

MORI Pipeline

Last updated 2/6/2019

Upload

- 1) Run → `./gowild`, navigates to WildThings folder
- 2) Run the masking script → `./MaskAllOwlOrientUsingTreehouse`
 - command outputs new files to upload into `/WildThings/3c_MaskedOwlOrient_tree`
- 3) Go to → `braingps.anatomyworks.org`
 - U/P: `ll@gmail / mnd####`
 - My Job Status → see completed jobs, available to download
 - Segmentation → upload new files
- 4) Upload new scans
- 5) Segmentation → T1 Multiatlas Batch
- 6) Drag & drop file
- 7) Highlight filename (w/o zip ending)
- 8) Saggital Data converted to Axial
- 9) Select correct atlas
 - `Ucdavis3yrs_289Labels_13atlases_picsl_v7A`
 - `Pediatric4-8yrs_289Labels_10atlases_picsl_v7A`
 - `Pediatric8-12yrs_289Labels_28atlases_picsl_v7A`
 - `Adult_289Labels_45atlases_picsl_v7a`
- 10) Upload each atlas individually → 4 for each case
- 11) Paste in filename with correct atlas → `_ucd`, `_ped48`, `_ped812`, `_adult`

Download

- 1) Log into → `braingps.anatomyworks.org` → My Job Status
- 2) Scroll to bottom → most recently completed jobs
- 3) Copy filename
- 4) Right click → Download Result → Save Link As
- 5) Go to → `data/arch/WildThings/4_BrainGPS_Outputs_wt/1_Output_Zips`
- 6) Paste filename → Save
- 7) Repeats these download steps for each atlas and case
- 8) Log into Treehouse → run `./gowild`
- 9) Unpack download cases with → `./AllUnpackMoriZip`
- 10) Command outputs to `WildThings/4_BrainOutputs_wt/3_Awaiting_QC`
 - copy filenames to RoiEdit google sheet

Recording Pass/Fail

- 1) Pass or Fail scans using script → `<script_name> <scan_name_atlas>`
 - helps to ctrl + c from RoiEdit sheet
 - `./FailQC.py #####-###_OwlOrient_ucd3`
 - `./PassQC.py #####-###_OwlOrient_ped48`
- 2) Pull MORI results using → `./PullMori.py`
- 3) Email .csv results as need