# 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, segmentation, and surface extraction. While various specialized tools exist for individual steps, integrating them into robust, reproducible, and user-friendly workflows that go from raw images to processed volumes 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** (including brain extraction using Fetal-BET (Faghihpirayesh et al., 2024), non-local means denoising (Manjón et al., 2010) and N4 bias-field correction (Tustison et al., 2010), all wrapped into a single container built at https://github.com/fetpype/utils_container), **super-resolution reconstruction** (NeSVoR (Xu et al., 2023), SVRTK (Kuklisova-Murgasova et al., 2012; Uus et al., 2022), or NiftyMIC (Ebner et al., 2020)), **segmentation** (BOUNTI (Uus

42 et al., 2023) or the developing human connectome project pipeline (Makropoulos et
43 al., 2018)) and **cortical surface extraction** (using a custom implementation available at
44 https://github.com/fetpype/surface_processing based on (Bazin & Pham, 2005, 2007;
45 Ma et al., 2022)).

46 The objective underlying the conceptualization of `Fetpype` is to provide the fetal MRI com-
47 munity with a standardized, reproducible, and flexible open-source platform for preprocessing
48 and analysis. By providing a modular `Nipype`-based framework, it facilitates the integration of
49 custom community tools through containerized interfaces and clear contribution guidelines.
50 Fetpype aims to advance research by improving comparability across studies and fostering
51 community collaboration by facilitating the dissemination of new image processing methods
52 for clinical applications. The pipeline is publicly available on GitHub (https://github.com/fet-
53 pype/fetpype).

54 In the future, we plan to supplement `Fetpype` with an automated reporting library containing
55 automated quality control (Sanchez et al., 2024, 2025), subject-wise and population-wise
56 biometry and volumetry (Esteban et al., 2017), as well as spectral analysis of surfaces
57 (Germanaud et al., 2012). We welcome contributions of authors desiring to integrate their
58 method to `Fetpype`.
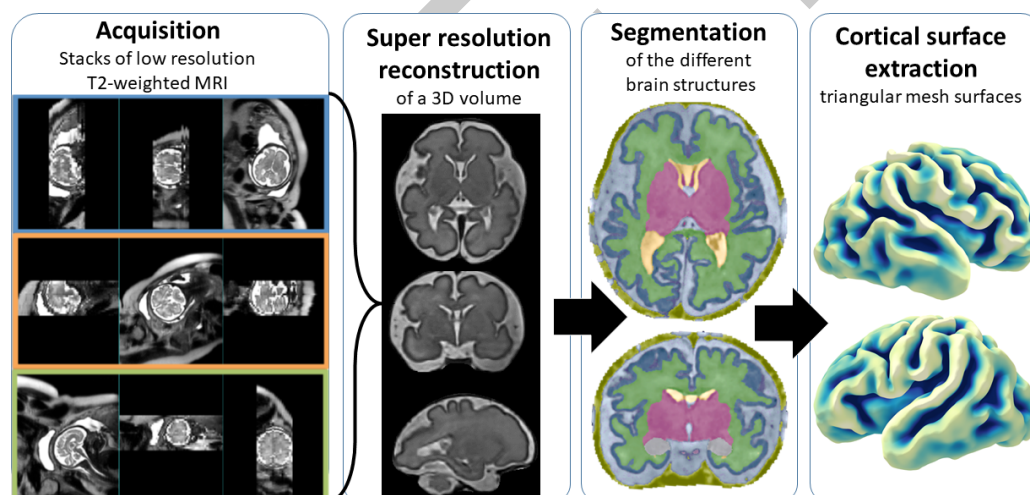
Figure 1: The different steps covered by `Fetpype`. Starting from several T2-weighted stacks of thick slices of the fetal brain (*acquisition*), `Fetpype` pre-processes data before feeding them to a *super-resolution reconstruction* algorithm that fuses them in a single high-resolution volume. This volume then underegoes *segmentation*, before moving to cortical *surface extraction*.

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