

# <sup>1</sup> Fetpipe: An Open-Source Pipeline for Reproducible <sup>2</sup> Fetal Brain MRI Analysis

<sup>3</sup> **Thomas Sanchez**  <sup>1,2\*</sup>, **Gerard Martí-Juan**  <sup>3\*</sup>, **David Meunier**  <sup>4</sup>, **Miguel**  
<sup>4</sup> **Angel Gonzalez Ballester**  <sup>3,5</sup>, **Oscar Camara**  <sup>3</sup>, **Elisenda Eixarch**  <sup>6,7</sup>,  
<sup>5</sup> **Gemma Piella**  <sup>3</sup>, **Meritxell Bach Cuadra**  <sup>1,2</sup>, and **Guillaume Auzias**  <sup>4</sup>

<sup>6</sup> 1 CIBM – Center for Biomedical Imaging, Switzerland 2 Department of Diagnostic and Interventional  
<sup>7</sup> Radiology, Lausanne University Hospital and University of Lausanne, Switzerland 3 BCN MedTech,  
<sup>8</sup> Department of Engineering, Universitat Pompeu Fabra, Spain 4 Aix-Marseille Université, CNRS, Institut  
<sup>9</sup> de Neurosciences de La Timone, France 5 ICREA, Barcelona, Spain 6 BCNatal | Fetal Medicine  
<sup>10</sup> Research Center (Hospital Clínic and Hospital Sant Joan de Déu, Universitat de Barcelona), Barcelona,  
<sup>11</sup> Spain 7 Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain and  
<sup>12</sup> Centre for Biomedical Research on Rare Diseases (CIBERER), Barcelona, Spain \* These authors  
<sup>13</sup> contributed equally.

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

## Software

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

Editor: 

Submitted: 09 October 2025

Published: unpublished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](https://creativecommons.org/licenses/by/4.0/)).<sup>23</sup><sup>24</sup><sup>25</sup>

## <sup>14</sup> Summary

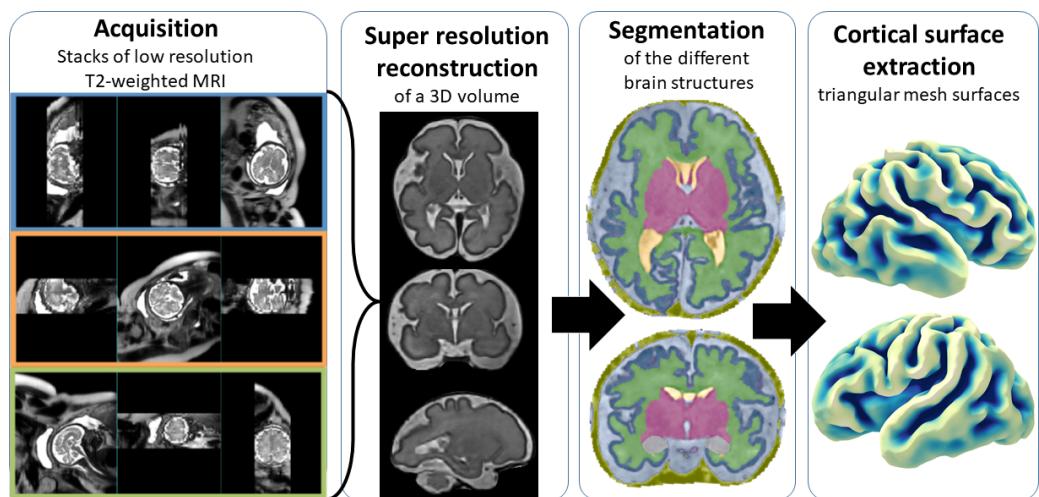
<sup>15</sup> Fetal brain magnetic resonance imaging (MRI) is crucial for assessing neurodevelopment *in*  
<sup>16</sup> *utero*. However, fetal MRI analysis remains technically challenging due to fetal motion, low  
<sup>17</sup> signal-to-noise ratio, and the need for complex multi-step processing pipelines. These pipelines  
<sup>18</sup> typically include motion correction, super-resolution reconstruction, tissue segmentation, and  
<sup>19</sup> cortical surface extraction. While specialized tools exist for each individual processing step,  
<sup>20</sup> integrating them into a robust, reproducible, and user-friendly end-to-end workflow remains  
<sup>21</sup> difficult. This fragmentation limits reproducibility across studies and hinders the adoption of  
<sup>22</sup> advanced fetal neuroimaging methods in both research and clinical contexts.

<sup>23</sup> Fetpipe addresses this gap by providing a standardized, modular, and reproducible framework  
<sup>24</sup> for fetal brain MRI preprocessing and analysis, enabling researchers to process raw T2-weighted  
<sup>25</sup> acquisitions through to derived volumetric and surface-based outputs within a unified workflow.

## <sup>26</sup> Statement of need

<sup>27</sup> Fetpipe is an open-source Python package designed to streamline and standardize the  
<sup>28</sup> preprocessing and analysis of T2-weighted fetal brain MRI data. The package targets the  
<sup>29</sup> fetal neuroimaging community, where methodological heterogeneity and complex software  
<sup>30</sup> dependencies have historically limited reproducibility and comparability across studies.

<sup>31</sup> Existing fetal brain MRI tools typically focus on individual processing steps and require  
<sup>32</sup> customized code for pre- and post-processing, as well as to connect different modules, making  
<sup>33</sup> it difficult to reproduce processing results across studies. Fetpipe addresses these challenges  
<sup>34</sup> by providing a configurable, containerized, and Nipype-driven solution that integrates state-  
<sup>35</sup> of-the-art fetal MRI processing tools into a cohesive pipeline. By emphasizing reproducibility,  
<sup>36</sup> extensibility, and ease of use, Fetpipe lowers the barrier to applying advanced fetal MRI  
<sup>37</sup> analysis methods and facilitates consistent processing across sites, scanners, and studies. In  
<sup>38</sup> doing so, Fetpipe improves comparability across studies and supports community collaboration  
<sup>39</sup> by facilitating the dissemination of new image processing methods for clinical applications.  
<sup>40</sup> 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*.

## 41 State of the field

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

54 Fetpipe was built to address these limitations by providing a unified, Python-based framework to  
 55 integrate existing containerized tools for fetal brain MRI analysis. By enforcing data formatting  
 56 following the widely-used Brain Imaging Data Structure (BIDS) standard (Gorgolewski et  
 57 al., 2016), and leveraging containerized execution and Nipype-based workflow management  
 58 (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  
 59 analysis on both local workstations and large-scale computing clusters.  
 60

## 61 Software design

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

- 64 1. **Data Standardization:** Fetpipe expects input data organized according to the BIDS  
 65 standard (Gorgolewski et al., 2016), promoting interoperability and simplifying data  
 66 management.
- 67 2. **Containerization:** Individual processing tools are encapsulated within Docker or Singularity  
 68 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](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](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](#).

## 91 Research impact statement

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

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

103 In the future, we plan to supplement Fetpype with an automated reporting library containing  
104 automated quality control (Sanchez, Zalevskyi, et al., 2026; Sanchez et al., 2024), subject-wise  
105 and population-wise biometry and volumetry (Esteban et al., 2017; Neves Silva et al., 2025),  
106 as well as spectral analysis of surfaces (Germanaud et al., 2012). We welcome community  
107 contributions, particularly implementations of new methods that can be integrated into the  
108 existing containerized workflow framework.

## 109 AI usage disclosure

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

## <sup>114</sup> Acknowledgements

<sup>115</sup> This work was funded by Era-net NEURON MULTIFACT project (TS: Swiss National  
<sup>116</sup> Science Foundation grants 31NE30\_203977, 215641; GA: French National Research  
<sup>117</sup> Agency, Grant ANR-21-NEU2-0005; EE: Instituto de Salud Carlos III (ISCIII) grant  
<sup>118</sup> AC21\_2/00016; GMJ, GP, OC, MAGB: Ministry of Science, Innovation and Universities:  
<sup>119</sup> MCIN/AEI/10.13039/501100011033/), the SulcalGRIDS Project, (GA: French National  
<sup>120</sup> Research Agency Grant ANR-19-CE45-0014), the pediatric domain shifts project (TS: SNSF  
<sup>121</sup> 205320-215641), and NVIDIA research grants with the use of NVIDIA RTX6000 ADA  
<sup>122</sup> GPUs. We acknowledge the CIBM Center for Biomedical Imaging, a Swiss research center of  
<sup>123</sup> excellence founded and supported by CHUV, UNIL, EPFL, UNIGE and HUG.

## <sup>124</sup> References

- <sup>125</sup> Bazin, P.-L., & Pham, D. L. (2005). Topology correction using fast marching methods and its  
<sup>126</sup> application to brain segmentation. *International Conference on Medical Image Computing*  
<sup>127</sup> and Computer-Assisted Intervention, 484–491. [https://doi.org/10.1007/11566489\\_60](https://doi.org/10.1007/11566489_60)
- <sup>128</sup> Bazin, P.-L., & Pham, D. L. (2007). Topology correction of segmented medical images using a  
<sup>129</sup> fast marching algorithm. *Computer Methods and Programs in Biomedicine*, 88(2), 182–190.  
<sup>130</sup> <https://doi.org/10.1016/j.cmpb.2007.08.006>
- <sup>131</sup> Ebner, M., Wang, G., Li, W., Aertsen, M., Patel, P. A., Aughwane, R., Melbourne, A., Doel, T.,  
<sup>132</sup> Dymarkowski, S., De Coppi, P., & others. (2020). An automated framework for localization,  
<sup>133</sup> segmentation and super-resolution reconstruction of fetal brain MRI. *NeuroImage*, 206,  
<sup>134</sup> 116324. <https://doi.org/10.1016/j.neuroimage.2019.116324>
- <sup>135</sup> Esteban, O., Birman, D., Schaefer, M., Koyejo, O. O., Poldrack, R. A., & Gorgolewski, K. J.  
<sup>136</sup> (2017). MRIQC: Advancing the automatic prediction of image quality in MRI from unseen  
<sup>137</sup> sites. *PloS One*, 12(9), e0184661. <https://doi.org/10.1371/journal.pone.0184661>
- <sup>138</sup> Faghihpirayesh, R., Karimi, D., Erdoğmuş, D., & Gholipour, A. (2024). Fetal-BET: Brain  
<sup>139</sup> extraction tool for fetal MRI. *IEEE Open Journal of Engineering in Medicine and Biology*.  
<sup>140</sup> <https://doi.org/10.1109/ojemb.2024.3426969>
- <sup>141</sup> Germanaud, D., Lefèvre, J., Toro, R., Fischer, C., Dubois, J., Hertz-Pannier, L., & Mangin,  
<sup>142</sup> J.-F. (2012). Larger is twistier: Spectral analysis of gyration (SPANGY) applied to  
<sup>143</sup> adult brain size polymorphism. *NeuroImage*, 63(3), 1257–1272. <https://doi.org/10.1016/j.neuroimage.2012.07.053>
- <sup>145</sup> Gorgolewski, K. J., Auer, T., Calhoun, V. D., Craddock, R. C., Das, S., Duff, E. P., Flandin,  
<sup>146</sup> G., Ghosh, S. S., Glatard, T., Halchenko, Y. O., & others. (2016). The brain imaging data  
<sup>147</sup> structure, a format for organizing and describing outputs of neuroimaging experiments.  
<sup>148</sup> *Scientific Data*, 3(1), 1–9. <https://doi.org/10.1038/sdata.2016.44>
- <sup>149</sup> Gorgolewski, K. J., Burns, C. D., Madison, C., Clark, D., Halchenko, Y. O., Waskom, M. L.,  
<sup>150</sup> & Ghosh, S. S. (2011). Nipype: A flexible, lightweight and extensible neuroimaging data  
<sup>151</sup> processing framework in python. *Frontiers in Neuroinformatics*, 5, 13. <https://doi.org/10.3389/fninf.2011.00013>
- <sup>153</sup> Kuklisova-Murgasova, M., Quaghebeur, G., Rutherford, M. A., Hajnal, J. V., & Schnabel, J.  
<sup>154</sup> A. (2012). Reconstruction of fetal brain MRI with intensity matching and complete outlier  
<sup>155</sup> removal. *Medical Image Analysis*, 16(8), 1550–1564. <https://doi.org/10.1016/j.media.2012.07.004>
- <sup>157</sup> Ma, Q., Li, L., Robinson, E. C., Kainz, B., Rueckert, D., & Alansary, A. (2022). CortexODE:  
<sup>158</sup> Learning cortical surface reconstruction by neural ODEs. *IEEE Transactions on Medical  
<sup>159</sup> Imaging*, 42(2), 430–443. <https://doi.org/10.1109/tmi.2022.3206221>

- 160 Makropoulos, A., Robinson, E. C., Schuh, A., Wright, R., Fitzgibbon, S., Bozek, J., Counsell, S.  
161 J., Steinweg, J., Vecchiato, K., Passerat-Palmbach, J., & others. (2018). The developing  
162 human connectome project: A minimal processing pipeline for neonatal cortical surface  
163 reconstruction. *Neuroimage*, 173, 88–112. <https://doi.org/10.1016/j.neuroimage.2018.01.054>
- 165 Manjón, J. V., Coupé, P., Martí-Bonmatí, L., Collins, D. L., & Robles, M. (2010). Adaptive  
166 non-local means denoising of MR images with spatially varying noise levels. *Journal of*  
167 *Magnetic Resonance Imaging*, 31(1), 192–203. <https://doi.org/10.1002/jmri.22003>
- 168 Neves Silva, S., Uus, A., Waheed, H., Bansal, S., St Clair, K., Norman, W., Aviles Verdera, J.,  
169 Cromb, D., Woodgate, T., Van Poppel, M., & others. (2025). Scanner-based real-time  
170 automated volumetry reporting of the fetus, amniotic fluid, placenta, and umbilical cord for  
171 fetal MRI at 0.55 t. *Magnetic Resonance in Medicine*. <https://doi.org/10.1002/mrm.70097>
- 172 Sanchez, T., Esteban, O., Gomez, Y., Pron, A., Koob, M., Dunet, V., Girard, N., Jakab,  
173 A., Eixarch, E., Auzias, G., & others. (2024). FetMRQC: A robust quality control  
174 system for multi-centric fetal brain MRI. *Medical Image Analysis*, 97, 103282. <https://doi.org/10.1016/j.media.2024.103282>
- 176 Sanchez, T., Mihailov, A., Martí-Juan, G., Girard, N., Manchon, A., Milh, M., Eixarch, E.,  
177 Dunet, V., Koob, M., Pomar, L., & others. (2026). Data quality biases normative models  
178 derived from fetal brain MRI. *bioRxiv*, 2026–2001. <https://doi.org/10.64898/2026.01.22.700996>
- 180 Sanchez, T., Zalevskyi, V., Mihailov, A., Martí-Juan, G., Eixarch, E., Jakab, A., Dunet, V.,  
181 Koob, M., Auzias, G., & Cuadra, M. B. (2026). Automatic quality control in multi-centric  
182 fetal brain MRI super-resolution reconstruction. *Perinatal, Preterm and Paediatric Image*  
183 *Analysis*, 3–14. [https://doi.org/10.1007/978-3-032-05997-0\\_1](https://doi.org/10.1007/978-3-032-05997-0_1)
- 184 Tustison, N. J., Avants, B. B., Cook, P. A., Zheng, Y., Egan, A., Yushkevich, P. A., & Gee, J.  
185 C. (2010). N4ITK: Improved N3 bias correction. *IEEE Transactions on Medical Imaging*,  
186 29(6), 1310–1320. <https://doi.org/10.1109/TMI.2010.2046908>
- 187 Uus, Alena U., Grigorescu, I., Poppel, M. P. van, Steinweg, J. K., Roberts, T. A., Rutherford,  
188 M. A., Hajnal, J. V., Lloyd, D. F., Pushparajah, K., & Deprez, M. (2022). Automated  
189 3D reconstruction of the fetal thorax in the standard atlas space from motion-corrupted  
190 MRI stacks for 21–36 weeks GA range. *Medical Image Analysis*, 80, 102484. <https://doi.org/10.1016/j.media.2022.102484>
- 192 Uus, Alena U., Kyriakopoulou, V., Makropoulos, A., Fukami-Gartner, A., Cromb, D., Davidson,  
193 A., Cordero-Grande, L., Price, A. N., Grigorescu, I., Williams, L. Z. J., Robinson, E. C.,  
194 Lloyd, D., Pushparajah, K., Story, L., Hutter, J., Counsell, S. J., Edwards, A. D., Rutherford,  
195 M. A., Hajnal, J. V., & Deprez, M. (2023). BOUNTI: Brain vOlumetry and aUtomatic  
196 parcellatioN for 3D feTal MRI. <https://doi.org/10.7554/elife.88818.1>
- 197 Xu, J., Lala, S., Gagoski, B., Abaci Turk, E., Grant, P. E., Golland, P., & Adalsteinsson, E.  
198 (2023). NeSVoR: Implicit neural representation for slice-to-volume reconstruction in MRI.  
199 *IEEE Transactions on Medical Imaging*. <https://doi.org/10.1109/tmi.2023.3236216>
- 200 Yadan, O. (2019). *Hydra - a framework for elegantly configuring complex applications*. Github.  
201 <https://github.com/facebookresearch/hydra>