

BiolmageVision

User Guideline

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User Notice

i. System Requirements

Operating System	Windows 10
Pyramid Data Generation Module	RAM>=128 GB
Data Visualization Module	Graphics memory>=4GB

ii. Overview of Functionality

As shown in the red box in Figure 1, click **File** → **Open** to import data; **Help** contains the developer's contact information.

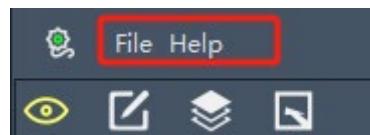


Figure 1.

Convert the original 2D sequence images into Biomedical Video Stream (Bio-VS) format or Ome-Zarr format; More details can be seen in [chapter 1](#).

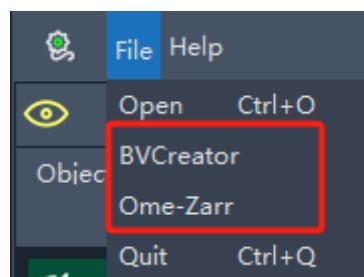


Figure 2.

As shown in Figure 2:

- 1) is Data Visualization Module; More details can be seen in [chapter 2](#).
- 2) is Visualization module of branch browsing, see in [chapter 3](#).
- 3) is 2D View module of arbitrary slice, see in [chapter 4](#).
- 4) is Maximum Intensity Projection; see in [chapter 5](#).



Figure 2.

iii. Toolbar for visualization

Toolbar for visualization as showed in Figure 3.



Figure 3

- 1) Reset the camera view to the XY/YZ/XZ directions.
- 2) will capture a screenshot of the visualization area to the local system.
- 3) allows you to annotate the visualization area data; for details, see in [chapter 2.6](#).
- 4) **2D View:** switch of 2D/3D view, see in [chapter 2.7](#).
- 5) **Multi Volume:** Visualization of multi-channel data, see in [chapter 2.8](#).

iv. Description of modules

- 1) Pyramid Data Generation Module

Convert the original 2D sequence images into Bio-VS format data or Ome-Zarr format data. See in [chapter 1](#).

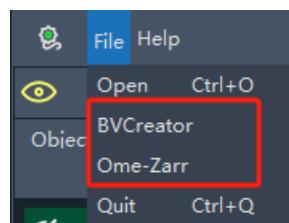


Figure 4

- 2) Visualization module

As shown in Figure 5, the red box represents the rendering list, the orange box represents the main scene of visualization area, and the blue box represents the rendering object properties. For detailed information, please refer to [chapter 2](#).

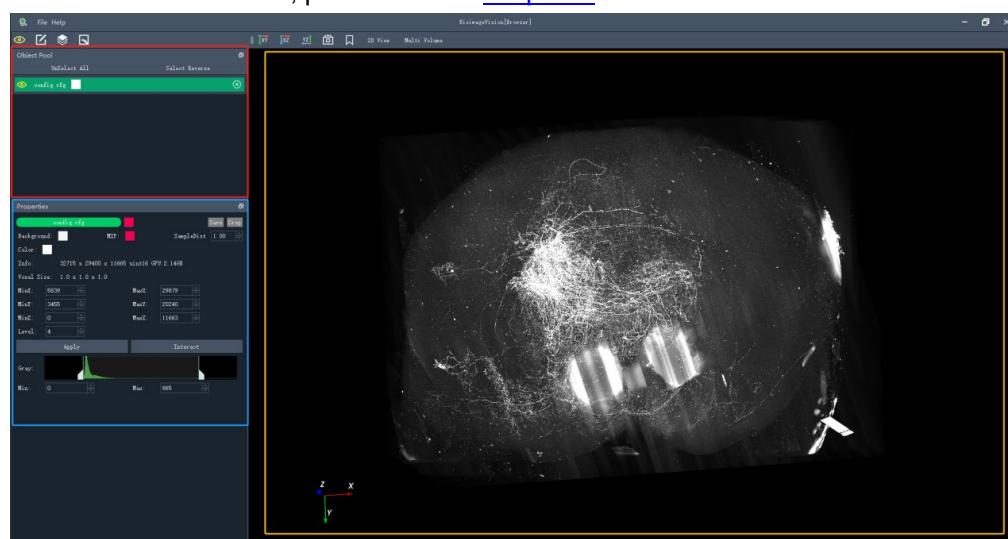


Figure 5

3) Visualization of branch browsing

As shown in Figure 6, the red box indicates the data properties, the orange box shows the number of fiber branches, and the blue box represents the visualization area. For detailed information, please refer to [chapter 3](#).

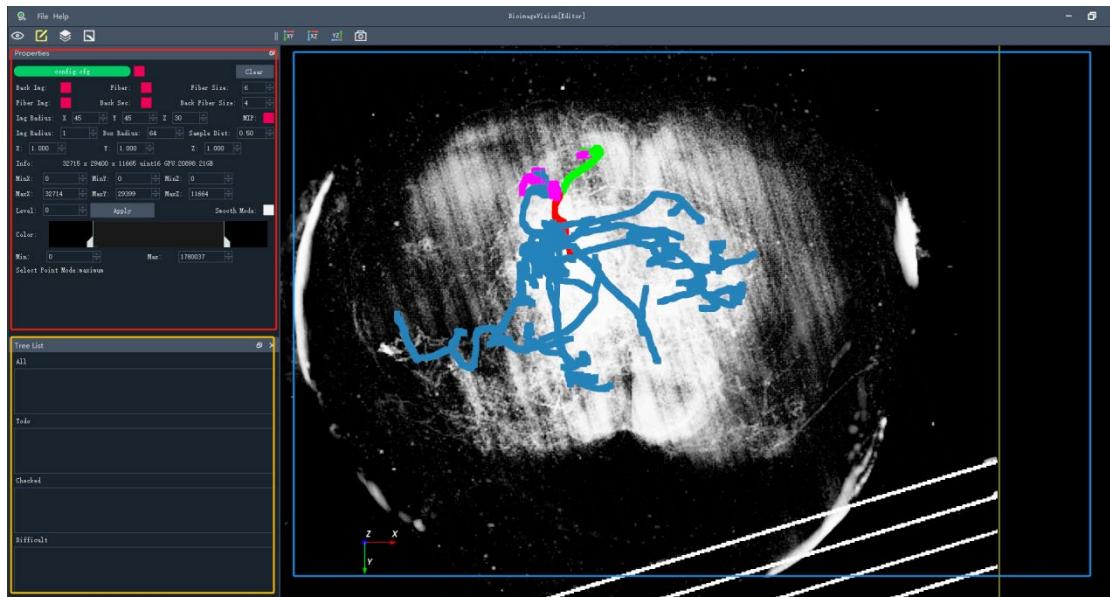


Figure 6

4) 2D view of arbitrary slice

As shown in Figure 7, the red area represents the properties of the Bio-VS format data, the blue box contains the list of annotation categories and annotations, and the green box shows the 2D data visualization area. For detailed information, please refer to [chapter 4](#).

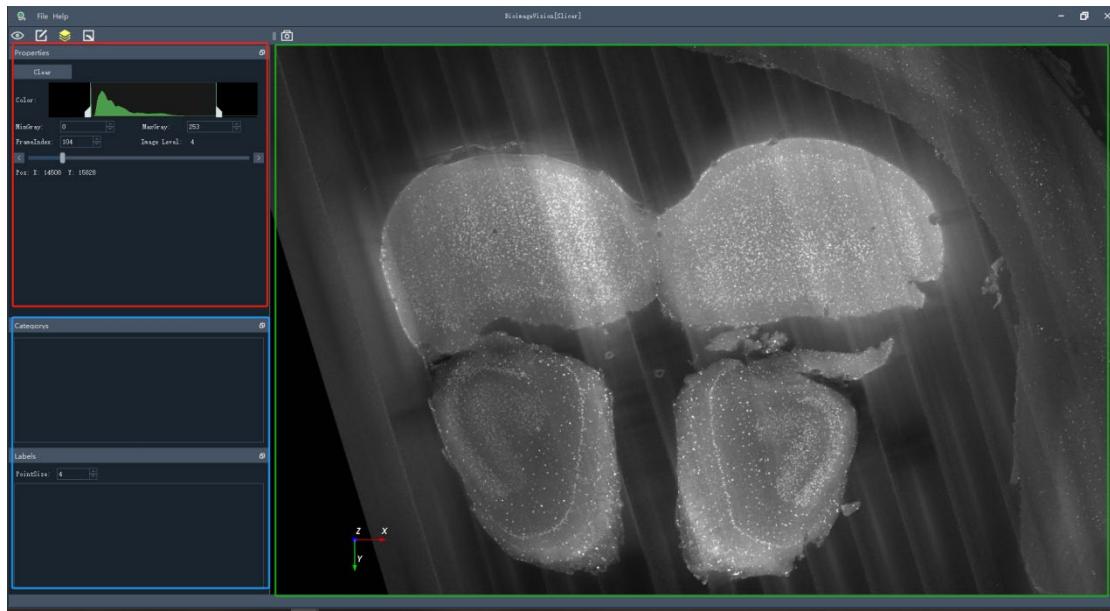


Figure 7

5) Maximum Intensity Projection

As shown in Figure 8, the red box shows the list of 2D sequence images generated by the maximum intensity projection, the orange box displays the data properties, and the blue box is the data visualization area. For detailed information, please refer to [chapter 5](#).

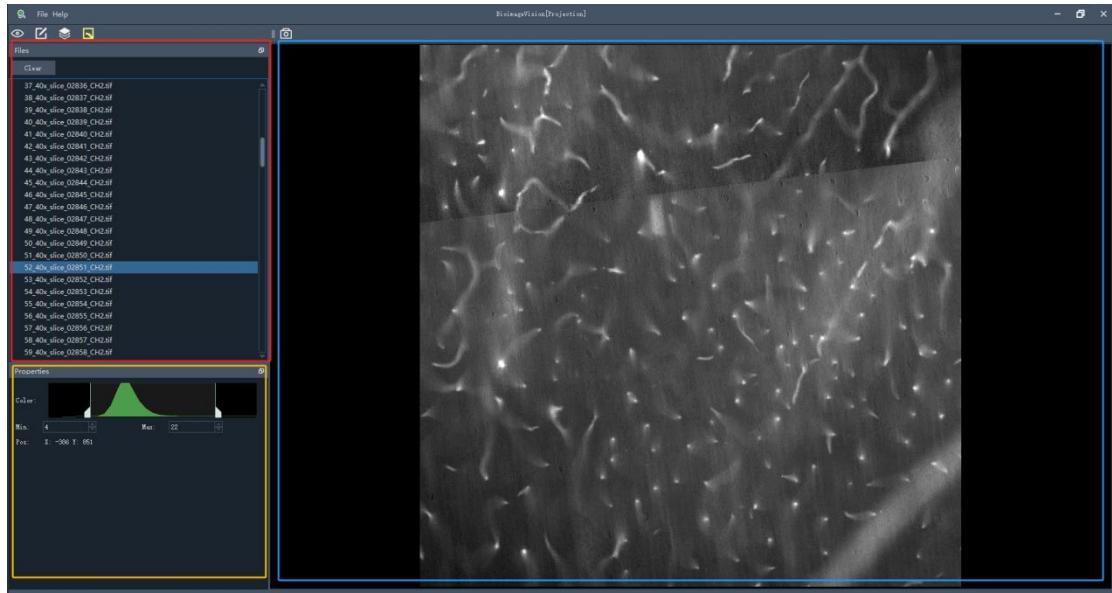


Figure 8

1. Pyramid Data Generation Module

In the visualization area, click **File**, and the contents in the orange box shown in Figure 1.1.1 will appear; **BVCreator** is for creating Bio-VS format big data; **Ome-Zarr** is for creating Ome-Zarr format big data.

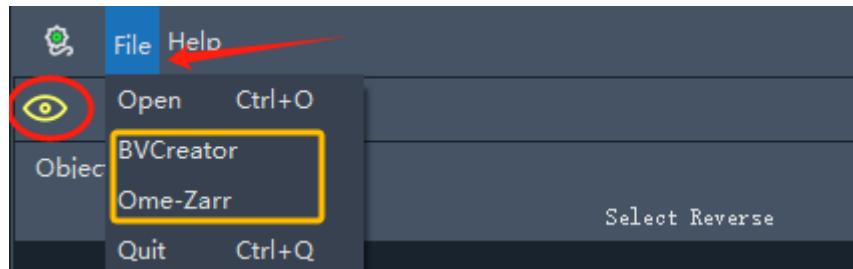


Figure 1.1.1

1.1 Generation of Bio-VS format data

1.1.1 Enter the Bio-VS format data generation module

Click **BVCreator** in Figure 1.1.1 to enter the Bio-VS format data generation module, as shown in Figure 1.1.2.

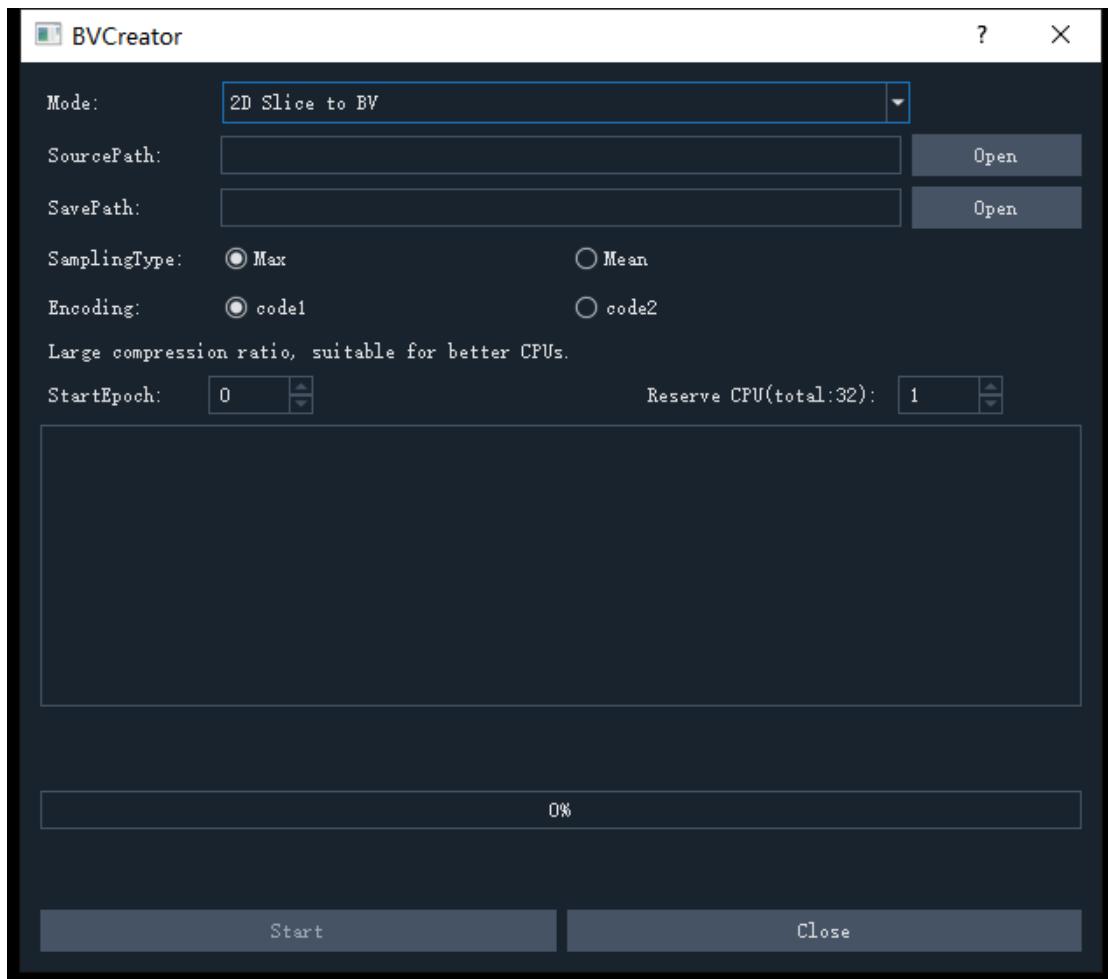


Figure 1.1.2

1.1.2 Introduction to the parameters of Bio-VS format data generation module

The following paths do not support Chinese:

- **SourcePath:** Data input path, the input data format is raw 2D sequence images in TIF format.
- **SavePath:** Data output path, the output is Bio-VS format (Input and output data should be stored on separate hard drives for faster read and write speeds).
- **SamplingType:** Sampling method, **Max** (maximum value sampling) or **Mean** (mean value sampling), default is maximum value sampling.
- **Encoding:** Encoding method.
- **StartEpoch:** The starting epoch number for format creation, default is 0. (If the creation process fails due to power outages or other reasons, the **startEpoch.txt** file can be found in the **SavePath** directory. The number in this file can be entered here to continue the creation process).
- **Reserve CPU (total: 32):** The number of CPU cores reserved for the system.

1.1.3 Process of generating Bio-VS format

The following paths do not support Chinese

- 1) Select the input path for the raw 2D sequence and the output path for the Bio-VS format data; other parameters remain unchanged. Click the **Start** button at the bottom left shown in Figure 1.1.3. The input and output paths should be on separate hard drives to maximize the utilization of the resources.

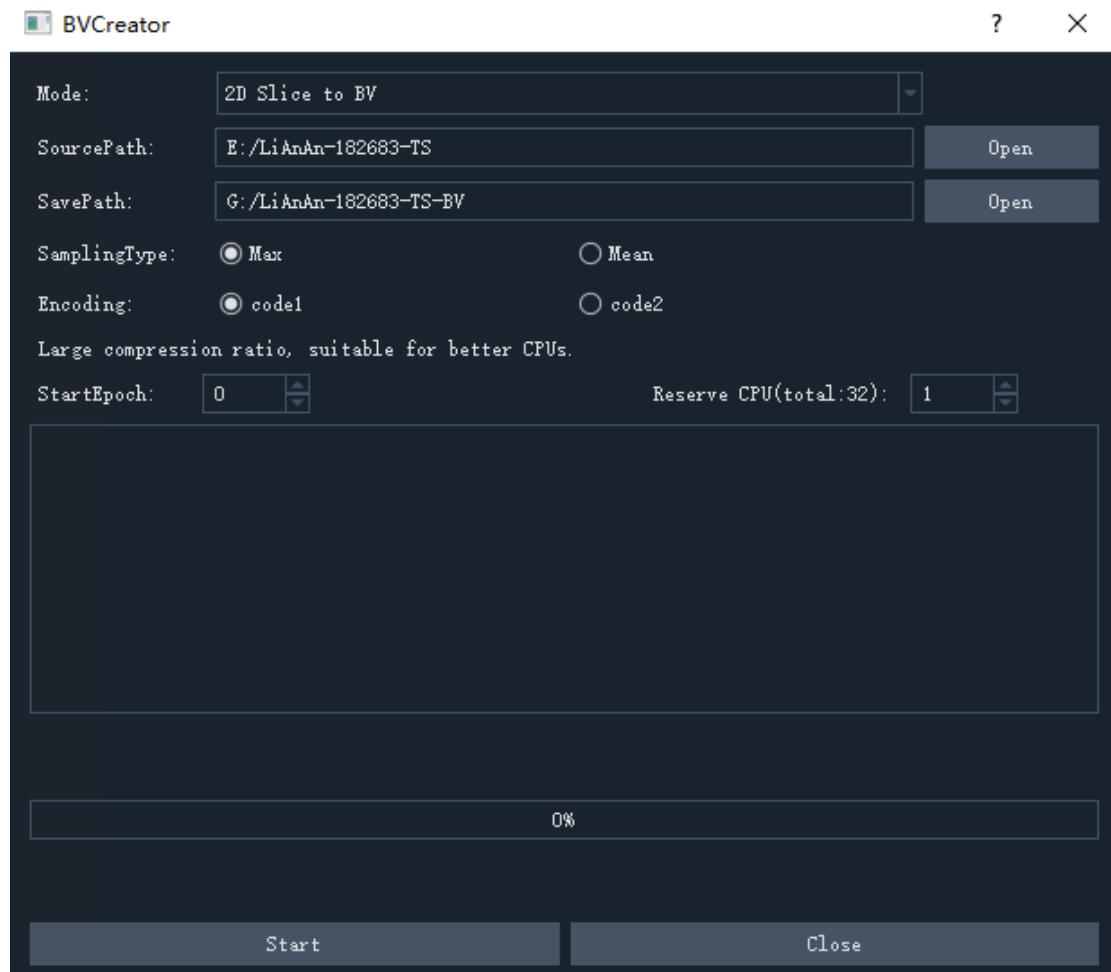


Figure 1.1.3

- 2) After clicking **Start**, the following prompt box will appear (shown in Figure 1.1.4). Click the **OK** button at the bottom.

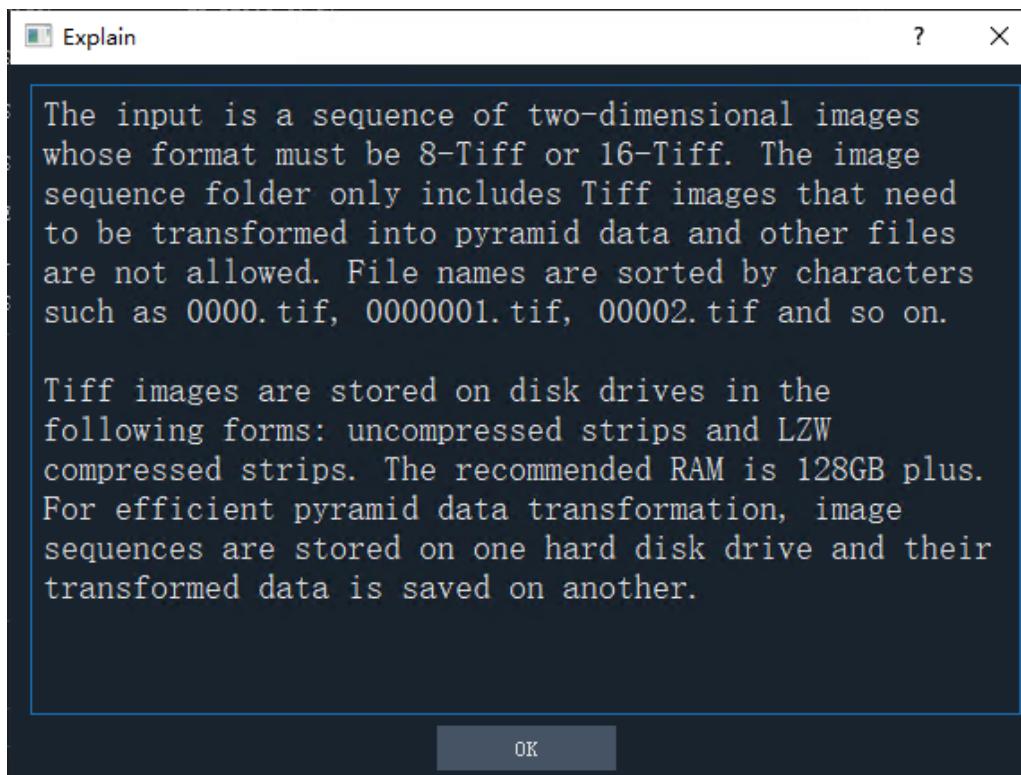


Figure 1.1.4

- 3) After clicking **OK**, if there are [other files \(other than the 2D sequence images\)](#) in the [directory](#), a prompt box as shown in Figure 1.1.5 will appear. **Click Auto Delete to delete the file. Please confirm carefully before clicking** (or move the files elsewhere). Then, continue by clicking the **OK** button in the prompt box shown in Figure 1.1.6.

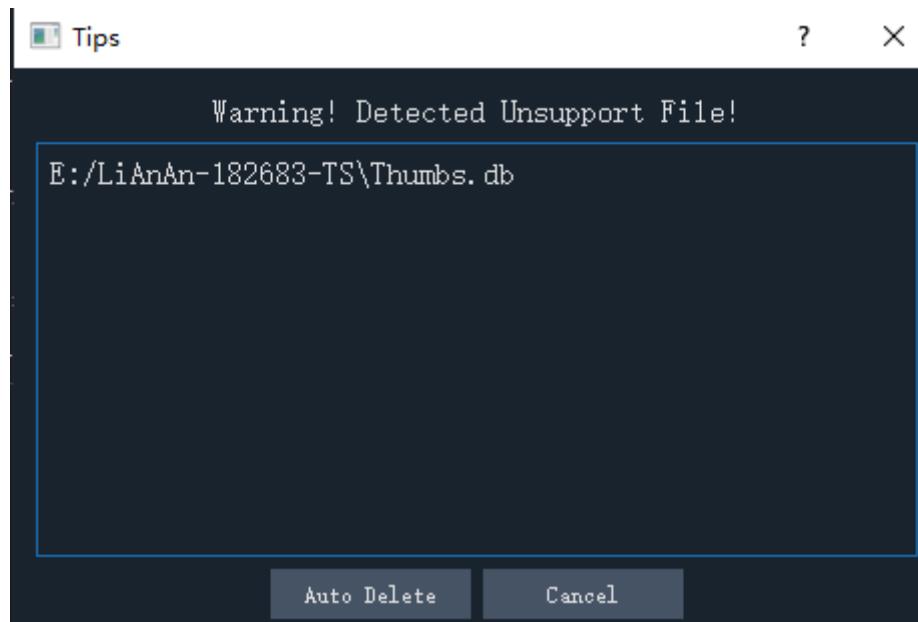


Figure 1.1.5

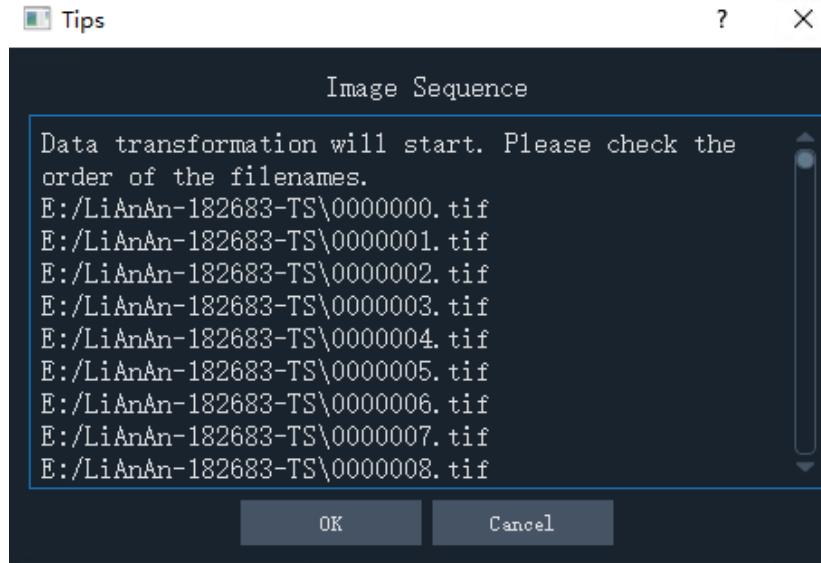


Figure 1.1.6

- 4) After clicking the **OK** button, as shown in Figure 1.1.7, the Bio-VS format data is being generated (the processing time depends on the type of hard drive and the size of the raw data).

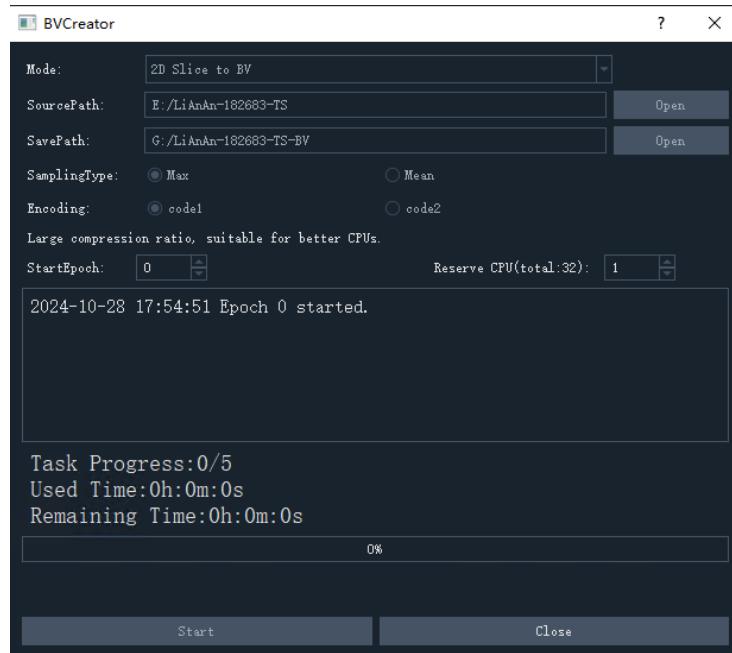


Figure 1.1.7

- 5) As shown in Figure 1.1.8, the intermediate result indicates that the first round of processing is complete, taking 1 hour and 43 minutes. An estimated 6 hours and 54 minutes are still needed to finish the entire process.

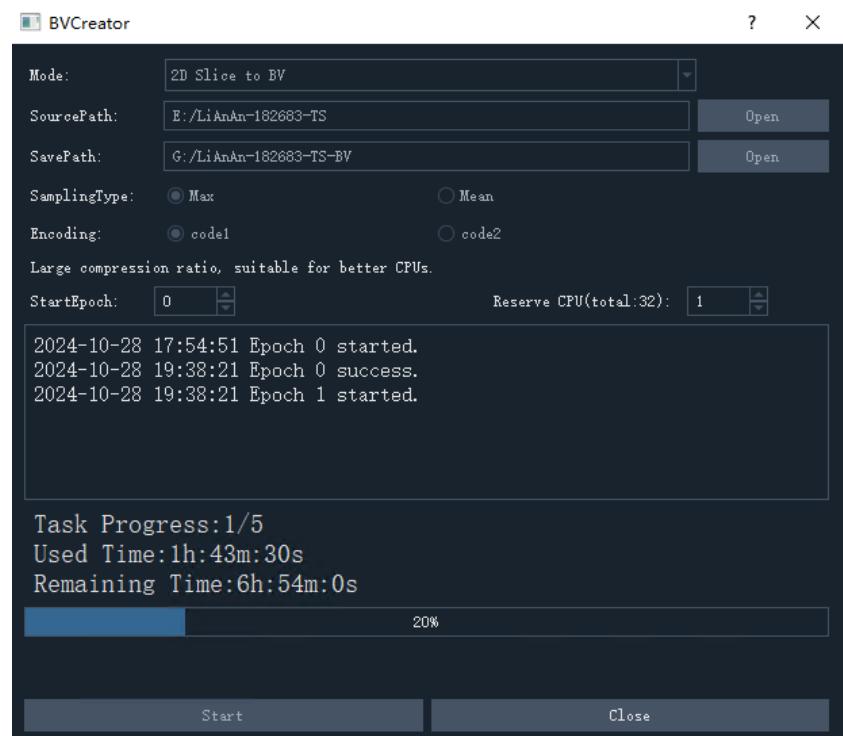


Figure 1.1.8

- 6) As shown in Figure 1.1.9, the Bio-VS format data generation is complete, taking 14 hours, 43 minutes, and 33 seconds. Click **OK** to proceed.

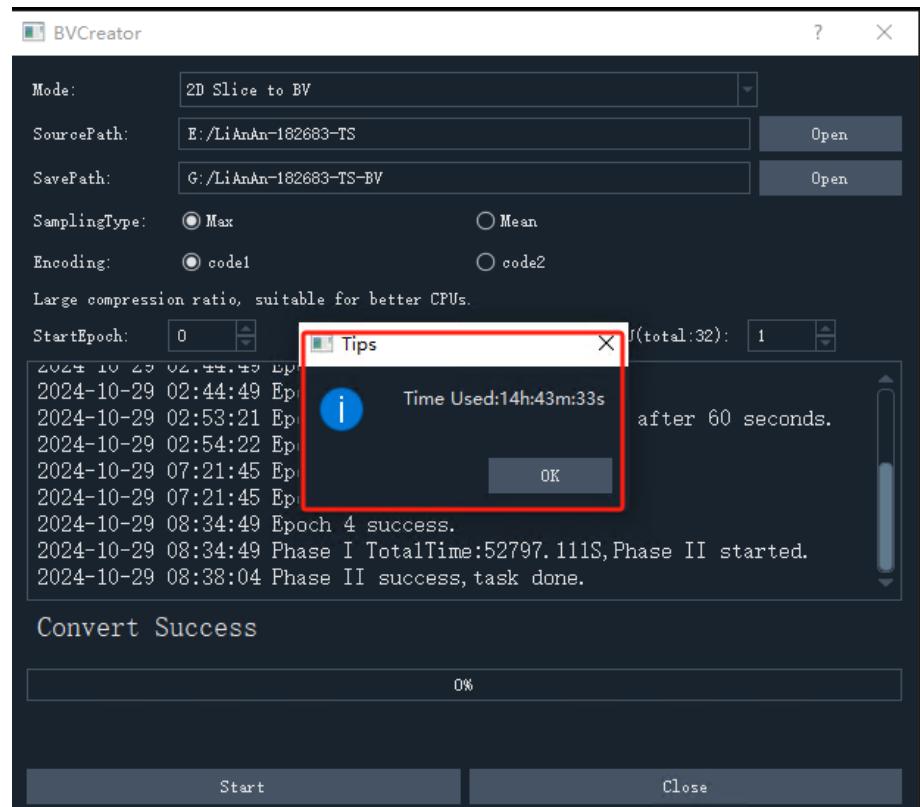


Figure 1.1.9

7) As shown in Figure 1.1.10, click **Close**.

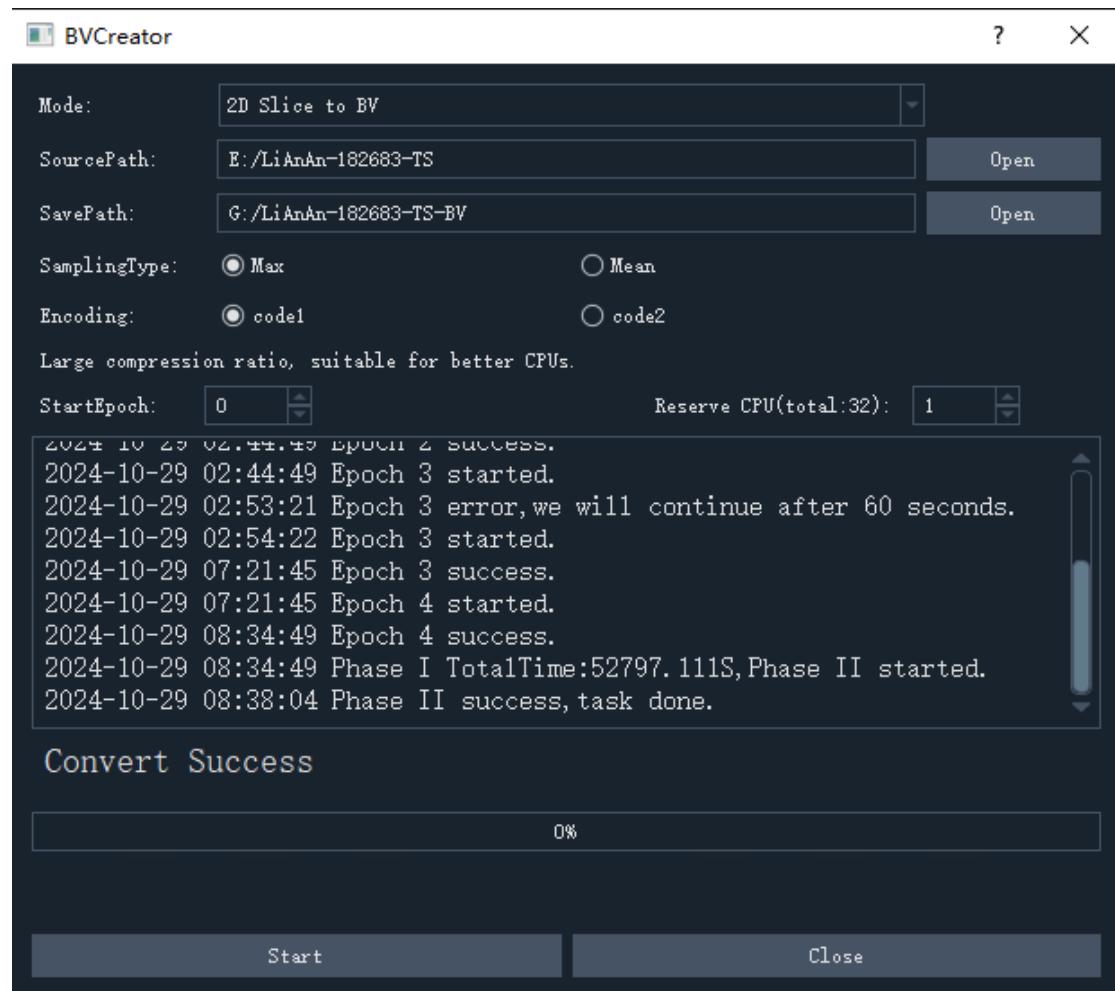


Figure 1.1.10

8) Enter the Bio-VS format data output path, the directory where the generated data is stored as shown in Figure 1.1.11.

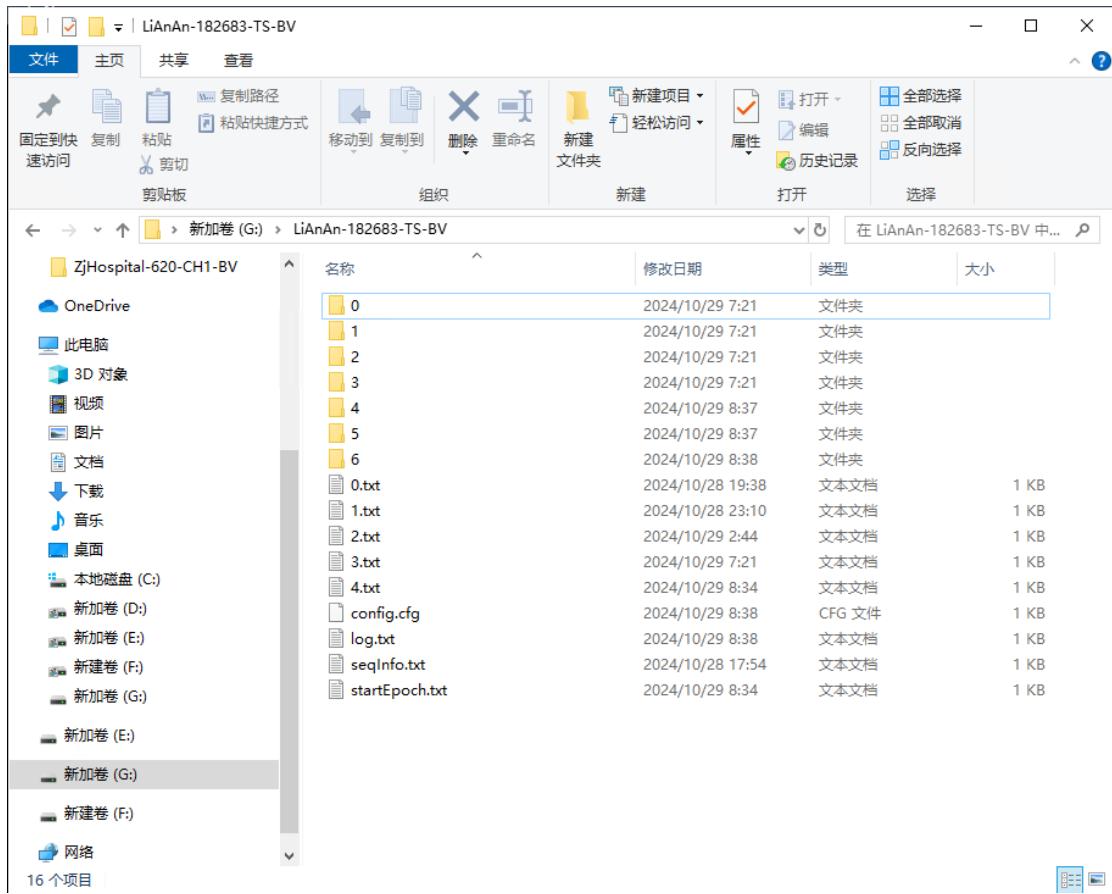


Figure 1.1.11

9) Import the successfully generated Bio-VS format data into the Data Visualization Module for viewing, as shown in Figure 1.1.12.

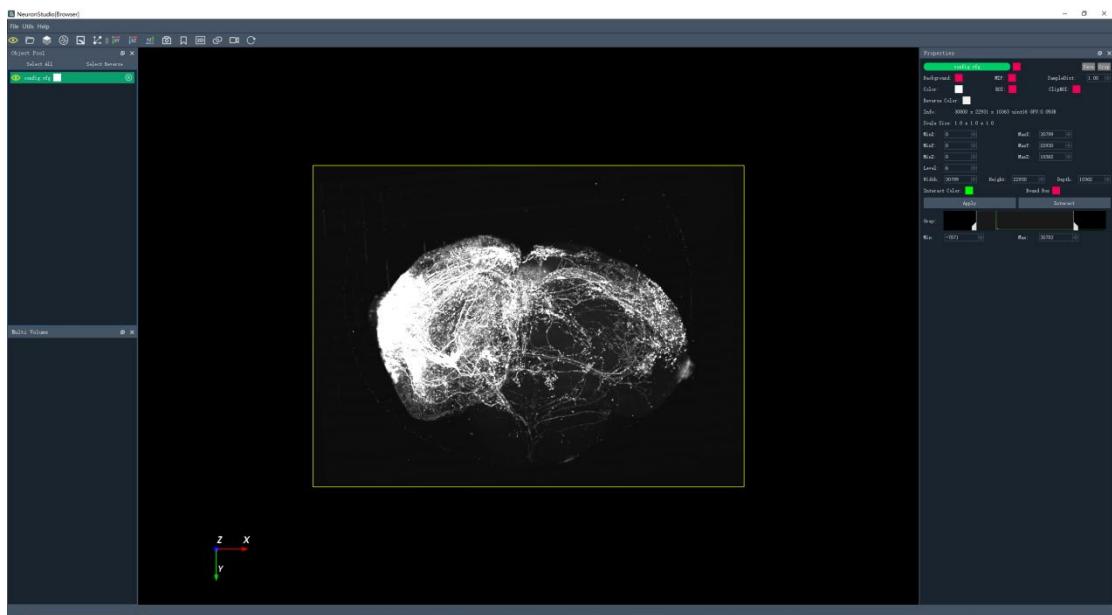


Figure 1.1.12

1.2 Generation of Ome-Zarr format data

1.2.1 Enter the Ome-Zarr format data generation module

Click **Ome-Zarr** in Figure 1.2.1 to enter the Ome-Zarr format data generation module, as shown in Figure 1.2.1.

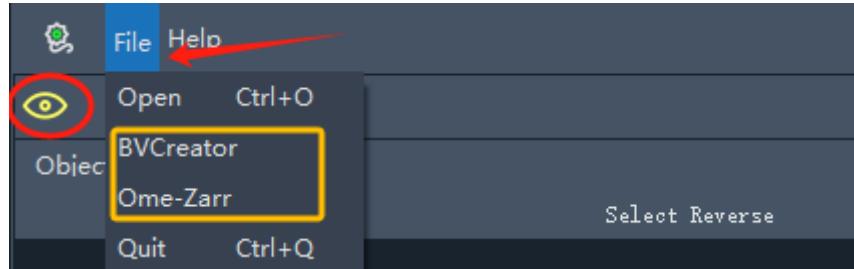


Figure 1.2.1

1.2.2 Introduction to the parameters of Ome-Zarr format data generation module

The following paths do not support Chinese

- **ImagePath**: Data input path, the input data format is raw 2D sequence images in TIF format.
- **Save Path**: Data output path, the output is Ome-Zarr format (Input and output data should be stored on separate hard drives for faster read and write speeds).
- **SamplingType**: Sampling method, **Max** (maximum value sampling) or **Mean** (mean value sampling), default is maximum value sampling.
- **StartEpoch**: The starting epoch number for format creation, default is 0. (If the creation process fails due to power outages or other reasons, the **startEpoch.txt** file can be found in the **SavePath** directory. The number in this file can be entered here to continue the creation process).
- **Reserve CPU (total: 12)**: The number of CPU cores reserved for the system.
- **SmallSize**: Base block size in the big data pyramid, it is recommended to set **X, Y, Z** to 512 (Do not modify unless necessary).

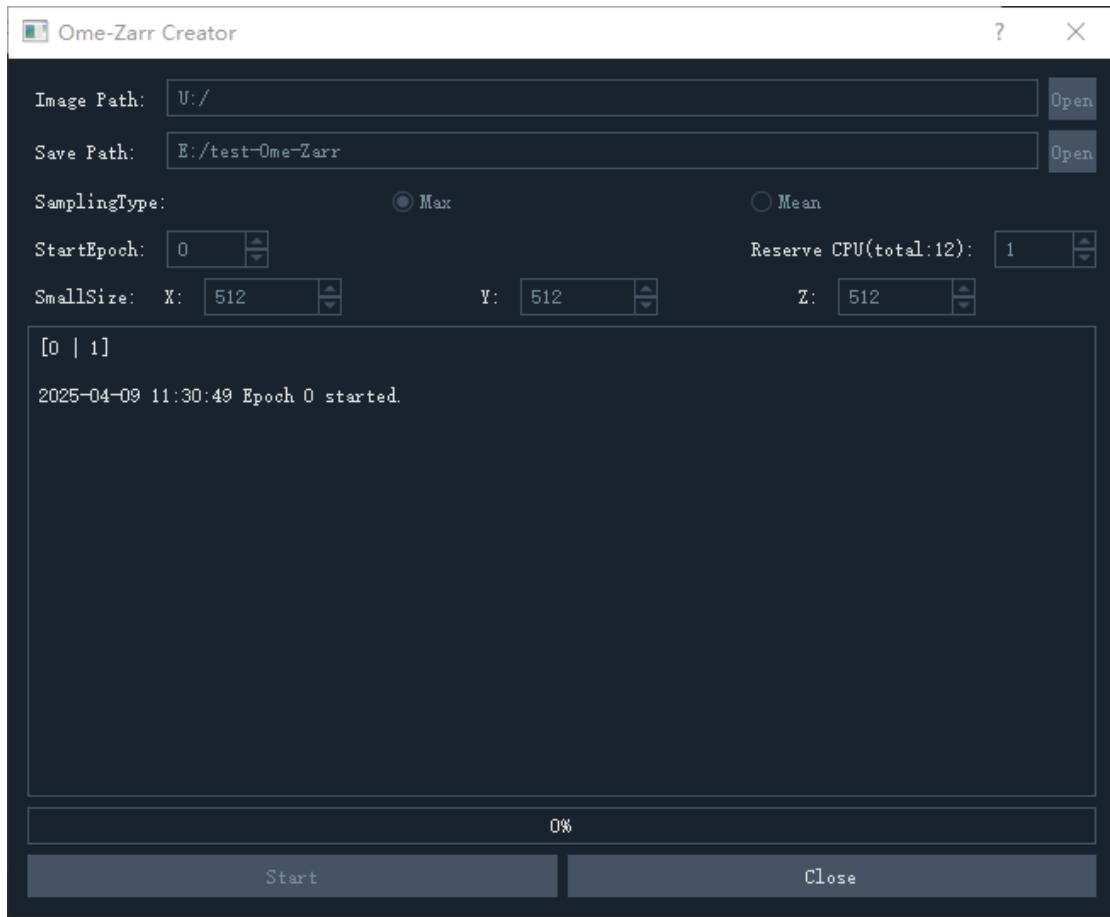


Figure 1.2.2

1.2.3 Process of generating Ome-Zarr format

The following example uses a small dataset, so the creation process is relatively fast. (For regular datasets, the process may take longer. Please be patient).

- 1) Select the path to the raw 2D sequence images and choose the save path.
- 2) Click **Start** to begin the generation process.
- 3) When the progress bar reaches 100%, the creation is complete.
- 4) You can then view the generated Ome-Zarr format data in the save path, as shown in Figure 1.2.4.

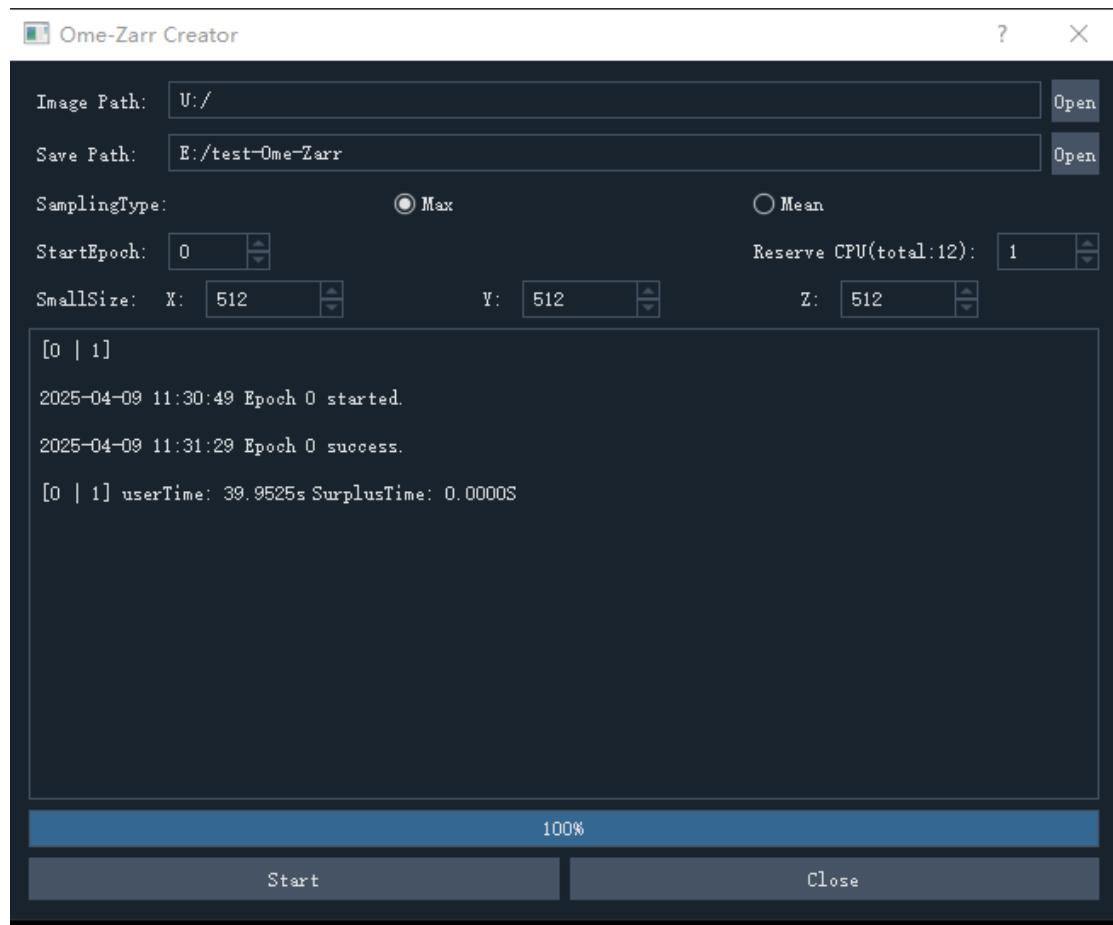


Figure 1.2.3

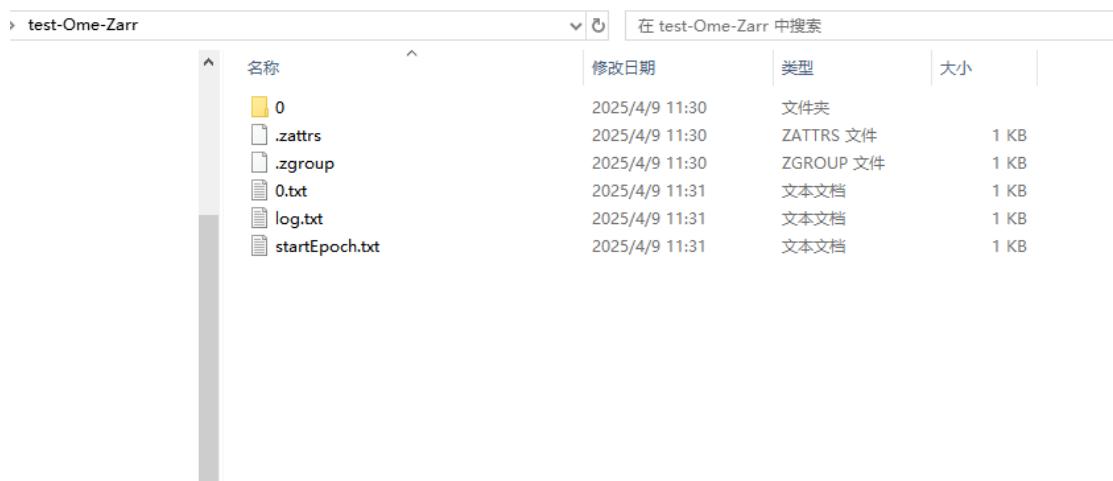


Figure 1.2.4

2. Data Visualization Module

2.1 Visualization for Bio-VS format

2.1.1 Enter the visualization module

Click  in the top-left toolbar to enter the data visualization module. In the menu bar, click **File → Open** to import data (Alternatively, you can directly drag the data into the render object list.).

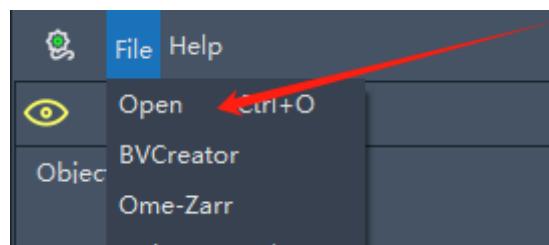


Figure 2.1.1

2.1.2 Data import

Import the successfully generated Bio-VS format data, click **Config** and select **Open**. (For details on how to create BV big data, see Section [chapter 1.1](#)).

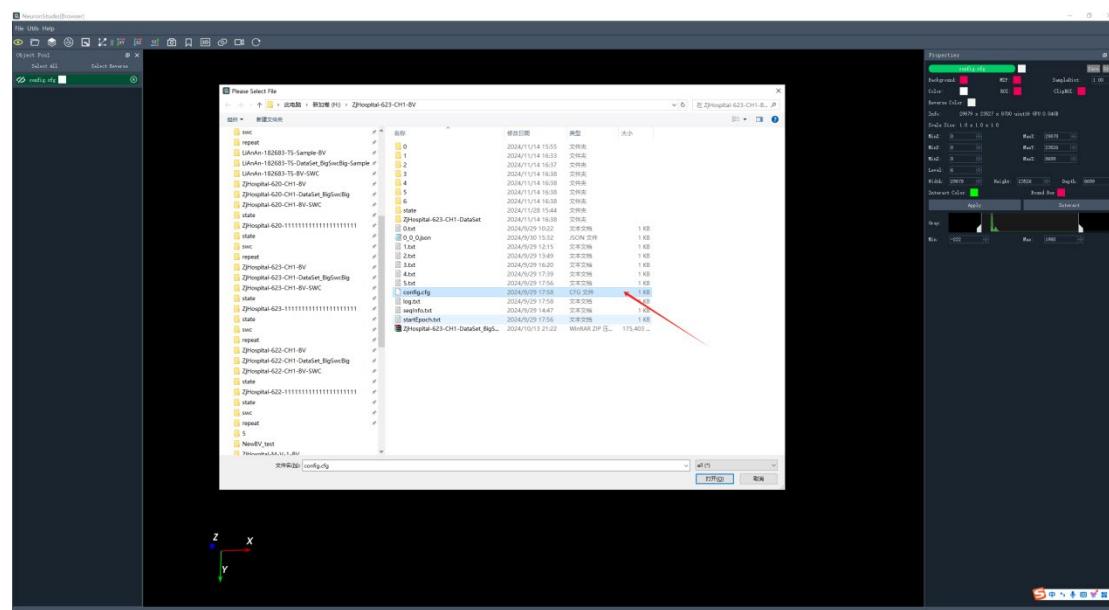


Figure 2.1.2

2.1.3 Introduction to the data rendering list

The **Object Pool** contains the list of imported data for rendering.  indicates that the data can be visualized in the display area on the right. Clicking it will change to , disabling the visualization. Clicking the  will remove the data from the list. You can also select or deselect all items in the list.

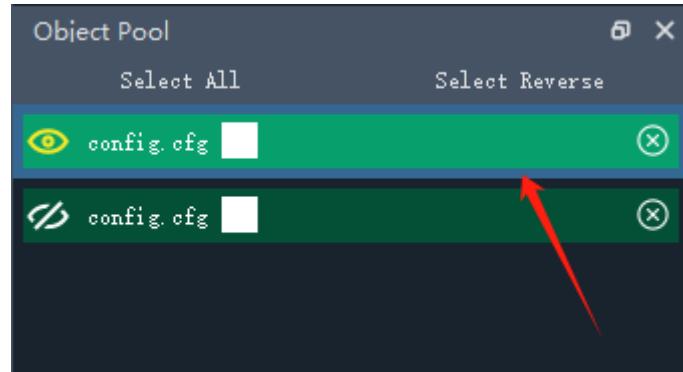


Figure 2.1.3

2.1.4 Introduction to data properties

The **Properties** panel displays the attributes corresponding to the imported data. Click on a data item in the **Object Pool** (as shown in Figure 2.1.3, a blue border around the data name indicates it is selected), and the attributes of the selected data will appear on the right side of the page (as shown in Figure 2.1.4).

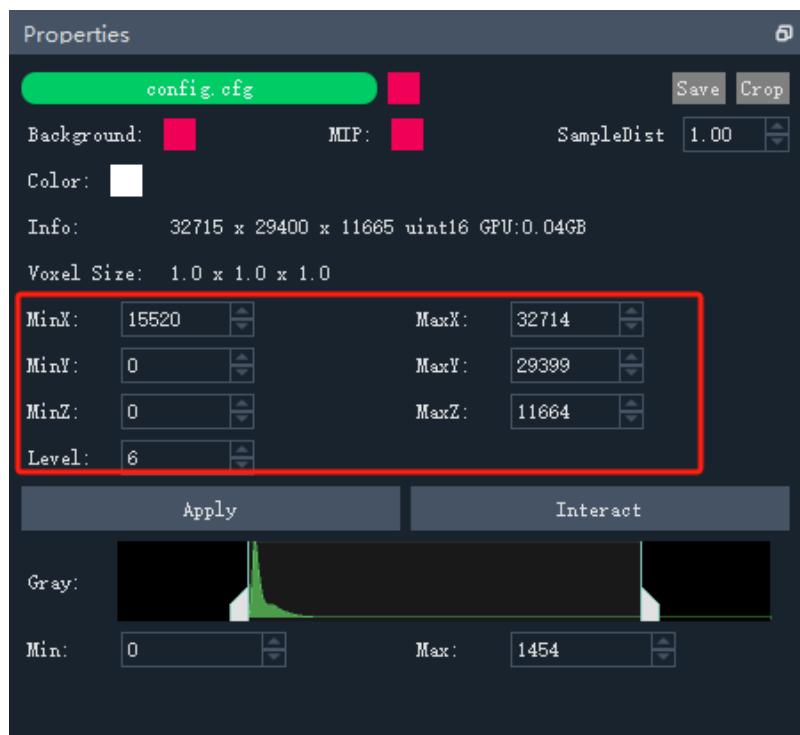


Figure 2.1.4

Notes:

- 1) Click the red square next to the data name  to hide the entire image.
- 2) Click the red square next to **Background** to hide all parts of the image outside the region of interest (ROI).
- 3) **MIP** stands for Maximum Intensity Projection. Click the red square next to **MIP** to disable the MIP mode.
- 4) **SampleDist**: Sampling distance, the smaller the value, the higher the image quality, but the more laggy the interaction (the default value is recommended).
- 5) **Color**: Set the image color mapping.
- 6) **Info** shows the image size. **unit16** indicates 16-bit data; **GPU: 0.06GB** shows the current GPU memory used for visualization.
- 7) **Save**: Saves the current ROI image of the viewed data. For ROI image settings, see steps 9, 10, and 11 below.
- 8) **Voxel Size** refers to the image resolution. Click **Crop** in the upper-right corner of the Properties panel to open the window shown in Figure 2.1.5, where you can adjust the resolution under **Resolution**.

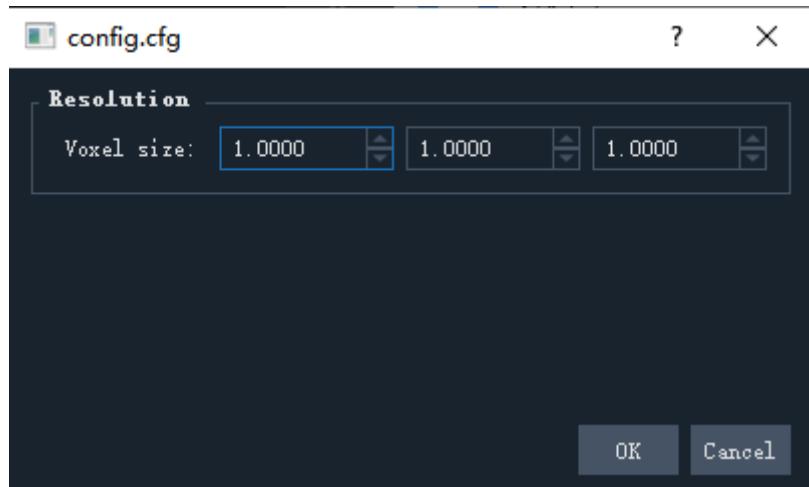


Figure 2.1.5

- 9) As shown in the red box in Figure 2.1.4, you can either manually enter the ROI coordinates or click **Interact** to select the ROI region (see the red arrow in Figure 2.1.6. left-click and hold the small spheres, then drag to adjust the region).

You can also press and hold the middle mouse button to move the ROI bounding box. Click **Apply** to confirm the selected region (as shown in the rectangular box). Click **Interact** again to hide the ROI bounding box.

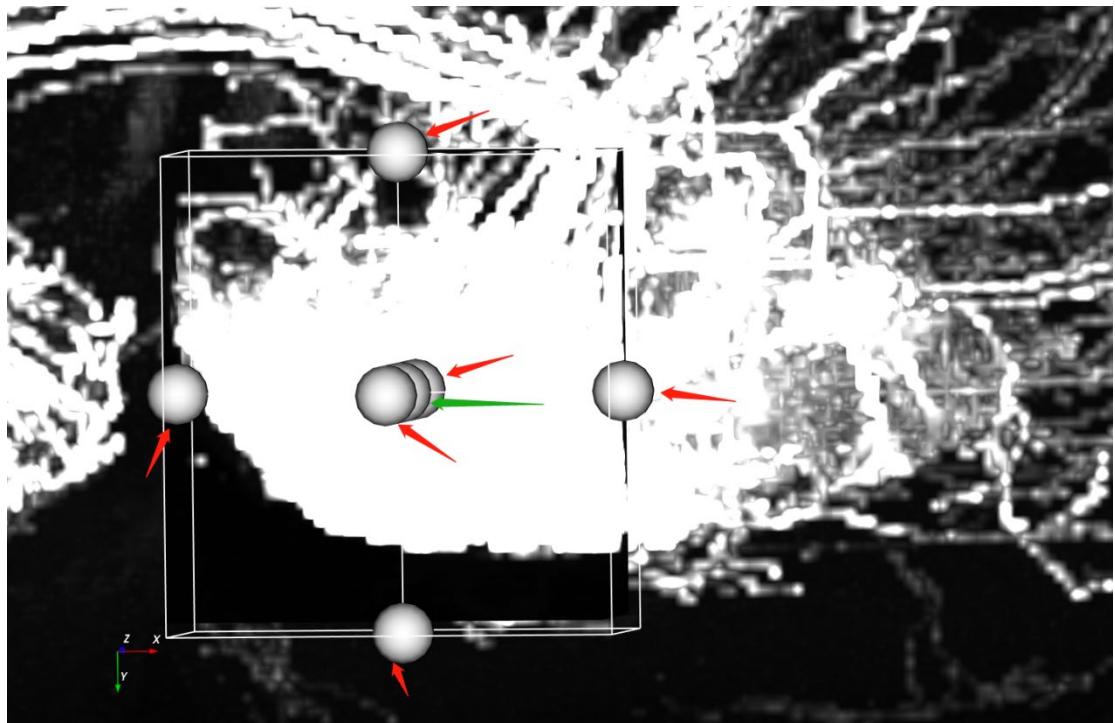


Figure 2.1.6

10) **Level:** Set a level value (the default is the maximum level defined in the configuration file) to adjust the display resolution of the image. The smaller the Level value, the clearer the image. For example, level value in Figure 2.1.6 is 6, while 1 in Figure 2.1.7.

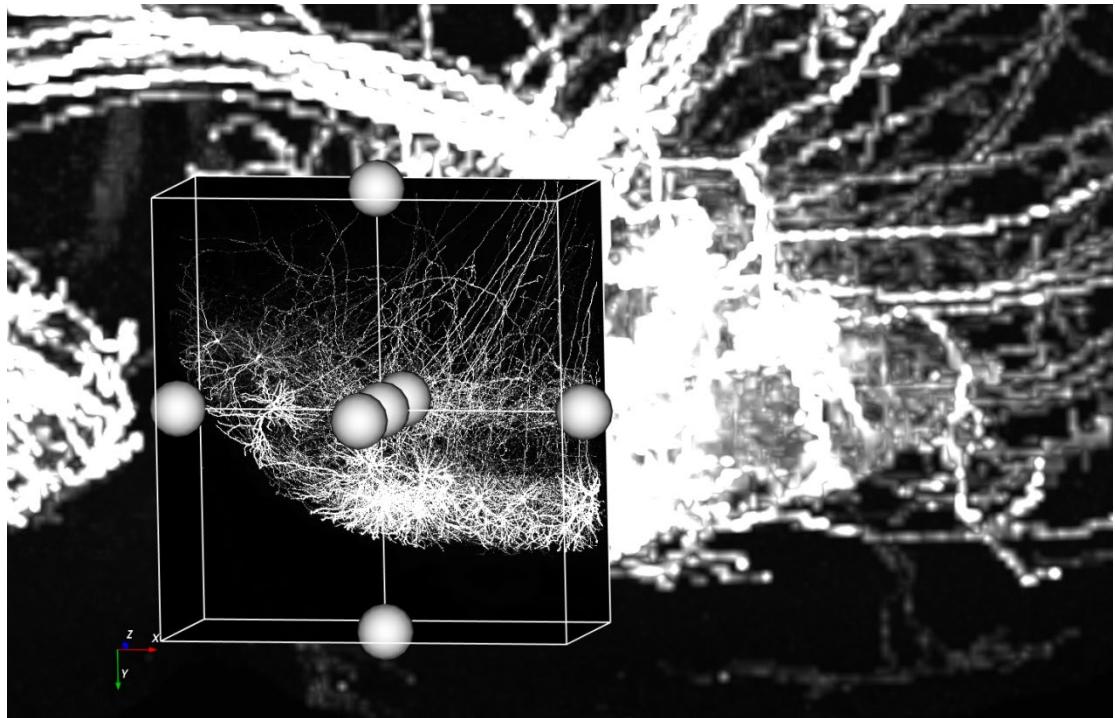


Figure 2.1.7

Note: When the selected region is too large and the Level value is set too low, there may not be enough GPU memory. In this case, a small window will appear to alert you, as shown in Figure 2.1.8.

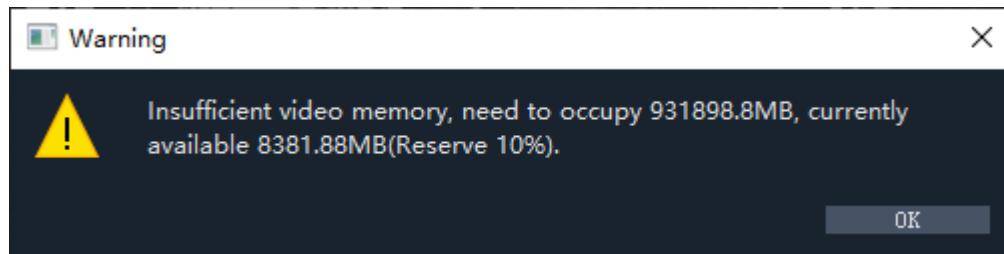


Figure 2.1.8

11) As shown in Figure 2.1.9, you can directly enter the ROI width, height, and depth (set the level to 0). Click **Apply** to load the current ROI image, and the visualization area will display the image with the corresponding size. Click **Save** to save the currently loaded ROI image.

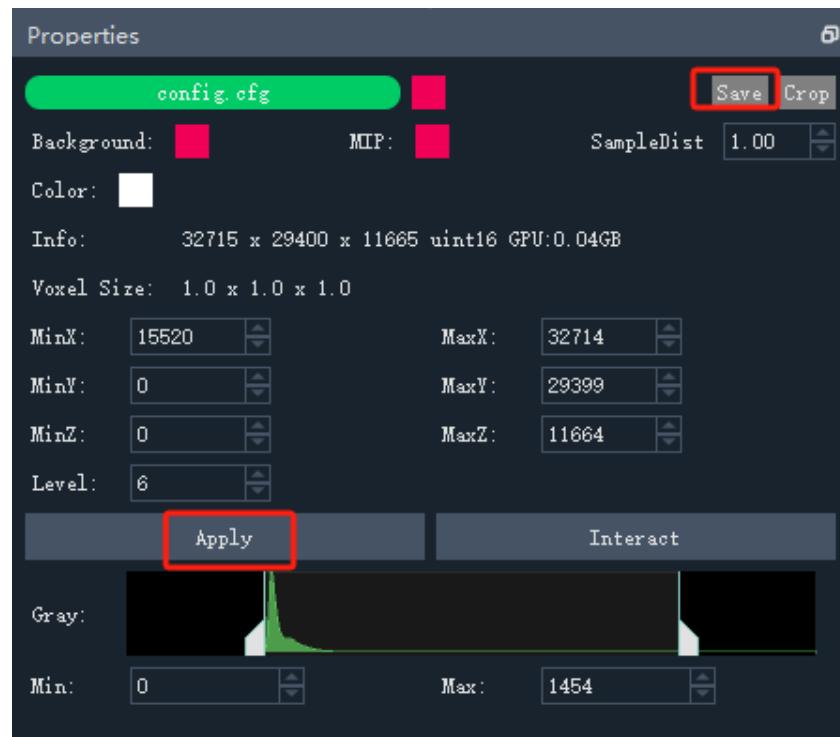


Figure 2.1.9

12) You can adjust the gray values by dragging within the histogram range in the **Color** section. Alternatively, you can input values directly into the **Min** or **Max** input fields and press Enter after entering the value.

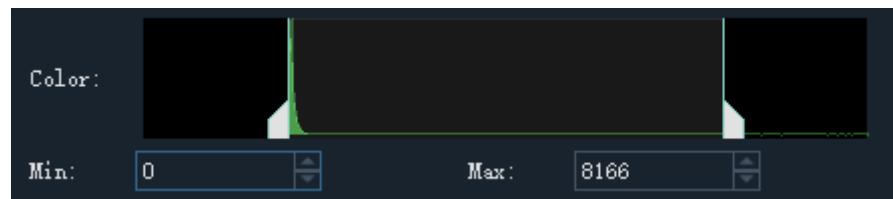


Figure 2.1.10

2.2 Visualization of 3D TIF data

2.2.1 Data import

Click  to enter the data visualization module. In the menu bar, click **File** → **Open** to import data (Alternatively, you can directly drag the data into the render object list.). The **Object Pool** area contains the list of rendering data.

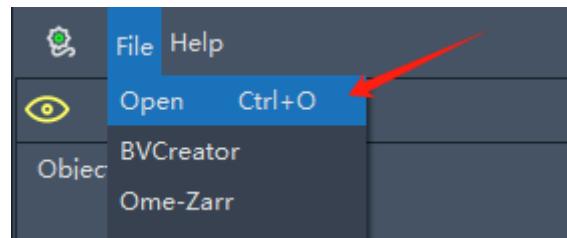
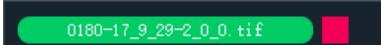


Figure 2.2.1

2.2.2 Introduction to data properties



Figure 2.2.2

-  The red square shows/hides the data block (shortcut key **A**).

- **UseMIP :**  The red square enables/disables the MIP mode.
- **Bound Box:** Displays/hides the image bounding box.
- Click **Crop** to adjust the resolution. The **Image Crop** function allows you to crop the current data, which will change the visualization range of the image (As show in Figure 2.2.3).

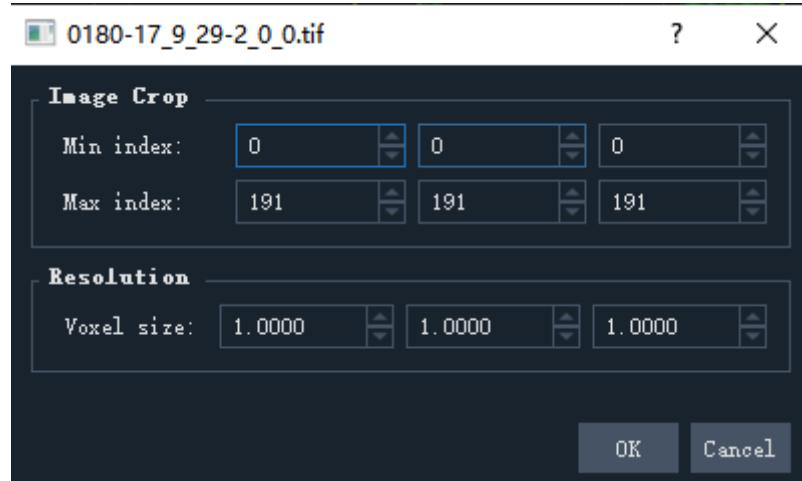


Figure 2.2.3

- **Interpolation:** The interpolation method, **Nearest** (nearest neighbor interpolation) or **Linear** (linear interpolation). Nearest interpolation results in a pixelated effect. (Used in the 2D module).
- **Projection:** Projection along the corresponding X, Y, or Z direction.
- **Info:** Information about the image.
- **Voxel Size:** The resolution of the image.
- **Surface:** Surface extraction.
- **Color:** The color of the image.
- **Reverse Color:** Inverts the colors. For Golgi-stained data, the image appears black. Reversing colors is necessary while visualizing and analyzing these kinds of data.
- **Gray:** The grayscale histogram.
- The original image is showed in Figure 2.2.4. After applying surface extraction (color set to green and adjust the image gray scale), the effect is displayed in Figure 2.2.5.

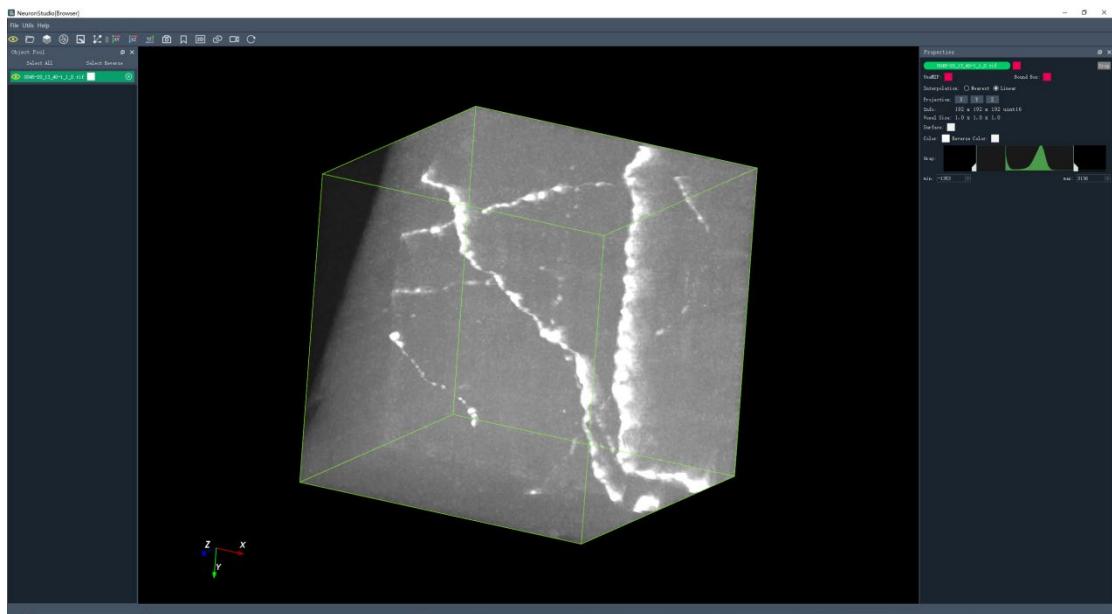


Figure 2.2.4

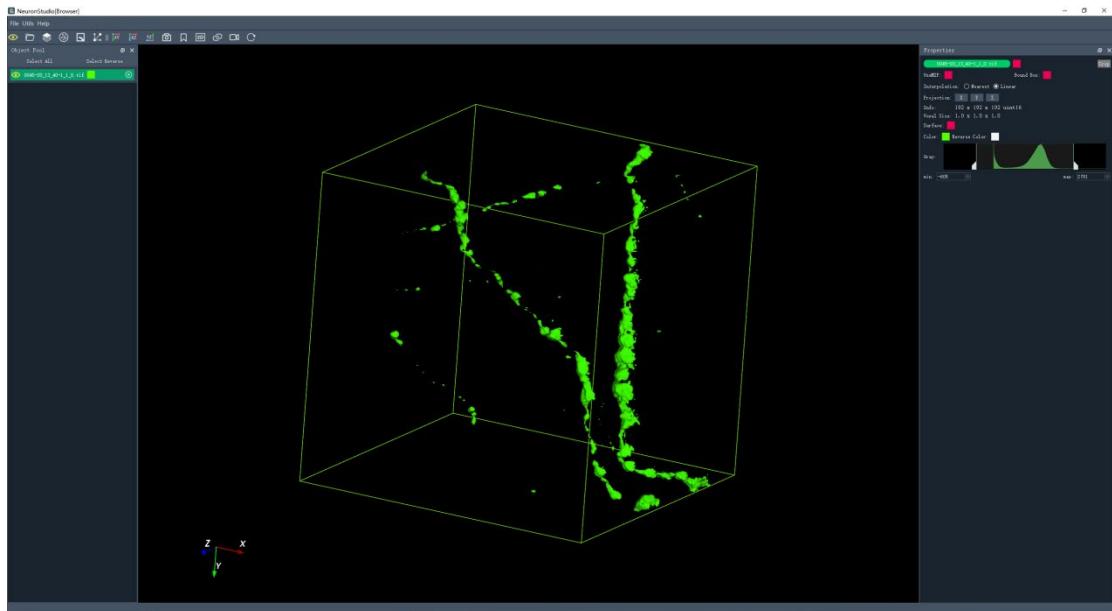


Figure 2.2.5

2.3 Visualization of Bio-VS block data

2.3.1 Data import

As shown in Figure 2.3.2, this is the location of the Bio-VS block data (within the subdirectory of the successfully created Bio-VS format data). Click  to enter the data visualization module. In the menu bar, click **File** → **Open** to import data (Alternatively, you can directly drag the data into the render object list, as shown in Figure 2.3.2 green arrow). The **Object Pool** area contains the list of rendering data.

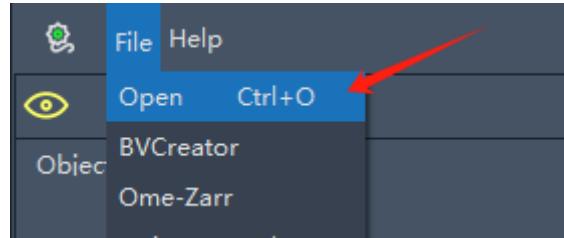


Figure 2.3.1

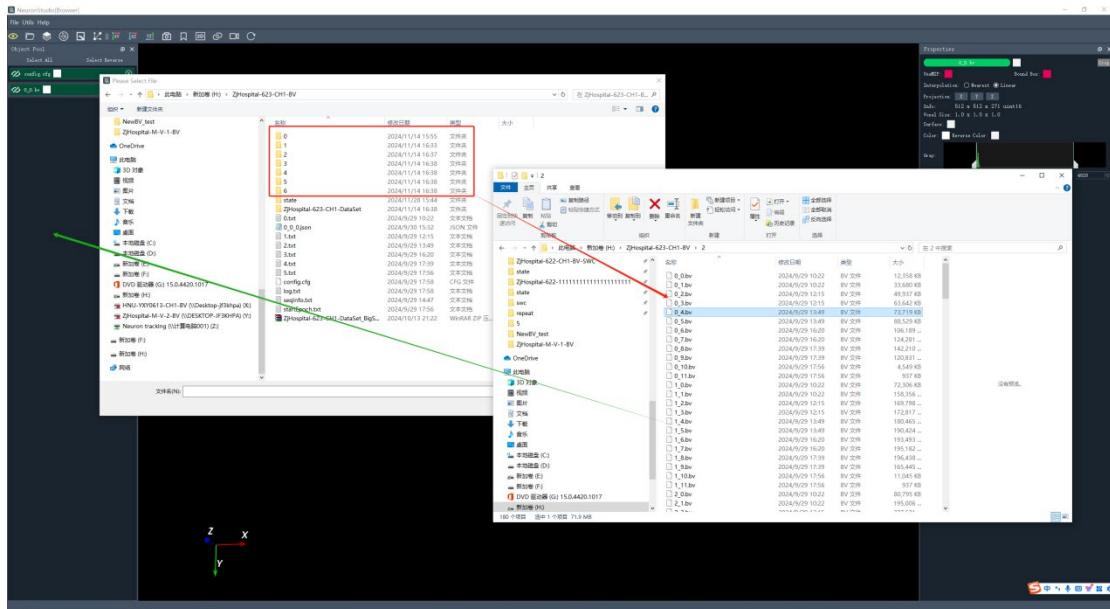


Figure 2.3.2

2.3.2 Introduction to data properties

The functionality is the same as for TIF data, see in [chapter 2.2.2](#).

2.4 Visualization of SWC data

2.4.1 Data import

- 1) Click to enter the data visualization module. In the menu bar, click **File** → **Open** to import data (Alternatively, you can directly drag the data into the render object list.). The **Object Pool** area contains the list of rendering data. Multiple SWC files can be viewed at once (as shown in Figure 2.4.2, different colors represent different SWC files).

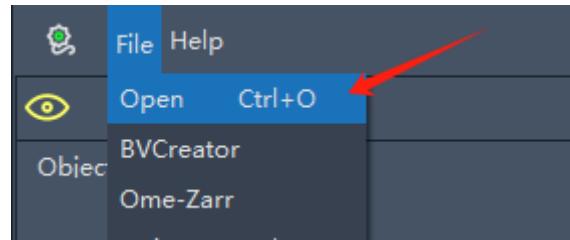


Figure 2.4.1



Figure 2.4.2

2) Left-click the small color box next to the SWC file name, and a window will appear as shown in Figure 2.4.3. Select the color you want to use, and click **OK** to change the visualization color of the SWC file.

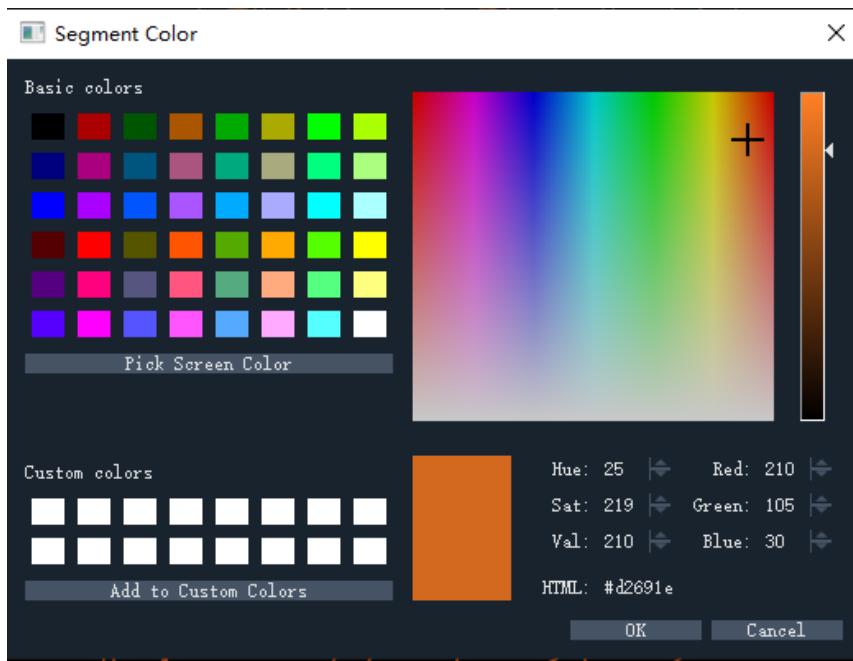


Figure 2.4.3

3) In Figure 2.4.2, multiple SWC files are viewed, but each SWC file contains only one root node, so each displays as a single tree structure. In Figure 2.4.4, one SWC file is imported, but it contains multiple root nodes, resulting in multiple tree structures being displayed.

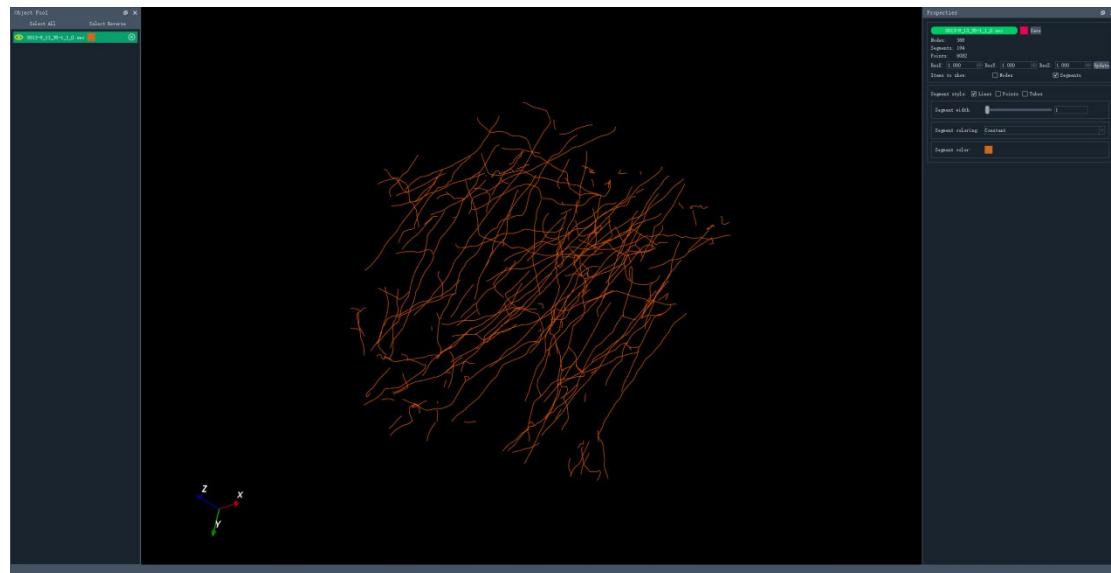


Figure 2.4.4

2.4.2 Introduction to data properties

Left-click the data in the **Object Pool** list on the left side of Figure 2.4.4, and the corresponding property information will be displayed as shown in Figure 2.4.5.

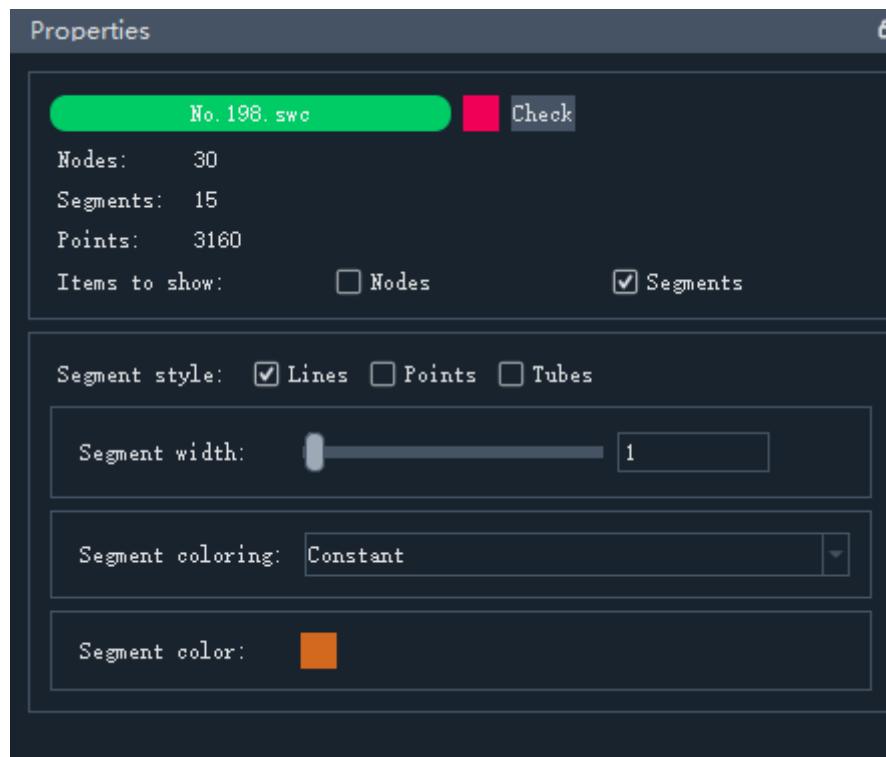
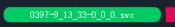


Figure 2.4.5

-  The red square shows/hides the SWC (shortcut key **A**).
 - **Nodes: 196** indicates that the data contains 196 nodes; **Segments: 98** means there are 98 segments; **Points: 5319** means the data contains 5319 points.
 - **Item to show** indicates the display style of the data.
- 1) When **Nodes** is selected, **Node scale** indicates the size of the nodes, and **Node color** indicates the color of the nodes. As shown in Figure 2.4.7, this is the visualization of the SWC displayed with **Nodes**.

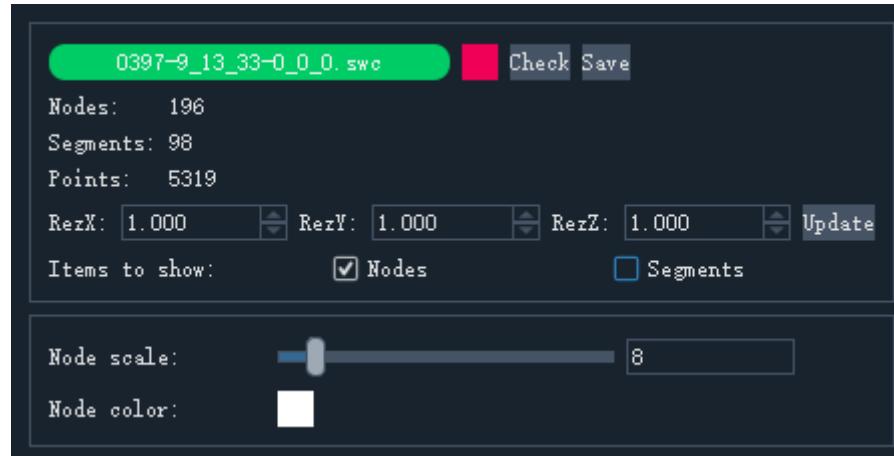


Figure 2.4.6

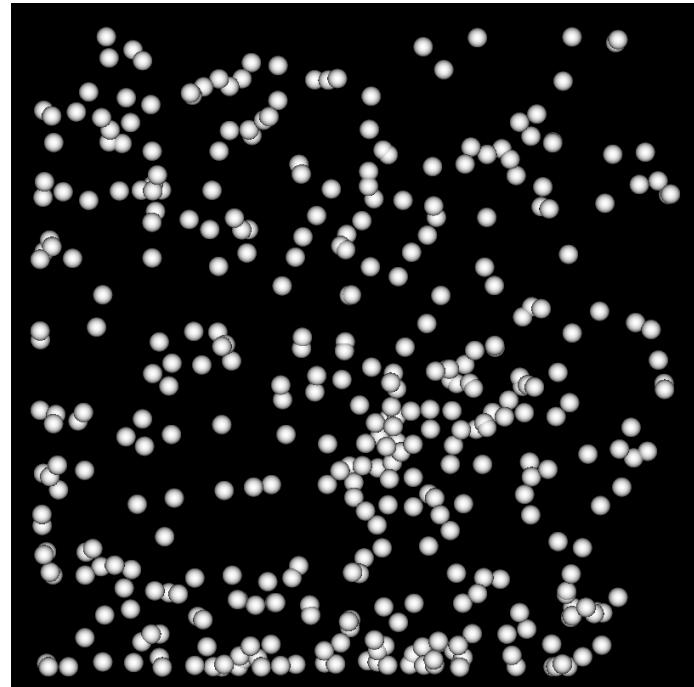


Figure 2.4.7

- 2) When **Segments** is selected, there are three display modes: **Lines**, **Points**, and **Tubes**, corresponding to the visualizations in Figures 2.4.8, 2.4.9, and 2.4.10 respectively. For **Lines** and **Points**, you can adjust the **Segment width**, **Segment coloring**, and **Segment color**. In **Tubes** mode, in addition to the above settings, you can also adjust **Tube scale** and **Tube scale factor**.

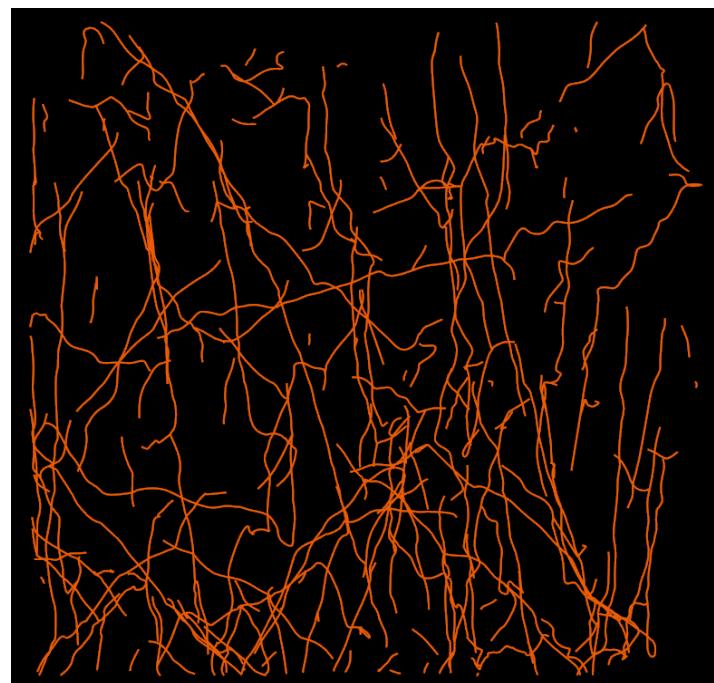


Figure 2.4.8

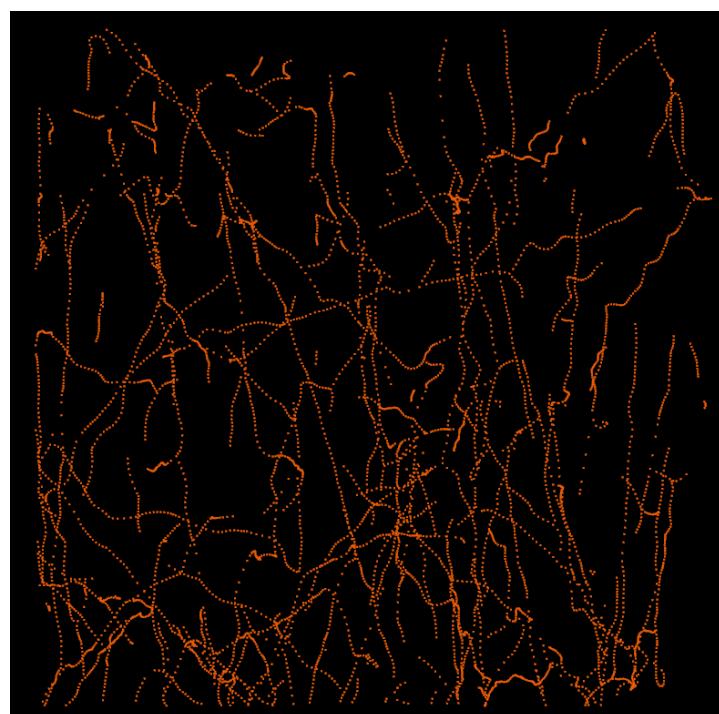


Figure 2.4.9

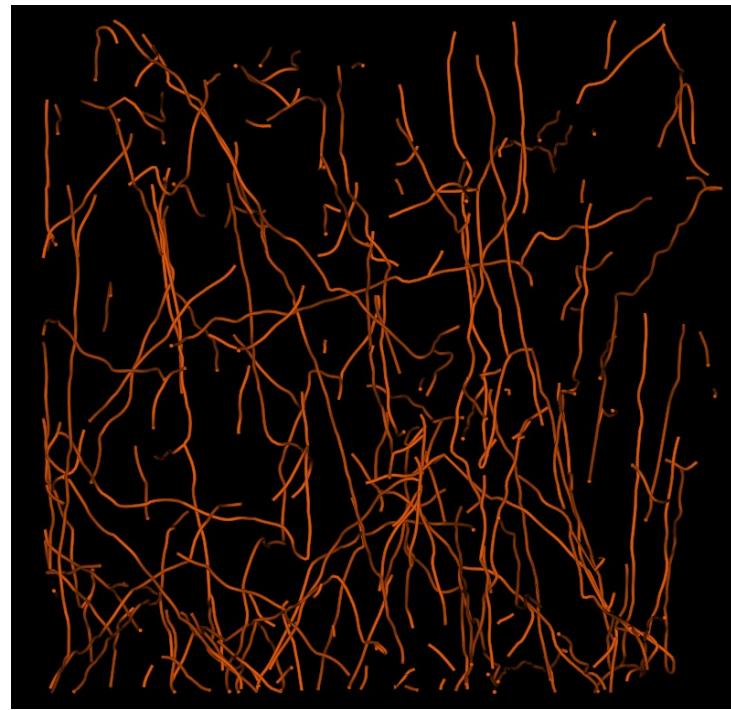
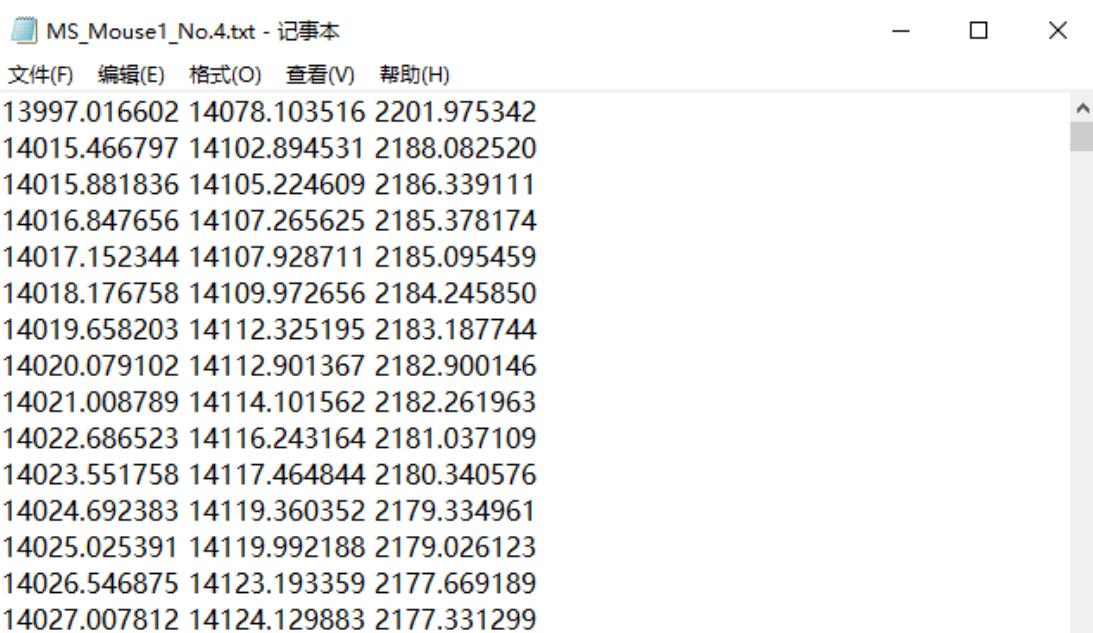


Figure 2.4.10

2.5 Visualization of pointcloud TXT data

2.5.1 Data import

- 1) Introduction to pointcloud TXT data: As shown in Figure 2.5.1, each row represents a point, and the three columns represent the 3D coordinates of that point. The values are separated by spaces.



MS_Mouse1_No.4.txt - 记事本

文件(F) 编辑(E) 格式(O) 查看(V) 帮助(H)

```
13997.016602 14078.103516 2201.975342
14015.466797 14102.894531 2188.082520
14015.881836 14105.224609 2186.339111
14016.847656 14107.265625 2185.378174
14017.152344 14107.928711 2185.095459
14018.176758 14109.972656 2184.245850
14019.658203 14112.325195 2183.187744
14020.079102 14112.901367 2182.900146
14021.008789 14114.101562 2182.261963
14022.686523 14116.243164 2181.037109
14023.551758 14117.464844 2180.340576
14024.692383 14119.360352 2179.334961
14025.025391 14119.992188 2179.026123
14026.546875 14123.193359 2177.669189
14027.007812 14124.129883 2177.331299
```

Figure 2.5.1

2) Click  to enter the data visualization module. In the menu bar, click **File** → **Open** to import data (Alternatively, you can directly drag the data into the render object list.). The **Object Pool** area contains the list of rendering data.

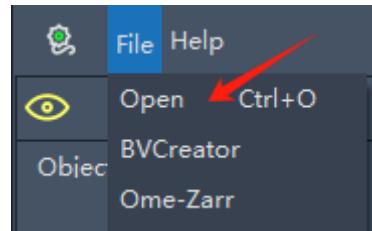


Figure 2.5.2

3) After importing the data, a prompt window will pop up, as shown in Figure 2.5.3, asking you to set the point cloud delimiter (default is space). Since the delimiter for this TXT point cloud data is a space, simply click **OK** to proceed.

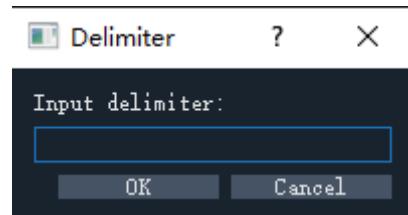


Figure 2.5.3

2.5.2 Introduction to data properties

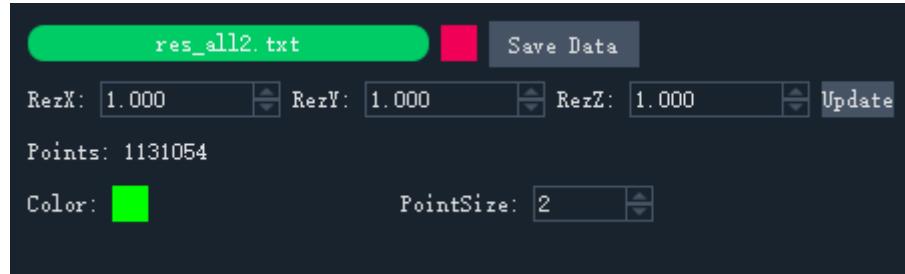


Figure 2.5.4

-  The red square shows/hides the pointcloud (shortcut key **A**).
- **Points: 1,131,054** indicates the current pointcloud contains 1,131,054 points.
- **Color:** Represents the current visualization color of the pointcloud, and can be modified.
- **PointSize:** Indicates the current size of the pointcloud points.
- As shown in Figure 2.5.5, the resolution of the data can be modified here. Click **Update** for the changes to take effect. In Figure 2.5.6, the resolution is **1:1:1**; in Figure 2.5.7, the resolution is **0.35:0.35:1**. After editing, click **Save Data** to store the result locally, as shown by the red arrow in Figure 2.5.8.



Figure 2.5.5

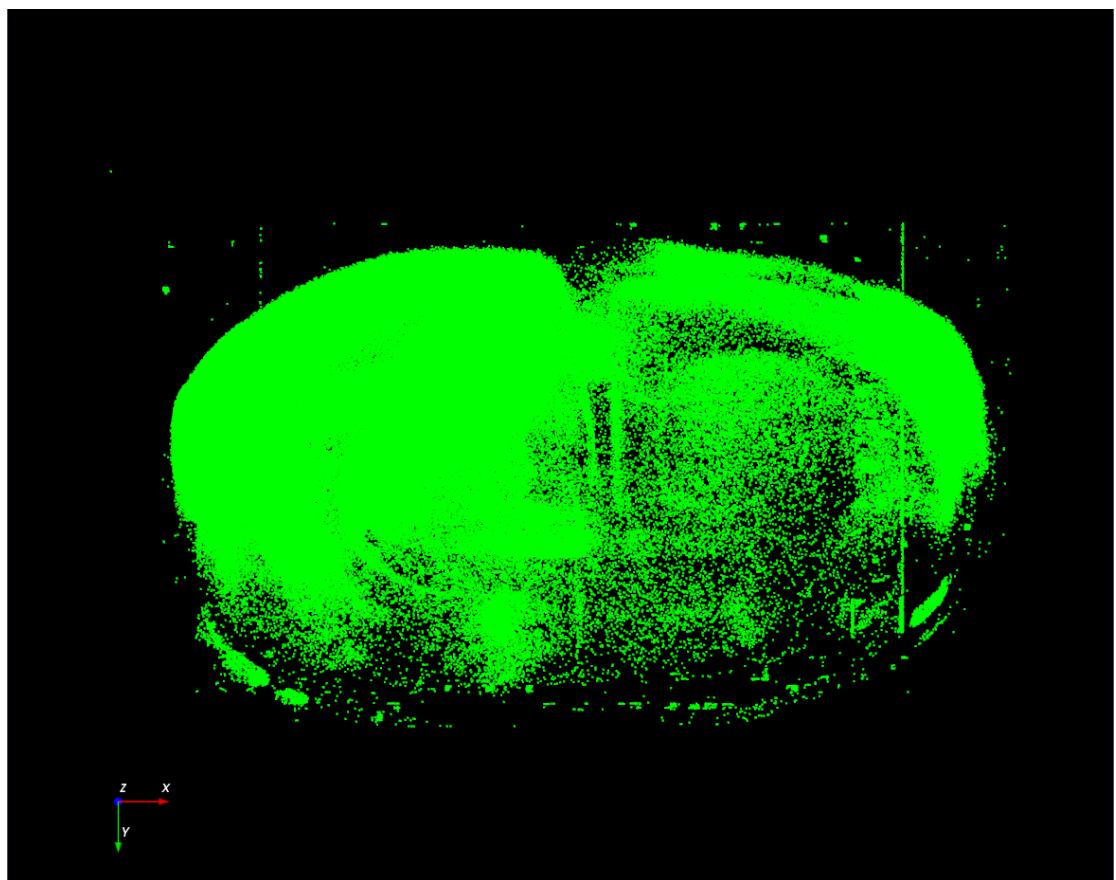


Figure 2.5.6

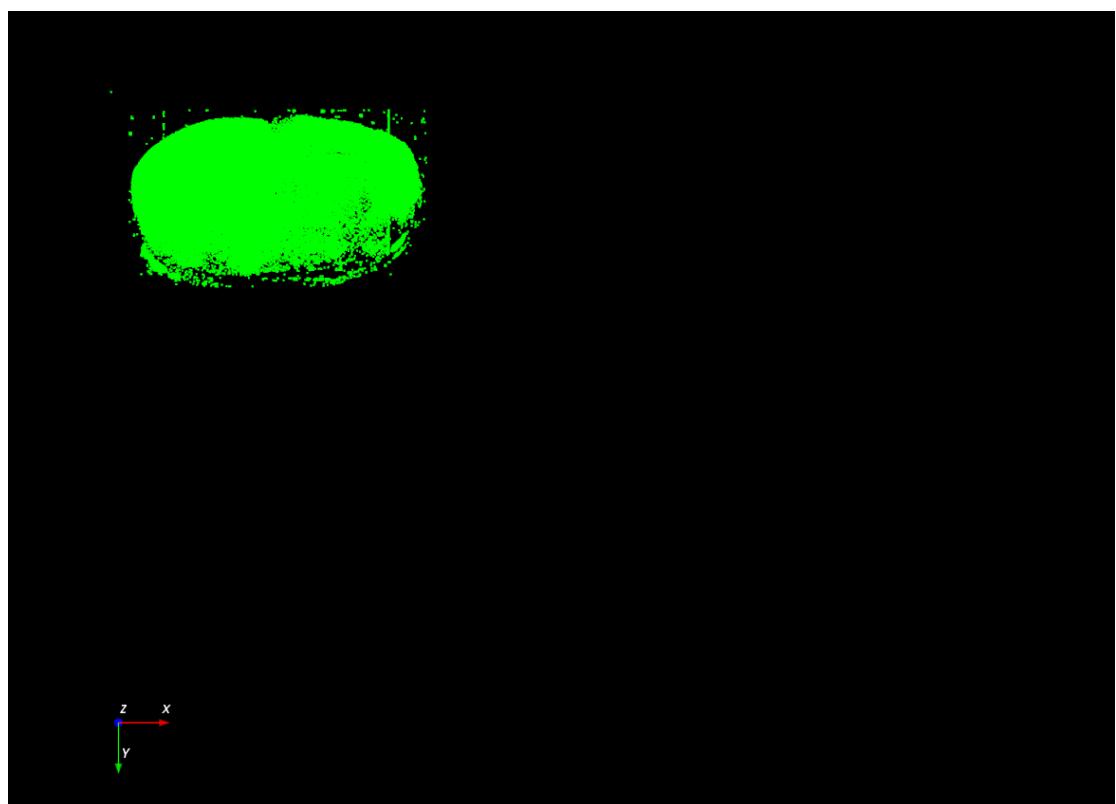


Figure 2.5.7



Figure 2.5.8

2.5.3 Clipping of pointcloud TXT data

- 1) Some points in the pointcloud need to be deleted. You can delete them directly in the visualization interface.
- 2) Press **N** to enter the clipping mode. Left-click the points to mark points. After marking, press **D** to delete the region enclosed by the marked points, as shown by the red area in Figure 2.5.9 (points within this area, which are not needed by the user, will be deleted).
- 3) During the marking process, press **Ctrl+Z** to undo the last step, and press **Z** to undo all marked points.
- 4) Press **S** to enter the normal mode. In this mode, **Ctrl+Z** will undo the last clipping result.
- 5) After completing the clipping, click **Save Data** to save the result, as indicated by the red arrow in Figure 2.5.8.

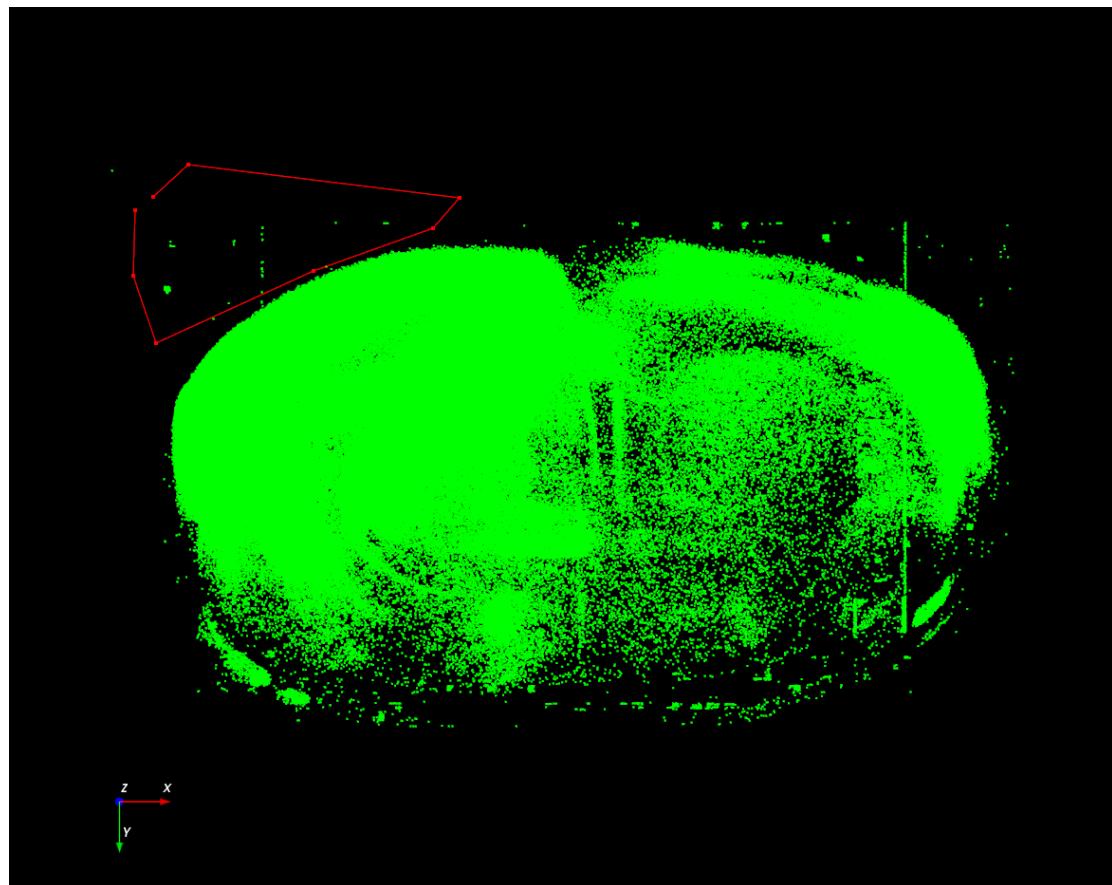


Figure 2.5.9

2.6 Data annotation

Supports annotation of ROI regions in pyramid data, 3D TIF data, and Bio-VS block data, facilitating data analysis and retrieval.

2.6.1 Introduction to annotation configuration file

1) First, import the data, then click the  annotation button in the toolbar. A dialog will pop up to save the JSON file. Choose the desired save location.

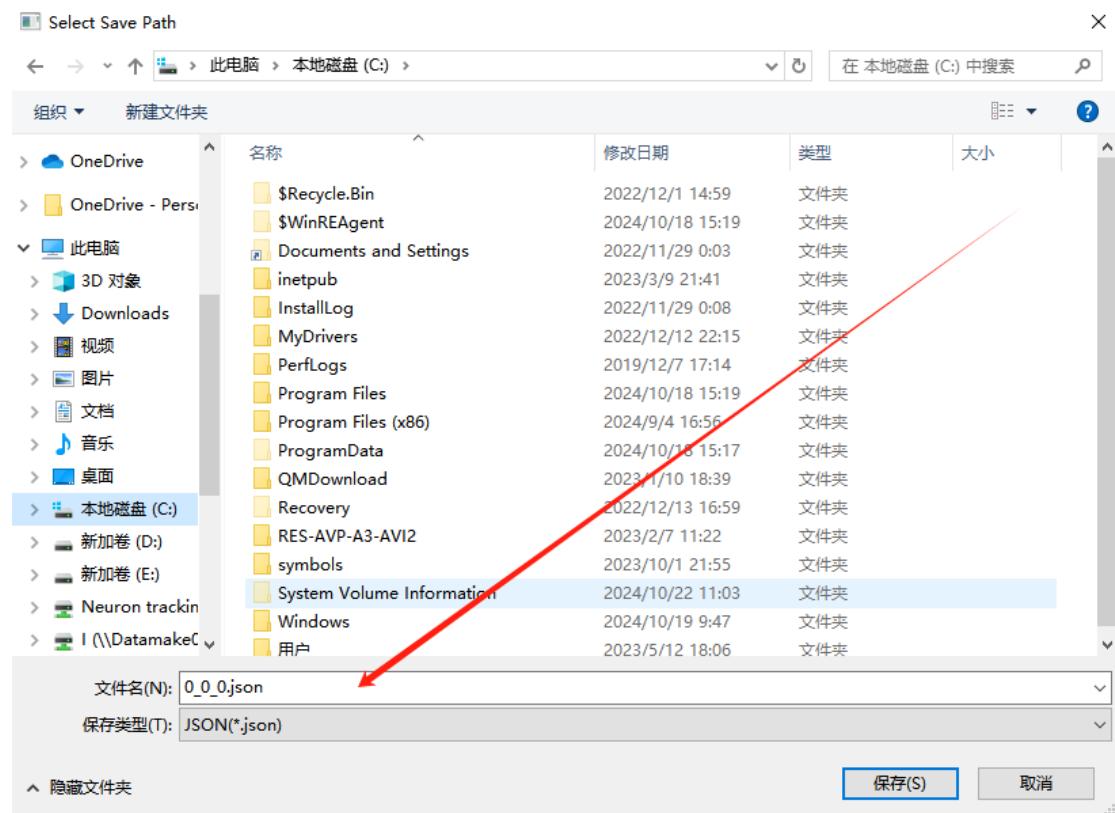


Figure 2.6.1

2) After saving, click the JSON file. The corresponding JSON properties will appear on the right side, as shown in Figure 2.6.3.

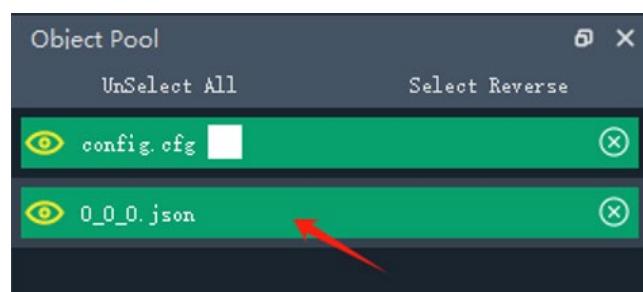


Figure 2.6.2

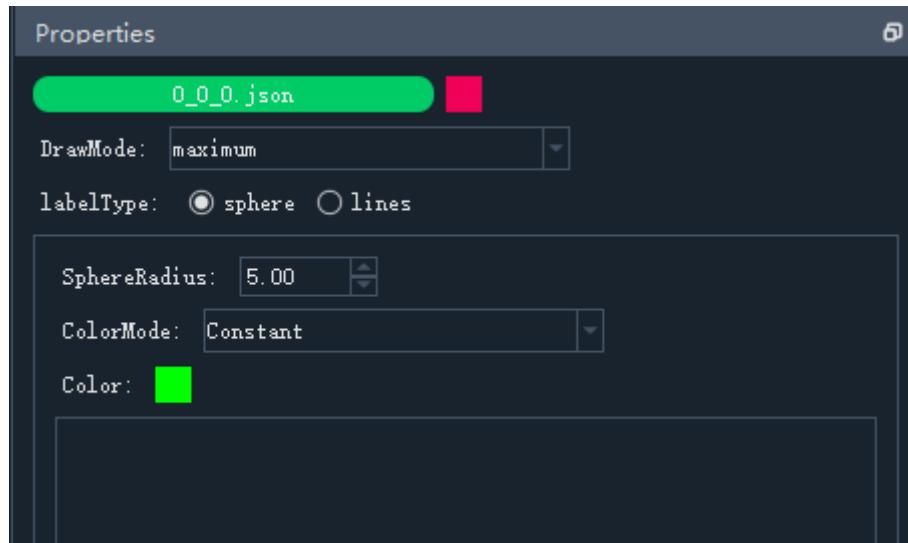


Figure 2.6.3

- 3) Click the red square next to the data name to display/hide the marked data.
- 4) Press **Ctrl+S** to save the marked content.

2.6.2 Annotation Types

Includes sphere annotation and lines annotation.

2.6.2.1 Sphere annotation

It must be done within the ROI. Press **V** on the keyboard to enter annotation mode (press **S** to return to normal mode). Left-click to select points. The **DrawMode** can be set to either **Maximum** or **Line** mode.

- **Maximum:** Directly selects the brightest point in the direction of the current click. As shown in Figure 2.6.4, the list in the red box on the right displays the 3D position information of the sphere.
- **Line:** Used for points with weaker signals. As shown in Figure 2.6.5, first left-click to draw a line segment, then left-click on the points along the line to select and confirm the 3D position at the intersection. Right-click the sphere to delete it.
- **SphereRadius:** The radius of the sphere.
- **ColorMode:** The color mode, **Random** (random color) or **Constant** (fixed color) can be set.
- **Color:** The fixed color of the sphere, which can be selected by clicking the green box.
- Press **Ctrl+S** to save the marked content. As shown in Figure 2.6.6, the JSON file will display the 3D coordinates of the 7 spheres.

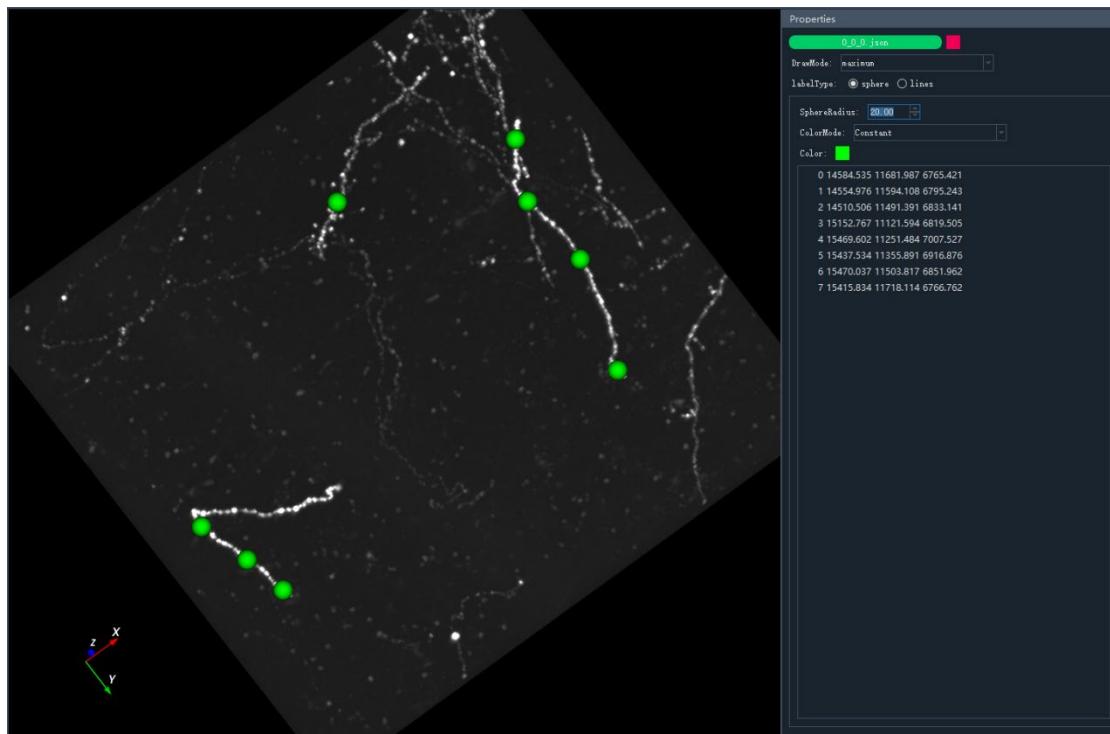


Figure 2.6.4

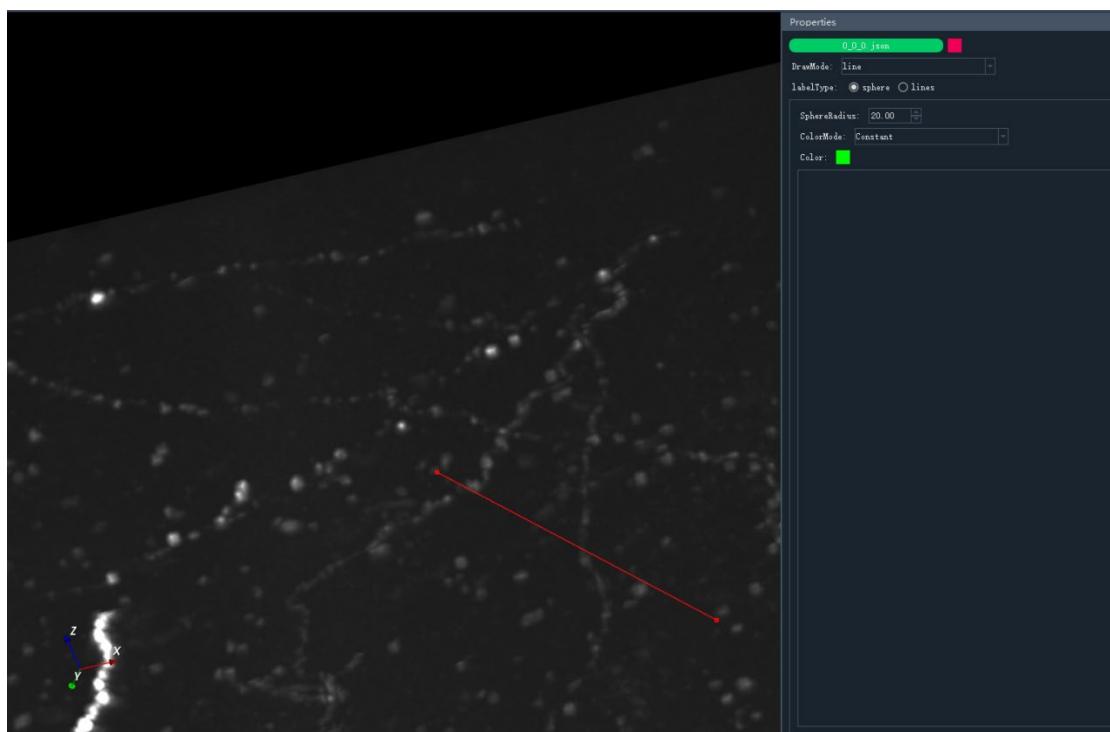


Figure 2.6.5

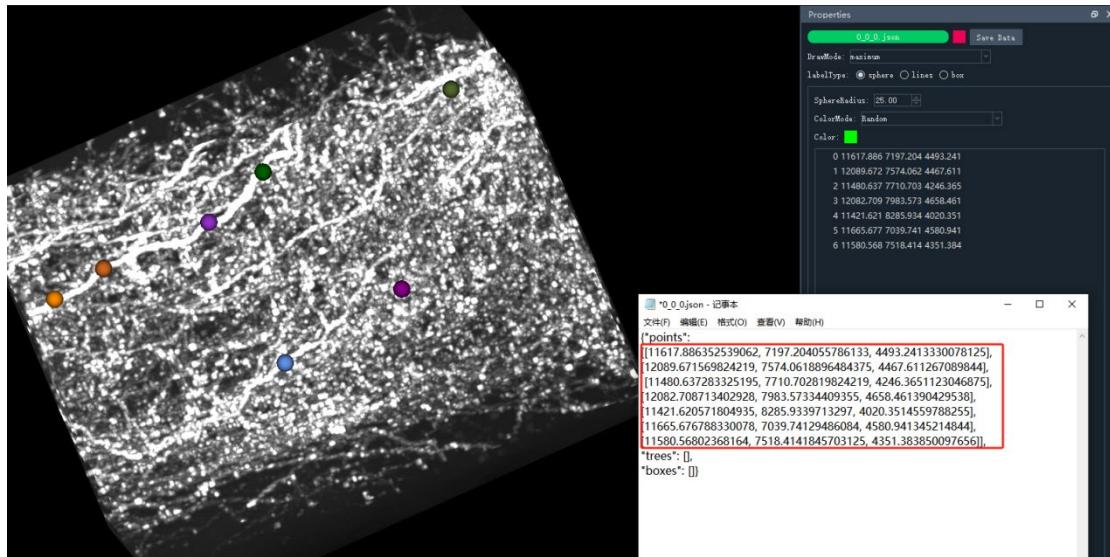


Figure 2.6.6

2.6.2.2 Lines annotation



Figure 2.6.7

Select **labelType** as **lines**. **DrawMode** only supports **maximum**.

- Press **V** on to enter the drawing line mode (press **S** to return to normal mode). Draw a line segment on the nerve fiber. After drawing, press **S** to save. A new entry will appear in the list on the right, as shown in Figure 2.6.8.
- To cut a line segment, hold down **Alt** on the keyboard and left-click to select the point where you want to cut. Release **Alt** to successfully cut. (After cutting, the line segment will be automatically deleted, press **Ctrl+Z** to undo the delete operation). Two entries will appear in the list on the right, as shown in Figure 2.6.9.
- To merge line segments, hold down **Alt** on the keyboard and left-click the two terminal points from the line segments you want to merge (as shown by the blue and orange circles in Figure 2.6.10). Release **Alt** to successfully merge them.
- **Delete Line Segment:** Left-click to select the line segment you want to delete (it will turn red), then press the "d" key to delete it.
- **pointSize:** The size of the endpoints of the line segments.
- After completing the annotation, press **Ctrl + S** to save. You can view the annotation position information in the generated JSON file.

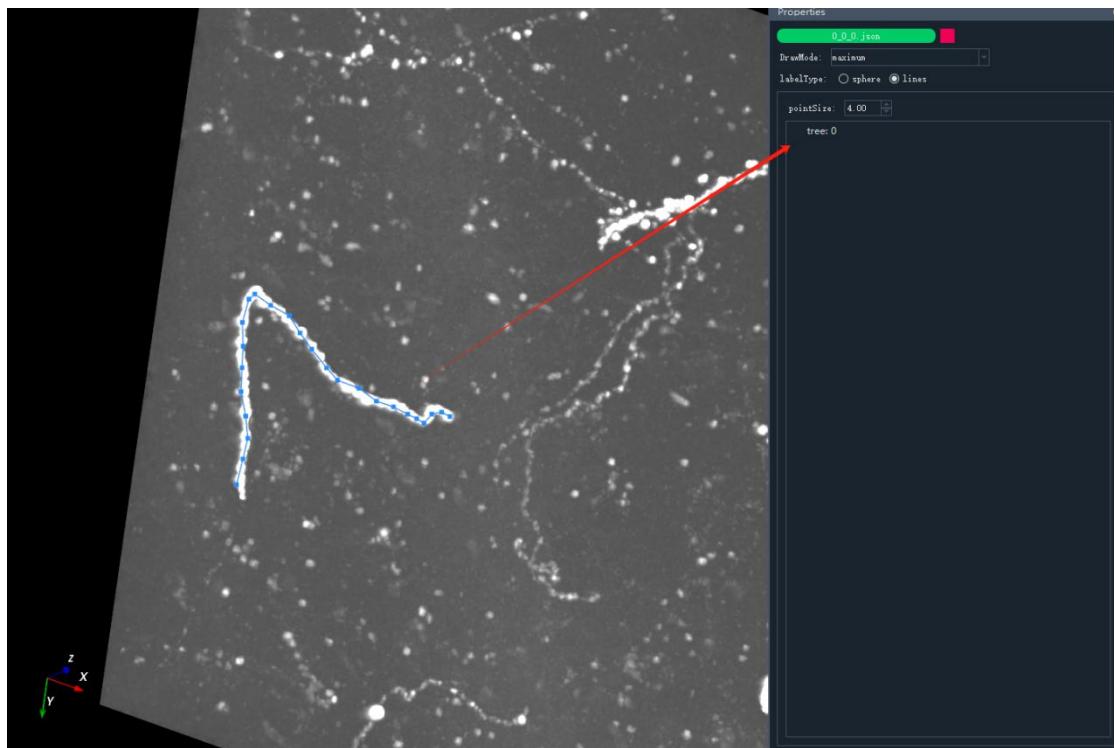


Figure 2.6.8

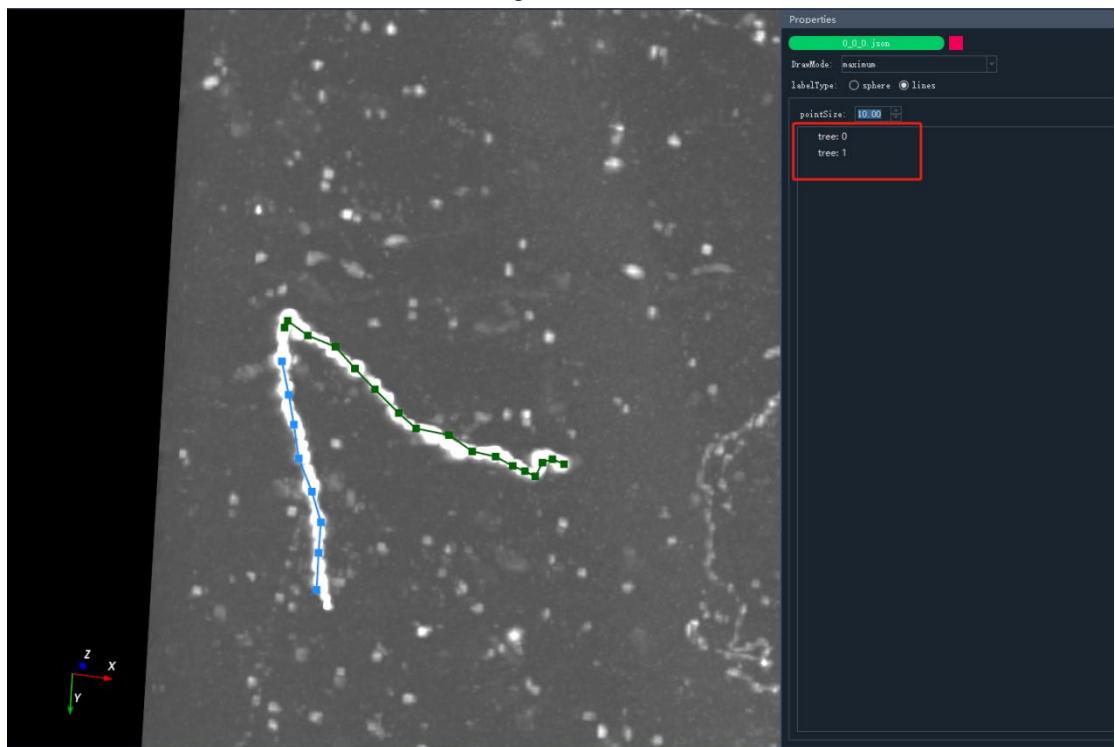


Figure 2.6.9

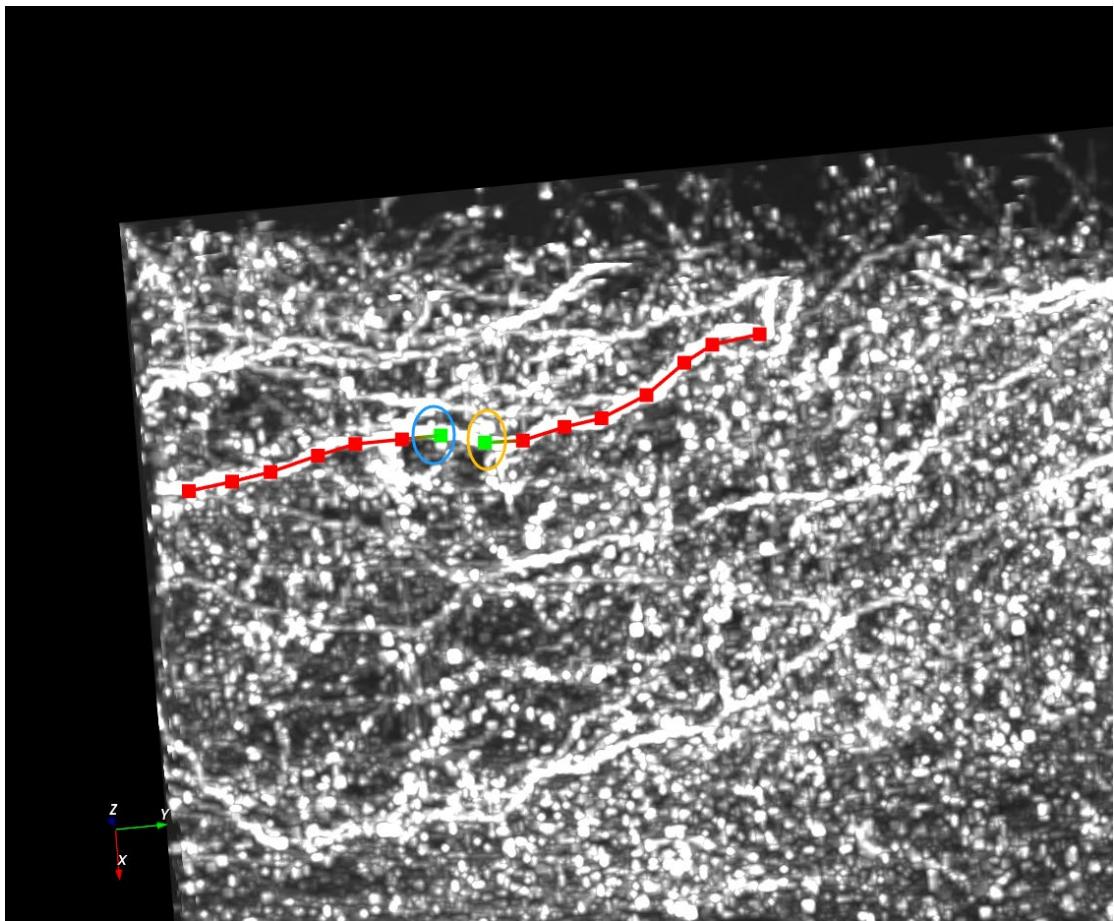


Figure 2.6.10

2.7 2D/3D Visualization

Supports Bio-VS format, 3D TIF data, Bio-VS block data, SWC data and pointcloud TXT data.

2.7.1 Data import

Take 3D TIF data and SWC data for examples. Import the data into the **Object Pool** (data rendering list), then click the "2D View" button in the toolbar to enter 2D mode.

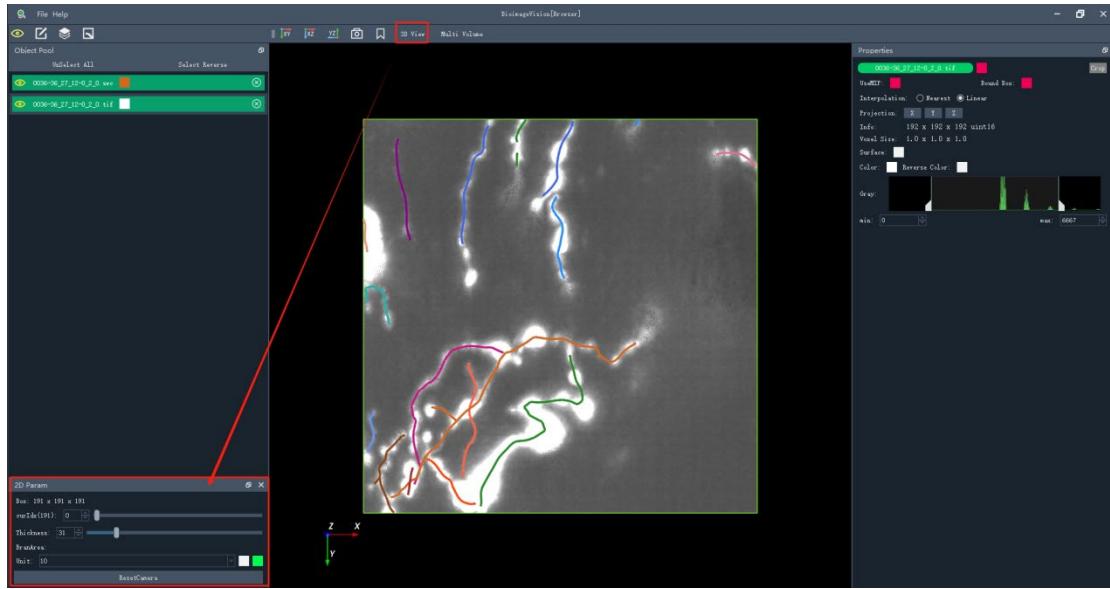


Figure 2.7.1

2.7.2 Introduction to data properties

Set the parameter information under **2D Param**.



Figure 2.7.2

- **Box:** Current size in X*Y*Z.
- **curIdx:** Current frame id. Click the toolbar options **XY**, **YZ**, or **XZ** to switch the visualization view direction. You can switch the frame using the slider or mouse scroll wheel.
- **Thickness:** Frame thickness. Drag the slider to adjust, greater thickness shows more layers. (Also adjustable with mouse scroll wheel).
- **BrainArea:** Brain region registration display. (This feature is only supported for standard Allen Brain Atlas, see in [chapter 2.7.3](#)).
- **ResetCamera:** Reset the visualization view (Use after zooming in or out of the image).
- Click **3D View** to return to 3D view mode.

2.7.3 Visualization of standard Allen Brain Atlas

1) Import the standard Allen Brain Atlas (10 μ m), as shown in Figure 2.7.3.

The operation is the same as in section 2.7.2.

- **Unit:** Dropdown menu for brain region resolution; select the 10 μ m brain region data. (Default is 10 μ m. Options include 10 μ m, 25 μ m, 50 μ m, and 100 μ m).
- The **first white square** next to "Unit" toggles the display of the brain atlas. (It is off by default—click to turn it red to enable display, as shown in Figure 2.7.4.).
- The **second green square** allows you to choose the color for the brain atlas display (As shown in Figure 2.7.4, the atlas appears yellow after color adjustment).



Figure 2.7.3

2) Zoom in/out image in 2D view: Hold **Ctrl** and use the **middle mouse wheel**.

3) Move in 2D view: Press and hold the **middle mouse button** while moving the mouse.

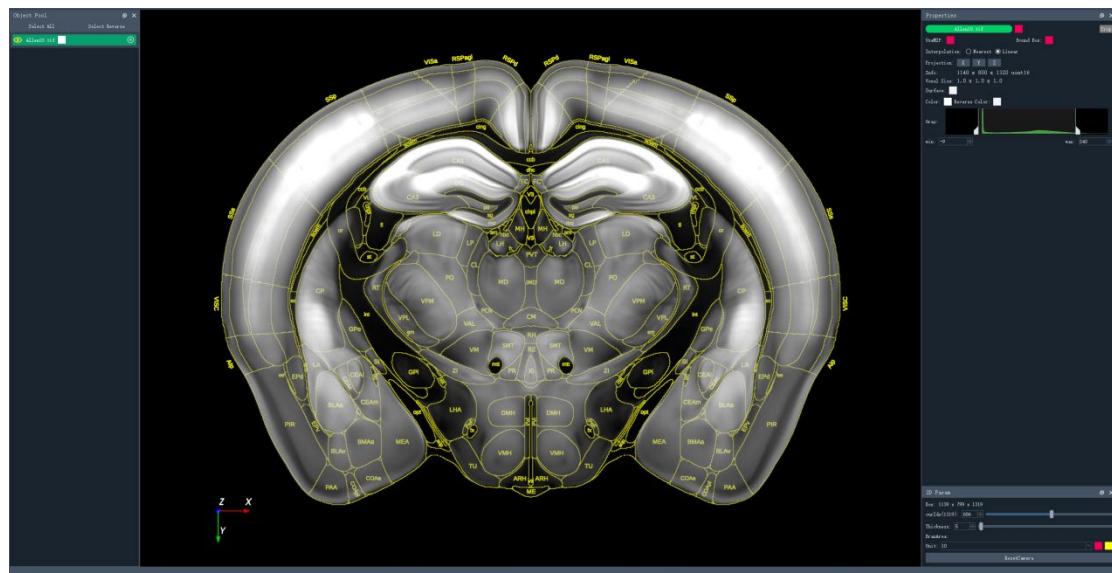


Figure 2.7.4

2.8 Visualization of Multi-channel data

Currently, only multi-channel visualization of 3D TIF data and Bio-VS block data are supported. A maximum of 4 channels can be viewed simultaneously, and all 4 channels must have the same bit depth.

2.8.1 Enter the visualization module

Click on the **Multi Volume** button in the toolbar, as shown by the red arrow in Figure 2.8.1. Once clicked successfully, the **Multi Volume** module will appear at the bottom left of the interface, as indicated by the red box in Figure 2.8.2.



Figure 2.8.1

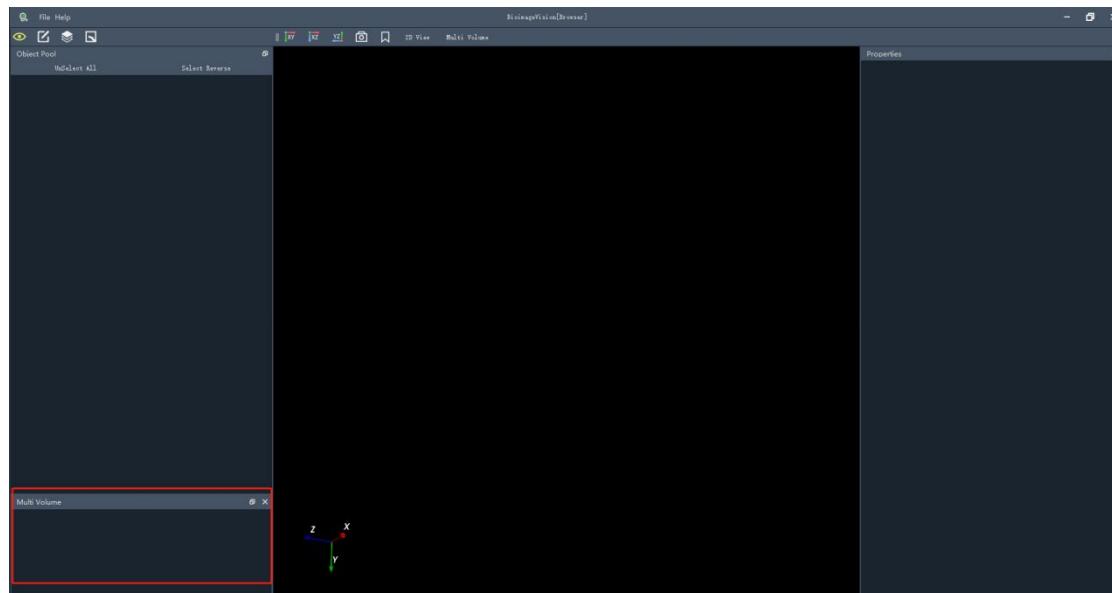


Figure 2.8.2

2.8.2 Data import

First, import the data into the **Object Pool** list; adjust the color and grayscale of the two 3D data sets (as shown in Figure 2.8.3). Then, drag the data from the **Object Pool** list into the Multi Volume module (First, left-click to select the data, then press and hold the left mouse button to drag it into the Multi Volume module), as shown by the yellow arrow in Figure 2.8.4.

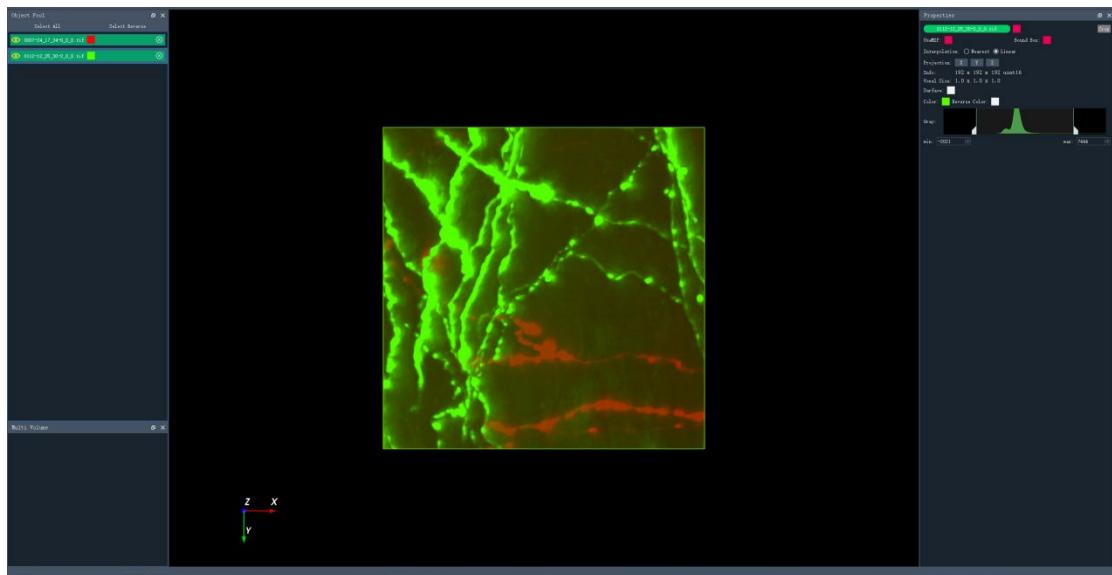


Figure 2.8.3

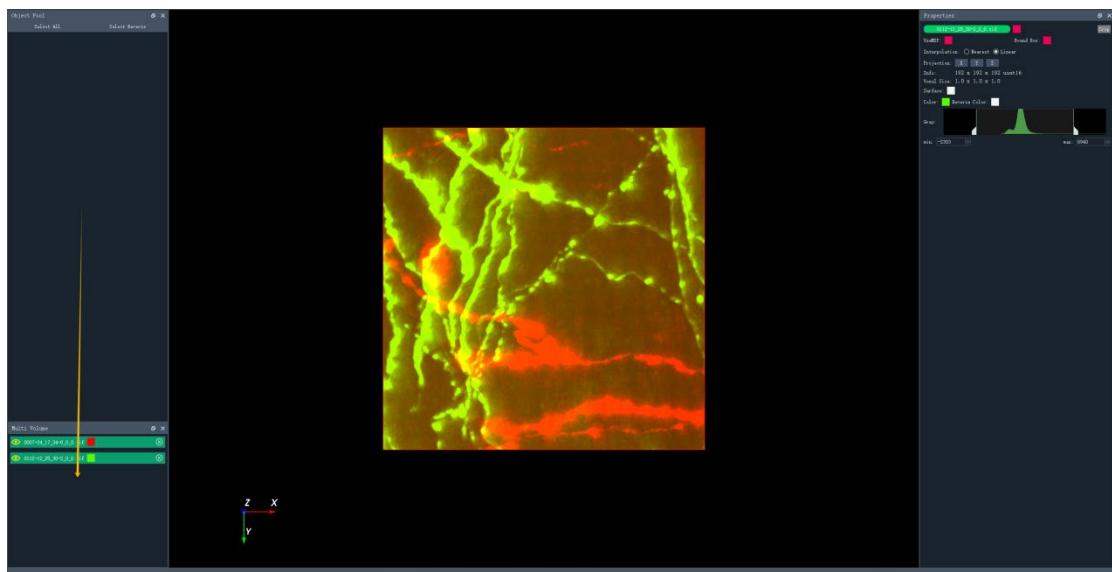


Figure 2.8.4

2.8.3 Introduction to data properties

The functionality is consistent with [chapter 2.2.2](#) (except for the inability to modify image resolution (**Crop**), use maximum intensity projection (**UseMIP**), or perform surface extraction (**Surface**) in the multi-channel module). For the remaining attribute descriptions, please refer to [chapter 2.2.2](#).



Figure 2.8.5

2.8.4 Difference between multi-channel visualization and single-channel visualization

As shown in Figure 2.8.6, the visualization mode is single-channel display, with red representing the first channel and green representing the second channel. In this case, some of the signal from the green channel is obscured.

As shown in Figure 2.8.7, the visualization mode is multi-channel display, with red representing the first channel and green representing the second channel. Both signals are displayed properly, and the image appears brighter compared to the single-channel display.

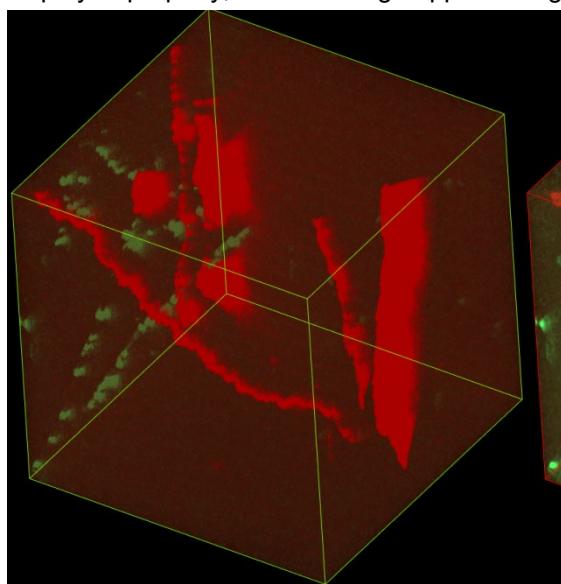


Figure 2.8.6

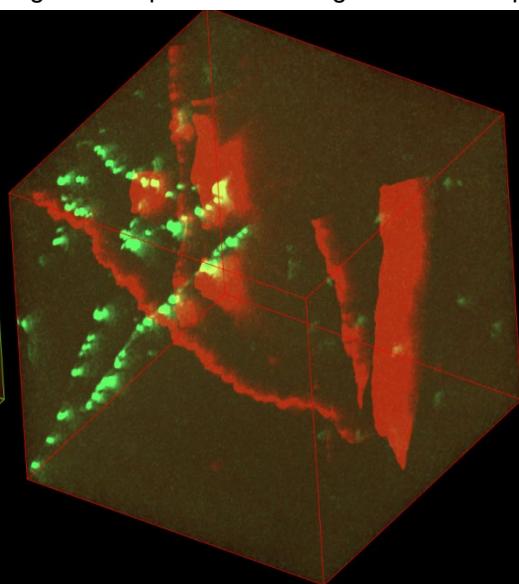


Figure 2.8.7

2.8.5 Exit multi-channel visualization

Drag the data from the Multi Volume module back to the Object Pool list (first, left-click to select the data, then press and hold the left mouse button to drag it into the Object Pool list). Alternatively, you can directly click the  next to the data name to remove the data from software.

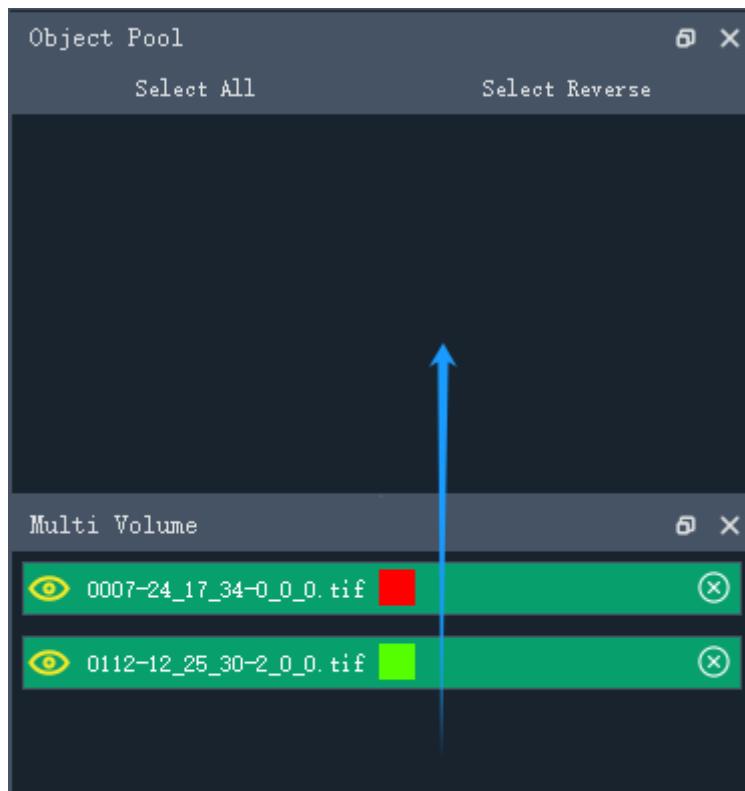


Figure 2.8.8

3. Visualization of branch browsing

View the corresponding image information of the fiber branch real-time.

3.1 Data import

Click the red arrow in Figure 3.1.1 to enter the module. Click **File** → **Open** to open the dialog box shown in Figure 3.1.3. Select the Config path (the Bio-VS format data generated in [chapter 1.1](#), and select the config.cfg configuration file), then select the SWC path (corresponding to the reconstructed neuron SWC data for the entire brain). After clicking OK, the content shown in Figure 3.1.5 will appear.

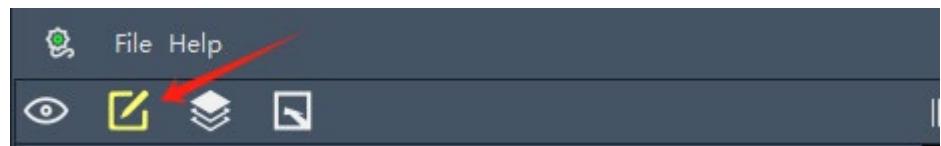


Figure 3.1.1

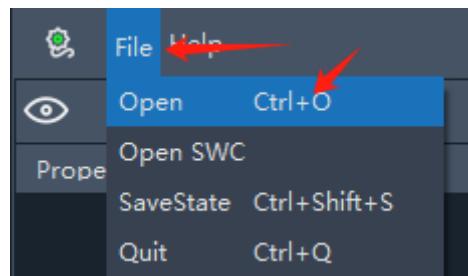


Figure 3.1.2

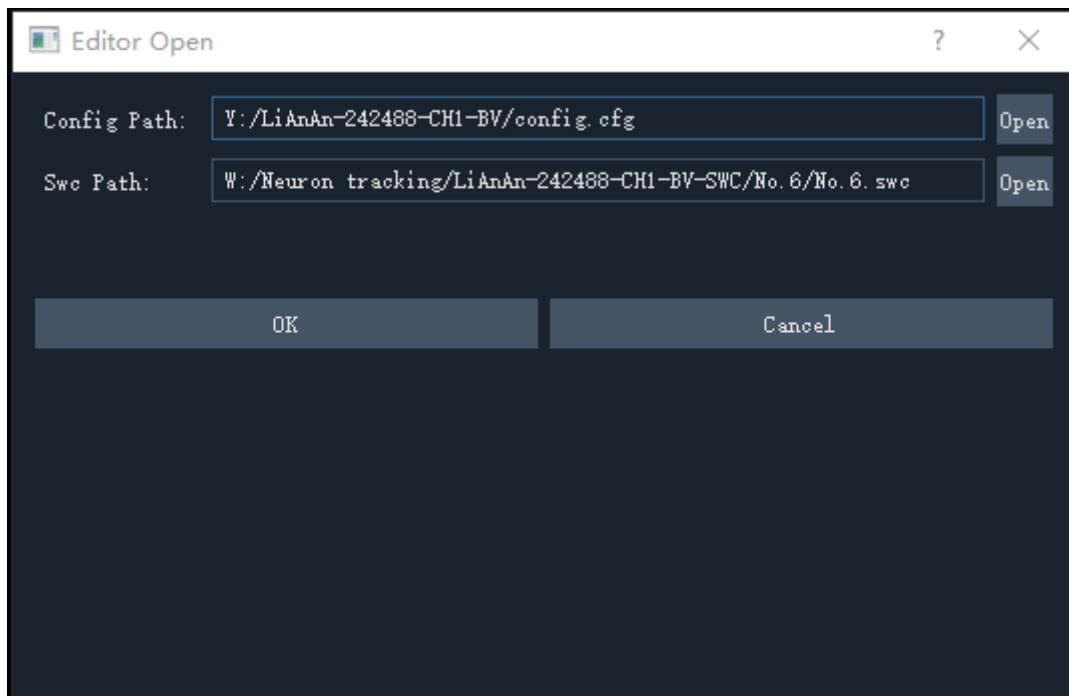


Figure 3.1.3

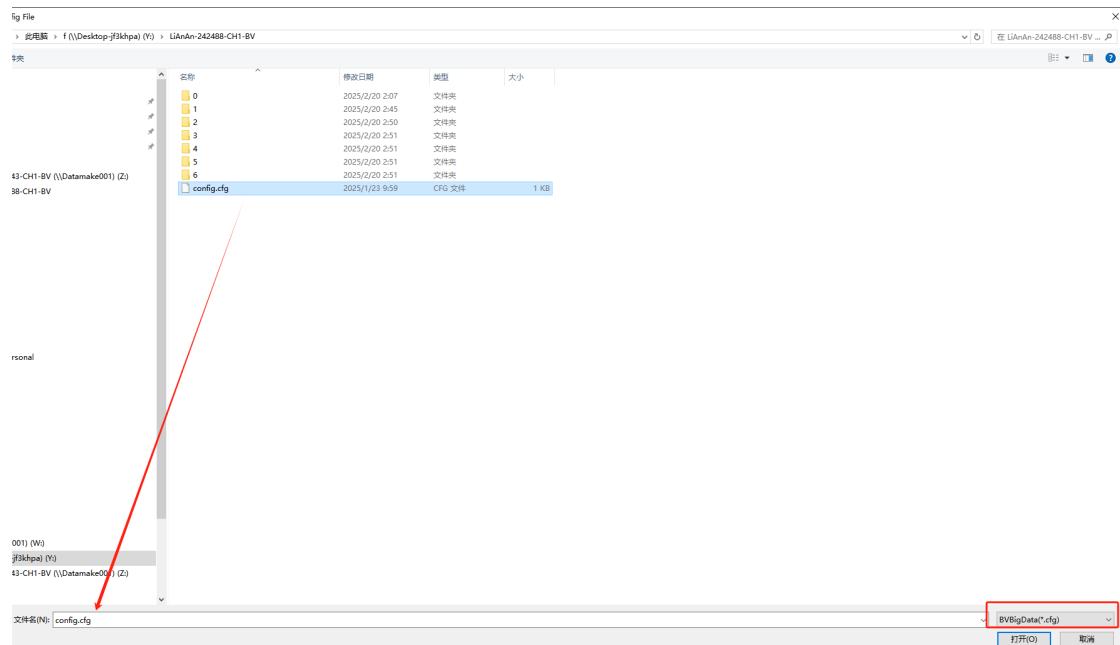


Figure 3.1.4

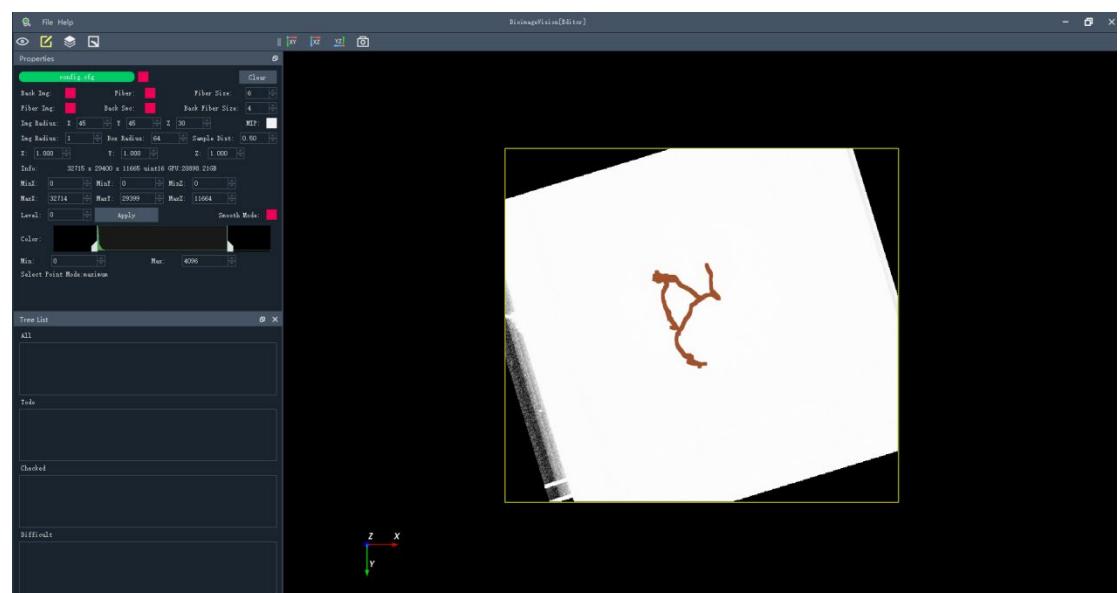


Figure 3.1.5

3.2 Visualization of branch browsing

- 1) Hide whole brain data and display at a lower resolution.

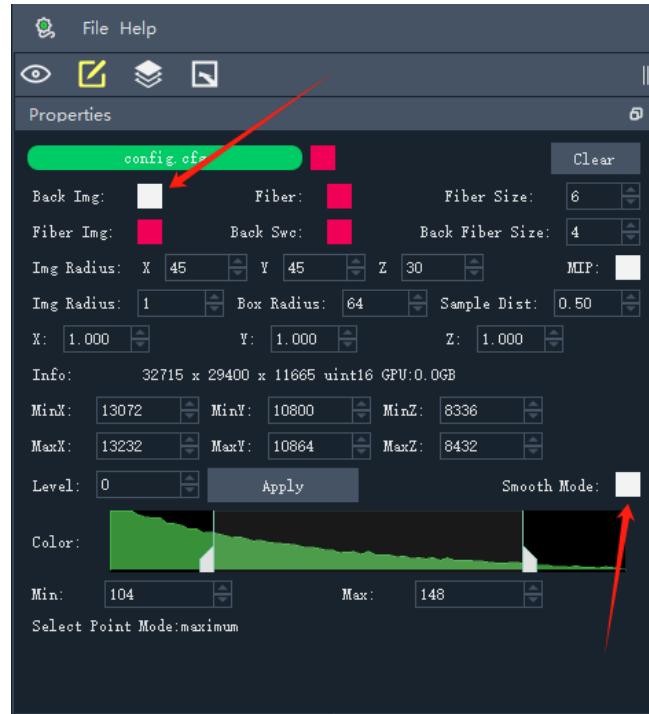


Figure 3.1.6

- 2) Select the soma location in the Swc, press **Y** to set it as the main branch; press **Ctrl+F** to bring up the corresponding box and adjust the grayscale to view the data (press **G** to automatically adjusts the grayscale, or it can be adjusted based on the grayscale histogram).

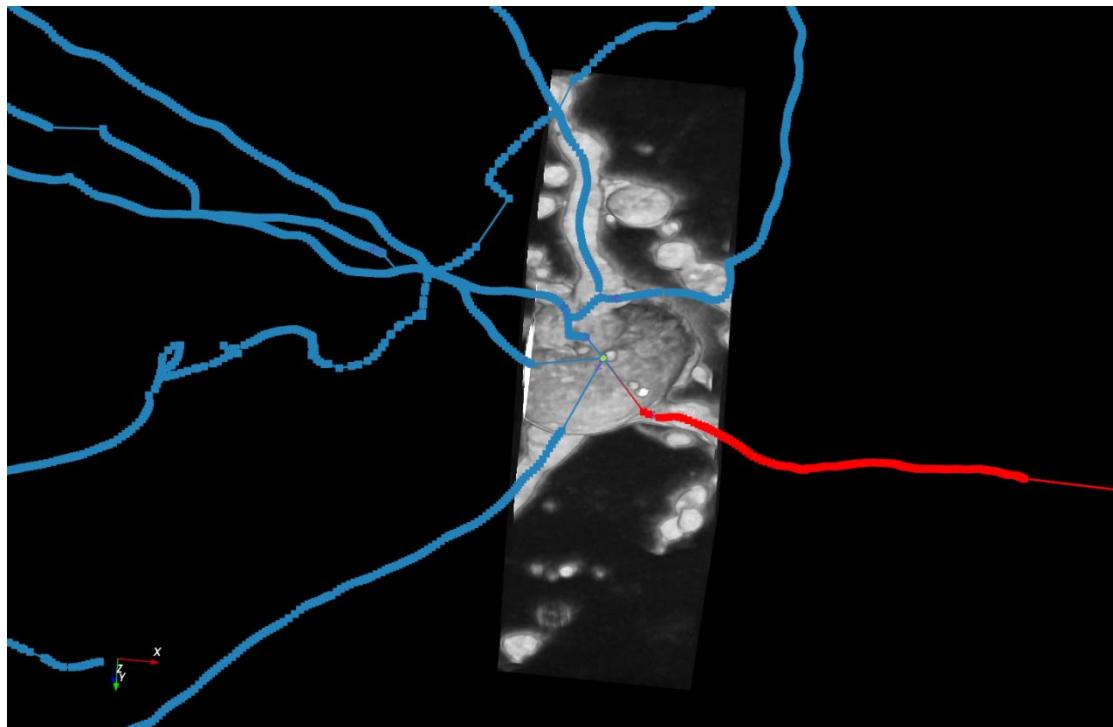


Figure 3.1.7

- 3) Browse along the branches of the soma, and press **Ctrl + left mouse button** click on the fibers to display the corresponding image.

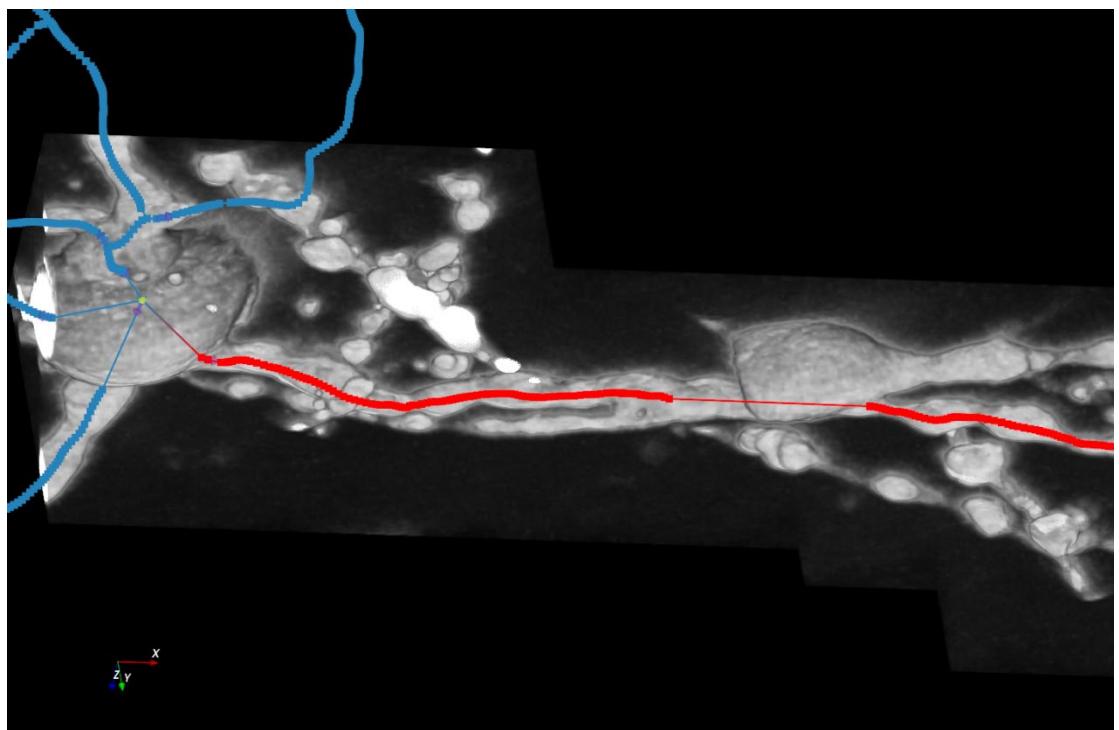


Figure 3.1.8

- 4) Press **Ctrl + Space** to automatically browse along the branch towards the end. Once the browsing of the current branch is complete, you can continue browsing other branches.

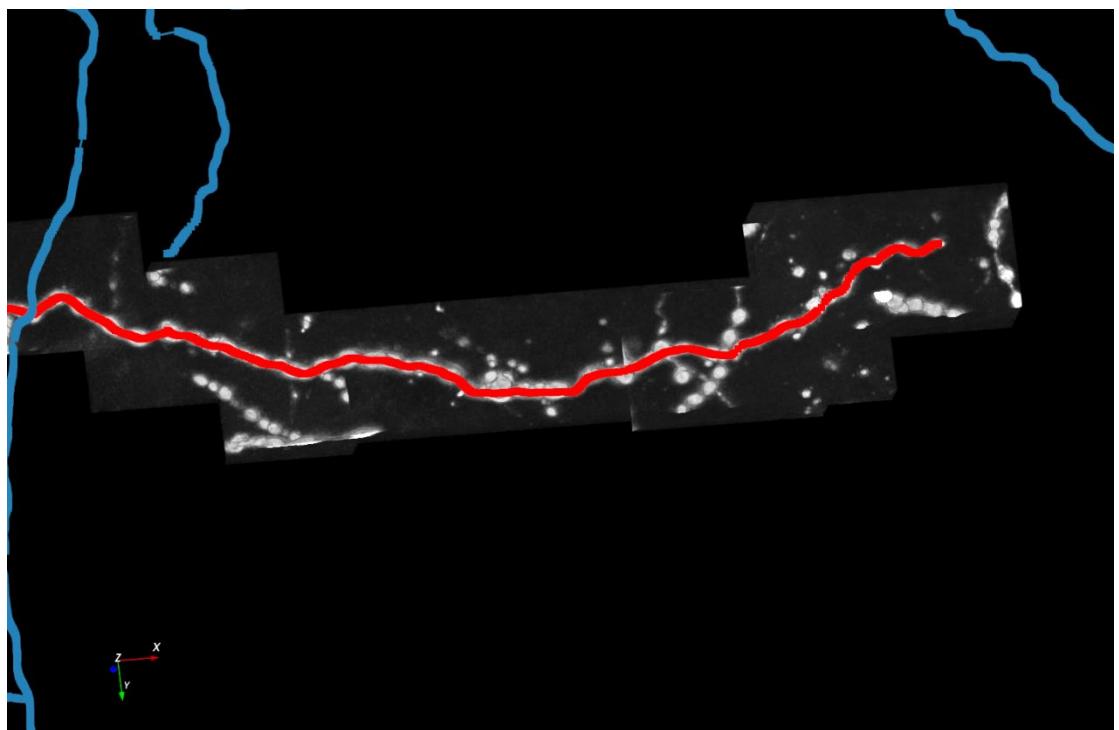


Figure 3.1.9

4. 2D view of arbitrary slice

Perform visualization on 2D single slice.

4.1 Visualization of single slice

4.1.1 Data import

Currently only support Bio-VS format data. Click  in toolbar to enter the single slice browsing mode (as shown in Figure 4.1.1). Then, click **File** → **Open** in the menu bar to import the Bio-VS format data generated in [chapter 1.1](#) (as shown in Figure 4.1.2). The interface after successful import is shown in Figure 4.1.3.

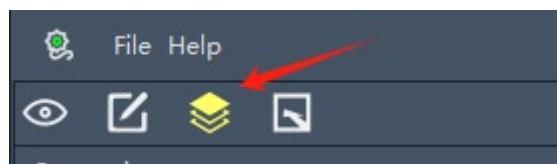


Figure 4.1.1

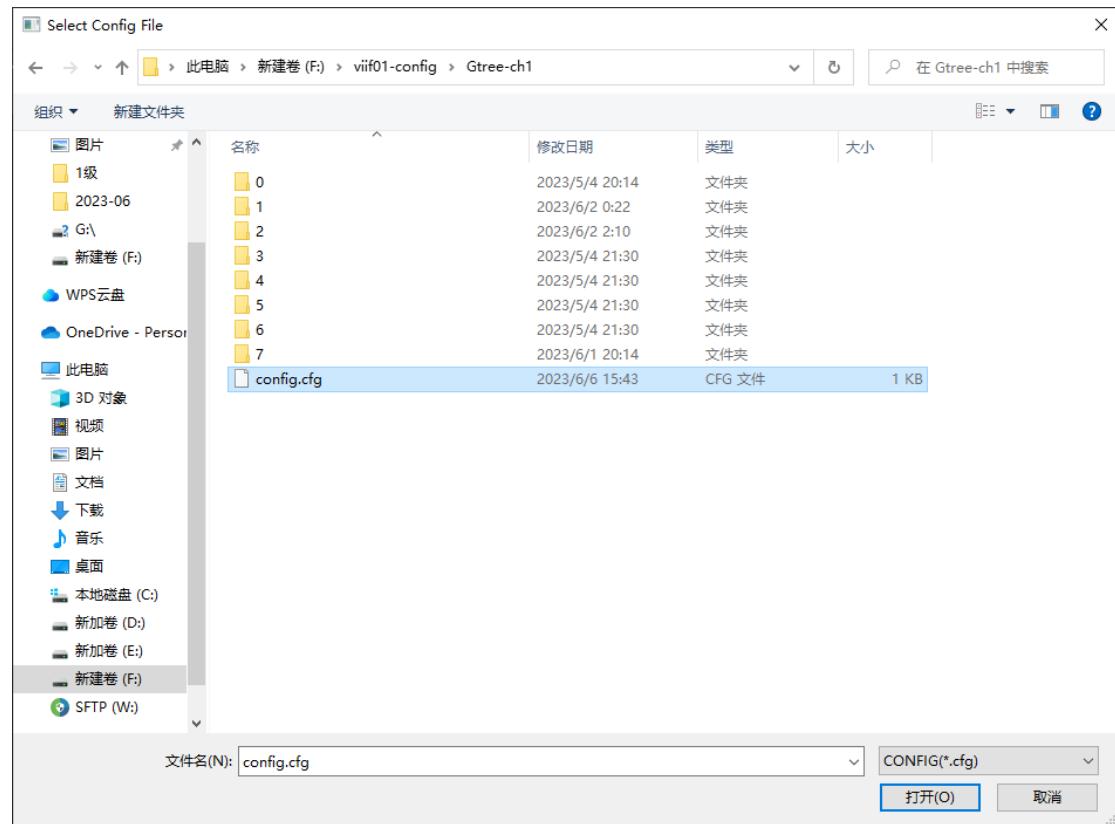


Figure 4.1.2

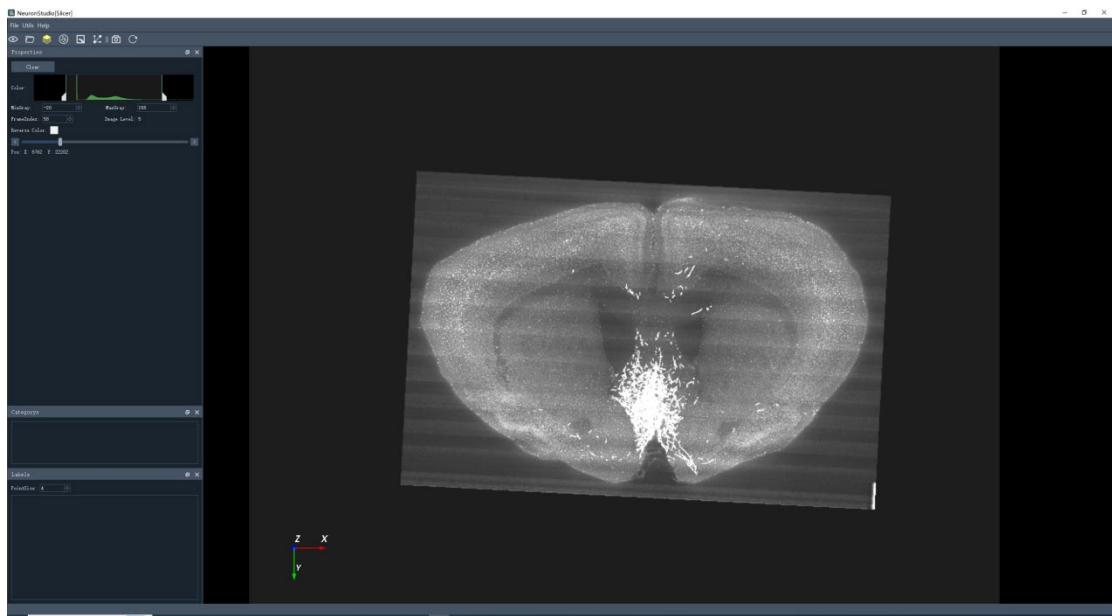


Figure 4.1.3

4.1.2 Introduction to data properties

The **Properties** section contains the following attributes for the imported data:

- **Clear:** Clears the data in the module.
- **Color:** Represents the grayscale histogram, which can be adjusted. **MinGray** and **MaxGray** represent the minimum and maximum grayscale values.
- **FrameIndex:** Adjusts the Z-axis frame index of the current displayed image.
- **Image Level:** Represents the current image level. The image level can be automatically changed by scrolling with the mouse wheel. The larger the zoom, the clearer the image, and the lower the image level.
- As shown in the red box in Figure 4.1.4, clicking will automatically play the next frame image; clicking will automatically play the previous frame image (Shortcut keys **A** for previous frame, **D** for next frame).
- **Pos: X: -14786 Y:10729:** Represents the current position of the mouse on the image.

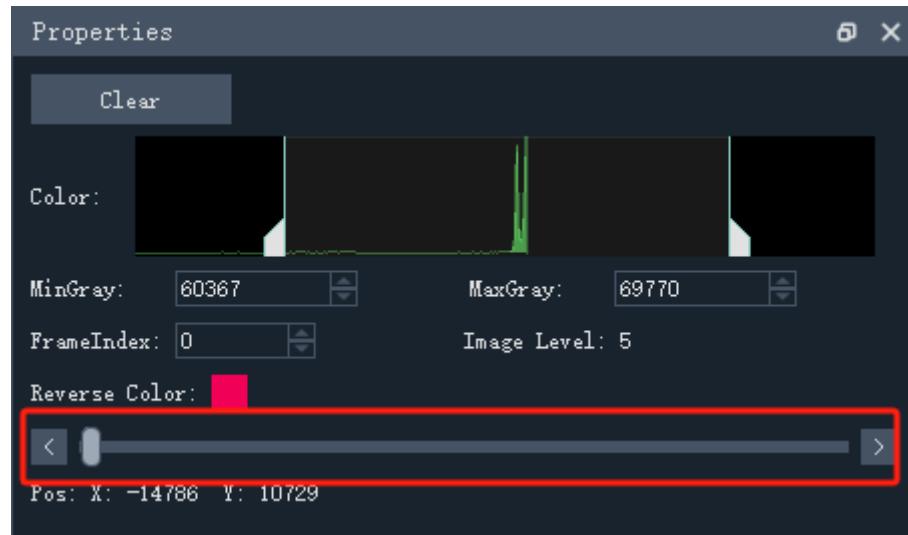


Figure 4.1.4

4.1.3 Mouse Operation

The mouse scroll wheel can zoom in or out of the 2D image. Left-click can be used to drag the 2D image.

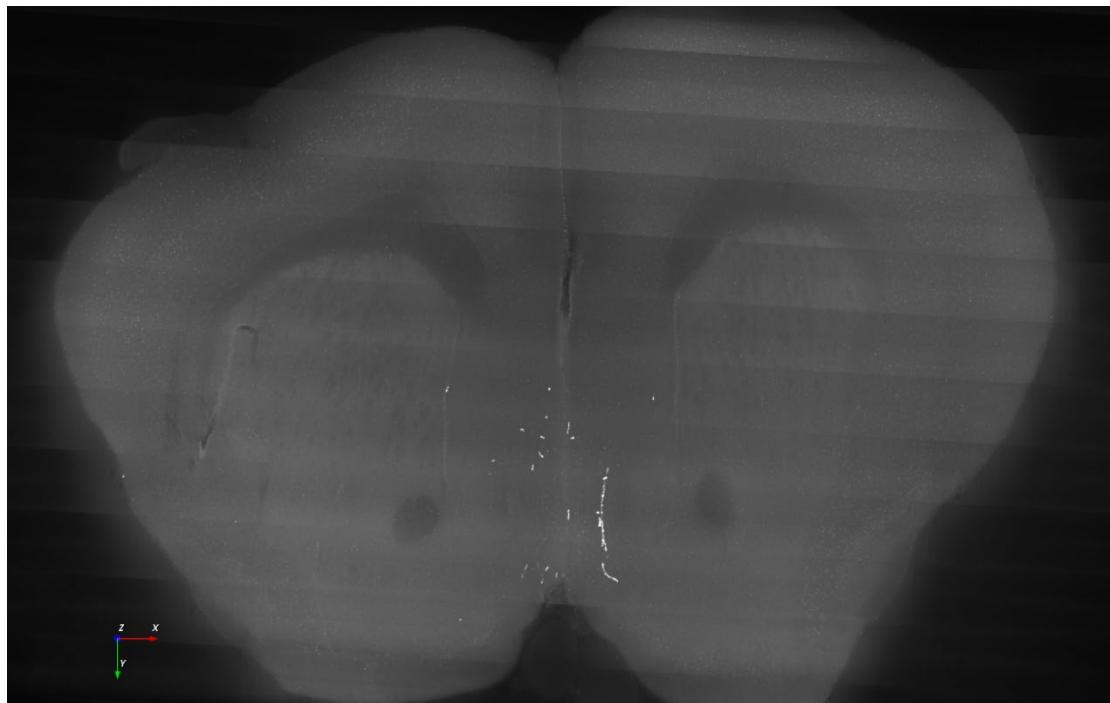


Figure 4.1.5

4.1.4 Data Annotation

Polygon boundary annotation can only be made when the **Image Level** is set to level 0.

- **Categorys:** Records the annotation types that have been created; as shown in the red box in Figure 4.1.6.

- **Labels:** Records all annotations based on the annotation type. Clicking on an annotation item will navigate to the selected annotation. Right-clicking on an annotation item in the list allows you to choose to delete it.
- **PointSize:** The size of the annotation points.

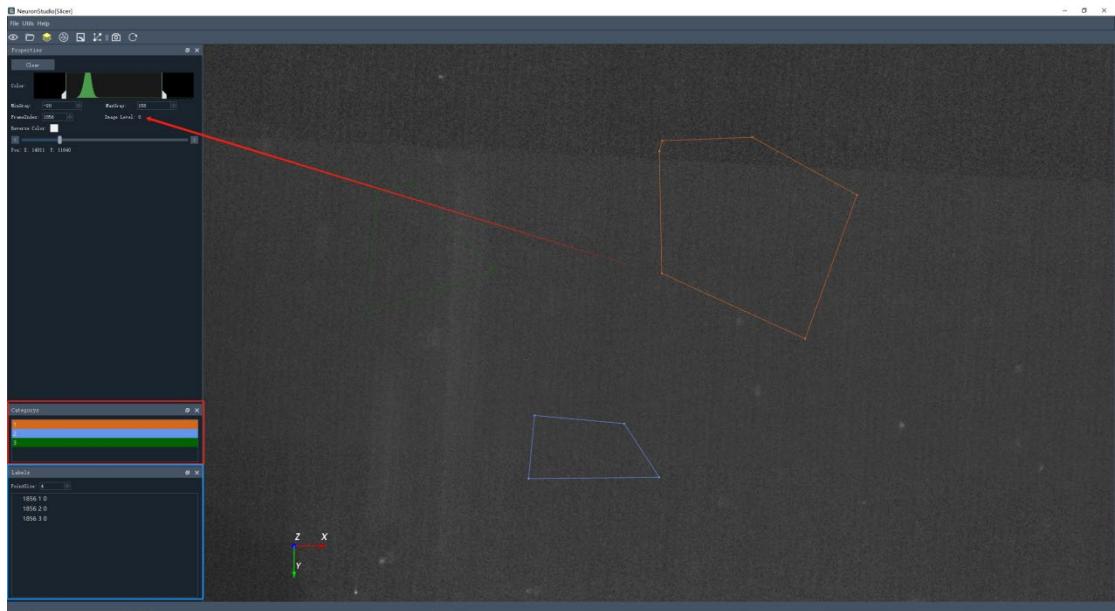


Figure 4.1.6

Annotation Operation:

- 1) Available at image level 0. Press **V** to enter annotation mode, left-click to create points. After drawing is done, press **S** to save the annotation. If the input category does not exist, a new type will be created.

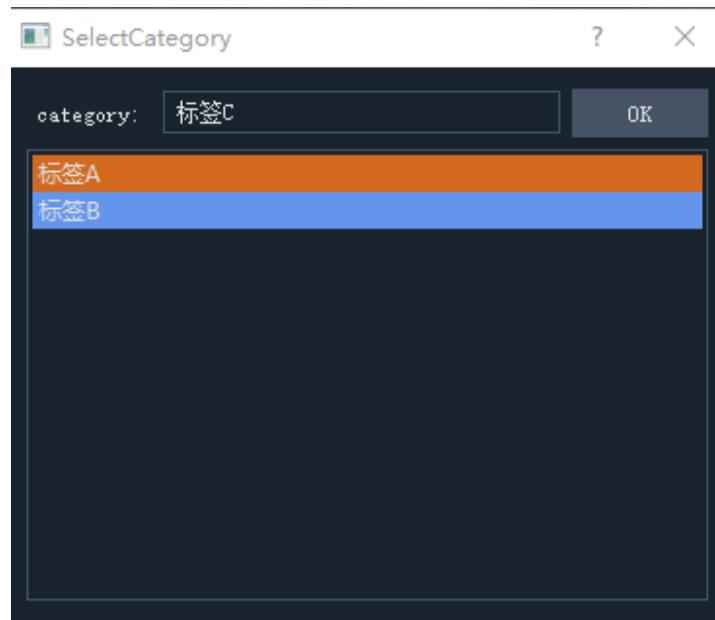


Figure 4.1.7

- 2) Press **S** to enter the normal mode. Press **Ctrl + S** to save all annotations, which will generate a Json file locally.

- 3) After importing the Bio-VS data format next time, import the saved Json file, and the corresponding polygon annotations will appear on the image. Click **File** and **OpenLabel** to open the labels, as shown in Figure 4.1.8.

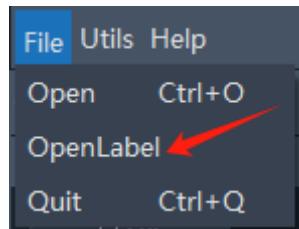


Figure 4.1.8

5. Maximum Intensity Projection

5.1 Generation of maximum intensity projection

- 1) Click  in the toolbar to enter the maximum intensity projection mode. Then click **File** → **ProjectionCreator** in the menu bar to create the maximum intensity projection.

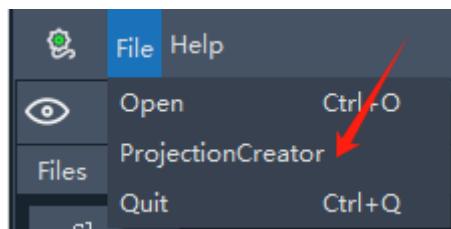


Figure 5.1.1

- 2) In the **ConfigPath**, select the “config.cfg” path of the Bio-VS format data generated in [chapter 1.1](#).
- 3) Set the save path.
- 4) **Axis** refers to the projection direction, **Level** is the image level, and **Space** is the projection interval. **Data Size** refers to the size of the image.

(Note: The **Level** is generally between 0-6, and it is recommended that the projection interval in the X and Y directions be a multiple of 512, while in the Z direction, the projection interval should be a multiple of 16).

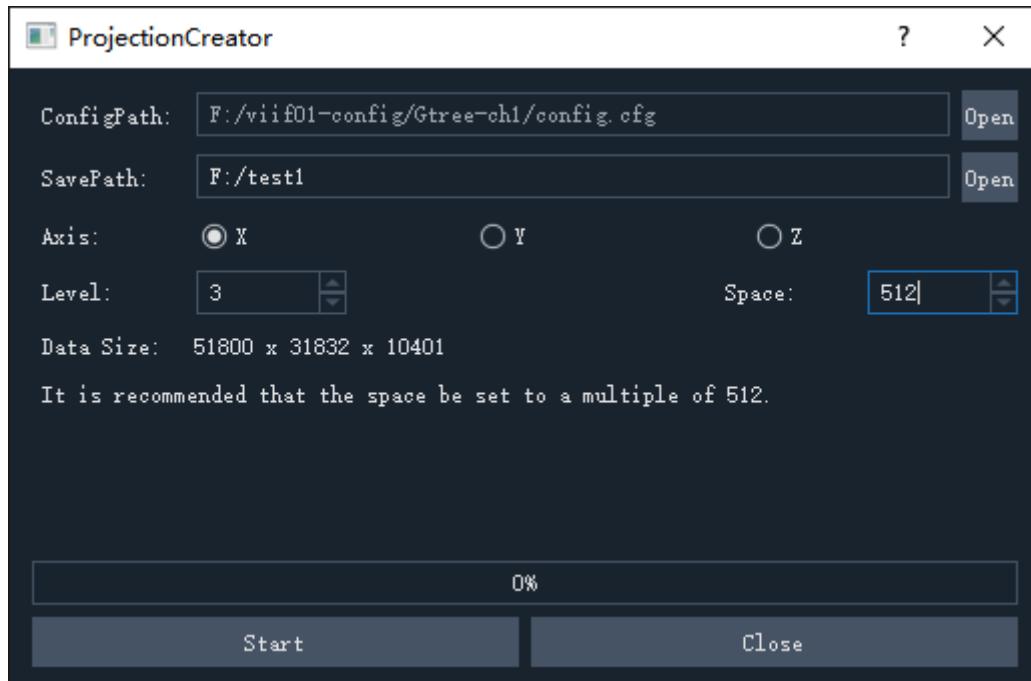


Figure 5.1.2

- 5) Click **Start** to begin the maximum intensity projection creation. The process is shown in Figure 5.1.3. **Task Progress** shows the progress of the task. **Used Time** indicates the time elapsed. **Remaining Time** shows the estimated time left for completion.

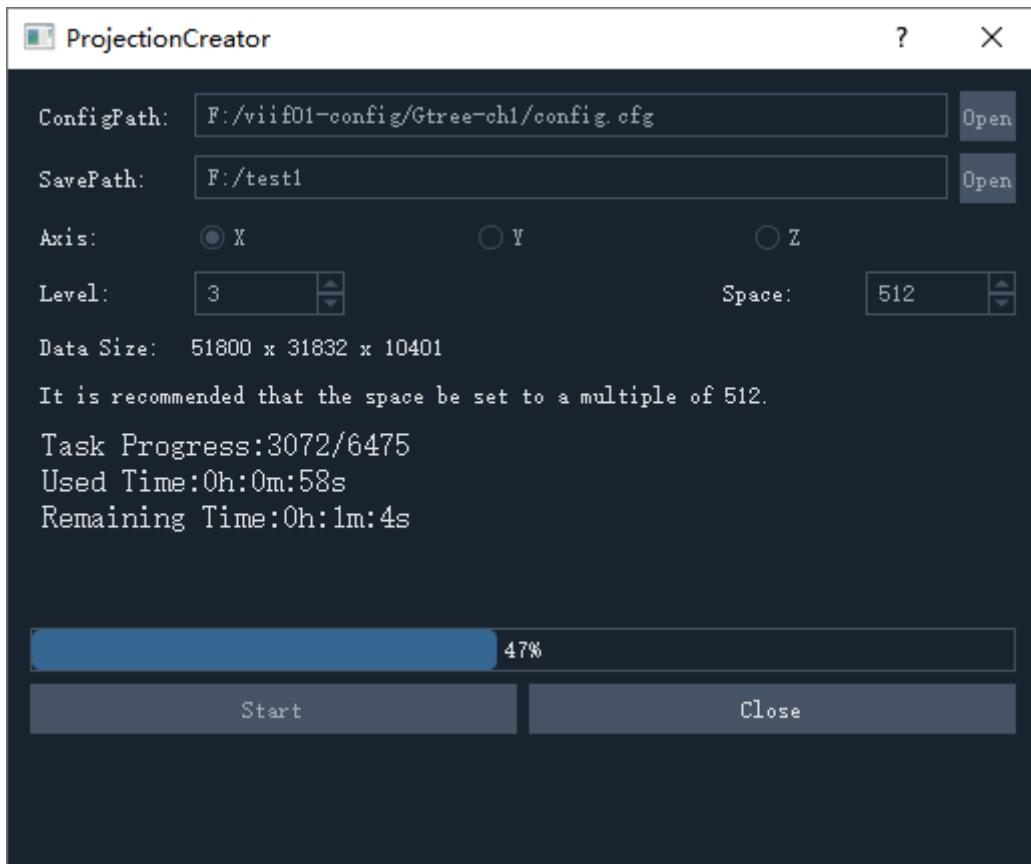


Figure 5.1.3

- 6) Once the generation is complete, the current window will display the information in the red box as shown in Figure 5.1.4, indicating that the process is finished. Click **Close** to close the window.

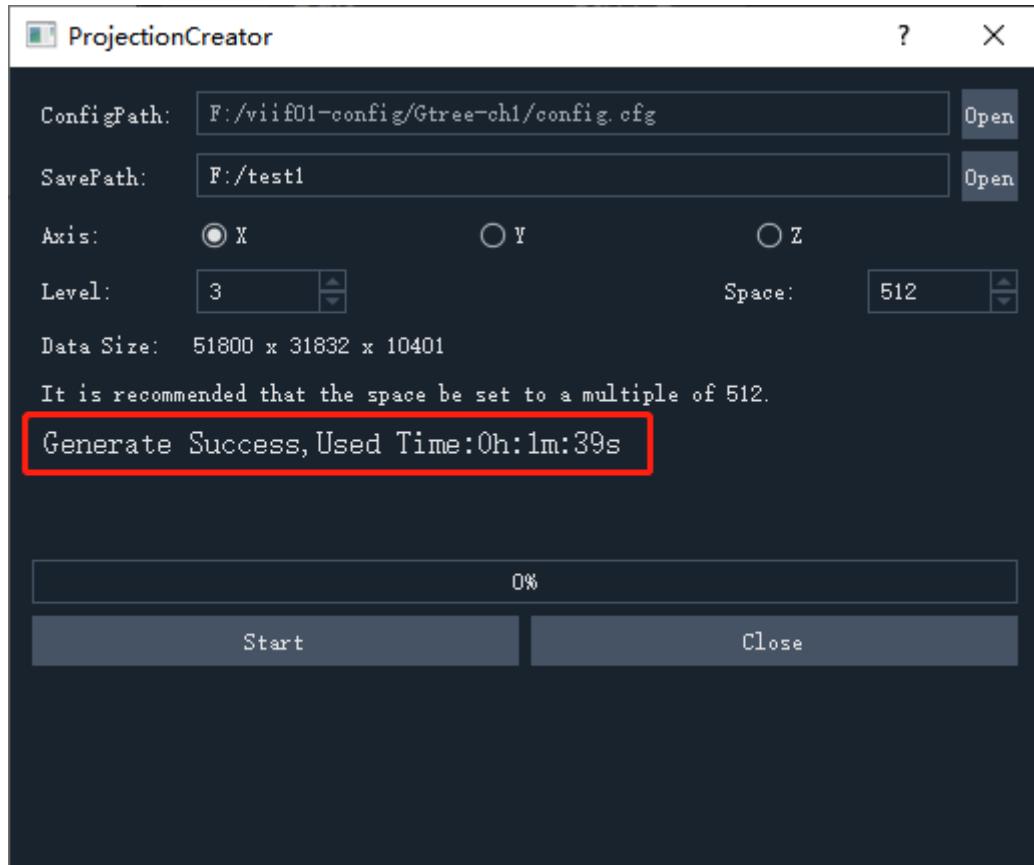


Figure 5.1.4

5.2 Visualization of maximum intensity projection

- 1) Click on the menu bar **File** → **Open** and select the image from the saved path of the maximum intensity projection generation.

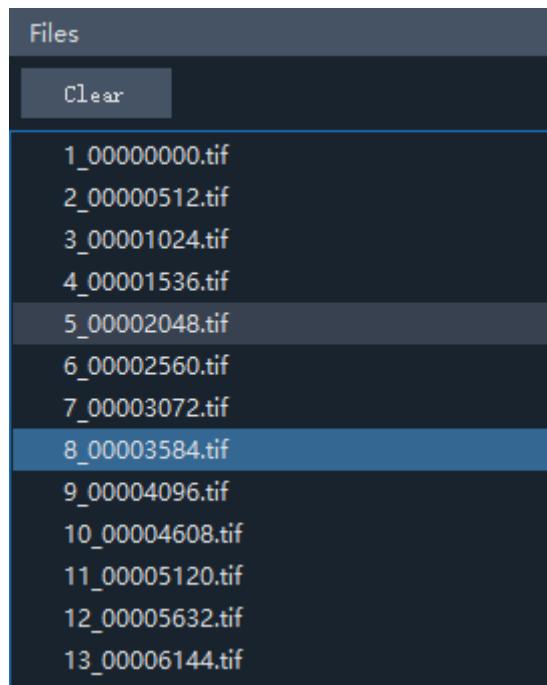


Figure 5.2.1

- 2) Grayscale values of the image can be adjusted in the grayscale histogram. **Pos** represents the coordinates of the current mouse position in the visualization area. **Clear** clears the current data in module.



Figure 5.2.2

- 3) Click on the image name in the list at the top left, and the corresponding image will be visualized on the right side. (When the mouse stays on the data list, the shortcut keys for switching data are the → key to go to the next image and the ← key to go to the previous image).

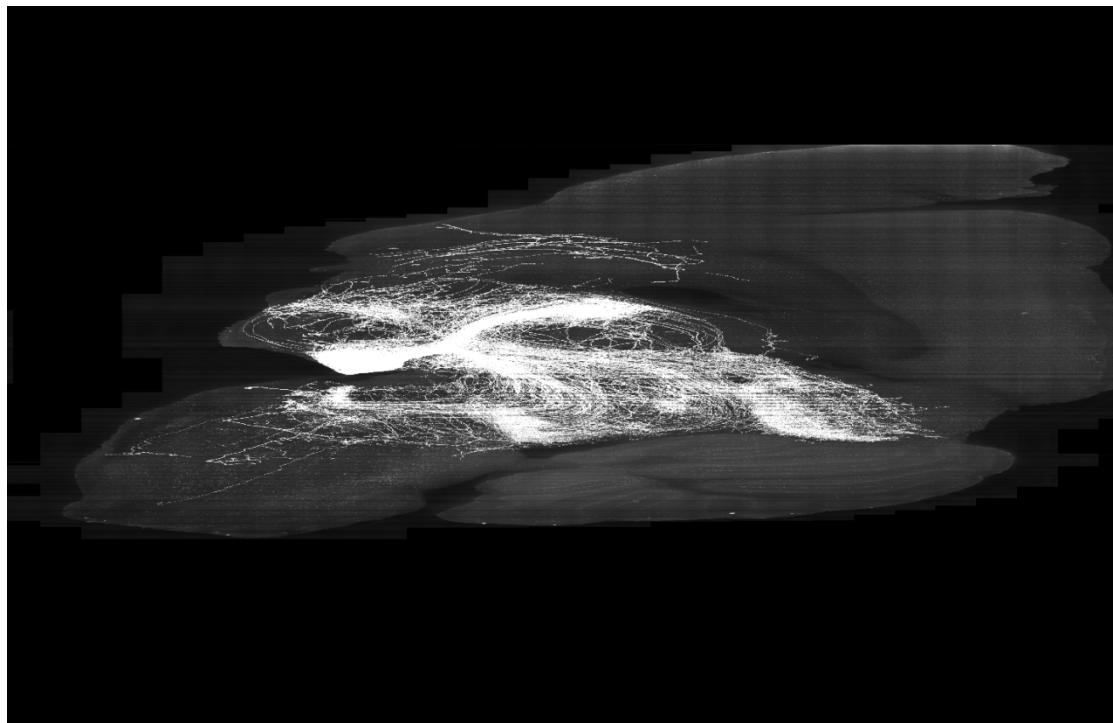


Figure 5.2.3

Mouse Instructions

- **Pan Image:** Hold the mouse wheel to move the mouse.
- **Zoom In:** Scroll the mouse wheel forward.
- **Zoom Out:** Scroll the mouse wheel backward.
- **Rotate Image:** Hold the left mouse button and move the mouse.
- **Reset Image:** Use the **XY**, **XZ**, or **YZ** button.