

Histology-Based Average Template of the Marmoset Cortex With Probabilistic Localization of Cytoarchitectural Areas

Piotr Majka, Sylwia Bednarek, Jonathan M. Chan, Natalia Jermakow, Cirong Liu, Gabriela Saworska, Katrina H. Worthy,
Afonso C. Silva, Daniel K. Wójcik, Marcello G.P. Rosa

Accessing the Nencki-Monash template files with ITK-SNAP

The following short tutorial demonstrates how to download and view the Nencki-Monash template package using the ITK-SNAP software. For detailed tutorials on ITK-SNAP, please consult the ITK-SNAP documentation (<http://www.itksnap.org/pmwiki/pmwiki.php?n=Documentation.SNAP3>)

Step 1: Download the template package: Please visit the Nencki-Monash template supplementary material website (http://www.marmosetbrain.org/nencki_monash_template) and download the 1) *The main data layers of the Nencki-Monash template*, and 2) *Probability maps for 116 cytoarchitectural areas* datasets. Alternatively, you can use the following links:

- 1) http://www.marmosetbrain.org/static/materials/Nencki_Monash_main_template_files.zip
- 2) http://www.marmosetbrain.org/static/materials/Nencki_Monash_probability_maps.zip

Step 2: If you don't have ITK-SNAP installed yet, we recommend you install the latest version (available for Linux, Windows, and MacOS) from: <http://www.itksnap.org/pmwiki/pmwiki.php?n=Downloads.SNAP3>.

Step 3: Run ITK-SNAP

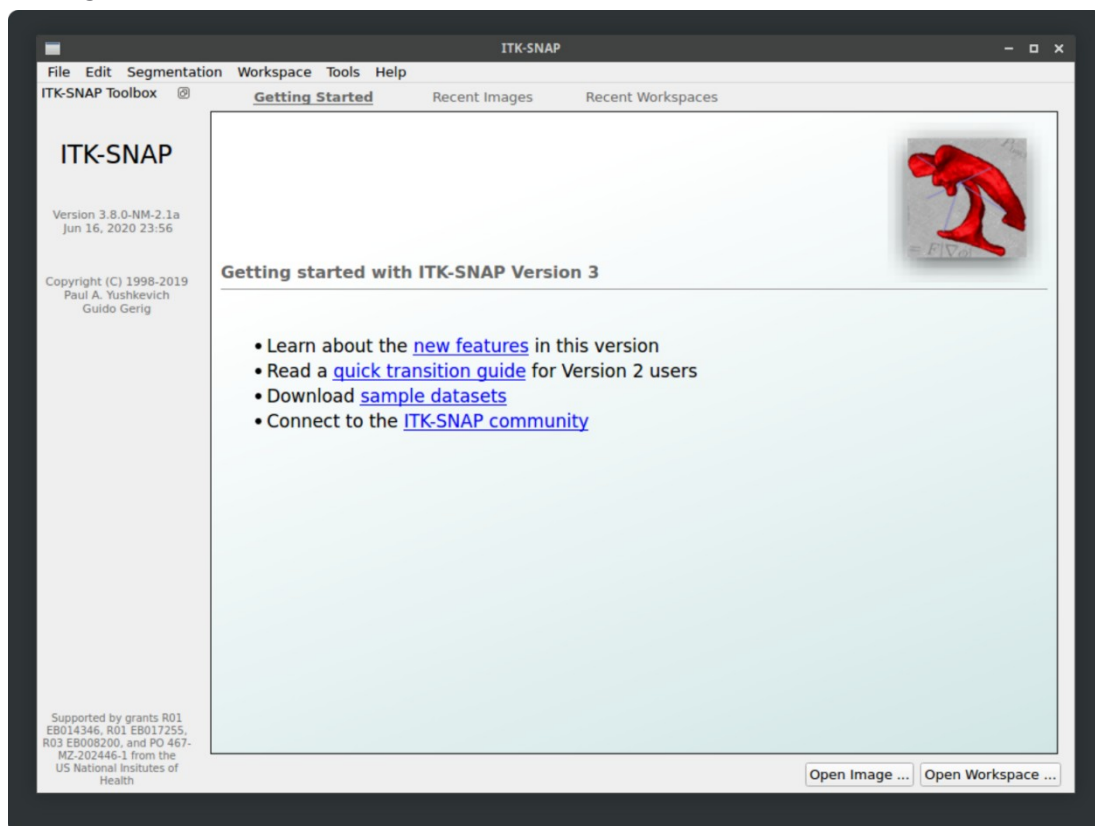


Fig. 1: Empty view of ITK-SNAP on first run.

Step 4: Open the Nencki-Monash template (`average_nissl.nii.gz`) for viewing:

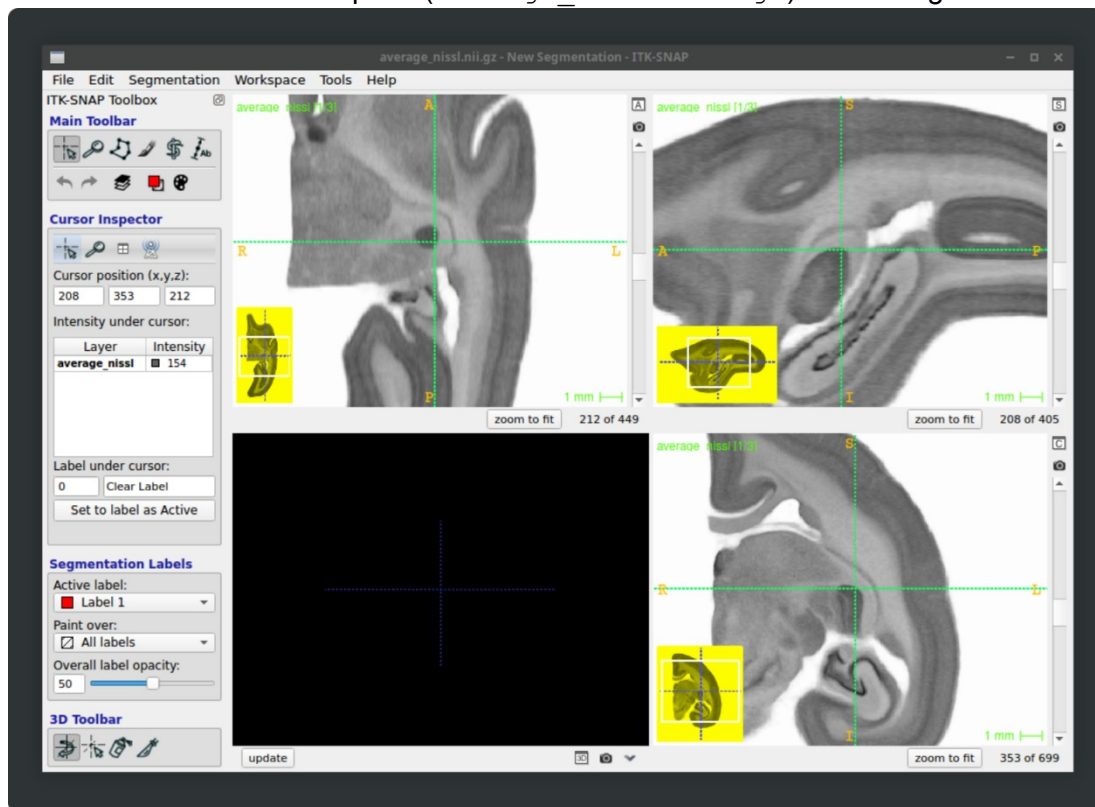


Fig. 2: Drag and drop the `average_nissl.nii.gz` file into the view area to open it, or press `Ctrl+G` to browse for the file in your system.

Step 5: You can change the display to RGB (color) mode:

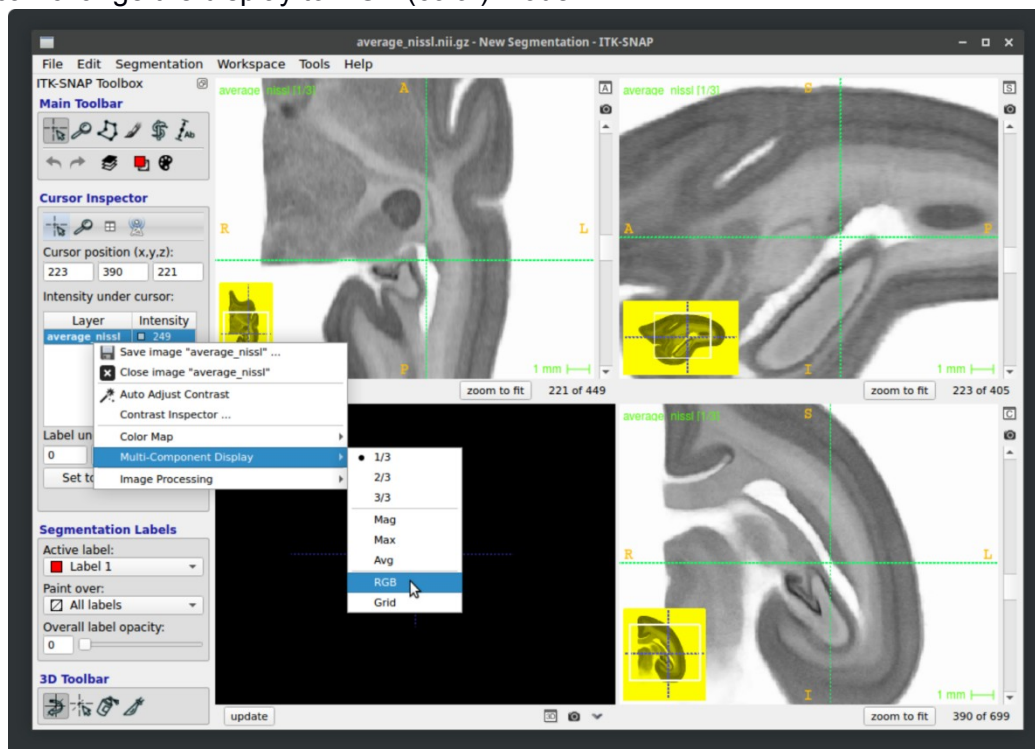


Fig. 3: Right click on `average_nissl` layer and change the Multi-Component Display to RGB.

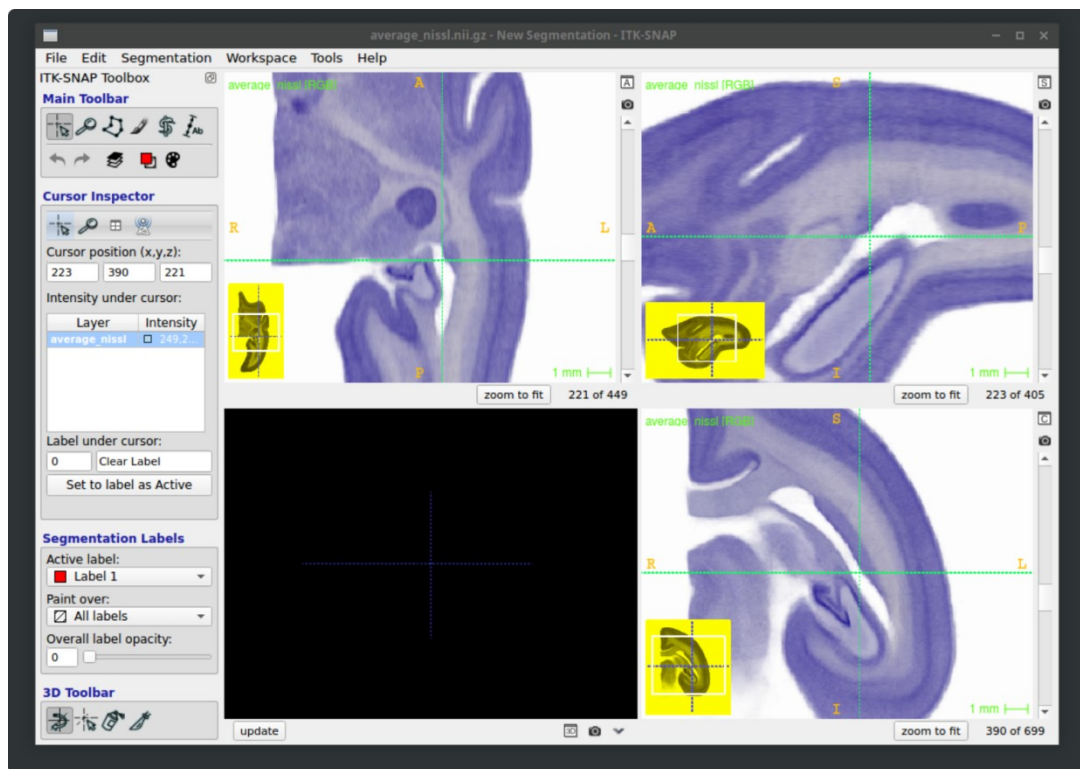


Fig. 4: RGB view of the Nencki-Monash template.

Step 6: Load the maximum probability segmentation of the cerebral cortex:

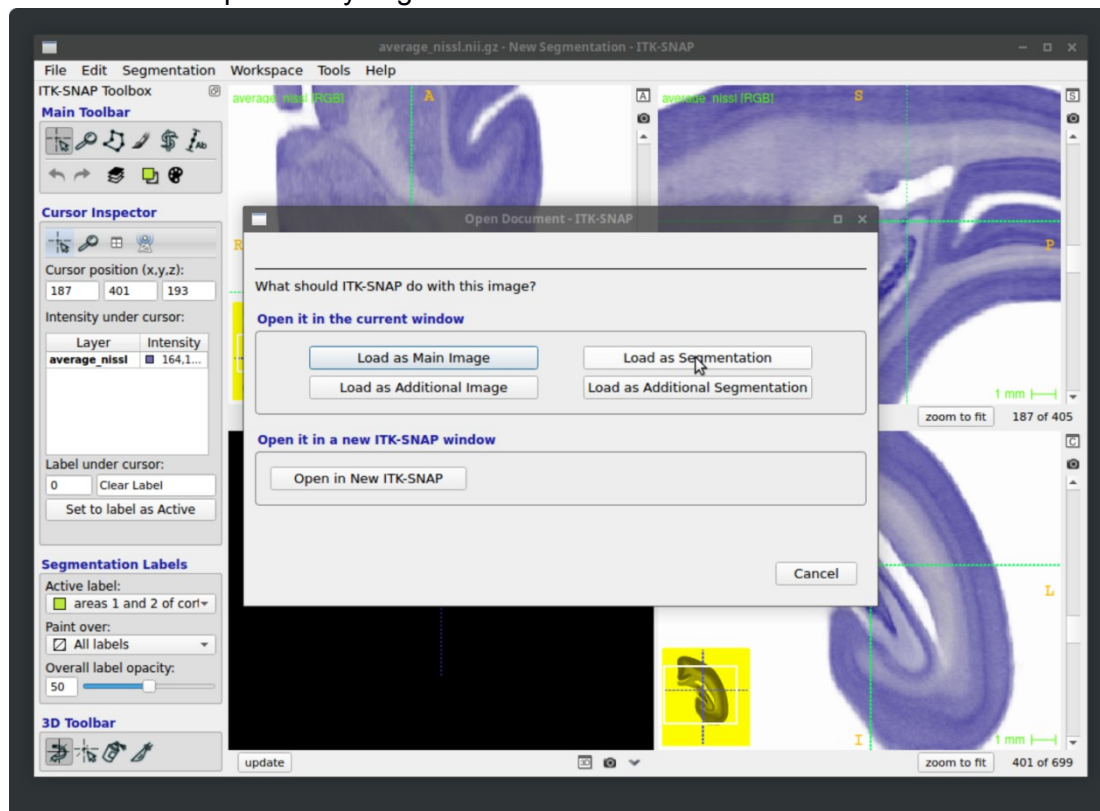


Fig. 5: Drag and drop the `maximum_probability_segmentation_streamlines.nii.gz` file into the view area and select **Load as segmentation** in the pop-up menu.

Step 7: Import Atlas labels:

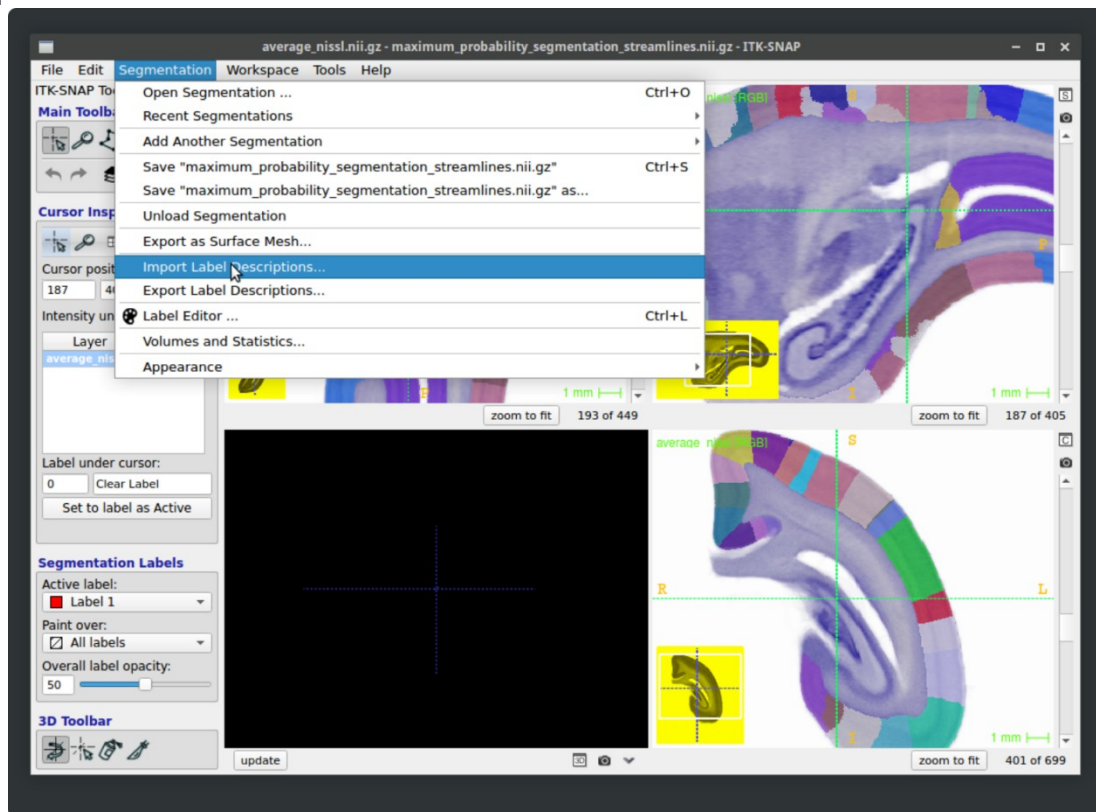


Fig. 6: Select *Import Label Descriptions* from the *Segmentation* menu, and browse for the atlas_labels.txt file.

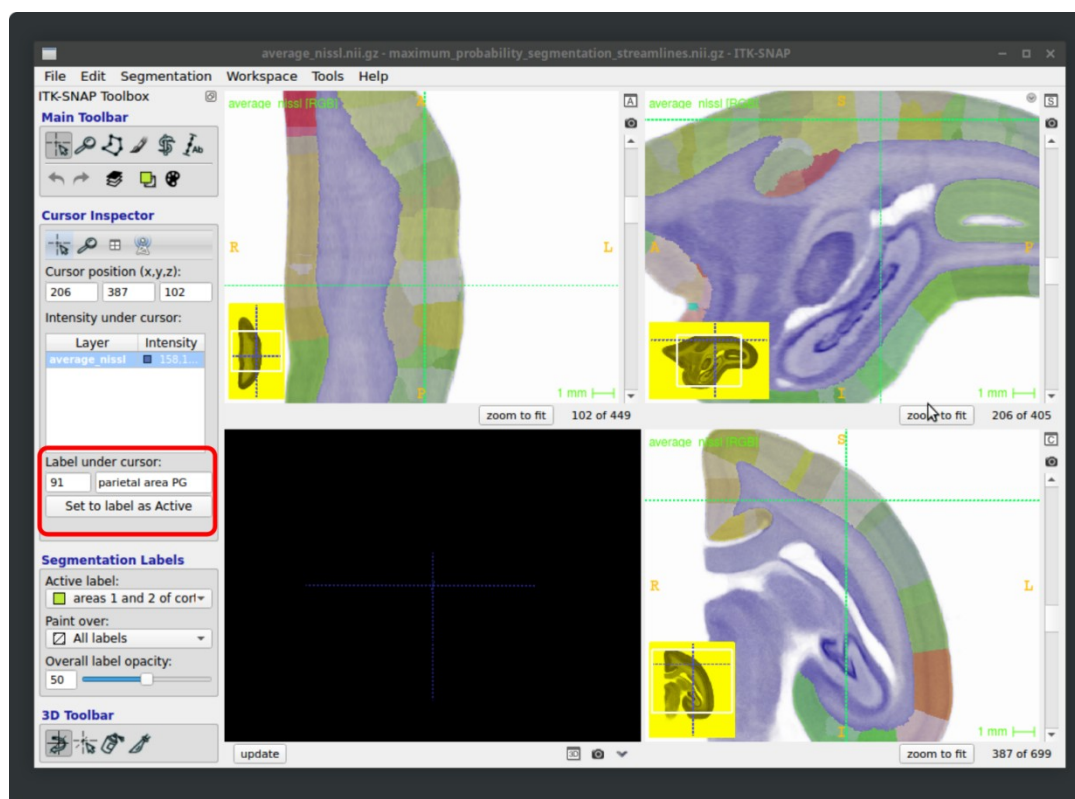


Fig. 7: After loading the label descriptions, label ID and description for the area under cursor will be displayed in the left panel of the ITK-SNAP window (highlighted in red).

Segmentation confidence level map

To view the segmentation confidence level map side by side with the Nencki-Monash template, open the `average_nissl.nii.gz` in ITK-SNAP as the main image, and drag and drop the `segmentation_confidence_streamlines.nii.gz` file, selecting **Load as Additional Image** option from the pop-up menu. You can also load the segmentation as previously, and display the confidence level map as an overlay (right-click on **segmentation_confidence_streamlines** and select **display as overlay**). The color map can be adjusted in **Color Map Inspector Window**. The value of the confidence level under the cursor appears in the **Cursor Inspector** panel as intensity value for the **segmentation_confidence_streamlines** layer (marked with a red box in Fig. 8).

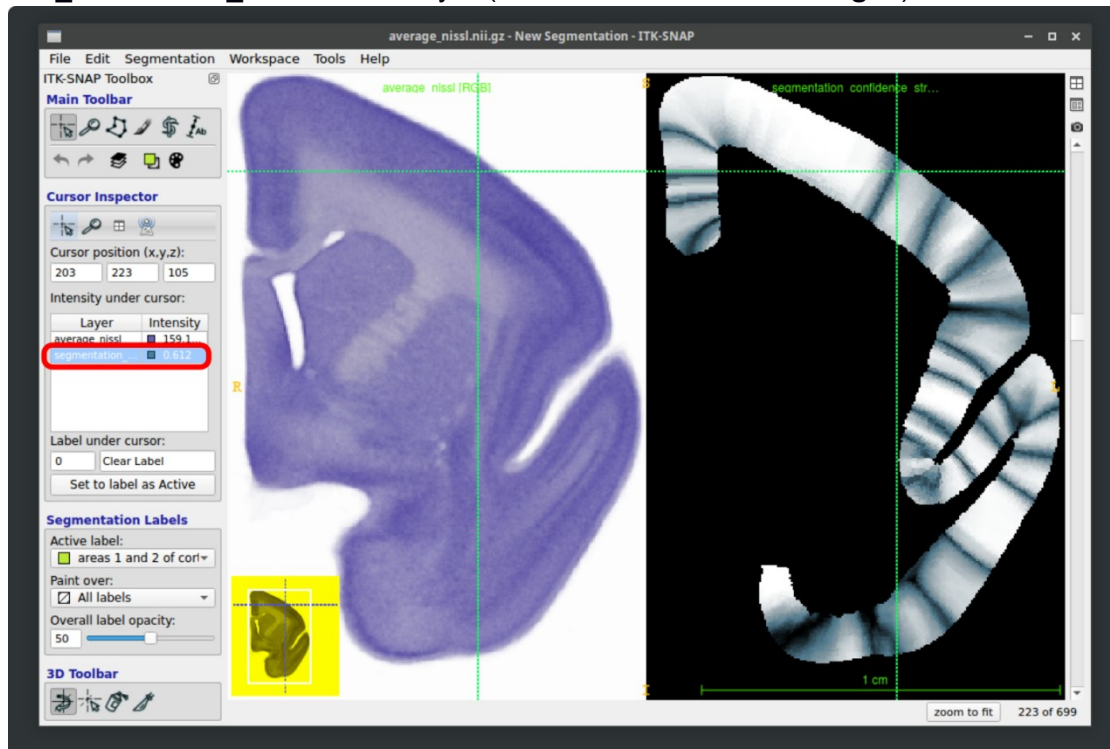


Fig. 8: Synchronized view of the Nencki-Monash template and confidence level map for cortical segmentation.

Probability maps for boundaries of cortical areas

When viewing multiple images, segmentation will be overlaid over all of them. Additionally, an interactive 3D model of the segmentation can be generated (**Update** button in the left lower quadrant of the ITK-SNAP window), as shown in Fig. 9.

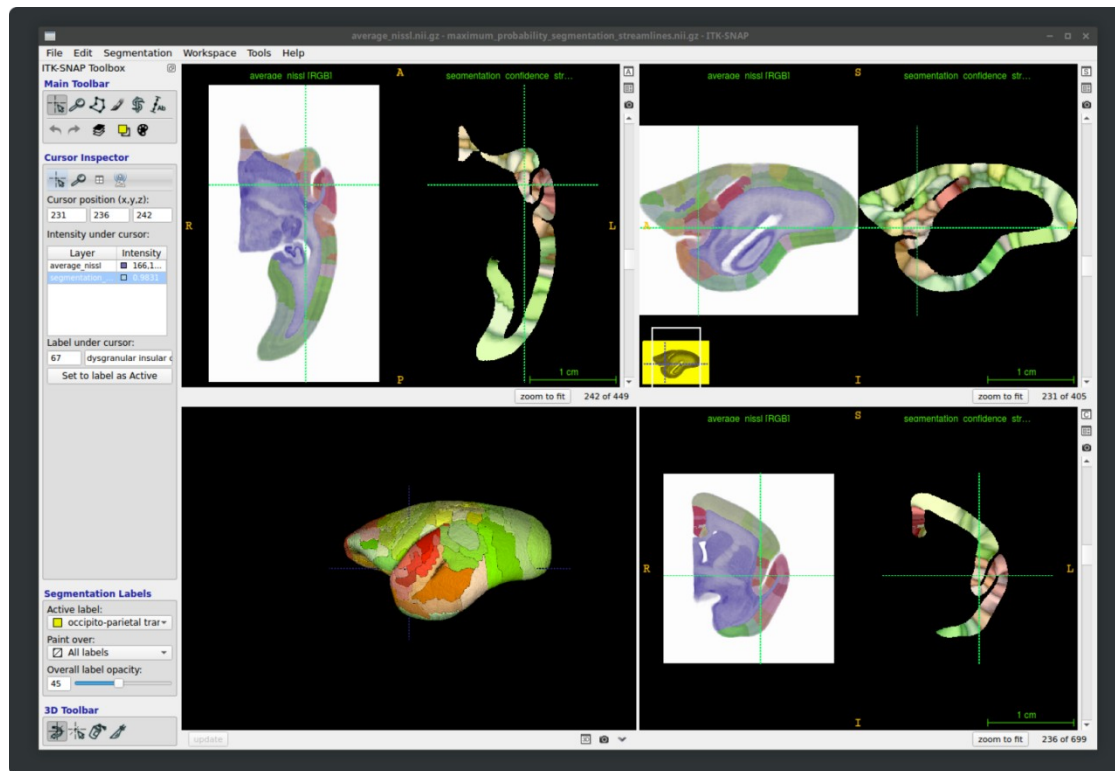


Fig. 9: A view of the Nencki-Monash template cross-sections in the three cardinal directions, with the segmentation overlay and concurrent view of segmentation confidence map. A 3D model of cortical parcellation is also displayed (bottom left panel).

As another exercise, open the Nencki-Monash template and add probability maps for areas A3b, LIP, A4ab and MT in ITK-SNAP as additional images. Right-click on each probability map layer and select **Display as Overlay**. After adjusting color map for each area, you can obtain results similar to those presented in **Fig. 10** and inspect values of probability maps across the brain.

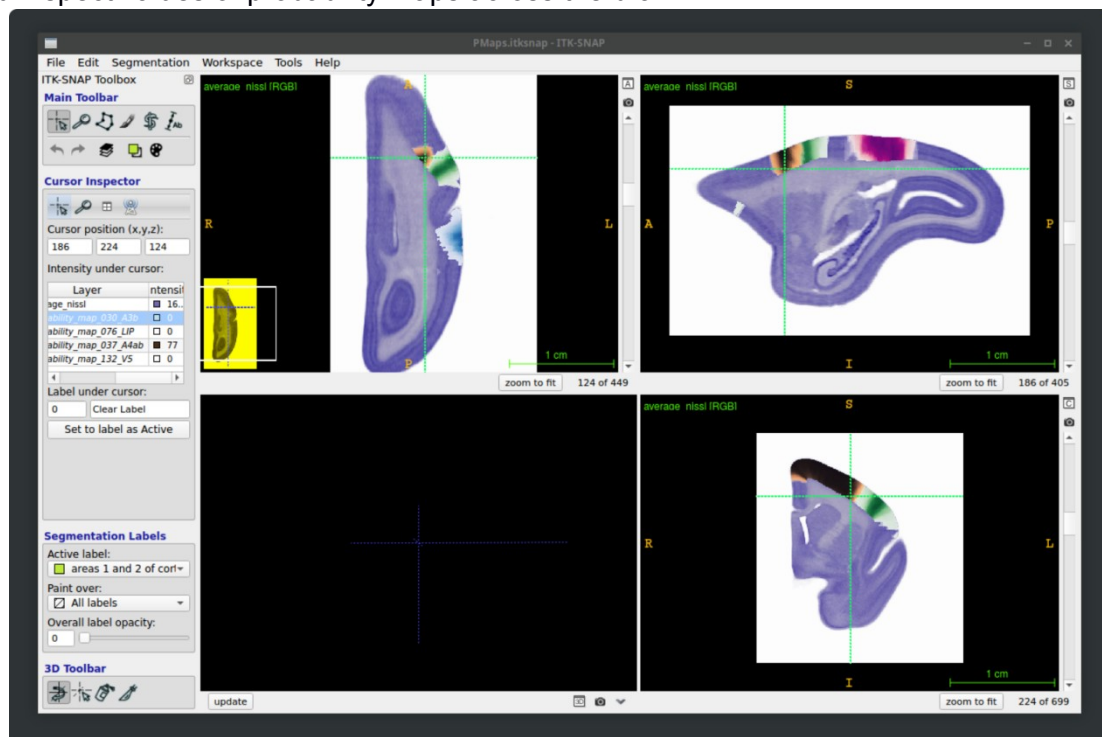


Fig. 10: Probability maps for regions **A3b**, **LIP**, **A4ab**, and **MT (V5)** displayed on top of the Nencki-Monash template.

Cortical thickness map

The cortical thickness maps can be accessed in a similar way: Open the Nencki-Monash template and the `full_thickness.nii.gz` file. The value representing the cortical thickness under the cursor (in mm) appears in the **Cursor Inspector** panel as **Intensity** value for layer **full_thickness**. Then, open the `thickness.nii.gz` file to display relative depth (in mm) below the pial surface. The intensity value for the **thickness** layer corresponds to the distance between the outer (pial) and inner (white matter border) perimeters of the cortex for a given point under the cursor. ITK-SNAP allows for concurrent viewing of multiple image files, which can be used to display several data layers simultaneously. All images are located in the same physical coordinate space ensuring synchronized data exploration. Note that separate instances (windows) of ITK-SNAP also support spatial synchronization by default.

Fig. 11 shows simultaneous view of the Nencki-Monash template, and three cortical maps: cortical thickness, distance from the pial surface, and the normalized thickness. The latter represents a fraction of thickness (the distance from pial surface) divided by full thickness ($\text{thickness} / \text{full_thickness}$).

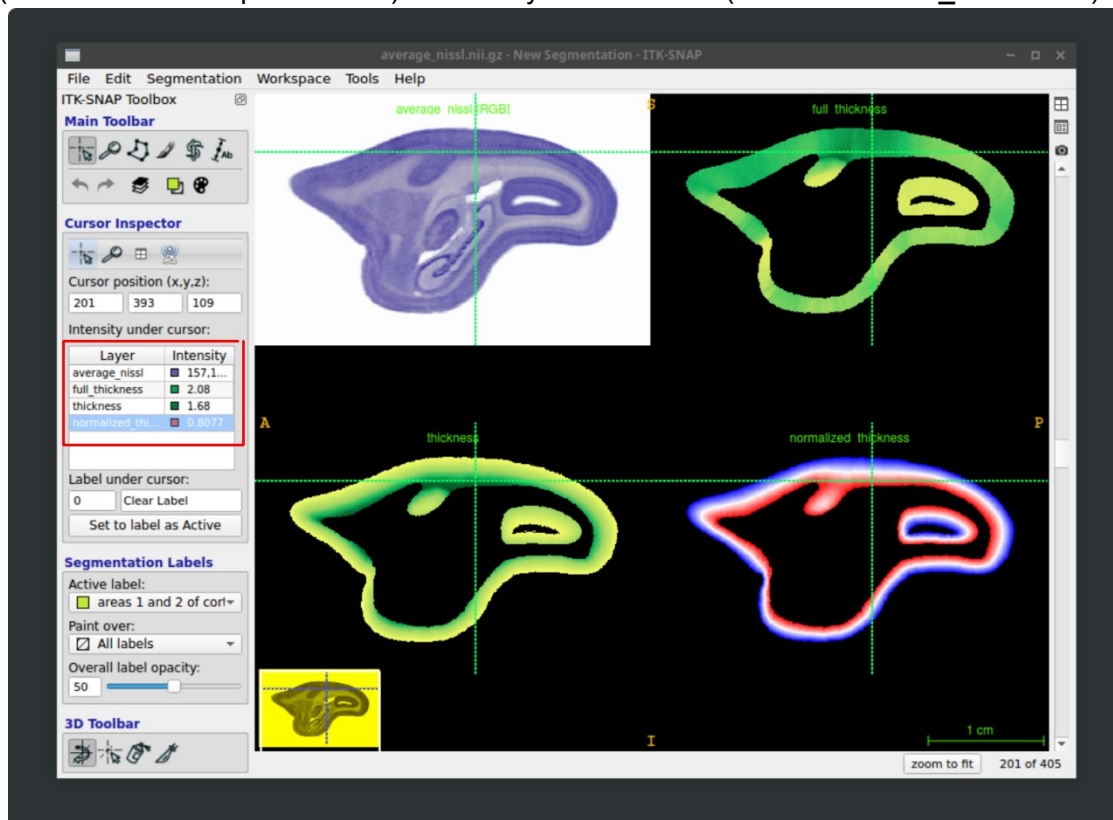


Fig. 11: Parasagittal view of the Nencki-Monash template and three data layers: cortical thickness map (**full_thickness**), distance from the pial surface (**thickness**), and normalized thickness (**normalized_thickness**) map.