

2025 Activity Report

RESEARCH CENTRE: Inria Centre at Rennes University

IN PARTNERSHIP WITH: INSERM, Institut Curie

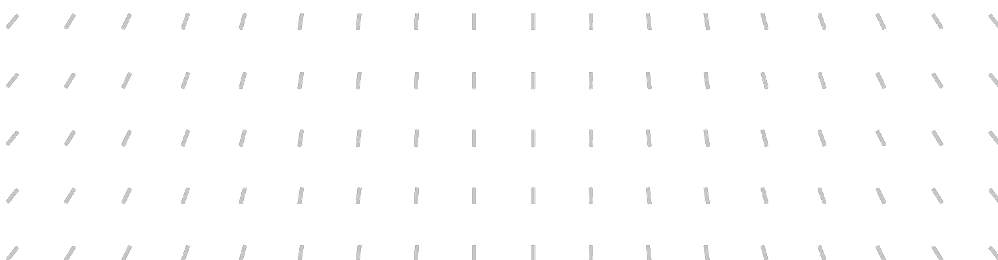

Project-Team

SAIRPICO

Space-time imaging, artificial intelligence and
computing for cellular and chemical biology



In collaboration with Chimie et Biologie du Cancer



Project-Team SAIRPICO

Creation of the Project-Team: 2023 April 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

- A3.1.1. – Modeling, representation
- A3.3. – Data and knowledge analysis
- A3.3.3. – Big data analysis
- A3.4. – Machine learning and statistics
- A5.3. – Image processing and analysis
- A5.3.2. – Sparse modeling and image representation
- A5.3.3. – Pattern recognition
- A5.3.4. – Registration
- A5.9.1. – Sampling, acquisition
- A5.9.2. – Estimation, modeling
- A5.9.3. – Reconstruction, enhancement
- A5.9.5. – Sparsity-aware processing
- A5.9.6. – Optimization tools
- A6.1.2. – Stochastic Modeling
- A6.1.3. – Discrete Modeling (multi-agent, people centered)
- A6.1.4. – Multiscale modeling
- A6.1.5. – Multiphysics modeling
- A6.2.3. – Probabilistic methods
- A6.2.4. – Statistical methods
- A6.2.6. – Optimization
- A6.3. – Computation-data interaction
- A6.3.1. – Inverse problems
- A6.3.2. – Data assimilation
- A6.3.3. – Data processing
- A6.3.4. – Model reduction
- A6.3.5. – Uncertainty Quantification
- A9.2. – Machine learning
- A9.2.1. – Supervised learning
- A9.2.5. – Bayesian methods
- A9.2.6. – Neural networks
- A9.2.7. – Kernel methods
- A9.2.8. – Deep learning
- A9.3. – Signal processing
- A9.12.1. – Object recognition
- A9.12.4. – 3D and spatio-temporal reconstruction
- A9.12.5. – Object tracking and motion analysis
- A9.12.6. – Object localization

Other research topics and application domains

B1.1.1. – Structural biology

B1.1.7. – Bioinformatics

B1.1.8. – Mathematical biology

B2.2.3. – Cancer

B2.6. – Biological and medical imaging

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1 Team members, visitors, external collaborators

Research Scientists

- Charles Kervrann [Team leader, INRIA, Senior Researcher, HDR]
- Anais Badoual [INRIA, Researcher]
- Vincent Briane [INRIA, Starting Research Position, from Feb 2025]
- Ludger Johannes [INSERM, Senior Researcher]
- Massiullah Shafaq-Zadah [INSERM, Researcher]
- Christian Wunder [INSERM, Researcher]

Post-Doctoral Fellows

- Xingyi Cheng [INRIA, Post-Doctoral Fellow, from Nov 2025]
- Ilyes Hamitouche [INSTITUT CURIE, Post-Doctoral Fellow]

PhD Students

- Chencheng Gu [INRIA]
- Leo Maury [INRIA]
- Mounir Messaoudi [INRIA]
- Ferdinand Plesse–Costa [INRIA]
- Quentin Rapilly [INRIA, until Nov 2025]

Technical Staff

- Estelle Dransart [Institut Curie, Engineer]
- Arthur Masson [INRIA, Engineer]
- Caio Vaz Rimoli [INSERM, Engineer]

Interns and Apprentices

- Matteo Audigier [INRIA, Intern, from Jun 2025 until Aug 2025]
- Enzo Choffat [INRIA, Intern, from Apr 2025 until Aug 2025]
- Maelys Hanoire [INRIA, Intern, from Apr 2025 until Aug 2025]
- Carel Ntsoumou Lihoula [INRIA, Intern, from Mar 2025 until Sep 2025]

Administrative Assistant

- Caroline Tanguy [INRIA]

External Collaborator

- Frédéric Lavancier [ENSAI, HDR]

2 Overall objectives

During the past two decades many ground-breaking technologies emerged and allowed the visualization of tissues, cells, proteins, viruses, and macromolecular structures at all levels of spatial resolution (from 10 nm to 150 nm). The discovery of fluorescent labeling probes (Green fluorescence Protein, Nobel Prize in chemistry 2008) and recent advances in optics and digital sensors (e.g., Photo-Activated Localization Microscopy (PALM), Stimulated Emission Depletion (STED) microscopy, and Structured Illumination Microscopy (SIM)) have been key developments which have served to overcome the theoretical optical diffraction limit (200 nm) established in the 19th century. Because of these technological breakthroughs and their impacts in life sciences, contemporary microscopy has been praised through prestigious awards, such as the Nobel Prizes awarded to inventors of the concepts of super-resolution microscopy (2014) and cryo-electron microscopy (2017). Fluorescent microscopy imaging has become the spearhead of modern biology as it is able to generate videos comprising dozens of Gigabytes of data within an hour, and can depict long-term 4D nanoscale cell behaviors with low photo-toxicity. The ability to follow nanoscale cellular events is also proving to be of immense clinical relevance, especially for the study of cancer progression and viral infections. All these technological advances in microscopy have created new challenges for researchers in signal-image processing, and have even modified conventional paradigms once digital processing became a key component in the surmounting of the diffraction barrier (e.g., PALM and SIM).

All fluorescence microscopy systems record fluorescent signals emitted by molecules tagged with genetically engineered or chemically coupled proteins within cells. In a conventional setup photons are collected and registered at a given pixel (or voxel in 3D imaging). The measured fluorescence intensity is a scalar value, generally proportional to the density of tagged-molecules representing a few dozens of nanometers within a pixel/voxel. However, fluorescence necessarily includes intensity (biomolecule density), wavelength (absorption and emission spectrum), time (fluorescence decay lifetime) and polarization (which arises from the dipole orientation). Nevertheless, it is worth noting that the orientation of dipoles cannot be measured by conventional fluorescence microscopy setups. **The next generation technology will be able to provide the missing directional information which is required to better reveal the structure and function of biomolecules and organelles in cells. Among the recent progress, let us mention polarized microscopy that has the potential to probe the dipole orientation of fluorophores linked to proteins or lipids of interest and thereby, to report valuable information about the orientation and diffusive behavior of the molecule.** Light polarization technology is also very flexible since it can be advantageously combined with super-resolution microscopy to characterize the nanometric structural organization of filamentous assemblies (actin filaments, microtubules), of membrane lipid orientations or the global architecture of local assembly of both proteins and lipids. Given their promising potential in terms of flexibility and production of information at high spatial resolution in vivo, **polarized microscopy vector-valued images are likely to be in the future as common as confocal scalar-valued images.**

As the resulting image data are 3D+time multi-valued signals, potentially depicting several fluorescently tagged molecular species, the analysis and the interpretation of these signals represents a new challenge in signal image processing and statistical machine learning, and one for which several scientific barriers must be overcome. **A first barrier is to reduce the high level of noise and blur observed in 3D+time vector-valued data, which encompass information about density and orientation of biomolecules.** As the processing of very large temporal series of images considerably slows down the analysis, special attention must be paid to the feasibility and scalability of the developed algorithms. **A second barrier is the interpretation of dynamic and structural information content of such vector-valued images,** for which no general method currently exists. **A third barrier relates to the possibility of producing 3D spatial high-resolution maps of molecular motions from data generated by conventional polarized microscopy instruments.** These barriers translate into unsolved digital challenges which need to be surmounted in order for this technology to be adopted in large-scale biological studies.

As the current methods are limited in handling polarized images, **SAIRPICO aims to create the next generation of information processing techniques** required to overcome the aforementioned barriers, and to solve challenging image processing problems induced by the **acquisition of 3D+time vector-valued images. The resulting algorithms will serve to characterize the dynamics of biomolecules (e.g., proteins, lipids, ...) and to decipher the molecular transport pathways or the motion (e.g., migration) and deformation of cells,** which is of considerable of interest in fundamental cell biology and for precision medicine.

3 Research program

Four complementary Research Axes will be investigated with scientists who develop chemical methods (e.g. advanced imaging probes such as non-natural clickable amino acids, linker chemistry) to improve the rigidity of linkers and the photo-stability of fluorophores required for robust estimation of orientation of single molecules and components of cytosolic machinery, as well as single-molecule FRET techniques to infer and quantify interactions between membrane proteins.

Methodological Research Axis 1 - Modeling and reconstruction of multi-valued images. Development of cutting-edge computational strategies and mathematical frameworks for reconstructing multi-valued images. Structure-based sparse representations of multi-value images will be established from the analysis of the spatiotemporal correlations and the inherent redundancy of data in multiple images. We will investigate statistical nonparametric methods and aggregation techniques, variational Bayesian methods, including shape-based models, as well as machine learning strategies to solve the underlying inverse problems.

Methodological Research Axis 2 - Methods for high-resolution spatial quantification of molecular mobility and interactions. Characterization of molecular mobility at the nanoscale from multi-valued images. We intend to fully exploit the rich contents of microscopy images in order to build single-molecule (e.g., endocytic ligands) and biomolecule (e.g., cytosolic machinery, metabolic sensors) tracking algorithms, derive robust estimators of molecular mobility, and quantify spatially-variable interactions between molecular species and cytoskeleton. The resulting algorithms will be used to produce high-resolution spatial maps of molecular mobility given stochastic motion models and sparse representations.

Methodological Research Axis 3 - Spatiotemporal modeling of 3D shapes, motions and deformations. Development of shape models and descriptors to capture 3D motion and deformation of macromolecular complexes (cryo-electron tomography (cryo-ET), single particle analysis (SPA)) on one hand, and on the other hand, intracellular components and tumor cells, at the scale of a single cell and tissues. We intend to represent 3D shapes by parametric surfaces controlled by key points and to segment and track structures in 3D microscopy. The main originality will be to exploit annotations and/or high-level priors to derive features for classifying molecular conformations in cryo-ET, and phenotypes induced by drugs (single cell), or controlled hypoxia conditions (tissue scale) in 3D+time fluorescence microscopy.

Transversal Research Axis 4 - Analysis of case-studies in cell biology and cancer research. Demonstration that the methods and algorithms related to the three previous methodological axes allow one to perform image reconstruction for several 3D instruments (TIRFM, Lattice Light Sheet Microscopy, Multi-Focus Microscopy, cryo-ET), and accurately quantify the shape and motion of cell components and biomolecules that interact with membranes and the cytoskeleton. The resulting images and features will be helpful to better decipher the intracellular dynamics of trafficking and signaling events in living cells, especially membrane mechanics at the cell surface, endocytosis, as well as signal transduction to the nucleus. The methods will be developed for investigation in cellular and chemical biology, and extended further to perform analysis at the tissue scale.

4 Application domains

The advances in SAIRPICO will result in a new generation of algorithms for multi-valued microscopy instruments, which will be widely used in the future in fundamental and applied cellular and chemical biology. The team gathers researchers developing new imaging modality and computational methods, biophysicists to develop and provide adapted experimental and theoretical models, chemist to design adapted probes and cell biologists. In collaboration with other teams of U1143 and the help of dedicated engineers (to be recruited) who will stimulate the interface between experiment and data sciences, we expect to build a general approach based on theories and tools in optics, chemistry, cell biology, biophysics, statistics, and machine learning.

Our case studies in cellular and chemical biology will be related to the analysis of intracellular transport and signaling pathways, and the migration of tumor cells in organoids, as they represent a

major contributory factor to a number of diseases such as cancer and viral infection. For instance, we wish to study in detail the causal link between lectin-driven glycolipid reorganization in biological membranes and the formation of endocytic sites from which clathrin-independent endocytic carriers are generated. Since a series of pathogens (e.g., polyoma and noroviruses), pathogenic factors (e.g., Shiga and cholera toxins) and cellular proteins (integrins, CD44...) are concerned by this mechanism we expect that this study will have a general impact in the life science and membrane biophysics communities. Understanding and exploring diverse and alternative cellular entry mechanisms, by gathering as many as possible molecular information in fundamental membrane biology research, paves the way for the development of innovative cancer therapy or vaccine strategies. We expect that our results will be helpful in the design of therapeutic compounds delivered to precise intracellular locations within specialized cells for immunotherapy, or to tumors for targeted therapy.

Meanwhile, **the ambition of SAIRPICO is to become the reference team in computational polarized bioimaging, with a focus on the development of advanced signal-image processing techniques for cell imaging.** To that end, we will create a centralized polarized image database and disseminate the results through dedicated workshops, summer schools, mini-symposia, on-line tutorials, and publications in high-visibility journals. It is worth noting that the interdisciplinary team will be bi-localized in Rennes and Paris and therefore will benefit from the scientific environment of both Inria (Applied mathematics, artificial intelligence) and Institut Curie (chemical biology, optics).

5 Social and environmental responsibility

Cancer is the second most common cause of death in EU countries, after cardiovascular disease, and Europe accounts for a quarter of all cancer cases worldwide, despite representing less than 10% of the world's population: it is therefore clear that cancer has a considerable impact on our society, putting pressure on national healthcare and social protection systems, public budgets and economic growth. Research policies in cancer control and diagnosis are increasingly based on results obtained in artificial intelligence applied to cellular imaging. Action to prevent cancer also contributes to the fight against obesity and other diseases such as cardiovascular disease and diabetes, since they share common risk factors.

6 Highlights of the year

6.1 Publications in high impact factor journals

- M. Shafaq-Zadah, E. Dransart, I. Hamitouche, C. Wunder, V. Chambon, C.A. Valades-Cruz, L. Leconte, N. Kumar Sarangi, J. Robinson, S.-K. Bai, R. Regmi, A. Di Cicco, A. Hovasse, R. Bartels, U. J. Nilsson, S. Cianféroni-Sanglier, H. Leffler, T.E. Keyes, D. Lévy, S. Raunser, D. Roderer, L. Johannes. **Spatial N-glycan rearrangement on $\alpha 5\beta 1$ integrin nucleates galectin-3 oligomers to determine endocytic fate.** *Nature Communications*, **16**, 9461, 2025 – In this paper, we discovered a molecular switch that exploits dynamic spatial rearrangements of N-glycans during such conformational transitions to control protein function. Our findings revealed the dynamic regulation of the glycan landscape at the cell surface to achieve oligomerization of galectin-3. Galectin-3 oligomers are thereby identified as functional decoders of defined spatial patterns of N-glycans on specifically the bent-closed conformational state of $\alpha 5\beta 1$ integrin and possibly other integrin family members.
- E. MacDonald, A. Forrester, C.A. Valades-Cruz, T.D. Madsen, J. Hetmanski, E. Dransart, Y. Ng, R. Godbole, A. Akhil Shp, L. Leconte, V. Chambon, D. Ghosh, A. Pinet, D.D. Bhatia, B. Lombard, D. Loew, M.R. Larson, H. Leffler, D.J. Lefeber, H. Clausen, P. Caswell, M. Shafaq-Zadah, S. Mayor, R. Weigert, C. Wunder, L. Johannes. **Growth factor-induced desialylation for the fast control of endocytosis.** *Nature Cell Biology*, **27(3)**, 2025 – Glycolipid-lectin (GL-Lect) driven endocytosis controls the formation of clathrin-independent carriers (CLICs) and the internalization of various cargos such as integrin. Whether this process is regulated in a dynamic manner remained unexplored. In this paper, we demonstrated that within minutes, the epidermal growth factor triggers the galectin-driven endocytosis of cell surface glycoproteins, such as integrins, that are key regulators of cell adhesion and migration. Furthermore, we showed that glycosylation at the cell surface thereby emerges as a dynamic

and reversible regulatory post-translational modification that controls a highly adaptable trafficking pathway.

- M. Harastani, G. Patra, C. Kervrann, M. Eltsov. **Template Learning: Deep learning with domain randomization for particle picking in cryo-electron tomography.** *Nature Communications*, **16, 8833, 2025** – In this paper, we presented "Template Learning", a technique that combines deep learning accuracy with the convenience of training on biomolecular templates via domain randomization. Template Learning automates synthetic dataset generation, modeling molecular crowding, structural variability, and data acquisition variation, thereby reducing or eliminating the need for annotated experimental data. We showed that models trained using "Template Learning", and optionally fine-tuned with experimental data, outperformed those trained solely on annotations.

7 Latest software developments, platforms, open data

7.1 Latest software developments

7.1.1 DCT2Net

Name: Trained shallow CNN (convolution neural network)-based DCT (Discrete Cosine Transform) denoiser

Keywords: Deep learning, Denoising, Convolutional Neural Network, Deconvolution

Functional Description: DCT2net software, based on the well-known DCT (Discrete Cosine Transform) image denoising algorithm, is dedicated to noise removal from images. The traditional DCT denoiser can be seen as a shallow CNN and thereby its original linear transform can be tuned through gradient descent in a supervised manner, improving considerably its performance. Consequently, DCT2net is a shallow and interpretable convolution network, whose parameters optimization allows to improve very significantly the performances of the traditional DCT denoiser. To deal with the remaining artifacts induced by DCT2net, an original hybrid solution between DCT and DCT2net is proposed, combining the best of what these two methods can offer. Experiments on artificially noisy images show that the two-layer DCT2net method provides results comparable to the BM3D method and is as fast as the DnCNN algorithm composed of more than a dozen of layers.

Inter Deposit Digital Number: IDDN.FR.001.460033.000.S.P.2021.000.21000 21

URL: <https://team.inria.fr/serpico/software/dct2net>

Publication: hal-03511641

Contact: Charles Kervrann

Participants: Sebastien Herbreteau, Charles Kervrann, Leo Maury

7.1.2 DeepFinder

Name: Deep learning for macromolecule identification within 3D cellular cryo-electron tomograms

Keywords: Image analysis, Deep learning, Cryo-electron microscopy, Object detection

Functional Description: DeepFinder is a computational approach that uses artificial neural networks to accurately and jointly localize multiple types and/or states of macromolecules in 3D cellular cryo-electron tomograms. DeepFinder leverages deep learning and outperforms the commonly-used template matching method on ideal data. On synthetic image data (SHREC 2019, 2020, and 2021 challenges), DeepFinder is very fast and produces superior detection results when compared to other competitive deep learning methods, especially on small macromolecules. On experimental cryo-ET data depicting ribosomes, the detection results obtained by DeepFinder are consistent with expert annotations. We have got a high overlap of detection (86%) and a similar structure resolution that those determined by subtomogram averaging.

Inter Deposit Digital Number: IDDN.FR.001.460030.000.S.P.2021.000.21000

URL: <https://github.com/deep-finder/deep-finder>

Publication: [hal-03509223](https://hal.archives-ouvertes.fr/hal-03509223)

Contact: Emmanuel Moebel

Participants: Arthur Masson, Mounir Messaoudi, Emmanuel Moebel, Charles Kervrann

Partners: Max Planck Institute Martinsried, Fondation Fourmentin-Guilbert, Helmholtz Pioneer Campus, Université de Strasbourg

7.1.3 ExoDeepFinder

Name: A Deep learning method for exocytosis event detection in fluorescence TIRF microscopy movies

Keywords: Image analysis, Deep learning, Fluorescence microscopy, Live-cell microscopy, Anomaly detection

Functional Description: ExoDeepFinder is a software for the detection of rare dynamic exocytosis events observed in temporal series of 2D Total Internal Reflection Fluorescent Microscopy (TIRFM) images. This U-net, originally designed for analyzing 3D cryo-electron tomography images (DeepFinder), achieved good absolute performances with a relatively small training dataset of 60 cells/12000 events. ExoDeepFinder method uses hybrid annotations performed manually by experts (more than 10,000 spatiotemporal coordinates of annotated exocytosis events) and automatically annotated bright spots that are not bona fide exocytosis events, with no data curation. By gathering the manual and automatic datasets, we significantly boosted the performance in order to detect very rare events in the volumes (< 1 event per frame in average), even if the automatic spot detector (ATLAS) potential produces annotation errors. ExoDeepFinder outcompeted the unsupervised conventional methods on a benchmark composed of several dozen experimental movies of one thousand frames with variable signal-to-background ratios, while exhibiting a greater plasticity to the experimental conditions when tested under drug treatments and after changes in cell line or imaged reporter. This robustness to unseen experimental conditions did not require re-training demonstrating generalization capability of ExoDeepFinder. The algorithm, designed for large 2D+time volume processing, takes about 30 seconds to process a video of 300 x 300 x 1000 voxels with no parameter adjustment, as compared to 10 to 20 minutes required with the two conventional image analysis algorithms. The method, as well as the annotated training datasets, were made transparent and available through an open-source software as well as a Napari plugin and can directly be applied to custom user data.

URL: <https://github.com/deep-finder/tirfm-deepfinder>

Publication: [hal-04874728](https://hal.archives-ouvertes.fr/hal-04874728)

Contact: Arthur Masson

Participants: Charles Kervrann, Arthur Masson, Hugo Lachuer, Anne-Sophie Mace, Kristin Schauer, Emmanuel Moebel

Partners: Institut Jacques Monod, Institut Gustave Roussy, UMR 144 CNRS - Institut Curie

7.1.4 LICH

Name: Linear and Iterative Combinations of patches for Image denoising

Keywords: Image analysis, Denoising

Functional Description: In the past decade, deep neural networks have revolutionized image denoising in achieving significant accuracy improvements by learning on datasets composed of noisy/clean image pairs. However, this strategy is extremely dependent on training data quality, which is a well-established weakness. To alleviate the requirement to learn image priors externally, single image (a.k.a., self-supervised or zero-shot) methods perform denoising solely based the analysis of the input

noisy image without external dictionary or training dataset. This work investigates the effectiveness of linear combinations of patches for denoising under this constraint. Although conceptually very simple, we show that linear combinations of patches are enough to achieve state-of-the-art performance. The proposed parametric approach relies on quadratic risk approximation via multiple pilot images to guide the estimation of the combination weights. Experiments on images corrupted artificially with Gaussian noise as well as on real-world noisy images demonstrate that our method is on par with the very best single-image denoisers, outperforming the recent neural network-based techniques, while being much faster and fully interpretable.

URL: <https://github.com/sherbret/lichi>

Publication: hal-03894346

Contact: Charles Kervrann

Participants: Sebastien Herbreteau, Charles Kervrann

Partner: Airbus Defense and Space

7.1.5 NL-Ridge

Name: A unified framework of non-local parametric methods for image denoising

Keywords: Image analysis, Denoising

Functional Description: We propose a unified view of non-local methods for single-image denoising, for which BM3D is the most popular representative, that operate by gathering noisy patches together according to their similarities in order to process them collaboratively. Our general estimation framework is based on the minimization of the quadratic risk, which is approximated in two steps, and adapts to photon and electronic noises. Relying on unbiased risk estimation (URE) for the first step and on “internal adaptation”, a concept borrowed from deep learning theory, for the second, we show that our approach enables to reinterpret and reconcile previous state-of-the-art non-local methods. Within this framework, we propose a novel denoiser called NL-Ridge that exploits linear combinations of patches. While conceptually simpler, we show that NL-Ridge can outperform well-established state-of-the-art single-image denoisers.

URL: <https://github.com/sherbret/NL-Ridge/>

Publication: hal-04472406

Contact: Charles Kervrann

Participants: Sebastien Herbreteau, Charles Kervrann

Partner: Airbus Defense and Space

7.1.6 DeepCristae

Name: A CNN for the restoration of mitochondria cristae in live microscopy images

Keywords: Image analysis, Deep learning, Deconvolution, Denoising, Live-cell microscopy, Fluorescence microscopy, Convolutional Neural Network

Functional Description: DeepCristae is a CNN specifically developed to restore mitochondria cristae in low spatial resolution microscopy images. The main specificities of the method are 1) a new training loss dedicated to the restoration of specific pixels of interest, 2) a random image patch sampling focusing on areas of mitochondria to increase the size of the training set, and 3) metrics for objective assessment of cristae restoration. DeepCristae was applied to several microscopy modalities and different biological scenarios capturing live mitochondria at high speed with low illumination and thus low phototoxicity. It allows long-term/fast dynamic observation of cristae behavior and organization.

URL: <https://gitlab.inria.fr/anbadoua/DeepCristae>

Publication: [hal-04295317](https://hal.archives-ouvertes.fr/hal-04295317)

Contact: Anais Badoual

Participants: Anais Badoual, Ludovic Leconte, Cesar Augusto Valades Cruz, Jean Salamero, Salome Papereux, Charles Kervrann

Partner: UMR 144 CNRS - Institut Curie

7.1.7 BDM-Generator4BioImaging

Name: A generative "Birth-Death-Move" model to simulate spatiotemporal dynamics of biomolecules in cells

Keywords: Live-cell microscopy, Stochastic models, Image analysis, Multi-Object Tracking, Multi-physics simulation, Marked Point Process

Functional Description: Generators of space-time dynamics in bioimaging have become essential to build ground truth datasets for image processing algorithm evaluation such as biomolecule detectors and trackers, as well as to generate training datasets for deep learning algorithms. In this contribution, we leverage a stochastic model, called birth-death-move (BDM) point process, in order to generate joint dynamics of biomolecules in cells. This particle-based stochastic simulation method is very flexible and can be seen as a generalization of well-established standard particle-based generators. In comparison, our approach allows us: (1) to model a system of particles in motion, possibly in interaction, that can each possibly switch from a motion regime (e.g., Brownian) to another (e.g., a directed motion), (2) to take into account finely the appearance over time of new trajectories and their disappearance, these events possibly depending on the cell regions but also on the current spatial configuration of all existing particles. This flexibility enables to generate more realistic dynamics than standard particle-based simulation procedures, by for example accounting for the colocalization phenomena often observed between intracellular vesicles.

URL: <https://github.com/balsollier-lisa/BDM-generator-for-bioimaging>

Publication: [hal-04021538](https://hal.archives-ouvertes.fr/hal-04021538)

Contact: Frédéric Lavancier

Participants: Lisa Balsollier, Frédéric Lavancier, Charles Kervrann

Partners: Université de Nantes, ENSAI, UMR 144 CNRS - Institut Curie

7.1.8 NAGINI-3D

Name: N-Active shapes for seGmentINg 3D biological Images

Keywords: Image segmentation, Active contours, Convolutional Neural Network

Functional Description: NAGINI-3D is a method for segmenting 3D biological images that combines the advantages of active contours and deep learning. The general idea is to train a convolutional network to estimate the position of objects within images and, for each of them, to predict a set of parameters that can be used to generate a surface that delineates the edges of the object. This method allows one to represent 3D objects as continuous shapes and to compute differential geometry features such as local curvature of object surfaces.

URL: <https://github.com/QuentinRapilly/NAGINI-3D>

Publication: [hal-04978619](https://hal.archives-ouvertes.fr/hal-04978619)

Contact: Quentin Rapilly

Participants: Quentin Rapilly, Anais Badoual, Charles Kervrann

7.1.9 Wetlands

Keywords: Python, Library, Virtual environment

Functional Description: Wetlands can create Conda environments on demand, install dependencies, and execute arbitrary code within them. This makes it easy to build plugin systems or integrate external modules into an application without dependency conflicts, as each environment remains isolated.

For example, if your application needs to use both Stardist and Cellpose, installing them in the same environment may not work due to conflicting dependencies. With Wetlands, you can create a dedicated environment for each library and run them both as needed from your main script.

The name Wetlands comes from the tropical environments where anacondas thrive.

URL: <https://arthursw.github.io/wetlands/latest/>

Contact: Arthur Masson

Participant: Arthur Masson

7.2 New platforms

Participants: Charles Kervrann, Arthur Masson.

BioImageIT for bioimage management and processing – New image acquisition systems generate large number of images and large volume images. Such data sets are hard to store, to process and to analyze for in a workstation. Many solutions exist for data management (e.g. Omero, OpenImadis), image analysis (e.g. Fiji, Icy, CellProfiler) and statistics (e.g R software). Each of them has its specificities and several bridges have been developed between pieces of software. Nevertheless, in many use-cases, we need to perform analysis using tools that are available in different pieces of software and different languages. It is then tedious to create a workflow that brings the data from one tool to another. This process requires programming skills and most of the time, custom scripts are developed to handle data processing management. To overcome these difficulties, we have already developed a framework – BioImageIT (bioimageit.github.io) – to create a middleware application that allow any scientist to process, and analyze data using only one single high level application, while keeping track of metadata. This BioImageIT application is based on 3 components:

- an interoperability with existing databases;
- an image processing and analysis tools integration method based on packaging and wrapping techniques;
- an application with a graphical interface to easily annotate data, run processing tools, and visualize data and results.

This software architecture has three main goals. First, data are annotated with open formats and experiment can then be stored in different architectures or servers. Second, the processing tools are used as binary packages managed by the Conda technology. This enable to gently handle dependencies and several versions of the same tool. Any existing tool can then be integrated in its native programming language. Third, using a single middleware application allows to automatically generate metadata for any processed data, improving the traceability and the repeatability of any experimental result (FAIR principles).

We envision to continue to promote BioImageIT in the forthcoming years, initiated in the frame of the France-BioImaging research infrastructure (france-bioimaging.org) in order to provide a standardized image processing tool set and data management for the imaging facilities.

8 New results

Note: In this section, we provide details of the "scientific production". Each paragraph summarizes a published or submitted paper.

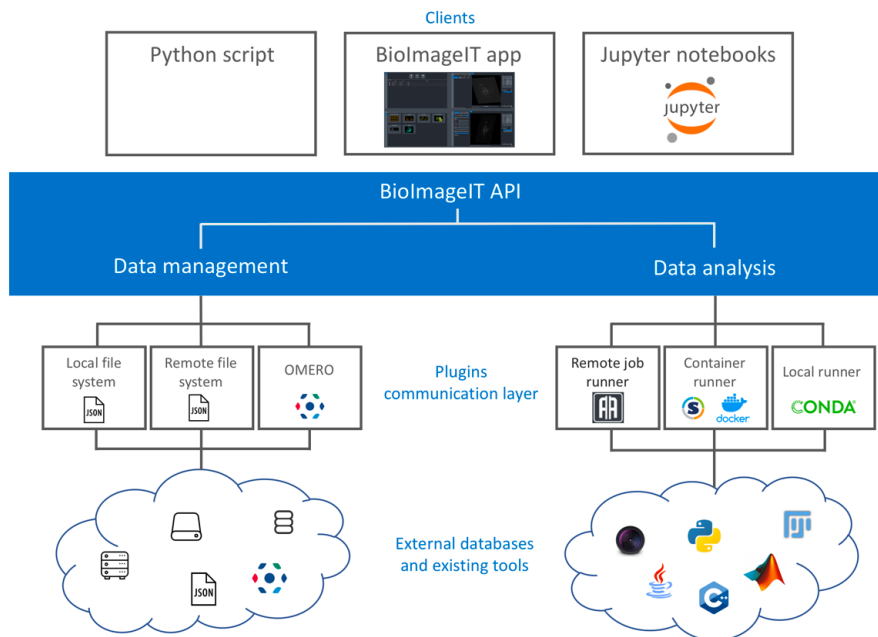


Figure 1: Scheme of the BioImageIT components interactions.

8.1 Methods for image restoration and computational microscopy

A unified framework of non-local parametric methods for image denoising

Participant: Charles Kervrann.

In [9], we proposed a unified view of non-local methods for single-image denoising, for which BM3D is the most popular representative, that operate by gathering noisy patches together according to their similarities in order to process them collaboratively. Our general estimation framework is based on the minimization of the quadratic risk, which is approximated in two steps, and adapts to photon and electronic noises. Relying on unbiased risk estimation (URE) for the first step and on “internal adaptation”, a concept borrowed from deep learning theory, for the second, we show that our approach enables to reinterpret and reconcile previous state-of-the-art non-local methods. Within this framework, we proposed a novel denoiser called NL-Ridge that exploits linear combinations of patches. While conceptually simpler, we showed that NL-Ridge can outperform well-established state-of-the-art single-image denoisers. (*in collaboration with S. Herbreteau, ENSAI, Bruz, France; R. Fraisse, AIRBUS Defence and Space, Toulouse, France*)

S. Herbreteau, C. Kervrann. *A unified framework of non-local parametric methods for image denoising*. SIAM J. Imaging Sciences, 18(1): 89-119, 2025, DOI:[10.1137/24M1630967](https://doi.org/10.1137/24M1630967), [hal-04472406](https://hal.archives-ouvertes.fr/hal-04472406), [9]. (NL-Ridge software)

Image processing and image analysis in microscopy

Participant: Anaïs Badoual.

In recent years, microscopy images have played a crucial part in the life sciences. They are the privileged witnesses for the observation at the molecular level of the great many and very complex intra-cellular interactions. As a corollary, the quantitative analysis of these images has become essential to improve the

understanding of this cellular machinery. While the acquisition of microscopic information varies greatly from one microscopy modality to another, they all now share a common denominator: the digital world. Indeed, since the 2000s, behind every microscope there are now automated systems, digital sensors, digital cameras and of course one or more computers. The latter are present throughout the entire process from image acquisition to the interpretation of their content. As explained in [20], the nature of experiments has therefore evolved from purely qualitative observations to quantitative analyses on computers. (*in collaboration with D. Sage, EPFL, BIG Group, Lausanne, Switzerland*)

D. Sage, A. Badoual. *Image Processing and Image Analysis in Microscopy*. In *Photonic Imaging for Biology: From Conventional Microscopy to Super-Resolution*, Chapter 10, 2025-237, John Wiley and Sons Inc., J.-B. Sibarita (editor), 2025, ISBN: 978-1-394-41788-9, hal-05469062, [20].

DeepCristae, a CNN for the restoration of mitochondria cristae in live microscopy images

Participants: Anaïs Badoual, Charles Kervrann.

Mitochondria play an essential role in the life cycle of eukaryotic cells. However, we still do not know how their ultrastructure, like the cristae of the inner membrane, dynamically evolves to regulate these fundamental functions, in response to external conditions or during interaction with other cell components. Although high-resolution fluorescent microscopy coupled with recently developed innovative probes can reveal this structural organization, their long-term, fast and live 3D imaging remains challenging. To address this problem, we have developed a convolutional neural network (CNN), called DeepCristae [14], to restore mitochondrial cristae in low spatial resolution microscopy images. Our CNN is trained from 2D STED images using a novel loss specifically designed for cristae restoration. Random sampling centered on mitochondrial areas was also developed to improve training efficiency. Quantitative assessments were carried out using metrics we derived to give a meaningful measure of cristae restoration. Depending on the conditions of use indicated, DeepCristae works well on broad microscopy modalities (STED, Live-SR, AiryScan and LLSM). It is ultimately applied in the context of mitochondrial network dynamics during interaction with endo/lysosomes membranes. (*in collaboration with J. Salamero, L. Leconte, C.A. Valades-Cruz, CNRS-UMR144, Institut Curie; T. Liu, Z. Chen, PKU University, Institute of Molecular Medicine, Beijing, People Republic of China*) S. Papereux, L. Leconte, C.A. Valades-Cruz, T. Liu, J. Dumont, Z. Chen, J. Salamero, C. Kervrann, A. Badoual. *DeepCristae, a CNN for the restoration of mitochondria cristae in live microscopy images*, *Communications Biology*, 8, 320, 2025, DOI:10.1038/s42003-025-07684-x, hal-04295317, [14].

Polarization MultiFocus Microscopy for volumetric super-resolution and orientation imaging of biofilaments

Participant: Caio Vaz Rimoli.

Accessing molecular orientation in single molecule localization microscopy (SMLM) offers valuable insights into molecular ordering and organization in biological structures. Conventional single-molecule orientation-localization microscopy (SMOLM) methods typically rely on either engineering the microscope's point-spread function (PSF) to encode the orientation information or on polarization-resolved detection. While PSF engineering enables detailed orientation analysis, it often requires complex computational analysis and suffers from reduced performance in dense cellular environments due to PSF spreading and overlap. In contrast, polarization-based approaches are easier to implement and are more fit when imaging dense samples but are typically unable to retrieve the axial information of single molecules.

To overcome this limitation, we introduced the Polarization MultiFocus Microscope (PoIMFM), a novel method for simultaneously retrieving the orientation and 3D position of single molecules [24]. PoIMFM combines the orientation measurement capabilities of a 4-polarization splitting scheme with a 3-planes multifocus microscope (MFM) enabling the reconstruction of molecular 2D orientation, wobble, and axial localization in a single acquisition. Through simulations, we demonstrated that PoIMFM accurately recovers

both orientation and 3D position, despite PSF defocusing. Experimental validation with reference samples shows that PolMFM matches the orientation precision of 4-Polar STORM, while uniquely adding axial information.

Moreover, we demonstrated the power of PolMFM by resolving the orientation and 3D positions of molecules in actin filaments in fixed cells, and by revealing that chromatin in crickets undergoes major reorganization and increased ordering during spermiogenesis. These findings highlight the potential of PolMFM for high-precision, multidimensional super-resolution imaging in complex and crowded biological environments. (*in collaboration with B. Hajj, CNRS-UMR168, Institut Curie, Paris, France; S. Brasselet, Institut Fresnel, Marseille, France*)

L. Régnier, C. V. Rimoli, S. Dey, F.C. Tsai, G.A. Orsi, S. Brasselet, B. Hajj . *Polarization Multi-Focus Microscopy for volumetric super-resolution and orientation imaging of biofilaments*, BioRxiv DOI:[10.1101/2025.11.19.687997](https://doi.org/10.1101/2025.11.19.687997), [hal-05392077](https://hal.archives-ouvertes.fr/hal-05392077), [24].

8.2 Supervised deep-learning for detection, segmentation, classification, and motion analysis in imaging

Template Learning: deep learning with domain randomization for particle picking in cryo-electron tomography

Participant: Charles Kervrann.

Cryo-electron tomography (cryo-ET) enables the three-dimensional visualization of biomolecules and cellular components in their near-native state. Particle picking, a crucial step in cryo-ET data analysis, is traditionally performed by template matching—a method utilizing cross-correlations with available biomolecular templates. Despite the effectiveness of recent deep learning-based particle picking approaches, their dependence on initial data annotation datasets for supervised training remains a significant limitation. In this work, we proposed a technique that combines the accuracy of deep learning particle identification with the convenience of the model training on biomolecular templates enabled through a tailored domain randomization approach. Our technique, named Template Learning [8], automates the simulation of training datasets, incorporating considerations for molecular crowding, structural variabilities, and data acquisition variations. This reduces or even eliminates the dependence of supervised deep learning on annotated experimental datasets. We demonstrated that models trained on simulated datasets, optionally fine-tuned on experimental datasets, outperform those exclusively trained on experimental datasets. Also, we illustrated that Template Learning used as an alternative to template matching, can offer higher precision and better orientational isotropy, especially for picking small non-spherical particles. Template Learning software is open-source, Python-based, and GPU and CPU parallelized. (*in collaboration with M. Eltsov and M. Harastani, IGBMC Strasbourg and Institut Pasteur Paris, France*)

M. Harastani, G. Patra, C. Kervrann, M. Eltsov. *Template Learning: deep learning with domain randomization for particle picking in cryo-electron tomography*, Nature Communications, 16, 8833, 2025, DOI:[10.1038/s41467-025-63895-0](https://doi.org/10.1038/s41467-025-63895-0), [hal-04874266](https://hal.archives-ouvertes.fr/hal-04874266), [8].

Deep learning detection of dynamic exocytosis events in fluorescence TIRF microscopy

Participants: Charles Kervrann, Arthur Masson.

Segmentation and detection of biological objects in fluorescence microscopy is of paramount importance in cell imaging. Deep learning approaches have recently shown promise to advance, automatize and accelerate analysis. However, most of the interest has been given to the segmentation of static objects of 2D/3D images whereas the segmentation of dynamic processes obtained from time-lapse acquisitions has been less explored. Here we adapted DeepFinder, a U-net originally designed for 3D noisy cryo-electron tomography (cryo-ET) data, for the detection of rare dynamic exocytosis events (termed ExoDeepFinder [10]) observed in

temporal series of 2D Total Internal Reflection Fluorescent Microscopy (TIRFM) images. ExoDeepFinder achieved good absolute performances with a relatively small training dataset of 60 cells/12000 events. We rigorously compared deep learning performances with unsupervised conventional methods from the literature. ExoDeepFinder outperformed the tested methods, but also exhibited a greater plasticity to the experimental conditions when tested under drug treatments and after changes in cell line or imaged reporter. This robustness to unseen experimental conditions did not require re-training demonstrating generalization capability of ExoDeepFinder. ExoDeepFinder, as well as the annotated training datasets, were made transparent and available through an open-source software as well as a Napari plugin and can directly be applied to custom user data. The apparent plasticity and performances of ExoDeepFinder to detect dynamic events open new opportunities for future deep-learning guided analysis of dynamic processes in live-cell imaging. (*in collaboration with H. Lachuer, Institut Jacques Monod, Paris, France; K. Schauer, Institut Gustave-Roussy; A.S. Macé, CNRS-UMR144, PICT-IBiSA, Institut Curie, Paris, France*)

H. Lachuer, E. Moebel, A.S. Macé, A. Masson, K. Schauer, C. Kervrann. *Deep learning detection of dynamic exocytosis events in fluorescence TIRF microscopy*, PLoS Computational Biology, 21(10): e1013556, 2025, DOI:[10.1371/journal.pcbi.1013556](https://doi.org/10.1371/journal.pcbi.1013556), [hal-04874728](https://hal.archives-ouvertes.fr/hal-04874728), [10].

H. Lachuer, E. Moebel, A.S. Macé, A. Masson, K. Schauer, C. Kervrann. *Deep learning detection of dynamic exocytosis events in TIRF microscopy*, In Colloque Français d'Intelligence Artificielle en Imagerie Biomédicale (IABM), Nice, France, 2025, [hal-05470418](https://hal.archives-ouvertes.fr/hal-05470418), [26]. (poster)

Ensembling Unets for rare chromosomal aberration detection in metaphase images, uncertainty quantification, and ionizing radiation dose estimation

Participant: Charles Kervrann.

In biological dosimetry a radiation dose is estimated using the average number of chromosomal aberrations per peripheral blood lymphocytes [17, 19, 22]. This analysis is still manually performed on 2D metaphase images depicting the 23 pairs of chromosomes because the false discovery rate of current automated detection systems is too high and variable because of sensitivity to small variations in image quality (chromosome spread, illumination variations ...). Therefore, the current systems are only used to assist human experts. Designing more performant automatic and reliable chromosomal aberration detection systems has become of paramount importance to improve diagnosis speed and reduce human expertise time. In this work, we proposed a novel deep-learning method for automatic rare chromosomal aberration detection and uncertainty quantification. We formulate the problem as a unique regression problem requiring the minimization of a sparsity-promoting loss to reduce the false alarm rate. Furthermore, we select checkpoints at the end of each epoch during training to form a model ensemble. The resulting artificial experts are further analyzed to derive a consensus voting, similar to an agreement of human annotator rating, to provide trustworthy aberration detections and confidence intervals. We also propose in this work an approach to visualize training dynamics using low-dimension representation to better interpret the relationships between training stochasticity and ensemble diversity [17]. A radiation dose curve is finally derived from deep learning-assisted counting of dicentric and fragments in metaphase images, in high agreement with the reference hand-crafted curve in biological dosimetry with a promising dose estimation validation. This approach provided a convenient explainable artificial intelligence tool to understand the mechanism of the chromosomal aberration detection of the model. (*in collaboration with M.A. Benadjaoud, ASNR, PSE-SANTE/SERAMED/LRacc, Fontenay-aux-Roses, France*)

A. Deschemps, E. Grégoire, J.S. Martinez, A. Vaurijoux, P. Fernandez, D. Dugue, L. Bobyk, M. Valente, G. Gruel, E. Moebel, M.A. Benadjaoud, C. Kervrann. *Ensembling Unets for rare chromosomal aberration detection in metaphase images, uncertainty quantification, and ionizing radiation dose estimation*, 2024, [hal-04874432](https://hal.archives-ouvertes.fr/hal-04874432). (submitted to "Cytometry Part A, in revision)

A. Deschemps, E. Grégoire, J.S. Martinez, A. Vaurijoux, P. Fernandez, D. Dugue, L. Bobyk, M. Valente, G. Gruel, E. Moebel, M.A. Benadjaoud, C. Kervrann. *Explainable artificial intelligence approach using low-dimensional visualization and ensembling uncertainty quantification for rare chromosomal aberration detection in cytogenetic imaging*, Proc. of Int. Conf. on Image Processing, Theory, Tools and Applications (IPTA), Istanbul, Turkiye, 2025, DOI:[10.1109/IPTA66025.2025.11222058](https://doi.org/10.1109/IPTA66025.2025.11222058), [hal-05446156v1](https://hal.archives-ouvertes.fr/hal-05446156v1), [17].

Prediction of parametric surfaces for multi-object segmentation in 3D biological imaging

Participants: Quentin Rapilly, Anaïs Badoual, Charles Kervrann.

Multi-object segmentation algorithms are of great interest in a very large range of fields. Deep learning brought major improvements in terms of processing speed or prediction accuracy. Nevertheless, some traditional methods such as active surfaces have features that conventional deep learning methods cannot provide, especially representing the object in a continuous geometrical way and encoding prior information on the shapes to segment. Those features are of particular interest in biology to efficiently segment noisy and poorly resolved data, and then understand the interactions between segmented cells. We introduced NAGINI-3D (N-Active shapes for seGmentINg 3D biological Images) [18, 21], a new hybrid segmentation method dedicated to multi-object segmentation of 3D images that combines the efficiency of deep learning and the powerful representation of active surfaces. We evaluated our method on real and synthetic 3D datasets of fluorescence microscopy. (*in collaboration with P. Maindron and G. Bouet, SAINBIOSE - Santé Ingénierie Biologie, Saint-Etienne, France*)

Q. Rapilly, A. Badoual, P. Maindron, G. Bouet, C. Kervrann. *Prediction of parametric surfaces for multi-object segmentation in 3D biological imaging*, In Proc. of Int. Conf. on Scale Space and Variational Methods in Computer Vision (SSVM), Totnes, United Kingdom, 2025, DOI:[10.1007/978-3-031-92366-1_20](https://doi.org/10.1007/978-3-031-92366-1_20), [hal-04978619](https://hal.archives-ouvertes.fr/hal-04978619), [18].

Q. Rapilly. *A hybrid CNN-snake approach for localization, segmentation, and shape representation in 3D biological imaging*, PhD Thesis, University of Rennes, December 2025, [tel-05502320](https://tel.archives-ouvertes.fr/tel-05502320), [21].

Q. Rapilly, P. Maindron, G. Bouet-Chalon, A. Badoual, C. Kervrann. *Segmentation multi-objets par prédiction de surfaces paramétriques pour l'imagerie biologique 3D*, In Colloque Français d'Intelligence Artificielle en Imagerie Biomédicale (IABM), Nice, France, 2025, [hal-05467429](https://hal.archives-ouvertes.fr/hal-05467429), [27]. (poster)

8.3 Analysis of spatiotemporal biological mechanisms and processes

Acidification on the plasma membrane

Participants: Ludger Johannes, Christian Wunder.

The pH balance between extracellular and intracellular space is crucial for a multitude of cellular processes. Real-time observation of pH fluctuations in the range 4-9 in live cells and tissues in a sensitive, non-invasive manner has become feasible with advances in pH quantification by organic dyes, genetically encoded fluorescent proteins, and DNA-based probes. In this work [12], we discussed mechanisms through which pH affects cell cycle, transcription, senescence, neurotransmission, glycolipid-lectin driven endocytosis, tissue remodelling, immune responses, and GPCR signalling. Growth factor-stimulated acidification of the extracellular space notably triggers enzymatic reactions like desialylation at the plasma membrane that control processes involving cell migration and bone resorption. Research into the role of pH in cellular physiology continues to be a fertile ground for discovery that underscores its fundamental importance. (*in collaboration with E. MacDonald, CRBM - Centre de recherche en Biologie cellulaire de Montpellier*)

E. MacDonald, L. Johannes, C. Wunder. *Acidification on the plasma membrane*, Current Opinion in Cell Biology, 95, 2025, DOI:[10.1038/s42003-025-07684-x](https://doi.org/10.1038/s42003-025-07684-x) [10.1016/j.ceb.2025.102531](https://doi.org/10.1016/j.ceb.2025.102531), [hal-05328086](https://hal.archives-ouvertes.fr/hal-05328086), [12].

Membrane glycoproteins get another go: the GlycoSwitch

Participants: Ludger Johannes, Christian Wunder.

The glycan makeup of membrane glycoproteins and glycosphingolipids at the cell surface is traditionally viewed as mature and static. Recent findings challenge this view, showing that selective glycan remodeling can redirect membrane glycoproteins back to the Golgi for another go. In this review we discussed the glycosylation processes in cells, with a focus on the terminal glycan chains on proteins and lipids that are capped by sialic acid sugars, and that engage the glycan-binding proteins of the galectin family. We highlighted new studies demonstrating that growth factors trigger the removal of sialic acid by endogenous neuraminidases at the cell surface, leading to glycolipid–lectin driven endocytosis and retrograde traffic to the Golgi. This molecular circuit, termed the GlycoSwitch, introduces new perspectives on glycan-mediated regulation of cellular functions. (*in collaboration with R. Weigert, CI-NIH Bethesda, USA; H. Clausen, University of Copenhagen, Department of Cellular and Molecular Medicine, Denmark*)

L. Johannes, R. Weigert, C. Wunder, H. Clausen, K. Schjoldager. *Membrane glycoproteins get another go: the GlycoSwitch*, Trends in Cell Biology, 2025, DOI:[10.1016/j.tcb.2025.09.005](https://doi.org/10.1016/j.tcb.2025.09.005). (In Press)

Galectin-3 mediated endocytosis of the orphan G-protein-coupled receptor GPRC5A

Participants: Ludger Johannes, Christian Wunder.

Galectins, a family of glycan-binding proteins, play crucial roles in various cellular functions, acting at both intracellular and extracellular levels. Among them, Galectin-3 (Gal-3) stands out as a unique member, possessing an intrinsically unstructured N-terminal oligomerization domain and a canonical carbohydrate-recognition domain (CRD). Gal-3 binding to glycosylated plasma membrane cargo leads to its oligomerization and membrane bending, ultimately resulting in the formation of endocytic invaginations. An interactomic assay using proteomic analysis of endogenous Gal-3 immunoprecipitates identified the orphan G protein-coupled receptor GPRC5A as a novel binding partner of Gal-3. GPRC5A, also known as Retinoic Acid-Induced protein 3 (RAI3), is transcriptionally induced by retinoic acid. Our results further demonstrated that extracellular recombinant Gal-3 stimulates GPRC5A internalization. In SW480 colorectal cancer cells, glycosylated GPRC5A interacts with Gal-3. Interestingly, while GPRC5A expression was upregulated by the addition of all-trans retinoic acid (ATRA), its endogenous internalization in SW480 cells was specifically triggered by extracellular Gal-3, but not by ATRA. This study provided new insights into the endocytic mechanisms of GPRC5A, for which no specific ligand has been identified to date. Further research may uncover additional Gal-3-mediated functions in GPRC5A cellular signaling and contribute to the development of innovative therapeutic strategies. (*in collaboration with University of Strasbourg, France and University of Jijel, Algeria*)

A. Boucheham, J. Mallor Franco, S. Bär, E. MacDonald, S. Zuttion, L. Blagec, B. Rinaldi, J. Chicher, L. Kuhn, P.e Hammann, C Wunder, L. Johannes, H. Recherche, S. Friant. *Galectin-3 mediated endocytosis of the orphan G-protein-coupled receptor GPRC5A*, Cells, 14(19):1571, 2025, DOI:[10.3390/cells14191571](https://doi.org/10.3390/cells14191571).

Next-generation small molecule inhibitors of clathrin function acutely inhibit endocytosis

Participants: Ludger Johannes, Massiullah Shafaq-Zadah, Estelle Dransart.

Clathrin-mediated endocytosis (CME) is the predominant endocytic pathway in eukaryotic cells and a major regulator of cell physiology as it facilitates the internalization of receptors, channels, and transporters and viral entry. The clathrin terminal domain acts as a central protein interaction hub within the endocytic protein network. Previously described inhibitors of CME display off-target activities that result in cytotoxicity, providing limitations to their use. Here, we reported the development and characterization of next-generation small molecule inhibitors of clathrin terminal domain function. These compounds termed Pitstop 2c and Pitstop 2d occupy the binding site within the clathrin terminal domain for endocytic protein ligands including epsin, resulting in potent inhibition of receptor-mediated endocytosis and reduced entry of vesicular stomatitis virus (VSV) with minimal cytotoxic side effects. Next-generation Pitstops thus provide an improved toolset to address clathrin function in cell physiology with potential applications as inhibitors of virus and pathogen entry.

(in collaboration with Leibniz-Forschungsinstitut für Molekulare Pharmakologie (FMP), Berlin, Germany; Department of Biology, Chemistry, Pharmacy, Freie Universität Berlin, Germany; Helmholtz-Zentrum Berlin für Materialien und Energie, Macromolecular Crystallography, Berlin, Germany; Chemistry, School of Environmental and Life Sciences, The University of Newcastle, Callaghan, Australia)

A. Horatscheck, M. Krauß, H. Bulut, V. Chambon, M. Shafaq-Zadah, E. Dransart, K. Peloza, K.F. Santos, M.J. Robertson, K. Prichard, S. Miksche, S. Radetzki, J.-P. von Kries, M.C. Wahl, A. McCluskey, L. Johannes, V. Haucke, M. Nazaré. *Next-generation small molecule inhibitors of clathrin function acutely inhibit endocytosis*, *Structure*, 33:878-890, 2025, DOI: [10.1016/str.2025.02.011](https://doi.org/10.1016/str.2025.02.011).

Growth factor-triggered desialylation controls glycolipid-lectin driven endocytosis

Participants: Ludger Johannes, Christian Wunder, Massiullah Shafaq-Zadah, Estelle Dransart.

Glycolipid-lectin (GL-Lect) driven endocytosis controls the formation of clathrin-independent carriers (CLICs) and the internalization of various cargos such as integrin. Whether this process is regulated in a dynamic manner remained unexplored. In this work [11], we demonstrated that within minutes, the epidermal growth factor triggers the galectin-driven endocytosis of cell surface glycoproteins, such as integrins, that are key regulators of cell adhesion and migration. The onset of this process, mediated by the Na⁺/H⁺ antiporter NHE-1 and the neuraminidases Neu1/3, requires the pH-triggered enzymatic removal of sialic acids whose presence otherwise prevents galectin binding. Desialylated glycoproteins are then retrogradely transported to the Golgi apparatus where their glycan makeup is reset to regulate EGF-dependent invasive cell migration. Further evidence is provided for a role of neuraminidases and galectin-3 in acidification-dependent bone resorption. Glycosylation at the cell surface thereby emerges as a dynamic and reversible regulatory post-translational modification that controls a highly adaptable trafficking pathway. (in collaboration with R. Weigert, CI-NIH Bethesda, USA; H. Clausen, University of Copenhagen, Department of Cellular and Molecular Medicine, Denmark; S. Mayor, National Centre for Biological Sciences, Bangalore, India; H. Leffler, Lund University, Division of Microbiology, Immunology and Glycobiology, Sweden)

E. MacDonald, A. Forrester, C.A. Valades-Cruz, T.D. Madsen, J. Hetmanski, E. Dransart, Y. Ng, R. Godbole, A. Akhil Shp, L. Leconte, V. Chambon, D. Ghosh, A. Pinet, D.D. Bhatia, B. Lombard, D. Loew, M.R. Larson, H. Leffler, D.J. Lefeber, H. Clausen, P. Caswell, M. Shafaq-Zadah, S. Mayor, R. Weigert, C. Wunder, L. Johannes. *Growth factor-induced desialylation for the fast control of endocytosis*, *Nature Cell Biology*, 27(3), 2025, DOI: [10.1038/s41556-025-01616-x](https://doi.org/10.1038/s41556-025-01616-x), [11].

Spatial N-glycan rearrangement on $\alpha5\beta1$ integrin nucleates galectin-3 oligomers to determine endocytic fate

Participants: Ludger Johannes, Christian Wunder, Massiullah Shafaq-Zadah, Estelle Dransart.

Membrane glycoproteins frequently adopt different conformations when altering between active and inactive states. In this work [15], we discovered a molecular switch that exploits dynamic spatial rearrangements of N-glycans during such conformational transitions to control protein function. For the conformationally switchable cell adhesion glycoprotein $\alpha5\beta1$ integrin, we found that only the bent-closed state arranges N-glycans to nucleate the formation of up to tetrameric oligomers of the glycan-binding protein galectin-3. We proposed a structural model of how these galectin-3 oligomers are assembled and how they clamp the bent-closed state to prime it for endocytic uptake and subsequent retrograde trafficking to the Golgi for polarized distribution in cells. Our findings highlighted an unexpectedly dynamic regulation of the glycan landscape at the cell surface to achieve oligomerization of galectin-3. Galectin-3 oligomers are thereby identified as decoders of defined spatial patterns of N-glycans and as functional extracellular interactors of specifically the bent-closed conformational state of $\alpha5\beta1$ integrin and possibly other family members. (in collaboration with H. Leffler, Lund University, Division of Microbiology, Immunology and Glycobiology,

Sweden; D. Roderer and S. Raunser, Leibniz-Forschungsinstitut für Molekulare Pharmakologie, Berlin, Germany)

M. Shafaq-Zadah, E. Dransart, C. Wunder, V. Chambon, C.A. Valades-Cruz, L. Leconte, N.K. Sarangi, J. Robinson, S. Bai, R. Regmi, A.D. Cicco, A. Hovasse, R. Bartels, U.J. Nilsson, S. Cianférani-Sanglier, H. Leffler, T.E. Keyes, D. Lévy, S. Raunser, D. Roderer, L. Johannes. *N-glycan rearrangement on $\alpha5\beta1$ integrin nucleates galectin-3 oligomers to determine endocytic fate*, Nature Communications, 16, 9461, 2025, DOI:10.1038/s41467-025-64523-7, hal-05335689, [15].

9 Bilateral contracts and grants with industry

Participants: Charles Kervrann.

9.1 Bilateral Grants with French State Operators

9.1.1 Contract with ASNR – Localization of chromosomal aberrations and detection of gene translocation between chromosomes induced by nuclear radiation dose excess in light microscopy images

Participant: Charles Kervrann.

Funding: ASNR (Autorité de Sûreté Nucléaire et Radioprotection)

Duration: (2020 – 2028)

Collaborator: M. Benadjaoud (ASNR, Direction de la Recherche et de l'Expertise en Santé, SERAMED/LRAcc, Fontenay-aux-Roses)

The first goal of this project was to develop statistical and deep-learning methods for localizing and classifying chromosomal aberrations observed in 2D microscopy images (blood test) and estimating radiation dose following a postulated nuclear reactor accident (PhD thesis of Antonin Deschemps).

The second goal was to develop supervised deep-learning classification and score-based diffusion methods and algorithms for the identification of gene translocation between chromosomes observed in FISH (Fluorescence in situ hybridization) microscopy images (PhD thesis of Quentin Tallon).

The third goal will consist in deploying generative AI and transfer learning methods in three areas: 1) The development of an AI model for the preselection of metaphases in Glemsa/Fish3 modalities; 2) the conversion of the automatic aberration counting in 3-Fish imaging into radiation dose, taking into account confounding factors and associated uncertainties; 3) the development of a new AI model for the automatic counting of chromosomal aberrations in M-Fish imaging (PhD thesis of Amine Banani).

This project funded by the ASNR, Région-Bretagne, ANR (ASTRID program), and AID (Agence de l'Innovation de Defense) concerned the PhD theses of Antonin Deschemps (2020-2023), Quentin Tallon (2022-2025), and Amine Banani (2026-2028) and the post-doc of Emmanuel Moebel (2022-2023).

10 Partnerships and cooperations

10.1 International initiatives

10.1.1 Participation in other International Programs

Informal international partners

Participants: Charles Kervrann, Ludger Johannes, Anaïs Badoual, Christian Wunder, Massiullah Shafaq-Zadah, Estelle Dransart, Caio Vaz Rimoli, Arthur Masson, Vincent Briane.

- Collaboration with Kyoto University Graduate School of Medicine (M. Arizono), Kyoto, Japan: *analysis of astrocytic calcium activity*. (with A. Badoual)
- Collaboration with EPFL (D. Sage), Biomedical Imaging Group, Lausanne, Switzerland: *Writing of a book chapter for image processing and image analysis in microscopy; preparation and conduct of a workshop for Mifobio 2025* (with D. Sage). (with A. Badoual)
- Collaboration with EPFL (J. Fageot), Lausanne, Switzerland: *Spline-based representation of time-evolving closed 3D shapes*. (with A. Badoual)
- Collaboration with the Institute of Hydrobiology (C.A. Valades-Cruz), Chinese Academy of Sciences, Wuhan, China: *Statistical analysis of molecule transport in cells in 3D lattice light sheet microscopy*. (with C. Kervrann, V. Briane)
- Collaboration with Advanced Bioimaging Unit (L. Leconte, L. Malacrida), Institut Pasteur, Montevideo Uruguay: *Deployment of BioImageIT software for the design of microscopy image analysis pipelines*. (with C. Kervrann, A. Masson)
- Collaboration with University of Campinas - UNICAMP (A. M. Dos Santos), Campinas, São Paulo State, Brazil: *Novel spectral confocal imaging and super-resolution microscopy studies of membrane organization in clathrin-independent endocytosis processes with Galectin3*. (with C.V. Rimoli, L. Johannes, E. Dransart, M. Shafaq-Zadah, C. Wunder)
- Collaboration with NCI-NIH Bethesda (R. Weigert), USA: *EGF-induced desialylation for the fast control of endocytosis*. (with L. Johannes, M. Shafaq-Zadah, C. Wunder, E. Dransart)
- Collaboration with Samuel Lunenfeld Research Institute (J.W. Dennis), Toronto, Canada: *SLC3A2 N-glycosylation and Golgi remodeling regulate SLC7A amino acid exchangers and stress mitigation*. (with L. Johannes, M. Shafaq-Zadah, C. Wunder, E. Dransart)
- Collaboration with University of Copenhagen, Department of Cellular and Molecular Medicine (H. Clausen), Denmark: *EGF-induced desialylation for the fast control of endocytosis; EGF-induced desialylation for the fast control of endocytosis*. (with L. Johannes, M. Shafaq-Zadah, C. Wunder, E. Dransart)
- Collaboration with National Centre for Biological Sciences (S. Mayor), Bangalore, India: *EGF-induced desialylation for the fast control of endocytosis*. (with L. Johannes, M. Shafaq-Zadah, C. Wunder, E. Dransart)
- Collaboration with Lund University, Division of Microbiology, Immunology and Glycobiology (H. Leffler), Sweden: *Spatial N-glycan rearrangement on $\alpha 5\beta 1$ integrin nucleates galectin-3 oligomers to determine endocytic fate; Endocytic roles of glycans on proteins and lipids; EGF-induced desialylation for the fast control of endocytosis*. (with L. Johannes, M. Shafaq-Zadah, C. Wunder, E. Dransart)
- Collaboration with Leibniz-Forschungsinstitut für Molekulare Pharmakologie (D. Roderer, S. Raunser), Berlin, Germany: *Spatial N-glycan rearrangement on $\alpha 5\beta 1$ integrin nucleates galectin-3 oligomers to determine endocytic fate*. (with L. Johannes, M. Shafaq-Zadah, C. Wunder, E. Dransart)
- Collaboration with University of Namur, Department of Biology-Faculty of Sciences (H.-F. Renard), Belgium: *N-BAR and F-BAR proteins - endophilin-A3 and PSTPIP1 - control the clathrin-independent endocytosis of LICAM*. (with L. Johannes, M. Shafaq-Zadah, C. Wunder, E. Dransart)

10.2 International research visitors

10.2.1 Visits of international scientists

Other international visits to the team

Lucia Hradecká**Status** (PhD))**Institution of origin:** Centre for Biomedical Image Analysis, Faculty of Informatics, Masaryk University**Country:** Czech Republic**Dates:** from June 3rd to June 20th, 2025**Context of the visit:** Collaboration about the development of methods for the segmentation and tracking of collectively developing cells in large-scale multidimensional image data using deep learning.**Mobility program/type of mobility:** research stay**10.2.2 Visits to international teams****Research stays abroad****Massiullah Shafaq-Zadah****Visited institution:** Leibniz-Forschungsinstitut für Molekulare Pharmakologie (D. Roderer), Berlin**Country:** Germany**Dates:** September 2025 (one week)**Context of the visit:** Project management and samples preparation for cryo-electron microscopy.**Mobility program/type of mobility:** research stay**10.3 European initiatives****10.3.1 Other european programs/initiatives****ESFRI initiative program:** EuroBioImaging**Participants:** Charles Kervrann, Arthur Masson.**Coordinator:** J. Eriksson (Turku University, Finland)**Funding:** Member states of the European Union**Partners:** 18 European countries in 2022 (+1 observer)

As a member of the National Research Infrastructures (RI) France BioImaging, SAIRPICO is involved in the [ESFRI Euro-BioImaging](#) project, and now in the ERIC EuroBioImaging (since November 2019), one of the landmarks of biomedical science Research Infrastructures in the roadmap of the European Strategic Forum on Research Infrastructures (ESFRI 2018). The mission of Euro-BioImaging is to provide access, service and training to state-of-the-art imaging technologies and foster the cooperation and networking at the European level including multidisciplinary scientists, industry, regional, national and European authorities.

10.4 National initiatives**10.4.1 France-BioImaging project**

Participants: Charles Kervrann, Arthur Masson.

Duration: 2011 – 2030

Funding: Investissement d’Avenir, ANR INBS-PIA1 2011 and “FBI Next Generation” (ANR program 2020-2030)

Coordinator: R.-M. Mège (Institut Jacques Monod, CNRS)

Partners: CNRS, Aix-Marseille Université, Collège de France, Ecole Normale Supérieure, Ecole Polytechnique, Inria, Institut Curie, Institut Pasteur, INSERM, Université de Bordeaux, Université de Montpellier, Université de Nantes, Université de Paris, Université de Rennes, Université de Rouen, Université de Strasbourg, Université de Lyon, Université de Grenoble, Université de Toulouse.

SAIRPICO (previously SERPICO 2010-2023) is member of the French initiative, the so-called “France-BioImaging” (FBI) National Research Infrastructure which gathers several outstanding cellular imaging centers (microscopy, spectroscopy, probe engineering and signal processing). FBI is on the [French Roadmap of Research Infrastructure](#). The mission of FBI is to build a distributed coordinated French infrastructure for photonic and electronic cellular bioimaging, dedicated to innovation, training and technology transfer. High-computing capacities are needed to exhaustively analyze image flows.

SAIRPICO is head of the IPDM (Image Processing and Data Management) node of the FBI network composed of 11 nodes since Jan 2024. In this context, we address the following scientific problems: i/ exhaustive analysis of bioimaging data sets; ii/ deciphering of key steps of biological mechanisms at organ, tissular, cellular and molecular levels through the systematic use of time-lapse 3D microscopy and image processing methods; iii/ storage and indexing of extracted and associated data and metadata through an intelligent data management system. The team recruited R&D engineers to disseminate image processing software for large scale computing and data sets processing.

This project concerned the two internships of E. Choffat (Master 2) and C. Ntsoumou Lihoula (Master 2) (supervised by A. Masson) in 2025.

10.4.2 ANR POLARISCOPIA project: Next generation information processing of microscopy vector-valued images : application in cell polarized imaging

Participants: Charles Kervrann, Luuger Johannes, Caio Vaz Rimoli, Arthur Masson, Vincent Briane, Chencheng Gu, Leo Maury, Ferdinand Plesse–Costa.

Duration: 48 months (Oct 2022 – Sept 2026)

Funding: ANR (Agence Nationale de la Recherche) PRME

Coordinator: Charles Kervrann

The objective of the project is to create the next generation of information processing techniques required to overcome the three aforementioned barriers, and to solve challenging image processing problems induced by the acquisition of 3D+Time vector-valued images. This will be achieved here by integrating concepts in statistical signal-image processing and machine learning, combined with innovative developments in fluorescence microscopy. The resulting algorithms will serve to characterize the dynamics of biomolecules and to decipher the molecular transport pathways, which are of considerable of interest in fundamental cell biology and for future precision medicine.

This project concerned the postdoc position of Vincent Briane and the PhD positions of Léo Maury and Chencheng Gu (supervised by C. Kervrann) in 2025.

10.4.3 ANR DEEPNER project: Deciphering chromatin rearrangements in response to UV irradiation using new deep learning based cryo-electron tomography data analysis tools

Participants: Charles Kervrann, Mounir Messaoudi.

Duration: 48 months (Oct 2023 – Sept 2027)

Funding: ANR (Agence Nationale de la Recherche) PRC

Coordinator: Mikhail Eltsov (IGBMC, Strasbourg)

Partners: Sorbonne University (IMPMC), Inria Rennes (SAIRPICO Team)

The goal is to reveal, with unprecedented resolution, chromatin reorganization during genotoxic stress. We will analyze the following three structural levels of the chromatin: (1) spatial organization of chromatin domains (nucleosome distribution, density, local order); (2) geometry of DNA linkers and (3) conformation and disassembly of nucleosomes. This analysis will reveal the chromatin structure-based mechanisms enabling detection and repair of UV-induced lesions in the chromatin context. To enable this analysis, we will develop appropriate DL approaches and software, in particular those for in situ cryo-ET data annotation and analysis. The added value of this research will be cryo-ET data analysis methods and algorithms embedded in software enabling not only an automated in situ annotation and analysis of nucleosomes but also other molecular complexes, in health and disease.

This project concerned the PhD position of Mounir Messaoudi (supervised by C. Kervrann) in 2025.

10.4.4 ANR OMEGA-MEMDO: Orientation microscopy and cryo-electron tomography to study glycan-dependent assembly of membrane nanodomains

Participants: Ludger Johannes, Charles Kervrann, Massiullah Shafaq-Zadah, Caio Vaz Rimoli, Estelle Dransart, Xingyi Cheng, Ferdinand Plesse-Costa, Ilyes Hamitouche.

Duration: 48 months (Oct 2025 – Sept 2029)

Funding: ANR (Agence Nationale de la Recherche) PRC

Coordinator: Ludger Johannes

Partners: UMR168 (B. Hajj, D. Levy, Julien Maufroid, Amaury Autric) - Institut Curie

With the OMEGA-MEMDO program, we will use forefront techniques to monitor the membrane nanodomain construction process from cellular to molecular scales. Oligomerization site mutants of Gal3 and glycosylation site mutants of $\alpha 5 \beta 1$ integrin will be tested on cells by lattice light sheet microscopy for endocytic uptake, and by Single Molecule Orientation-Localization Microscopy (SMOLM) for orientation and order of lipids and proteins at the nanoscale. Purified Gal3, $\alpha 5 \beta 1$ integrin, and mutants will be analyzed by cryo-electron tomography (cryo-ET) on model membrane systems to visualize individual proteins and their conformation, spatial organization, and membrane environment. Developments in image processing and artificial intelligence will be performed to extract and correlate cellular and molecular information from SMOLM and cryo-ET datasets.

This project concerned the postdoc position of Xingyi Cheng and the PhD position of Ferdinand Plesse-Costa (supervised by C. Kervrann, B. Hajj (UMR168 - Institut Curie), and C. Vaz Rimoli) in 2025.

10.4.5 Fondation ARC Programmes labellisés (PGA): Dysregulation of sialoglycans via the GlycoSwitch pathway controls immune modulation during tumor progression

Participants: Ludger Johannes, Christian Wunder, Massiullah Shafaq-Zadah, Estelle Dransart, Ilyes Hamitouche.

Duration: 36 months (Oct 2025 – Sept 2028)

Funding: Fondation ARC

Coordinator: Ludger Johannes

Define changes in sialic acid and GlycoSwitch component expression during tumor progression in a mouse model of HNSCC and in vitro, determine the stage at which the impairment of the GlycoSwitch results in inhibition of tumor progression through blockage of immune evasion, and transpose findings from the mouse model to patient samples.

10.5 Regional initiatives

10.5.1 Allocations d'Installation Scientifique (AIS)

Participant: Anaïs Badoual.

Funding: Rennes Métropole

Duration: 36 months (Oct 2022 – Sep 2025)

This project concerned the internships of two Master 1 students in 2025.

- Maelys Hanoire (4 months, from April 2025 to August 2025) – "*Classification of astrocytic calcium signals observed with 3D lattice light sheet fluorescence microscopy*". The goal of the internship was to develop a method to classify segmented astrocytic calcium signals into those that are localized within microdomains and those that propagate throughout the astrocyte. Due to the lack of reliable labeled annotations, the work primarily focused on unsupervised 3D approaches, using either applied mathematics techniques (such as PCA) or deep learning methods.
- Matteo Audigier (3 months from June 2025 to August 2025) – "*Development of Python modules for image processing in 3D+time fluorescence microscopy images*". The goal of the internship was to rewrite an existing method, originally developed in Java by Anaïs Badoual, for detecting and segmenting calcium signals in 3D+time LLSM images into modular Python code. The work also focused on optimizing the method through parallelization and alternative mathematical algorithms, as well as adding the extraction of new quantitative metrics and improving the visualization of the results.

11 Dissemination

11.1 Promoting scientific activities

11.1.1 Scientific events: organisation

Participant: Ludger Johannes.

General chair, scientific chair

- Ludger Johannes :
 - > Henrik Clausen, Copenhagen Center of Glycomics (Denmark) on May 20, 2025: "*New strategies to study recognition and functions of glycans – more than meets the eye !*"
 - > Helge Ewers, Breie Universität Berlin (Germany) on July 4th, 2025: "*Adhesion energy controls lipid binding-mediated endocytosis*".

11.1.2 Scientific events: selection

Participants: Charles Kervrann.

Member of the conference program committees

- Charles Kervrann was member of the scientific committee of IABM'2025 (Colloque Français d'Intelligence Artificielle en Imagerie Biomédicale (IABM)).

11.1.3 Journal

Participants: Charles Kervrann, Ludger Johannes, Anaïs Badoual, Christian Wunder, Frédéric Lavancier.

Member of the editorial boards

- Charles Kervrann is Associate Editor for the "IEEE Transactions on Image Processing" journal (since 2021).
- Ludger Johannes is member of the Editorial Board of the "Biology of the Cell" journal (since 2010) and "Toxins" (since 2015), and Academic Editor for the "PLoS ONE" journal (since 2013).
- Frédéric Lavancier is Associate Editor for the "Scandinavian Journal of Statistics" (since 2024) and for "Stateco" (since 2023).

Reviewer - reviewing activities

- Charles Kervrann was reviewer for "IEEE Transactions on Image Processing" and "IEEE Transactions on Computational Imaging" in 2025.
- Ludger Johannes was reviewer for "Nature" "Nature Communications", "Science Adv", "Cell Reports", "Proc. Natl Acad Sci. USA", "J Cell Biol", "Biol Cell", "PLoS One", "Frontiers", "EMBO J", "Biochem Soc Trans, Science", "Biochem Cell Biol", "ACS Nano", and "Trends in Celle Biology".
- Anaïs Badoual was reviewer for "Nature Methods" and "Signal Procesing" in 2025.
- Frédéric Lavancier was reviewer for "J. American Statistical Association" (JASA), and "Sports Analytics" in 2025.
- Christian Wunder was reviewer for "Communications Biology" in 2025.

11.1.4 Invited talks

Participants: Charles Kervrann, Ludger Johannes, Massiullah Shafaq-Zadah, Es-telle Dransart, Frédéric Lavancier, Quentin Rapilly.

- Charles Kervrann:
 - > *"Statistical and artificial methods for live-cell fluorescence imaging and cryo-electron tomography"*, IMPMC–CNRS UMR 7590 Sminar, Sorbonne University, Paris, France, January 2025. (seminar)
 - > *"Machine learning for molecule identification in 3D cryo-cellular tomograms"*, Journées de la Société Française des Microscopies (SF μ), Toulouse, France, July 2025. (invited talk)
 - > *"Deep learning to detect and identify molecules in 3D microscopy images"*, Journées INRAE Scientifiques et Techniques R μ I (JST R μ I), Versailles, France, November 2025. (invited talk)
 - > *"Deep learning to detect and identify molecules in 3D microscopy images"*, INRAE DIGIT-BIO Webinar, October 2025. (seminar)
 - > *"Deep learning to detect and identify molecules in 3D microscopy images"*, Interdisciplinary School MIFOBIO, Seignosse, France, October 2025. (invited talk)
 - > *"Deep learning and convolutional neural network for macromolecule detection and identification in 3D cryo-cellular tomograms"*, FRISBI webinar, November 2025. (seminar)
- Ludger Johannes:

- > *"GlycoSwitch: a novel signaling circuit to control endocytosis"*, 5 FEBS Special Meeting on Sphingolipid Biology/XIII International Ceramide Conference, Varna, Bulgaria, May 2025.
 - > *"Glycan-based membrane remodeling for endocytic uptake into cells"*, 5th Jacques Monod meeting on Membrane Organization and Remodeling in Roscoff, France, May 2025.
 - > *"GlycoSwitch: A novel signaling circuit to control endocytosis"*, Annual meeting of National Synchrotron Radiation Research Center in Hsinchu, Taiwan, September 2025. (Keynote lecture)
 - > *"GlycoSwitch: A novel signaling circuit to control endocytosis"*, Biomembrane Days, biannual conference series of the Max Planck Institute of Colloids and Interfaces, Berlin, Germany, September 2025.
 - > *"GlycoSwitch — a novel signaling circuit to control endocytosis"*, Annual GDR APPICOM meeting, Dourdan, France, November 2025.
 - > *"GlycoSwitch: a novel signaling circuit to control endocytosis"*, Annual meeting of the Department of Cellular and Molecular Medicine of the University of Copenhagen, Denmark, November 2025. (Keynote lecture).
 - > *"GlycoSwitch: a novel signaling circuit to control endocytosis"*, Université de Namur, Belgium, March 2025. (seminar)
 - > *"GlycoSwitch: a novel signaling circuit to control endocytosis"*, National Taiwan University, Taipei, Taiwan, 1st and 8th September 2025. (seminar)
 - > *"GlycoSwitch: a novel signaling circuit to control endocytosis"*, Chang Gung University, Taoyuan City, Taiwan, September 2025. (seminar)
- – Massiullah Shafaq-Zadah and Estelle Dransart:
 - > GlycoMADNESS Symposium, Paris, France, September 2025. (invited talk)
- Frédéric Lavancier:
 - > *"Estimating the hyperuniformity exponent of spatial point processes"*, SSIAB, Smögen, Sweden, June 2025. (invited talk)
 - Quentin Rapilly:
 - > *"NAGINI-3D: N-Active shapes for segmenting 3D biological images"*, RTMFM-MAIIA workshop webinar, December 2025. (seminar)

11.1.5 Leadership within the scientific community

Participants: Charles Kervrann, Ludger Johannes.

- Charles Kervrann is head of the "BioImage Informatics" node (ANR [France-BioImaging](#) project since January 2024, National Research Infrastructure" for Biology and Health) (co-head since 2011). He is member of the IEEE Signal Processing Society (since 2010).
- Ludger Johannes is member of the American Society for Cell Biology (since 1996), Société de Biologie Cellulaire de France (since 1996), French Society for Biophysics (SFB) and Membrane Study Group (GEM) (since 2012), Société de Chimie Thérapeutique (SCT) (since 2014), Biophysical Society (since 2015), Société Française pour l'Etude des Toxines (SFET) (since 2021), Société Française du Cancer (SFC) (since 2022), Société Chimique de France (SCF) (since 2023).

11.1.6 Scientific expertise

Participants: Ludger Johannes, Christian Wunder, Frédéric Lavancier.

- Ludger Johannes is:
 - > member of the scientific council of the Indo-French Centre for the Promotion of Advanced Research (IFCPAR/CEFIPRA since 2021,
 - > member of the permanent SVE3 HCERES expert panel (independent agency for the reviewing of research structures in France) (2021-2025),
 - > HCERES mission IAB, Grenoble (November 2025),
 - > member of the Scientific Council of the "Membrane Study Group" (since 2021),
 - > Member of the scientific council of the Chemical Biology Interest Group (GDR Chémobiologie) since 2021,
 - > member of the scientific committee of the Cellular and Tissular Imaging Platform (PICT) at CurieCoreTech of Institut Curie since 2021,
 - > member of the scientific council of Doctoral School BIOSIGNE (ED568) since 2014.
 - > scientific expert for the reviewing of projects for the European Innovation Council (EIC), European Research Council (ERC), Cancéropôle PACA, HCERES, CEFIPRA, Fondation Maladies Rares, Israel Science Foundation, and ANR in 2025,
 - > member of the reviewing body of the Hellenic Foundation for Research and Innovation (HFRI) since 2021.
- Christian Wunder was :
 - > Vice-chair for Evaluation of Marie Skłodowska-Curie Actions (MSCA) in HorizonEurope since 2012
 - > reviewer for CEFIPRA calls on DNA-origami in 2025,
 - > reviewer for the proposal evaluation of HORIZON-HLTH-2025-01-TOOL-03 ("Leveraging multimodal data to advance Generative Artificial Intelligence applicability in biomedical research" (GenAI4EU)) in 2025.
- Frédéric Lavancier was scientific expert for the reviewing of projects from the Swiss National Science Foundation in 2025.

11.1.7 Research administration

Participants: Charles Kervrann, Ludger Johannes, Massiullah Shafaq-Zadah.

- Charles Kervrann:
 - > Head of the SAIRPICO Project-Team since 2023.
 - > Head of the "BioImage Informatics" node (ANR [France-BioImaging](#) project, National Research Infrastructure" for Biology and Health) since Jan 2024 (co-head since 2011).
- Ludger Johannes:
 - > Deputy director of Chemical Biology of Cancer unit (INSERM-U1339 / CNRS-UMR3666) since January 2025.
 - > Head of Traffic, Signaling and Delivery team at Curie Institute since 2001.

- > Scientific director of the Metabolomics and Lipidomics Platform at CurieCoreTech of Institut Curie since 2021.
- > Representative of Doctoral School BIOSIGNE (ED568) in the Doctoral College of PSL University since 2016.
- > Institut Curie coordinator of institutional partnership between Institut Curie, CNRS and the National Centre for Biological Sciences (NCBS) à Bangalore (India) since 2012.
- Massiullah Shafaq-Zadah:
 - > Member of the laboratory council of UMR3666.

11.2 Teaching - Supervision - Juries - Educational and pedagogical outreach

Participants: Charles Kervrann, Ludger Johannes, Anaïs Badoual, Massiullah Shafaq-Zadah, Estelle Dransart, Caio Vaz Rimoli, Arthur Masson, Frédéric Lavancier.

11.2.1 Supervision

- PhD supervision
 - > Quentin Rapilly (PhD defended in December 2025, Inria grant): *"Hybrid CNN-Snake algorithms for quantitative analysis of 3D+time live-cell images"* (started in December 2022, supervised by A. Badoual and C. Kervrann).
 - > Léo Maury (PhD in progress, ANR Polariscaopia grant): *"Machine learning and optimization methods for 3D vector-valued microscopy image reconstruction"* (started in January 2024, supervised by C. Kervrann).
 - > Chencheng Gu (PhD in progress, ANR Polariscaopia grant): *"Spatial statistics and machine learning for molecular dynamics analysis in polarized microscopy"* (started in March 2024, supervised by C. Kervrann).
 - > Mounir Messaoudi (PhD in progress, ANR DeepNer grant): *"Machine learning for 3D cryo-electron tomogram analysis: localization, identification, and spatial organization of macromolecules in cells"* (started in May 2024, supervised by C. Kervrann).
 - > Ferdinand Plesse-Costa (PhD in progress, Inria grant): *"Statistical and machine learning for image reconstruction and super-resolution in fluorescence polarized microscopy"* (started in November 2024, supervised by C. Kervrann, B. Hajj (CNRS-UMR168 - Institut Curie), and C. Vaz Rimoli).
- Postdoc supervision
 - > Ilyes Hamitouche (INSERM grant), since June 2023, supervised by M. Shafaq-Zadah, E. Dransart, C. Kervrann, and L. Johannes.
 - > Xingyi Cheng (ANR Omega-MEMDO), since November 2025, supervised by C. Kervrann.
- Master supervision
 - > Matteo Audigier, Grenoble INP – ENSIMAG, Master 1, from Jun 2025 until Aug 2025, supervised by A. Badoual.
 - > Enzo Choffat, ESIEA – Laval, Master 2, from Apr 2025 until Aug 2025, supervised by A. Masson
 - > Maelys Hanoire, ESIEA – Laval, Master 1, from Apr 2025 until Aug 2025, supervised by A. Badoual.
 - > Carel Ntsoumou Lihoula, Ecole Nationale Supérieure d'Ingénieurs du Mans (ENSIM), Master 2, from Mar 2025 until Sep 2025, supervised by A. Masson.

11.2.2 Juries

Participants: Charles Kervrann, Ludger Johannes.

– Charles Kervrann:

- > President of the PhD defense committee of :
 - * X. Cheng - "*Automated image processing of membranes and membrane proteins in cryo-electron tomography*". UMR168 Institut Curie, University PSL, supervised by M. Dezi and D. Levy. (defense in June 2025)
 - * H. Barral - "*Self-supervised learning for infrared video enhancement*". Centre Borelli, ENS Paris-Saclay, University Paris-Saclay, supervised by P. Arias and A. Davy (defense in October 2025)
- > Reviewer for the PhD theses of :
 - * E. Grandgirard - "*Simulation-based deep learning for 3D nuclei segmentation and cell type classification in label-free imaging*". University of Toulouse, supervised by C. Sengès and M. Serrurier. (defense in November 2025)
 - * F. Robert - "*3D semantic cell segmentation via propagation of 2D results and integration of intercellular priors*". University of Bordeaux, supervised by B. Denis de Senneville and C.F. Grosset. (defense in September 2025)
- > Member of the PhD defense committee of :
 - * T. Bonte - "*Computer vision for the phenotypic profiling of the cell cycle*". Mines ParisTech, University PSL, supervised by T. Walter. (defense in April 2025)

– Ludger Johannes:

- > Reviewer and President of the PhD thesis of :
 - * S. Salame - "*A comprehensive characterization of lysophospholipid acyltransferases reveals the regulation and functions of glycerophospholipid lipid tails*". Université Nice Côte d'Azur, supervised by T. Harayama. (defense in May 2025)
- > Member of the PhD defense of:
 - * S. Ruggiero - "*Characterisation of the functions of the protein arginine methyltransferase PRMT4/CARM1 in triple-negative breast cancer*". Université Paris Sciences et Lettres, supervised by T. Dubois. (defense in November 2025)

11.2.3 Educational and pedagogical outreach

Participants: Charles Kervrann, Ludger Johannes, Anaïs Badoual, Frédéric Lavancier, Quentin Rapilly.

– Charles Kervrann:

- > Master 2: "*From Bioimage Processing to BioImage Informatics*", 3 hours (4.5 hours TD), coordinator of the module (30 hours / equiv 45 hours TD), Master 2 Research IRIV, Telecom-Physique Strasbourg and University of Strasbourg.
- > Engineer Degree (3rd year) and Master 2 Statistics and Mathematics: "*Statistical Models and Image Analysis*", 30 hours (45 hours TD), Ecole Nationale de la Statistique et de l'Analyse de l'Information (ENSAI), Bruz.
- > "*Basics in deep learning and convolutional neural networks for microscopy image analysis*", 1 hour, Interdisciplinary School MIFOBIO (300 participants), Seignosse, France, October 2025.

- > *"Statistical and artificial methods for live-cell fluorescence imaging and cryo-electron tomography"*, 2 hours, Master 2 Research "Digital Health", University of Rennes, France, November 2025.
- Ludger Johannes
 - > Master 2: *"Endocytic trafficking"* for "Chemical Frontiers of Living Cells", 2 hours, PSL Research University.
 - > Lecture *"Molecular Biology of the Cell"*, 2 hours, Institut Pasteur/Curie, lectures and lab training.
 - > Lecture *"Lipids and Glycans"* for "Chemical Frontiers of Living Cells" course, 2 hours, PSL Research University.
- Anaïs Badoual:
 - > Master 2 degree: *"Analysis of Image Sequences"*, 9 hours (13.5 hours TD) and 3 hours Practical Courses (2 hours TD), Master 2 Research SiVos, ISTIC & University of Rennes.
 - > Master 2 degree: *"Object Tracking in microscopy"*, 1.75 hours (2.63 hours TD), Master 2 Research IRIV, Telecom-Physique Strasbourg.
 - > Engineer Degree (3rd year) and Master 2 Statistics and Mathematics: *"Statistical Models and Image Analysis"*, 7.5 hours practical course (5 hours TD), Ecole Nationale de la Statistique et de l'Analyse de l'Information (ENSAI), Bruz.
 - > *"Human-in-the-loop for cell image segmentation"*, workshop, 2 1h45-sessions, Interdisciplinary School MIFOBIO, Seignosse, France, October 2025.
 - > Examiner in a Selection Committee of 1st year-students, Mines-Telecom, 2 days, 2025.
- Frédéric Lavancier:
 - > Engineer degree (2nd year) : *"Generalized and linear regression models"*, 24 hours (36 hours TD), coordinator, ENSAI.
 - > Engineer degree (2nd year) : *"Markovian models"*, 21 hours (31.5 hours TD), coordinator, ENSAI.
 - > Doctoral course : *"A short introduction to models and inference for spatial point processes"*, 4 hours, Cotonou, Benin, January 2025.
- Quentin Rapilly:
 - > Licence (L2) degree: *"Introduction to probabilities theory"*, 20 hours (TD), INSA Rennes
 - > Licence (L1) degree: *"Introduction to mathematics for engineering"*, 16 hours (Lecture/TD), INSA Rennes/ENSAB

11.3 Popularization

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

E. MacDonald, C. Nuges, L. Johannes. *Casser du sucre sur le dos des cellules cancéreuses*, 42(1): 36-28, Médecine/Sciences, 2026, DOI: [10.1051/medsci/2025249](https://doi.org/10.1051/medsci/2025249).

12 Scientific production

12.1 Major publications

- [1] S. Arumugam, S. Schmieder, W. Pezeshkian, U. Becken, C. Wunder, D. Chinnapen, J. H. Ipsen, A. Kenworthy, W. Lencer, S. Mayor and L. Johannes. 'Ceramide structure dictates glycosphingolipid nanodomain assembly and function'. In: *Nature Communications* 12.1 (Dec. 2021), p. 3675. DOI: [10.1038/s41467-021-23961-9](https://doi.org/10.1038/s41467-021-23961-9). URL: <https://hal.science/hal-04092098>.

- [2] V. Briane, C. Kervrann and M. Vimond. ‘Statistical analysis of particle trajectories in living cells’. In: *Physical Review E* 97.6 (11th June 2018), pp. 1–20. DOI: [10.1103/PhysRevE.97.062121](https://doi.org/10.1103/PhysRevE.97.062121). URL: <https://inria.hal.science/hal-01961971>.
- [3] A. Forrester, S. Rathjen, M. Daniela Garcia-Castillo, C. Bachert, A. Couhert, L. Tepshi, S. Pichard, J. Martinez, M. Munier, R. Sierocki, H.-F. Renard, C. Augusto Valades-Cruz, F. Dingli, D. Loew, C. Lamaze, J.-C. Cintrat, A. Linstedt, D. Gillet, J. Barbier and L. Johannes. ‘Functional dissection of the retrograde Shiga toxin trafficking inhibitor Retro-2’. In: *Nature Chemical Biology* 16.3 (Mar. 2020), pp. 327–336. DOI: [10.1038/s41589-020-0474-4](https://doi.org/10.1038/s41589-020-0474-4). URL: <https://hal.inrae.fr/hal-03321166>.
- [4] S. Herbreteau and C. Kervrann. ‘DCT2net: an interpretable shallow CNN for image denoising’. In: *IEEE Transactions on Image Processing* 31 (17th June 2022), pp. 4292–4305. DOI: [10.1109/TIP.2022.3181488](https://doi.org/10.1109/TIP.2022.3181488). URL: <https://inria.hal.science/hal-03511641>.
- [5] F. Lavancier, T. Pécot, L. Zengzhen and C. Kervrann. ‘Testing independence between two random sets for the analysis of colocalization in bioimaging’. In: *Biometrics* 76.1 (1st Mar. 2020), pp. 36–46. DOI: [10.1111/biom.13115](https://doi.org/10.1111/biom.13115). URL: <https://hal.science/hal-02369555>.
- [6] E. Moebel, A. Martinez-Sanchez, L. Lamm, R. D. Righetto, W. Wietrzynski, S. Albert, D. Larivière, E. Fourmentin, S. Pfeffer, J. Ortiz, W. Baumeister, T. Peng, B. D. Engel and C. Kervrann. ‘Deep Learning Improves Macromolecule Identification in 3D Cellular Cryo-Electron Tomograms’. In: *Nature Methods* 18.11 (21st Oct. 2021), pp. 1386–1394. DOI: [10.1038/s41592-021-01275-4](https://doi.org/10.1038/s41592-021-01275-4). URL: <https://inria.hal.science/hal-03509223>.
- [7] S. Prigent, C. A. Valades-Cruz, L. Leconte, L. Maury, J. Salamero and C. Kervrann. ‘BioImageIT: Open-source framework for integration of image data-management with analysis’. In: *Nature Methods* 19 (1st Nov. 2022), pp. 1328–1330. DOI: [10.1038/s41592-022-01642-9](https://doi.org/10.1038/s41592-022-01642-9). URL: <https://inria.hal.science/hal-03474512>.

12.2 Publications of the year

International journals

- [8] M. Harastani, G. Patra, C. Kervrann and M. Eltsov. ‘Template Learning: deep learning with domain randomization for particle picking in cryo-electron tomography’. In: *Nature Communications* 16.8833 (3rd Oct. 2025), pp. 1–15. DOI: [10.1038/s41467-025-63895-0](https://doi.org/10.1038/s41467-025-63895-0). URL: <https://inria.hal.science/hal-04874266> (cit. on p. 17).
- [9] S. Herbreteau and C. Kervrann. ‘A unified framework of non-local parametric methods for image denoising’. In: *SIAM Journal on Imaging Sciences* 18.1 (6th Jan. 2025), pp. 89–119. DOI: [10.1137/24M1630967](https://doi.org/10.1137/24M1630967). URL: <https://inria.hal.science/hal-04472406> (cit. on p. 15).
- [10] H. Lachuer, E. Moebel, A.-S. Macé, A. Masson, K. Schauer and C. Kervrann. ‘Deep learning detection of dynamic exocytosis events in fluorescence TIRF microscopy’. In: *PLoS Computational Biology* 21.10 (14th Oct. 2025), e1013556. DOI: [10.1371/journal.pcbi.1013556](https://doi.org/10.1371/journal.pcbi.1013556). URL: <https://inria.hal.science/hal-04874728> (cit. on pp. 17, 18).
- [11] E. Macdonald, A. Forrester, C. Valades-Cruz, T. D. Madsen, J. H. Hetmanski, E. Dransart, Y. Ng, R. Godbole, A. A. Shp, L. Leconte, V. Chambon, D. Ghosh, A. Pinet, D. Bhatia, B. Lombard, D. Loew, M. Larsen, H. Leffler, D. J. Lefeber, H. Clausen, A. Blangy, P. Caswell, M. Shafaq-Zadah, S. Mayor, R. Weigert, C. Wunder and L. Johannes. ‘Growth factor-triggered de-sialylation controls glycolipid-lectin-driven endocytosis’. In: *Nature Cell Biology* 27.3 (21st Feb. 2025), pp. 449–463. DOI: [10.1038/s41556-025-01616-x](https://doi.org/10.1038/s41556-025-01616-x). URL: <https://hal.science/hal-05304119> (cit. on p. 21).
- [12] E. Macdonald, L. Johannes and C. Wunder. ‘Acidification on the plasma membrane’. In: *Current Opinion in Cell Biology* 95 (Aug. 2025), p. 102531. DOI: [10.1016/j.ceb.2025.102531](https://doi.org/10.1016/j.ceb.2025.102531). URL: <https://hal.science/hal-05328086> (cit. on p. 19).
- [13] E. Meunier and P. Bouthemy. ‘Segmenting the motion components of a video: A long-term unsupervised model’. In: *IEEE Transactions on Pattern Analysis and Machine Intelligence* Early access (Sept. 2025), pp. 1–12. DOI: [10.1109/TPAMI.2025.3608065](https://doi.org/10.1109/TPAMI.2025.3608065). URL: <https://hal.science/hal-04937203>.

- [14] S. Papereux, L. Leconte, C. A. Valades-Cruz, T. Liu, J. Dumont, Z. Chen, J. Salamero, C. Kervrann and A. Badoual. ‘DeepCristae, a CNN for the restoration of mitochondria cristae in live microscopy images’. In: *Communications Biology* 8.1 (26th Feb. 2025), p. 320. DOI: [10.1038/s42003-025-07684-x](https://doi.org/10.1038/s42003-025-07684-x). URL: <https://hal.science/hal-04295317>. In press (cit. on p. 16).
- [15] M. Shafaq-Zadah, E. Dransart, I. Hamitouche, C. Wunder, V. Chambon, C. A. Valades-Cruz, L. Leconte, N. K. Sarangi, S. Cianfèrani-Sanglier, J. Robinson, R. Regmi, A. D. Cicco, S.-K. Bai, R. Bartels, A. Hovasse, U. J. Nilsson, H. Leffler, T. E. Keyes, D. Lévy, S. Raunser, D. Roderer and L. Johannes. ‘Spatial N-glycan rearrangement on $\alpha_5\beta_1$ integrin nucleates galectin-3 oligomers to determine endocytic fate’. In: *Nature Communications* 16.1 (2025), p. 9461. DOI: [10.1038/s41467-025-64523-7](https://doi.org/10.1038/s41467-025-64523-7). URL: <https://hal.science/hal-05335689> (cit. on pp. 21, 22).
- [16] P. Ucla, J. L -Chesnais, H. Ver Hulst, X. Ju, I. Calvente, E. Nematollahi, L. Leconte, J. Salamero, I. Bonnet, C. Monnot, H. D. Moreau, J. Landoulsi, V. Semetey and S. Coscoy. ‘Quantifying cell traction forces at the single-fiber scale in 3D: An approach based on deformable photopolymerized fiber arrays’. In: *Proceedings of the National Academy of Sciences of the United States of America* 122.42 (13th Oct. 2025). DOI: [10.1073/pnas.2507677122](https://doi.org/10.1073/pnas.2507677122). URL: <https://hal.science/hal-05317446>.

International peer-reviewed conferences

- [17] A. Deschemps, E. Gr goire, J. Martinez, A. Vaurijoux, P. Fernandez, D. Dugue, E. Moebel, G. Gruel, M.-a. Benadjaoud and C. Kervrann. ‘Explainable Artificial Intelligence Approach Using Low-Dimensional Visualization and Ensembling Uncertainty Quantification for Rare Chromosomal Aberration Detection in Cytogenetic Imaging’. In: *2025 Fourteenth International Conference on Image Processing, Theory, Tools & Applications (IPTA)*. IPTA 2025 - Fourteenth International Conference on Image Processing, Theory, Tools & Applications. Istanbul, Turkey: IEEE, 2025, pp. 1–6. DOI: [10.1109/ipta66025.2025.11222058](https://doi.org/10.1109/ipta66025.2025.11222058). URL: <https://asnr.hal.science/hal-05446156> (cit. on p. 18).
- [18] Q. Rapilly, A. Badoual, P. Maindr n, G. Bouet and C. Kervrann. ‘Prediction of Parametric Surfaces for Multi-Object Segmentation in 3D Biological Imaging’. In: *Lecture Notes in Computer Science (LNCS)*. SSVM 2025 - 10th International Conference on Scale Space and Variational Methods in Computer Vision. Vol. 15667. Totnes, United Kingdom: Springer, 2025, pp. 255–268. DOI: [10.1007/978-3-031-92366-1_20](https://doi.org/10.1007/978-3-031-92366-1_20). URL: <https://hal.science/hal-04978619> (cit. on p. 19).
- [19] Q. Tallon, J. Martinez Guerrero, E. Gregoire, P. Fernandez, D. Dugue, G. Gruel, C. Kervrann and M.-a. Benadjaoud. ‘Diffusion model uniform manifold filtering for classification of small datasets with underrepresented classes: Application to chromosomal aberration microscopy detection’. In: *Proceedings Volume Seventeenth International Conference on Machine Vision (ICMV 2024)*. ICMV 2024 - 17th International Conference on Machine Vision. Vol. 13517. Edinburgh, Scotland, United Kingdom: SPIE Digital Library, 24th Feb. 2025, 135170K. DOI: [10.1117/12.3055038](https://doi.org/10.1117/12.3055038). URL: <https://inria.hal.science/hal-04900898> (cit. on p. 18).

Scientific book chapters

- [20] D. Sage and A. Badoual. ‘Image Processing and Image Analysis in Microscopy’. In: *Photonic Imaging for Biology: From Conventional Microscopy to Super-Resolution*. Chapitre 10. Ed., Wiley, 1st Oct. 2025, pp. 205–237. URL: <https://inria.hal.science/hal-05469062> (cit. on p. 16).

Doctoral dissertations and habilitation theses

- [21] Q. Rapilly. ‘A hybrid CNN-snake approach for localization, segmentation, and shape representation in 3D biological imaging’. Universit  de rennes, 18th Dec. 2025. URL: <https://theses.hal.science/tel-05502320> (cit. on p. 19).
- [22] Q. Tallon. ‘Artificial Intelligence for the automatic detection of chromosomal translocations : application to retrospective dosimetry based on FISH imaging’. Universit  de Rennes, 16th Jan. 2025. URL: <https://theses.hal.science/tel-05058122> (cit. on p. 18).

Reports & preprints

- [23] Y. Hachani, P. Bouthemy, E. Fromont, S. Ruffini, L. Laffont and A. de Paula Reis. *Supervised contrastive learning for cell stage classification of animal embryos*. 2025. URL: <https://hal.science/hal-04937720>.
- [24] L. Régnier, C. V. Rimoli, S. Dey, F.-C. Tsai, G. A. Orsi, S. Brasselet and B. Hajj. *Polarization MultiFocus Microscopy for volumetric super-resolution and orientation imaging of biofilaments*. 19th Nov. 2025. DOI: [10.1101/2025.11.19.687997](https://doi.org/10.1101/2025.11.19.687997). URL: <https://hal.science/hal-05392077> (cit. on pp. 16, 17).

Other scientific publications

- [25] A. Badoual, M. Arizono, M. Ducros, U. V. Nägerl and C. Kervrann. ‘Analysis of astrocytic Ca²⁺ signaling revealed by LLSM’. In: IABM 2025 - Colloque Français d’Intelligence Artificielle en Imagerie Biomédicale. Nice, France, 2025. URL: <https://hal.science/hal-05446286>.
- [26] H. Lachuer, E. Moebel, A.-S. Macé, A. Masson, K. Schauer and C. Kervrann. ‘Deep learning detection of exocytosis events in TIRF microscopy’. In: IABM 2025 - Colloque français d’Intelligence Artificielle pour le Bio-Médical. Nice, France, 2025. URL: <https://hal.science/hal-05470418> (cit. on p. 18).
- [27] Q. Rappilly, A. Badoual, P. Maindron, G. Bouet and C. Kervrann. ‘Prediction of Parametric Surfaces for Multi-Object Segmentation in 3D Biological Imaging (Poster)’. In: IABM 2025 - Colloque français d’Intelligence Artificielle pour le Bio-Médical. Nice, France, 2025. URL: <https://hal.science/hal-05467429> (cit. on p. 19).