

Registration of a 3D mouse brain atlas with brain microstructure data

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Abstract

Exploring the Brain Forest, providing visualization support for the *Brain Tissue Scanner* [6], explores the topology and geometry of brain's architecture at two levels: its gross anatomy and microstructure. A three-dimensional atlas of mouse brain partitions the gross anatomical structures of brain by a finite element model. The finite element model, when registered with the microstructure data, serves to organize and index the microstructure data. We contend that such a finite element partitioning of the mouse brain data can provide a common coordinate framework for visualization and morphological modeling of neurons and can also serve as containers to grow synthetic neurons for anatomically-correct models of mouse brain.

1. Objectives

Our objectives are to

- build a finite element model (3D atlas) of a mouse brain gross anatomy,
- register this model with the brain microstructure data, and thereby
- organize and index the microstructure data.

2. Introduction

Exploring the Brain Forest, currently under development concurrently with the *Brain Tissue Scanner* [6], explores the topology and geometry of brain's architecture at two levels: microstructure and gross anatomy. At the microstructure level, the exoskeleton microstructure database [4] supports 3D reconstruction and modeling of neurons and cortical networks. At the gross anatomy level, we are building a finite element model of cortical areas and brain nuclei, that can also accommodate the gross description of connections of encapsulated fibers in nerve tracts and blood vasculature.

We build a hexahedral finite element model of a mouse brain that can organize and index the microstructure data. We partition the finite element model following the gross anatomical structures of brain. We contend that such a finite element partitioning of the 3-dimensional mouse brain model can provide a common coordinate framework for visualization and morphological modeling of neurons [1, 7], and can also serve as containers to grow the synthetic neurons. The global indexing and organization of the microstructure data at the gross anatomy level are possible because we assign each neuron to the finite element that houses its soma, and position each finite element within a 3D model of brain.

For rat and mouse brains, there are 2D brain atlases (e.g., Jacobowitz [3], Paxinos [13, 14], Swanson [17], the Mouse Brain Library [8]), some with more than 1000 individual structures listed. We will construct three-dimensional atlases, modeled from both the 2D structures and additional partitioning by hexahedral finite elements [1]. Solid three-dimensional modeling, based on neuroanatomical nomenclature, will facilitate later integration of our system with other anatomical, electrophysiological, and neurochemical database systems (e.g., NeuronDB [11], ORDB [12], XANAT [19]).

3. Methods

3.1 Collection of the volume data

The mouse brain is embedded in a brain blocker (13.125mm A-P x 10mm M-L x 6.25mm D-V). The *Brain Tissue Scanner* [6] concurrently sections and scans the brain tissue at 0.5 μ m thickness with 0.625mm effective knife width. For horizontal scanning, the volumetric data is obtained from scanning a total of 200,000 aligned sections.

3.2 Data acquisition from image sequence

The *Brain Tissue Scanner* [6] uses knife-edge scanning to generate aligned image stacks from mouse tissue. The effective knife width of 0.625mm represents the digitized portion of the field of view (FoV) of the objective, i.e., the diameter of the largest circular area that can be simultaneously viewed by the linear sensor array of a line-scan camera. For horizontal monochrome scanning, each section (13.125mm x 0.625mm x 0.5 μ m) line sampled at 250nm yields an image that is 52,500 line samples of 4,096 pixels (2,500 after binning)—for color, 2,048 pixels per line sample are used. Assuming one byte per pixel, each monochrome image then contains 0.215GB of data in the worst case. This data size is less than 2GB (the memory size on our servers), and therefore the data can be kept concurrently in memory for filtering and extraction of the regions of interest (ROIs). Moreover, when the strips are cut parallel to M-L or D-V axes, the data size contained in each image section decreases, and the data acquisition can be easily adapted.

3.3 Organization of the volume data

The volumetric data is organized as a collection of 3360 *big voxels* where each big voxel is cubic and 0.625mm x 0.625mm x 0.625mm in size. This collection of big voxels forms a block (13.125 mm x 10 mm x 6.25 mm) whose dimensions are identical to those of the brain blocker in which the mouse brain was embedded for scanning. Following the conventions employed by the National Library of Medicine's Visible Human Project [10], we can then visualize our volume data as serial coronal slices (perpendicular to the A-P axis) [5]. We can also assemble sagittal slices (perpendicular to the M-L axis) or horizontal slices (perpendicular to the D-V axis). The big voxels located at the outer boundaries of the block are treated as “dark” big voxels, i.e., as big voxels that contain no data but that facilitate storage and organization of the big voxels.

The FoV of the objective determines the big voxel dimensions of 0.625mm. Hence, when the volumetric data is obtained from confocal or two-photon microscopy, or from the BTS with a different effective knife width, the physical dimensions of the big voxel and the total number of big voxels would change depending on the objective.

3.4 Finite element partitioning and refinement

For the mouse brain that is embedded in a 13.125mm x 10mm x 6.25mm block, we initially decompose it into a collection of 168 hexahedrons where each hexahedron is 1.875mm x 1.875mm x 1.875mm in size. That is, each hexahedron is a collection of 27 big voxels as defined above. Each hexahedron is defined by 8 vertices and 56 additional control points that define the tricubic B-splines [2] representing the curved boundaries of the hexahedral finite element.

Our initial finite elements are equal sized. To accommodate the anatomical structures that are finer than our initial finite element size, we use an octree-based refinement algorithm that is an extension of the grid based algorithm [16]. The octree is a well-known tool for organizing spatial data with applications in solid modeling, mesh generation and various other fields [18]. We use a modified octree concept [15, 18] where we start with a hexahedron from the initial decomposition above. The hexahedron is then split up into 27 sub-hexahedrons (octants) which are refined recursively until the sizes of all octants fall below a predefined threshold that is set by the size of the smallest anatomical structure to be represented. In the standard octree decomposition method, an octant is split up into 8 sub-octants. We choose the “27-tree” method

[15] because the control points for the refined tricubic B-splines and their data storage can be derived more easily from this structure.

3.5 Registration of the finite element model with the microstructure data

A solid model of brain cortical areas and nuclei is reconstructed from the contours extracted from the image scans, where the image scans can be oriented perpendicular to any of the three axes. The reconstructed microstructure data is then organized and indexed by the 3D finite element model. By superimposing our finite element model over the mesh of big voxels, we register the microstructure data with our finite element model. We use the open source toolkit, Insight Toolkit (ITK) [9], being developed for the segmentation and registration of data sets from the Visible Human Project [10].

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