissues including partial volume effect handling. Coordinated views between spatial slice-based visualizations and multidimensional metabolite spaces allow for the selection of individual voxels, certain anatomical regions, or groups of voxels with similar concentrations for a comparative analysis in the linked views as well as in further linked statistical plots. We apply our method to the analysis of brain tumors and surrounding tissue.

1. Introduction

In 2012, WHO reported 256,213 brain cancer cases from which 189,382 deaths are recorded [NIH15]. Magnetic Resonance Spectroscopy Imaging (MRSI) allows for an improved diagnosis of the type of tumor and the infiltration of surrounding tissues that is otherwise hard to examine [BTBJ04]. While magnetic resonance imaging (MRI) provides location, shape, and size of a tumor, MRSI allows for a better classification into the more than 100 tumor types and a rating between most malignant to benign. MRSI is a non-invasive bio-medical technique used by radiologist and neurosurgeons for in-vivo brain studies to quantitatively analyze the concentrations of affecting bio-chemicals (called metabolites) [VDMCW94]. While most analyses of MRSI data focus on individual metabolites, we present an approach to visually analyze the entire multi-dimensional metabolite space in conjunction with the imaging space, thus, exploiting the full potential of the imaging method.

2. Related Work

In clinical practice, tools like jMRUI [SDCA*09] are used that includes various pre-processing algorithms for MRSI data and a slice-based visualization, where for some selected metabolites the concentration of a metabolite is color-coded and the color map is overlaid with the MR image. Commercial tools like SyngoMR and SpectroView that are distributed with scanners provide similar functionality. Kinoshita et al. [KY97] showed in in-vitro experiments on the human brain that the list of metabolites are active in certain type of tumors goes beyond what is provided by standard tools. Feng et al. [FKLTI10] and Nunes et al. [NRS*14] proposed first approached to use multidimensional data visualization methods such as scatter plots and parallel coordinates for visualizing metabolite concentrations. We build upon such methods and extend in various directions including coupling it with segmentation results, visualizing the multidimensional feature space with projections which allows for a selection of voxels with similar metabolic concentrations in the multi-dimensional space, and comparative visual analysis of individual voxels and/or groups of interest.

3. Visual Encodings and Interaction Mechanisms

The spatial visualizations are based on the MR images with overlaid color maps or glyphs. We support an automatic segmentation algorithm (MICO) [LGD14] for segmenting the MR image, but a manual segmentation is also possible by simply marking respective regions in the slice. As the MR image has a substantially higher resolution than the MRS image, the MRSI voxels exhibit a partial volume effect when compared to the MRI segmentation. We visualize the segmentation result at an MRSI-voxel resolution using pixel-map glyphs, where each MRSI voxel is visualized as a rectangle that is filled with colored bars according to the segmentation result of the covered MRI voxels. As each segment is assigned one distinct color, each glyph consists of respective portions of those colors, see Figure 1a.

We pre-process the MRSI data with Tarquin [RWPA06] to extract all metabolite concentrations. The multidimensional space is visualized using linear projections, which can be modified using a star coordinate widgets, see Figures 1b and 1d. Layouts by automatic projection methods such as Principal Component Analysis are also supported. Each MRSI voxel is represented by one circular

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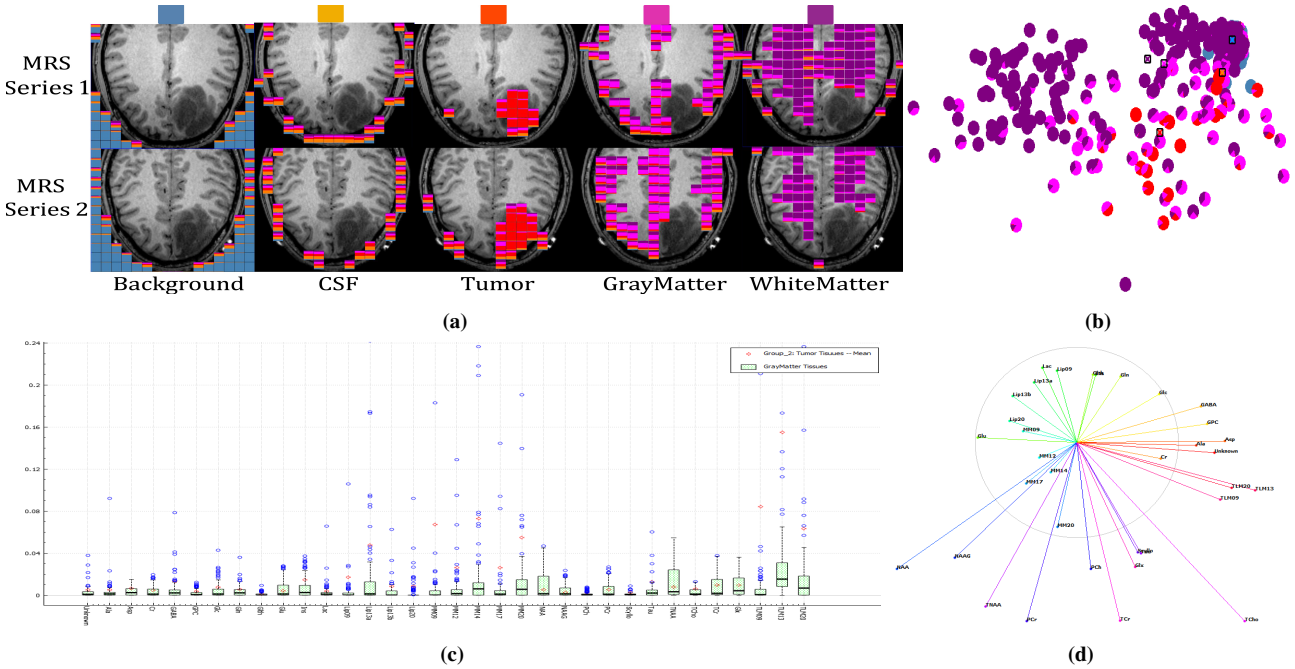

Figure 1: *(a) Automatic MRI segmentation result impose on MRSI voxels using pixel-map glyphs for encoding partial volume effect. (b) Linear projection of multidimensional metabolite space with interactive separation of clusters by control points (black boxes). Voxels are encoded by pie-chart glyphs of segmentation result. (c) Box plots of all metabolite concentrations for one reference group (grey matter) when compared to the tumor voxels (here average) shown as red dots. (d) Star coordinate widget showing long axes of dominant metabolites.*

glyph, where the glyph is a pie chart that shows the same colors and proportions as the glyphs in the spatial slice-based view.

When investigating the multidimensional data projection, one can observe the different colors reflecting different tissue types. One can also impose a hard segmentation, where each voxel is assigned to the segment that contributes most. A respective classification defines groups of voxels. In the projected view, the centroid of each view is computed and the classes can be separated (if possible, at all, with a linear projection) by pulling apart those control points following the approach by Mochanov and Linsen [ML14]. Voxels or regions of interest can be selected both in the slice-based view and in the projected view for further comparative investigations.

Further investigations can be performed with additional linked statistical plots such as scatterplots for a pair of selected metabolites and, in particular, by a bar chart plot over all present metabolites, see Figure 1c. Comparisons between two selections are possible by selecting a reference group, which is depicted using bar charts for its metabolite concentrations, and a test object like a voxel or a group of voxels, which can be depicted by individual dots (or also bar charts).

4. Brain Tumor Study Results

We applied our visual analysis tool to data from a ^{1}H MRSI scan (3T Siemens scanner, TR/TE/flip = 1700ms/135ms/90) of a 26-year-old male patient with a brain tumor. (Data courtesy of Miriam Bopp and Christopher Nimsky, Universitätsklinikum, Marburg, Germany.) The MRI volume is $224 \times 256 \times 144 mm^3$ with 1 *mm* slice thickness and the two MRSI series each have a $160 \times 160 \times 12 mm^3$ FoV (Field of View). Each MRSI voxel stretches over $10 \times 10 \times 12$ MRI voxels. Figure 1a shows the automatic segmentation result at the MRSI-voxel level with pixel-map glyphs encoding the partial volume effect. The segmentation result is not perfect and would require manual fine-tuning, but the tumor is clearly visible. Figures 1b and 1d show the respective projection and star coordinate configuration of the multi-dimensional metabolite space with pie-chart glyphs. The segments have been interactively separated. The long star coordinate axes indicate, which metabolites are mainly responsible for the separation. The typical suspects show up plus some other metabolites. Figure 1c shows a comparison of the tumor voxels (represented by their mean) against grey matter to investigate for which metabolites the concentrations differ. This indicates what type of tumor this may be. In a next step, one would select neighboring voxels to the tumor to investigate their concentrations and judge whether they are already partially infiltrated by the tumor.

5. Conclusions

We have presented a novel tool for the investigation of all metabolite concentrations measured by MRSI to exploit its full capacity. Visual encodings in spatial dimensions and metabolic space allowed for coordinated interaction and comparative visual analyses. The tool showed potential in supporting the analysis of tumor types and voxels surrounding the tumor area.

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