

2025 Activity Report

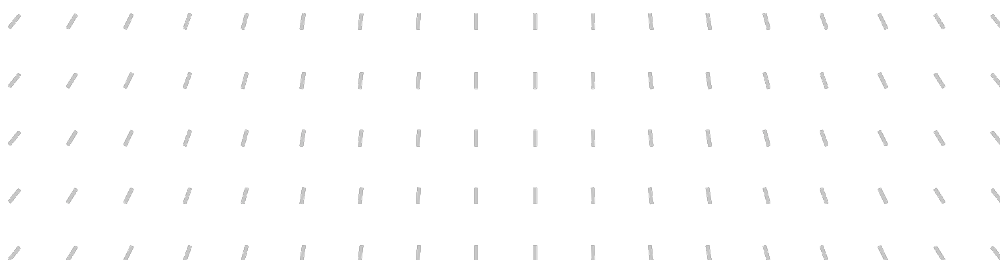
RESEARCH CENTRE: Inria Paris Centre at Sorbonne University
IN PARTNERSHIP WITH: CNRS, INSERM, Sorbonne Université

Project-Team

ARAMIS

Algorithms, models and methods for images and
signals of the human brain

In collaboration with Institut du Cerveau et de la Moelle Epinière



Project-Team ARAMIS

Creation of the Project-Team: 2014 July 01

Each year, Inria research teams publish an Activity Report presenting their work and results over the reporting period. These reports follow a common structure, with some optional sections depending on the specific team. They typically begin by outlining the overall objectives and research programme, including the main research themes, goals, and methodological approaches. They also describe the application domains targeted by the team, highlighting the scientific or societal contexts in which their work is situated. The reports then present the highlights of the year, covering major scientific achievements, software developments, or teaching contributions. When relevant, they include sections on software, platforms, and open data, detailing the tools developed and how they are shared. A substantial part is dedicated to new results, where scientific contributions are described in detail, often with subsections specifying participants and associated keywords. Finally, the Activity Report addresses funding, contracts, partnerships, and collaborations at various levels, from industrial agreements to international cooperations. It also covers dissemination and teaching activities, such as participation in scientific events, outreach, and supervision. The document concludes with a presentation of scientific production, including major publications and those produced during the year.

Keywords

Computer sciences and digital sciences

- A3.4. – Machine learning and statistics
- A5.3. – Image processing and analysis
- A5.9. – Signal processing
- A6.2.4. – Statistical methods
- A9. – Artificial intelligence
 - A9.2. – Machine learning
 - A9.2.1. – Supervised learning
 - A9.2.2. – Unsupervised learning
 - A9.2.4. – Optimization and learning
 - A9.2.6. – Neural networks
 - A9.2.8. – Deep learning
 - A9.3. – Signal processing
 - A9.6. – Decision support
 - A9.12. – Computer vision

Other research topics and application domains

- B2. – Digital health
 - B2.2.6. – Neurodegenerative diseases
- B2.6. – Biological and medical imaging
 - B2.6.1. – Brain imaging

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1 Team members, visitors, external collaborators

Research Scientists

- Olivier Colliot [Team leader, CNRS, Senior Researcher, HDR]
- Ninon Burgos [CNRS, Senior Researcher, HDR]
- Stanley Durrleman [INRIA, Senior Researcher, HDR]
- Benjamin Glemain [INRIA, Starting Research Position, from Nov 2025]

Faculty Members

- Didier Dormont [SORBONNE UNIVERSITE, Professor, Emeritus, HDR]
- Daniel Racoceanu [SORBONNE UNIVERSITE, Professor, HDR]
- Sophie Tezenas Du Montcel [SORBONNE UNIVERSITE, Associate Professor, HDR]

Post-Doctoral Fellows

- Elise Delzant [ICM, Post-Doctoral Fellow, from Nov 2025]
- Ravi Hassanaly [CNRS, Post-Doctoral Fellow, until Mar 2025]
- Thomas Nedelec [ICM]
- Juliette Ortholand [CNRS, from Apr 2025 until May 2025]
- Arya Yazdan Panah [CNRS, from Mar 2025 until Aug 2025]

PhD Students

- Lea Aguilhon [INRIA, from Oct 2025]
- Pascaline Andre [CNRS]
- Gabrielle Casimiro [INRIA, from Oct 2025]
- Elise Delzant [INRIA, until Aug 2025]
- Marc Dibling [ICM]
- Guanghui Fu [ICM, until Sep 2025]
- Octave Guinebretiere [ICM, until Aug 2025]
- Ayse Gungor [Hôpital Fondation Adolphe de Rothschild]
- Mehdi Hamadache [INSERM, from Oct 2025]
- Manon Heffernan [ICM]
- Charles Heitz [CNRS]
- Matthieu Joulot [ICM]
- Sofia Kaisaridi [INRIA]
- Esther Kozłowski [ICM]
- Hugues Roy [ICM]

- Swann Ruyter [SORBONNE UNIVERSITE]
- Ilias Sarbout [Hôpital Fondation Adolphe de Rothschild]
- Maelys Solal [SORBONNE UNIVERSITE]
- Maylis Tran [ICM]
- Arya Yazdan Panah [ICM, until Feb 2025]

Technical Staff

- Lea Aguilhon [INRIA, Engineer, until Sep 2025]
- Camille Brianceau [ICM, Engineer, until Sep 2025]
- Thibault De Varax [ICM, Engineer]
- Nicolas Gensollen [INRIA, Engineer, until Jun 2025]
- Charlotte Godard [ICM, Engineer, from May 2025]
- Leo Guillon [INRIA, Engineer, until Nov 2025]
- Adam Ismaili [ICM, Engineer, from Mar 2025]
- Alice Joubert [ICM, Engineer]
- Sebastian Mendez Pineda [INRIA, Engineer, from Nov 2025]
- Charlotte Nijhoff [ICM, Project manager]
- Juliette Ortholand [INRIA, Engineer, until Mar 2025]
- Caglayan Tuna [INRIA, Engineer, until Oct 2025]

Interns and Apprentices

- Gabrielle Casimiro [INSERM, Intern, until Jul 2025]
- Emma Deloupy [ICM, Intern, until Jan 2025]
- Mehdi Hamadache [SORBONNE UNIVERSITE, Intern, from Feb 2025 until Aug 2025]
- Mathis Krause [ICM, Intern, from Jul 2025 until Sep 2025]
- Hanna Malet [ICM, Intern, until Jul 2025]
- Willow Scott [SORBONNE UNIVERSITE, Intern, from Apr 2025 until Sep 2025]

Administrative Assistant

- Helene Milome [INRIA]

External Collaborator

- Baptiste Couvy-Duchesne [Other]

2 Overall objectives

2.1 Context

ARAMIS is an Inria project-team based in the Paris Brain Institute (*Institut du Cerveau, ICM*¹) at the Pitié-Salpêtrière hospital in Paris, with joint affiliation to Inria, CNRS, Inserm and Sorbonne Université.

The Pitié-Salpêtrière hospital, the largest adult hospital in Europe, is France's leading centre for neurological diseases. The Paris Brain Institute brings together all neuroscience and neurology research at the hospital and hosts 32 research teams, state-of-the-art technical facilities, and over 800 staff. This unique position allows ARAMIS to collaborate closely with neuroscientists and clinicians, providing access to valuable clinical data, fostering new methodological developments, and facilitating the translation of research results into clinical applications.

2.2 General aim

ARAMIS develops **computational, mathematical, and statistical methods for the analysis of multimodal patient data in brain disorders**, with a strong focus on imaging. The team unites expertise in mathematics, computer science, engineering, and medicine to design tools at the intersection of machine learning, statistics, and medical image analysis. Our work is organised along four main axes:

- **Neuroimaging biomarkers and decision support:** Developing advanced methods for segmentation, lesion detection, and diagnosis support from brain images, with special attention to heterogeneous and large-scale clinical datasets.
- **Disease progression modelling:** Building predictive models of neurodegenerative disease evolution to inform clinical trials and patient stratification.
- **Computational pathology and high-content microscopy:** Leveraging deep learning and advanced image analysis to extract biomarkers from histopathology and cellular imaging, with a focus on model explainability and robust analysis.
- **High-dimensional multimodal data analysis:** Developing scalable methods to integrate and analyse large datasets combining genetics, imaging, and environmental variables.

Our applications cover a wide range of neurological disorders (including Alzheimer's, Parkinson's, multiple sclerosis, rare diseases, brain tumours, and psychiatric disorders), through collaborations at the Paris Brain Institute and with external partners.

Our impact is reinforced through the development and open distribution of software tools (Clinica, ClinicaDL, Leaspy), active engagement in open science, and participation in community initiatives and standards. ARAMIS operates in a mature, highly competitive international landscape, with innovative contributions in disease modelling, deep learning for medical images, and reproducible research. Its integration within the Paris Brain Institute and hospital secures access to unique clinical resources and facilitates rapid methodological translation to clinical research.

3 Research program

3.1 Neuroimaging biomarkers and clinical decision support systems

Benchmarking and improving deep generative models for unsupervised anomaly detection in brain FDG PET We have developed and validated deep generative modelling approaches for unsupervised anomaly detection in brain FDG PET, targeting early dementia biomarkers. To enable evaluation without manual annotation, we introduced a simulation-based framework for generating realistic anomalies and benchmarking pseudo-healthy image reconstruction methods (Hassanly et al., MELBA, 2024 [23]). We also conducted the first large-scale benchmarking of 20 VAE variants for 3D PET anomaly detection (Hassanly et al., JMI, 2025 [24]). To enhance robustness, we leveraged population variability using Z-score approaches

¹parisbraininstitute.org

(Solal et al., SPIE Medical Imaging, 2024 [125]) and proposed model aggregation and normalisation strategies (Solal et al., SPIE Medical Imaging, 2026 [96]). In addition, we introduced the first Bayesian flow network-based method for medical imaging, which outperformed existing models and reduced false positives in Alzheimer’s disease detection (Roy et al., DGM@MICCAI, 2025 [95]). Together, these contributions advance robust, scalable biomarker detection for clinical neuroimaging.

Machine learning for clinical MRI: quality control, harmonisation, and computer-aided diagnosis We have advanced a suite of machine learning approaches tailored for the unique challenges of routine clinical brain MRI available in large-scale clinical data warehouses. For quality control, we developed convolutional neural networks for the automatic quality control of 3D T1-weighted MRI (Bottani et al., MedIA, 2022 [4]). Building on this foundation, we implemented a simulation-based transfer learning strategy, pre-training on research data with simulated artefacts and fine-tuning on clinical images, which substantially improved the detection of motion artefacts (Loizillon et al., MedIA, 2024 [38]) and overall quality assessment (Loizillon et al, MELBA, 2024 [37]) in 3D T1-weighted MRIs. Quality control was extended to 3D FLAIR images through a semi-supervised domain adaptation technique (Loizillon et al., MedIA, 2025 [75]). To address dataset heterogeneity, we demonstrated that image-to-image translation could convert contrast-enhanced to non-contrast-enhanced images, supporting the harmonisation of clinical datasets and enabling reliable downstream analysis (Bottani et al., BMC Medical Imaging, 2024 [5]). In the domain of computer-aided diagnosis, we evaluated standard MRI-based machine learning models for dementia diagnosis and found that their performance drops markedly and can be confounded by quality and contrast agent effects when transitioning from curated research cohorts to complex clinical data (Bottani et al., MedIA, 2023 [3]). Lastly, we assessed unsupervised anomaly detection for identifying age-related white matter hyperintensities in routine FLAIR MRI, showing promise and robustness to quality variation, but also underscoring current limitations for clinical implementation (Loizillon et al., MIDL, 2024 [39]). Collectively, these studies chart both the significant progress and the outstanding barriers in deploying robust automated neuroimaging tools in routine clinical settings.

Deep learning-based segmentation of Parkinson’s disease-related brain structures and lymphomas

While deep learning has enabled significant progress in automatic segmentation of anatomical and pathological brain structures, key challenges for clinical robustness remain. We developed a pooling loss function introducing soft topology constraints, which reduced topological errors and improved segmentation accuracy when annotations are scarce (Fu et al, SPIE Medical Imaging, 2023 [120]). We also proposed a frequency disentangled learning strategy, separating image components during training, that boosted performance for Parkinsonian nuclei segmentation in some settings (Fu et al, SPIE Medical Imaging, 2024 [119]; Fu et al, Journal of Medical Imaging, 2024 [118]). For primary central nervous system lymphoma, our comprehensive comparison showed that specialised nnU-Net models outperform general foundation models, and we released a validated open-source nnU-Net tool that demonstrated robust performance across several centres (Fu et al, SPIE Medical Imaging, 2025 [91]; Fu et al, Radiology: Imaging Cancer, 2025 [71]). These works highlight the need for anatomical priors, novel training methods, and comprehensive validation for reliable neuroimaging segmentation.

Confidence intervals for performance evaluation in medical image segmentation

In medical image segmentation, the lack of systematic reporting on the precision of performance metrics, especially confidence intervals, undermines the reliability and clinical translation of artificial intelligence models. We have shown that small test sets, often used in the field, result in very wide confidence intervals for metrics such as the Dice coefficient, which limits interpretability and comparability (El Jurdi and Colliot, IEEE ISBI, 2023 [122]). Our empirical and simulation studies in brain MRI segmentation indicate that parametric and bootstrap methods produce similar confidence intervals, and that segmentation typically requires fewer cases than classification to reach a given precision (El Jurdi et al., MedIA, 2025 [70]). Analysing major conferences with our international collaborators, we found that confidence intervals are seldom reported, and differences between top-performing models are often not statistically significant when these intervals are considered (Christodoulou et al., MICCAI, 2024 [9]). We further identified that for median estimates, some bootstrap approaches provide unreliable coverage, highlighting the need for careful methodological choices (André et

al., BRIDGE MICCAI Workshop, 2025 [89]). Overall, our work strongly supports transparent and systematic confidence interval reporting to improve the evaluation and clinical translation of segmentation models.

3.2 Disease progression modelling for trial design

Disease course mapping We designed a new class of mixed-effects models to learn distributions of trajectories from a longitudinal dataset. The successive observations of a subject are seen as successive points along a curve drawn on a multivariate Riemannian manifold. The subjects' curves all derive from a common geodesics on the manifold, which summarises the progression scenario in the population. The derivation comprises a time-reparameterisation of the geodesics to account for variations in the dynamics of changes and exp-parallelisation to account for the distribution of the data at a given stage of progression. The theoretical and computational foundations of these approaches were set up in the thesis and articles of J.-B. Schiratti (Schiratti et al, JMLR, 2017 [54]). During the PhD thesis of J. Ortholand, the model was extended to consider events in addition to longitudinal data. This was first done for a model with one feature and then the model was extended to consider several features. In both cases, the model was validated on simulated data with good performance in comparison with other existing models. Modelling the heterogeneous progression of chronic diseases requires methods that extend beyond standard mixed-effects assumptions. We proposed a probabilistic mixture extension of the *Disease Course Mapping* model to capture distinct disease progression subtypes within a population. This framework provided a robust and interpretable approach for clustering patients according to spatiotemporal disease dynamics, offering a valuable tool for potential insights into precision medicine (Kaisaridi et al, ISCB, 2025 [104]).

Disease progression modelling for trial design Disease progression models can effectively model the progression of diseases using a great variety of multimodal longitudinal data and provide valuable insights into the disease's clinical manifestations and progression. The estimations obtained thanks to these models can inform clinical trial design and facilitate more accurate prognosis and individualised treatment strategies. In particular, we evaluated AD Course Map, a statistical model predicting the progression of neuropsychological assessments and imaging biomarkers for a patient from current medical and radiological data at early disease stages of Alzheimer's disease. We showed that enriching the population with the predicted progressors decreased the required sample size by 38% to 50%, depending on trial duration, outcome, and targeted disease stage, from asymptomatic individuals at risk of AD to subjects with early and mild AD (Maheux et al, Nature Communications, 2023 [40]). We also explored prediction-powered inference (PPI) and its subsequent development, PPI++, which provide a novel approach to standard statistical estimation by leveraging machine learning systems to enhance unlabelled data with predictions. We use this paradigm in clinical trials, where the predictions are provided by disease progression models such as those produced by Leaspy, providing prognostic scores for all the participants as a function of baseline covariates. The proposed method would empower clinical trials by providing untreated digital twins of the treated patients while remaining statistically valid (Poulet et al, BMC Medical Research Methodology, 2025 [81]).

Methods for real-world health data Our team has developed rigorous methodological frameworks for leveraging large-scale administrative health databases in neuroepidemiology research. We established algorithms for disease identification and created novel approaches to quantify diagnostic and encoding delays, providing empirical tools to address temporal biases inherent in real-world data. Through transnational collaborations across multiple healthcare systems (France, Sweden, UK, Australia), we standardised case identification methods and developed comparative analytical frameworks to distinguish genuine epidemiological trends from database artefacts (Wei et al, EBioMedicine, 2025 [86]). Our work on prodromal phases combined large-scale case-control designs with temporal trajectory analysis to identify early disease markers while controlling for multiple comparisons (Guinebretiere, thesis [108]). We applied target trial emulation methodology to draw causal inferences from observational data, exploiting natural experiments like policy changes as sources of quasi-random treatment variation. We also analysed the care pathway of patients from several diseases (Dibling et al, Neuroepidemiology, 2024 [19]). We finally contributed to open-source infrastructure development in R (sndsTools) to standardise data processing and promote reproducibility.

Applications in chronic neurological diseases The methodological advances were applied to a range of chronic neurological diseases, including amyotrophic lateral sclerosis, Parkinson’s disease, CADASIL, and cerebellar ataxia. These studies revealed key factors influencing disease progression, such as sex, onset site, genetic modifiers, and comorbidities, and uncovered heterogeneity in the trajectories of clinical symptoms and decline. The models provided new insights into early and distinct patterns of progression, paving the way for better patient stratification and precision medicine in these disorders [17, 74, 43].

3.3 Computational pathology and high-content microscopy

Virtual staining and generative modelling A central scientific contribution is the invention of algorithms and methods for generating multiple virtual immunohistochemical (IHC, antibody-reaction-based) stain images from a single H&E whole-slide image (mainly structural), using paired and unpaired generative approaches. This patent formalises a scalable, trustworthy GenAI framework for virtual multi-staining in computational pathology, enabling accurate prediction of immunostains (CD3, CD8, GIEMSA, CD163, AE1AE3, CD117, D2-40, CD15) directly from routine H&E slides. The underlying model integrates explainable diffusion and specialised CycleGAN-based architectures constrained by biophysical priors to ensure plausibility and interpretability. The foundational publication (Ounissi et al, PLoS Computational Biology, 2025 [46]) underpinning these technologies demonstrates the scalability and reliability of our methods across multiple tissue types and staining protocols.

High-content microscopy and neurodegenerative pathology Quantifying phagocytosis in dynamic, unstained cells is crucial for studying neurodegenerative diseases, yet extremely challenging due to rapid cellular interactions, low contrast, and acquisition artefacts in phase-contrast time-lapse microscopy. We introduced a scalable, real-time, end-to-end framework combining data quality control, robust segmentation, and two complementary explainability modules that reveal deep learning decisions through visual attribution and model simplification. This demonstrates that interpretability can enhance, rather than hinder, performance, yielding a more efficient architecture and optimised execution. Applied to microglial phagocytosis in frontotemporal dementia (FTD), the method reveals statistically significant alterations (FTD mutant cells being larger and more aggressive than controls) and achieves state-of-the-art results across public benchmarks. To accelerate translational research, we have released the full pipeline and a unique phagocytosis dataset, providing a reproducible foundation for future interpretable AI developments in neurodegenerative disease characterisation. The methods and results were published in Ounissi et al, Scientific Reports, 2024 [45], together with the computational foundation for PhagoStat (github.com/ounissimehdi/PhagoStat), a framework enabling interpretable quantification of cell phagocytosis and neuroinflammation dynamics.

Tauopathy analysis for refined Alzheimer’s disease patient stratification Quantifying the distribution and morphology of tau protein structures in brain tissue is essential for diagnosing Alzheimer’s disease (AD) and its variants and for refining patient stratification. We introduce a deep learning framework for semantic segmentation of tau lesions, particularly neuritic plaques, in WSI from post-mortem data provided by the NEURO-CEB AP-HP / ICM human brain tissue repository. We released ADNP-15, an open-source whole-slide image dataset for neuritic plaque segmentation and stain normalisation (Zhao et al, IRBM, 2025 [62]), after a preliminary dataset and methodological publication (Jiménez et al, MICCAI, 2022 [121]). Complementary work in Ingrassia et al, J. Neuropathol. Exp. Neurol., 2024 [26] has established new quantitative methods for the interpretable segmentation of pathological structures such as tau tangles and neuritic plaques using frugal, explainable architectures.

Physics-informed modelling and multi-scale integration We contributed to the development of mechanistic models of tumour oxygenation and hypoxia based on coupled PDEs constrained by spatial imaging data (Kumar et al, Physics Medicine and Biology, 2024 [35]). This work exemplifies our broader approach of integrating data-driven deep learning with mesoscopic physical modelling to enhance biological realism, interpretability, and generalisation of predictive models. Such physics-guided generative frameworks are being extended to longitudinal tumour modelling and multi-scale image registration, linking MRI, histology, and spatial transcriptomics in a consistent computational space.

Responsible and frugal AI frameworks The foundation of this line of research is synthesised in Racoceanu et al, *Techniques de l'Ingénieur*, 2022 [50], which formalises the concept of Responsible AI as applied to computational pathology, integrating explicability, traceability, and human oversight, and demonstrates that explainability and performance can coexist through frugal architectures (Ounissi et al, *Scientific Reports*, 2024 [45]). This framework underpins ongoing developments in multi-virtual staining (Ounissi et al, *PLoS Computational Biology*, 2025 [46]), as well as agentic AI architectures for multi-modal integration (Kumar et al, *Physics in Medicine and Biology* 2024 [35]).

Our results demonstrate a consistent research trajectory, from theoretical foundations of responsible generative AI to patented applications in virtual staining and multi-scale biomedical data modelling, thereby solidifying our contributions at the intersection of computational pathology, physics-informed AI, and clinical translation.

3.4 High-dimensional multimodal data (genetic, imaging)

High-dimensional statistics for brain imaging Our group's contributions in high-dimensional neuroimaging statistics are highlighted by three major articles, each addressing foundational challenges with innovative solutions and far-reaching implications for research and clinical practice. In a first-of-its-kind analysis, we systematically quantified how different cortical atlases capture trait-related brain variance, revealing that atlas selection profoundly affects the proportion of phenotypic variance explained by brain structure, i.e. the morphometricity (Fürtjes et al, *Cortex*, 2023 [21]). This work provides a rigorous, data-driven framework for choosing atlases, directly impacting the reproducibility and biological interpretability of neuroimaging findings across studies. The second study pioneers a comprehensive benchmarking of MRI processing pipelines, demonstrating for the first time how pipeline choice influences morphometricity, replicability, and predictive power (Delzant et al, *Human Brain Mapping*, 2025 [68]). By identifying volume-based pipelines (e.g., FSLVBM) as optimal for robustness and surface-based pipelines as sources of unique but less consistent signals, it sets a new standard for pipeline selection in high-dimensional neuroimaging, ensuring more reliable and generalisable results. The third article translates these methodological advances into clinical impact by synthesising grey matter biomarkers for Alzheimer's disease progression and cognitive decline (Couvry-Duchesne et al, *Human Brain Mapping*, 2024 [13]). Its meta-analytic approach not only identifies robust, early-detection biomarkers but also bridges the gap between high-dimensional statistics and real-world applications, offering actionable insights for early intervention and personalised medicine. Collectively, these studies redefine best practices in neuroimaging analysis, from atlas and pipeline selection to clinical translation. Their originality lies in providing empirical, scalable solutions to longstanding challenges in high-dimensional data, while their significance is amplified by their direct impact on reproducibility, biological insight, and the potential for early disease detection, particularly in neurodegenerative disorders like Alzheimer's.

Combining deep learning and advanced statistics to unveil the genetic underpinnings of imaging and clinical phenotypes Combining deep learning for imaging and advanced statistics for omics data, we were able to unveil the genetic bases of various phenotypes that are highly relevant neuroscientifically and/or clinically but had never been studied so far, due to lack of adequate tools. We built a deep learning tool to measure choroid plexuses (Yazdan-Panah et al, *NeuroImage: Clinical* [61]), a structure which is highly relevant to multiple sclerosis and neuroinflammation, and used this tool to perform the first corresponding genome-wide association (GWAS) that unveiled their complex genetic architecture (Yazdan-Panah, PhD thesis, 2025 [109]; Yazdan-Panah et al, In preparation). In a similar spirit, we built a tool for automatic rating of incomplete hippocampal inversion and extensively validated it across multiple cohorts and over 1,000 participants (Hemforth et al, *MELBA*, 2024 [25]). Its application allowed us to perform a GWAS which robustly identified various genetic variants associated with this phenotype (Hemforth et al, under revision at *Imaging Neuroscience*). We studied other intriguing anatomical variations of the basal temporal lobe, in particular topological sulcal connections. We demonstrated their heritability and unveiled a sexual dimorphism as well as association with incomplete hippocampal inversions (De Matos et al, *Brain Structure and Function*, 2023 [42]).

Learning multimodal representations of imaging and transcriptomic data We introduced a deep learning framework learn joint representations that can integrate multimodal data from neuroimaging and transcriptomics. To that purpose, we proposed a multimodal variational autoencoder formulation. An original feature of this approach is the introduction of a weak supervision to constraint the latent space structure to reflect disease severity. The approach was applied to study the progression of genetic forms of frontotemporal dementia and amyotrophic lateral sclerosis. It allowed building disease progression scores that were validated against disease stage (Kmetzsch et al, *IEEE J. Biomed. Health. Inf.*, 2022 [31]).

4 Application domains

Our applications cover a wide range of neurological disorders through collaborations at the Paris Brain Institute and with external partners.

4.1 Core neurodegenerative disease projects

Neurodegenerative diseases were and still are a central focus of our clinical research activities.

Alzheimer’s disease We performed unique real-world data analyses using more than 80,000 medical records in France and the UK. These analyses identified specific drug consumption patterns before Alzheimer’s disease (AD) onset (Ansart et al, *Alzheimer’s Dement.: Transl. Res. Clin. Interv.*, 2021 [2]) and ten health conditions significantly associated with AD in the 2 to 10 years before diagnosis (Nédélec et al, *The Lancet Digital Health*, 2022 [44]). This landmark study provided new insights into risk factors and prodromal symptoms of AD and attracted substantial media attention.

Genetic frontotemporal dementia Building on a decade-long research programme on genetic forms of frontotemporal dementia [117, 116, 126, 124], we coordinated MRI acquisition and analysis for the multicentre studies PredictPGRN and PREVDEMALS (PIs: A. Brice and I. Le Ber). Recently, we advanced two critical areas: first, plasma-based biomarkers using circulating microRNAs to track disease progression (Kmetzsch et al, *Ann. Clin. Transl. Neurol.*, 2022 [32]); second, quantification of longitudinal imaging changes in the presymptomatic phase (Saracino et al, *Alzheimer’s & Dementia*, accepted).

Parkinson’s disease and related disorders We strengthened our activities on Parkinson’s disease through several complementary approaches. In collaboration with genetics specialists at ICM and internationally, we identified genetic determinants of cognitive decline (Faouzi et al, *npj Parkinson’s disease*, 2024 [20]). During Lydia Chougar’s Inria-funded secondment (neuroradiologist), we identified imaging biomarkers to differentiate Parkinsonian syndromes (Chougar et al, *Park & Rel Dis*, 2023 [8]) and demonstrated that MRI markers significantly improve diagnostic performance compared to standard clinical diagnosis (Chougar et al, *Movement Disorders*, 2024 [7]).

4.2 Disease progression modelling across neurological diseases

We applied our disease progression modelling framework to diverse neurological conditions, demonstrating its versatility and capacity to reveal disease-specific temporal patterns and heterogeneity.

Amyotrophic lateral sclerosis Using a multivariable disease modelling approach, we showed that sex and onset site are important drivers of the progression of motor function, BMI, and FVC decline in ALS patients (Ortholand et al, *ENCALS*, 2022 [123]).

Parkinson’s disease progression and heterogeneity We reconstructed the temporal cascade of Parkinson’s disease, finding that the first changes occurred in the contralateral putamen 13 years before diagnosis, followed by changes in motor symptoms, dysautonomia, and sleep (all before diagnosis), and finally cognitive decline at diagnosis. The model revealed earlier disease onset, earlier non-motor and later motor symptoms, and more rapid cognitive decline in PD patients with REM sleep behavioural disorder compared to those without. Understanding this heterogeneity is key to deciphering underlying pathophysiology and selecting homogeneous subgroups for precision medicine (Di Folco et al, *Movement Disorders*, 2023 [17]).

CADASIL In cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL), the most frequent genetic small artery brain disease, we demonstrated gradual and heterogeneous decline in different clinical and cognitive performances over patients' lifetimes. Two progression profiles emerged: one rapid and early, the other delayed and slower. Male gender, low educational level, pathogenic variant location in EGF α 1 to 6 domains, smoking, and arterial hypertension were identified as factors affecting clinical progression (Kaisaridi et al, *Neurology*, 2025 [74]).

Ataxias Studying the scale for the assessment and rating of ataxia (SARA), the reference clinical scale for cerebellar ataxia, we found that seven of eight items showed non-linear progression while the total score progressed linearly. Progression speed differed between most items, providing crucial information for clinical trial design in upcoming therapeutic trials (Moulaire et al, *Movement Disorders*, 2023 [43]).

4.3 Emerging clinical applications

Recently, we initiated research in two new clinical domains, expanding our expertise beyond neurodegenerative diseases.

Neuro-oncology: primary brain lymphomas During Lucia Niccheli's Inria-funded secondment (neuroradiologist), we launched a new research programme on primary central nervous system lymphoma, a rare, highly malignant brain tumour. We developed an open source model for automatic segmentation of such tumours with extensive internal and external validation (Fu et al, *Radiology: Imaging Cancer*, 2025 [71]). Current work builds on this foundation to develop approaches for predicting treatment response.

Neuro-ophthalmology AI-based stroke detection Through collaborative PhD supervision of Ayse Gungor and Ilias Sarbout, and leveraging neuro-ophthalmology expertise at the Adolphe de Rothschild Foundation Hospital, we developed deep learning models for rapid detection of hyperacute central retinal artery occlusion from retinal fundus photographs (*J. American Heart Association*, 2025 [22]). Our results suggest that AI-based analysis of retinal photographs could support emergency stroke pathways, facilitate timely fibrinolysis decisions, and improve secondary stroke prevention pending further validation.

5 Social and environmental responsibility

The team is attentive to the environmental impact of its activities and encourages responsible practices. Members are free to decline submissions or travel to distant conferences if they wish to limit air travel, and train travel is systematically encouraged for national and nearby international events. Computing resources are used efficiently through shared institute and national clusters, reducing the need for individual high-power machines. Software developments are designed with reproducibility and reusability in mind, limiting redundant computations and promoting sustainable research practices. In terms of equipment, the team aims to extend the lifetime of computers and, when they are no longer needed, donates them to Emmaüs Connect for refurbishment and redistribution to people in need. These measures reflect a collective effort to integrate environmental responsibility into the team's research and day-to-day operations.

6 Highlights of the year

- Olivier Colliot became Deputy Scientific Director of the Paris Brain Institute.
- Daniel Racoceanu registered two world patents WO2025/168731 (paired images) and WO2025/168729A1 (unpaired images, published on 14 Aug 2025, entitled "Device and method for generating n virtual IHC stain images from one H&E image").

6.1 Awards

- Maylis Tran received the best oral presentation award at ISCB 2025 - 46th Annual Conference of the International Society for Clinical Biostatistics.

7 Latest software developments, platforms, open data

7.1 Latest software developments

7.1.1 Clinica

Name: Clinica

Keywords: Neuroimaging, Brain MRI, MRI, Clinical analysis, Image analysis, Machine learning

Functional Description: Clinica is a software platform for clinical neuroscience research, enabling multimodal brain image analysis of large-scale datasets. It facilitates the application of advanced analysis pipelines to diverse clinical studies. To this end, it integrates a comprehensive set of processing tools for the main neuroimaging modalities: anatomical MRI, diffusion MRI, and PET.

For each modality, Clinica enables the extraction of various types of features (regional measures, parametric maps, surfaces,...). These features can then be used as input for statistical modeling or machine learning methods. Processing pipelines are based on combinations of open-source tools developed by the community. Clinica follows the BIDS specification for input data and proposes one for the storage of processed outputs. Clinica is written in Python and leverages the Nipype system for pipelining. It combines widely-used software for neuroimaging data analysis (SPM, Freesurfer, ANTs, FSL, MRtrix...), and machine learning (scikit-learn).

URL: <http://www.clinica.run>

Publications: [hal-02308126](#), [hal-04278898](#), [hal-03728243](#), [hal-03513920](#), [hal-02549242](#), [hal-02132147](#), [hal-02562504](#), [hal-01518785](#), [hal-01578479](#), [hal-01858384](#), [hal-01907482](#), [hal-01654000](#), [hal-02566361](#), [hal-01950933](#)

Contact: Ninon Burgos

Participants: Ninon Burgos, Olivier Colliot, Alice Joubert, Adam Ismaili, Matthieu Joulot, Maelys Solal, Hugues Roy, Michael Bacci, Simona Bottani, Mauricio Diaz, Stanley Durrleman, Sabrina Fontanella, Nicolas Gensollen, Pietro Gori, Jeremy Guillon, Ravi Hassanaly, Thomas Jacquemont, Sophie Loizillon, Pascal Lu, Arnaud Marcoux, Tristan Moreau, Alexandre Routier, Omar El Rifai, Jorge Samper Gonzalez, Elina Thibeau-Sutre, Ghislain Vaillant, Junhao Wen

Partners: Institut du Cerveau et de la Moelle épinière (ICM), CNRS, INSERM, Sorbonne Université

7.1.2 ClinicaDL

Keywords: Deep learning, Neuroimaging, Reproducibility

Scientific Description: As deep learning faces a reproducibility crisis and studies on deep learning applied to neuroimaging are contaminated by methodological flaws, there is an urgent need to provide a safe environment for deep learning users to help them avoid common pitfalls that will bias and discredit their results. Several tools have been proposed to help deep learning users design their framework for neuroimaging data sets. ClinicaDL has been developed to bring answers to three common issues encountered by deep learning users who are not always familiar with neuroimaging data: (1) the format and preprocessing of neuroimaging data sets, (2) the contamination of the evaluation procedure by data leakage and (3) a lack of reproducibility. The combination of ClinicaDL and its companion project Clinica allows performing an end-to-end neuroimaging analysis, from the download of raw data sets to the interpretation of trained networks, including neuroimaging preprocessing, quality check, label definition, architecture search, and network training and evaluation.

Functional Description: ClinicaDL is a Python open-source software for neuroimaging data processing with deep learning. This software includes many functionalities, such as neuroimaging preprocessing, synthetic dataset generation, label definition, data split with similar demographics, architecture search, network training, performance evaluation and trained network interpretation. The three main objectives of ClinicaDL are to (1) help manipulate neuroimaging data sets, (2) prevent data leakage from biasing results and (3) reproduce deep learning experiments.

URL: <http://clinicadl.aramislab.fr/>

Publications: [hal-03351976](#), [hal-02562504](#), [hal-04279014](#), [hal-04419141](#)

Contact: Ninon Burgos

Participants: Ninon Burgos, Olivier Colliot, Thibault De Varax, Maelys Solal, Hugues Roy, Camille Brianceau, Mauricio Diaz, Ravi Hassanaly, Alexandre Routier, Elina Thibeau-Sutre

Partners: Institut du Cerveau et de la Moelle épinière (ICM), CNRS, INSERM, Sorbonne Université

7.1.3 leaspy

Name: Learning spatiotemporal patterns in python

Keywords: Clinical analysis, Medical applications, Personalized medicine

Functional Description: Leaspy, standing for LEARning Spatiotemporal Patterns in Python, has been developed to analyze longitudinal (or sequential) data that correspond to the measurements of a long-term progression. Said differently, each sequence of repeated observations derives from a portion of the global process, with a certain variability between sequence.

Release Contributions: 1.The new structure is a result of a global refactoring: o This breaking change is the result of a major refactoring of how model parameters and variables are handled. o The new architecture is more modular and is designed to simplify the definition and extension of models compared to v1. o The codebase has been structured to closely mirror the mathematical formulation of the models. o At its core, distinct classes are implemented, following a well-defined hierarchy of dependencies and inheritance, for the model and the algorithm class, using a Directed Acyclic Graph (DAG) and a 'family' concept. o This modular and transparent architecture ensures clarity, extensibility, and consistency, while its straightforward structure greatly simplifies the development and integration of new model or algorithm variants. o A State builds on this structure: it is a DAG with an additional mapping between node names and their current values, effectively holding both the model's blueprint and the values currently loaded.

2.New models are added: o joint: for the joint modelisation of patient outcomes and events o mixture: for the clustering of patients with similar spatiotemporal profiles

3.Documentation is updated and completed. The documentation page that comes with this release provides a detailed description of the mathematical intuition behind leaspy, the models and the algorithms implemented and the interpretation of the results. It also comes with an example gallery with complete notebooks fitting different models with synthetic data.

Publications: [hal-01540367](#), [hal-01964821](#), [hal-03877293](#), [hal-04319442](#), [hal-04023781](#), [hal-03831598](#), [tel-04770912](#), [hal-04095450](#), [hal-04216957](#), [hal-04848392](#)

Contact: Sophie Tezenas Du Montcel

Participants: Lea Aguilhon, Gabrielle Casimiro, Raphaël Couronné, Némo Fournier, Nicolas Gensollen, Sofia Kaisaridi, Igor Koval, Etienne Maheux, Sebastian Mendez Pineda, Juliette Ortholand, Pierre-Emmanuel Poulet, Maylis Tran, Caglayan Tuna, Arnaud Valladier

Partners: Université Paris Cité, INSERM

7.1.4 sndsTools

Name: Extraction of healthcare utilisation data from the SNDS with R

Keywords: Electronic Medical Records, Real world data

Functional Description: sndsTools is a community-driven R package designed to streamline the extraction, cleaning, and harmonisation of healthcare utilisation data from the French National Health Data System (SNDS), which is a crucial resource for large-scale real-world evidence research. Initiated after multidisciplinary discussions at the Emoïs congress in March 2024, and coordinated by T. Nedelec (ARAMIS) alongside collaborators from the French Health Authority (HAS) and AP-HM, sndsTools addresses core challenges in SNDS data management. The package greatly simplifies recurring steps in SNDS-based studies, making routine data extraction and reproducibility accessible for a growing community of users in epidemiology and medical data science. With a modular, evolving design and long-term support ambitions, sndsTools is released under the EUPL licence to foster open, collaborative development and ensure compatibility with the wider public health research ecosystem.

URL: <https://sndstoolers.github.io/sndsTools/>

Contact: Thomas Nedelec

Participants: Thomas Nedelec, Antoine Belloir, Marc Dibling, Matthieu Doutreligne, Leo Guillon, Thomas Soeiro

7.1.5 PhagoStat

Name: Efficient quantification of cell phagocytosis in neurodegenerative disease studies

Keywords: Explainable Artificial Intelligence, Deep learning, Scalability, Live-cell microscopy, Microscopy

Scientific Description: This pipeline is an integrated, end-to-end solution for data-sequence handling, video-based analysis, noise management, quantitative analysis, and statistical reporting. To the best of our knowledge, unique in its scope and functionality, we have made this innovative tool publicly available on GitHub. As an added feature, especially beneficial for less technical users, we included a pre-coded, user-friendly UX and a framework for an HPC environment, it operates with a single command line. User-friendly UX and HPC support components are optional for highly technical users. Given that the source code for all modules, along with the UX and HPC framework, is publicly accessible, it allows for usage, modification, and potential enhancements by the community. Applying the PhagoStat pipeline to microglial cells has yielded statistically significant findings. Our discovery that Frontotemporal Dementia (FTD) mutant cells exhibit increased size and activity compared to wild-type cells is a novel insight, contributing significantly to our understanding of neurodegenerative diseases and potentially catalyzing further research in this domain.

Functional Description: The PhagoStat pipeline is able to process large data-sets and includes a data quality verification module to counteract potential perturbations such as microscope movements and frame blurring. We also propose an explainable cell segmentation module to improve the interpretability of deep learning methods compared to black-box algorithms. This includes two interpretable deep learning capabilities: visual explanation and model simplification. We demonstrate that interpretability in deep learning is not the opposite of high performance, by additionally providing essential deep learning algorithm optimization insights and solutions. Besides, incorporating interpretable modules results in an efficient architecture design and optimized execution time. We apply this pipeline to quantify and analyze microglial cell phagocytosis in frontotemporal dementia (FTD) and obtain statistically reliable results showing that FTD mutant cells are larger and more aggressive than control cells. The method has been tested and validated on several public benchmarks by generating state-of-the-art performances. To stimulate translational approaches and future studies, we release an open-source end-to-end pipeline and a unique microglial cells phagocytosis dataset for immune system characterization in neurodegenerative diseases research. This pipeline and the associated dataset will consistently crystallize future advances in this field, promoting the development of efficient and effective interpretable algorithms dedicated to the critical domain of neurodegenerative diseases' characterization.

Release Contributions: Initial version 1.0

URL: <https://github.com/ounissimehdi/PhagoStat>

Publication: [hal-04067345v3](#)

Contact: Daniel Racoceanu

Participants: Daniel Racoceanu, Medhi Ounissi

7.2 Open data

ADNP-15

Contributors: Chenxi Zhao, Jianqiang Li, Qing Zhao, Jing Bai, Susana Boluda, Benoit Delatour, Lev Stimmer, Daniel Racoceanu, Gabriel Jimenez, Guanghui Fu

Description: The ADNP-15 dataset [88] represents a unique open-source resource for the quantitative analysis of Alzheimer’s disease histopathology. Unlike existing collections, it provides expertly annotated whole-slide images of neuritic plaques, lesions that combine amyloid deposits with surrounding tau-positive dystrophic neurites, captured across realistic staining and acquisition conditions. Its dual focus on lesion segmentation and stain variability makes it the first dataset specifically designed to benchmark both deep-learning architectures and stain normalisation methods for AD pathology. By releasing all images, annotations, and code openly, ADNP-15 establishes a reproducible foundation for developing and comparing algorithms, filling a critical gap in large-scale, high-quality data for computational neuropathology.

Dataset DOI: [doi:10.5281/zenodo.15009434](https://doi.org/10.5281/zenodo.15009434)

Publication: Chenxi Zhao, Jianqiang Li, Qing Zhao, Jing Bai, Susana Boluda, et al.. ADNP-15: An Open-Source Histopathological Dataset for Neuritic Plaque Segmentation in Human Brain Whole Slide Images with Frequency Domain Image Enhancement for Stain Normalization. *Innovation and Research in BioMedical engineering*, 2025, 46 (6), pp.100913. ([10.1016/j.irbm.2025.100913](#)). ([hal-05286275](#))

8 New results

8.1 Automatic segmentation of primary central nervous system lymphoma at clinical routine postcontrast T1-weighted MRI

Participants: Guanghui Fu, Lucia Nichelli, Olivier Colliot (*Correspondant*).

We developed and validated a deep learning model for automatic segmentation of primary central nervous system lymphoma (PCNSL) on postcontrast T1-weighted MRI. Retrospective data were collected from immunocompetent patients with pathologically confirmed PCNSL between September 2010 and February 2022. A model based on the nnU-Net framework was trained using a single-center dataset with manual neuroradiologist segmentations as reference and evaluated on both internal and multi-center external test sets comprising seven additional institutions. Segmentation performance was assessed using the Dice score, mean average surface distance, and F1 score, with statistical comparisons performed using the Mann–Whitney U test and bootstrap-based confidence intervals. The study included 135 patients (68 female, 66 male, one unspecified; internal dataset mean age \pm SD, 67.0 ± 12.0 years; external dataset mean age, 75.5 ± 13.6 years). The model achieved a mean Dice score of 0.84 (95% CI, 0.79–0.88) on the internal test set ($n = 44$) and 0.88 (95% CI, 0.84–0.91) on the external test set ($n = 48$), with no evidence of a difference between test sets ($P = 0.59$). Performance was highest for homogeneous, well-defined lesions and decreased modestly in the presence of numerous poorly defined infracentimetric lesions. Automatic and manual segmentations showed strong volumetric agreement (internal $r = 0.99$, external $r = 0.98$, both $P < 0.001$), indicating robust performance across centers with heterogeneous MRI acquisition protocols.

More details in [71].

8.2 Confidence intervals for performance estimates in brain MRI segmentation

Participants: Rosana El Jurdi, Gaël Varoquaux, Olivier Colliot (*Correspondant*).

Medical segmentation models are evaluated empirically. As such an evaluation is based on a limited set of example images, it is unavoidably noisy. Beyond a mean performance measure, reporting confidence intervals is thus crucial. However, this is rarely done in medical image segmentation. The width of the confidence interval depends on the test set size and on the spread of the performance measure (its standard-deviation across of the test set). For classification, many test images are needed to avoid wide confidence intervals. Segmentation, however, has not been studied, and it differs by the amount of information brought by a given test image. In this paper, we study the typical confidence intervals in medical image segmentation. We carry experiments on 3D image segmentation using the standard nnU-net framework, two datasets from the Medical Decathlon challenge and two performance measures: the Dice accuracy and the Hausdorff distance. We show that the parametric confidence intervals are reasonable approximations of the bootstrap estimates for varying test set sizes and spread of the performance metric. Importantly, we show that the test size needed to achieve a given precision is often much lower than for classification tasks. Typically, a 1% wide confidence interval requires about 100-200 test samples when the spread is low (standard-deviation around 3%). More difficult segmentation tasks may lead to higher spreads and require over 1000 samples.

More details in [70].

8.3 Choice of processing pipelines for T1-weighted brain MRI impacts association and prediction analyses

Participants: Élise Delzant (*Correspondant*), Olivier Colliot, Baptiste Couvy-Duchesne.

The growing availability of large neuroimaging datasets, such as the UK Biobank, provides new opportunities to improve robustness and reproducibility in brain imaging research. However, little is known about the extent to which MRI processing pipelines influence results. Using 39,655 T1-weighted MRI scans from the UK Biobank, we systematically compared five widely used gray-matter representations derived from three major software packages: FSL (volume-based), CAT12/SPM (volume- and surface-based), and FreeSurfer (cortical and subcortical surface-based). We assessed their impact on morphometricity (trait variance explained by brain features), susceptibility to imaging confounders, false positives, association findings, and prediction accuracy across 29 diverse traits, including lifestyle, metabolic, and disease-related variables. We found that all pipelines were sensitive to imaging confounders such as head motion, brain position, and signal-to-noise ratio, and many produced non-normal voxel or vertex distributions. FSL and FreeSurfer generally yielded higher morphometricity estimates, but each captured partially unique signals, leading to inconsistencies in brain regions identified across methods. Volume-based approaches tended to outperform surface-based ones, detecting more significant clusters, achieving higher replication rates, and producing stronger predictive performance. Small clusters (single voxels or vertices) were less reliable, suggesting caution in their interpretation. Among all methods, FSLVBM emerged as the most consistent all-rounder, maximizing morphometricity, replicability, and predictive accuracy. Our results highlight the strengths and limitations of commonly used processing pipelines, offering benchmarks to guide researchers in method selection. They further suggest that combining multiple pipelines may improve brain-based prediction by leveraging unique, complementary signals, and that careful treatment of imaging confounders is essential for robust large-scale neuroimaging analyses.

More details in [68].

8.4 Automatic quality control of brain 3D FLAIR MRIs for a clinical data warehouse

Participants: Sophie Loizillon, Simona Bottani, Lydia Chougar, Didier Dormont, Olivier Colliot, Ninon Burgos (*Correspondant*).

Clinical data warehouses, which have arisen over the last decade, bring together the medical data of millions of patients and offer the potential to train and validate machine learning models in real-world scenarios. The quality of MRIs collected in clinical data warehouses differs significantly from that generally observed in research datasets, reflecting the variability inherent to clinical practice. Consequently, the use of clinical data requires the implementation of robust quality control tools. By using a substantial number of pre-existing manually labelled T1-weighted MR images (5,500) alongside a smaller set of newly labelled FLAIR images (926), we present a novel semi-supervised adversarial domain adaptation architecture designed to exploit shared representations between MRI sequences thanks to a shared feature extractor, while taking into account the specificities of the FLAIR thanks to a specific classification head for each sequence. This architecture thus consists of a common invariant feature extractor, a domain classifier and two classification heads specific to the source and target, all designed to effectively deal with potential class distribution shifts between the source and target data classes. The primary objectives of this paper were: (1) to identify images which are not proper 3D FLAIR brain MRIs; (2) to rate the overall image quality. For the first objective, our approach demonstrated excellent results, with a balanced accuracy of 89%, comparable to that of human raters. For the second objective, our approach achieved good performance, although lower than that of human raters. Nevertheless, the automatic approach accurately identified bad quality images (balanced accuracy >79%). In conclusion, our proposed approach overcomes the initial barrier of heterogeneous image quality in clinical data warehouses, thereby facilitating the development of new research using clinical routine 3D FLAIR brain images.

More details in [75].

8.5 Benchmarking 3D generative autoencoders for pseudo-healthy reconstruction of brain ^{18}F -fluorodeoxyglucose positron emission tomography

Participants: Ravi Hassanaly, Maelys Solal, Olivier Colliot, Ninon Burgos (*Correspondant*).

Many deep generative models have been proposed to reconstruct pseudo-healthy images for anomaly detection. Among these models, the variational autoencoder (VAE) has emerged as both simple and efficient. While significant progress has been made in refining the VAE within the field of computer vision, these advancements have not been extensively applied to medical imaging applications. We present a benchmark that assesses the ability of multiple VAEs to reconstruct pseudo-healthy neuroimages for anomaly detection in the context of dementia. We first propose a rigorous methodology to define the optimal architecture of the vanilla VAE and select through random searches the best hyper-parameters of the VAE variants. Relying on a simulation-based evaluation framework, we thoroughly assess the ability of 20 VAE models to reconstruct pseudo-healthy images for the detection of dementia-related anomalies in 3D brain ^{18}F -fluorodeoxyglucose (FDG) positron emission tomography (PET) and compare their performance. This benchmark demonstrated that the majority of the VAE models tested were able to reconstruct images of good quality and generate healthy looking images from simulated images presenting anomalies. Even if no model clearly outperformed all the others, the benchmark allowed identifying a few models that perform slightly better than the vanilla VAE. It further showed that many VAE-based models can generalize to the detection of anomalies of various intensities, shapes and locations in 3D brain FDG PET.

More details in [73].

8.6 Unsupervised anomaly detection using Bayesian flow networks: application to brain FDG PET in the context of Alzheimer's disease

Participants: Hugues Roy, Reuben Dorent, Ninon Burgos (*Correspondant*).

Unsupervised anomaly detection (UAD) plays a crucial role in neuroimaging for identifying deviations from healthy subject data and thus facilitating the diagnosis of neurological disorders. In this work, we focus on Bayesian flow networks (BFNs), a novel class of generative models, which have not yet been applied to medical imaging or anomaly detection. BFNs combine the strength of diffusion frameworks and Bayesian inference. We introduce AnoBFN, an extension of BFNs for UAD, designed to: i) perform conditional image generation under high levels of spatially correlated noise, and ii) preserve subject specificity by incorporating a recursive feedback from the input image throughout the generative process. We evaluate AnoBFN on the challenging task of Alzheimer’s disease-related anomaly detection in FDG PET images. Our approach outperforms other state-of-the-art methods based on VAEs (β -VAE), GANs (f-AnoGAN), and diffusion models (AnoDDPM), demonstrating its effectiveness at detecting anomalies while reducing false positive rates.

More details in [95].

8.7 Determining Clinical Disease Progression in Symptomatic Patients With CADASIL

Participants: Sofia Kaisaridi, Sophie Tezenas du Montcel (*Correspondant*).

Cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL) is the most frequent small artery brain disease caused by pathogenic variants of the NOTCH3 gene. During the disease, we still do not know how the various deficits progress and develop with each other at different stages of the disease. We aim to model disease progression and identify possible progressive subgroups and the effects of different covariates on clinical worsening.

Data were obtained from patients followed in the French CADASIL referral center, who were aged 25-80 years and had completed at least 2 visits and one of 14 clinical scores. Progression and variability were assessed using a disease course model (Leaspy). A Gaussian mixture model was used to identify different progression subgroups. Logistic regressions were used to compare the characteristics between groups.

In 395 patients along 2,007 visits, the follow-up ranged from 6 months to 19 years, with a mean of 7.5 years. They were 45% men with a mean age of 52.2 years. The evolution curves of the different scores showed that clinical manifestations develop heterogeneously and can vary considerably depending on the disease stage. We identified an early-onset, rapidly progressing subgroup of patients with earlier motor symptoms and focal neurologic deficits (median time shift 59 [Q1-Q3 48.9-66.3], median acceleration rate 0.84 [0.07-1.31]) and a late-onset slowly progressing group with earlier cognitive symptoms (median time shift 69.2 [63.4-75.1], median acceleration rate -0.18 [-0.48 to 0.14]). Male sex, lower education level, hypertension, and NOTCH3 pathogenic variant location within epidermal growth factor-like repeat (EGFr) 1-6 were found to be associated with this group difference.

Our results suggest a gradual and heterogeneous decline in different clinical and cognitive performances over the lifetime of patients with CADASIL. Two progression profiles—one rapid and early and the other, more delayed and slower—are possible after the onset of symptoms. A major limitation of our study is that the clusters were assessed post hoc, which may induce some bias. Overall, male sex, low level of education, pathogenic variant location in EGFr 1 to 6 domains, smoking, and/or arterial hypertension may affect the clinical progression of the disease.

More details in [74].

8.8 How Reliable Is the G41 Discharge Code for Status Epilepticus?

Participants: Sophie Tezenas du Montcel.

Medico-administrative databases are increasingly used to study the epidemiology of status epilepticus (SE), targeting hospitalizations with the SE G41 ICD-10 code. However, the positive predictive value (PPV) of the G41 code, which measures the percentage of true cases among those identified by the code, is unknown.

We identified all hospitalizations with a primary or secondary diagnosis coded as G41 in five different hospitals. Medical reports for each hospitalization were reviewed to classify the stays as really related to SE or not, using two distinct approaches (sensitive and specific). The clinical characteristics of SE cases were also extracted.

Among the 797 hospitalizations identified, the PPV ranged from 85.7% using the sensitive approach to 70.6% with the specific approach. Hospitalizations coded with G41 as the main diagnosis had the highest PPV, whereas codes G411 and G418 showed the lowest PPV. Of the 400 hospitalizations with a G410 (generalized convulsive SE) code, 72.7% were classified as generalized convulsive SE, while 76.5% of the 149 hospitalizations with a G412 (focal SE) code were classified as focal SE.

Our findings highlight that PPV varies by G41 subtype and diagnostic position. Studies requiring a higher PPV should exclude certain codes or hospitalizations with G41 code only as an associated diagnosis. Further studies are needed to estimate the sensitivity and specificity of G41 code.

More details in [66].

8.9 Prediction-powered Inference for Clinical Trials: application to linear covariate adjustment

Participants: Pierre-Emmanuel Poulet, Maylis Tran, Sophie Tezenas du Montcel, Stanley Durrleman.

Prediction-powered inference (PPI) [1] and its subsequent development called PPI++ [2] provide a novel approach to standard statistical estimation, leveraging machine learning systems, to enhance unlabeled data with predictions. We use this paradigm in clinical trials. The predictions are provided by disease progression models, providing prognostic scores for all the participants as a function of baseline covariates. The proposed method would empower clinical trials by providing untreated digital twins of the treated patients while remaining statistically valid. The potential implications of this new estimator of the treatment effect in a two-arm randomized clinical trial (RCT) are manifold. First, it leads to an overall reduction of the sample size required to reach the same power as a standard RCT. Secondly, it advocates for an imbalance of controls and treated patients, requiring fewer controls to achieve the same power. Finally, this technique directly transfers any disease prediction model trained on large cohorts to practical and scientifically valid use. In this paper, we demonstrate the theoretical properties of this estimator and illustrate them through simulations. We show that it is asymptotically unbiased for the Average Treatment Effect and derive an explicit formula for its variance. We then compare this estimator to a regression-based linear covariate adjustment method. An application to an Alzheimer's disease clinical trial showcases the potential to reduce the sample size.

More details in [81].

8.10 Spastic Ataxia Composite (SPAXCOM): a composite scale to evaluate the progression of subjects with spasticity and ataxia

Participants: Cécile Di Folco, Sophie Tezenas du Montcel (*Correspondant*).

Current clinical scales that track disease progression are more tailored to spasticity or ataxia, with limited sensitivity to change. Objectives The aim was to develop a sensitive and valid scale specifically geared towards optimized sensitivity to change and adapted to patients presenting with both spasticity and ataxia. Longitudinal data from 127 spastic paraplegia type 7 (SPG7) and 112 autosomal recessive spastic ataxia Charlevoix-Saguenay (ARSACS) patients were collected within the multicenter PROSPAX study. Sensitivity to change over 2 years of 30 items from the Scale for the Rating and Assessment of Ataxias (SARA), Spastic Paraplegia Rating Scale (SPRS), and the Activities of Daily Living subscale of the Friedreich's Ataxia Rating

Scale (FARS-ADL) was evaluated. Items that demonstrated the highest sensitivity to change were used to build the Spastic Ataxia Composite scale (SPAXCOM). With seven items, the SPAXCOM showed an effect size of 0.71, higher than reference scales (SARA: 0.43, SPRS: 0.42, FARS-ADL: 0.27). The SPAXCOM had a similar sensitivity to change for both genotypes and was more sensitive in participants with a SARA lower than 10 and within the intermediate disease stage (FARS-Disease Staging: 2-3.5). The SPAXCOM showed a high correlation with disease duration ($r = 0.67$ [0.60; 0.72]) and disease stage ($r = 0.86$ [0.83; 0.89]). Perception of improvement, stagnation, and worsening were associated with a mean yearly SPAXCOM change of 0.44 (-0.14; 1.01), 0.61 (0.19; 1.03), and 1.22 (0.96; 1.49), respectively. The SPAXCOM is more sensitive to change and homogeneous across genotypes than the reference scales, allowing a reduction of the required sample size in future clinical trials.

More details in [69].

8.11 Predictive models for ataxia progression and conversion in spinocerebellar ataxia type 1 and 3

Participants: Sophie Tezenas du Montcel.

The READISCA study aims to prepare for clinical trials in SCA1 and SCA3. Hence, we searched for predictive variables of ataxia onset (phenoconversion) and progression. Individuals with SCA1 or SCA3 and controls were enrolled from 2018-2021 in US and Europe. Clinical scores, MRI measures and NfL levels were assessed annually for 5 years. In the pre-ataxic group at baseline, we compared phenoconverters with non-converters. A Bayesian mixed model was used to model the longitudinal progression of clinical scores and NfL levels. The impact of data-driven selected baseline variables (demographic, clinical, MRI) on the expected SARA progression was tested. Forty-three controls, 55 SCA1 and 124 SCA3 carriers were included; a subset of the cohort ($n=109$) had MRI data. Converters from pre-ataxic to ataxic stages represented 5/22 (22%) and 12/38 (32%) for SCA1 and SCA3. Converters were more depressed (PHQ9: 3.9 ± 2.9 vs 2.3 ± 2.6 $p = 0.04$), had higher plasma NfL levels (17.6 ± 5.7 pg.mL⁻¹ vs 11.1 ± 5.9 , $p < 0.0001$), more cerebellar white matter atrophy ($1.44 \pm 0.12\%$ of total intracranial volume vs 1.54 ± 0.16 , $p = 0.032$) and more INAS signs (1.8 ± 1.3 vs 0.7 ± 0.8 , $p = 0.002$). All clinical scores except CCAS significantly worsened during the study. NfL levels significantly increased in non-converters and ataxic SCA3 (1.06 ± 0.33 pg.mL⁻¹/year, $p = 0.002$ and 0.57 ± 0.21 , $p = 0.01$) but not in controls and ataxic SCA1 (0.31 ± 0.26 , $p = 0.24$ and 0.26 ± 0.42 , $p = 0.55$). In the best predictive model of SARA progression after 1 year ($R^2 = 0.54$), factors linked with faster progression were higher functional stage ($p < 0.001$), higher CCFS score ($p = 0.002$), and higher total creatine in cerebellar white matter ($p = 0.026$). Factors significantly linked to conversion, namely NfL levels, depression, and lower motor neuron involvement, differ from those driving disease progression. NfL levels and lower motoneuron signs could be used as predictors of phenoconversion and MRI variables as ataxia progression predictors. Psychological care should be provided in the pre-ataxic phase of the disease.

More details in [79].

8.12 Scalable, trustworthy generative model for virtual multi-staining from H&E whole slide images

Participants: Mehdi Ounissi, Ilias Sarbout, Daniel Racoceanu.

Chemical staining methods, while reliable, are time consuming and can be resource-intensive, involving costly chemical reagents and raising environmental concerns. This underscores the compelling need for alternative solutions such as virtual staining, which not only accelerates the diagnostic process but also enhances the flexibility of stain applications without the associated physical and chemical costs. Generative artificial intelligence technologies prove to be immensely useful in addressing these challenges. However, in healthcare, particularly within computational pathology, the high-stakes nature of decisions complicates the

adoption of these tools due to their often opaque processes. Our work introduces an innovative approach that harnesses generative models for virtual stain transformations, improving performance, trustworthiness, scalability, and adaptability within computational pathology. The core of the proposed methodology involves a singular Hematoxylin and Eosin (H&E) encoder that supports multiple stain decoders. This design prioritizes critical regions in the latent space of H&E tissues, leading to a richer representation that enables precise synthetic stain generation by the decoders. Tested to simultaneously generate eight different stains from a single H&E slide, our method also offers significant scalability benefits for routine use by loading only necessary model components during production. We integrate label-free knowledge during training, using loss functions and regularization to minimize artifacts, thereby enhancing the accuracy of virtual staining in both paired and unpaired settings. To build trust in these synthetic stains, we employ a real-time self-inspection methodology using trained discriminators for each stain type, providing pathologists with confidence heatmaps to aid in their evaluations. In addition, we perform automatic quality checks on new H&E slides to ensure that they conform to the trained H&E distribution, guaranteeing the generation of high-quality synthetic stained slides. Recognizing the challenges pathologists face in adopting new technologies, we have encapsulated our method in an open-source, cloud-based proof-of-concept system. This system enables users to easily and virtually stain their H&E slides through a browser, eliminating the need for specialized technical knowledge and addressing common hardware and software challenges. It also facilitates real-time user feedback integration. Lastly, we have curated a novel dataset comprising eight different paired H&E/stains related to pediatric Crohn's disease at diagnosis, providing 30 whole slide images (WSIs) for each stain set (total of 480 WSIs) to stimulate further research in computational pathology.

More details in [78].

NB: two international patents (WO2025168731A1 (paired images) and WO2025168729A1 (unpaired images)) have been submitted concerning this methodology (Priority 2024-02-09, Filed 2025-02-06, Published 2025-08-14).

8.13 ADNP-15: An Open-Source Histopathological Dataset for Neuritic Plaque Segmentation in Human Brain Whole Slide Images with Frequency Domain Image Enhancement for Stain Normalization

Participants: Daniel Racoceanu, Gabriel Jimenez, Guanghui Fu.

Alzheimer's Disease (AD) is a neurodegenerative disorder characterized by amyloid- β plaques and tau neurofibrillary tangles, which serve as key histopathological features. The identification and segmentation of these lesions are crucial for understanding AD progression but remain challenging due to the lack of large-scale annotated datasets and the impact of staining variations on automated image analysis. Deep learning has emerged as a powerful tool for pathology image segmentation; however, model performance is significantly influenced by variations in staining characteristics, necessitating effective stain normalization and enhancement techniques. In this study, we address these challenges by introducing an open-source dataset (ADNP-15) of neuritic plaques (i.e., amyloid deposits combined with a crown of dystrophic tau-positive neurites) in human brain whole slide images. We establish a comprehensive benchmark by evaluating five widely adopted deep learning models across four stain normalization techniques, providing deeper insights into their influence on neuritic plaque segmentation. Additionally, we propose a novel image enhancement method that improves segmentation accuracy, particularly in complex tissue structures, by enhancing structural details and mitigating staining inconsistencies. Our experimental results demonstrate that this enhancement strategy significantly boosts model generalization and segmentation accuracy. All datasets and code are open-source, ensuring transparency and reproducibility while enabling further advancements in the field.

More details in [88].

NB: an open-source dataset (ADNP-15) is associated to this publication.

8.14 Unravelling the topographical organization of brain lesions in variants of Alzheimer's disease progression

Participants: Gabriel Jimenez, Daniel Racoceanu.

In this study, we propose and evaluate a graph-based framework to assess variations in Alzheimer’s disease (AD) neuropathologies, focusing on classic (cAD) and rapid (rpAD) progression forms. Histopathological images are converted into tau-pathology-based (i.e., amyloid plaques and tau tangles) graphs, and derived metrics are used in a machine-learning classifier. This classifier incorporates SHAP value explainability to differentiate between cAD and rpAD. Furthermore, we test graph neural networks to extract topological embeddings from the graphs and use them in classifying the progression forms of AD. The analysis demonstrates denser networks in rpAD and a distinctive impact on brain cortical layers: rpAD predominantly affects middle layers, whereas cAD influences both superficial and deep layers of the same cortical regions. These results suggest a unique neuropathological network organization for each AD variant.

More details in [93].

8.15 Prediction of biochemical prostate cancer recurrence from any Gleason score using robust tissue structure and clinically available information

Participants: Laura Marin, Daniel Racoceanu, Fanny Casado.

Biopsy information and protein Prostate-Specific Antigen (PSA) levels are the most robust information available to oncologists worldwide to diagnose and decide therapies for prostate cancer patients. However, prostate cancer presents a high risk of recurrence, and the technologies used to evaluate it demand more complex resources. This paper aims to predict Biochemical Recurrence (BCR) based on Whole Slide Images (WSI) of biopsies, Gleason scores, and PSA levels. A U-net model was used to segment phenotypic features and trained on images from the Prostate Cancer Grade Assessment (PANDA) database to segment tumorous regions from pre-processed and scored WSI of biopsies. Then, the model was tested on data from publicly available repositories achieving an Intersection over Union of 87%. Tissue features, Gleason scores, and PSA levels provided high accuracy and precision in classifying patients according to their risk of presenting recurrence, for any Gleason score sampled. The trained classifier model demonstrated a 79.2% relative accuracy, and a precision of 69.7% for patients experiencing recurrences before 24 months. Our results provide a robust, cost-efficient approach using already available information to predict the risk of BCR.

More details in [76].

8.16 Artificial Intelligence-Based Detection of Central Retinal Artery Occlusion Within 4.5 Hours on Standard Fundus Photographs

Participants: Ayse Gungor, Ilias Sarbout, Daniel Racoceanu, Dan Milea.

Prompt diagnosis of acute central retinal artery occlusion (CRAO) is crucial for therapeutic management and stroke prevention. However, most stroke centers lack onsite ophthalmic expertise before considering fibrinolytic treatment. This study aimed to develop, train, and test a deep learning system to detect hyperacute CRAO on retinal fundus photographs within the critical 4.5-hour treatment window and up to 24 hours after visual loss to aid in secondary stroke prevention. Our retrospective, cross-sectional study included 1322 color fundus photographs from 771 patients with acute visual loss due to CRAO, central retinal vein occlusion, nonarteritic anterior ischemic optic neuropathy, and healthy controls. Photographs were collected from 9 expert neuro-ophthalmology centers in 6 countries, including 3 randomized clinical trials. Training included 1039 photographs (517 patients), followed by testing on 2 data sets: (1) hyperacute CRAO (54 photographs, 54 patients) and (2) CRAO within 24 hours after visual loss (110 photographs, 109 patients). The deep learning system achieved an area under the receiver operating characteristic curve of 0.96 (95% confidence

interval (CI), 0.95-0.98), a sensitivity of 92.6% (95% CI, 87.0-98.0), and a specificity of 85.0% (95% CI, 81.8-92.8) for detecting CRAO at hyperacute stage, with similar results within 24 hours. The deep learning system outperformed stroke neurologists on a subset of hyperacute testing data set (120 photographs, 120 patients). A deep learning system can accurately detect hyperacute CRAO on retinal photographs within a time window compatible with urgent fibrinolysis. If further validated, such systems could improve patient selection for fibrinolytic trials and optimize secondary stroke prevention. Registration URL: [NCT06390579](#).

More details in [72]

8.17 Visual Prostheses in the Era of Artificial Intelligence Technology

Participants: Ilias Sarbout, Ayse Gungor, Mehdi Ounissi, Daniel Racoceanu, Dan Milea.

Over the past few decades, technological advancements have transformed invasive visual prostheses from theoretical concepts into real-world applications. However, functional outcomes remain limited, especially in visual acuity. This review aims to summarize current developments in retinal and cortical prostheses (RCPs) and critically assess the role of artificial intelligence (AI) in advancing these systems. To describe current RCPs and provide a systematic review on image and signal processing algorithms designed for improved clinical outcomes. **Patients and Methods:** We performed a systematic review of the literature related to AI subserving prosthetic vision, using mainly PubMed, but also, Elicit, a dedicated AI-based reference research assistant. A total of 455 studies were screened on PubMed, of which 23 were retained for inclusion. An additional 5 studies were identified and included through Elicit. The analysis of current RCPs highlights various limitations affecting the quality of the visual flow provided by current artificial vision. Indeed, the 28 reviewed studies on AI covered two applications for RCPs including extraction of saliency in camera captured images, and consistency between electrical stimulation and perceived phosphenes. A total of 14 out of 28 studies involved the use of artificial neural networks, of which 12 included model training. Evaluation with data from a visual prosthesis was conducted in 7 studies, including 1 that was prospectively assessed with a human RCP. Validation with empirical data from human or animal data was performed in 22 out of 28 studies. Out of these, 15 were validated using simulated prosthetic vision. Finally, out of 22 studies leveraging a mathematical model for phosphenes perception, 14 used a symmetrical oversimplified modeling. AI algorithms show promise in optimizing prosthetic vision, particularly through enhanced image saliency extraction and stimulation strategies. However, most current studies are based on simulations. Further development and validation in real-world settings, especially through clinical testing with blind patients, are essential to assess their true effectiveness.

More details in [83]

9 Bilateral contracts and grants with industry

VICO

Participants: Sophie Tezenas du Montcel (*Correspondant*).

Description: VO659 Strategic Advisory Board.

Coordinator: Sophie Tezenas Du Montcel

Date: Started in 2023

10 Partnerships and cooperations

10.1 International initiatives

10.1.1 Inria associate team not involved in an IIL or an international program

Brainetics

Title: Multi-modal analyses of brain magnetic resonance images and genetics for neurodegenerative and psychiatric disorders

Duration: 2023 – 2025

Coordinator: N. Wray

Partners: University of Queensland Brisbane (Australia)

Inria contacts: Olivier Colliot, Baptiste Couvy-Duchesne

Description: The general objective of the associate team is to develop multi-modal methods and analyses, that combine genetics and neuroimaging data. Each member of the associate team is specialised in a data modality (genetics for PCTG, neuroimaging for ARAMIS) and both teams have a strong track record in method and software development.

10.2 European initiatives

10.2.1 Horizon Europe

CLARA

Participants: Olivier Colliot, Ninon Burgos, Charlotte Nijhoff, Charlotte Godard, Adam Ismaili.

Title: CLARA: Centre for Artificial Intelligence and Quantum Computing in System Brain Research

Partner Institution(s):

- International Neurodegenerative Disorders Research Centre, Czechia
- VSB-Technical University of Ostrava, Czechia
- Czech Technical University in Prague, Czechia
- International Clinical Research Centre - St. Anne's University Hospital, Czechia
- Paris Brain Institute, France
- Bayerische Akademie der Wissenschaften - Leibniz-Rechenzentrum (Leibniz Supercomputing Centre), Germany

Duration: 2024–2030

Description: CLARA, the Centre for Artificial Intelligence and Quantum Computing in System Brain Research, is an interdisciplinary centre of excellence focused on next-generation artificial intelligence/machine learning applications and quantum-centric supercomputing tools to advance neurodegeneration research, particularly Alzheimer's disease. Building a domain-specific hybrid computing and data infrastructure platform based on emerging EuroHPC Joint Undertaking computing resources, CLARA will significantly contribute to development of the European computing and data ecosystem in system brain research. CLARA will be established as an autonomous division of the International Neurodegenerative Disorders Research Centre in Prague, Czech Republic, with prominent European partners including Paris Brain Institute (France) and Leibniz Supercomputing Centre (Germany).

10.2.2 Other European programs/initiatives

JPND project Lemerend

Participants: Stanley Durrleman (*Correspondant*), Baptiste Couvy-Duchesne, Thomas Nedelec.

Project acronym: Lemerend

Project title: Leveraging medical records to identify patients at risk of neurodegenerative disease

Duration: 2022–2025

Amount: 260k€

Coordinator: Stanley Durrleman

Other partners: Aix-Marseille université, Karolinska Institute, University of Queensland

Description: Neurodegenerative diseases represent a major public health challenge requiring prevention policies, with key needs being identification of at-risk patients long before disease onset. LeMeReND uses electronic health records from millions of patients followed for at least 10 years before diagnosis across 4 healthcare systems (Australia, France, UK, Sweden) and 4 diseases (Alzheimer's, Parkinson's, dementia with Lewy bodies, motor neuron diseases) to identify biomedical risk factors and stratify patients based on risk factor progression profiles. The project will design screening tools giving propensity scores for developing neurodegenerative diseases, whilst identified prodromal factors will be studied using UK BioBank and GWAS data to advance understanding of genetic and imaging markers. LeMeReND will provide invaluable insights for health policies, therapeutic targets, and unique screening tools for large-scale patient recruitment in secondary prevention trials.

EJP-RD project CADANHIS

Participants: Sophie Tezenas du Montcel, Lea Aguilhon, Benjamin Glemain.

Project acronym: CADANHIS

Project title: CADASIL-Natural HIStory

Duration: 2024–2026

Amount: 2058k€

Coordinator: H. Chabriat (ASSISTANCE PUBLIQUE - HOPITAUX DE PARIS)

Other partners: Fundació Institut de Recerca de l'Hospital de la Santa Creu i Sant Pau, Karolinska Institutet, LMU University Hospital, Klinikum der Universität München

Description: CADASIL is a rare hereditary small vessel disease leading to stroke and progressive motor and cognitive decline with no therapy to prevent progression. CADANHIS aims to understand current management practices across European countries, make a quantum leap in predicting individual disease progression through natural history modelling, develop patient reported outcomes, and determine relevant imaging or clinical outcomes for future trials. The project will identify circulating biomarkers associated with white-matter lesions at earliest disease stages and sensitive blood or CSF biomarkers for monitoring vascular disease progression and measuring therapeutic efficacy. The consortium assembles patients, families, clinicians and researchers from five European countries with data from cohorts totalling over 1000 patients.

10.3 National initiatives

10.3.1 IHU

General program

Participants: Olivier Colliot, Stanley Durrleman, Didier Dormont, Ninon Burgos, Sophie Tezenas du Montcel, Baptiste Couvy-Duchesne, Daniel Racoceanu.

Project acronym: IHU-A-ICM

Project title: Institute of Translational Neuroscience

Duration: Since 2011

Description: The IHU-A-ICM programme was selected, in 2011, in a highly competitive national call for projects. A 10-year, 55M€ program, has been implemented by a recently created foundation for scientific cooperation. Based on the clinical and scientific strengths of the ICM and the hospital Department of Nervous System Diseases, it mainly supports neuroscience research, but is also invested in improving care and teaching.

10.3.2 3IA Institutes & IA-Clusters

PRAIRIE

Participants: Ninon Burgos, Olivier Colliot, Stanley Durrleman.

Project acronym: PRAIRIE

Project title: Paris Artificial Intelligence Research Institute

Duration: Since 2019

Director: Isabelle Ryl

Website: [PRAIRIE](#)

Description: PRAIRIE is one of the four selected French Institutes of AI. It was selected within a call for creation of interdisciplinary AI research institutes (or “3IAs” for “Instituts Interdisciplinaires d’Intelligence Artificielle”), as part of the national French initiative on Artificial Intelligence (AI). PRAIRIE aspires to become within five years a world leader in AI research and higher education, with an undeniable impact on economy and technology at the French, European and global levels. ARAMIS team members N. Burgos, O. Colliot and S. Durrleman hold a chair at PRAIRIE.

PRAIRIE-PSAI

Participants: Ninon Burgos, Olivier Colliot, Stanley Durrleman.

Project acronym: PRAIRIE-PSAI

Project title: Paris Artificial Intelligence Research Institute - School of AI

Duration: Since 2024

Director: Isabelle Ryl

Website: PRAIRIE

Description: Four years after its creation, the 3IA Institute PR[AI]RIE has become PR[AI]RIE - Paris School of AI (PR[AI]RIE-PSAI), expanding its scope to unite all interdisciplinary research and training initiatives of its partners, based on three fundamental pillars: education, research, and innovation. It was selected within the “AI Cluster: World-Class Research and Training Hubs in Artificial Intelligence” call, as part of the national French initiative on Artificial Intelligence (AI). ARAMIS team members N. Burgos, O. Colliot and S. Durrleman hold a chair/fellowship at PRAIRIE-PSAI.

10.3.3 ANR

ANR JCJC ANO-NEURO

Participants: Ninon Burgos (*Correspondant*), Matthieu Joulot, Alice Joubert.

Project acronym: ANO-NEURO

Project title: Anomaly Detection in Multimodal Neuroimaging for the Computer-aided Diagnosis of Dementia

Duration: 2024–2027

Amount: 272k€

Coordinator: Ninon Burgos

Description: This project develops innovative computational imaging tools to improve differential diagnosis and prognosis in neurological disorders by modelling brain abnormalities as deviations from normal variability using multimodal brain imaging. Deep generative models will generate pseudo-healthy images from patients’ images across different modalities (MRI, PET), with comparisons producing individual abnormality maps that highlight pathological changes to assist clinicians. These maps will be evaluated both as features for classification algorithms and through clinical assessment in collaboration with clinical partners from the Paris Brain Institute. All methodological developments will be integrated into the open-source platforms Clinica and ClinicaDL to facilitate transfer of advanced image analysis and deep learning tools to clinical research.

10.3.4 PEPR

PEPR Santé Numérique – Project REWIND

Participants: Stanley Durrleman (*Correspondant*), Sophie Tezenas du Montcel, Caglayan Tuna, Sebastian Mendez Pineda, Gabrielle Casimiro.

Project acronym: REWIND

Project title: Médecine de précision avec données longitudinales

Duration: 2023–2028

Coordinator: Stéphanie Allasonnière

Other partners: Université de Paris Cité, Université Grenoble-Alpes, Université Claude Bernard Lyon 1, Sorbonne Université, CNRS, INRIA, INSERM, CHU Pitie-Salpêtrière, Hospices Civils de Lyon

Description: This project develops new mathematical and statistical approaches for analysing multimodal multiscale longitudinal data to improve understanding of chronic disease progression and enable earlier diagnosis, precise prognosis, and treatment prediction. The work integrates time-to-event prediction models, spatio-temporal models with AI tools, Bayesian frameworks incorporating expert knowledge, and interpretable deep-learning architectures combining data-driven and model-based approaches. The resulting models will be implemented in an easy-to-use platform for researchers and physicians, contributing to precision medicine and next-generation clinical decision support systems.

10.3.5 RHU

RHU – Project Secret Gift

Participants: Sophie Tezenas du Montcel (*Correspondant*), Maylis Tran.

Project acronym: Secret Gift

Project title: Platelet repair system-based biotherapy of Amyotrophic Lateral Sclerosis combining theraagnostic biomarkers

Duration: 2024–2029

Amount: 8.3m€

Coordinator: David Devos

Other partners: Université de Lille, InVenis Biothérapies, INSERM Nord-Ouest, CHU Lille, EFS AuRA, INSERM Occitanie, Institut du Cerveau (ICM), CHU Montpellier

Description: Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disease with progressive muscle paralysis and median survival of 3 years, requiring more potent therapeutic strategies beyond current treatments that show only modest effects. The team has developed and patented HPPL (human platelet pellet lysate), a unique clinical-grade platelet lysate containing multiple neurotrophic factors, neurotransmitters, and anti-inflammatory proteins that has shown neuroprotective effects in various animal models of CNS diseases including ALS. HPPL overcomes challenges of previous platelet preparations by eliminating protein loading, fibrinogen toxicity, and neuroinflammation issues while maintaining significant neuroprotection. Continuous intracerebroventricular administration will ensure full CNS biodistribution over time, addressing the limitations of engineered stem cell therapies that are restricted to single transplantation sites. The SECRET-GIFT project aims to demonstrate the feasibility, safety, and initial efficacy of HPPL biotherapy with continuous i.c.v. administration in early-stage ALS patients.

10.3.6 Other national programs

Inserm MESSIDORE – GALAN

Participants: Olivier Colliot (*Correspondant*), Ninon Burgos, Manon Heffernan.

Project acronym: GALAN

Project title: Artificial intelligence-based tools to harness the full potential of clinical data warehouses in neuroimaging

Duration: 2024–2028

Amount: 1m€

Coordinator: Olivier Colliot

Other partners: Neuroradiology Department, Hôpital Pitié-Salpêtrière, AP-HP; Neuroradiology Department, Lille University Hospital; Inserm U1172 (Lille)

Abstract: The general objective of this project is to develop a comprehensive set of AI-based tools to harness the full potential of neuroimaging data in clinical data warehouses, to make these tools available to other researchers and clinicians and to demonstrate that they can be used to develop trustworthy and unbiased AI-assisted reading systems for neuroradiology. This is a joint project between teams from Paris and Lille and involves two clinical data warehouses (AP-HP in Paris, INCLUDE in Lille).

France 2030 – MEDITWIN – Use Case Alzheimer

Participants: Ninon Burgos (*Correspondant*), Hugues Roy, Alice Joubert.

Project acronym: MEDITWIN

MEDITWIN partners: Dassault Systèmes, Inria, IHUs (Institut Imagine, LIRYC, ICAN, FOrReSIGHT, IHU Strasbourg, PRISM), CHU Nantes, start-ups

Project title: Task ‘Detection of anomalies for the analysis of individual brain images’ within the WP ‘Early diagnosis of Alzheimer’s and vascular dementia’

Duration: 2024–2029

Amount for the task: ~500k€

Task coordinator: Ninon Burgos

Task objectives: The objectives of the task are to develop innovative image processing tools to model anomalies, defined as deviations from normal variability, from brain images. To this end, deep generative models will be used to generate pseudo-healthy images from real patient images. Comparison of pseudo-sound and real images will provide individual maps of abnormalities. The abnormality maps obtained will be made available to clinicians to help them locate pathological areas and quantify their degree of abnormality.

MIC 2025 programme - Interdisciplinary approaches in oncogenic processes and therapeutic perspectives: Contributions of mathematics and informatics to oncology

Participants: Daniel Racoceanu (*Correspondant*).

Project acronym: SIMAI

Project title: Synergising Mechanistic and AI Approaches for Modelling the Impact of Microenvironment Heterogeneity on Immunotherapy efficacy

Duration: 2025–2029

Budget: 528k€

Coordinator: Ovidiu Radulescu

Other partners: University of Montpellier (LPHI - UMR CNRS 5235, LIRMM - UMR CNRS 5506), the Montpellier Cancer Research Institute (IRCM, Inserm U1194) and Paris Brain Institute (CNRS UMR 7225, Inserm U 1127).

Description: SIMAI addresses the challenge that immune checkpoint inhibitors (ICIs) remain effective in only 30–40% of advanced melanoma patients, with tumour-associated tertiary lymphoid structures (TLS) playing a crucial role in modulating ICI response. Building on findings that metabolic changes enhance melanoma immunogenicity and ICI outcomes, the project aims to understand how metabolic zonation within the tumour microenvironment affects TLS function and immunotherapy success. SIMAI integrates mathematical modelling and artificial intelligence to investigate this relationship, combining 3D reconstructions with mechanistic modelling, spatial transcriptomics and proteomics, and high-dimensional partial differential equation models to simulate cell population dynamics. The project seeks to improve predictive accuracy and develop strategies to enhance immunotherapy efficacy.

11 Dissemination

11.1 Promoting scientific activities

11.1.1 Scientific events: selection

Chair of conference program committees

- Olivier Colliot was Conference Chair of the [SPIE Medical Imaging: Image Processing conference 2025](#).

Member of the conference program committees

- Olivier Colliot was Programme Committee member SPIE Medical Imaging: Image Processing conference 2025.
- Ninon Burgos was Programme Committee member of the SPIE Medical Imaging: Image Processing conference 2025.

Reviewer

- Ninon Burgos acted as a reviewer for the international conferences Neural Information Processing Systems (NeurIPS), International Conference on Learning Representations (ICLR), Medical Image Computing and Computer-Assisted Intervention (MICCAI), Image Processing in Medical Imaging (IPMI), SPIE Medical Imaging: Image Processing, Organisation for Human Brain Mapping (OHBM), the international workshops on Simulation and Synthesis in Medical Imaging (SASHIMI) and Deep Generative Models (DGM4MICCAI), and the national conferences Intelligence Artificielle en Imagerie Biomédicale (IABM) and Groupe de Recherche et d'Etudes de Traitement du Signal et des Images (GRETSI).
- Olivier Colliot acted as a reviewer for the international conference Medical Image Computing and Computer-Assisted Intervention (MICCAI) and the national conference Intelligence Artificielle en Imagerie Biomédicale (IABM).

11.1.2 Journal

Member of the editorial boards

- Olivier Colliot is an Associate Editor of the journal Medical Image Analysis, a Senior Area Editor and an Associate Editor of the journal IEEE Transactions on Medical Imaging, and an Associate Editor of the journal SPIE Journal of Medical Imaging.
- Ninon Burgos is an Associate Editor of the journal Pattern Recognition.

Reviewer - reviewing activities

- Ninon Burgos acted as a reviewer for Medical Image Analysis, IEEE Transactions on Medical Imaging, Machine Learning for Biomedical Imaging (MELBA), Computer Methods and Programs in Biomedicine, and IEEE Journal of Biomedical and Health Informatics.
- Sophie Tezenas Du Montcel acted as a reviewer for Human Genetics, Journal of NeuroEngineering and Rehabilitation, Annals of Neurology, Movement Disorders, eClinicalMedicine, Annals of Clinical and Translational Neurology, IEEE Journal of Biomedical and Health Informatics, The Cerebellum, Plos One, Brain, BMC Medical Genetics, Journal of Neurology, Neurosurgery and Psychiatry, Journal of Huntington's Disease, and Therapeutic advances in Rare Disease.
- Daniel Racoceanu acted as a reviewer for Medical Image Analysis and Nature Scientific Reports.

11.1.3 Invited talks

- Olivier Colliot was invited to give a talk at the Annual French Conference on Artificial Intelligence for Biomedical Imaging (IABM), Nice, France, 2025.
- Olivier Colliot was invited to give a talk at the Indo-French Dialogue on AI in Healthcare, Paris, France, 2025.
- Olivier Colliot was invited to give a talk at MICCAI webinar series, online, 2025.
- Ninon Burgos was invited to give a talk at the AI4Health Summer School (Paris, France).
- Ninon Burgos was invited to give a talk at the Deep Learning for Medical Imaging School (Lyon, France).
- Ninon Burgos was invited to give a talk at the Journée des ingénieurs du Programme National de Recherche en Intelligence Artificielle (Paris, France).
- Ninon Burgos was invited to give a talk at the Journées scientifiques Inria handicap et numérique (Paris, France).
- Ninon Burgos was invited to give a talk at Radiologie Aujourd'hui et Demain (Angers, France).
- Ninon Burgos was invited to give a talk at the Symposium Citadel Franco-Québécois (Montreal, Canada).
- Ninon Burgos was invited to give seminars in the context of the CONNExIN (Comprehensive Neuroimaging aNalysis Experience In resource constraiNed settings) programme (online), COMPASS (COncnecting Minds to Progress AI in Medicine Seminar Series) (online) and the McConnell Brain Imaging Centre seminar (Montreal, Canada).
- Sophie Tezenas Du Montcel was invited to give a talk at the meeting Human trajectories: models and applications (Paris, France).
- Daniel Racoceanu was invited speaker at the Journées Ouvertes en Biologie, Informatique et Mathématiques (JOBIM), Bordeaux, France.
- Daniel Racoceanu was invited spaker at the Computer Vision for Drug Discovery (CVDD) workshop, IEEE/CVF Conference on Computer Vision and Pattern Recognition (CVPR), Nashville, TN, USA.

11.1.4 Leadership within the scientific community

- Olivier Colliot is founding member of the board of IABM (The French Society for Artificial Intelligence in Biomedical Imaging) (since 2025).
- Olivier Colliot is a member of the board and the treasurer of the MICCAI Special Interest Group on Challenges in AI (since 2024).
- Daniel Racoceanu is a member of the Advisory Board of the European Society of Integrative Digital Pathology (ESDIP).
- Sophie Tezenas Du Montcel is a member of the Critical Path to Therapeutics for the Ataxias.

11.1.5 Scientific expertise

- Ninon Burgos reviewed grant applications for the Fonds de recherche du Québec, MIAI Cluster Chair, KU Leuven Industrial Research Fund Council and ANR PRCI.
- Ninon Burgos was a member of the committee for the Inserm/IReSP MESSIDORE Programme (2025).
- Ninon Burgos was a member of the jury for the Health Data Hub Data Challenges en Santé.
- Ninon Burgos is a member of the Scientific and Ethical Committee of the Paris university hospital trust's clinical data warehouse (EDS AP-HP) (2024–).
- Ninon Burgos was a member of the jury for the recruitment of PR[AI]RIE-PSAI Fellows in Artificial Intelligence.
- Daniel Racoceanu is elected member of the Inria Evaluation Committee (Inria CE) for the quadriennial mandate 2023–2027.
- Daniel Racoceanu was a member of the Scientific Evaluation Committee “Interfaces: mathematics, digital sciences - biology, health” (CE45) of the French National Research Agency ANR (2025).
- Daniel Racoceanu participated, as reviewer to the recruitment jury for the Junior Professorship (CPJ) position at MINES Paris - PSL.
- Daniel Racoceanu participated, as reviewer to the recruitment jury for the Junior Professorship (CPJ) position at the University of Montpellier.
- Daniel Racoceanu participated, as reviewer to the recruitment jury for the Full Professor position at the Sorbonne University.
- Daniel Racoceanu participated, as reviewer to the recruitment jury for the Full Professor position at Polytech Sorbonne engineering school.
- Sophie Tezenas Du Montcel is member of the Ataxia Advisory Committee for Therapeutics (ACT of Ataxia Global Initiative).
- Sophie Tezenas Du Montcel is a member of the scientific board of the National Bank for Rare Diseases (Banque Nationale de Données Maladies Rares, BNDMR).
- Sophie Tezenas Du Montcel is a member of scientific board of the CERMOI study.

11.1.6 Research administration

- Olivier Colliot is Deputy Scientific Director of the ICM (since 2025).
- Olivier Colliot is Inaugural Director of the Centre for Artificial Intelligence and Data Science of the ICM (since 2025).
- Olivier Colliot is a member of the Executive Committee (CODIR) of the ICM (since 2025).
- Olivier Colliot is a member of the “Bureau du Comité des Projets” of the Inria Paris Centre.

11.1.7 Research committees

- Sophie Tezenas Du Montcel is a member of the bureau of the Conseil national des universités 4604.
- Ninon Burgos is the scientific secretary of the Institute Scientific Board of CNRS Informatics.

11.2 Teaching - Supervision - Juries - Educational and pedagogical outreach

11.2.1 Teaching

University teaching

- Master: Olivier Colliot coordinates the course “Deep Learning for Medical Imaging” of the Master 2 MVA (Mathematics, Vision, Learning) of ENS Paris-Saclay, University of Paris, Centrale-Supelec and teaches 15 hours (CM).
- Master: Olivier Colliot coordinates the course “Artificial Intelligence” of the Master 2 Bioentrepreneur of Paris-Descartes University and teaches 20 hours (CM).
- Engineering school: Olivier Colliot, 5 hours (eqTD), Mines ParisTech
- DU: Ninon Burgos gives lectures (1h) on deep learning for medical imaging as part of the DU IA appliquée en santé (Paris Cité and Université de Lille).
- Master: Daniel Racoceanu coordinates the teaching module (UE) “Introduction to Artificial Intelligence” of the Master 1 : Control Sciences and Robotics (AR - Automatique, Robotique) and Electronics, Electrical Energy, Control Sciences (E3A - Électronique, Énergie Électrique, Automatique) at Sorbonne University, Faculty of Science and Engineering (110 students / 3 ECTS) and teaches 30 hours (CM/courses and TP/labs) - courses in English.
- Master: Daniel Racoceanu coordinates the teaching module (UE) “Computer Vision for Biomedical” of the Master 1 : Electronics, Electrical Energy, Control Sciences (E3A - Électronique, Énergie Électrique, Automatique) at Sorbonne University, Faculty of Science and Engineering (30 students / 3 ECTS) and teaches 32 hours (CM/courses and TP/labs).
- Master: Daniel Racoceanu coordinates the teaching module (UE) “Image Processing” of the Master 1 : Control Sciences and Robotics (AR - Automatique, Robotique) at Sorbonne University, Faculty of Science and Engineering (110 students / 3 ECTS) and teaches 36 hours (CM/courses and TP/labs) - courses in English.
- Master: Daniel Racoceanu coordinates the teaching module (UE) “3D Computer Graphics” of the Master 1 : Computer Sciences (Informatique) at Sorbonne University, Faculty of Science and Engineering (22 students / 3 ECTS) and teaches 24 hours (CM/courses and TP/labs) - courses in English (within the european programme EIT Health) - courses in English.
- Master: Daniel Racoceanu gives labs (22 hours - TP/labs) in “Machine Learning” - Master 1 : Control Science and Robotics (AR - Automatique, Robotique) at Sorbonne University, Faculty of Science and Engineering (50 students).
- Master: Daniel Racoceanu gives labs/seminars (12 hours - TP/labs and 12 hours - TD/seminars) in “Information Theory” - Master 1 : Control Science and Robotics (AR - Automatique, Robotique) at Sorbonne University, Faculty of Science and Engineering (50 students).
- Master: Daniel Racoceanu gives courses and labs (4 hours of course and 4 hours of TP/labs) in “Visual Perception for Robotics” - Master 2 : Control Science and Robotics (AR - Automatique, Robotique) at Sorbonne University, Faculty of Science and Engineering (22 students).
- Master: Sophie Tezenas du Montcel coordinates the Master 1 of Public Health of Sorbonne University.
- Master: Sophie Tezenas du Montcel coordinates the course of Biostatistics of the Master 1 of Health of Sorbonne University and teaches 20 hours (CM).

- Master: Sophie Tezenas du Montcel coordinates the course of “Bases de données médico-administratives: aspects épidémiologiques” of the Master 2 of Public Health of Sorbonne University and teaches 9 hours (CM).
- Medical school: Sophie Tezenas du Montcel gives Biostatistics courses for Medical students (First year, 32 hours TD).

Summer/winter schools, courses at conferences

- Ninon Burgos was invited to give lectures on deep learning for medical imaging as part of the CENIR courses at the Paris Brain Institute, Deep Learning for Medical Imaging spring school (Lyon), and the AI4Health summer school (Paris).
- Daniel Racoceanu was invited to give a teaching lesson about explainable and interpretable artificial intelligence in front of master students from Mines, Dauphine, ENS and ESPCI, at Paris Sciences et Lettres (PSL), Paris, France.

Educational material ARAMIS has developed several comprehensive tutorials to support the research community and facilitate the adoption of our methodological and software contributions. These materials have been prepared for thematic schools, workshops, and to assist users of our software tools. We delivered a practical session on code and data versioning using Git and DVC at the Open Neuro Workshop 2023², introducing best practices for reproducible research. At the AI4Health summer school 2025, we provided a hands-on tutorial on diffusion models with applications to medical imaging, covering implementations from scratch in PyTorch and anomaly detection in brain MRI³. To support users of our Leaspy software for disease course mapping, we have created a series of three progressive tutorials⁴ that guide researchers from the limitations of linear mixed-effects models to real-world applications with their own data. Finally, we developed a comprehensive tutorial on deep learning classification from brain MRI⁵, demonstrating the use of Clinica and ClinicaDL for differentiating Alzheimer’s disease patients from healthy controls while highlighting methodological pitfalls to avoid.

11.2.2 Supervision

- PhD in progress: Charles Heitz, “Deep learning for assisting clinical decisions in brain imaging: trustworthy validation and benchmarking”, started in 2025, supervisors: Olivier Colliot
- PhD in progress: Pascaline Andre, “Statistical evaluation of models and machine learning procedures in medical imaging”, started in 2024, supervisors: Olivier Colliot and Sophie Tezenas du Montcel
- PhD completed in 2025: Guanghui Fu, “Segmentation, classification and generative models for computer-aided diagnosis of neurological diseases from neuroimaging data”, started in 2021, supervisors: Olivier Colliot and Didier Dormont
- PhD completed in 2025: Arya Yazdan-Panah, “Deep learning for multimodal image analysis in multiple sclerosis”, started in 2021, supervisors: Olivier Colliot and Bruno Stankoff
- PhD in progress: Manon Heffernan, “Artificial intelligence tools for clinical data warehouses in neuroimaging”, started in 2024, supervisors: Olivier Colliot and Ninon Burgos
- PhD in progress: Matthieu Joulot, “Longitudinal processing of multimodal brain imaging for the study of neurodegenerative diseases”, started in 2024, supervisors: Ninon Burgos and Olivier Colliot
- PhD in progress: Maëlys Solal, “Robust anomaly detection in multimodal neuroimaging”, started in 2023, supervisor: Ninon Burgos

²aramislab.paris.inria.fr/workshops/NOW/2023

³github.com/HuguesRoy/AI4Health_TP_diff

⁴disease-progression-modelling.github.io/pages/notebooks/disease_course_mapping/disease_course_mapping.html#tutorials

⁵aramislab.paris.inria.fr/clinicadl/tuto/2023/html

- PhD in progress: Hugues Roy, “Pseudo-healthy image synthesis for the detection of anomalies in the brain, a multi-modal approach”, started in 2024, supervisor: Ninon Burgos
- PhD completed in 2025: Élise Delzant, “Methods for big-data neuroimaging analyses”, started in 2022, supervisors: Baptiste Couvy-Duchesne and Olivier Colliot
- PhD in progress: Maylis Tran, “Optimisation du design d’essai clinique à l’aide de données d’histoire naturelle”, started in 2024, supervisor: Sophie Tezenas Du Montcel
- PhD in progress: Marc Dibling, “Parcours de soin des patients atteints de maladies neurodégénératives rares”, started in 2023, supervisor: Sophie Tezenas Du Montcel
- PhD in progress: Sofia Kaisaridi, “Modélisation multimarqueurs de l’évolution clinique et en imagerie cérébrale de patients CADASIL et de son influence sur un évènement censure”, started in 2022, supervisor: Sophie Tezenas Du Montcel
- PhD in progress: Ayse Gungor, “Correlation between eye and brain pathologies”, started in 2023, supervisors: Dan Milea and Daniel Racoceanu
- PhD in progress: Ilias Sarbout, “Artificial Vision by fMRI analysis and XAI approaches”, started in 2023, supervisors: Dan Milea and Daniel Racoceanu
- PhD in progress: Esther Kozlowski, “A responsible artificial intelligence framework for modeling the progression of Parkinson’s disease”, started in 2023, supervisors: Marie Vidailhet and Daniel Racoceanu
- PhD in progress: Swann Ruyter, “ComPath: Next Generation Computational Pathomics for Personalized Medicine. Explainable Deep Learning Integration of Computational Pathology and Spatial Transcriptomics”, started in 2024, supervisor: Daniel Racoceanu
- PhD in progress: Mehdi Hamadache, “Physics Informed AI meets Mechanistic Modeling: Predicting Cancer Immunotherapy Outcomes using Multimodal Computational Pathology”, started in 2025, supervisor: Daniel Racoceanu
- PhD completed in 2025: Octave Guinebretiere, “Early prediction of neurodegenerative diseases using large transnational electronic health records databases for better prevention”, started in 2022, supervisors: Stanley Durrleman and Thomas Nedelec

11.2.3 Juries

- Ninon Burgos participated, as reviewer, to the PhD committee of Juliette Moreau, Université Claude Bernard Lyon 1.
- Ninon Burgos participated, as reviewer, to the PhD committee of Ashay Patel, King’s College London.
- Ninon Burgos participated, as reviewer, to the PhD committee of Aghiles Kebaili, Université de Rouen.
- Ninon Burgos participated, as reviewer, to the PhD committee of Élodie Piot, Université Grenoble Alpes.
- Ninon Burgos participated to the individual PhD student monitoring committee of Florencia Boccarato, Université Côte d’Azur.
- Ninon Burgos participated to the individual PhD student monitoring committee of Baptiste Pierrard, Université de Lyon.
- Ninon Burgos participated to the individual PhD student monitoring committee of Daniele Falchetta, EURECOM .
- Ninon Burgos participated to the individual PhD student monitoring committee of Trang Nguyen, Université Côte d’Azur .

- Ninon Burgos participated to the individual PhD student monitoring committee of Franklin Sierra, Institut Polytechnique de Paris, France & Universidad Industrial de Santander, Colombia.
- Daniel Racoceanu participated, as reviewer, to the PhD committee of Alexandre Martin, Université Côte d’Azur.
- Daniel Racoceanu participated, as president, to the PhD committee of Victorien Quevit, University of Rennes.
- Daniel Racoceanu participated to the individual PhD student monitoring committee of Marie Arrivat, Institut Polytechnique de Paris.
- Daniel Racoceanu participated to the individual PhD student monitoring committee of Tiziana Tocci, Institut Curie, Paris.
- Daniel Racoceanu participated to the individual PhD student monitoring committee of Paul Barthe, University of Caen.
- Olivier Colliot participated, as president, to the PhD committee of Marianne Golse, Sorbonne University.
- Sophie Tezenas Du Montcel participated, as reviewer, to the PhD committee of Niels Hendrickx, Université Paris Cité.
- Sophie Tezenas Du Montcel participated, as reviewer, to the PhD committee of Théo Silvestre, Université Paris Saclay.

11.3 Popularization

11.3.1 Productions (articles, videos, podcasts, serious games, ...)

- Olivier Colliot contributed to the popular science book “Tout comprendre (ou presque) sur l’intelligence artificielle” (CNRS éditions).

12 Scientific production

12.1 Major publications

- [1] M. Ansart, S. Epelbaum, G. Bassignana, A. Bône, S. Bottani, T. Cattai, R. Couronné, J. Faouzi, I. Koval, M. Louis, E. Thibeau-Sutre, J. Wen, A. Wild, N. Burgos, D. Dormont, O. Colliot and S. Durrleman. ‘Predicting the Progression of Mild Cognitive Impairment Using Machine Learning: A Systematic, Quantitative and Critical Review’. In: *Medical Image Analysis* 67 (Jan. 2021), p. 101848. DOI: [10.1016/j.media.2020.101848](https://doi.org/10.1016/j.media.2020.101848). URL: <https://hal.archives-ouvertes.fr/hal-02337815>.
- [2] M. Ansart, S. Epelbaum, M. Houot, T. Nedelec, B. Lekens, L. Gantzer, D. Dormont and S. Durrleman. ‘Changes in the use of psychotropic drugs during the course of Alzheimer’s disease: A large-scale longitudinal study of French medical records’. In: *Alzheimer’s & Dementia: Translational Research & Clinical Interventions* 7.1 (14th Sept. 2021), e12210. DOI: [10.1002/trc2.12210](https://doi.org/10.1002/trc2.12210). URL: <https://hal.sorbonne-universite.fr/hal-03351244> (cit. on p. 12).
- [3] S. Bottani, N. Burgos, A. Maire, D. Saracino, S. Stroër, D. Dormont and O. Colliot. ‘Evaluation of MRI-based machine learning approaches for computer-aided diagnosis of dementia in a clinical data warehouse’. In: *Medical Image Analysis* 89 (Oct. 2023), p. 102903. DOI: [10.1016/j.media.2023.102903](https://doi.org/10.1016/j.media.2023.102903). URL: <https://hal.science/hal-03656136> (cit. on p. 8).
- [4] S. Bottani, N. Burgos, A. Maire, A. Wild, S. Ströer, D. Dormont and O. Colliot. ‘Automatic quality control of brain T1-weighted magnetic resonance images for a clinical data warehouse’. In: *Medical Image Analysis* 75 (2022). DOI: [10.1016/j.media.2021.102219](https://doi.org/10.1016/j.media.2021.102219). URL: <https://inria.hal.science/hal-03154792> (cit. on p. 8).

- [5] S. Bottani, E. Thibeau-Sutre, A. Maire, S. Ströer, D. Dormont, O. Colliot and N. Burgos. ‘Contrast-enhanced to non-contrast-enhanced image translation to exploit a clinical data warehouse of T1-weighted brain MRI’. In: *BMC Medical Imaging* 24.1 (20th Mar. 2024), p. 67. DOI: [10.1186/s12880-024-01242-3](https://doi.org/10.1186/s12880-024-01242-3). URL: <https://hal.science/hal-03497645> (cit. on p. 8).
- [6] S. Brice, S. Reyes, A. Jabouley, C. Machado, C. Rogan, N. Gastellier, N. Alili, S. Guey, E. Jouvent, D. Hervé, S. Tezenas Du Montcel and H. Chabriat. ‘Trajectory Pattern of Cognitive Decline in Cerebral Autosomal Dominant Arteriopathy With Subcortical Infarcts and Leukoencephalopathy’. In: *Neurology* 99.10 (5th Sept. 2022), e1019–e1031. DOI: [10.1212/WNL.000000000000200805](https://doi.org/10.1212/WNL.000000000000200805). URL: <https://hal.inria.fr/hal-03774149>.
- [7] L. Chougar, A. Faucher, J. Faouzi, F.-x. Lejeune, G. Gama Lobo, C. Jovanovic, F. Cormier, G. Dupont, M. Vidailhet, J.-c. Corvol, O. Colliot, S. Lehericy, D. Grabli and B. Degos. ‘Contribution of MRI for the Early Diagnosis of Parkinsonism in Patients with Diagnostic Uncertainty’. In: *Movement Disorders* 39.5 (14th Mar. 2024), pp. 825–835. DOI: [10.1002/mds.29760](https://doi.org/10.1002/mds.29760). URL: <https://hal.science/hal-04675671> (cit. on p. 12).
- [8] L. Chougar, F.-X. Lejeune, J. Faouzi, B. Morino, A. Faucher, N. Hoyek, D. Grabli, F. Cormier, M. Vidailhet, J.-c. Corvol, O. Colliot, B. Degos and S. Lehericy. ‘Comparison of mean diffusivity, R2* relaxation rate and morphometric biomarkers for the clinical differentiation of parkinsonism’. In: *Parkinsonism & Related Disorders* 108 (Mar. 2023), p. 105287. DOI: [10.1016/j.parkreldis.2023.105287](https://doi.org/10.1016/j.parkreldis.2023.105287). URL: <https://hal.sorbonne-universite.fr/hal-04041736> (cit. on p. 12).
- [9] E. Christodoulou, A. Reinke, R. Houhou, P. Kalinowski, S. Erkan, C. H. Sudre, N. Burgos, S. Boutaj, S. Loizillon, M. Solal, N. Rieke, V. Cheplygina, M. Antonelli, L. D. Mayer, M. D. Tizabi, M. J. Cardoso, A. Simpson, P. F. Jäger, A. Kopp-Schneider, G. Varoquaux, O. Colliot and L. Maier-Hein. ‘Confidence intervals uncovered: Are we ready for real-world medical imaging AI?’ In: *Lecture Notes in Computer Science. MICCAI 2024 - 27th International Conference on Medical Image Computing and Computer-Assisted Intervention. Vol. LNCS-15010. Medical Image Computing and Computer Assisted Intervention – MICCAI 2024 27th International Conference, Marrakesh, Morocco, October 6–10, 2024, Proceedings, Part X. Marrakech, Morocco: Springer Nature Switzerland, 3rd Oct. 2024*, pp. 124–132. DOI: [10.1007/978-3-031-72117-5_12](https://doi.org/10.1007/978-3-031-72117-5_12). URL: <https://hal.science/hal-04715638> (cit. on p. 8).
- [10] G. Coarelli, A. Heinzmann, C. Ewencyk, C. Fischer, M. Chupin, M.-L. Monin, H. Hurmic, F. Calvas, P. Calvas, C. Goizet, S. Thobois, M. Anheim, K. Nguyen, D. Devos, C. Verny, V. a. G. Ricigliano, J.-F. Mangin, A. Brice, S. Tezenas Du Montcel and A. Durr. ‘Safety and efficacy of riluzole in spinocerebellar ataxia type 2 in France (ATRIL): a multicentre, randomised, double-blind, placebo-controlled trial’. In: *The Lancet Neurology* 21 (18th Jan. 2022), pp. 225–233. DOI: [10.1016/s1474-4422\(21\)00457-9](https://doi.org/10.1016/s1474-4422(21)00457-9). URL: <https://hal.science/hal-03852287>.
- [11] O. Colliot. *Machine Learning for Brain Disorders*. Vol. 197. Neuromethods. Springer, 2023. DOI: [10.1007/978-1-0716-3195-9](https://doi.org/10.1007/978-1-0716-3195-9). URL: <https://hal.science/hal-04225627>.
- [12] O. Colliot, E. Thibeau-Sutre and N. Burgos. ‘Reproducibility in machine learning for medical imaging’. In: *Machine Learning for Brain Disorders*. Springer, 2023. URL: <https://hal.science/hal-03957240>.
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