




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

Thomas Sanchez ^{1,2*}, Gerard Martí-Juan ^{3*}, David Meunier ⁴, Miguel Angel Gonzalez Ballester ^{3,5*}, Oscar Camara ^{3*}, Gemma Piella ³, Meritxell Bach Cuadra ^{1,2}, and Guillaume Auzias ⁴

¹ CIBM – Center for Biomedical Imaging, Switzerland ² Department of Diagnostic and Interventional Radiology, Lausanne University Hospital and University of Lausanne, Switzerland ³ BCN MedTech, Department of Engineering, Universitat Pompeu Fabra, Spain ⁴ Aix-Marseille Université, CNRS, Institut de Neurosciences de La Timone, France ⁵ ICREA, Barcelona, Spain * These authors contributed equally.

DOI: [10.xxxxx/draft](https://doi.org/10.xxxxx/draft)

Software

- [Review](#) 
- [Repository](#) 
- [Archive](#) 

Editor: [Open Journals](#) 

Reviewers:

- [@openjournals](#)

Submitted: 01 January 1970

Published: unpublished

License

Authors of papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License ([CC BY 4.0](#)).

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:
 - a. **Data preprocessing:** including brain extraction using Fetal-BET ([Faghihpouryesh 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/utis_container,

- b. **Super-resolution reconstruction:** implementing three widely used pipelines: NeSVoR (Xu et al., 2023), SVRTK (Kuklisova-Murgasova et al., 2012; Alena U. Uus et al., 2022), and NiftyMIC (Ebner et al., 2020),
- c. **Segmentation:** implementing BOUNTI (Alena U. Uus et al., 2023) and the developing human connectome project pipeline (Makropoulos et al., 2018) and
- d. **Cortical surface extraction:** using a custom implementation available at https://github.com/fetpype/surface_processing based on (Bazin & Pham, 2005, 2007; Ma et al., 2022).

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

In the future, we plan to supplement Fetpype with an automated reporting library containing automated quality control (Sanchez et al., 2026, 2024), subject-wise and population-wise biometry and volumetry (Esteban et al., 2017; Neves Silva et al., 2025), as well as spectral analysis of surfaces (Germanaud et al., 2012). We welcome contributions of authors desiring to integrate their method to Fetpype.

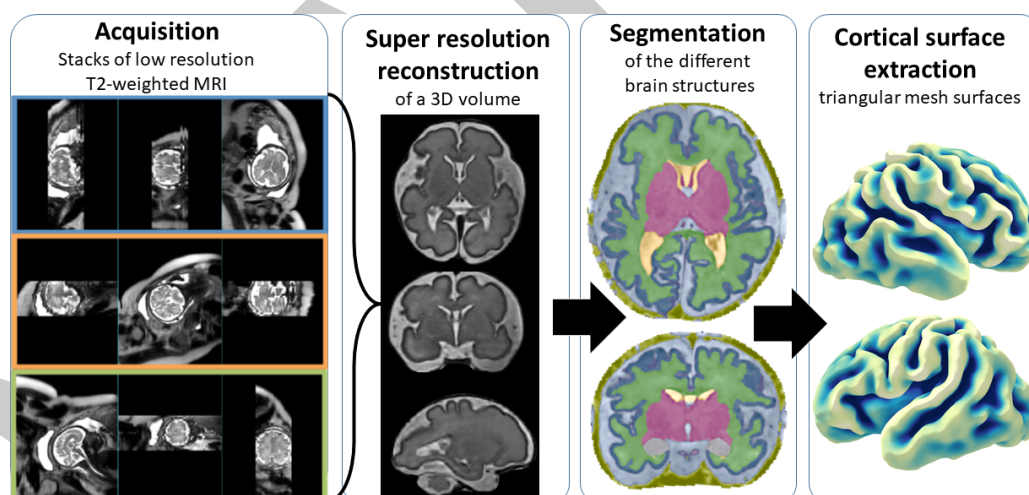


Figure 1: The different steps covered by Fetpype. Starting from several T2-weighted stacks of thick slices of the fetal brain (*acquisition*), Fetpype pre-processes data before feeding them to a *super-resolution reconstruction* algorithm that fuses them in a single high-resolution volume. This volume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

Acknowledgements

This work was funded by Era-net NEURON MULTIFACT project (TS: Swiss National Science Foundation grants 31NE30_203977, 215641; GA: French National Research Agency, Grant ANR-21-NEU2-0005; GMJ, GP, OC, MAGB: Ministry of Science, Innovation and Universities: MCIN/AEI/10.13039/501100011033/), and the SulcalGRIDS Project, (GA: French National Research Agency Grant ANR-19-CE45-0014). We acknowledge the CIBM Center for Biomedical Imaging, a Swiss research center of excellence founded and supported by CHUV, UNIL, EPFL, UNIGE and HUG. This research was also supported by grants from NVIDIA and utilized NVIDIA RTX6000 ADA GPUs.

References

- 72
- 73 Bazin, P.-L., & Pham, D. L. (2005). Topology correction using fast marching methods and its
74 application to brain segmentation. *International Conference on Medical Image Computing
75 and Computer-Assisted Intervention*, 484–491. https://doi.org/10.1007/11566489_60
- 76 Bazin, P.-L., & Pham, D. L. (2007). Topology correction of segmented medical images using a
77 fast marching algorithm. *Computer Methods and Programs in Biomedicine*, 88(2), 182–190.
78 <https://doi.org/10.1016/j.cmpb.2007.08.006>
- 79 Ebner, M., Wang, G., Li, W., Aertsen, M., Patel, P. A., Aughwane, R., Melbourne, A., Doel, T.,
80 Dymarkowski, S., De Coppi, P., & others. (2020). An automated framework for localization,
81 segmentation and super-resolution reconstruction of fetal brain MRI. *NeuroImage*, 206,
82 116324. <https://doi.org/10.1016/j.neuroimage.2019.116324>
- 83 Esteban, O., Birman, D., Schaer, M., Koyejo, O. O., Poldrack, R. A., & Gorgolewski, K. J.
84 (2017). MRIQC: Advancing the automatic prediction of image quality in MRI from unseen
85 sites. *PloS One*, 12(9), e0184661. <https://doi.org/10.1371/journal.pone.0184661>
- 86 Faghihpirayesh, R., Karimi, D., Erdoğan, D., & Gholipour, A. (2024). Fetal-BET: Brain
87 extraction tool for fetal MRI. *IEEE Open Journal of Engineering in Medicine and Biology*.
88 <https://doi.org/10.1109/ojemb.2024.3426969>
- 89 Germanaud, D., Lefèvre, J., Toro, R., Fischer, C., Dubois, J., Hertz-Pannier, L., & Mangin,
90 J.-F. (2012). Larger is twistier: Spectral analysis of gyrification (SPANGY) applied to
91 adult brain size polymorphism. *NeuroImage*, 63(3), 1257–1272. <https://doi.org/10.1016/j.neuroimage.2012.07.053>
- 93 Gorgolewski, K. J., Auer, T., Calhoun, V. D., Craddock, R. C., Das, S., Duff, E. P., Flandin,
94 G., Ghosh, S. S., Glatard, T., Halchenko, Y. O., & others. (2016). The brain imaging data
95 structure, a format for organizing and describing outputs of neuroimaging experiments.
96 *Scientific Data*, 3(1), 1–9. <https://doi.org/10.1038/sdata.2016.44>
- 97 Gorgolewski, K. J., Burns, C. D., Madison, C., Clark, D., Halchenko, Y. O., Waskom, M. L.,
98 & Ghosh, S. S. (2011). Nipype: A flexible, lightweight and extensible neuroimaging data
99 processing framework in python. *Frontiers in Neuroinformatics*, 5, 13. <https://doi.org/10.3389/fninf.2011.00013>
- 101 Kuklisova-Murgasova, M., Quaghebeur, G., Rutherford, M. A., Hajnal, J. V., & Schnabel, J.
102 A. (2012). Reconstruction of fetal brain MRI with intensity matching and complete outlier
103 removal. *Medical Image Analysis*, 16(8), 1550–1564. <https://doi.org/10.1016/j.media.2012.07.004>
- 105 Ma, Q., Li, L., Robinson, E. C., Kainz, B., Rueckert, D., & Alansary, A. (2022). CortexODE:
106 Learning cortical surface reconstruction by neural ODEs. *IEEE Transactions on Medical
107 Imaging*, 42(2), 430–443. <https://doi.org/10.1109/tmi.2022.3206221>
- 108 Makropoulos, A., Robinson, E. C., Schuh, A., Wright, R., Fitzgibbon, S., Bozek, J., Counsell, S.
109 J., Steinweg, J., Vecchiato, K., Passerat-Palmbach, J., & others. (2018). The developing
110 human connectome project: A minimal processing pipeline for neonatal cortical surface
111 reconstruction. *NeuroImage*, 173, 88–112. <https://doi.org/10.1016/j.neuroimage.2018.01.054>
- 113 Manjón, J. V., Coupé, P., Martí-Bonmatí, L., Collins, D. L., & Robles, M. (2010). Adaptive
114 non-local means denoising of MR images with spatially varying noise levels. *Journal of
115 Magnetic Resonance Imaging*, 31(1), 192–203. <https://doi.org/10.1002/jmri.22003>
- 116 Neves Silva, S., Uus, A., Waheed, H., Bansal, S., St Clair, K., Norman, W., Aviles Verdera, J.,
117 Cromb, D., Woodgate, T., Van Poppel, M., & others. (2025). Scanner-based real-time
118 automated volumetry reporting of the fetus, amniotic fluid, placenta, and umbilical cord for

- 119 fetal MRI at 0.55 t. *Magnetic Resonance in Medicine*. <https://doi.org/10.1002/mrm.70097>
- 120 Sanchez, T., Esteban, O., Gomez, Y., Pron, A., Koob, M., Dunet, V., Girard, N., Jakab,
121 A., Eixarch, E., Auzias, G., & others. (2024). FetMRQC: A robust quality control
122 system for multi-centric fetal brain MRI. *Medical Image Analysis*, 97, 103282. <https://doi.org/10.1016/j.media.2024.103282>
123
- 124 Sanchez, T., Zalevskyi, V., Mihailov, A., Martí-Juan, G., Eixarch, E., Jakab, A., Dunet,
125 V., Koob, M., Auzias, G., & Cuadra, M. B. (2026). Automatic quality control in multi-
126 centric fetal brain MRI super-resolution reconstruction. *Perinatal, Preterm and Paedi-*
127 *atric Image Analysis*, 3–14. [https://doi.org/https://link.springer.com/chapter/10.1007/](https://doi.org/https://link.springer.com/chapter/10.1007/978-3-032-05997-0_1)
128 [978-3-032-05997-0_1](https://doi.org/https://link.springer.com/chapter/10.1007/978-3-032-05997-0_1)
- 129 Tustison, N. J., Avants, B. B., Cook, P. A., Zheng, Y., Egan, A., Yushkevich, P. A., & Gee, J.
130 C. (2010). N4ITK: Improved N3 bias correction. *IEEE Transactions on Medical Imaging*,
131 29(6), 1310–1320. <https://doi.org/10.1109/TMI.2010.2046908>
- 132 Uus, Alena U., Grigorescu, I., Poppel, M. P. van, Steinweg, J. K., Roberts, T. A., Rutherford,
133 M. A., Hajnal, J. V., Lloyd, D. F., Pushparajah, K., & Deprez, M. (2022). Automated
134 3D reconstruction of the fetal thorax in the standard atlas space from motion-corrupted
135 MRI stacks for 21–36 weeks GA range. *Medical Image Analysis*, 80, 102484. <https://doi.org/10.1016/j.media.2022.102484>
136
- 137 Uus, Alena U., Kyriakopoulou, V., Makropoulos, A., Fukami-Gartner, A., Cromb, D., Davidson,
138 A., Cordero-Grande, L., Price, A. N., Grigorescu, I., Williams, L. Z. J., Robinson, E. C.,
139 Lloyd, D., Pushparajah, K., Story, L., Hutter, J., Counsell, S. J., Edwards, A. D., Rutherford,
140 M. A., Hajnal, J. V., & Deprez, M. (2023). *BOUNTI: Brain vOlumetry and aUtomated*
141 *parcellatioN for 3D feTal MRI*. <https://doi.org/10.7554/elife.88818.1>
- 142 Xu, J., Lala, S., Gagoski, B., Abaci Turk, E., Grant, P. E., Golland, P., & Adalsteinsson, E.
143 (2023). NeSVoR: Implicit neural representation for slice-to-volume reconstruction in MRI.
144 *IEEE Transactions on Medical Imaging*. <https://doi.org/10.1109/tmi.2023.3236216>
- 145 Yadan, O. (2019). *Hydra - a framework for elegantly configuring complex applications*. Github.
146 <https://github.com/facebookresearch/hydra>