Title:
3D Model for Representation and Visualization of Magnetic Resonance Spectroscopy Data

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Introduction:
Magnetic resonance spectroscopy (MRS) is a noninvasive technique to explore in vivo biological tissues during brain magnetic resonance imaging (MRI) examination. MRS can give information about the chemical composition of brain tissues, and thus combined with anatomical images, it can be helpful for diagnosis and the following of pathologies (tumors, Alzheimer's diseases, stroke...) [?]. This metabolic information, which is a relative concentration of different molecules, is stored inside a single or multiple MRS voxels, that are precisely localized in the brain [1]. Each voxel encompasses several MRI slices and can be composed of multiple tissues: White matter (WM), gray matter (GM) or cerebrospinal fluid (CSF) at least, and, possibly, different type of lesions due to diseases. Metabolites are known not to be uniformly distributed between anatomical structures. Yet, a single concentration value for each metabolite is given for the whole volume whatever the tissues present in it. This clinical representation is therefore limited to visualise the impact of the anatomical structures in a fine way.

Methodologies have been proposed to improve the accuracy of the acquired values without having to lengthen or complicate clinical protocols. Those are based on the use of partial volume effect (PVE), which gives, for each voxel in a MRI scan, the probability that it belongs to one of the tissue type [2]. Basic interpolation algorithms can be applied on the data in order to improve the spatial resolution of the result. However, the volume composition of a spectroscopy voxel is not taken into consideration. The visualization and representation of concentrations of metabolite dispatch between all different tissues of the brain remains a challenge.

A voxel-based model can be created directly through the segmentation of MRI images, assigning each voxel to a specific physiological element corresponding to an anatomical tissue segment. However, using this discrete representation for modelling brain tissues close to reality exhibits several drawbacks: (1) addressing holes and cavities becomes challenging, (2) the boundaries lack smoothness, and (3) the calculation of geometric properties is constrained by the voxel size. In order to conduct a comprehensive analysis of the anatomical composition of the brain, it is necessary to work with a continuous and coherent

3D mesh. This mesh should consist of compact volumes without overlaps or empty spaces (volumes not associated to any type). The understanding of the topological relations, such as adjacency and inclusion, is also crucial at this stage. This description corresponds to the partitioning of 3D space into volumes, with known neighborhood information (topology).

We propose a new modelling method that produces a precise model to represent and compute spectroscopic data, based on a reconstruction method offering a 3D topological mesh. The proposed method relies, at first, on a robust, topologically-consistent, volumetric mesh of a brain reconstructed from MRI images, producing a partition of 3D space. The 3D object is then iteratively cut by several planes to extract the part of the mesh included in each MRS voxel. One important point of the method is that it explicitly handles the inclusion of volumes during the cut phase. The new topological model is enhanced by spectroscopic data, and then used to better calculate and visualise the metabolic concentrations by exploiting information of each anatomical volume.

Standard Modelling Approach:

In this section, we introduce the current approach for visualizing the concentration of a metabolite in individual voxels within a well-defined grid in the brain. This grid is specifically localized to the region where the spectroscopic data acquisition took place. Practitioners use both segmented MRI images and MRS grid to visualize a specific metabolite concentration (Fig 1). However, the spectroscopic resolution is significantly less refined compared to the resolution used in MRI. As a comparison, the voxel size of a spectroscopic grid is typically $6.875x6.875x20mm^3$, compared with $0.89x0.89x0.9mm^3$ for segmented anatomical images (standard T3 scan).
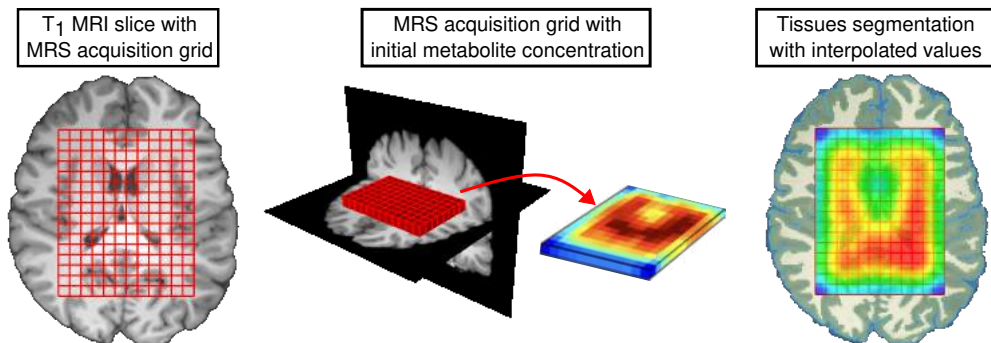

Fig. 1: Basic Visualization Method (from left to right): MRS grid [red colored] on a T1 MRI slice; 3D view of the acquisition grid into the brain and the concentration distribution inside it, from the higher concentration [red colored] to the lower concentration [dark blue colored]; linear interpolation on the estimated concentration values on a MRI slice segmented into three brain tissues: cerebrospinal fluid [blue colored], white matter [white colored] and gray matter [green colored].

Traditional interpolation methods found in typical processing tools rely on interpolation algorithms directly on the images without considering the composition of the brain (Fig 1). These algorithms overlook the heterogeneity within a volume composed of various tissues, potentially resulting in inaccuracies when quantifying metabolite concentrations in smaller voxels. It is possible to work only with a discrete model, but this implies oversampling the coarser grid in order to work with a resolution compatible with both grids. Nevertheless, additional considerations include the fact that MRI and MRS grids cannot be naturally superimposed, either because the MRS grid is not aligned with the MRI images, or because of the size of the voxels, one not being a multiple of the other.

Our new Modelling Method

The first step of the proposed method consists in producing a 3D model that corresponds to the anatomical images. For that purpose, a topological 3D reconstruction from the segmented MRI images of the brain tissues is performed [3]. The different reconstructed volumes are associated with the chosen topological model which formalizes the partitioning of space into cells (vertex, edges, faces, volumes) and their neighborhood relationships. This formalization allows the cells to be associated with semantic information, such as the tissue from which they come. The geometric, topological and semantic information of the model is used for a multi-criteria classification of the volumes to remove the volumes deemed as artifacts (typically, volumes generated by acquisition noise). Then, all the reconstructed segments are integrated in the same space, by linking the common faces of adjacent volumes. Thanks to topological properties, we correct locally all remaining inconsistencies and empty spaces, using PVE maps and anatomical constraints. Finally, coordinates of each vertex of the 3D mesh are slightly modified using PVE maps in order to deform the model to best match the acquired MRI data.

The 3D topological spectroscopic model we want to build corresponds to the corefinement of a reconstructed brain model by the MRS voxel grid. Given a soup of faces, the corefinement operation consists in reconstructing a set of volumes representing the fusion of input meshes [4]. Thus, from two meshes, the corefinement process generates a final mesh, without adding overlapping or empty spaces, by cutting the intersecting faces and edges of each input mesh. Since a grid is a particular mesh, built with infinite planes oriented along three perpendicular directions, it is possible to design a dedicated corefinement process relying on a single operation: the cutting of a mesh by a plane. This operation guarantees that cut volumes are closed, but faces an issue in case of nested volumes.

Fig. 2: Example of the cutting by plane operation for two different meshes, the results of which, at the right of each red arrow, are in topological view to observe the different volumes generated. On the right, Stanford bunny; on the left, a cerebral cortex, made up of several nested volumes (inclusion information are circled in red).

Our method is based on a topological and geometrical process that deals with volume inclusion (Fig 2) and preserves topological and semantic information. Once a cutting plane is defined, we compute its intersection with the edges of each face and generate *separation lines* representing face/plane intersections. In degenerated cases where the separation line coincides with the vertex of a face of the mesh, we consider that the latter is cut out a little before its vertex (using a very small epsilon). Indeed, the intersection calculation and, as a consequence the coordinates of the new points to be inserted are sensitive to numerical precision. Besides, two faces that share a common edge may not position the point of intersection at exactly the same position in space because of a very small offset. To avoid this problem, we rely on the model's adjacency relations, so that an intersection point on an edge of a face is computed only once and used again when an adjacent face is processed. After adding all intersection vertices, a separation line is inserted to split each intersected face. To avoid creating open volumes, a topological closure operation is called to create a face representing the footprint of the cutting plane for each cut

volume. To deal with inclusion information explicitly, we consider the newly-created face of the nested volume is included in the one of the container volume. We therefore only detect this face inclusion to introduce an inclusion information (as a topological link) between the volumes (Fig 2).

Application on Spectroscopic Data

Applied to the context of MRS, we have a 3D topologiwcal model that accurately represents the volumes contained in the study area of the MRS acquisition (Fig 3). We can now enhance the model by spectroscopic information. Since the plane cuts were used to separate the volumes to represent the grid voxels acquired by MRS, each reconstructed volume has the voxel identifier and the initial relative concentration of the metabolite. Also, for each volume in the final model, we know the nature of the associated anatomical tissue (semantics), the identifier of the spectropscopic voxel and the adjacent volumes (topological neighbourhood). Thus it encompasses all necessary information to compute and represent accurate metabolic concentration and dispatch it between every anatomical volume. To give a more precise example, the concentration of a metabolite present in a single tissue can be reinterpreted by the actual volume covered by the tissue and not the whole volume of the voxel, so the concentration obtained is higher. The molecular concentration is thus recalculated for each volumes based on mass conservation, the concentration of a given metabolite in each tissue related to its distribution rates, and the exact volume size, more details regarding these calculations can be found in [5]. The topological definition of volumes allows all computations to be performed locally, which greatly reduces the processing time. The study of metabolic concentration inside the brain using our 3D model is shown in Fig 4.
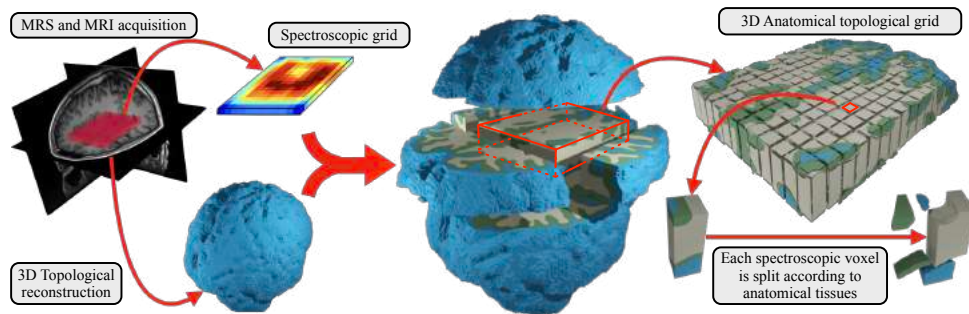

Fig. 3: 3D Anatomical topological construction matching the spectroscopy grid. Using the information of the spectroscopy grid and its voxels, the 3D brain model is split in accordance with the number of rows and columns of the initial grid. The resulting model is composed of identified volumes, from a specific spectroscopy voxel and brain tissue.

We tested our model on real spectroscopic data to show the variation in the concentration of a metabolite in each tissue on healthy patients. Within distinct volumes, a minor variation in metabolite concentration is noted for identical tissue types. This variation arises from the impact of both the tissue's inherent characteristics and its specific position within the brain on the concentration values [6] and our results correspond to the literature. In comparison, conventional methods yield a consistent concentration value throughout the entire depth of a voxel acquisition for a given 2D position, which does not give information about the impact of a tissue on the metabolism. By giving continuous volumes, we offer more details about the changes in metabolic concentration, mainly at the borders between the reconstructed tissues. Also, our model does not contain any ambiguous volumes by exploiting PVE maps, compared to voxel-based representation. By discretizing our model, we can produce 2D slices that display a metabolite concentration contain in each corresponding 3D volume. The resolution of the visualization can be chosen arbitrarily, thus giving higher definition at the boundaries between tissues.
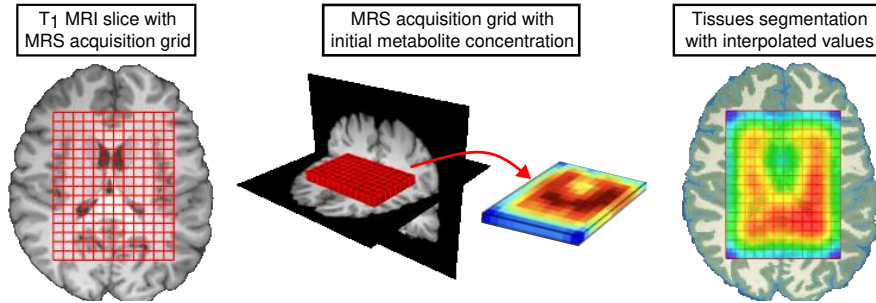
Fig. 4: Metabolites computation on the spectroscopy voxel grid: The concentration of a spectroscopy voxel is distributed in an anatomical voxel according to its tissue.

Conclusion:

In this work, we have proposed a new modeling method to produce a model that represent and visualize in a finer way spectroscopic data. Our method apply a specific corefinement process between the acquired MRS grid and the anatomical 3D mesh. Our model ensures that the geometry of the tissue covered by each voxel is well defined and topologically coherent. Using the well-identified volumes, distribution of a metabolite concentration takes into account the real nature of the underlying tissues based on distribution rates evaluated in clinical studies. Our 3D topological model is an adaptive tool to represent anatomical structures and their impact on the metabolism as close as possible to the real data.

Acknowledgement:

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