

# Synaptome Explorer v1.0 User Manual

University of Edinburgh, Centre for Clinical Brain Sciences

June 21, 2018

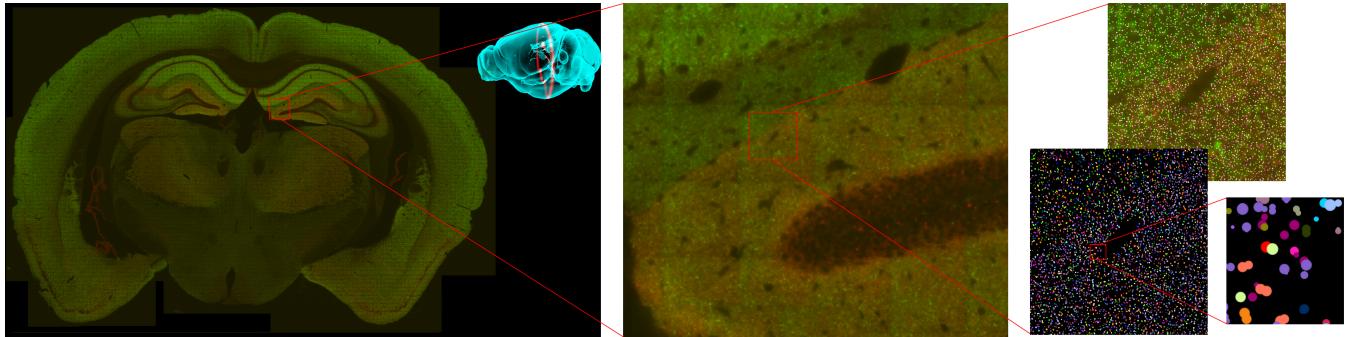


Figure 1: Exploring the synaptome in multiple resolution scales. On the left, a whole section image is shown, including a thumbnail of the 3D model with the location of the section marked. In the middle, a zoomed-in area of the hippocampus is shown. On the right, further zoomed-in individual SAP102/PSD95 puncta are displayed as overlays on the original image (top image) or shown exclusively using subtype colors (bottom images).

## 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.

### 1.1 Basic usage

Run the application, click on "Load dataset folder" and select one of the dataset folders: "0005", "0036", "0048", "0065" or "0096".

### 1.2 Requirements

- Any modern CPU, e.g. Intel i5 processor
- At least 4GB of RAM
- A graphics card supporting at least OpenGL 4.3, e.g. NVIDIA GTX 760 or AMD R9 200

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 at the following url:

[our.datashare.link](http://our.datashare.link)

Each dataset represents a single section, and includes section image data, calculated puncta, delineation hierarchy and a delineation map.

## 2 User 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 CA1

First expand the section "Section view". Expanding and folding GUI controls works by either double-clicking on the control text, or by single-clicking on the control's filled arrow. 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 CA1. The exact location is in "Cerebrum", then "Cerebral cortex", then "Cortical plate", then "Hippocampal Formation", then CA1. 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 CA1 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 stop the highlighting, select "None" in the "Highlight region" radio buttons.

### Show PSD95 only puncta in "CA2so left"

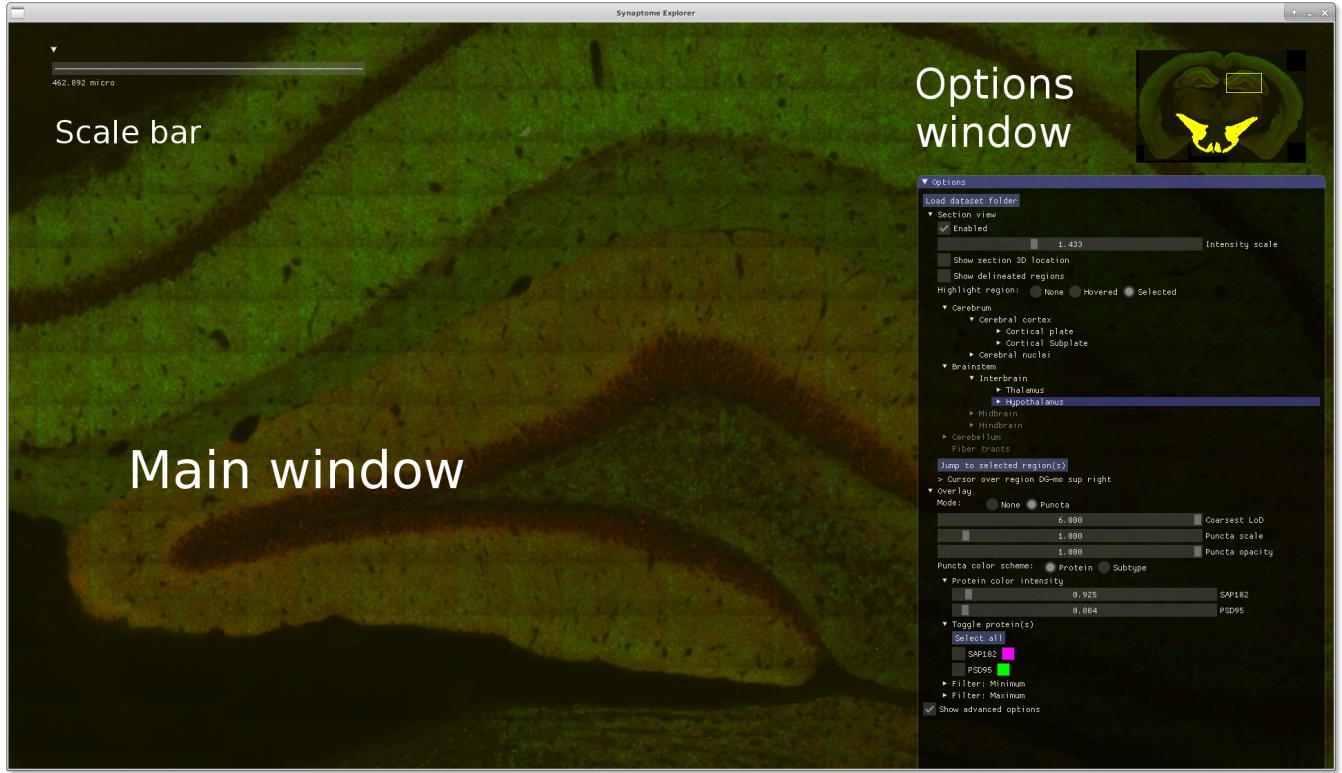
Find the "Hippocampal Formation" area as described above. Then expand the "Overlay" GUI control, located at the bottom of the "Options" window entries. Select the "Puncta" radio button to display puncta-related controls. At this point, the individual puncta should also display on top of the section image. To enhance the visualization of the puncta, we need to turn off the section image. To do that, we uncheck the checkbox "Enabled", which is the first option in the "Section view" expandable GUI control. This will disable the background image. To enhance the visualization , we can expand the "Protein color intensity" control, located under the "Overlay" control, and move both sliders to the right. Finally, to disable SAP102 so that we can only see PSD95, expand the "Toggle protein(s)" control, located under "Protein color intensity", and uncheck SAP102.

### Show Colocalized subtypes in "SSp-tr right"

First locate the area in Isocortex as described above. Similar to the puncta visualization, expand the "Overlay" control and select the "Puncta" radio button. Now, select the "Subtype" radio button in the "Puncta color scheme" line. This will automatically disable the background section image to allow clarity in the visualization of the different subtype colors. Expand the "Toggle subtype(s)" GUI control; this will display a list of checkboxes, 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.

## 3 User interface manual

The user interface is comprised of 3 elements: the *main window*, the *scale bar* 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. A thumbnail of section showing the current viewport (mini-map) is shown on the top-right. Users can optionally toggle a 3D visualization of a translucent mouse brain, showing the location of the current section in the brain with red color.

#### 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. ↕
- **Zooming:** Roll the mouse wheel to zoom in and out.

### 3.2 Scale bar

The scale bar is a draggable GUI window that can be moved and resized. It shows the scale corresponding to the length of the horizontal line at the current zoom level. The scale bar window, as any other GUI window, can be folded/unfolded by double-clicking on its title bar.

### 3.3 Options window

The options window displays the current section and bregma position and lists several controls. Below, all the controls are described (marked with the symbol ►), in order of appearance.

#### ► "Load dataset folder" button

Pressing the button brings up a folder selection dialog. By selecting a dataset folder, the associated dataset will be loaded.

#### 3.3.1 "Section view" options group

This group controls the view of the section image and the delineation selection.

#### ► "Enabled" checkbox

Toggles the display of the section image.

#### ► "Intensity scale" slider

Adjust the intensity of the section image.

#### ► "Show section 3D location" checkbox

Enables a 3D visualization of a translucent mouse brain on the top-right of the screen, showing the location of the current section in the brain with red color. When disabled, a thumbnail of section showing the current viewport (mini-map) is shown instead.

#### ► "Show delineated regions" checkbox

Enables an overlay of the user-defined delineation boundaries atop the section image.

#### ► "Highlight region" radio group

Selects between modes of region highlighting.

- **None:** No region is being highlighted.
- **Hovered:** Highlight the region that the mouse cursor is over. While a region is highlighted in this mode, holding the right mouse button will display a tooltip with the name of the region that is being highlighted.
- **Selected:** Display a hierarchical view of user-defined delineations. Single-click selects (and highlights) a node, while double-click expands/collapses a node if it's not a leaf. Ctrl + click adds a node into the current selection, if the node is under the same parent. A button "Jump to selected region(s)" appears, that, when pressed, zooms and pans the view so that the selected region(s) fit exactly into view.

Regardless of the highlight region option, the name of the region under the cursor is displayed at the bottom of the "Section view" options group.

#### 3.3.2 "Overlay" options group

There is a single overlay type: "Puncta", selectable via the radio button. Using the puncta overlay mode, calculated puncta are overlaid on top of the section image if the view at least at a given zoom level. Puncta are displayed as circles of varying radius, color and intensity (the latter for the *Protein* color scheme only). The radius is approximated from a punctum's area using the circle area formula  $A = \pi R^2$ , while the intensity used is the mean intensity of the puncta.

When the "Puncta" overlay type is selected, the following options are activated.

#### ► "Puncta color scheme" radio group

Selects between two ways of colorizing puncta: **Protein** and **Subtype**.

When the *Protein* radio button is active, SAP102 puncta use magenta color, while PSD95 puncta use green color. Additionally, the below two controls are displayed, unique to the Protein option.

#### ► "Protein color intensity" sliders

Adjusts the intensity for each protein type individually, in order to aid visualization.

#### ► "Toggle protein(s)" checkboxes

Allows visualization of each protein individually.

When the *Subtype* radio button is active, puncta are colorized based on their respective subtype color. As this visualization mode is intended to demonstrate the classification results, brightness is unaffected by the calculated puncta intensities. Additionally, for the same reason, the original section image is not displayed, even if it is enabled. Additionally, the below control is displayed, unique to the Subtype option.

#### ► "Toggle subtype(s)" checkboxes

Allows visualization of a custom subset of subtypes. There are additional buttons to aid selection, by toggling all or no subtypes, all or no PSD95-specific subtypes (1-11), all or no SAP102-specific subtypes (12-18) and all or no Colocalized subtypes (19-37). The buttons change color depend on how many subtypes per group are active: it is brightest when *all* subtypes of a group are active, dark when *some* subtypes of a group are active, and darkest when *none* of the subtypes of the group are active.

## License

This software is licensed under the MIT License - see the LICENSE.txt file for details.

## Software and data used

- **SDL2:** <https://www.libsdl.org/>
- **GLEW:** <http://glew.sourceforge.net/>
- **Dear ImGui:** <https://github.com/ocornut/imgui/>
- **Mouse brain model by Scalable Brain Atlas:** [https://scalablebrainatlas.incf.org/templates/ABA\\_v3/wholebrain.x3d](https://scalablebrainatlas.incf.org/templates/ABA_v3/wholebrain.x3d)

## Contact

Seth Grant: [seth.grant@ed.ac.uk](mailto:seth.grant@ed.ac.uk)

Babis Koniaris: [ckoniari@ed.ac.uk](mailto:ckoniari@ed.ac.uk)

Ricky Qiu: [z.qiu@ed.ac.uk](mailto:z.qiu@ed.ac.uk)