The Journal of Open Source Software

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

David Meunier [1], **Kep Kee Loh** [4], **Bastien Cagna** [2,3], **Regis Trapeau** [1], **Julien Sein** [1], and **Olivier Coulon** [1]

1 Aix Marseille Univ, CNRS, INT, Inst Neurosci Timone, Marseille, France **2** CATI, US52-UAR2031, CEA, ICM, Sorbonne Université, CNRS, INSERM, APHP, Ile de France, France **3** Paris Brain Institute - Institut du Cerveau (ICM), Inserm U1127, CNRS UMR 7225, Sorbonne Universités UMR S 1127, ICM, F-75013 Paris, France. **4** Department of Psychology, National University of Singapore, Singapore

DOI: 10.xxxxxx/draft

Software

- Review
- Repository
- Archive

Editor: Adam Tyson

Submitted: 05 September 2025
Published: unpublished

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.

State of the field

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 NHP 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.

Software design

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 upon Nipype, a widely used Python framework for human MRI analysis.

The Journal of Open Source Software

The Macapype package was specifically designed to provide wrappers of custom tools specific to NHP anatomical MRI preprocessing, as well as pipelines and workflows to achieve high-quality automated tissue segmentation of NHP anatomical images. In particular, the tuning of parameters for different species, should be possible if needed via the use of parameter files.

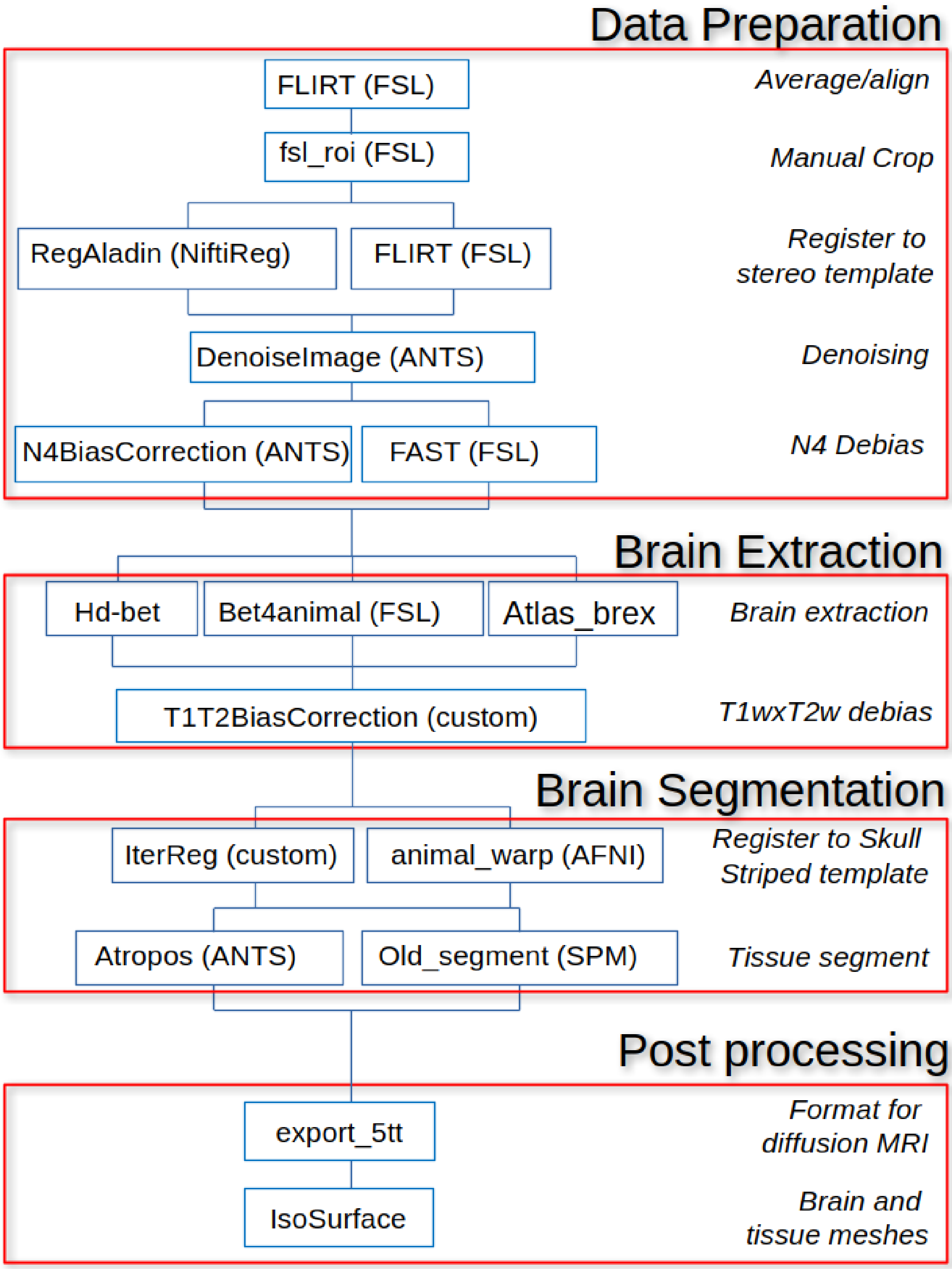

Figure 1: Different pipelines are chained

Pipelines

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

- Data Preparation Pipeline

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

- Brain Extraction Pipeline

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

- Tissue Segmentation Pipeline

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

- Post-Processing Pipeline

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

Research impact statement

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

AI usage disclosure

No generative AI tools were used in the development of this software, or the preparation of supporting materials. This manuscript has been written with the help of Mistral AI for formatting, as well as syntax and language checking.

Acknowledgements

We are grateful to Adrien Meguerditchian, Paul Apicella, and Guilhem Ibos for providing MRI datasets for testing.

References

Avants, B., Tustison, N., & others. (2011). A reproducible evaluation of ANTs similarity metric performance in brain image registration. *NeuroImage*, *54*, 2033–2044. https://doi.org/10.1016/j.neuroimage.2010.09.025

Cox, R. (1996). AFNI: Software for analysis and visualization of functional magnetic resonance neuroimages. *Computers and Biomedical Research*, *29*, 162–173. https://doi.org/10.1006/cbmr.1996.0014

Fischl, B. (2012). FreeSurfer. *NeuroImage*, *62*, 774–781. https://doi.org/10.1016/j.neuroimage.2012.01.021

Frackowiak, R., Friston, K., Frith, C., Dolan, R., & Mazziotta, J. (1997). *Human brain function*. Academic Press USA. https://psycnet.apa.org/doi/10.1027/0269-8803.14.2.128

Isensee, F., Schell, M., & others. (2019). Automated brain extraction of multisequence MRI using artificial neural networks. *Human Brain Mapping*, *40*(17), 4952–4964. https://doi.org/10.1002/hbm.24750

Lepage, C., Wagstyl, K., & others. (2021). CIVET-macaque: An automated pipeline for MRI-based cortical surface generation and cortical thickness in macaques. *Neuroimage*, *227*, 117622. https://doi.org/10.1016/j.neuroimage.2020.117622

Lohmeier, J., Kaneko, T., & others. (2019). AtlasBREX: Automated template-derived brain extraction in animal MRI. *Sci Rep*, *9*(1), 12219. https://doi.org/10.1038/s41598-019-48489-3

Messinger, A., Sirmpilatze, N., & others. (2021). A collaborative resource platform for non-human primate neuroimaging. *NeuroImage*, *226*, 117519. https://doi.org/10.1101/2020.07.31.230185

Milham, M., Ai, L., & others. (2018). An open resource for non-human primate imaging. *Neuron*, *100*, 61–74. https://doi.org/10.1016/j.neuron.2018.08.039

Smith, S., Jenkinson, M., & others. (2004). Advances in functional and structural MR image analysis and implementation as FSL. *NeuroImage*, *23*, 208–219. https://doi.org/10.1016/j.neuroimage.2004.07.051

Tournier, J.-D., Smith, R., & others. (2019). MRtrix3: A fast, flexible and open software framework for medical image processing and visualisation. *NeuroImage*, *202*, 116–137. https://doi.org/10.1016/j.neuroimage.2019.116137

Zhong, T., Wu, X., & others. (2024). nBEST: Deep-learning-based non-human primates brain extraction and segmentation toolbox across ages, sites and species. *NeuroImage*, *295*, 120652. https://doi.org/10.1016/j.neuroimage.2024.120652