

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

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Summary

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

Statement of Need

Non-human primates (NHPs) are increasingly used for neuroimaging studies due to the progress of MR acquisitions and the promises it holds in the field of neuroscience (Milham et al., 2018). Despite the standardization of MRI processing in humans with several well-known software 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 anatomical image segmentation remains difficult.

Related Packages

Two categories of methods have been proposed to address the issue of NHP anatomical MR image segmentation. The first category corresponds to particular implementations for PNH images of existing human-MRI softwares such as NHP-Freesurfer and CIVET-Macaque, 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 techniques, such as U-Nets, for example nBEST to provide brain mask, segmentation of GM, WM and subcortical nuclei (Zhong et al., 2024). The latter requires the use of GPUs, most existing softwares performs relatively badly on small NHP species such as marmoset due to the lack of flexibility in the processing steps and the variability of brain peculiarities among NHP species.

Presentation of the Package

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

The Macapype package was specifically designed to provide wraps of custom tools specific to 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

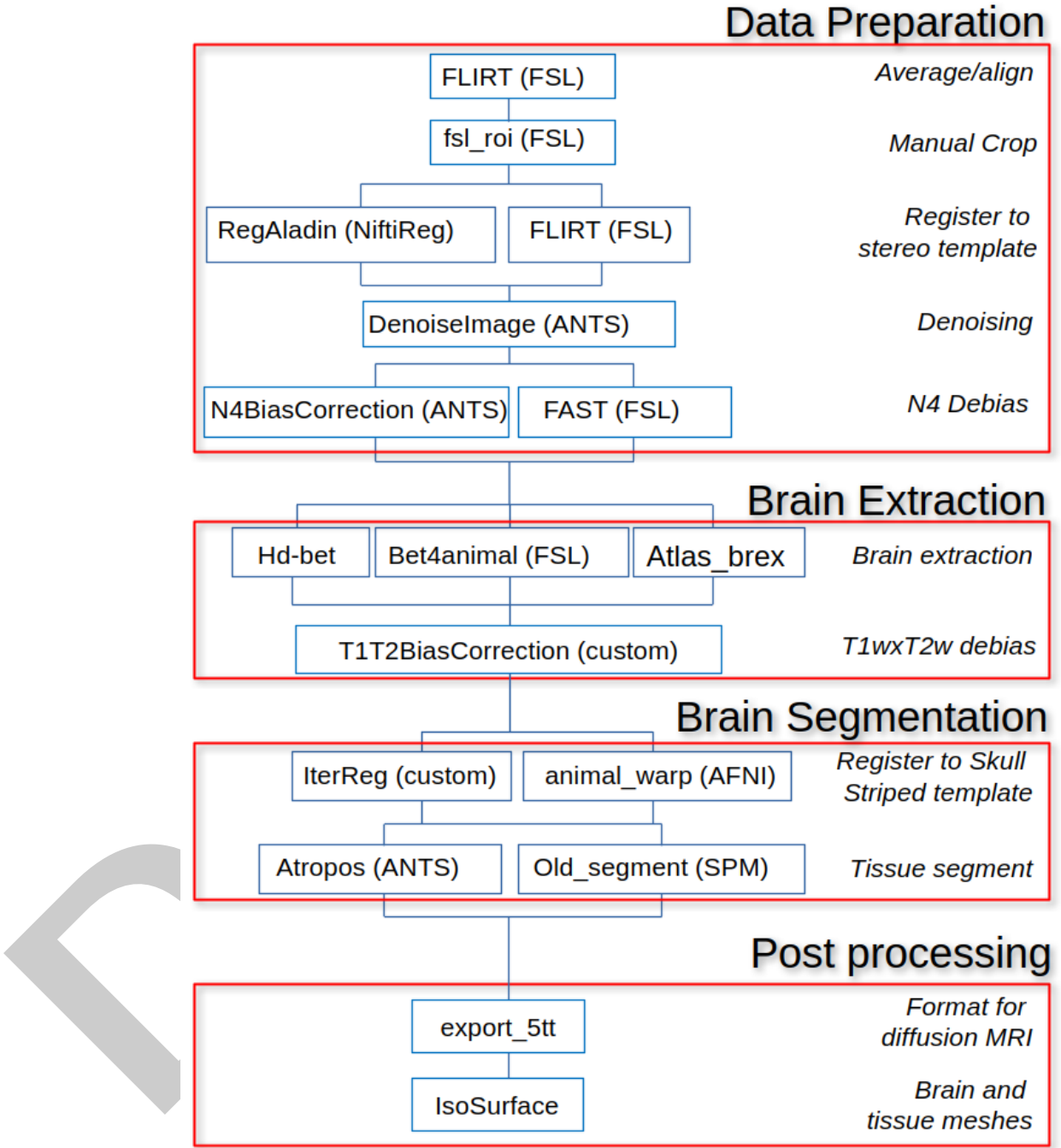


Figure 1: Different pipelines are chained

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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