

¹ Macapype: An open multi-software framework for non-human primate brain anatomical MRI processing

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²²

⁹ Summary

¹⁰ Although brain anatomical Magnetic Resonance Imaging (MRI) processing is largely standard-
¹¹ ized and functional in humans, it remains a challenge to define robust processing pipelines
¹² for the segmentation of non-human primate (NHP) images. To unify the processing of NHP
¹³ anatomical MRI, we propose Macapype, an open-source framework to create custom pipelines
¹⁴ for data preparation, brain extraction, and brain segmentation.

¹⁵ Statement of Need

¹⁶ Non-human primates (NHPs) are increasingly used for neuroimaging studies due to the progress
¹⁷ of MR acquisitions and the promises it holds in the field of neuroscience ([Milham et al., 2018](#)).
¹⁸ Despite the standardization of MRI processing in humans with several well-known software
¹⁹ options available, such as AFNI ([Cox, 1996](#)), FSL ([Smith et al., 2004](#)), SPM12 ([Frackowiak et al., 1997](#)), and ANTS ([Avants et al., 2011](#)), defining robust processing pipelines for NHP
²⁰ anatomical image segmentation remains difficult.

²² Related Packages

²³ Two categories of methods have been proposed to address the issue of NHP anatomical
²⁴ MR image segmentation. The first category corresponds to particular implementations for
²⁵ PNH images of existing human-MRI softwares such as **NHP-Freesurfer** and **CIVET-Macaque**,
²⁶ respectively relying on human-MRI softwares Freesurfer ([Fischl, 2012](#)) and CIVET ([Lepage et al., 2021](#)). The second category relies on the use of deep-learning and machine learning
²⁷ techniques, such as **U-Nets**, for example **nBEST** to provide brain mask, segmentation of GM,
²⁸ WM and subcortical nuclei ([Zhong et al., 2024](#)). The latter requires the use of GPUs, most
²⁹ existing softwares performs relatively badly on small NHP species such as marmoset due to
³⁰ the lack of flexibility in the processing steps and the variability of brain peculiarities among
³¹ NHP species.
³²

³³ Presentation of the Package

³⁴ In this context, we propose a general framework for the tissue segmentation of non-human
³⁵ primate brain MR images that can provide multiple pipelines to adapt to a variety of image
³⁶ qualities and species. This open-source framework, named Macapype, is built on the Nipype
³⁷ ([Gorgolewski et al., 2011](#)), a widely used Python framework for human MRI analysis.

³⁸ The Macapype package was specifically designed to provide wraps of custom tools specific to
³⁹ NHP anatomical MRI preprocessing, as well pipelines and workflows to achieve high-quality

⁴⁰ automated tissue segmentation of NHP anatomical images. In particular, the tuning of
⁴¹ parameters for different species, should be possible if needed via the use parameters files

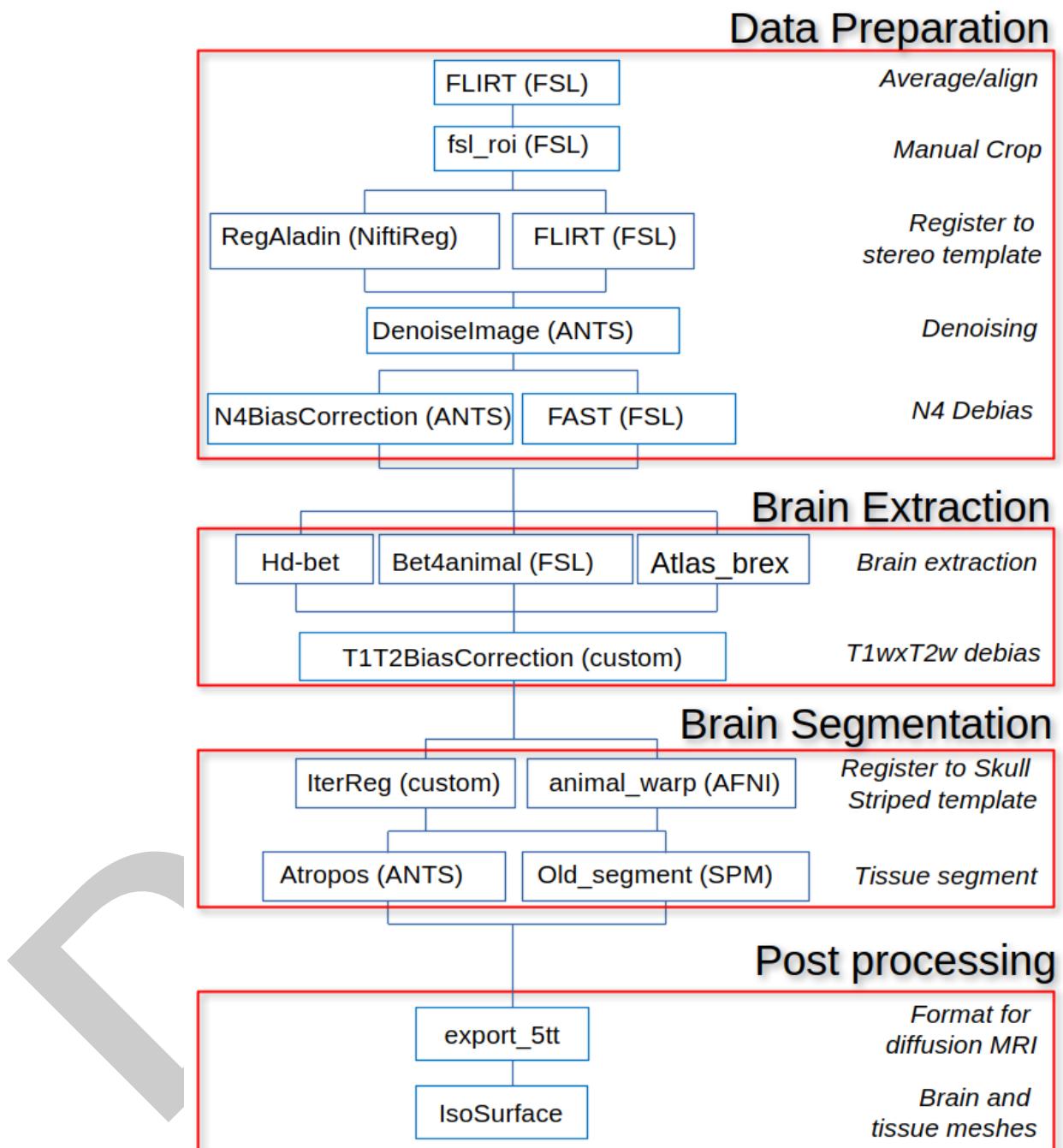


Figure 1: Different pipelines are chained

⁴² Pipelines

⁴³ Macapype provides configurable pipelines organized in three steps: data preparation, brain
⁴⁴ extraction, and brain segmentation. Post-processing allows for conversion to format for further
⁴⁵ processing outside Macapype.

46 **Data Preparation Pipeline**

47 The data preparation pipeline is specified in a JSON parameters file and depends on individual
48 parameters. If cropping parameters are absent, Macapype performs an automated but low-
49 precision crop. The input volume is reoriented in a standard space, and denoising and debiasing
50 steps are performed.

51 **Brain Extraction Pipeline**

52 For skull-stripping step, Macapype offers a choice between AtlasBREx (Lohmeier et al., 2019)
53 and bet4animal, an optimized version of brain extraction tool (BET in FSL) for NHP. HD-BET
54 (Isensee et al., 2019) is also available for deep-learning-based brain extraction.

55 **Tissue Segmentation Pipeline**

56 Tissue segmentation is template-based and can be done in template or native space. Macapype
57 provides templates for macaque, marmoset, baboon, and chimpanzee. T1xT2 debias is applied,
58 followed by normalization and segmentation using ANTS-based Atropos or SPM12-based old
59 segment.

60 **Post-Processing Pipeline**

61 For compatibility with further processing, Macapype provides formatting options, such as the
62 5tt file from MRTrix (Tournier et al., 2019) for further processing of diffusion MRI and meshes
63 in STL format for 3D printing.

64 **Discussion**

65 Macapype is compatible with FAIR principles, storing all processing steps and parameters in
66 a JSON file. It allows evaluation of results at different preprocessing steps and is tested on
67 images from the PRIME-DE database (Milham et al., 2018) and is listed as a software solution
68 on PRIME-RE (Messinger et al., 2021).

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