Synaptome Explorer v2.0 User Manual

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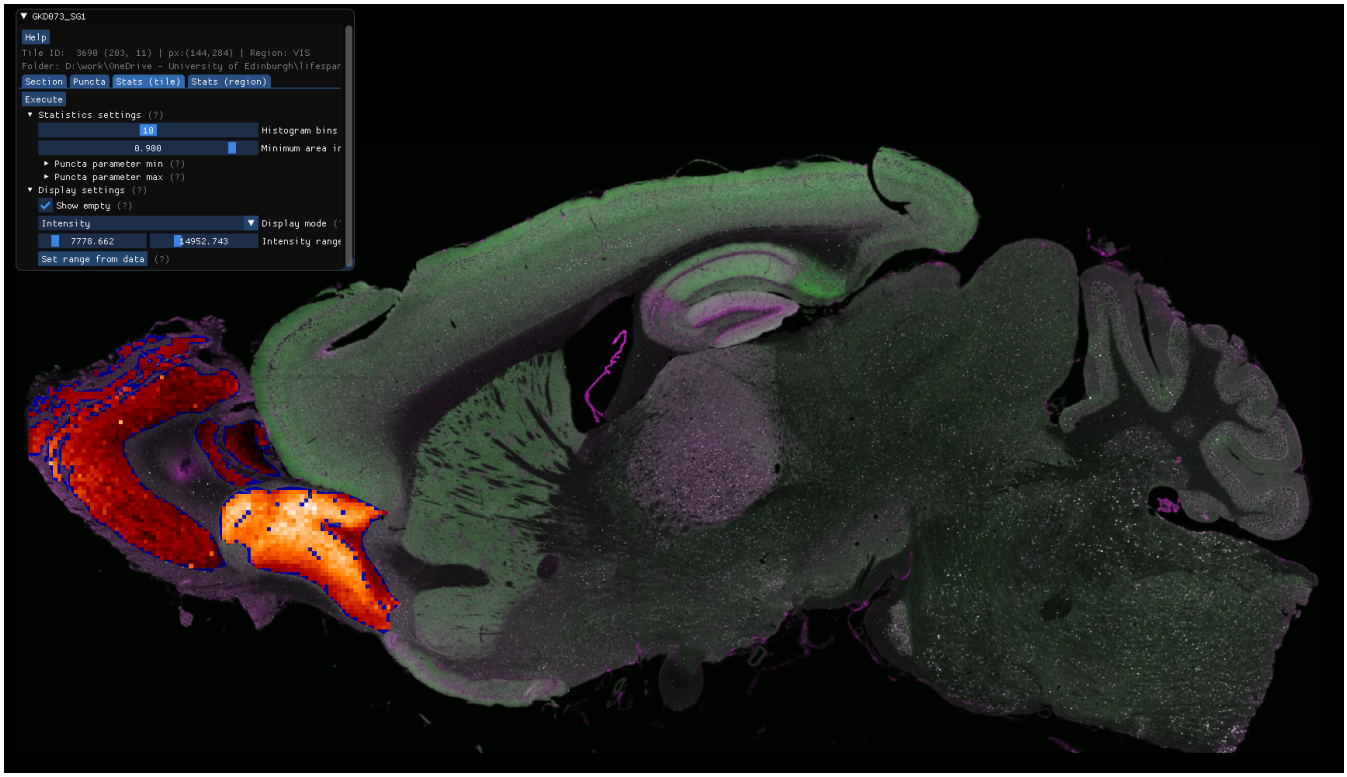

Figure 1: View of the synaptome, visualizing a heatmap of mean intensities in the olfactory areas.

1 Introduction

Synaptome Explorer is a viewer of mouse synaptome data from whole brain scale down to single synapse level, for a single section. It enables seamless interactive viewing of the original microscope-captured images and provides facilities for visualizing individual detected puncta and their properties, such as shape, size, intensity, protein type and subtypes. Additionally, provision of delineated region maps allows users to see and easily navigate to regions of interest.

This version of Synaptome Explorer (2.0) allows additional control over the displayed puncta (filtering via setting parameter ranges for each of the properties), selection and visualization of properties of individual puncta, and calculation of statistical properties of filtered puncta in selected regions. Finally, it allows visualization of the raw microscope data at its full resolution.

1.1 Basic usage

Run the application by dragging and dropping a configuration file on the executable. Configuration files are included in the datasets.

1.2 Requirements

- Any modern CPU, e.g. Intel i5 processor
- At least 4GB of RAM

- A graphics card supporting at least OpenGL 4.5

If the machine doesn't satisfy the requirements, the application will automatically exit soon after it has started.

1.3 Datasets

Sample datasets are provided in the zip file at the following url: [coming soon]

Each dataset represents a single section from a particular age point:

- PUP109_SG3 : 1D
- PUP145_SG2 : 1W
- PUP011_SG2 : 2W
- PUP068_SG3 : 3W
- PUP039_SG1 : 1M
- PUP058_SG3 : 2M
- GKD348_SG1 : 3M
- GKD180_SG2 : 6M
- GKD139_SG2 : 12M
- GKD173_SG1 : 18M

2 Use-case scenarios

Here, a few scenarios are outlined, demonstrating common use cases. All of the scenarios can be completed by using the mouse and interacting with GUI controls from the "Options" window.

Load dataset for section 0048

Press the "Load dataset folder" button. Then locate the folder named "0048" in the dataset folder tree, click on it and press ok. Loading section data is a data-intensive operation, and it needs several seconds to complete, depending on the performance of the hard drive of the machine that runs the software.

Find the area CA1so

First select the tab "Section". This will show a number of GUI elements. On the line that starts with "Highlight region:", click the "Selected" radio button. A tree-like GUI control will appear. Navigate through the tree by expanding nodes, to find CA1so. The exact location is in "HippocampalFormation", then CA1so. Select the node so that it is highlighted. Press the button "Jump to selected region(s)" below the hierarchy. This automatically moves the camera so that CA1so fits into view.

Alternatively, use panning-and-zooming to manually navigate to the desired location. Left-click and drag the mouse to pan, and use the scroll wheel to zoom.

To disable the highlighting, select "None" in the "Highlight region" radio buttons.

Show PSD95 only puncta in CA1so

Find the "HippocampalFormation" area as described above. Then select the tab "Puncta", to change options page. Enable "Show puncta". At this point, the individual puncta should also display on top of the section image. To enhance the visualization of the puncta, we need to turn off the section image. To do that, we need to go back to tab "Section" and uncheck "Show section", which is the first option. This will disable the background image. Back in the "Puncta" tab, to enhance the visualization, we can select the "Protein" tab and adjust sliders to the desired range. Finally, to disable SAP102 so that we can only see PSD95, in the "Toggle protein(s)" group uncheck SAP102.

Show Colocalized subtypes in "CA1so"

First locate the area as described above. Similar to the puncta visualization, select the "Puncta" tab. Now, select the "Subtype" tab. This will automatically disable the background section image to allow clarity in the visualization of the different subtype colors. At the "Toggle subtype(s)" GUI control a list of checkboxes appears, one per subtype. Above the checkboxes there are 4 buttons, labeled "All", "PSD95", "SAP102" and "Colocalized". Press the "All" button once to toggle all subtypes off. Press the "Colocalized" button once to toggle all colocalized subtypes on. These buttons switch the on-off state of all associated subtypes, acting as a shortcut to manually checking and unchecking a multitude of subtypes.

Show only puncta of subtype 32 with mean intensities between 10000 and 20000

First, enable puncta as described above. Select the "Puncta" tab and expand "Puncta min" and "Puncta max". In "Puncta min", reset to defaults by pressing button "Defaults (Global)", move the intensity slider to 10000 and the subtype slider to 32. Similartly, in "Puncta max" press the button "Defaults (Global)", move the intensity slider to 20000 and the subtype slider to 32.

Visualize unsupervised map of densities in the Hippocampus

In the "Section" tab, select area "HippocampalFormation" as described above. In the "Stats (tile)" tab, click "Execute" and then select "Density" from the display mode. Finally, click on "Set range from data" for clearer visualization.

Visualize supervised map of intensities in the entire brain

In the "Section" tab, select all areas by CTRL+click on every region. Select "Stats (region)" tab and ensure that granularity level is 1, and click "Execute". Since the query will use all data from the entire brain, the process will take several seconds to complete. Click on "Set range from data" for clearer visualization.

3 User interface manual

The user interface is comprised of 2 elements: the *main window* and the *options window*.

3.1 Main window

The main window shows the stitched section image, at 1/16th of the original resolution. Users can optionally display user-defined delineated regions and calculated puncta overlaid on the section image.

3.1.1 Navigation

- **Panning:** Hold the left mouse button and drag the mouse to pan the image towards the direction of the mouse cursor. ¡br¿
- **Zooming:** Roll the mouse wheel to zoom in and out.

3.2 Options window

The options window displays all options that can be used to modify visualizations in the main window. All controls are followed by "(?)", where if hovered, a tooltip will display information about use. Small buttons provide equivalent tooltips when hovered. A "Help" button shown in the top of the options window will display general help for using the application.

License

Software and data used

- **SDL2**: `https://www.libsdl.org/`
- **GLEW**: `http://glew.sourceforge.net/`
- **Dear ImGui**: `https://github.com/ocornut/imgui/`

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