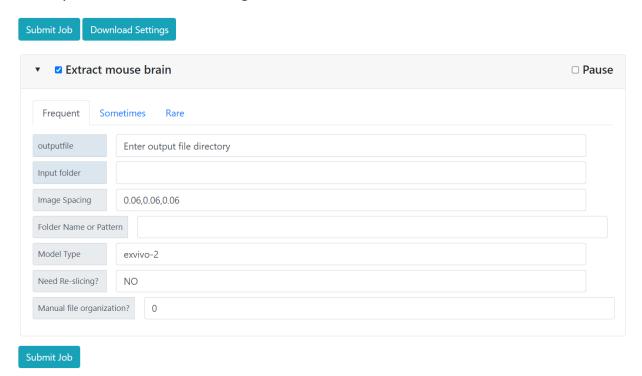
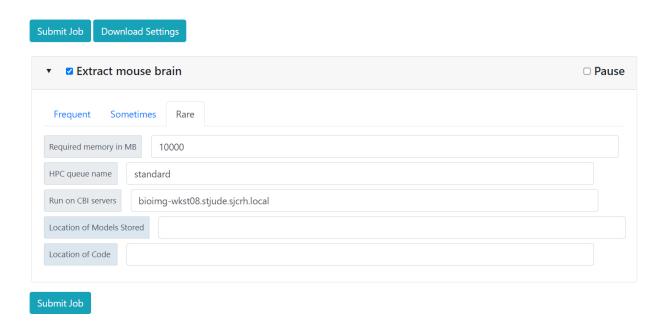
User's Manual for DeepBrainIPP

SKULL STRIPPING

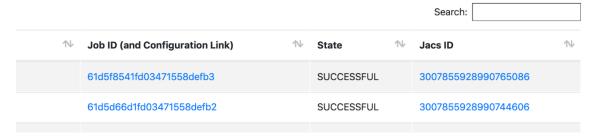
- 1. Collect URL and port information where IPP is installed
- 2. Login to http://hostname:port/step/skullstrip using your username and password. The following interface will be shown.



- 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 **exviovo-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.



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

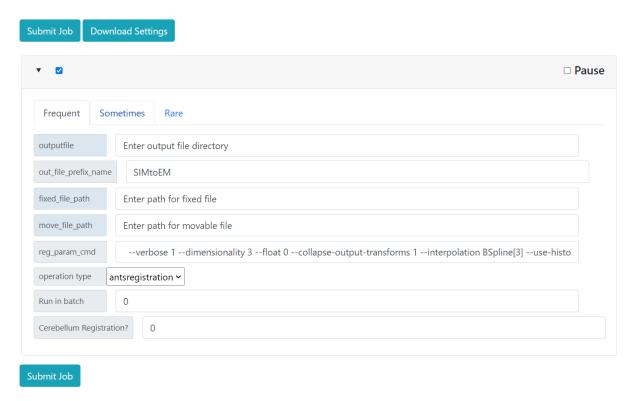


- 7. Skull stripping images will be stored in **final_segmentation** folder with measured volumes in **brain_measures.csv** file
- 8. Paraflocculous segmentation outcome will be stored in **PF_outer_final_segmentation** with measured volumes

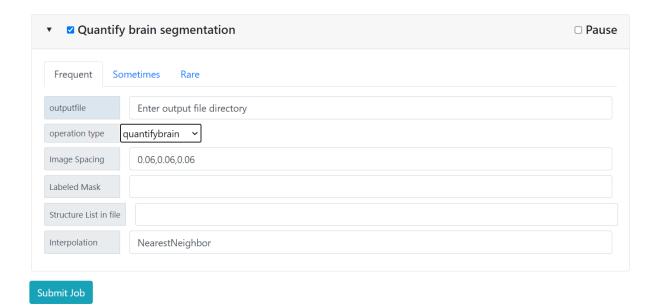
Brain/Cerebellum Image Registration

- 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



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



- 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-imageintensities [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 --smoothingsigmas 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 --smoothingsigmas 0x0x0x0vox