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p-HCP, Prenatal Human Connectome Patterns: multimodal imaging of human fetal brain development at the mesoscopic scale using 11.7 T ex vivo MRI

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p-HCP (Prenatal Human Connectome Patterns) is a high-resolution multimodal MRI dataset of human fetal brain development spanning the second half of gestation. Acquired ex vivo at ultra-high field strength (11.7 T), this dataset includes whole-hemisphere images at 100–200 µm isotropic resolution: anatomical scans, quantitative relaxometry maps, and high-angular-resolution diffusion imaging across multiple b-values. By offering whole-brain, isotropic, multimodal images at an unprecedented resolution, p-HCP will enable new insights into the spatiotemporal dynamics of prenatal brain development. It represents a valuable resource for building mesoscopic brain atlases and advancing our understanding of human neurodevelopment at a stage previously inaccessible to such detailed explorations.

The second half of gestation is a vital period of neurodevelopment involving processes such as neuronal migration, synaptogenesis, and axonal growth. Capturing these transient events in 3D across the whole brain has remained a challenge. While histological methods allow detailed microstructural insight, they typically lack whole-brain volumetric coverage. Conversely, in utero MRI has enabled full-brain 3D imaging but remains limited to macroscopic resolution (~1 mm) due to motion and safety limitations.

This dataset addresses a critical gap in developmental neuroimaging by capturing fetal brain development at a mesoscopic scale, which should help bridge the gap between in vivo fetal imaging and histological microscopy. Our approach leverages ex vivo MRI over extended scan times to acquire comprehensive multimodal 3D imaging at high resolution, allowing detailed visualization and quantitative assessment of developing brain structures. The few existing fetal studies that used ultra-high-field MRI have focused on the first and early second trimesters of gestation, because older brains are typically too large for small-bore preclinical scanners. To overcome this size limitation, we adapted a blockwise acquisition and digital reconstruction method, previously pioneered in an adult brain known as the Chenonceau dataset. The brains were sectioned into blocks, each block was imaged separately in a small-bore 11.7-tesla scanner, and a dedicated semi-automatic image registration and data fusion pipeline was used to reconstruct whole-hemisphere images.

The acquired imaging modalities provide rich information on the tissue composition and microstructure: with quantitative relaxometry, T_2^* is sensitive to iron content and myelin, T_1 reflects macromolecular environments, and T_2 informs on water content and microstructure. Multi-shell diffusion imaging (b = 1500, 4500, 8000 s/mm²) and high angular resolution (90 directions at b = 8000 s/mm²) will enable detailed tractography and multi-compartment diffusion models. The quantitative multimodality gives access to microstructural modelling, paving the way for a better understanding of the brain tissue composition and neurodevelopmental dynamics occurring during the last two trimesters of gestation.

The initial data release available on the EBRAINS platform features three brains at 18, 27, and 31 post-conceptional weeks, with a complete set of anatomical and relaxometry data, and metrics of the diffusion tensor imaging (DTI) model. Future data releases will include additional specimens covering the developmental timeline, multi-shell models of the diffusion signal, tractography, correlative histological data from the same brains, and segmentations of brain structures, turning this dataset into a full-featured developmental atlas.

Primary authors: Mr ARCAMONE, Lucas (UMR 1141 NeuroDiderot, Eq inDEV, INSERM, Université Paris Cité, Hôpital Robert-Debré, Paris, France; UNIACT, NeuroSpin, CEA, Université Paris-Saclay, F-91191, Gif-sur-Yvette, France); Dr POUPON, Cyril (BAOBAB, NeuroSpin, Université Paris-Saclay, CNRS, CEA, F-91191, Gif-sur-Yvette, France); Dr KHUNG-SAVATOVSKY, Suonavy (Unité fonctionnelle de foetopathologie, Département de Génétique, DMU BioGeMH, AP-HP, Hôpital Universitaire Robert-Debré, Paris, France); Prof. ALISON, Marianne (UMR 1141 NeuroDiderot, Eq inDEV, INSERM, Université Paris Cité, Hôpital Robert-Debré, Paris, France; Service d'Imagerie Pédiadrique, AP-HP, Hôpital Universitaire Robert-Debré, Paris, France); Prof. ADLE-BIASSETTE, Homa (UMR 1141 NeuroDiderot, Eq inDEV, INSERM, Université Paris Cité, Hôpital Robert-Debré, Paris, France; Service d'Anatomie Pathologique, DMU DREAM, Biobank BB-0033-00064, AP-HP, Hôpital Lariboisière, Paris, France); Dr DUBOIS, Jessica (UMR 1141 NeuroDiderot, Eq inDEV, INSERM, Université Paris Cité, Hôpital Robert-Debré, Paris, France; UNIACT, NeuroSpin, CEA, Université Paris-Saclay, F-91191, Gif-sur-Yvette, France); Dr HERTZ-PANNIER, Lucie (UMR 1141 NeuroDiderot, Eq inDEV, INSERM, Université Paris Cité, Hôpital Robert-Debré, Paris, France; UNIACT, NeuroSpin, CEA, Université Paris-Saclay, F-91191, Gif-sur-Yvette, France); Dr LEPRINCE, Yann (UNIACT, NeuroSpin, CEA, Université Paris-Saclay, F-91191, Gif-sur-Yvette, France; UMR 1141 NeuroDiderot, Eq inDEV, INSERM, Université Paris Cité, Hôpital Robert-Debré, Paris, France)

Presenter: Dr LEPRINCE, Yann (UNIACT, NeuroSpin, CEA, Université Paris-Saclay, F-91191, Gif-sur-Yvette, France; UMR 1141 NeuroDiderot, Eq inDEV, INSERM, Université Paris Cité, Hôpital Robert-Debré, Paris, France)

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