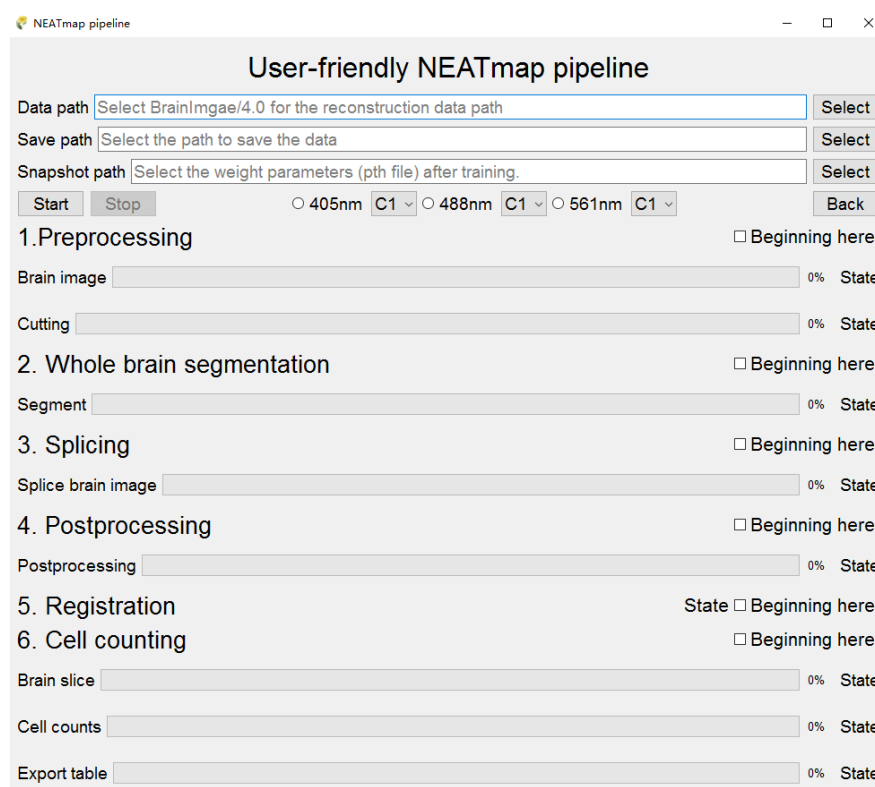
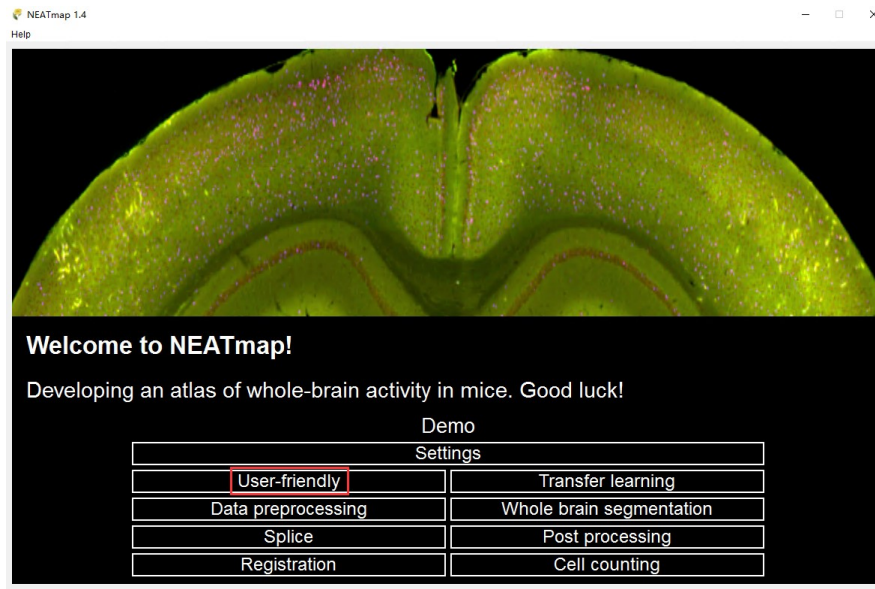


NEATmap Software User Guide

User-friendly



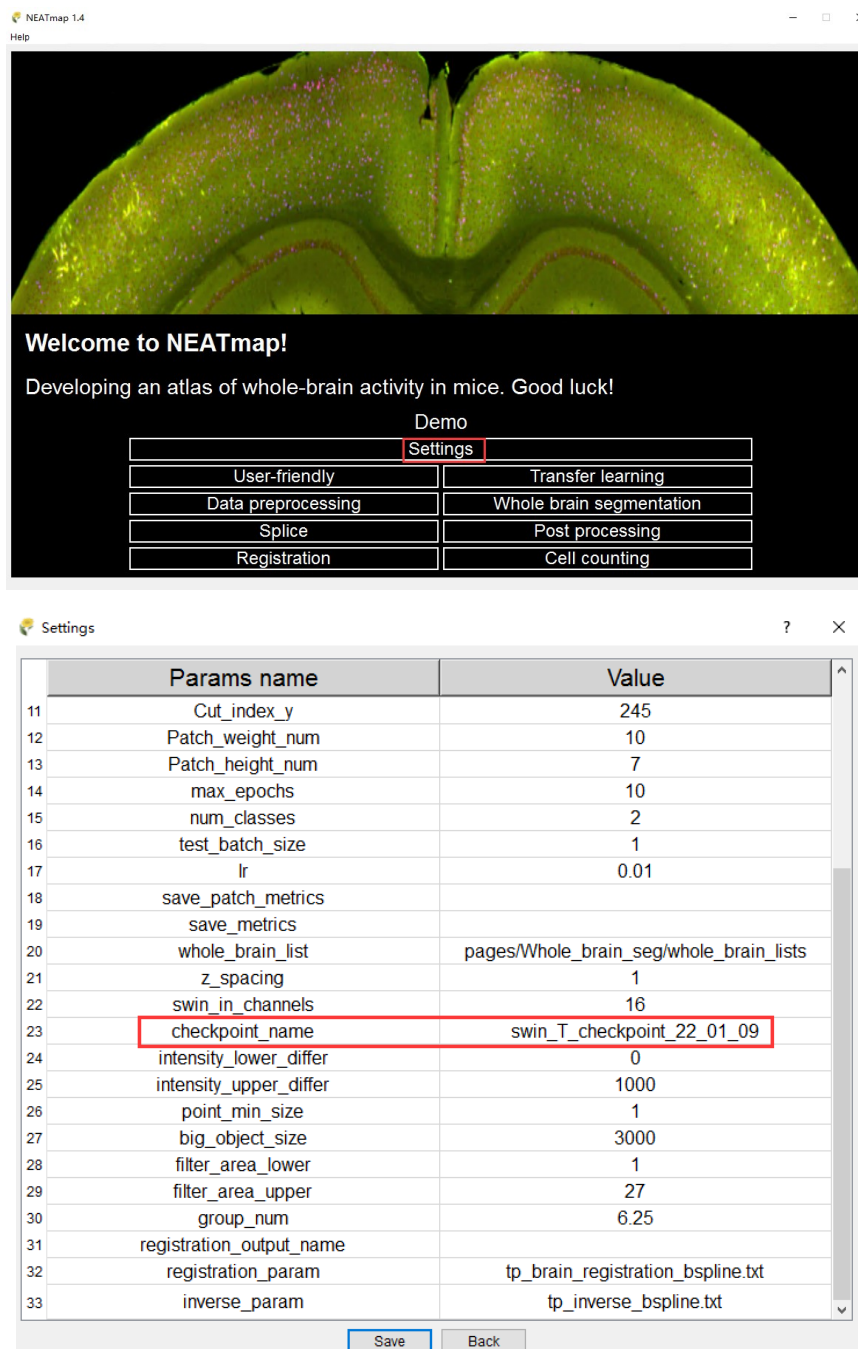
The **Data path** is BrainImage/4.0 after reconstruction.

Snapshot path is the path for loading the trained parameters of the

neural network. The default path for the trained parameters is:

pages\Whole_brain_seg\swin_T_checkpoint_22_01_09.

If you want to change the network parameters, you need to modify the checkpoint name on the **Settings** page to the name of the folder where the network parameters are located.



NEATmap 1.4

Help

Welcome to NEATmap!

Developing an atlas of whole-brain activity in mice. Good luck!

Demo

Settings	
User-friendly	Transfer learning
Data preprocessing	Whole brain segmentation
Splice	Post processing
Registration	Cell counting

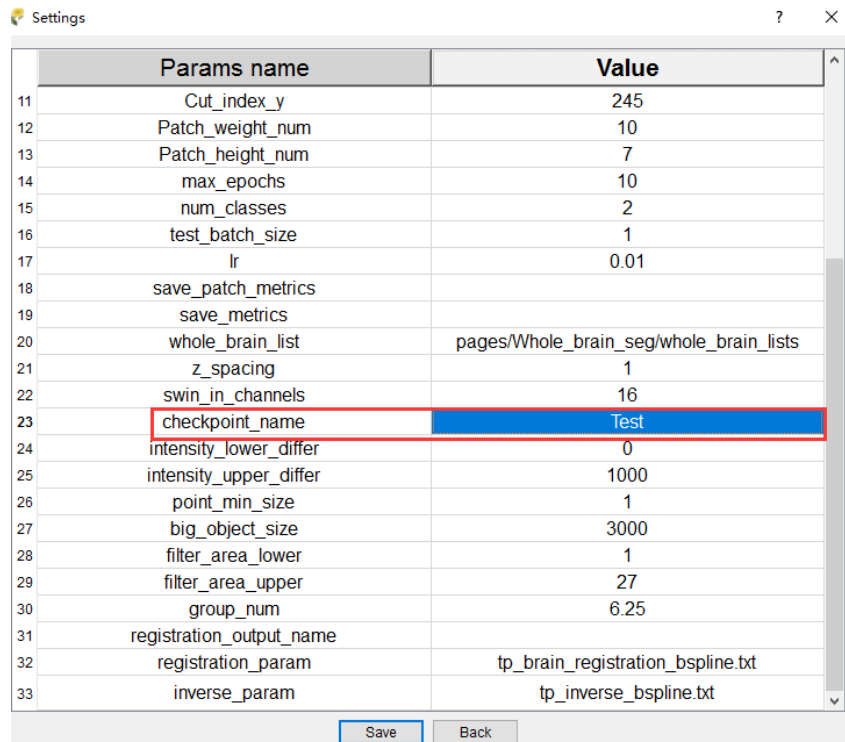
Settings

	Params name	Value
11	Cut_index_y	245
12	Patch_weight_num	10
13	Patch_height_num	7
14	max_epochs	10
15	num_classes	2
16	test_batch_size	1
17	lr	0.01
18	save_patch_metrics	
19	save_metrics	
20	whole_brain_list	pages/Whole_brain_seg/whole_brain_lists
21	z_spacing	1
22	swin_in_channels	16
23	checkpoint_name	swin_T_checkpoint_22_01_09
24	intensity_lower_differ	0
25	intensity_upper_differ	1000
26	point_min_size	1
27	big_object_size	3000
28	filter_area_lower	1
29	filter_area_upper	27
30	group_num	6.25
31	registration_output_name	
32	registration_param	tp_brain_registration_bspline.txt
33	inverse_param	tp_inverse_bspline.txt

Save Back

For example, if the network parameters you want to use are in the

folder name **Test**, modify them as shown below:



The screenshot shows a 'Settings' window with a table of parameters. The 'checkpoint_name' parameter is highlighted with a red box, and its value is 'Test'. The table has two columns: 'Params name' and 'Value'.

	Params name	Value
11	Cut_index_y	245
12	Patch_weight_num	10
13	Patch_height_num	7
14	max_epochs	10
15	num_classes	2
16	test_batch_size	1
17	lr	0.01
18	save_patch_metrics	
19	save_metrics	
20	whole_brain_list	pages/Whole_brain_seg/whole_brain_lists
21	z_spacing	1
22	swin_in_channels	16
23	checkpoint_name	Test
24	intensity_lower_differ	0
25	intensity_upper_differ	1000
26	point_min_size	1
27	big_object_size	3000
28	filter_area_lower	1
29	filter_area_upper	27
30	group_num	6.25
31	registration_output_name	
32	registration_param	tp_brain_registration_bspline.txt
33	inverse_param	tp_inverse_bspline.txt

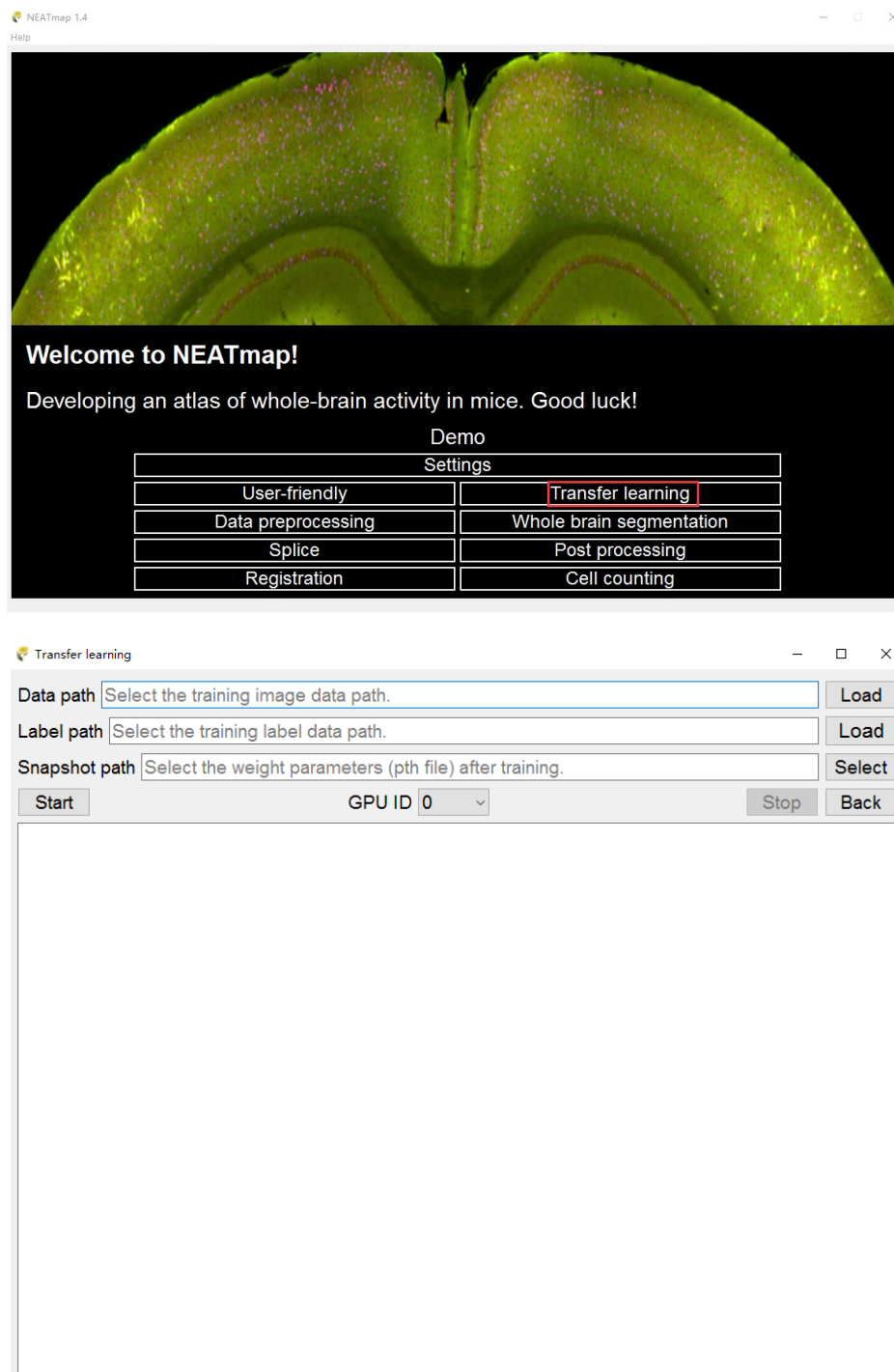
At the bottom of the window, there are two buttons: 'Save' and 'Back'.

Then, click **Save** to complete the modification of network parameters.

Finally, the number information of each channel must be selected correctly, and click **Start** to start running. On this page, Data preprocessing to export of cell counting results will be completed.

If you want to skip **Preprocessing**, you can check **Beginning here** to the right of **Whole brain segmentation**. Other operate similarly.

Transfer learning

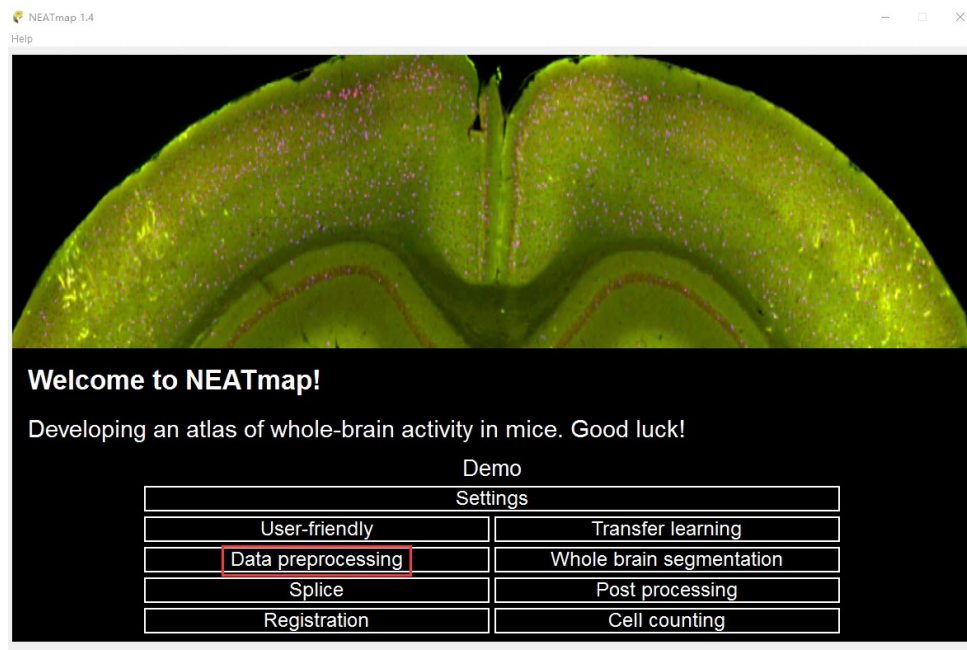


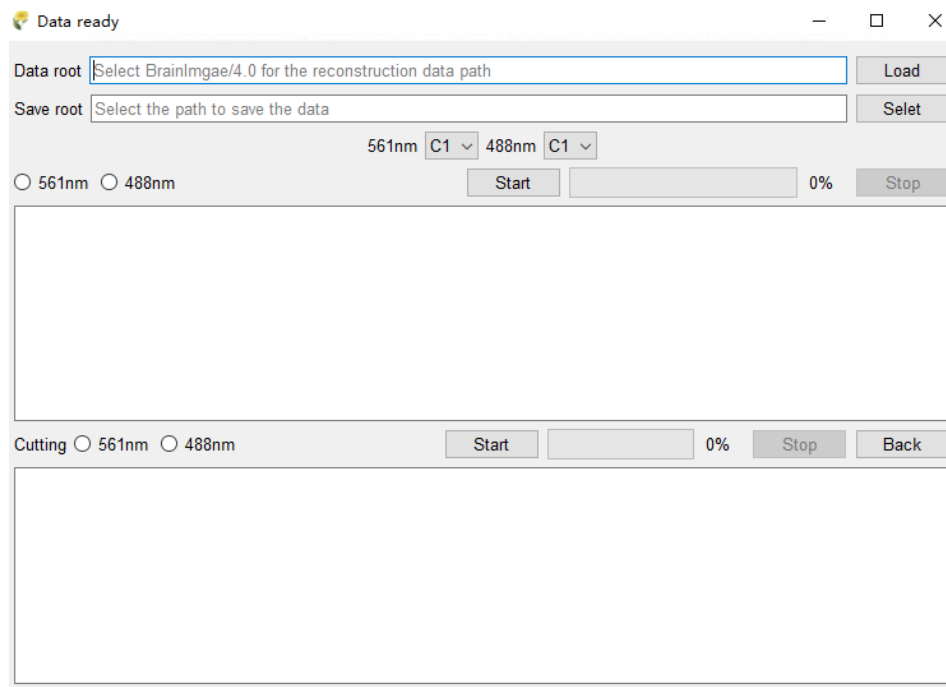
The **Data path** consists of training image data path that needs to be transferred for learning. The naming follows the rules: Z00001.tif, Z00002.tif, and so on.

The **Label path** contains training ground truth data path required for transfer learning. The naming follows these rules: Z00001_seg.tif, Z00002_seg.tif, and so on.

The **Snapshot path** is a weight parameter path that needs to be fine-tuned. The GPU ID allows you to choose which graphics card to use for transfer learning. If not applicable, you can select 'False'. The minimum configuration includes an NVIDIA Tesla V100S-PCIe with 32GB RAM.

1. Data preparation



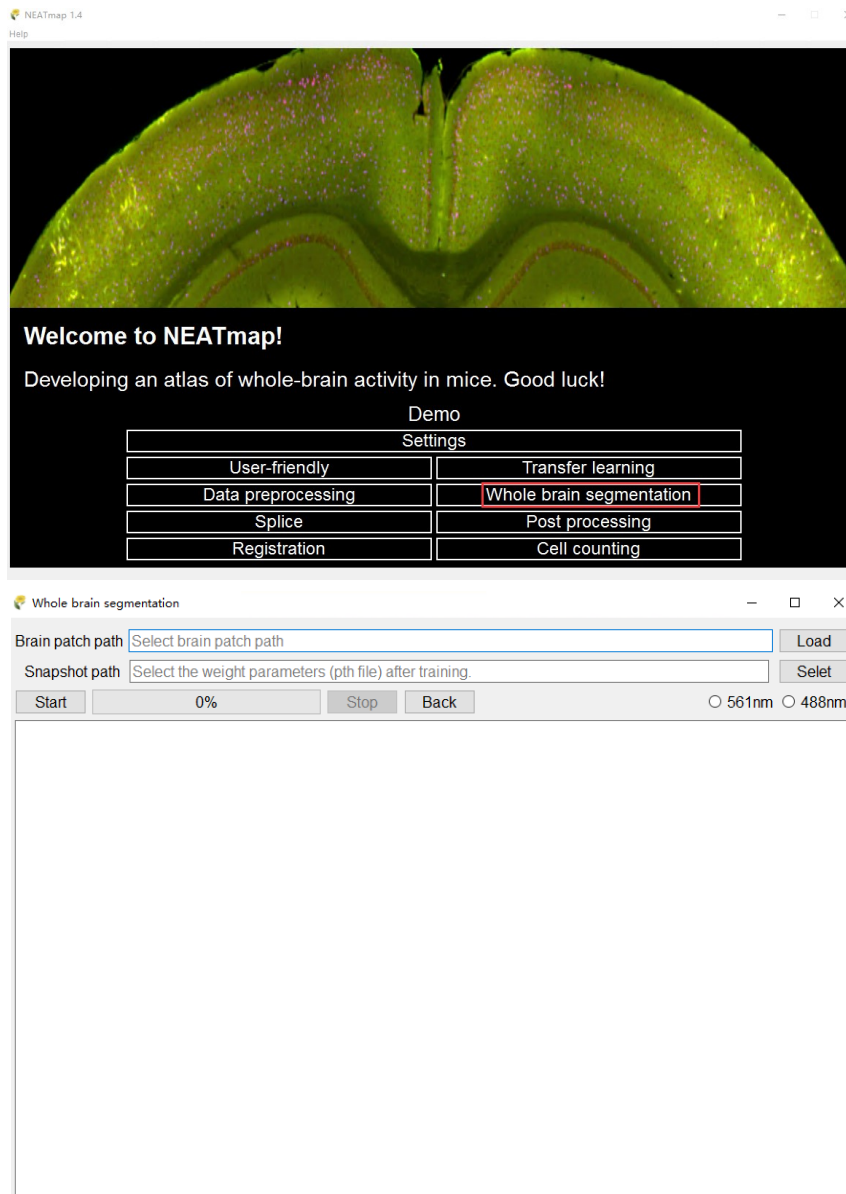


(1). Data preparation for 3D brain slices: The data root is BrainImage/4.0 after reconstruction. Select channels corresponding to 561nm and 488nm. By default, the 3D data size is (3500, 2500, 64) for (x, y, z) dimensions. Click **Start** to begin the preparation process for either 561nm or 488nm channels. **Stop** will change to **Finished** when a single data preparation is complete.

(2). After the 3D data preparation is complete, start cropping the data. Crop one data into 70 subvolume brain images with dimensions (256, 256, 64) for (x, y, z). Perform the operation as before, and click **Back** to return to the main page after completion.

2. Whole-brain immunolabeled signal segmentation

After cropping, start the whole-brain automated segmentation of c-Fos+ and spontaneous fluorescence signals in the whole brain.

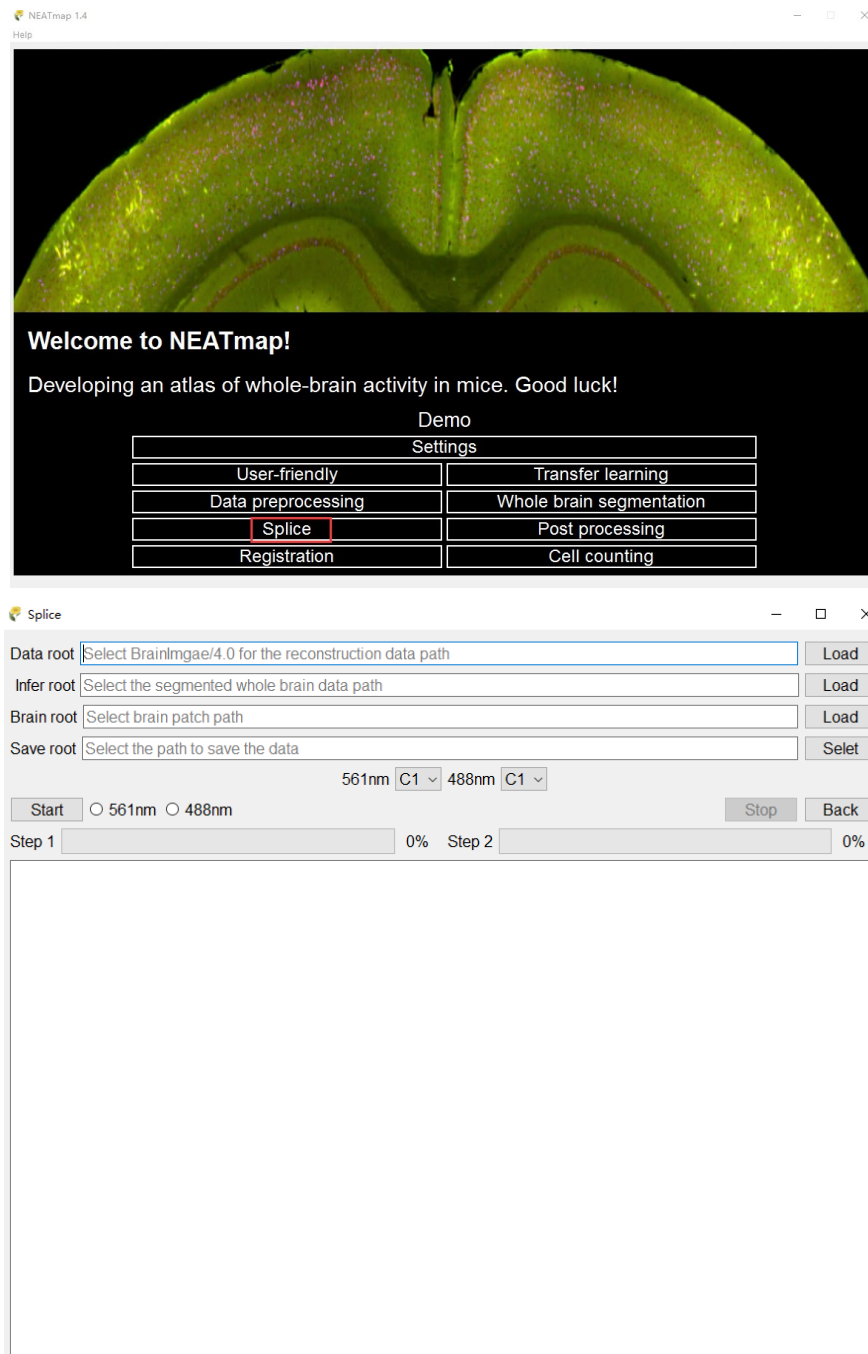


Brain patch path refers to the parent path of the Subvolume brain images after cropping. Snapshot path is the path for loading the trained parameters of the neural network. The default path for the trained parameters is:

pages\Whole_brain_seg\swin_T_checkpoint_22_01_09.

3. Whole brain splicing of segmentation results

After completing the whole-brain signal segmentation for the dual channels, it is necessary to restore the segmentation results of the Subvolume brain images to the original size of the brain slices.

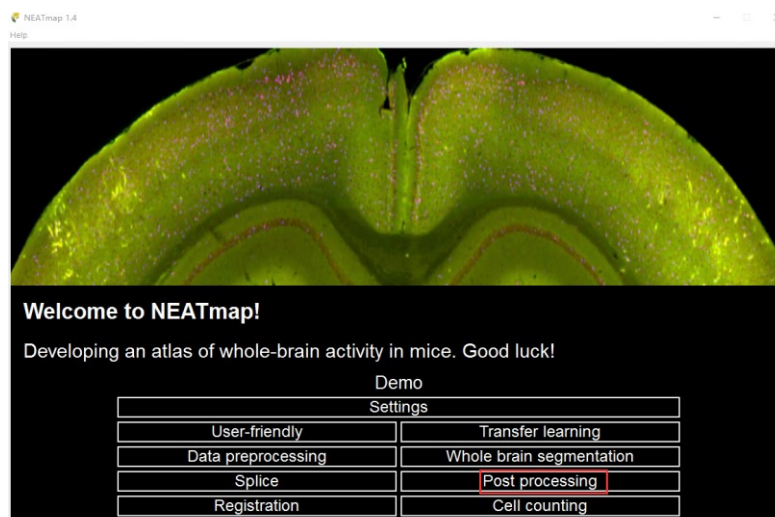


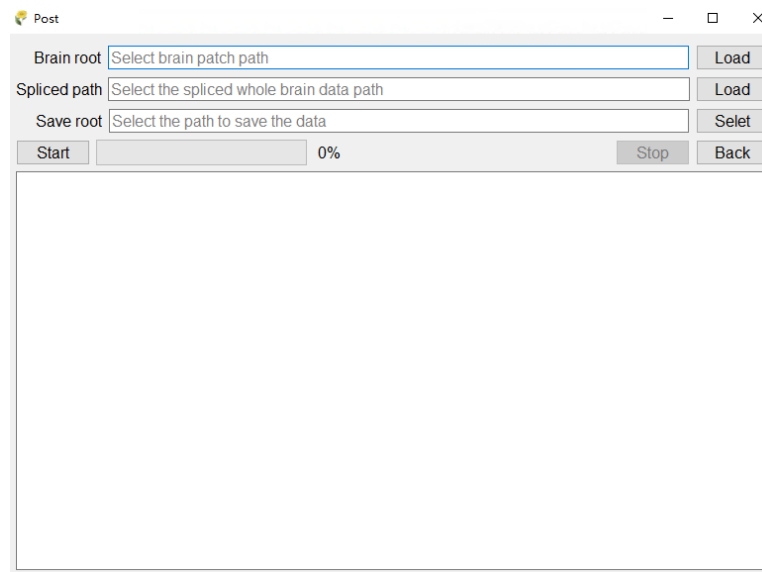
The data root path is as described above. The Infer root refers to the path of the whole-brain dual-channel segmentation results, and the Brain root refers to the parent path of the Subvolume brain images.

The stitching process consists of a total of 2 steps. The first step is to convert the 3D segmentation results to 2D and stitch them in a 2D layer-wise manner for the whole brain (3500, 2500). The second step is to combine all stitched 2D segmentation results to generate a 3D volume (3500, 2500, 64).

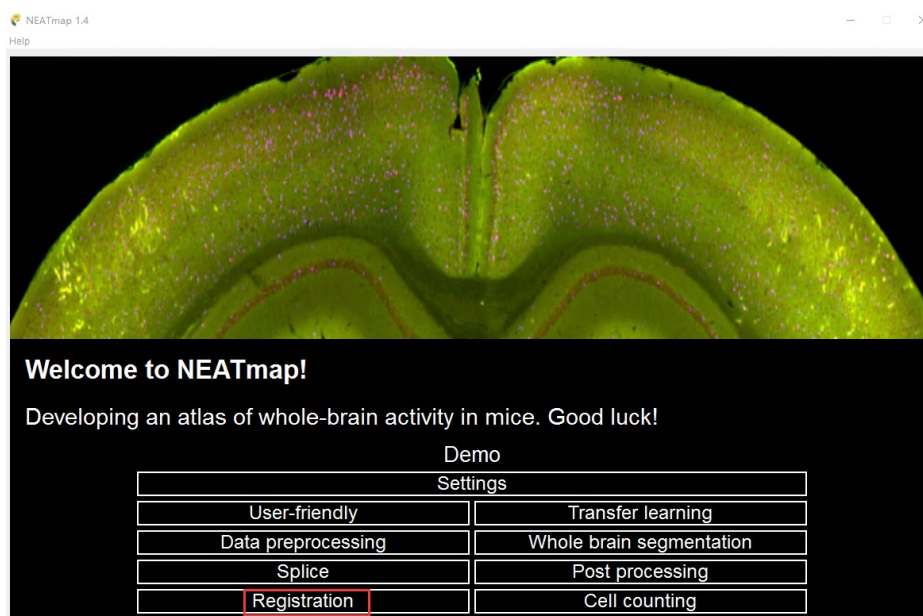
4. Post processing

After completing the whole-brain signal segmentation stitching, post-processing operations are performed. The splice path refers to the parent path of the stitched results.



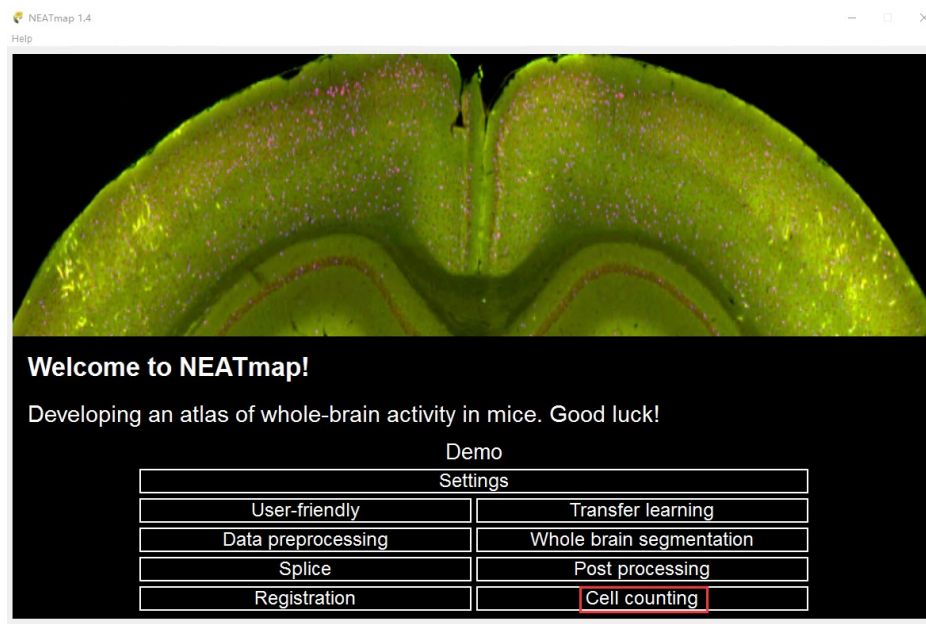


5. Registration

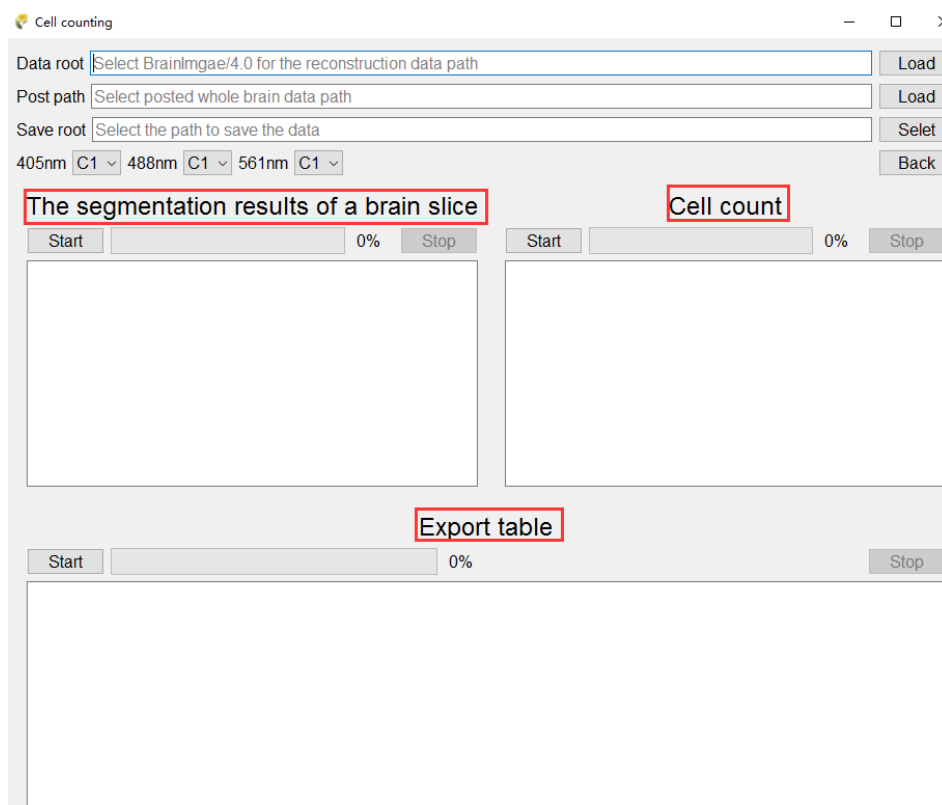


This module can register the whole brain to the Allen Common Coordinate Framework atlas. The operation is the same as above, and when finished, the **Stop** button displays **Finished**.

6. Cell counts



After registration and post-processing are completed, the segmentation results need to be mapped to the Allen CCFv3. The Post path refers to the parent path of the post-processing results.



(1) The module is used to restore the size of the segmentation results from (3500, 2500, 64) to (3500, 2500, 75), which corresponds to a thickness of 300 μm ($75 \times 4 \mu\text{m}$).

(2) Cell count. This module is used to count cells in the whole brain signal segmentation results.

(3) Export table. This module is used to generate a csv file that can be imported into Freesia, which records the centroid coordinates of each segmented c-Fos signal.

Exported file

brain_image_64_488nm	2022/11/13 22:37
brain_image_64_561nm	2022/11/13 22:19
BrainRegistration	2022/11/20 16:09
PatchImage_488nm	2022/11/19 18:11
PatchImage_561nm	2022/11/22 17:14
whole_brain_cell_counts	2022/11/23 22:26
whole_brain_pred_3d	2022/11/20 20:36
whole_brain_pred_488nm	2022/11/19 20:47
whole_brain_pred_561nm	2022/11/19 17:16
whole_brain_pred_post_filter	2022/11/20 10:00
whole_predications_488nm	2022/11/19 18:49
whole_predications_561nm	2022/11/18 19:41