

User's Manual for DeepBrainIPP

SKULL STRIPPING

1. Collect URL and port information where IPP is installed
2. Login to <http://hostname:port/step/skullstrip> using your username and password. The following interface will be shown.

▼ ☒ Extract mouse brain ☐ Pause

Frequent

Sometimes

Rare

outputfile

Enter output file directory

Input folder

Image Spacing

0.06,0.06,0.06

Folder Name or Pattern

Model Type

exvivo-2

Need Re-slicing?

NO

Manual file organization?

0

3. Enter the value for each parameter. The input and output directory must be accessible by HPC cluster. Enter the image spacing correctly. The folder name should follow same pattern for all images for a dataset. For Ex-vivo MRIs enter **exvivo-1** and In-vivo MRIs enter **invivo-2**. If you need re-slicing of MRIs, put **YES**. This is required when cerebellum is not at the beginning of Z slices.
4. Click on **Rare** tab. You will see following interface.

Submit Job

Download Settings

▼

☒ Extract mouse brain

☐ Pause

Frequent

Sometimes

Rare

Required memory in MB

10000

HPC queue name

standard

Run on CBI servers

bioimg-wkst08.stjude.sjcrh.local

Location of Models Stored

Location of Code

Submit Job

5. Enter HPC queue name such as **dgx**, **gpu** based on your preference and make sure that queue has GPUs
6. Submit the job. When the job is finished, **state** will be updated to **SUCCESSFUL**

Search:

↕	Job ID (and Configuration Link)	↕	State	↕	Jacs ID	↕
	61d5f8541fd03471558defb3		SUCCESSFUL		3007855928990765086	
	61d5d66d1fd03471558defb2		SUCCESSFUL		3007855928990744606	

7. Skull stripping images will be stored in **final_segmentation** folder with measured volumes in **brain_measures.csv** file
8. Paraflocculus segmentation outcome will be stored in **PF_outer_final_segmentation** with measured volumes

Brain/Cerebellum Image Registration

9. Select step equals **antsgenericregistration** from the dropdown list.
Following interface will be shown
- 10.Enter a directory where registration outcome will be stored

11. Enter the location of Atlas file
12. Enter the path of **final_segmentation** folder where skull stripped brain are stored
13. Change the registration command based on the dataset and image modalities
14. If you need to register and process multiple files, enter **1** in **Run in batch**

▼ ☒

☐ Pause

Frequent

Sometimes

Rare

outputfile

Enter output file directory

out_file_prefix_name

SIMtoEM

fixed_file_path

Enter path for fixed file

move_file_path

Enter path for movable file

reg_param_cmd

--verbose 1 --dimensionality 3 --float 0 --collapse-output-transforms 1 --interpolation BSpline[3] --use-histo

operation type

antsregistration ▼

Run in batch

0

Cerebellum Registration?

0

15. Once registration is done, click on **quantifysegmentation** from step dropdown list. You will see the following interface

▼

Quantify brain segmentation

☐ Pause

Frequent

Sometimes

Rare

outputfile

Enter output file directory

operation type

quantifybrain ▼

Image Spacing

0.06,0.06,0.06

Labeled Mask

Structure List in file

Interpolation

NearestNeighbor

Submit Job

16. Change **operation type** to **quantifybrain** in the dropdown
17. Enter image spacing. For exvivo, it would be 0.06,0.06,0.06 and Invivo would be 0.06,0.06,0.48
18. Enter path of label mask and structure list
19. Submit Job
20. The brain structures will be segmented and stored in **subregion** folder.
21. For cerebellum registration and subcerebral region extraction, follow the steps 13-18. Make sure you put **1** for **Cerebellum Registration** parameter

Registration command and sample parameter for Whole Brain:

```
--verbose 1 --dimensionality 3 --float 0 --collapse-output-transforms 1 --
interpolation BSpline[3] --use-histogram-matching 1 --winsorize-image-
intensities [0.005,0.995] --initial-moving-transform [fixed_file,move_file,1]
--transform Rigid[0.1] --metric MI[fixed_file,move_file,1,64,Regular,0.25] --
convergence [1000x500x250x100,1e-6,20] --shrink-factors 8x4x2x1 --smoothing-
sigmas 6x4x2x1vox --transform Affine[0.1] --metric
Mattes[fixed_file,move_file,1,64,Regular,0.25] --convergence
[1000x500x250x100,1e-6,20] --shrink-factors 8x4x2x1 --smoothing-sigmas
6x4x2x1vox --transform Syn[0.1,3,0] --metric CC[fixed_file,move_file,1,4] --
convergence [100x50x25x10,1e-6,20] --shrink-factors 8x4x2x1 --smoothing-
sigmas 6x4x2x1vox
```

Registration command and sample parameter for Cerebellum:

```
--verbose 1 --dimensionality 3 --float 0 --collapse-output-transforms 1 --  
interpolation BSpline[3] --use-histogram-matching 1 --winsorize-image-  
intensities [0.005,0.995] --initial-moving-transform [fixed_file,move_file,1]  
--transform Rigid[0.1] --metric MI[fixed_file,move_file,1,64,Regular,0.25] --  
convergence [1000x500x250x100,1e-6,20] --shrink-factors 8x4x2x1 --smoothing-  
sigmas 0x0x0x0vox --transform Affine[0.1] --metric  
Mattes[fixed_file,move_file,1,64,Regular,0.25] --convergence  
[1000x500x250x100,1e-6,20] --shrink-factors 8x4x2x1 --smoothing-sigmas  
0x0x0x0vox --transform Syn[0.1,3,0] --metric CC[fixed_file,move_file,1,4] --  
convergence [100x50x25x10,1e-6,20] --shrink-factors 8x4x2x1 --smoothing-  
sigmas 0x0x0x0vox
```