

Fetpipe: 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, Elisenda Eixarch  ^{6,7}, 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 **6** BCNatal | Fetal Medicine Research Center (Hospital Clínic and Hospital Sant Joan de Déu, Universitat de Barcelona), Barcelona, Spain **7** Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain and Centre for Biomedical Research on Rare Diseases (CIBERER), Barcelona, Spain * These authors contributed equally.

DOI: [N/A](#)

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Submitted: 01 January 1970

Published: 01 January 1970

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Summary

Fetal brain magnetic resonance imaging (MRI) is crucial for assessing neurodevelopment *in utero*. However, fetal MRI analysis remains technically challenging due to fetal motion, low signal-to-noise ratio, and the need for complex multi-step processing pipelines. These pipelines typically include motion correction, super-resolution reconstruction, tissue segmentation, and cortical surface extraction. While specialized tools exist for each individual processing step, integrating them into a robust, reproducible, and user-friendly end-to-end workflow remains difficult. This fragmentation limits reproducibility across studies and hinders the adoption of advanced fetal neuroimaging methods in both research and clinical contexts.

Fetpipe addresses this gap by providing a standardized, modular, and reproducible framework for fetal brain MRI preprocessing and analysis, enabling researchers to process raw T2-weighted acquisitions through to derived volumetric and surface-based outputs within a unified workflow.

Statement of need

Fetpipe is an open-source Python package designed to streamline and standardize the pre-processing and analysis of T2-weighted fetal brain MRI data. The package targets the fetal neuroimaging community, where methodological heterogeneity and complex software dependencies have historically limited reproducibility and comparability across studies.

Existing fetal brain MRI tools typically focus on individual processing steps and require customized code for pre- and post-processing, as well as to connect different modules, making it difficult to reproduce processing results across studies. Fetpipe addresses these challenges by providing a configurable, containerized, and Nipype-driven solution that integrates state-of-the-art fetal MRI processing tools into a cohesive pipeline. By emphasizing reproducibility, extensibility, and ease of use, Fetpipe lowers the barrier to applying advanced fetal MRI analysis methods and facilitates consistent processing across sites, scanners, and studies. In doing so, Fetpipe improves comparability across studies and supports community collaboration by facilitating the dissemination of new image processing methods for clinical applications. The pipeline is publicly available on GitHub (<https://github.com/fetpipe/fetpipe>).

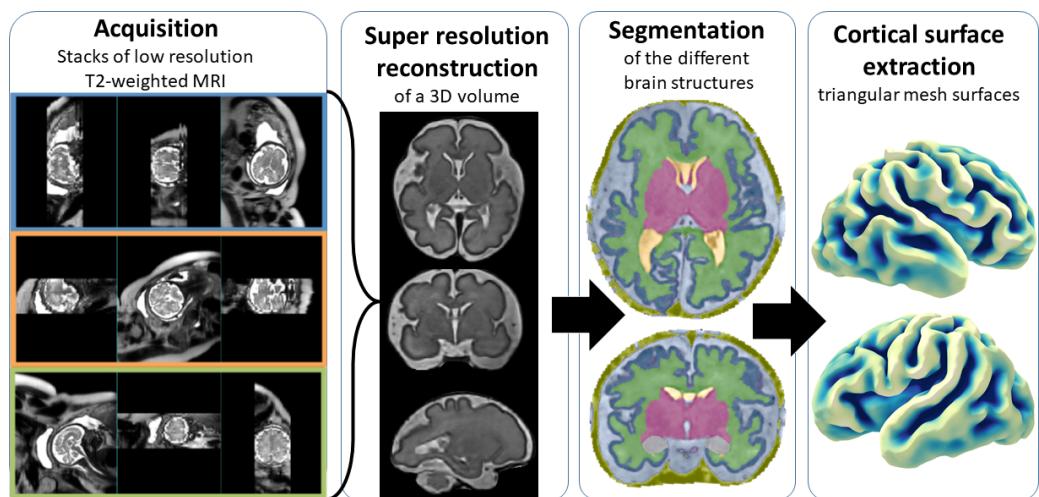


Figure 1: The different steps covered by Fetpipe. Starting from several T2-weighted stacks of thick slices of the fetal brain (*acquisition*), Fetpipe pre-processes data before feeding them to a *super-resolution reconstruction* algorithm that fuses them in a single high-resolution volume. This volume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

State of the field

Fetal brain MRI analysis relies on a range of specialized tools that address individual processing steps, particularly motion correction and super-resolution reconstruction. Widely used reconstruction frameworks include SVRTK (C++) (Kuklisova-Murgasova et al., 2012; Alena U. Uus et al., 2022), NiftyMIC (Python) (Ebner et al., 2020), and NeSvoR (Python/PyTorch) (Xu et al., 2023). While increasingly distributed as containers, these tools rely on distinct data organization schemes as well as custom pre- and post-processing steps. Downstream processing tools for brain extraction, segmentation, and surface reconstruction show similar diversity, combining Python scripts, compiled binaries, and domain-specific imaging libraries (Bazin & Pham, 2005; Faghihpirayesh et al., 2024; Makropoulos et al., 2018; Alena U. Uus et al., 2023). As a result, constructing an end-to-end fetal MRI workflow typically requires custom scripting to orchestrate multiple containers, manage data formats, and handle intermediate outputs, limiting reproducibility and accessibility.

Fetpipe was built to address these limitations by providing a unified, Python-based framework to integrate existing containerized tools for fetal brain MRI analysis. By enforcing data formatting following the widely-used Brain Imaging Data Structure (BIDS) standard (Gorgolewski et al., 2016), and leveraging containerized execution and Nipype-based workflow management (Gorgolewski et al., 2011) and Hydra-based configuration (Yadan, 2019), Fetpipe provides a standardized and scalable environment for reproducible end-to-end fetal brain MRI analysis on both local workstations and large-scale computing clusters.

Software design

Fetpipe is built around four core design principles: data standardization, containerization, workflow orchestration, and flexible configuration:

1. **Data Standardization:** Fetpipe expects input data organized according to the 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 ([Faghhihpirayesh 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,
 - 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 overall processing workflow is summarized in [Figure 1](#).

Research impact statement

Fetpype is the result of a longstanding collaboration within a European consortium of researchers specializing in fetal neuroimaging. Its default configurations and processing workflows have been the result of extensive testing to achieve robust processing on data acquired across multiple hospitals in France, Spain, and Switzerland, covering a range of scanners and acquisition protocols.

The framework has been used to process large-scale fetal MRI datasets within the consortium, has contributed to a first publication ([Sanchez, Mihailov, et al., 2026](#)), and is supporting ongoing research projects. Fetpype is used by multiple research groups and has begun to receive external contributions, including pull requests that integrate additional processing methods. This suggests that Fetpype addresses a clear methodological need and can serve as shared community infrastructure for fetal brain MRI research.

In the future, we plan to supplement Fetpype with an automated reporting library containing automated quality control ([Sanchez, Zalevskyi, et al., 2026](#); [Sanchez et al., 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 community contributions, particularly implementations of new methods that can be integrated into the existing containerized workflow framework.

AI usage disclosure

GitHub Copilot, integrated within Visual Studio Code, was used during software development to assist with code completion and implementation. ChatGPT (GPT-5.2) was used for proofreading and language refinement of the manuscript. The authors take full responsibility for the written content.

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; EE: Instituto de Salud Carlos III (ISCIII) grant AC21_2/00016; GMJ, GP, OC, MAGB: Ministry of Science, Innovation and Universities: MCIN/AEI/10.13039/501100011033/), the SulcalGRIDS Project, (GA: French National Research Agency Grant ANR-19-CE45-0014), the pediatric domain shifts project (TS: SNSF 205320-215641), and NVIDIA research grants with the use of NVIDIA RTX6000 ADA GPUs. We acknowledge the CIBM Center for Biomedical Imaging, a Swiss research center of excellence founded and supported by CHUV, UNIL, EPFL, UNIGE and HUG.

References

- Bazin, P.-L., & Pham, D. L. (2005). Topology correction using fast marching methods and its application to brain segmentation. *International Conference on Medical Image Computing and Computer-Assisted Intervention*, 484–491. https://doi.org/10.1007/11566489_60
- Bazin, P.-L., & Pham, D. L. (2007). Topology correction of segmented medical images using a fast marching algorithm. *Computer Methods and Programs in Biomedicine*, 88(2), 182–190. <https://doi.org/10.1016/j.cmpb.2007.08.006>
- Ebner, M., Wang, G., Li, W., Aertsen, M., Patel, P. A., Aughwane, R., Melbourne, A., Doel, T., Dymarkowski, S., De Coppi, P., & others. (2020). An automated framework for localization, segmentation and super-resolution reconstruction of fetal brain MRI. *NeuroImage*, 206, 116324. <https://doi.org/10.1016/j.neuroimage.2019.116324>
- Esteban, O., Birman, D., Schaer, M., Koyejo, O. O., Poldrack, R. A., & Gorgolewski, K. J. (2017). MRIQC: Advancing the automatic prediction of image quality in MRI from unseen sites. *PloS One*, 12(9), e0184661. <https://doi.org/10.1371/journal.pone.0184661>
- Faghihpirayesh, R., Karimi, D., Erdoğmuş, D., & Gholipour, A. (2024). Fetal-BET: Brain extraction tool for fetal MRI. *IEEE Open Journal of Engineering in Medicine and Biology*. <https://doi.org/10.1109/ojemb.2024.3426969>
- Germanaud, D., Lefèvre, J., Toro, R., Fischer, C., Dubois, J., Hertz-Pannier, L., & Mangin, J.-F. (2012). Larger is twistier: Spectral analysis of gyration (SPANGY) applied to adult brain size polymorphism. *NeuroImage*, 63(3), 1257–1272. <https://doi.org/10.1016/j.neuroimage.2012.07.053>
- Gorgolewski, K. J., Auer, T., Calhoun, V. D., Craddock, R. C., Das, S., Duff, E. P., Flandin, G., Ghosh, S. S., Glatard, T., Halchenko, Y. O., & others. (2016). The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments. *Scientific Data*, 3(1), 1–9. <https://doi.org/10.1038/sdata.2016.44>
- Gorgolewski, K. J., Burns, C. D., Madison, C., Clark, D., Halchenko, Y. O., Waskom, M. L., & Ghosh, S. S. (2011). Nipype: A flexible, lightweight and extensible neuroimaging data processing framework in python. *Frontiers in Neuroinformatics*, 5, 13. <https://doi.org/10.3389/fninf.2011.00013>
- Kuklisova-Murgasova, M., Quaghebeur, G., Rutherford, M. A., Hajnal, J. V., & Schnabel, J. A. (2012). Reconstruction of fetal brain MRI with intensity matching and complete outlier removal. *Medical Image Analysis*, 16(8), 1550–1564. <https://doi.org/10.1016/j.media.2012.07.004>
- Ma, Q., Li, L., Robinson, E. C., Kainz, B., Rueckert, D., & Alansary, A. (2022). CortexODE: Learning cortical surface reconstruction by neural ODEs. *IEEE Transactions on Medical Imaging*, 42(2), 430–443. <https://doi.org/10.1109/tmi.2022.3206221>

- Makropoulos, A., Robinson, E. C., Schuh, A., Wright, R., Fitzgibbon, S., Bozek, J., Counsell, S. J., Steinweg, J., Vecchiato, K., Passerat-Palmbach, J., & others. (2018). The developing human connectome project: A minimal processing pipeline for neonatal cortical surface reconstruction. *Neuroimage*, 173, 88–112. <https://doi.org/10.1016/j.neuroimage.2018.01.054>
- Manjón, J. V., Coupé, P., Martí-Bonmatí, L., Collins, D. L., & Robles, M. (2010). Adaptive non-local means denoising of MR images with spatially varying noise levels. *Journal of Magnetic Resonance Imaging*, 31(1), 192–203. <https://doi.org/10.1002/jmri.22003>
- Neves Silva, S., Uus, A., Waheed, H., Bansal, S., St Clair, K., Norman, W., Aviles Verdera, J., Cromb, D., Woodgate, T., Van Poppel, M., & others. (2025). Scanner-based real-time automated volumetry reporting of the fetus, amniotic fluid, placenta, and umbilical cord for fetal MRI at 0.55 t. *Magnetic Resonance in Medicine*. <https://doi.org/10.1002/mrm.70097>
- Sanchez, T., Esteban, O., Gomez, Y., Pron, A., Koob, M., Dunet, V., Girard, N., Jakab, A., Eixarch, E., Auzias, G., & others. (2024). FetMRQC: A robust quality control system for multi-centric fetal brain MRI. *Medical Image Analysis*, 97, 103282. <https://doi.org/10.1016/j.media.2024.103282>
- Sanchez, T., Mihailov, A., Martí-Juan, G., Girard, N., Manchon, A., Milh, M., Eixarch, E., Dunet, V., Koob, M., Pomar, L., & others. (2026). Data quality biases normative models derived from fetal brain MRI. *bioRxiv*, 2026–2001. <https://doi.org/10.64898/2026.01.22.700996>
- Sanchez, T., Zalevskyi, V., Mihailov, A., Martí-Juan, G., Eixarch, E., Jakab, A., Dunet, V., Koob, M., Auzias, G., & Cuadra, M. B. (2026). Automatic quality control in multi-centric fetal brain MRI super-resolution reconstruction. *Perinatal, Preterm and Paediatric Image Analysis*, 3–14. https://doi.org/10.1007/978-3-032-05997-0_1
- Tustison, N. J., Avants, B. B., Cook, P. A., Zheng, Y., Egan, A., Yushkevich, P. A., & Gee, J. C. (2010). N4ITK: Improved N3 bias correction. *IEEE Transactions on Medical Imaging*, 29(6), 1310–1320. <https://doi.org/10.1109/TMI.2010.2046908>
- Uus, Alena U., Grigorescu, I., Poppel, M. P. van, Steinweg, J. K., Roberts, T. A., Rutherford, M. A., Hajnal, J. V., Lloyd, D. F., Pushparajah, K., & Deprez, M. (2022). Automated 3D reconstruction of the fetal thorax in the standard atlas space from motion-corrupted MRI stacks for 21–36 weeks GA range. *Medical Image Analysis*, 80, 102484. <https://doi.org/10.1016/j.media.2022.102484>
- Uus, Alena U., Kyriakopoulou, V., Makropoulos, A., Fukami-Gartner, A., Cromb, D., Davidson, A., Cordero-Grande, L., Price, A. N., Grigorescu, I., Williams, L. Z. J., Robinson, E. C., Lloyd, D., Pushparajah, K., Story, L., Hutter, J., Counsell, S. J., Edwards, A. D., Rutherford, M. A., Hajnal, J. V., & Deprez, M. (2023). BOUNTI: Brain vOlumetry and aUtomatic parcellatioN for 3D feTal MRI. <https://doi.org/10.7554/elife.88818.1>
- Xu, J., Lala, S., Gagoski, B., Abaci Turk, E., Grant, P. E., Golland, P., & Adalsteinsson, E. (2023). NeSVoR: Implicit neural representation for slice-to-volume reconstruction in MRI. *IEEE Transactions on Medical Imaging*. <https://doi.org/10.1109/tmi.2023.3236216>
- Yadan, O. (2019). *Hydra - a framework for elegantly configuring complex applications*. Github. <https://github.com/facebookresearch/hydra>