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Architectonics-informed partition of the cortex at sub-millimetre resolution

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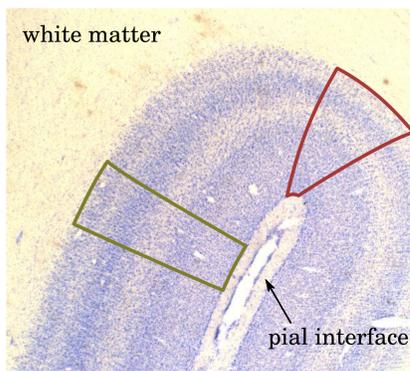
#3560 (OHBM 2014, Hamburg, 11. June 2014)

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Overview

We propose a method to partition the cortex into cortical traverses, in the geometry of the original image. Two properties make this a good basis for studying cortical lamination:

- each region contains samples from the whole cortical thickness;
- each voxel appears in one, and only one traverse.



Context

Magnetic resonance imaging at 7 T and beyond enables imaging the full cortex at resolutions below 0.5 mm isotropic, allowing the study of intra-cortical features such as lamination. In order to describe and analyse these features, the cortex needs to be described in ways that respect its local geometry across its whole thickness. One prominent aspect of the cortical micro-structure is its organization in cellular columns that are visible on histological images.

Cortical columns and layers are visible on this Nissl-stained histological slice of a baboon brain (courtesy of Thierry Delzescaux)

1 Preparing the data



Starting point of the method: **voxel-wise segmentation** in grey, white, and CSF compartments.

Built from the image below using an adapted Morphologist segmentation pipeline [www.brainvisa.info].



Test data set:

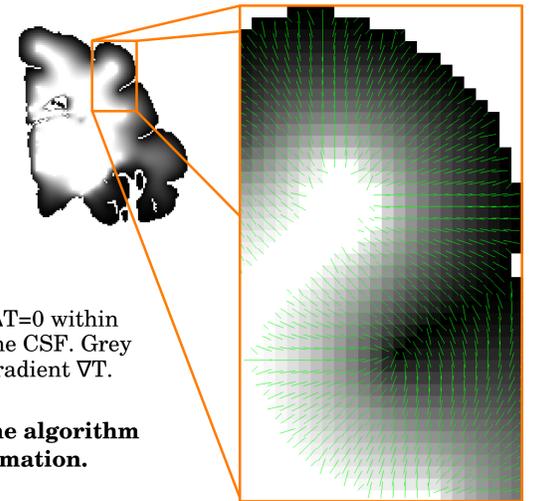
- post-mortem ferret brain
- 7 T small animal scanner
- quantitative T2 map
- 0.12 mm isotropic resolution
- whole brain 3D image

2 Modelling cortical columns

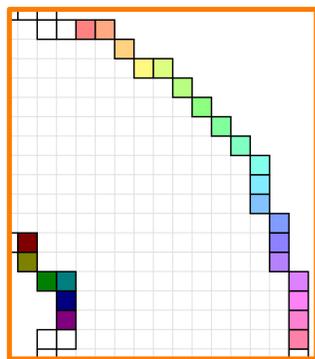
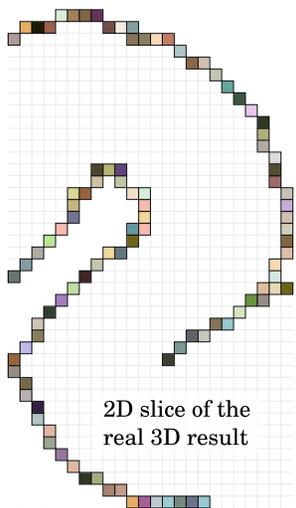
Cortical columns cannot be directly imaged with MRI. Previous evidence [Schleicher et al. 2005] suggests that the direction of cortical columns is well represented by the gradient of a Laplacian field, as introduced by [Jones et al. 2000].

The Laplacian field is defined by solving the Laplace equation $\Delta T=0$ within grey matter, by imposing $T=1$ in the white matter and $T=0$ in the CSF. Grey levels represent T , green arrows represent the direction of its gradient ∇T .

The results are shown on a single slice, but all steps of the algorithm work on volume images to utilize full 3D geometric information.

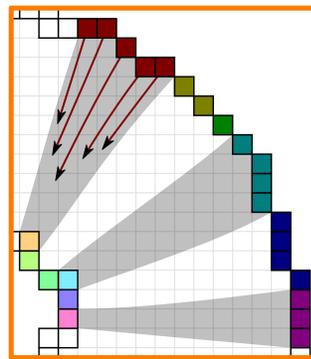


3 Labelling the interfaces



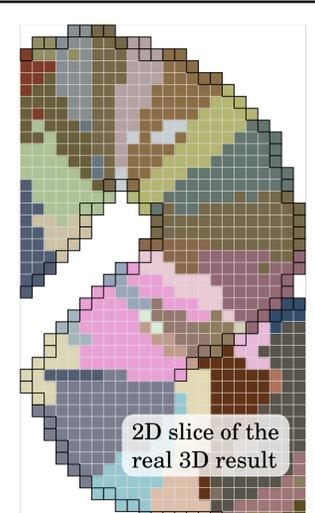
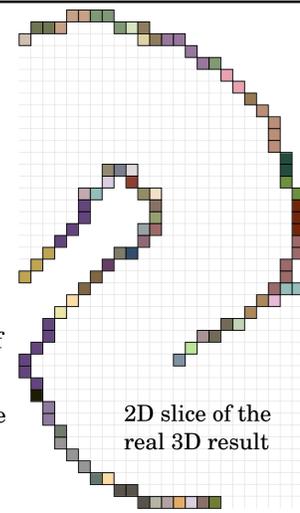
Each voxel of the grey-white and grey-CSF interfaces is assigned a unique label.

4 Grouping interface voxels



Each interface voxel is advected towards the other interface along ∇T towards the grey-white boundary. The label of the voxel reached is assigned to the voxel at the origin of the advection.

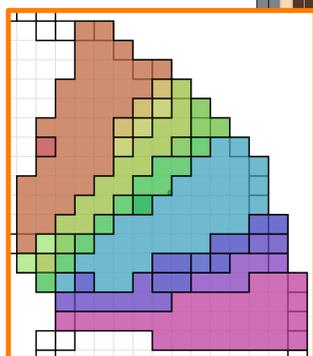
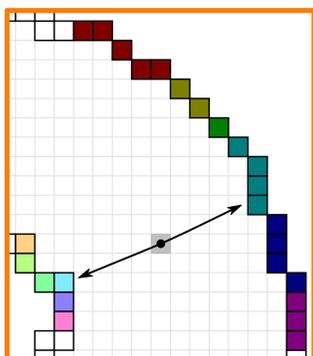
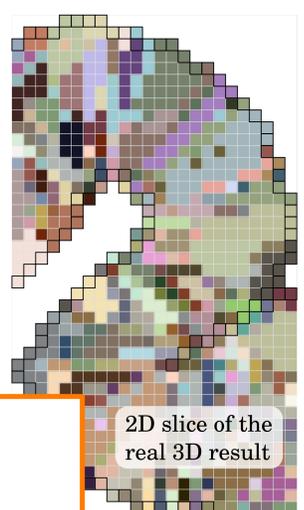
As a result, interface voxels are grouped at the exterior of curved regions.



5 Grouping cortical voxels

Each cortical voxel is advected towards both interfaces along ∇T . The labels at the end of these paths form a pair $(L_{\text{white}}, L_{\text{pial}})$. Cortical voxels associated with a same pair of labels are grouped together.

The resulting regions are aligned along the Laplacian field, but many of them are too small and do not traverse the whole cortical thickness.

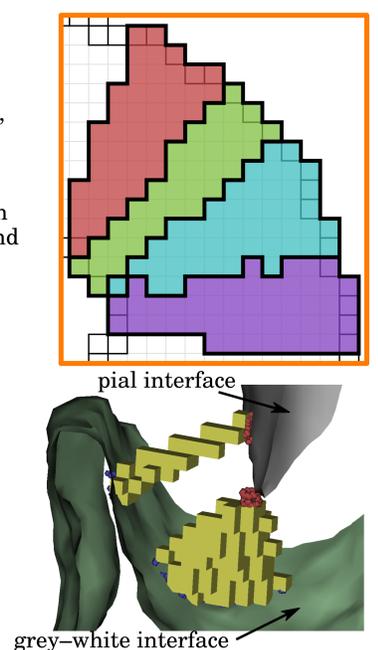
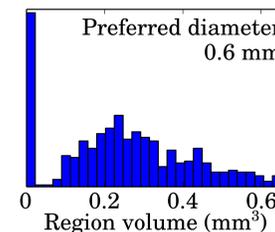
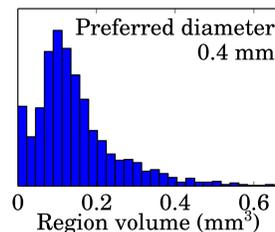


6 Merging regions

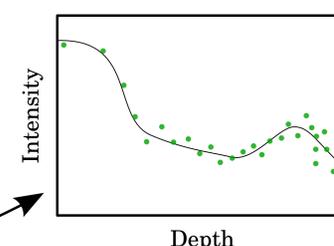
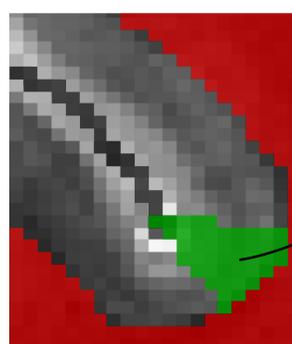
The regions are aggregated using an iterative merging algorithm, in order to reduce "over-parcellation" and obtain regions of a defined, configurable size.

The merging is based on the quality factor Q of the regions, which is defined as $V / (S_{\text{pial}} + S_{\text{white}})$, with V the volume of the region, and S_x the approximate surface projection of the region onto each interface, estimated by fitting an ellipsoid to the ends of the advection paths.

Resulting regions are dense and traverse the whole cortical thickness.



Perspective: cortical lamination analysis



Each region created by this method, when associated with a voxel-wise measurement of depth, can be used to characterize the evolution of signal intensity along cortical thickness.

This yields lamination profiles that reflect the local cytoarchitecture of the cortex.

The regions could be used as building blocks of a cortical parcellation based on the extracted cytoarchitectural data.