Fetpype: An Open-Source Pipeline for Reproducible Fetal Brain MRI Analysis

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Summary

Fetal brain Magnetic Resonance Imaging (MRI) is crucial for assessing neurodevelopment *in utero*. However, analyzing this data presents significant challenges due to fetal motion, low signal-to-noise ratio, and the need for complex multi-step processing, including motion correction, super-resolution reconstruction, and segmentation. While various specialized tools exist for individual steps, integrating them into robust, reproducible, and user-friendly workflows that go from raw image to volume and surface analysis is not straightforward. This lack of standardization hinders reproducibility across studies and limits the adoption of advanced analysis techniques for researchers and clinicians. To address these challenges, we introduce Fetpype, an open-source Python library designed to streamline and standardize the preprocessing and analysis of T2-weighted fetal brain MRI data as illustrated in (Figure 1).

Statement of need

Fetpype is a Python package integrating several established neuroimaging software principles and tools to create a cohesive and extensible framework, which we summarize in four points.

1. **Data Standardization**: Fetpype expects input data organized according to the Brain Imaging Data Structure (BIDS) standard (Gorgolewski et al., 2016), promoting interoperability and simplifying data management.
2. **Containerization**: Individual processing tools are encapsulated within Docker or Singularity containers. This ensures reproducibility and reduces installation issues, providing a better experience for the end user.
3. **Workflow Management**: The Nipype library (Gorgolewski et al., 2011) is used to construct processing workflows: it provides a robust interface for combining different steps from different containers or packages, facilitating data caching and parallelization, and allowing pipelines to be easily shareable.
4. **Configuration**: Pipeline configuration is managed using simple YAML files and the Hydra library (Yadan, 2019), allowing users to easily select between different modules or parameters without directly modifying the code. The current implementation of Fetpype integrates modules for **data preprocessing** (Fetal-BET (Faghihpirayesh et al., 2024), non-local means denoising (Manjón et al., 2010) and N4 bias-field correction (Tustison et al., 2010)), **super-resolution reconstruction** (NeSVoR (Xu et al., 2023), SVRTK (Kuklisova-Murgasova et al., 2012; Alena U. Uus et al., 2022), or NiftyMIC (Ebner et al., 2020)), **segmentation** (BOUNTI (Alena U. Uus et al., 2023) or the developing human connectome project pipeline (Makropoulos et al., 2018)) and **cortical surface extraction** (using a

⁴² custom implementation available at https://github.com/fetpype/surface_processing
⁴³ based on (Bazin & Pham, 2005, 2007; Ma et al., 2022)).

⁴⁴ The objective underlying the conceptualization of 'Fetpype' was to provide the fetal MRI com-
⁴⁵ munity with a standardized, reproducible, and flexible open-source platform for preprocessing
⁴⁶ and analysis. We believe this tool can facilitate research and improve the comparability across
⁴⁷ studies. We also intend to foster collaboration across research teams by providing Fetpype as a
⁴⁸ central framework that facilitates the dissemination of new image processing methods for clinical
⁴⁹ applications. The pipeline is publicly available on GitHub (https://github.com/fetpype/fet-
⁵⁰ pype), and its open-source nature and modular design facilitate community involvement:
⁵¹ researchers can integrate their own tools by creating corresponding `Nipype` interfaces and
⁵² container wrappers, following the package contribution guidelines.

⁵³ In the future, we plan to supplement `Fetpype` with an automated reporting library containing
⁵⁴ automated quality control (Sanchez et al., 2026, 2024), subject-wise and population-wise
⁵⁵ biometry and volumetry (Esteban et al., 2017), as well as spectral analysis (Germanaud et al.,
⁵⁶ 2012). We welcome contributions of authors desiring to integrate their method to `Fetpype`.
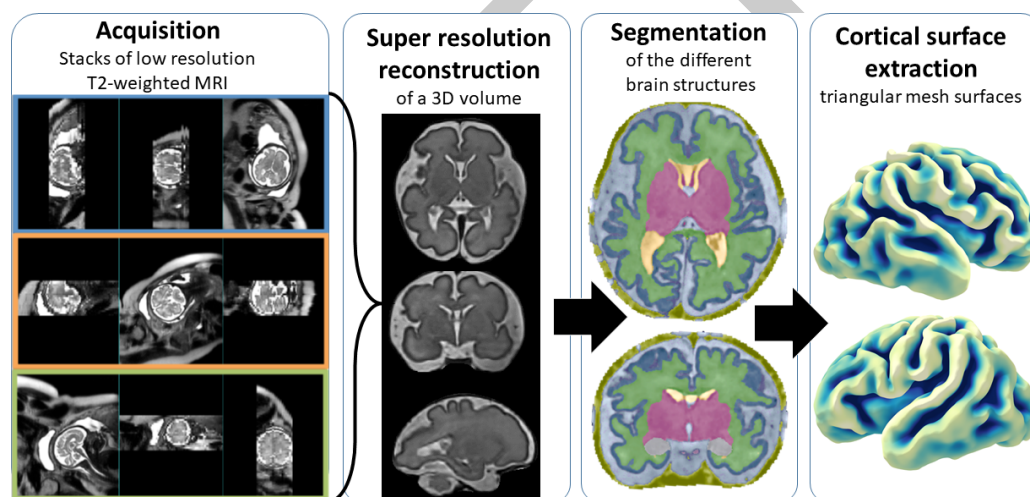

Figure 1: The different steps covered by `Fetpype`. Starting from several T2-weighted stacks of thick slices of the fetal brain (*acquisition*), `Fetpype` pre-processes data before feeding them to a *super-resolution reconstruction* algorithm that fuses them in a single high-resolution volume. This volume then underegoes *segmentation*, before moving to cortical *surface extraction*.

Acknowledgements

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