

NeuTu Proofreading Manual

Version Multi-scales

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Oct 17, 2017

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About NeuTu

NeuTu is a software package written by Ting Zhao for neuronal reconstruction and visualization from machine segmentation of serial electron microscopic images. It allows the user to observe segmentation and to split or merge if necessary. NeuTu users can also use the program for annotation and has many other features. In this manual you will have the chance to dive deeper into understanding proofreading and all that NeuTu offers.

About the dataset and DVID

Each dataset consists of a grayscale image stack and its associated machine segmentation and annotations. To provide good interactive performance for users, image and segmentation planes are divided into tiles at multiple resolutions and stored on a server. NeuTu loads tiles of the desired zoom on demand.

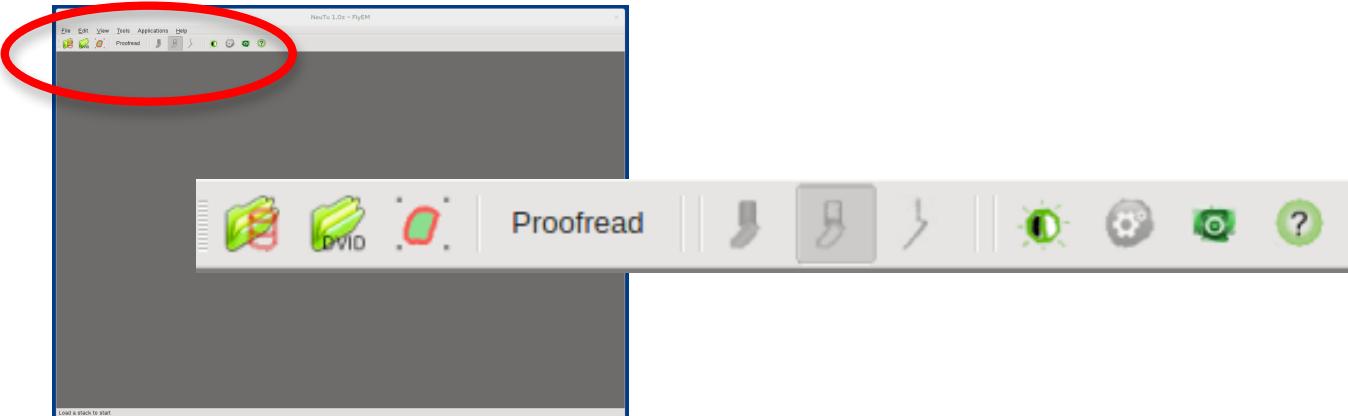
DVID was created to handle datasets that greatly exceed the memory available on a single computer and, moreover, allows multiple users to simultaneously work on a single dataset. DVID is a distributed, versioned, image-oriented data service designed by Bill Katz to support Janelia Research Campus's brain imaging, analysis and visualization efforts. For more details about DVID and what it offers please visit this site: <https://github.com/janelia-flyem/dvid/wiki>.

What is EM proofreading?

The goal is to reconstruct a neural circuit at an individual neuron level using electron images and machine segmentation. Parts of the neurons such as cell body, mitochondria, and synapses are classified and individual neurons are segmented. EM proofreading is the manual editing of machine segmentation of electron microscopic images. False merges and false splits are the two errors that could occur during machine segmentation. To extract neuronal bodies from our datasets, proofreaders will interpret the ultrastructure in grayscale images by identify axons, dendrites and synapses in order to edit segmentation to correct falsely merged and over-segmented or falsely split neurons. NeuTu has a suite of tools to identify and correct both types of errors.

How to launch the NeuTu application

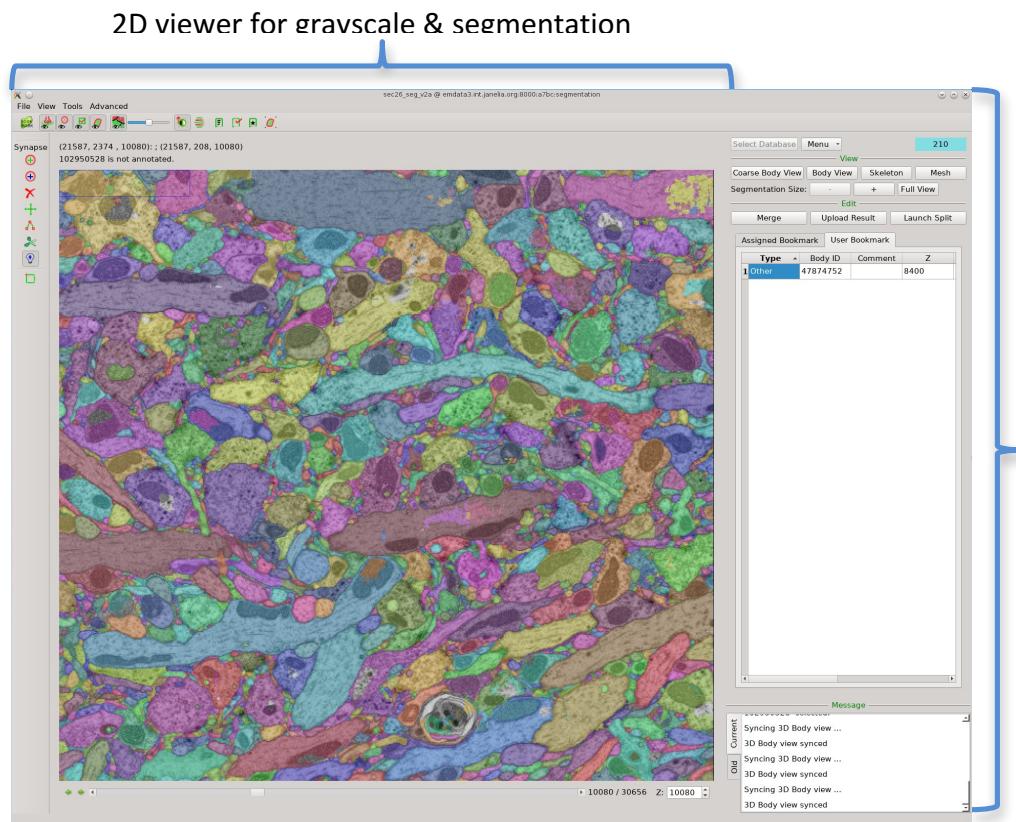
NeuTu is typically installed in the users home directory. Launch NeuTu from the terminal window by typing: /opt/bin/neutu and clicking enter. Click on <Proofread> in the menu bar to open the Main Proofreading Window.



How to launch proofreading functions in NeuTu.

Main Proofreading Window

This window has two main areas (Figure 2). On the left, the two-dimensional view of the data takes up most of the screen. A panel of visualization and proofreading tools is located on the right. The main window also has two menu bars in the top left corner and a status bar at the top center. In addition to the main proofreading window, NeuTu has two additional windows dedicated to 3D body visualization and splitting.



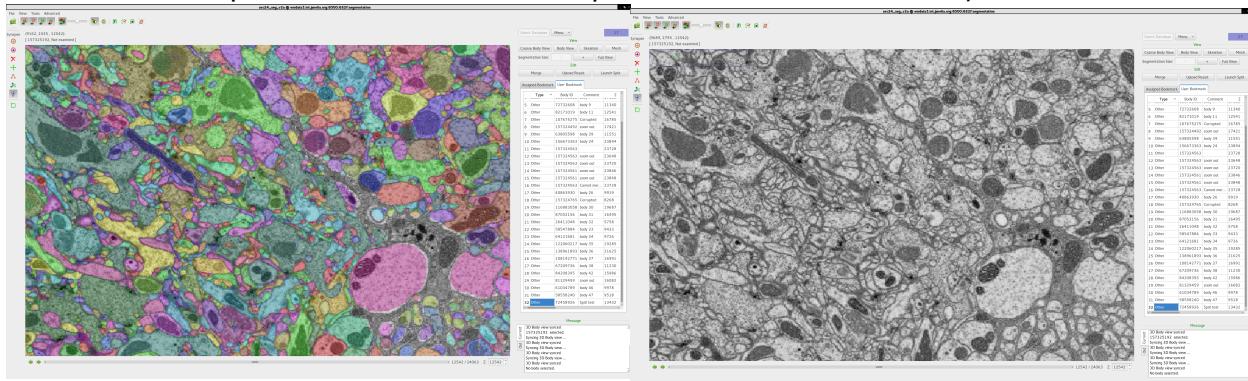
Main Proofreading Window consists of a 2D viewer and tool panel for proofreading and 3D visualization.

2D viewer for grayscale and segmentation

The user can zoom, pan and change planes with either the keyboard or mouse. Please refer to the *Keyboard Shortcuts and Mouse Operations* to learn more about how to use these functions. These operations will be faster if segmentation is toggled off.

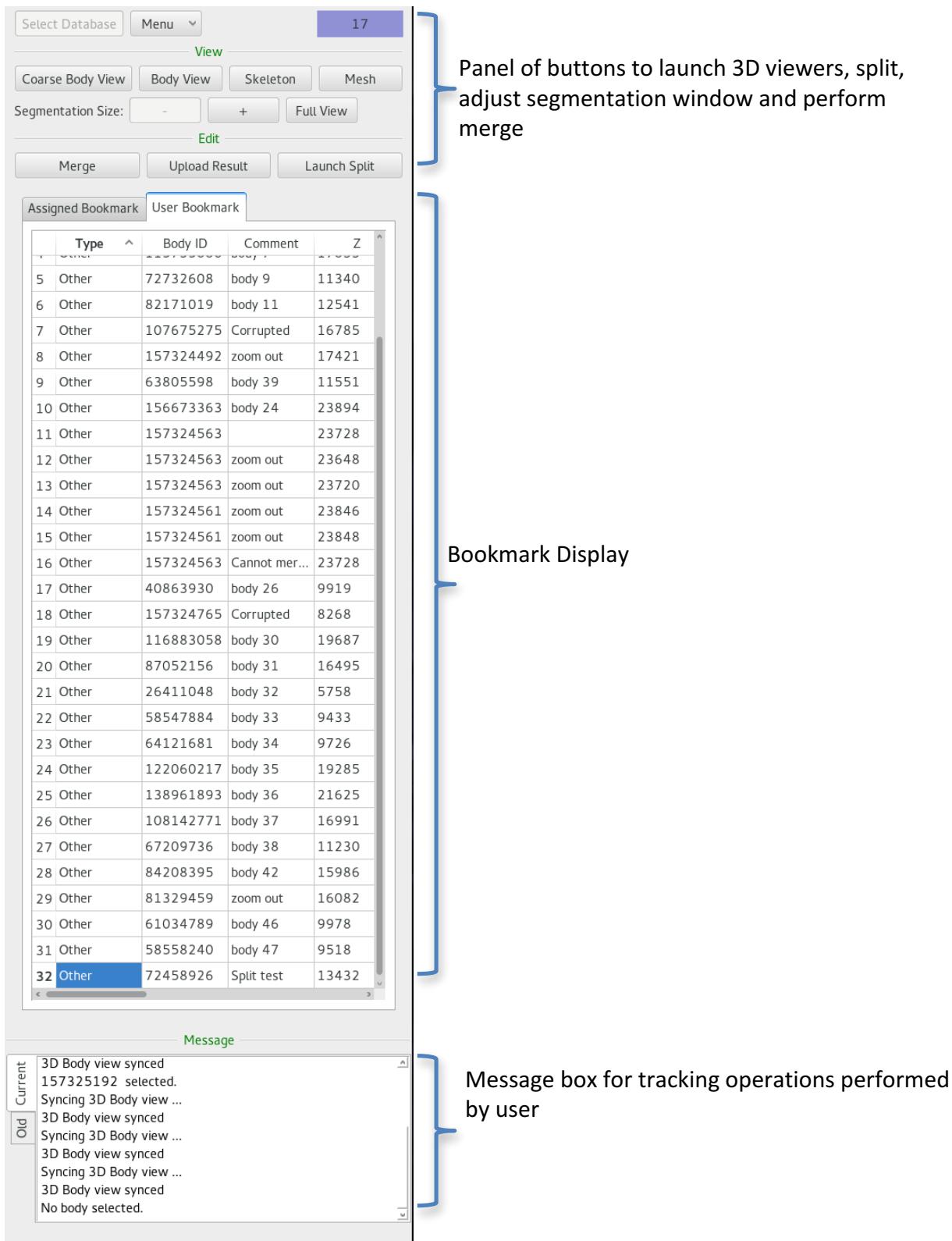
Upon viewing NeuTu's main window the segmentation window is fixed in the x-y view. The user must drag or pan the grayscale underneath the window to view the segmentation in that region. Users can toggle between the grayscale image and false-colored segmentation using keyboard shortcuts (**F key**) or the toggle buttons on the menu bar.

Segmentation can be viewed in three modes: normal, transparent and name (See Figure 4 for normal and transparent modes and *Color Maps* for details on name mode).



Segmentation can be viewed in two modes. In the normal mode, each body is colored and the selected body is white. In the transparent mode, the selected body is colored and user can see the gray scale imaging surrounding the selected body.

Visualization and Proofreading Tool Panel



Visualization and Proofreading Tool Panel.

1. Database Selection

Select the image stack for proofreading by clicking on <Select Database> in the Visualization and Proofreading Panel the DVID Server window opens (Figure 5). A window with blank field's to the server information will pop up (Figure 6). Users much input this information which is accessible by a google doc that contains the required database information.

Every database is associated with a Universally Unique Identifier (UUID). Users can select a database using the drop-down menu under Server, or enter the port number and UUID directly. For convenience, the UUID and other database info are also displayed.

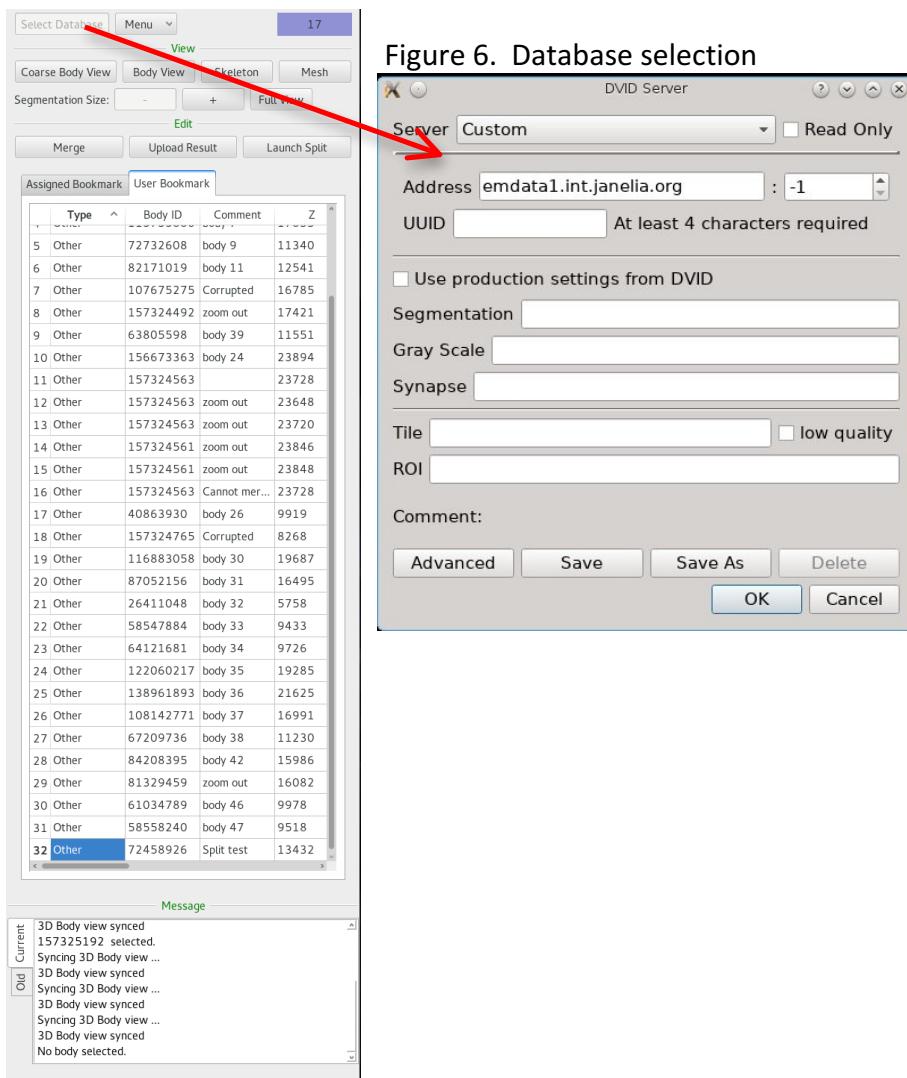
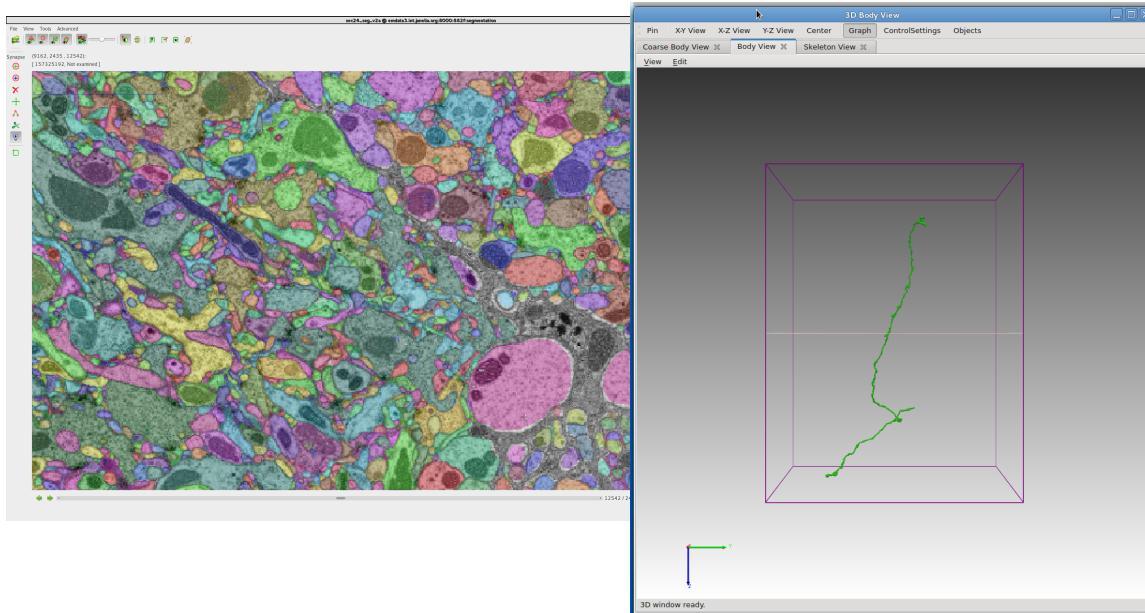


Figure 6. Database selection

2. 3D Body View Window

The user can select 3D Body View from a selected body for 3D visualization. Right-click on the segmentation to select a body for viewing in 3D. The selected body will be colored white or if in transparent mode the body will be colored. There are three types of 3D views: Coarse Body View, Body View or Skeleton which may be selected in the proofreading panel (see Figure 8 for comparison of different viewers). The 3D Body View window will open (Figure 7). By default, the graph mode is active. This mode shows the plane that is currently active in the 2D viewer.



3D Body View Window and selected body in 2D window.

The menu bar on the top contains toggles for the viewing orientation, graph, control settings and objects. Graph mode is on and shows location of plane (arrow) currently active in 2D window. X-Y-Z axis is conveniently located in the lower left hand corner.

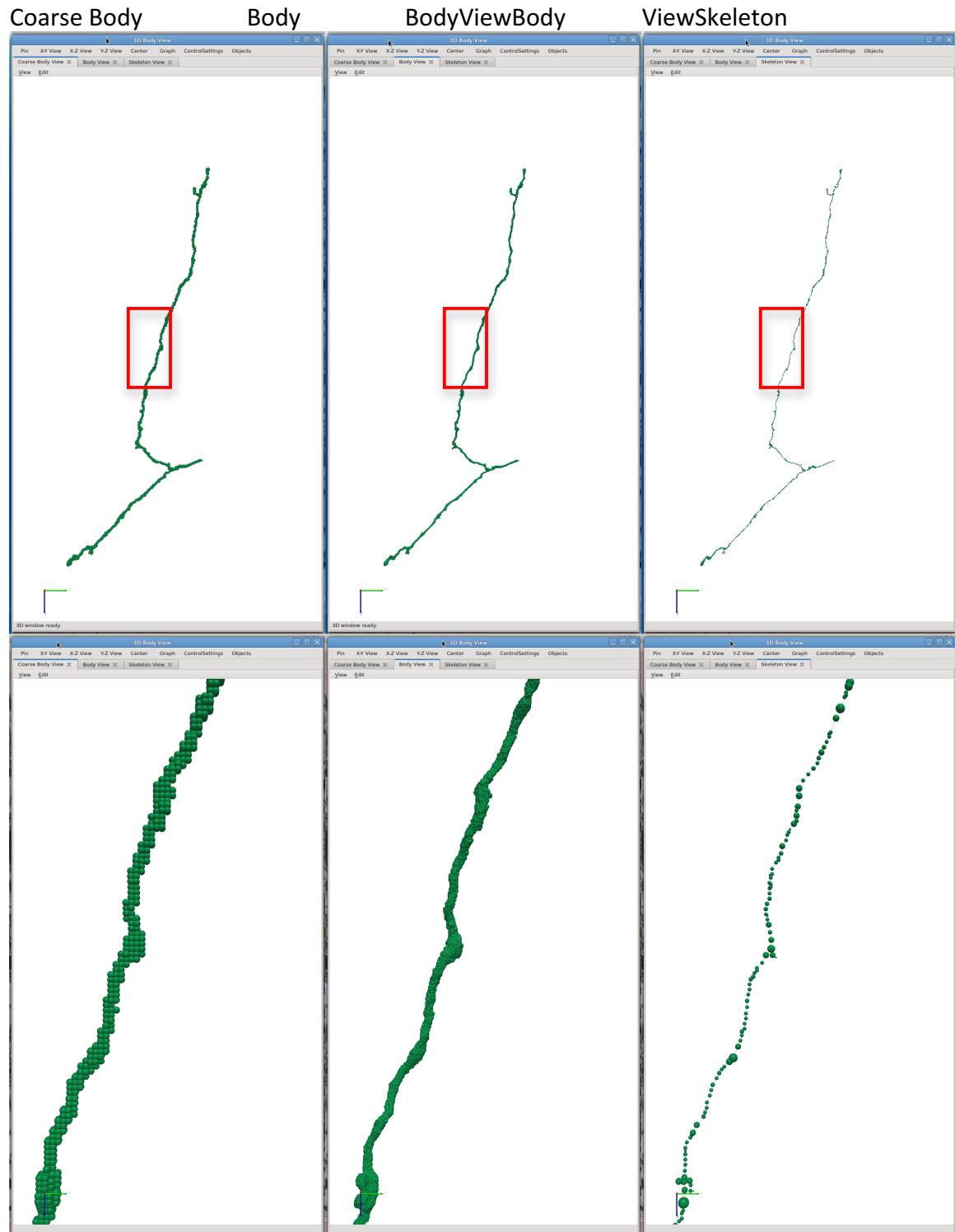
Keyboard and mouse are used to zoom, rotate and translate the image in the 3D window as follows:

- Mouse wheel to zoom
- Left click + drag to rotate
- Shift + drag to translate up or down

NeuTu allows users to sync the body in the 3D view with the grayscale/segmentation displayed in the 2D view. By hitting the "z" key and selecting any point in the 3D body, users can go to that plane in the 2D window. The graph mode also displays the location of the grayscale plane shown in the 2D window.

2-1. Three options for visualizing bodies in 3D

NeuTu provides three options for viewing bodies or neurons in 3D.



Models of 3D visualization.

2-2. Control Settings Panel to adjust image features

Click on *ControlSettings* to open a panel with following tabs:

- General (to adjust angle of lighting on the 3D object)
- Capture (to collect and save image)
- Image
- Graph (to show plane active in 2D window)
- Surface
- To Do
- Neurons
- Puncta (to show synapses on body)
- Background (to toggle or adjust background color)
- Axis (X-Y-Z)

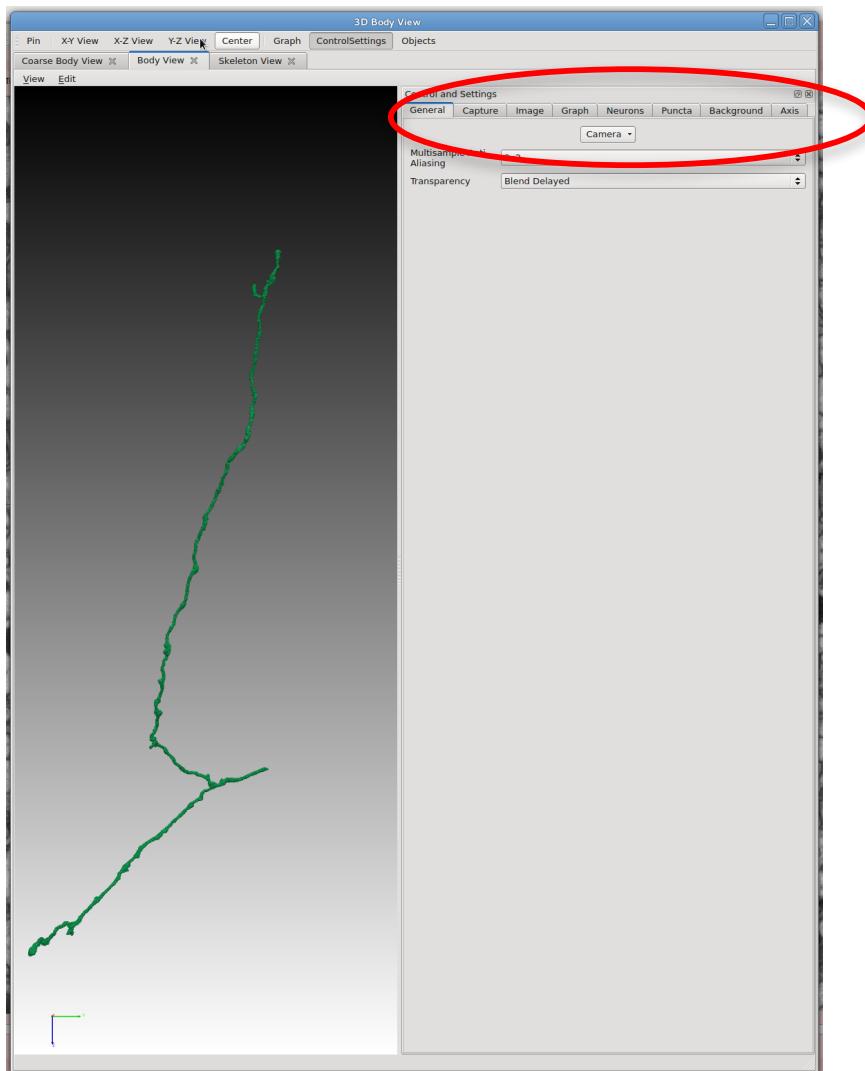


Figure 9. 3D Body Viewer + control settings panel.

2-3. Display synapses on body using the Puncta tab

NeuTu allows users to visualize the location of pre- and post-synaptic sites (also called T-bars and PSDs) on the 3D body. To use this feature, go to the Puncta tab on Control and Settings panel (Figure 10). Select “Visible” to show T-bars (yellow) and PSDs (gray). Some synapses may be buried in the body. Select “Always in front” to see distribution of all synapses.

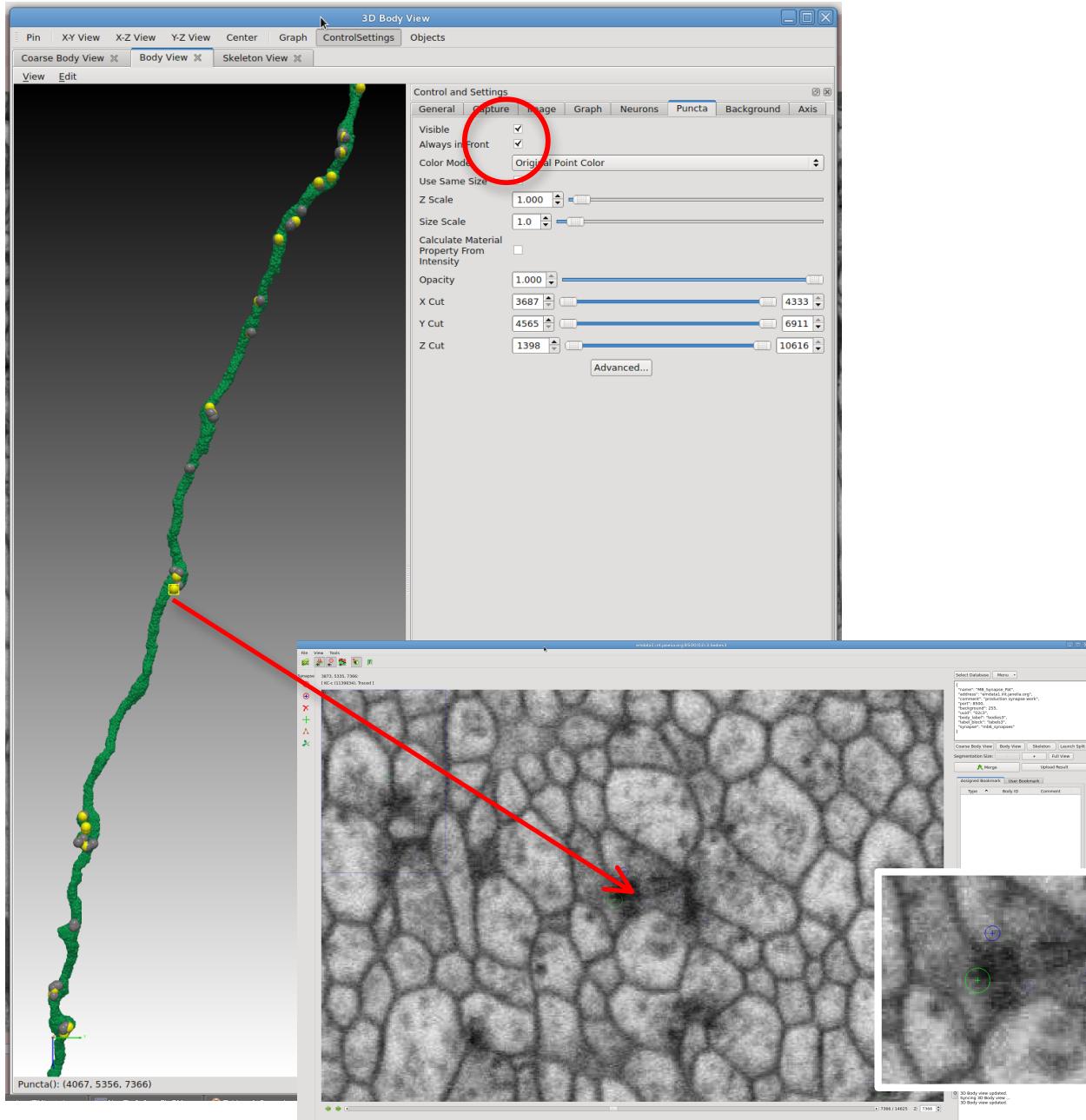


Figure 10. Puncta tab on Control Settings panel is used to display synapses in 3D body view. Select *Visible* and *Always in front* (red circle) to show all synapses. Note that individual synapse can be selected (yellow box) and synced with 2D window by hitting “z” key.

2-4. Objects Panel (toggle on-off)

The body and synapses (T-bars and PSDs) are classified as objects. Users can toggle off one or more objects in the image.

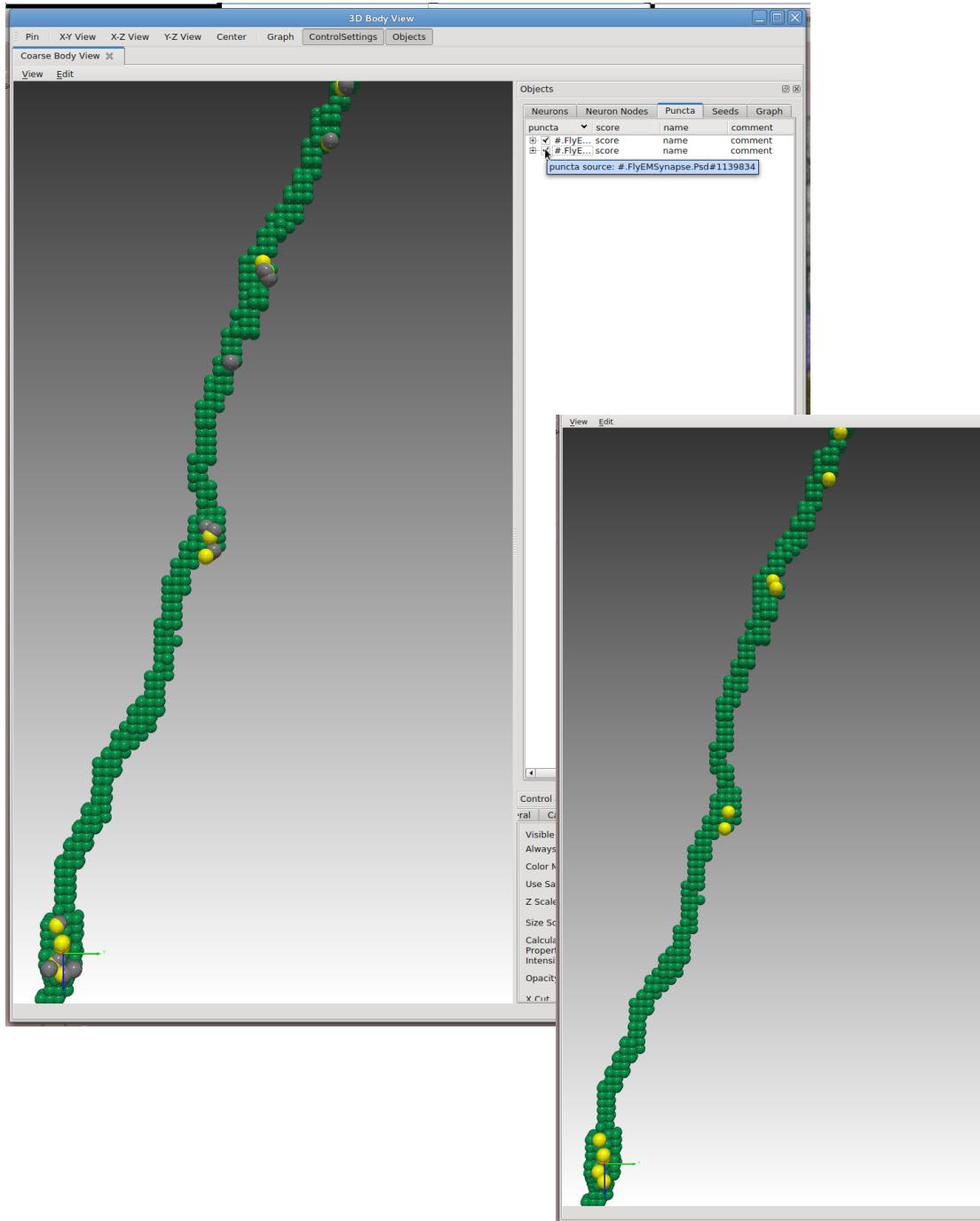


Figure 11. This panel can be used to toggle off an object class. In this case, PSDs (gray) were toggled off to better visualize the T-bars (yellow).

3. Launch Split

If a proofreader notices a mistake in segmentation they may use the Launch Split button to launch a suite of tools to place seeds in 2D and view the final split results in 3D. See section on *Correcting False Merge* for more details.

4. Merge and Upload Results

See section on *Correcting False Splits* for instructions on how to merge bodies in 3D.

5. Bookmarks

NeuTu uses a “bookmarking” system to mark bodies or areas of interest. Bookmarks are point annotations that can be imported as a list or added by the user. Bookmarks appear as red open circles in the 2D window.

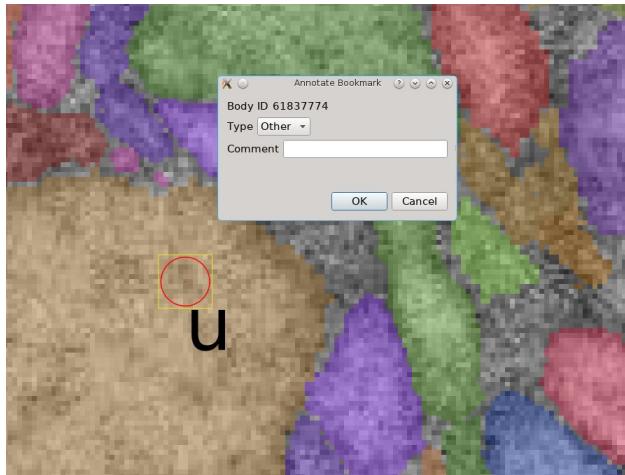
Bookmarks are classified into three types: Merge, Split and Other. Merge and Split bookmarks can be used to mark falsely merged bodies and falsely split bodies. Other-type bookmarks can be used to label specific bodies for proofreading assignments.

Users can import an “assigned” list of bookmarks using the Bookmark button in the top left menu bar. NeuTu also displays bookmarks and sorts them in ascending order by Z and shows the body ID and comments associated with each bookmark.

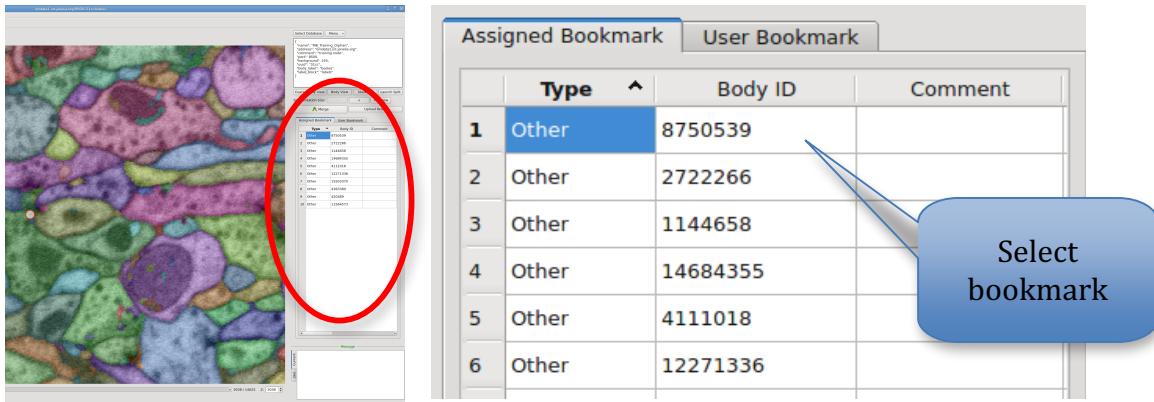
Assigned Bookmark		
Type	Body ID	Comment
1 Other	8750539	
2 Other	2722266	
3 Other	1144658	
4 Other	14684355	
5 Other	4111018	

Assigned bookmark list.

Users can add their own bookmarks to the database. To place a bookmark, the user must hit the “G” key to go to the bookmarking mode. Click on mouse to add bookmark and double-click to annotate with free form text. User bookmarks can be selected and deleted as well.



How to annotate a user bookmark.



How to use assigned bookmarks. Use menu bar to import bookmark list. Select bookmark in panel and 2D window goes to bookmark's location. Select body under bookmark for proofreading.

7. Message board

The message board displays current operations as well as past operations performed on the user's dataset.

Menu bars and drop-down

There are two menu bars (horizontal and vertical) on the main proofreading window in the top left corner. The *horizontal menu bar* contains buttons to perform the following actions:

- Import bookmarks
- Toggle on/off segmentation
- Toggle on/off synapse annotation
- Open Sequencer (see section XX for how to use sequencer)

The *vertical menu bar or synapse bar* contains tools for synapse annotation and is described in another section.

There is a drop-down menu on the Visualization/proofreading tool panel. After selecting a database, users can quickly navigate to a location in x-y-z or body ID of interest by using the dropdown menu located in the Visualization & Proofreading Tool Panel. Users can also select a Color Map (described in section Color maps).

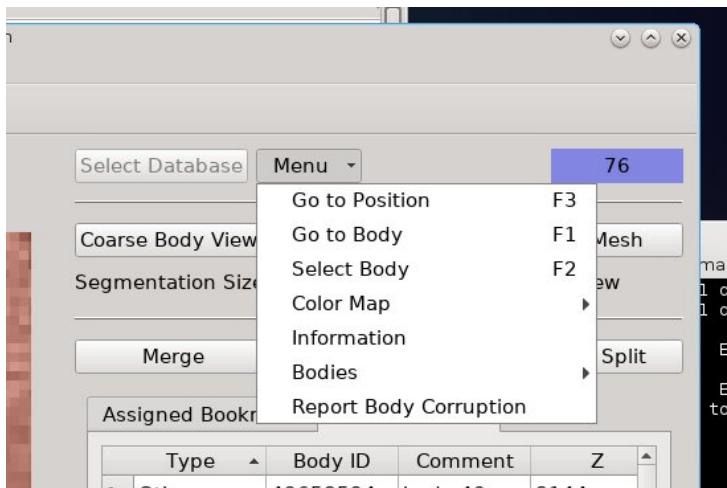


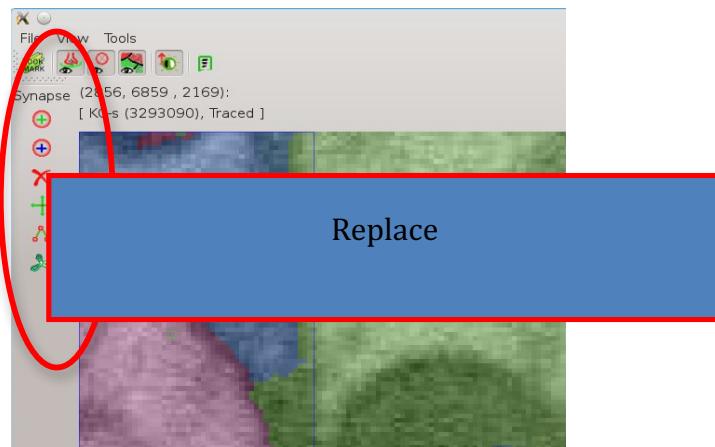
Figure 16. Go-to and Color Map menu.

Status bar

Located at the top center, this bar displays the name of the DVID database.

Synapse annotation tool bar

See Section on *Synapse annotations* for more details.

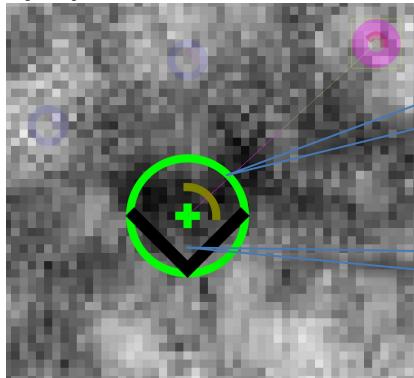


Synapse annotations

Basic Operations:

- Click to select a synapse.
- Ctrl + Click to unselect a selected synapse.

Synapse:



The quarter circle means this synapse is 'low confidence'

The V shape means this synapse is verified

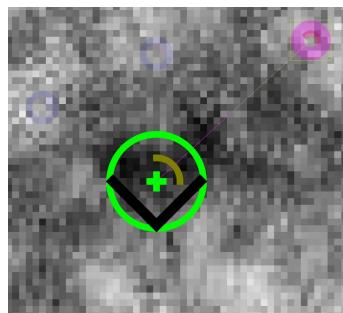
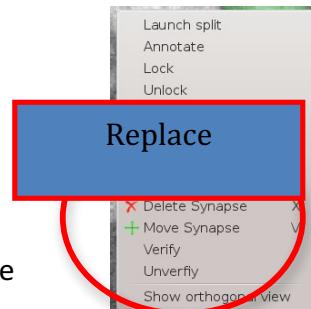
How to annotate/edit synapses:

1. Annotate pre-synapses

- Choose 'Add Tbar' from the tool menu or right click menu.
Click where you would like to place a pre-synapse glyph.

2. Annotate post-synapse (also called PSD)

- Choose the pre-synapse which you would like to link to PSDs.
Choose 'Add PSD' from the tool menu or right click menu.
Click where you would like to place a post-synapse. PSD will be automatically linked to the pre-synapse selected.



3. To delete the pre- or post-synapses

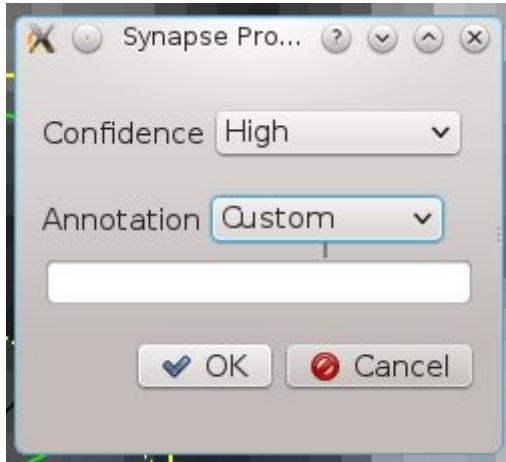
- Select the pre/post synapse, and choose 'Delete Synapse' from the tool menu or right click menu, or press 'X' as a short cut key.

4. To move pre- or post-synapse

Select the pre/post synapse, and choose ‘Move Synapse’ from the tool menu or right click menu, or press ‘V’ as a short cut key.

5. To manage the confidence and annotation

Double click the synapse. Window pops up to manage the confidence level (High or low/unsure) and annotations (add comment here).



Todo annotations and Todo list

Todo list and Todo annotations can be used for variety of purposes. Todo's are different from bookmarks in two ways: (1) they can be shared with other users, and (2) they are visible in 3D viewer. Like bookmarks, the status of the Todo can be changed from ‘merge later’,‘split later’,‘unchecked’ to ‘checked’.

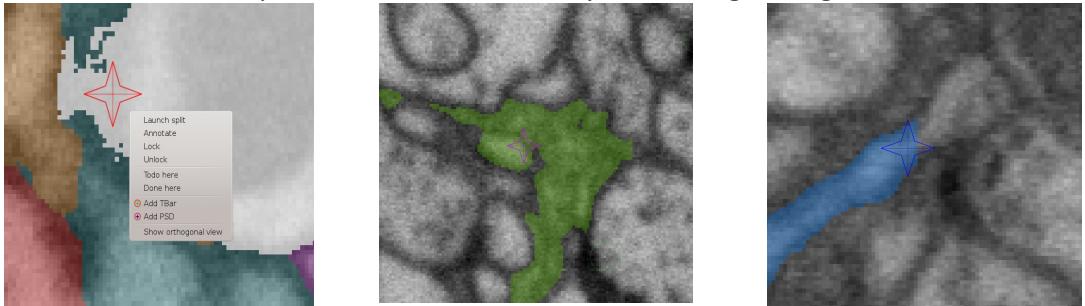
Suggested ways to use Todo's:

1. Put a Todo annotation on a spot and return to it later. Set the todo status to ‘checked’ or just delete when done.
2. Put a Todo on a terminal branch to notify other users that this branch has already been proofread or checked. (Comment function may be added in future.)

Basic operations

1. To place the Todo, right click and choose ‘Todo here’ ,‘split’ or ‘merge’. *Short -cut ‘Shift+g’ and click.
2. To change the Todo status to ‘checked’, click to choose the Todo, and right click to choose the menu ‘set checked’.

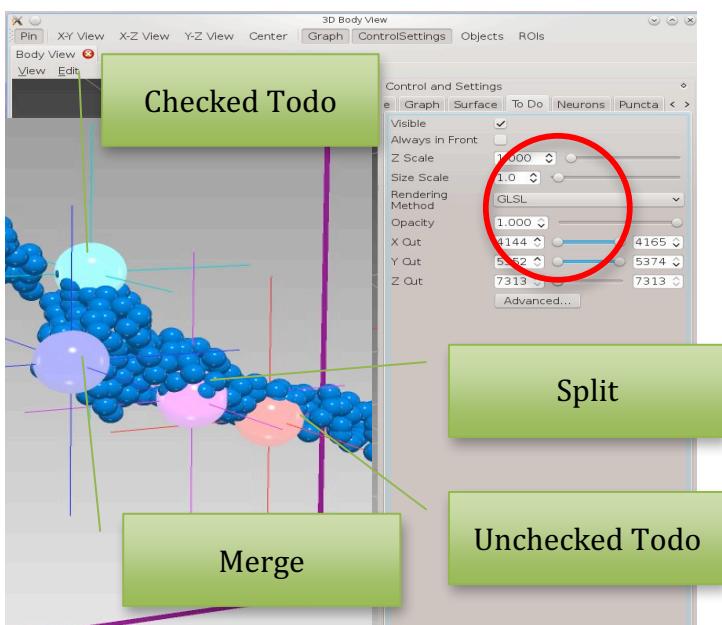
3. If you would like to place the 'Done' (already checked Todo) without the process of setting it checked, click to choose 'Done here' and click.
4. The user can also place Todo in the 3D body view using the right click menu.



Red = unchecked, Light blue = checked, pink= split, blue= merge.

Todo in the 3D viewer

Todo are also visible in the 3D viewer.



Click and press short-cut 'Z' to go to the location in the 2D viewer.

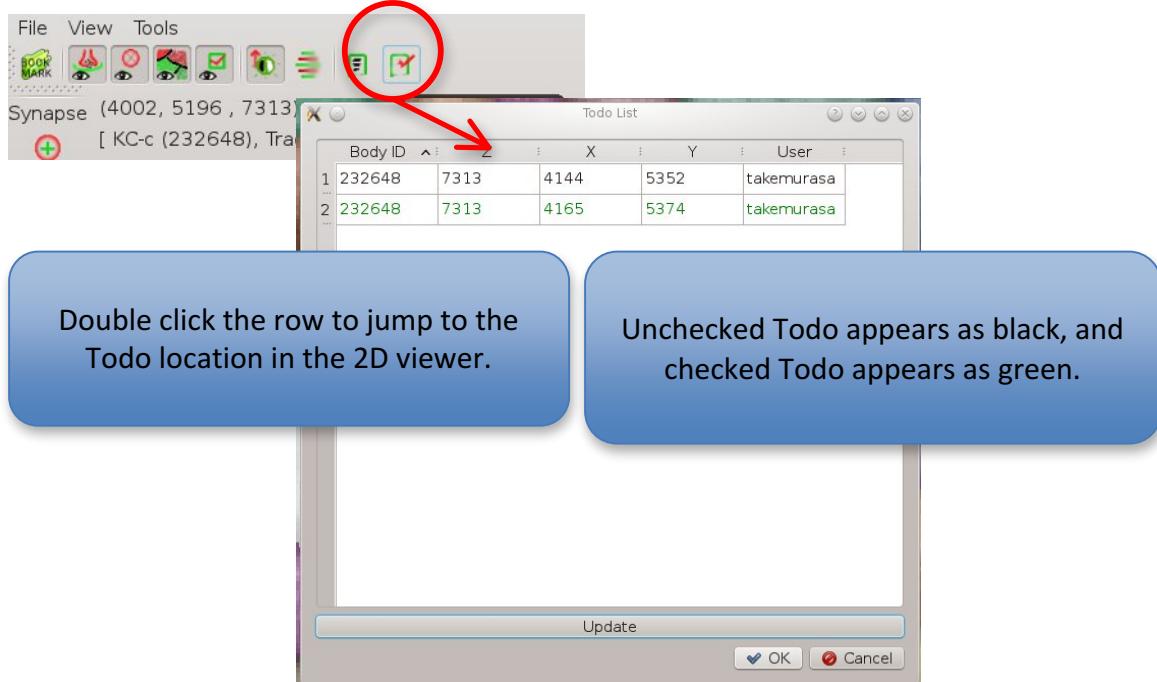
The user can change the setting, such as visible/invisible and size of the Todo in the control setting panel.

The user can also add Todo/Done directly in the 3D body view. To delete, press Delete key.

Todo List

1. To launch the todo list, click the  from the tool bar.

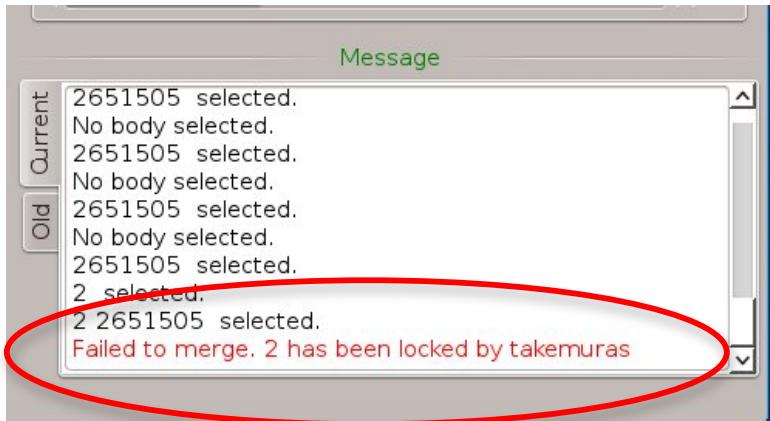
2. Press 'update' to see all the Todo on the selected body. A user needs to press 'update' every time he/she would like to see the latest information.
3. Double click the row to jump to the Todo location in the 2D viewer.



Intro to Locking Bodies

Users can collaborate by simultaneously editing the database instead of working separately. Although this strategy saves time, conflicts may occur when two or more users try to edit the same body. To manage this conflict, NeuTu “locks” bodies by user, so only one user can make and save changes to the body at a time. Once the changes are uploaded to the server, the body is automatically unlocked and another user can edit it!

When changes are saved to the server, any updates from other users are automatically refreshed. If a user tries to work on a locked body, NeuTu issues a warning and the user can not work on the body until it is unlocked.



NeuTu locks a body whenever the user makes changes to body by merging or splitting. NeuTu does not lock bodies that have been selected for viewing, so multiple users can view the same body at the same time!

Correcting False Splits

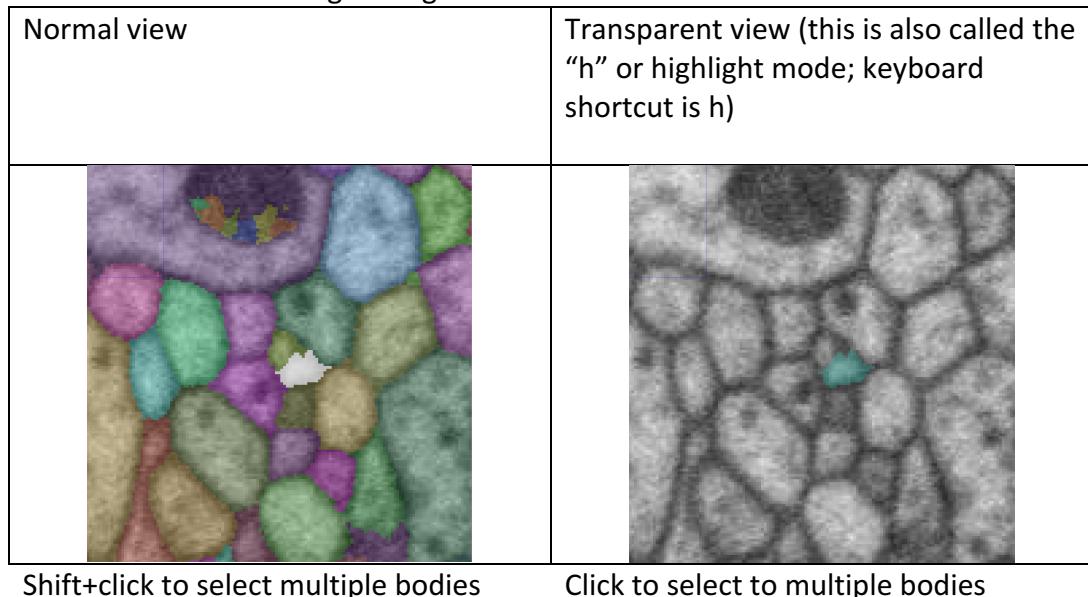
Neurons may be over-segmented or falsely split and proofreaders must identify and merge segments to create the neuron of interest. Three steps are required to correct false splits: (1) Select the bodies or segments for merging, (2) Execute the merge function, and (3) Upload the result. The user's ability to undo and the status of the body at each step is summarized in the table below.

Step	Action	Update Server	Lock the body	Ability to undo operation	Body ID
1	Select bodies for merging by clicking	No	N/A	Yes	Each segment has a different

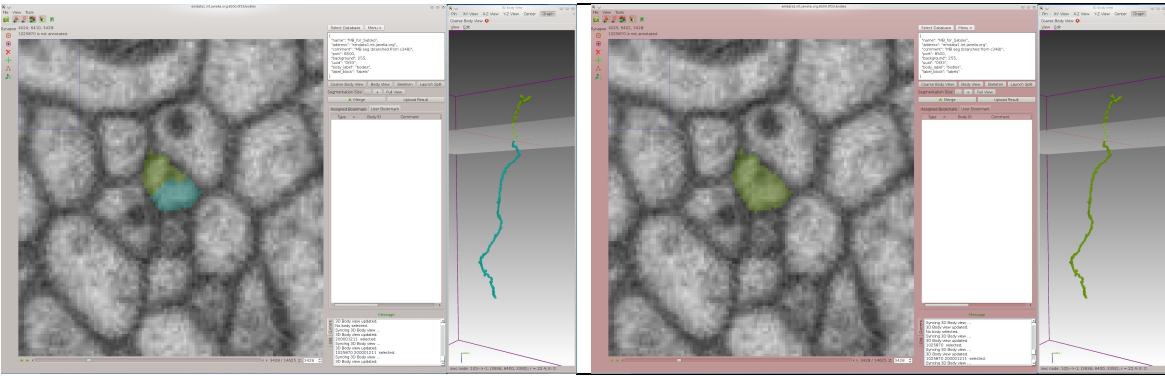
	and adding segments				body ID
2	Merge	No	Lock after merging	Yes	Each segment has a different body ID
3	Upload the result	Yes	Unlock after uploading	No	Segments have the same body ID (considered one body now).

Basic instructions for merging bodies

1. Select the body by either clicking on the body in the 2D image, double-clicking on a bookmark, or entering the body ID directly into the Go-to-Body function (short-cut for this option is F1).
2. Choose the normal view or transparent view (also called h mode) in 2D and open the 3D coarse view. Note that scrolling through z is much faster in h mode than normal view.

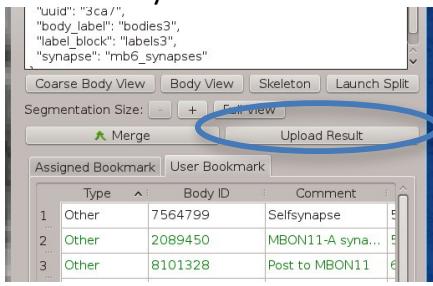


3. Select bodies or segments for merging by clicking directly on the segmentation or draw a bounding box around the bodies. Press Shift + r to draw a box and then press "s" to select all bodies in the bounding box. Before executing the merge, it is important to inspect the bodies in the 3D coarse body viewer. Remove any bodies that are inappropriate by clicking on the body in the 2D segmentation window. After approving the bodies for merging, click 'm' for merge or press <Merge>.



This operation doesn't save the result to the server. Even though the bodies are the same color, the body IDs have not been changed!

4. Click "Upload results" after approving the merge. The results will be uploaded to the server and you can not undo!



5. Annotate body with right mouse click as needed.
6. Add "user" bookmarks as needed.

Correcting False Merges

Split tools are hidden and appear in the main window when the split mode is launched (Figure 16). To split a falsely merged body, the user places different color seeds in the 2D view and NeuTu interpolates the split in 3D. Some false merges involve several bodies, so the user can select up to 9 seed colors (one color per body). Users also have the opportunity to inspect and amend the splitting results before finalizing them. Step-by-step instructions for splitting falsely merged bodies are provided in the next section.

Import bookmarks

Seed/split tools

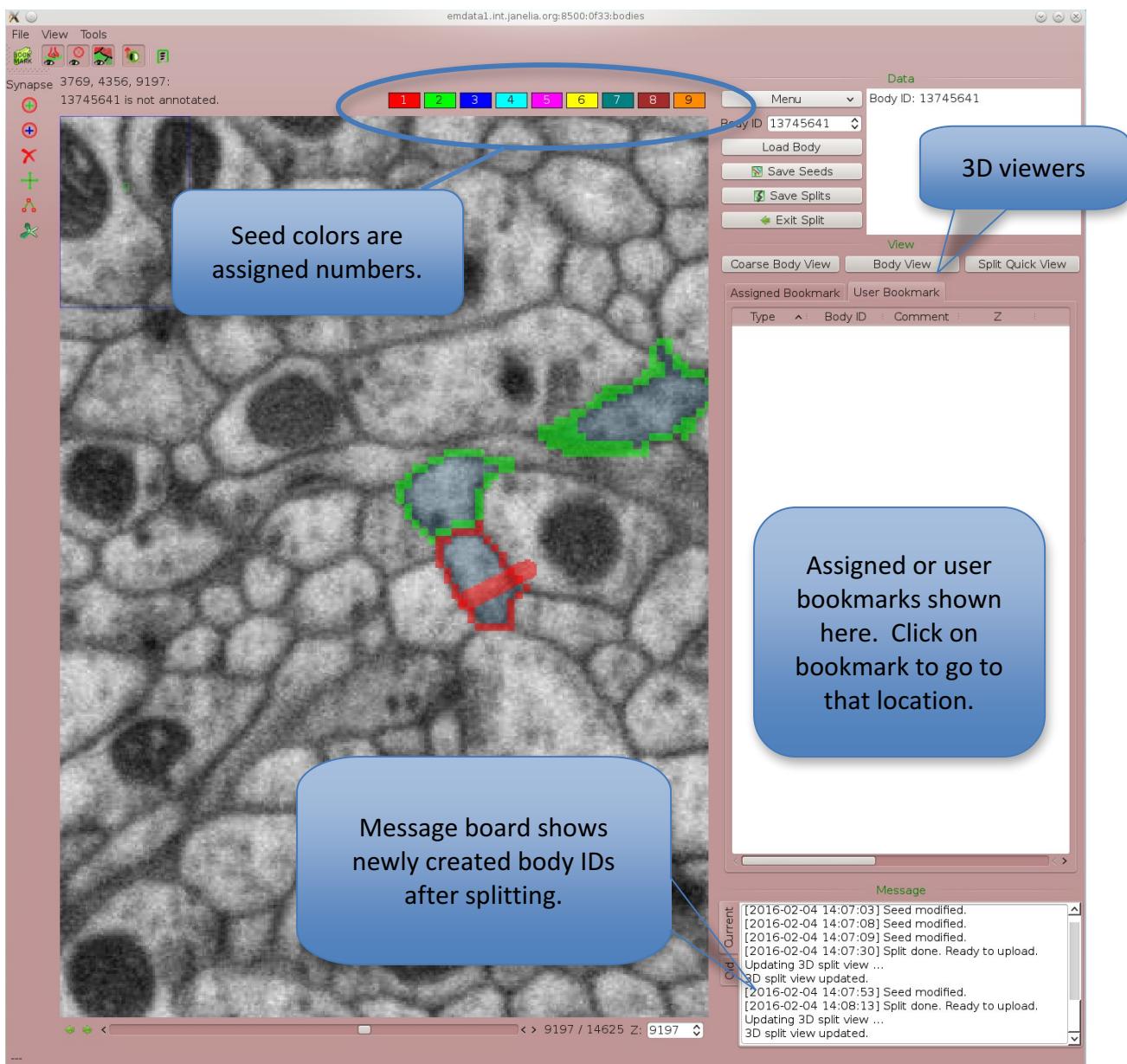


Figure 17. Split window. When the Split mode is launched, merge-specific tools are hidden and split-specific tools appear in the main window.

Basic instructions for splitting bodies

1. Launch the split mode

- Click to choose the body you would like to split in the normal mode (segmentation mode or transparent mode).
- Right click and choose 'Launch split' from the pop-up menu.

* There is another way to launch. The user might want to use it occasionally.



- Press <Launch Split> in the main window.

- B. A dialog box appears. Enter the body ID and press ‘OK’. If you don’t have a specific body ID, press ‘skip’.

2. Before you start splitting

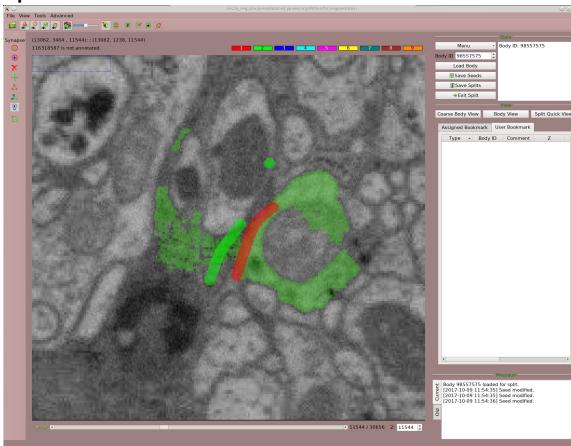
- A. Import bookmarks as needed.
- B. Note that user can add bookmarks while in the split window, but only “split” type bookmarks will be displayed in the user bookmark tab.

3. Find the false merge

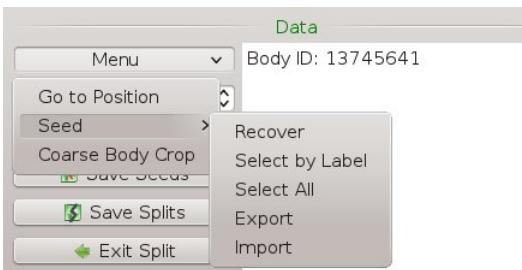
- A. If the assignment bookmarks are not provided, open the Body View (3D). Find the false merge by looking through 3D and 2D images. Also, click on the 3D view and hit the ‘z’ key to go to that location in the 2D window.

4. Place seeds

- B. Press ‘r’ key to use the mouse for seed mode.
- C. Place different color seeds on regions that you would like to split. Select the seed color using the ‘1’ through ‘9’ keys. See the color-key guide at the top of the 2D window.
Note that you will create at least two bodies during the split operation. The body marked by the red (#1) seeds will keep the original body ID. The non-red body will get a newly generated body ID. The message board displays all body IDs before and after the split.



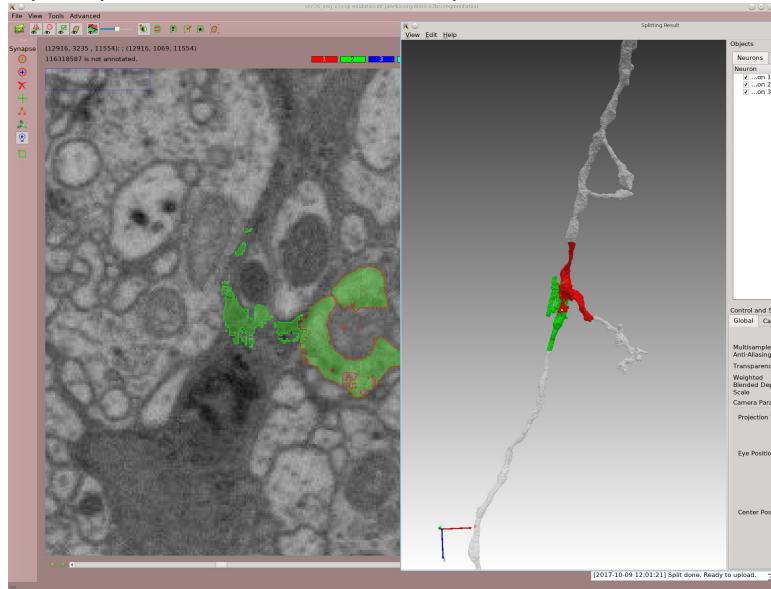
- D. To delete seeds, select the seed by clicking on it, then press the ‘delete’ key. You also have an option to select seeds by color or select all seeds from the drop-down menu.



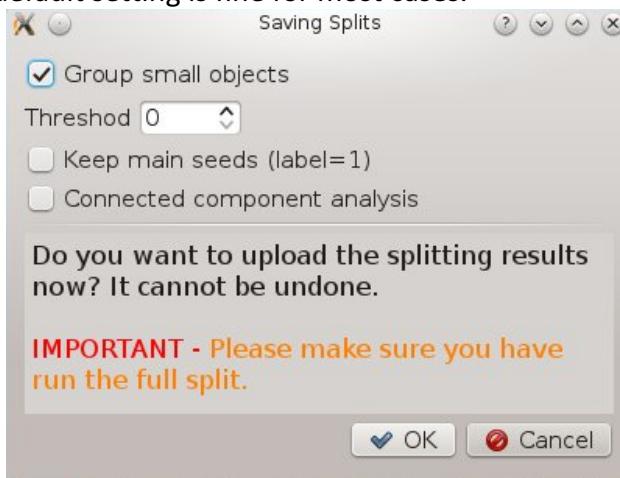
- E. A false merge may occur when boundaries (i.e. membranes) are not visible. You may have to draw seeds around the edges to fill this “leak”. If needed, draw seeds on multiple planes.

5. Execute splits

- A. Execute a split (Press Shift + Space). A progress bar appears as NeuTu propagates the split. Inspect the quality of the split and add more seeds as needed and repeat the split.
- B. Open *Split Quick View* to see the split bodies in 3D; rotate and inspect as needed.



- C. Repeat steps 1-3 as needed.
- D. Press <Save Split> when done. A dialog box shows up with options (see below). The default setting is fine for most cases.

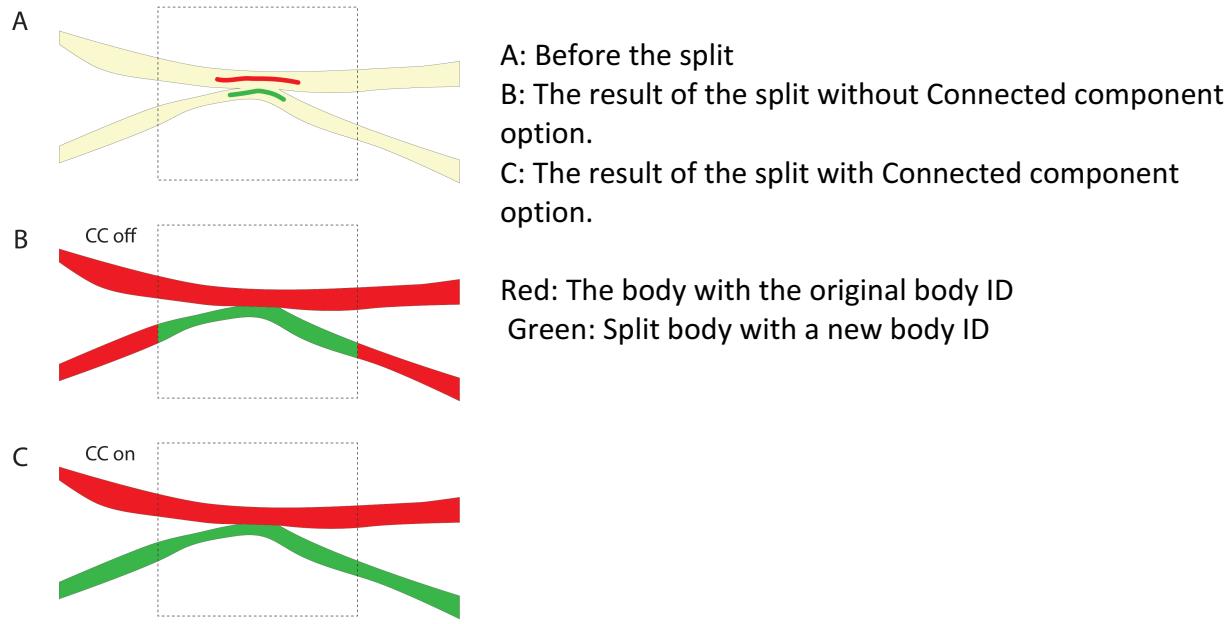


- E. New Body IDs are created for new bodies. These IDs are displayed in the message box.

Group small objects: When this option is checked, bodies smaller than the threshold size (in voxels) will be grouped as one body instead of assigning a unique body ID to each small body.

Keep main seeds (label = 1): When checked, the main seeds (red) will remain after the split. If not, all seeds will be removed automatically.

Connected component analysis: It propagates the analyses to the body which is of the bounding box, or approximately $x200*y200*z200$ from your seeds when you don't use the bounding box, and allocates the appropriate body ID for those parts of the body. If you don't use this option, any parts of the body out of the bounding box keep the original body ID.



Bounding Box Split: Split is performed in a bounding box drawn by the user. The split is restricted to a limited area and will save time.

- Shift + 'r' key to start the drawing tool
- Draw a box by dragging the mouse and place seeds on each body.
- When you execute the split (Shift + Space), it only splits in the box.
- The box can be expanded by Shift + click on area outside of the current box. Make sure you see the pointing finger icon. If not, shift + r again, and Shift click to expand the box.

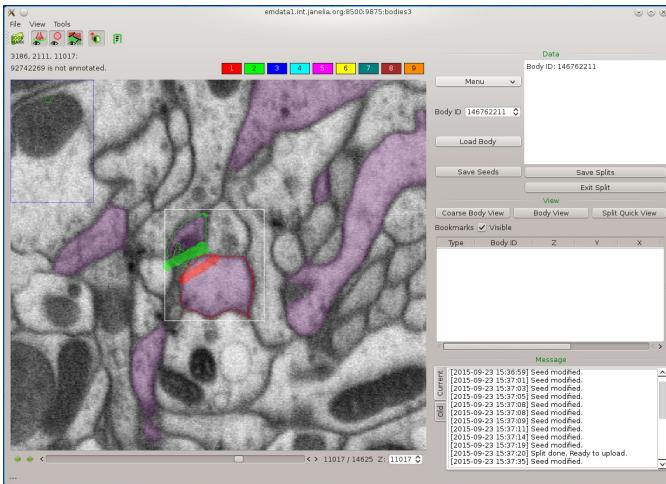


Figure 19. Bounding box split.

3D View Split: Split directly in the 3D Coarse Body Viewer.

- Press Shift + r to start the drawing tool.
- Draw a rectangle by dragging the mouse in the 3D Coarse Body View.
- Press 'x' key to execute the split. IMPORTANT: This action cannot be canceled by undo action (Ctrl + z).

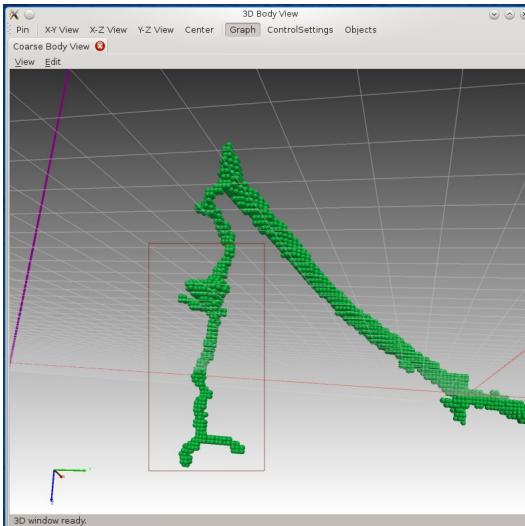


Figure 20. Side view split.

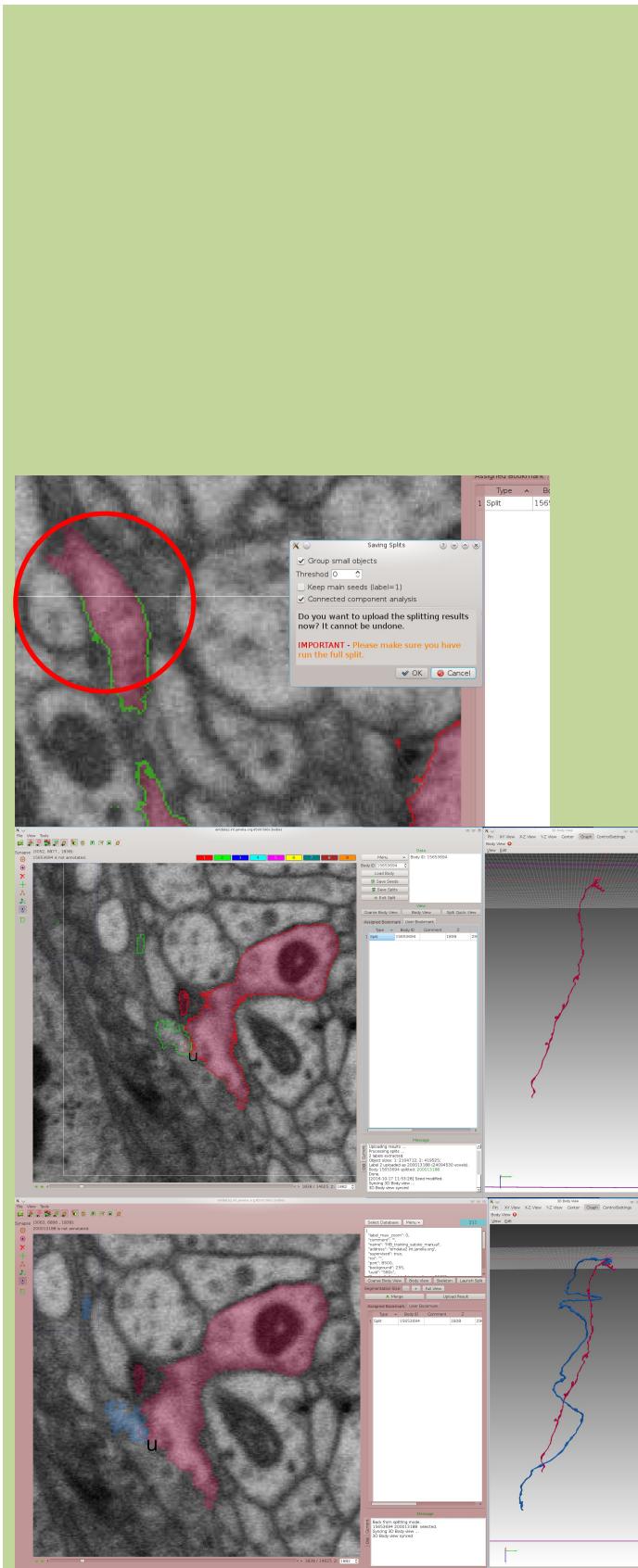
Examples of splitting

Case 1: Split two larger bodies using the bounding box.

When you have to split two bodies, it is faster to use the bounding box split method.

Press Shift + r to draw a box.

Draw a box around the false merge.



Locate the false merge and place seeds.

Press Shift + Space to see the results.

Inspect the result. Launch Split Quick View as needed.

*If the results are unsatisfactory, other false merges/leaks may exist. Place more seeds.

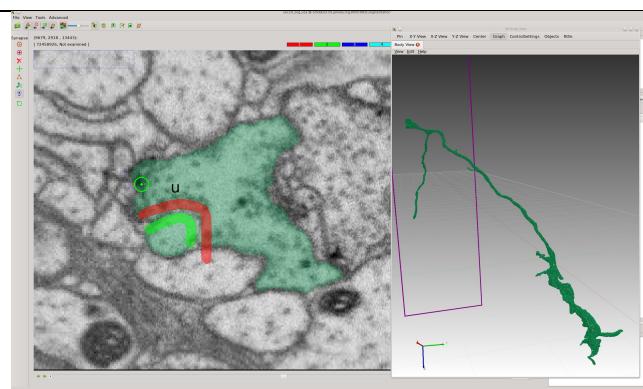
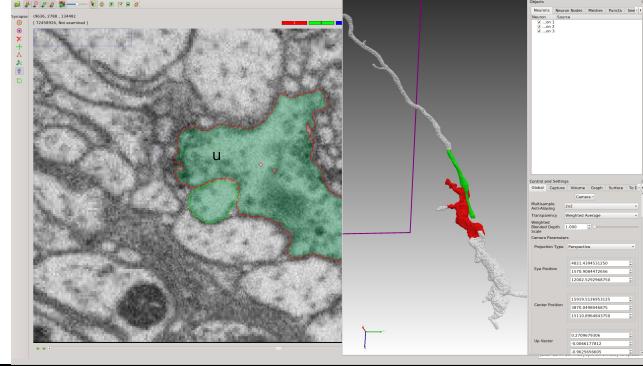
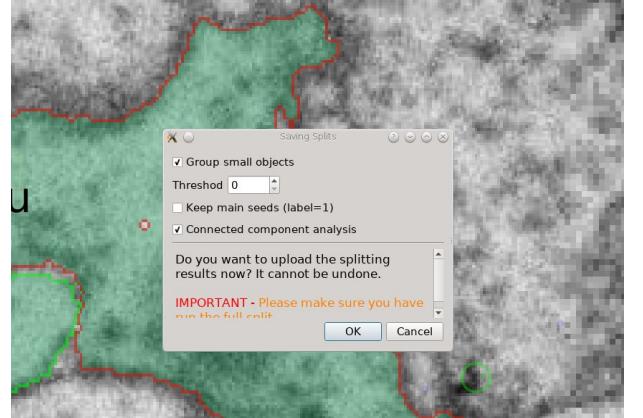
Press 'Save Splits'. Check 'Connected component analysis' because green seeded body goes out of the bounding box.

* If you don't choose the option, all the part of the body out of the bounding box will remain as the original body ID.

Split completed.

Exit Split mode, and two separated bodies exist.

Case 2: Fix the broken membranes

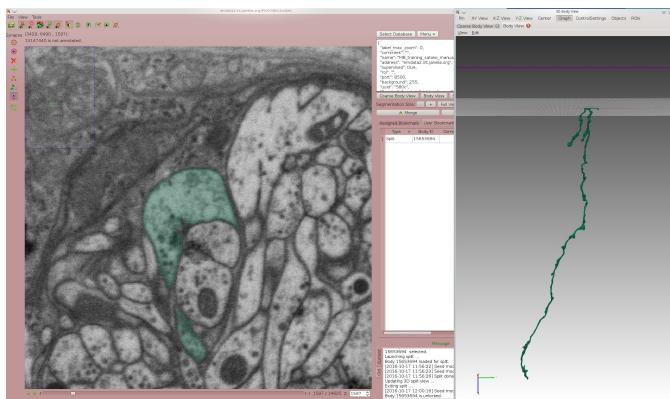
	<p>Place seeds around the 'leaks'. Press Shift + Space to see the results.</p>
	<p>Inspect the result. Launch Split Quick View as needed. *If the results are unsatisfactory, other false merges/leaks may exist. Place more seeds.</p>
	<p>Press 'Save Splits'. Check 'Connected component analysis'.</p>

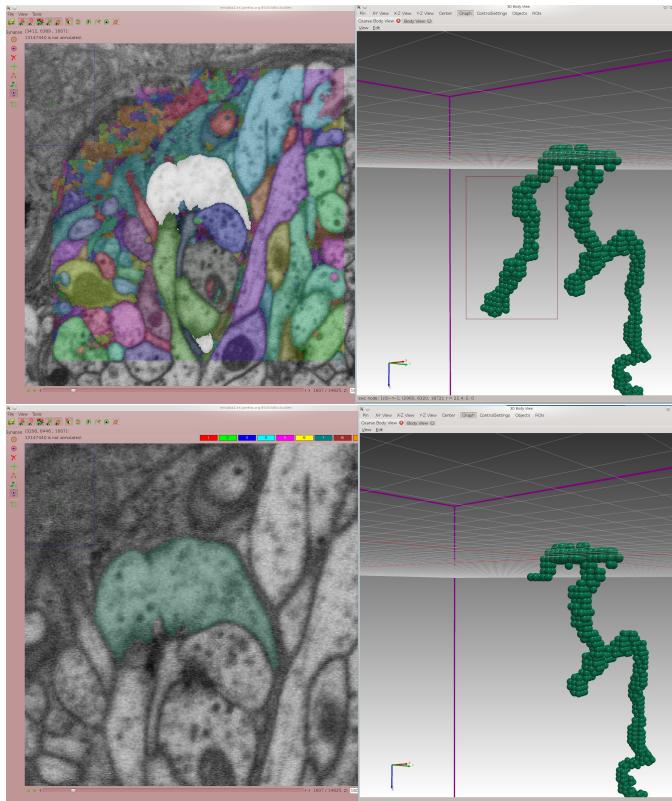
	Split completed.
	Exit Split mode, and two separated bodies exist.

Case 3.

	When you would like to cut out a small piece from the big merged body (such as a glia look body), using a bounding box is strongly recommended to save time.
	Use green seeds for the part you would like to cut out, and use red seeds the rest of the part. Shift + R to draw a box. Shift + space to execute the split. Make sure all the green body is in the box after the split.
	Save the split. This time, you don't have to use " option because the green body is small enough to be in the bounding box.
	Exit the split mode. Click the split body (green seeded).

Case 4. 3D view split





Open 'Coarse Body View' window, and click Shift + 'r' to draw a bounding box.

Draw a bounding box where to be cropped.

Press 'x' to crop

The part of bodies is cropped.
The cropped part has the new Body ID.

Keyboard shortcuts and mouse operations

2D view				
Operation		Shortcut (+ mouse)	Mouse control	Note
Undo		Ctrl + z		
Redo		Ctrl + Shift + z		
Clear body		c		
Go to Body		F1	Menu - Go to Body	Select the body by body ID
Select Body		F2	Menu – Select Body	Select multiple bodies by body ID
Toggle grayscale		f		
Toggle segmentation view and transparent mode		h		
Merge		m		
Go to top of the body		t		
Go to bottom of the body		b		
Pan	left	a	Mouse left drag	
	right	b		
	up	w		

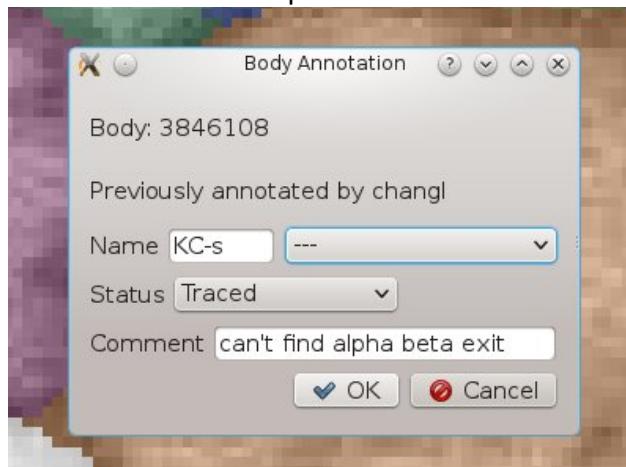
	down	s		
Change plane	up	e Right (arrow)	Mouse scroll wheel	Hold Shift key to increase the step of panning (Shift + A/S/D/W) or changing plane (Shift + Q/E/mouse scroll)
	down	q Left (arrow)		
Zoom in and out			Mouse right drag back and forth Ctrl+mouse scroll wheel	
User bookmark		g		Double click on user bookmark to edit bookmark annotation
Turn on measure tool		l		
3D view				
Draw a bounding box		Shift + r		
	Expand	Shift + click		Outside of current box
	Crop	x		Only in the split mode
Zoom in and out			Mouse scroll wheel	
Move the object vertically			Shift + mouse drag	
Find point in grayscale that corresponds with point on 3D model		Click + z		
Change skeleton geometry mode		Ctrl + g		
Split mode				
Draw a bounding box		Shift + r		
	expand	Shift + click		Outside of current box
Turn on seed painting		r		
Exit seed painting		Escape	Mouse right click	
Seed color change		1 to 7		
Quick seed color change		Shift + mouse click		
Projection		Ctrl + p		Use this to see a projection image of all seeds.
Zoom in and out			Mouse scroll wheel	
Move the object vertically			Shift + mouse drag	
Rotate the object			Mouse click + mouse drag	
Change paint brush size	smaller	q		
	larger	e		
Local split		Space		
Full split		Shift + Space		
Toggle split boundary		Ctrl + t		
Orthogonal View				
Toggle to grayscale; each window		f		
Toggle to grayscale; all windows (leave the cross hair)		d		

Body Annotations

After proofreading a body, users can edit the proofreading status or other biological information about the body/neuron.

How to annotate a body:

1. Select a body and choose 'Annotate' from the right click menu. The body annotation window opens.



User can edit Neuron Name, Status, and comment. For proofreaders, 'Status' is a very useful way to manage the proofreading status, such as 'Not examined, Traced, Partially traced'... etc.

Sequencer

By using Sequencer, users can see the list of bodies/neurons. It is also used for analyzing the neuron connections briefly. Click Sequencer button in the toolbar below or select <Tool>-<Open Sequencer> from Main menu. The window appears.

A screenshot of the Sequencer application. The main window shows a toolbar with icons for Bookmarks, Eyes, and other functions, followed by a list of synapses: 'Synapse (3361, 3239, 10656)'. A red circle highlights the 'Bodies' icon in the toolbar. An arrow points from this icon to a 'Body Information' panel on the right, which displays a table of body details. The table has columns for Body ID, name, # pre, # post, and status. The first few rows show:

Body ID	name	# pre	# post	status
13723880	PAM-sc5	154	334	Traced
14372907	PAM-10	130	336	Traced
13719714	PAM-4	123	386	Traced
14301234	PAM-sc4	118	281	Traced
15282447	PAM-13	116	332	Traced
16562174	PAM-8	106	658	Traced
16795383	PAM-9	101	264	Traced
14456457	PAM-sc1	98	271	Traced
13985691	PAM-sc3	97	204	Traced



Colors /Connections

Body information (Upper side of the window)

Body list: The list of all the bodies are shown in default.

#pre: Number of pre synapses on that body

#post: Number of post synapses on that body

Body filter: Filter the list of the result by any words or numbers in the columns

(Body ID, name, #pre, #post, or status)

Goto button: Selected bodies on the list will be sent to the main proofreading window.

Click on the body ID to select the body. Shift click to select multiple bodies.

Save color filter button: Refer “Color maps” in the next section.

Export bodies button:

Body Connection tab (Lower side of the window)

Body connection window shows Pre/Post synapse connections on a body.

1. Double click ‘#pre’ or ‘#post’ number in Body information list.
2. All the Outputs or Inputs bodies and numbers will be listed in the lower-left side of the window.
3. Double click “#” number in the list of Connections tab.
4. All the location (x, y, z) will be listed in the lower-right side of the window.
5. Double click “x”, “y” or “z” location on the list of Connections.
6. It will take you to the synapse location in Main Proofreading Window.

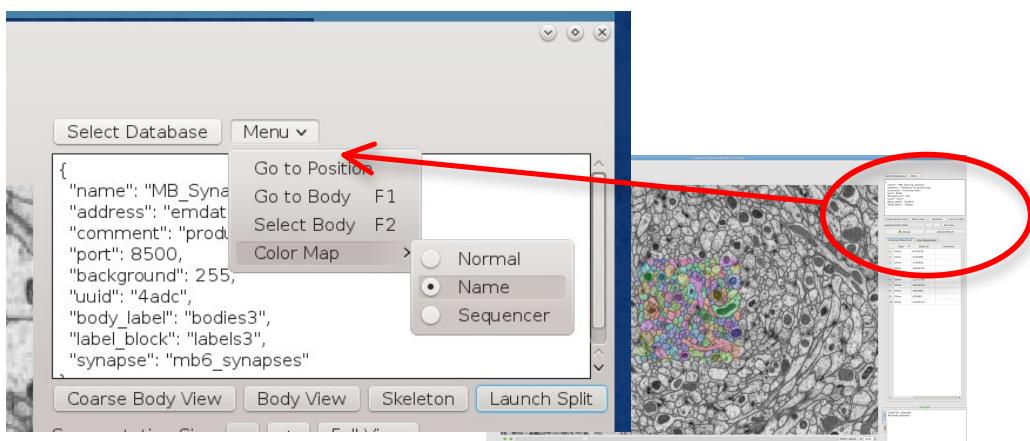
Colors tab

Refer “Color maps” in the next section.

Note: Information in Body information (upper side) is currently updated once a day. Body connection (lower side) is updated on time. Therefore it may show inconsistency between the numbers of each side of the window.

Color maps

Color maps highlight the bodies/neurons by name or status. The Color map is useful when you overview or analyze the result of proofreading.



Color Map by name: Neurons are highlighted by names. Currently the colors and the names are set by the software developer by requests.

- Press <Menu> -<Color Map>-<Name> in the main window. The named neurons are highlighted. Note that you need to be in the segmentation mode, not the transparent mode. (Press shortcut 'h' to toggle the mode)
- Press <Full View> in the main window as needed. Note that the full view ends when you change the section to avoid the poor performance due to the large data transmission.



Color Map by sequencer: Neurons are highlighted set by Sequencer.

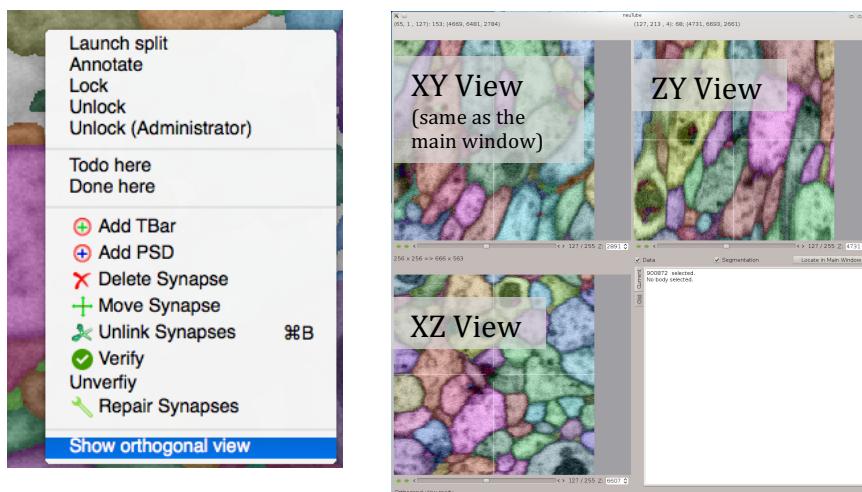
- Press <Menu> -<Color Map>-<Sequencer> in the main window.
- Open Sequencer in the main window.
- Search the neuron by Body filter in Sequencer. (See previous section 'Sequencer')
- Press <Save color filter> in Sequencer. Double click on the color to change the color scheme. User can save more than 2 color filters as needed. Press <Delete> to delete the color filter.
- In the main window, the neuron color is refreshed automatically.



- F. Save the color filter settings as a file as needed by <Save...>. Otherwise the setting is not saved after closing the sequencer window. If you want to load the saved color filter settings, press <Load...>.

Orthogonal View

Orthogonal viewer shows the image from different angle. To launch, right click on the 2D main window, and select menu ‘show orthogonal view’.



together, press D.

The user also can zoom in/out and put annotations.

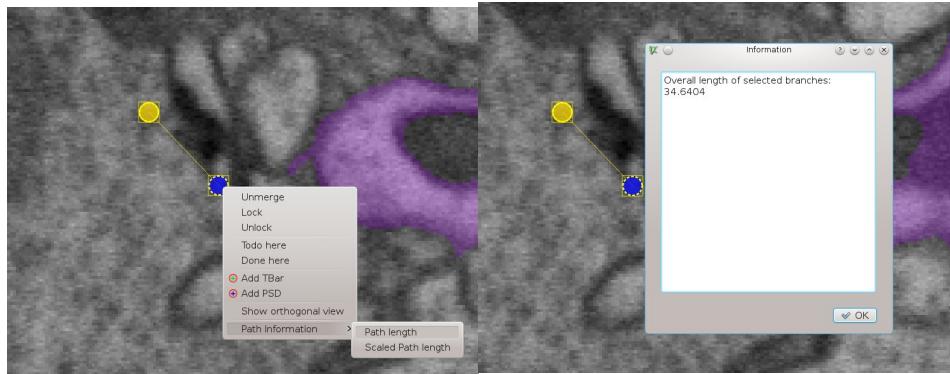
To toggle the segmentation and annotations on the individual view, press F on each view. To toggle to the transparent mode, press H.

To toggle the segmentation and annotations all

Measuring tool

By using measuring tool, the user can measure the distance between two points.

1. To launch, use the short-cut 'I' and click to place the first checkpoint.
2. Select the first checkpoint, and place other checkpoint(s). They are automatically linked. To stop placing the points, right click.
3. To see the length between checkpoints, select **ALL** the checkpoints you would like to measure by Ctrl+ click, and choose the right click menu 'Path information'- 'Path length'.



Settings

