

Homology Viewer User Manual

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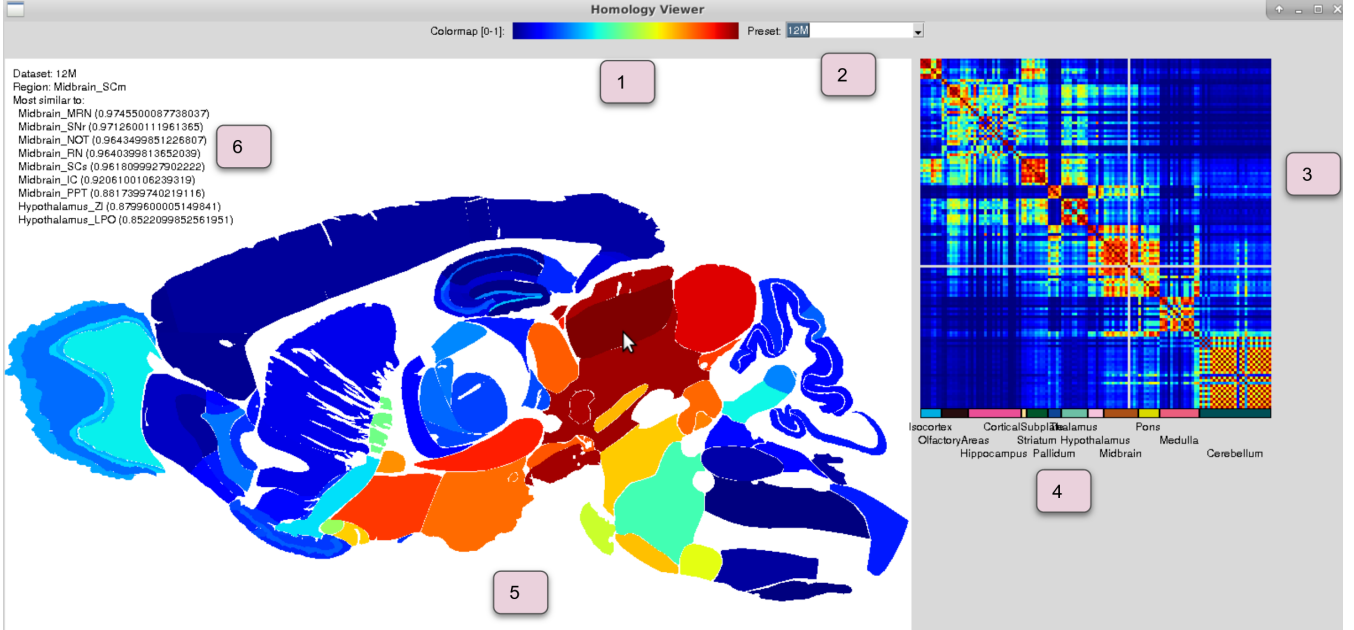


Figure 1: Visualizing the similarities between subregions. Labels mark points of interest, explained in section 1.1.

1 Introduction

Homology Viewer is a tool that enables interactive visualization of similarity matrices whose values correspond to brain regions/subregions, puts the data in a spatial context and allows simultaneous visualization of different brain section data that are delineated similarly. Users can hover over a brain region or a similarity matrix entry and immediately see how that region is similar to all other regions using a heatmap. Likewise, when using multiple brain regions, users can visualize how a hovered-over region in a brain section is similar to all other regions in all other brain sections. Thus, the tool makes the results of similarity matrices visually accessible owing to the direct mapping of the data on the brain section(s).

1.1 User interface

Figure 1 shows a typical screenshot from the script. Below are the descriptions for each of the numbered labels:

1. Color map used for image and matrix.
2. Preset selection dropdown in default execution mode (without providing arguments)
3. Homology matrix visualization. Rows/columns correspond to subregions, organized by regions (isocortex, olfactory areas, etc). If the cursor is over a region, the corresponding row/column is highlighted in the matrix
4. Each region has a specific color code, used for all columns that correspond to its subregions. The region name is centered under the colored rectangles
5. Section visualization. By hovering the mouse over a region, the image and matrix are colored based on the similarity values of the hovered-over region compared to all others, thus providing a spatial context for the homology matrix values.
6. When hovering over a region, the name of the dataset is displayed, in addition to the hovered over subregion and a list of most similar subregions and their corresponding similarity values.

1.2 Usage

By executing the script “homology_viewer.py”, a number of default configurations is loaded, that can be selected via a dropdown. the entries correspond to all 10 datasets, a comparison of all datasets using matrices only and a comparison of all datasets using images only.

The alternative execution mode of the script is by using command line arguments. “-help” shows usage information. Users can specify the datasets to be compared and if the image view, matrix view, or both, should be shown per dataset, for example:

- **homology_viewer.py -i -d 1W 2W 3W** Compares datasets for weeks 1, 2 and 3, showing section images only (no matrix)
- **homology_viewer.py -m -d 3W 1M** Compares datasets for 3 weeks and 1 month, showing matrices only (no section images)
- **homology_viewer.py -d 1M 2M** Compares datasets for months 1 and 2, showing both section images and matrices

1.3 Requirements

- Any modern CPU, e.g. Intel i5 processor
- Python 3 installation with the following libraries: tkinter, PIL, numpy, matplotlib

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