

RESEARCH CENTRE

**Inria Saclay Centre at Université
Paris-Saclay**

IN PARTNERSHIP WITH:

Université Paris-Saclay

2024

ACTIVITY REPORT

Project-Team

OPIS

**OPTimization for large Scale biomedical
data**

DOMAIN

Digital Health, Biology and Earth

THEME

**Computational Neuroscience and
Medicine**

Inria

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Project-Team OPIS

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Keywords

Computer sciences and digital sciences

- A3.4. – Machine learning and statistics
 - A3.4.1. – Supervised learning
 - A3.4.2. – Unsupervised learning
 - A3.4.3. – Reinforcement learning
 - A3.4.4. – Optimization and learning
 - A3.4.5. – Bayesian methods
 - A3.4.6. – Neural networks
 - A3.4.8. – Deep learning
- A6.2. – Scientific computing, Numerical Analysis & Optimization
 - A6.2.4. – Statistical methods
 - A6.2.6. – Optimization
- A8.2. – Optimization
- A8.7. – Graph theory
- A9.2. – Machine learning
- A9.3. – Signal analysis
- A9.7. – AI algorithmics

Other research topics and application domains

- B1. – Life sciences
 - B1.1. – Biology
 - B1.2. – Neuroscience and cognitive science
- B2.6. – Biological and medical imaging

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2 Overall objectives

Mathematical optimization is the key to solving many problems in science, based on the observation that physical systems obey a general principle of least action. While some problems can be solved analytically, many more can only be solved via numerical algorithms. Research in this domain has been steadily ongoing for decades.

In addition, many fields such as medicine continue to benefit from considerable improvements in data acquisition technology, based on sophisticated tools from optics and physics (e.g., new laser sources in microscopy, multi-coil systems in MRI, novel X-ray schemes in mammography, etc). This evolution is expected to yield significant improvements in terms of data resolution, making the interpretation and analysis of the results easier and more accurate for the practitioner. The large amounts of generated data must be analyzed by sophisticated optimization tools so that, in recent years, optimization has become a main driving force fostering significant advances in data processing. Previously hidden or hard to extract information can be pried from massive datasets by modern recovery and data mining methods. At the same time, automated decision and computer-aided diagnoses are made possible through optimal learning approaches.

However, major bottlenecks still exist. Recent advances in instrumentation techniques come with the need to minimize functions involving an increasingly large number of variables (at least one billion variables in 3D digital tomography modality), and with increasingly complex mathematical structure. The computational load for solving these problems may be too high for even state-of-the-art algorithms. New algorithms must be designed with computational scalability, robustness, and versatility in mind. In particular, the following severe requirements must be fulfilled: (i) ability to tackle high-dimensional problems in a reasonable computation time; (ii) low-requirements in terms of memory usage; (iii) robustness to incomplete or unreliable information; (iv) adaptivity to statistically varying environments; (v) resilience to latency issues arising in architectures involving multiple computing units.

These difficulties are compounded in the medical and biomedical areas. In these contexts, datasets are not easily available due to patient confidentiality and/or instrument limitations. Moreover, high-level expertise is necessary to interpret the data which can be of very high dimension. Finally, the developed analysis methods must be reliable and interpretable by the medical/biomedical community.

The objective of the OPIS project is to design advanced optimization methods for the analysis and processing of large and complex data. Applications to inverse problems and machine learning tasks in biomedical imaging are major outcomes of this research project. We seek optimization methods able to tackle data with both a large sample-size ("big N " e.g., $N = 10^9$) and/or many measurements ("big P " e.g., $P = 10^4$). The methodologies to be explored are grounded on nonsmooth functional analysis, fixed point theory, parallel/distributed strategies, and neural networks. The new optimization tools that are developed are set in the general framework of graph signal processing, encompassing both regular graphs (e.g., images) and non-regular graphs (e.g., gene regulatory networks).

More specifically, three main research avenues are explored, namely:

1. Accelerated algorithms for solving high-dimensional continuous optimization problems ;
2. Optimization over graphs ;
3. Toward more understandable deep learning.

In summary, the specificity of OPIS is to address problems involving high-dimensional biomedical data, e.g. 3D CT, PET, ultrasound images, and MRI, by making use of advanced computational optimization methods.

3 Research program

3.1 Accelerated algorithms for solving high-dimensional continuous optimization problems

Variational problems requiring the estimation of a huge number of variables have now to be tackled, especially in the field of 3D reconstruction/restoration (e.g. $\geq 10^9$ variables in 3D imaging). In addition

to the curse of dimensionality, another difficulty to overcome is that the cost function usually reads as the sum of several loss/regularization terms, possibly composed with large-size linear operators. These terms can be nonsmooth and/or nonconvex, as they may serve to promote the sparsity of the sought solution in some suitable representation (e.g. a frame) or to fulfill some physical constraints. In such a challenging context, there is a strong need for developing fast parallelized optimization algorithms for which sound theoretical guarantees of convergence can be established. We explore deterministic and stochastic approaches based on proximal tools, MM (Majorization-Minimization) strategies, and trust region methods. More generally, we are interested in using fixed point methods which provide a simplifying and unifying framework to model, analyze, and solve a great variety of problems. They constitute a natural environment to explain the behavior of advanced convex optimization methods as well as of recent nonlinear methods in data science which are formulated in terms of paradigms that go beyond minimization concepts and involve constructs such as Nash equilibria or monotone inclusions. Because of the versatility of the methods, a wide range of applications in image recovery are considered, such as dynamic positron emission tomography (PET), 3D ultrasound imaging, and two-photon microscopy. For example, in dynamic PET imaging (collaboration with CEA - Biomaps), we must solve a tomographic ill-posed inverse problem with Poisson noise of particularly high intensity. Our goal is to devise an efficient dose-dependent regularization scheme adapted to the dynamic protocol, with interpretable learned hyperparameters. In two-photon microscopy (collaboration with XLIM), our objective is to provide effective numerical solutions to improve the 3D resolution of the microscope, especially when cheap laser sources are used, with applications to bacteria imaging, and muscle disease screening.

3.2 Optimization over graphs

Graphs and hypergraphs are rich data structures for capturing complex, possibly irregular, dependencies in multidimensional data. Coupled with Markov models, they constitute the backbones of many techniques used in computer vision. Optimization is omnipresent in graph processing. Firstly, it allows the structure of the underlying graph to be inferred from the observed data, when the former is hidden. Second, it permits to develop graphical models based on the prior definition of a meaningful cost function. This leads to powerful nonlinear estimates of variables corresponding to unknown weights on the vertices and/or the edges of the graph. Tasks such as partitioning the graph into subgraphs corresponding to different clusters (e.g., communities in social networks) or graph matching, can effectively be performed within this framework. Finally, graphs by themselves offer flexible structures for formulating and solving optimization problems in an efficient distributed manner. On all these topics, our group has acquired a long-term expertise that we plan to further strengthen. In terms of applications, novel graph mining methods are proposed for gene regulatory and brain network analysis. For example, we plan to develop sophisticated methods for better understanding the gene regulatory network of various microscopic fungi, in order to improve the efficiency of the production of bio-fuels (collaboration with IFP Energies Nouvelles).

3.3 Toward more understandable deep learning

Nowadays, deep learning techniques efficiently solve supervised tasks in classification or regression by utilizing large amounts of labeled data and the powerful high level features that they learn by using the input data. Their good performance has caught the attention of the optimization community since currently these methods offer virtually no guarantee of convergence, stability or generalization. Deep neural networks are optimized through a computationally intensive engineering process via methods based on stochastic gradient descent. These methods are slow and they may not lead to relevant local minima. Thus, more efforts must be dedicated in order to improve the training of deep neural networks by proposing better optimization algorithms applicable to large-scale datasets. Beyond optimization, incorporating some structure in deep neural networks permits more advanced regularization than the current methods. This should reduce their complexity, as well as allow us to derive some bounds regarding generalization. For example, many signal processing models (e.g. those based on multiscale decompositions) exhibit some strong correspondence with deep learning architectures, yet they do not require as many parameters. One can thus think of introducing some supervision into these models in

order to improve their performance on standard benchmarks. A better mathematical understanding of these methods permits to improve them, but also to propose some new models and representations for high-dimensional data. This is particularly interesting in settings such as the diagnosis or prevention of diseases from medical images, because they correspond to critical applications where the made decision is crucial and needs to be interpretable. One of the main applications of this work is to propose robust models for the prediction of the outcome of cancer immunotherapy treatments from multiple and complementary sources of information: images, gene expression data, patient profile, etc (collaboration with Institut Gustave Roussy).

4 Application domains

4.1 Robustness of AI

4.1.1 Design of robust neural networks in safety critical industrial domains

Participants: Ana Neacsu, Kavya Gupta, Fragkiskos Malliaros, Jean-Christophe Pesquet (Collaboration: P. Combettes, North Carolina State University ; C. Burileanu, Polithenica University of Bucharest)

One of the main challenges faced today by companies like Thales or Schneider Electric designing advanced industrial systems, is to ensure the safety of new generations of products based on the use of neural networks. Since 2013, neural networks have been shown to be sensitive to adversarial perturbations. Deep neural networks can thus be fooled, in an intentional (security issue) or in undeliberate manner (safety issue), which raises a major robustness concern for safety-critical systems which need to be certified by an independent certification authority prior to any entry into production/operation. Techniques based on mathematical proofs of robustness are generally preferred by industrial safety experts since they enable a safe-by-design approach that is more efficient than a robustness verification activity done a posteriori with a necessarily bounded effort. Among the possible mathematical approaches, we focus on those relying upon the analysis of the Lipschitz properties of neural networks [64, 23]. Such properties play a fundamental role in the understanding of the internal mechanisms governing these complex nonlinear systems. Besides, they make few assumptions on the type of non-linearities used and are thus valid for a wide range of networks.

4.1.2 Certification of segmentation networks

Participants: Othmane Laousy, Maria Vakalopoulou (Collaboration: G. Chassagnon and M.-P. Revel, Paris Cité University ; N. Paragios, Therapanacea ; A. Araujo, S. Garg and F. Khorram, New York University)

The robustness of image segmentation has been an important research topic in the past few years as segmentation models have reached production-level accuracy. However, like classification models, segmentation models can be vulnerable to adversarial perturbations, which hinders their use in critical-decision systems like healthcare or autonomous driving. Recently, randomized smoothing has been proposed to certify segmentation predictions by adding Gaussian noise to the input to obtain theoretical guarantees. However, this method exhibits a trade-off between the amount of added noise and the level of certification achieved. In this topic, we address the problem of certifying segmentation prediction using a combination of randomized smoothing and diffusion models. We challenge our methods in both general computer vision and medical imaging dataset.

4.2 Radiology, hyper-progressive disease and immunotherapy

4.2.1 Imaging radiomics and pathomics to assess response to treatment

Participants: Maria Vakalopoulou, Hugues Talbot (Collaboration: E. Deutsh, Institut Gustave Roussy ; N. Paragios, Therapanacea)

The response of patients with cancer to immunotherapy can vary considerably, innovative predictors of response to treatment are needed to improve treatment outcomes. We aimed to develop and independently validate radiomics-based biomarkers of tumour-infiltrating cells in patients included in trials of the two most common, recent immunotherapy treatments: anti-programmed cell death protein (PD)-1 or anti-programmed cell death ligand 1 (PD-L1) monotherapy. We also aimed to evaluate the association between the biomarker, and tumour immune phenotype and clinical outcomes of these patients.

However, sometimes, not only do patient respond poorly, but immunotherapy seems to make things worse. Some patients see they tumoral load increase significantly faster after immunotherapy is started. These patients are called “hyper-progressors”. One of our project has been to clearly define and detect this class of patients. This is so novel that the very notion of hyperprogressive patient was still controversial when our work was published, but is accepted now.

In this axis we investigate powerful representations for radiological and pathological data that could be associated with interesting and important clinical questions.

4.2.2 Analysis of histopathology images for cancer treatment

Participants: Ségolène Martin, Nora Ouzir, Jean-Christophe Pesquet, Aymen Sardroui (Collaboration: A. Laurent-Bellue, C. Guettier: APHP, Hôpital du Kremlin-Bicêtre ; A. Beaufrère, K. Mondet, V. Paradis, APHP, Hôpital Beaujon)

The core focus of our research revolves around scrutinizing cancer through the utilization of digital slide images resulting from biopsies or surgical resection. Our exploration stands at the intersection of cutting-edge AI technology and its invaluable potential for advancing precision medicine, and more particularly liver cancer (hepatocellular carcinoma and intrahepatic cholangiocarcinoma) diagnosis and treatment. The challenges to be solved are related to the limited number of available annotated data and the large-size of whole slide images (WSIs) [53, 54].

4.2.3 Vision, machine learning and precision medicine

Participants: Younes Belkouchi, Loïc Le Bescond, Hugues Talbot (Collaboration: N. Lassau, Institut Gustave Roussy)

In March 2020, the PRISM institute of Gustave-Roussy was launched. The aim of this project, funded for 5 years, is to develop targeted treatments that are more likely to work on specific patients.

The mission of this “second-generation” precision medicine centre will be to model cancer on an individual scale by creating numerical avatars of tumours. The aim is to identify patients with the most aggressive cancers very early in the disease, without waiting for relapses, in order to offer them the most appropriate treatment from the start of treatment, using the huge volume of clinical, biological and molecular data and their analysis by artificial intelligence. PRISM will conduct large-scale clinical studies and develop molecular analysis technologies and data analysis methods.

Coordinated by Professor Fabrice André, Research Director of Gustave Roussy, Inserm Research Director and Professor at Paris-Saclay University, Prism aims to revolutionize the understanding of the molecular and biological mechanisms of cancer development and progression through artificial intelligence. Based on increasingly rich data of various types (clinical, genomic, microbiological, imaging, etc.), learning algorithms make it possible to develop finer diagnostic and prognostic tools, and thus to propose therapies that are personalised according to the characteristics of the individual.

Funded by the French National Research Agency, PRISM received the IHU label in 2018, followed by the National Center for Precision Medicine label.

4.2.4 Physics-informed, generative models for heart left ventricle perfusion analysis

Participants: Raoul Salle de Chou, Hugues Talbot (Collaboration: I. Vignon-Clementel, SIMBIOTX Team Inria ; L. Najman, Université Gustave-Eiffel, L. Papamanolis Stanford university, USA, California)

Coronary arteries feed the heart muscles with nutrients and oxygen. As such, they are some of the most critical blood vessel in the entire body. Coronary disease is difficult to diagnose especially when it

affects the smaller branches of these vessels, because direct imaging of these vessels is infeasible with current medical imaging technology. Instead, blood perfusion through the myocardium can be imaged and is correlated with both arterial and myocardium disease. However, perfusion imaging is challenging, invasive and expensive because it relies on radioactive tracers.

A previous model was developed for myocardial perfusion simulation for coronary artery disease in [\[link\]](#) to replace the actual exam with a numerical twin and conduct it via simulations. The model aims at reproducing $[^{15}\text{O}]\text{H}_2\text{O}$ PET imaging exam using only CT scans as input. The simulation is based on :

1. the detection, segmentation and simulation of blood flow through the coronary vessels visible on the injected CT scan;
2. a patient-specific method for generating small 3D vessels consistent with the vessels detected. The rules for the growth of these vessels are based on physiology and simulated blood flows;
3. a perfusion simulation model that considers the myocardium as a porous medium.

For this a linear Darcy model is used to simulate blood flow through the porous medium. However, in addition to a high computational cost, the simulation fails to accurately reproduce some diseases, particularly those that affect medium-size coronary branches.

The main goal of this project is to combine Machine Learning (ML) methods with physical simulations, in order to improve the current simulation pipeline. ML algorithms are used to learn from PET imaging exams while being guided by simulation hypothesis, thereby diminishing the dependency on patient data. To achieve this, each part of the simulation is to be replaced by an ML model. Following successful replication of simulation outcomes, the model will undergoes refinement using patient data.

A finite volume physics informed graph neural network was developed to solve the Darcy equations on irregular shapes serving as a substitute for the myocardium component in perfusion simulation. Preliminary results indicate superior performance of this model in terms of accuracy and generalization compared to classical ML approaches. In [\[55\]](#), we introduced a novel optimization framework for the generation of the synthetic small vessels utilizing the constructed constrained optimization (CCO) method. Our new approach simulated similar 2D vascular trees as the original CCO method in terms of morphometry while producing better optimal solutions at lower computational cost. This new approach is expected to be more readily reproducible using ML methods compared to the original CCO technique.

Additionally, work has been conducted towards the determination of the myocardium perfusion regions. Determining these regions, and their associated vessel is a crucial step in current simulation pipeline. However, the current calculation method is inaccurate and highly sensitive to the resolution of segmented vessels. A more robust and accurate model, employing graph neural networks (GNNs), has been developed for the determination of these regions.

4.3 Sparse inverse problems

4.3.1 Sparse signal processing in chemistry

Participants: Emilie Chouzenoux, Mouna Gharbi, Jean-Christophe Pesquet (Collaboration: L. Duval, IFPEN, Rueil Malmaison)

Peak-signal retrieval is a core challenge in separative analytical chemistry (AC). For instance, in chromatography, spectrometry, spectroscopy, peak localization, amplitude, width or area provide useful chemical quantitative information. We investigated this problem through the deep unrolling paradigm, in [\[40, 18\]](#), in collaboration with Dr. L. Duval, Research Engineer at IFP Energies Nouvelles, France.

4.3.2 Image restoration for multiphoton microscopy

Participants: Julien Adjenbaum, Emilie Chouzenoux, Jean-Baptiste Fest, Ségolène Martin, Jean-Christophe Pesquet (Collaboration: C. Lefort, XLIM, CNRS, Limoges ; M. Chalvidal, ANITI, Toulouse)

Through an ongoing collaboration with physicists from XLIM laboratory (CNRS, Limoges, France), we propose advanced mathematical and computational solutions for multiphoton microscopy (MPM) 3D

image restoration. This modality enjoys many benefits such as a decrease in phototoxicity and increase in penetration depth. However, blur and noise issues can be more severe than with standard confocal images. Our objective in [48, 1] was to drastically improve the quality of the generated images and their resolution by improving the characterization of the PSF of the system and compensating its effect. We consider the application of the improved MPM imaging tool to the microscopic analysis of muscle ultrastructure and composition, with the aim to help diagnosing muscle disorders including rare and orphan muscle pathologies, and to visualize bacteria and viral structures.

4.3.3 Reconstruction approaches in PET imaging

Participants: Emilie Chouzenoux, Alix Chazottes, Jean-Christophe Pesquet, Claire Rossignol (Collaboration: F. Sureau, CEA)

Positron emission tomography (PET) is a quantitative functional imaging modality used to track the fate and/or dynamics of a radiotracer previously injected into a patient. This technique is particularly used in oncology for diagnosis and therapeutic monitoring, in the study of neurodegenerative diseases, and in pharmacology. In dynamic PET, the temporal evolution of the spatial distribution of the radiotracer during the examination is taken into account for the estimation of physiological parameters allowing for a fine characterization of the molecular mechanisms at play (receptor concentration, absorption, dissociation constants, binding potential, etc.). In the PhD thesis of Alix Chazottes, in collaboration between OPIS and CEA, we aim to propose methodological developments in the fields of optimization and learning to address the problem of robust dynamic PET reconstruction [37].

4.4 Graph mining applications

4.4.1 Geometric Graph Neural Networks for molecular and chemical systems

Participants: Alexandre Duval, Fragkiskos Malliaros (Collaboration: V. Schmidt, Alex Hernandez, Y. Bengio, David Rolnick, Mila - Quebec AI Institute ; S. Miret, Intel Labs Berkeley)

Graph Neural Networks (GNNs) currently constitute state-of-the-art models for solving prediction tasks on graphs. Through the flexible formulation of the message passing mechanism, GNNs can learn informative latent representations of graph entities at different resolution levels (e.g., node-, edge-, graph-level). In many practical applications in molecular and chemical systems, the nodes of the graph have associated geometric attributes (e.g., coordinates, velocities) related to their position in the 3D space. In this context, *geometric graphs* represent the interaction of atoms in the 3D space, encapsulating a range of physical symmetries such as rotations and translations. Existing GNN models often overlook this aspect, rendering them ill-suited for prediction tasks on geometric graphs. Recently, Geometric GNN architectures tailored to respect physical symmetries have emerged as flexible models of atomic systems. Through an ongoing collaboration with Mila - Quebec AI Institute, Université de Montréal, McGill University, and Intel Labs, we study geometric GNN models, focusing both on design principles as well as on practical applications in materials modeling (e.g., property prediction and molecule generation).

4.4.2 Graph inference for gene regulation analysis

Participants: Fragkiskos Malliaros (Collaboration: A. Pirayre, F. Bidard, and L. Duval, IFPEN)

The discovery of novel gene regulatory processes improves the understanding of cell phenotypic responses to external stimuli for many biological applications, such as medicine, environment or biotechnologies. To this purpose, transcriptomic data are generated and analyzed from DNA microarrays or more recently RNAseq experiments. They consist in genetic expression level sequences obtained for all genes of a studied organism placed in different living conditions. From these data, gene regulation mechanisms can be recovered by revealing topological links encoded in graphs. In regulatory graphs, nodes correspond to genes. A link between two nodes is identified if a regulation relationship exists between the two corresponding genes. In our work, we propose to address this network inference problem with recently developed techniques pertaining to graph optimization. Given all the pairwise gene regulation

information available, we propose to determine the presence of edges in the considered GRN by adopting an energy optimization formulation integrating additional constraints. Either biological (information about gene interactions) or structural (information about node connectivity) a priori are considered to restrict the space of possible solutions. Different priors lead to different properties of the global cost function, for which various optimization strategies, either discrete and continuous, can be applied.

4.4.3 Graph machine learning for spatiotemporal data

Participants: Fragkiskos Malliaros (Collaboration: J. Castro-Correa, Mohsen Badiey, Univ. of Delaware ; J. H. Giraldo, Télécom Paris ;A. Mondal, Univ. of Surrey ; T. Bouwmans, La Rochelle Univ.)

Numerous real-world prediction problems involve spatiotemporal data. For example, consider sensors scattered across diverse geographical regions measuring environmental conditions (e.g., temperature, pollution) or functional magnetic resonance imaging (fMRI) data capturing brain activity. Both scenarios generate data inherently rich in spatiotemporal structure, benefiting from the relational inductive bias of graph-based modeling. In an ongoing collaboration with the University of Delaware, Télécom Paris, and La Rochelle Université, we have introduced a methodology that leverages graph-based modeling, enabling time series imputation with GNNs. Major challenges here concern inducing temporal and relational smoothness assumptions into the model as well as inferring the (often unknown) graph structure. Furthermore, an intriguing aspect involves enhancing spatiotemporal graph models with causal properties to capture causal influence effects among entities.

4.4.4 Graph representation learning for computational medicine

Participants: Emilie Chouzenoux, Fragkiskos Malliaros (Collaboration: A. Majumdar, IIIT Delhi ; G. Chierchia, ESIEE Paris ; B. Liu, D. Papadopoulos, G. Tsoumakas, A. Papadopoulos, Aristotle Univ. of Thessaloniki)

Following the Associate International Inria Team COMPASS (ended in 2023), led by Emilie Chouzenoux and Dr. A. Majumdar (IIIT Delhi), we pursue our research to investigate new models and inference tools to understand and predict optimal drug association, so as to tackle real-life problems of computational drug discovery. We introduced graph-based regularization techniques in order to incorporate expert knowledge and metadata in matrix completion tasks arising in the prediction of drug-virus and drug-drug associations. Our recent works apply the proposed methodology to drug repositioning [63].

The discovery of drug-target interactions is also explored by Fragkiskos Malliaros, in collaboration with Aristotle University of Thessaloniki. Accurately identifying reliable interactions among drugs and proteins via computational methods, which typically leverage heterogeneous information retrieved from diverse data sources, can boost the development of effective pharmaceuticals. We have considered multi-layered network modeling to handle diverse drug and target similarities, introducing an optimization framework called Multiple similarity DeepWalk-based Matrix Factorization (MDMF) for DTI prediction. Current efforts in this direction involve leveraging Graph Neural Networks and self-supervised learning tools.

4.4.5 Graph inference for time series analysis in earth and climate applications

Participants: Emilie Chouzenoux (Collaboration: V. Elvira, Univ. Edinburgh, UK)

Studying the causal inter-dependencies in complex dynamical systems is a critical challenge. We explore sparse graphical models to gain insight through observational causal discovery. We revisit Granger causality under a graphical perspective of state-space models. We investigate expectation-maximisation algorithms [35] [11] for estimating matrix parameters in the state equation of a linear-Gaussian state-space model under sparse priors, emphasizing both causal and correlation relationships among time series samples.

4.5 Other biomedical applications

4.5.1 Artificial intelligence for accessible eccentric photorefraction

Participants: Emilie Chouzenoux, Nguyen Vu, Jean-Christophe Pesquet, Clement Lavaud (Collaboration: P. Pinault, S. Boutinon, M. Peloux, R&D ESSILOR)

Affordable and accessible screening tools are crucial to diagnose and, hence, effectively address vision impairment. In collaboration with ESSILOR R&D, we developed novel pipelines based on photorefraction and advanced AI techniques which complies with these requirements [59]. Our results pave the way for a practical application of the proposed device for an accurate vision loss diagnostic in a real setting.

4.5.2 Imaging biomarkers and characterization for chronic lung diseases

Participants: Othmane Laousy, Maria Vakalopoulou (Collaboration: S. Christodoulidis, G. Chassagnon, M.-P. Revel, APHP ; N. Paragios, Therapanacea)

Diagnosis and staging of lung diseases is a major challenge for both patient care and approval of new treatments. Among imaging techniques, computed tomography (CT) is the gold standard for in vivo morphological assessment of lung anatomy currently offering the highest spatial resolution in lung diseases. Although CT is widely used its optimal use in clinical practice and as an endpoint in clinical trials remains controversial. Our goal in the PhD thesis of Othmane Laousy, is to provide automatic and accurate tools that could help clinicians with their everyday practice.

4.5.3 AI for small bowel obstruction diagnosis

Participants: Alix Chazottes, Emilie Chouzenoux, Maxence Gélard, Jean-Christophe Pesquet (Collaboration: Q. Vanderbecq, M. Zins, Hôpital Saint Joseph ; M. Wagner, LIB, Sorbonne Univ.)

Small bowel obstruction (SBO) is a common nontraumatic surgical emergency. All guidelines recommend computed tomography (CT) as the first-line imaging technique for patients with suspected mechanical SBO with a four-fold goal: (i) to confirm or refute the diagnosis of SBO and, when SBO is present, (ii) to locate the site of the obstruction, that is, the transition zone (iii) to identify the cause, and (iv) to look for complications such as strangulation or perforation. Identifying SBO and differentiating its causes (e.g., open-loop and closed-loop mechanisms) is time-consuming and subject to inter-observer and intra-observer variability.

The aim of this collaborative project between Inria Saclay OPIS, Hôpital St Joseph, and LIB, Sorbonne University, is to investigate AI approaches for a guided SBO diagnosis from 3D CT scans [33].

4.5.4 A generative model for heart left ventricle perfusion analysis

Participant: Hugues Talbot (Collaboration: L. Najman, ESIEE Paris ; I. Vignon-Clementel, REO Team leader, Inria ; C. Taylor, Heartflow Inc.)

Cardio-vascular diseases continue to be the leading cause of mortality in the world. Understanding these diseases is a current, challenging and essential research project. The leading cause of heart malfunction are stenoses causing ischemia in the coronary vessels. Current CT and MRI technology can assess coronary diseases but are typically invasive, requiring risky catheterization and renal-toxic contrast agents injection. In collaboration with the REO team headed by Irène Vignon-Clementel, and Heartflow, a US based company, we have in the past contributed to Heartflow's major product, that replaces these physical exams with image-based exams only, limiting the use of contrast agents and in the cases that do not require a stent insertion, eliminating catheterisation. Heartflow is current the market leader in non-invasive coronary exams and the owner of most of the relevant IP in this domain.

Unfortunately, current imaging technology is unable to assess coronary disease along the full length of coronary vessels. CT is limited to a resolution of about 1mm, whereas coronary vessels can be much smaller, down to about 10 micrometers in diameter. To assess blood vessel health down to the smallest

sizes, blood perfusion imaging technique throughout the heart muscle must be used instead. Perfusion imaging with PET or a Gamma camera, the current gold standard, is an invasive technology requiring the use of radioactive tracers. To avoid using these, a lower quality estimate of perfusion can be achieved using some ToF or injected gated MRI modalities.

We have investigated patient-specific vessel generation models together with porous model simulations in order to propose a direct model of perfusion imaging, based on the known patient data, computer flow dynamic simulations as well as experimental data consistent with known vessel and heart muscle physiology. The objective of this work is to both to provide a useful, complex forward model of perfusion image generation, and to solve the inverse problem of locating and assessing coronary diseases given a perfusion exam, even though the affected vessels may be too small to be imaged directly.

Continuing on our work from the period 2015-2019, this year we proposed a functional myocardial perfusion model consisting of the CT-derived segmented coronary vessels, a simulated vessel tree consisting of several thousands of terminal vessels, filling the myocardium in a patient-specific way, consistent with physiology data, physics-based and empirically-observed vessel growth rules, and a porous medium. We produced and validated a CFD code capable of simulating blood flow in all three coupled compartments, which allows us to simulate perfusion realistically.

5 Social and environmental responsibility

5.1 Footprint of research activities

The research carried out in OPIS aims at developing advanced techniques in the domain of data science for precision medicine. One of the main features of this research is to ensure that the proposed methods are not only efficient, but also grounded on sound mathematical foundations inherited from the areas of optimization and fixed point algorithms. In the biomedical domain, it appears indeed mandatory to guarantee the reliability and the explainability of the proposed approaches in their use by medical doctors or producers of medical imaging devices.

5.2 Impact of research results

OPIS participates in the design of innovative products developed by big companies working in the domain of medical imaging (GE Healthcare and Essilor) and several startups. Various application fields are targeted (breast cancer detection, surgical radiology, interventional surgery, coronary disease monitoring, vision correction, ...).

The methodological contributions of OPIS are far reaching, with impact going further the field of medical imaging. OPIS transfers its expertise in artificial intelligence, image processing, and optimization through collaboration with major industrial partners such as SNCF, Schneider Electrics, IFPEN, and Thales. The transfer activity typically goes through CIFRE PhD contracts or more dedicated partnerships.

In addition, OPIS has active collaborations with several hospitals, particularly Institut Gustave Roussy and public hospitals from APHP in Paris. The purpose of these collaborations is to develop artificial intelligence tools aiding medical doctors in their practice. A large part of this research activity is oriented toward fighting against cancer using different kinds of data (CT scans, MRI, genomic data, histopathology images,...). OPIS was also involved in several projects for helping to better diagnose and cure COVID-19 infection.

6 Highlights of the year

6.1 Awards

- Jean-Christophe Pesquet was nominated Fellow of the Asia-Pacific Artificial Intelligence Association (AAIA).
- Aymen Sadraoui and Loïc Le Bescond, advised by Mounir Kaaniche, Jean-Christophe Pesquet, and Hugues Talbot, won the DigilUT international challenge: *Diagnosing lung transplant rejection with*

AI. (Organizer: Foch Hospital, Suresnes) [Digilut 2024](#). This challenge was organized by Antoine Roux from Foch hospital, in collaboration with the Health Data Hub and funded by Bpifrance.

- The article [49] coauthored by Ségolène Martin and Jean-Christophe Pesquet on Transductive zero-shot and few-shot CLIP was selected as an highlight paper at CVPR (less than 10% of accepted papers).

7 New software, platforms, open data

7.1 New platforms

7.1.1 Prox Repository

Web site: [Prox Repository](#)

- Software Family: utility
- Audience: universe
- Evolution and maintenance: long term support
- Context/Role of OPIS: This website was created by E. Chouzenoux and J.-C. Pesquet from OPIS, along with P.L. Combettes, North Carolina State University, and G. Chierchia, ESIEE Paris. The maintenance is made by summer interns funded by OPIS, and by the authors of the website.
- Duration of the Development: The website was released in 2016, and is maintained regularly since then.
- Proximity operators have become increasingly important tools as basic building blocks of proximal splitting algorithms, a class of algorithms that decompose complex composite convex optimization methods into simple steps involving one of the functions present in the model. This website provides formulas for efficiently computing the proximity operator of various functions, along with the associated codes in Matlab/Python languages.
- The codes provided are distributed under the licence CeCill-B.

7.1.2 The PINK image library

Web site: [PINK](#)

- Software Family: utility
- Audience: universe
- Evolution and maintenance: long term support
- Context/Role of OPIS: H. Talbot is among the creators of this library and is still actively involved in its maintenance.
- Duration of the Development: This software has been developed and maintained since 2011.
- The PINK image library is a general-purpose, open-source, portable image processing library specializing in discrete geometry and mathematical morphology. It is the result of several decades of research in these domains and features state-of-the art algorithmic implementation of both classical and leading edge DG and MM operators. These include nD parallel thinning and skeletonization methods and efficient hierarchical morphological transforms.
- This code is distributed under the CeCILL license.

7.1.3 The Vivabrain AngioTK toolkit

Web site: [Vivabrain AngioTK toolkit](#)

- Software Family: `vehicle`
- Audience: `partners`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: H. Talbot participated to the programming of this software.
- Duration of the Development: This software has been released in 2018.
- AngioTK is a toolkit supported by Kitware (the authors of VTK) for the filtering, segmentation, generation and simulation of blood vessels. It was started in the context of the Vivabrain ANR project in 2012, but continues with the same as well as new partners. Applications are numerous, from the simulation and understanding of perfusion (see associated theme) to the simulation of realistic blood flow MRI images with associated ground truth, via the generation of blood vessel atlases.
- This code is distributed under the Apache License, Version 2.0.

7.1.4 A scientific image viewer

Web site: [imview](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: H. Talbot is the author of this software.
- Duration of the Development: This software has been released in 2001. His last version has been updated in 2014.
- This general-purpose and cross-platform scientific image viewing tool has been part of the Debian Linux distribution since 2001. This viewer is well adapted to display 2D with high-precision data images (floating-point, etc), as well as 3D and hyper-spectral data. It features an interactive segmentation tool for multispectral data and is scriptable.
- The codes provided are distributed under a GNU General Public License version 2.0 (GPLv2).

7.1.5 TCGA segmentation

Web site: [TCGA segmentation](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: This code was produced by the OPIS PhD student M. Le Rousseau.
- Duration of the Development: This software was developed during the PhD thesis of M. Le Rousseau, mostly during the year 2020.
- This is a Python/Pytorch code that implements an end-to-end Whole Slide Imaging pre-processing pipeline from The Cancer Genome Atlas download documents, as well as a complete implementation of deep learning tumor segmentation from WSI binary labels.
- The codes provided are distributed under a GNU Affero General Public License v3.0.

7.1.6 ScanCovIA

Web site: [ScanCovIA](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: This software is the product of the ScanCovIA collaborative project between OPIS, IGR, CentraleSupélec and the start-up Owkin. Several PhD students of OPIS were involved in the programming of this software.
- Duration of the Development: This software was developed during the year 2020.
- This is a Python/Pytorch code allowing to reproduce the results of the ScanCovIA project.
- The codes provided are distributed under a GPL v3.0 license.

7.1.7 Graphical inference in linear-Gaussian state-space models

Web site: [Graphical inference in linear-Gaussian state-space models](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: The code is produced by OPIS member Emilie Chouzenoux.
- Duration of the Development: This software has been developed from 2021. The most recent release is from July 2023.
- This is a set of Matlab codes, to reproduce the experimental results from the article [11].
- The codes provided are distributed under CeCILL-B V1 license.

7.1.8 Antibiotic bacteria interaction: dataset and benchmarking

Web site: [Antibiotic bacteria interaction: dataset and benchmarking](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: The code was produced by S. Chatterjee, PhD student at IIIT Delhi, in the context of the Inria International Associate Team COMPASS.
- Duration of the Development: This software has been developed during the year 2023.
- This is a database, and a set of Python codes, to reproduce the experimental results from the article [63].
- The codes provided are distributed through Github platform, under a General Public License v3.0.

7.1.9 Joint registration tumor segmentation

Web site: [Joint registration tumor segmentation](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: This code was produced by the OPIS PhD student T. Estienne.
- Duration of the Development: This software was developed during the PhD thesis of T. Estienne, mostly during the year 2019.
- This is a Python/Pytorch code that allows to reproduce the results of the paper [\[link\]](#).
- The codes provided are distributed under a General Public License v3.0.

7.1.10 U-HQ

Web site: [U-HQ](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: This code was produced by the OPIS PhD student Mouna Gharbi.
- Duration of the Development: This software was developed during the PhD thesis of M. Gharbi, mostly during the year 2023.
- This is a Python/Pytorch code allowing to reproduce the results of the paper [\[18\]](#).
- The codes provided are distributed under a GNU General Public License v3.0.

7.1.11 CITRUS

Web site: [CITRUS](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: This software is developed as part of a collaboration with Télécom Paris, in the context of the postdoctoral position of A. Einizade (co-supervised by F. Malliaros and J. Giraldo).
- This is a Python code allowing to reproduce the results of the paper [\[38\]](#).
- The codes provided are distributed under the licence GNU General Public License v3.0.

7.1.12 Missing Modalities in Multimodal Recommendations

Web site: [GitHub link](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: This software is developed in the context of the postdoctoral position of D. Malitesta, in collaboration with Politecnico di Bari (Italy).
- This is a Python code allowing to reproduce the results of the paper [47].
- The codes provided are distributed under the licence GNU General Public License v3.0.

7.1.13 Graph-based Uplift Modeling

Web site: [UMGNet](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: This software is developed in the context of a collaboration with the University of Luxembourg (G. Panagopoulos and J. Pang).
- This is a Python code allowing to reproduce the results of the paper [52].
- The codes provided are distributed under the licence GNU General Public License v3.0.

7.1.14 GegenGNN

Web site: [GegenGNN](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: This software is developed in the context of a collaboration with the University of Delaware (J Castro-Correa and M. Badiéy) and Télécom Paris (J. Giraldo).
- This is a Python code allowing to reproduce the results of the paper [8].
- The codes provided are distributed under the licence GNU General Public License v3.0.

8 New results

8.1 Theoretical advances for majorize-minimize algorithms

Participants: Emilie Chouzenoux, Jean-Baptiste Fest, Jean-Christophe Pesquet (Collaboration: University of Milan ; University of Modena and Reggio Emilia ; University of Helsinki ; TU Graz)

In the context of large-scale, differentiable optimization, an important class of methods relies on the principle of majorization-minimization (MM). MM algorithms are becoming increasingly popular in signal/image processing and machine learning. MM approaches are fast, stable, require limited manual settings, and are often preferred by practitioners in application domains such as medical imaging and

telecommunications. In the work [12], we give conditions under which the sequence generated by the resulting block majorize-minimize subspace algorithm converges to a critical point of the objective function, in the non-convex setting.

In the collaborative work [61], we investigate the training of SVMs through a smooth sparse-promoting-regularized squared hinge loss minimization. This choice paves the way to the application of quick training methods built on MM approaches, benefiting from the Lipschitz differentiability of the loss function. Moreover, the proposed approach allows us to handle sparsity-preserving regularizers promoting the selection of the most significant features, so enhancing the performance. Numerical tests and comparisons conducted on three different datasets demonstrate the good performance of the proposed methodology in terms of qualitative metrics (accuracy, precision, recall, and F1 score) as well as computational cost

8.2 Convergence analysis in stochastic optimization

Participants: Emilie Chouzenoux, Jean-Baptiste Fest (Collaboration: A. Repetti, Heriot-Watt Univ., Edinburgh)

Asymptotic analysis of generic stochastic algorithms often relies on descent conditions. In a convex setting, some technical shortcuts can be considered to establish asymptotic convergence guarantees of the associated scheme. However, in a non-convex setting, obtaining similar guarantees is usually more complicated, and relies on the use of the Kurdyka-Lojasiewicz (KL) property. In [69], we propose a new framework for using the KL property in a non-convex stochastic setting based on conditioning theory.

8.3 Fundamental problems in image reconstruction

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Fernando Marcelo Roldan Contreras

In inverse problems such as X-ray computed tomography, the applicability of the algorithm is dominated by the cost of applying the forward linear operator and its adjoint at each iteration. In practice, the adjoint operator is thus often replaced by an alternative operator with the aim to reduce the overall computation burden and potentially improve conditioning issues. In [13], we analyze the effect of such an adjoint mismatch on the convergence of a large set of primal-dual proximal algorithms. We derive conditions under which convergence of the algorithms to a fixed point is guaranteed. We also derive bounds on the error between this point and the solution to the original minimization problem. We illustrate our theoretical findings on image reconstruction tasks in computed tomography.

8.4 Deep unrolled algorithms for inverse problems in image and signal processing

Participants: Emilie Chouzenoux, Mouna Gharbi, Jean-Christophe Pesquet (Collaboration: S. Villa, Univ. Genoa ; L. Duval, IFPEN ; C. Della Valle, Sorbonne Univ.)

While model-based iterative methods can be used for solving inverse problems arising in image processing, their practicability might be limited due to tedious parameterization and slow convergence. In addition, inadequate solutions can be obtained when the retained priors do not perfectly fit the solution space. Deep learning methods offer an alternative approach that is fast, leverages information from large data sets, and thus can reach high reconstruction quality. However, these methods usually rely on black boxes not accounting for the physics of the imaging system, and their lack of interpretability is often deplored. At the crossroads of both methods, unfolded deep learning techniques have been recently proposed. They incorporate the physics of the model and iterative optimization algorithms into a neural network design, leading to superior performance in various applications.

In [18], we propose a deep neural network based on unrolling a Half-Quadratic algorithm to address the problem of sparse signal reconstruction arising in analytical chemistry. This allows us to build interpretable layers mirroring iterations, making it possible to learn automatically data-driven hyperparameters such as regularization and stepsizes. Furthermore, we propose a dictionary of custom activation functions derived from potentials used in the original variational model. This interpretation of activations can be useful for analyzing the stability of neural networks. The efficiency of our method in comparison to

iterative and learning-based methods is showcased through various experiments conducted on realistic mass spectrometry databases with various blur kernels and noise levels. Deep unrolling of primal-dual proximal algorithms has also been considered in [40], for the same application context.

In [64], we question the robustness of an unrolled neural network architecture designed to solve inverse problems where the degradation operator is linear and known. This architecture is constructed by unrolling a forward-backward algorithm derived from the minimization of an objective function that combines a data-fidelity term, a Tikhonov-type regularization term, and a potentially nonsmooth convex penalty. The robustness of this inversion method to input perturbations is analyzed theoretically.

8.5 Computational approaches for multiphotonic image restoration

Participants: Emilie Chouzenoux, Ségolène Martin, Jean-Christophe Pesquet (Collaboration: C. Lefort, XLIM, CNRS ; J. Ajdenbaum, Univ. Paris Saclay)

We investigate image restoration approaches in the context of the development of novel laser strategies in multiphoton microscopy (MPM). The resolution of the MPM device is quantified by a procedure of point-spread-function (PSF) assessment led by an original, robust, and reliable computational approach. The estimated values for the PSF width are shown to be comparable to standard values found in optical microscopy. Advanced optimization methods taking advantage of modern multicores computing devices have been developed these past years in our group. Recently, in [48][1], we present a novel approach for addressing the MPM image restoration inverse problem in an end-to-end fashion. Our comprehensive restoration pipeline revisits the conventional restoration protocol from acquisition to the final restored outcome.

8.6 Divergence minimization in statistical inference

Participants: Emilie Chouzenoux, Thomas Guilmeau (Collaboration: V. Elvira, N. Branchini, University of Edinburgh)

A wide class of problems in statistical inference, including proposal adaptation in Monte-Carlo, maximum likelihood estimation, and variational approximation, read as the minimization of a divergence over a set of parametric distributions. We investigate the resolution of such problems, with modern tools of convex analysis. In [20], we propose a theoretical and algorithmic framework to solve variational inference and maximum likelihood estimation problems over the lambda-exponential family. For the resolution, we introduce novel proximal-like algorithms that exploit the geometry underlying the lambda-exponential family. In [43], we propose an adaptive importance sampling Monte-Carlo algorithm that accurately approximates heavy tail targets by Student-t proposal distributions. The proposal adaptation relies on the minimization of a α -divergence, by a Bayesian optimization technique.

8.7 Monte-Carlo approaches for global optimization

Participants: Emilie Chouzenoux, Thomas Guilmeau (Collaboration: V. Elvira, University of Edinburgh)

Finding the global minimum of a nonconvex optimization problem is a notoriously hard task appearing in numerous applications, from signal processing to machine learning. In [19], we introduce a new framework, based on divergence-decrease conditions, to study and design black-box global optimization algorithms. Our approach allows to establish and quantify the improvement of sampling distributions at each iteration, in terms of expected value or quantile of the objective.

8.8 Computational approaches for drug discovery

Participant: Emilie Chouzenoux (Collaborations: S. Chatterjee, A. Majumdar, IIT Delhi)

The discovery of drug-target interactions (DTIs) is a very promising area of research with great potential. The accurate identification of reliable interactions among drugs and proteins via computational

methods, which typically leverage heterogeneous information retrieved from diverse data sources, can boost the development of effective pharmaceuticals.

We recently focused on computational models for repurposing drugs with the potential for treating drug resistant bacterial infections. In [63], we produced a dataset for drug-bacteria associations (DBA) that affects humans, and conduct genomic similarity computations for all known bacteria impacting humans and assess structural similarities for all antibiotic drugs.

8.9 Expectation-Maximization for time series modeling and inference

Participants: Emilie Chouzenoux (Collaboration: V. Elvira, University of Edinburgh)

Modeling and inference with multivariate sequences is central in a number of signal processing applications such as acoustics, social network analysis, biomedical, and finance, to name a few. The linear-Gaussian state-space model is a common way to describe a time series through the evolution of a hidden state, with the advantage of presenting a simple inference procedure due to the celebrated Kalman filter. A fundamental question when analyzing multivariate sequences is the search for relationships between their entries (or the modeled hidden states), especially when the inherent structure is a non-fully connected graph. In such context, graphical modeling combined with parsimony constraints allows to limit the proliferation of parameters and enables a compact data representation which is easier to interpret by the experts.

We recently introduced a novel perspective by relating this matrix to the adjacency matrix of a directed graph, also interpreted as the causal relationship among state dimensions in the Granger-causality sense. Under this perspective, we propose in [11], a novel approach introducing a joint graphical modeling framework that bridges the graphical Lasso model and a causal-based graphical approach for linear-Gaussian state-space model. We present DGLASSO (Dynamic Graphical Lasso), a new inference method within this framework that implements an efficient block alternating majorization-minimization algorithm. In [35], we extend the proposed methodology to deal with Markovian models with order higher than one (i.e., more than one-step-ahead causality). In [66], we propose GraphGrad, a fully automatic approach for obtaining sparse estimates of the state interactions of a non-linear state-space model via a polynomial approximation. This novel methodology unveils the latent structure of the data-generating process, allowing us to infer both the structure and value of a rich and efficient parameterisation of a general state-space model. Our method utilises a differentiable particle filter, combined with suitable proximal updates, to estimate the model parameters.

8.10 Advanced nonconvex priors for signal and image restoration

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Gabriele Scrivanti (Collaboration: M.-C. Corbineau, Preligens)

The core of many approaches for the resolution of variational inverse problems arising in signal and image processing consists of promoting the sought solution to have a sparse representation in a well-suited space. A crucial task in this context is the choice of a good sparsity prior that can ensure a good trade-off between the quality of the solution and the resulting computational cost.

In [10], we propose a novel nonsmooth and nonconvex variational formulation of the problem of joint problem of reconstruction/feature extraction. For this purpose, we introduce a versatile generalised Gaussian prior whose parameters, including its exponents, are space-variant. Secondly, we design an alternating proximal-based optimisation algorithm that efficiently exploits the structure of the proposed nonconvex objective function. We also analyze the convergence of this algorithm. As shown in numerical experiments conducted on joint segmentation/deblurring tasks, the proposed method provides high-quality results.

8.11 Interpretable ensembling rules

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Nguyen Vu (Collaboration: I. Ben-Ayed, ETS Montréal, Canada)

Ensemble learning leverages multiple models (i.e., weak learners) on a common machine learning task to enhance prediction performance. Basic ensembling approaches average the weak learners outputs, while more sophisticated ones stack a machine learning model in between the weak learners outputs and the final prediction. The work [78] fuses both aforementioned frameworks. We introduce an aggregated f-average (AFA) shallow neural network which models and combines different types of averages to perform an optimal aggregation of the weak learners predictions. We emphasise its interpretable architecture and simple training strategy, and illustrate its good performance on the problem of few-shot class incremental learning.

8.12 Boosting radiologist performance using machine learning, the usecase of parotid tumours diagnosis

Participants: Emilie Chouzenoux, Arnaud Quillent (Collaboration: Institut Gustave Roussy)

In the work [2], we develop a machine learning algorithm based on magnetic resonance images characteristics to automatically classify parotid gland tumours. We then compare its results with the diagnoses of junior and senior radiologists in order to evaluate its utility in routine practice. While automatic algorithms applied to parotid tumours classification have been developed in the past, we believe that our study is one of the first to leverage four different MRI sequences and propose a comparison with clinicians.

8.13 Convolutional transform learning for multi-view data clustering

Participants: Emilie Chouzenoux (Collaboration: A. Majumdar, P. Gupta, A. Goel, IIIT Delhi, G. Chierchia, ESIEE Paris)

Multi-view data clustering is essential for discovering patterns and exploiting information from different sources. In this context, we propose in [22] DeConFCluster, an unsupervised multi-view clustering fusion framework based on Deep Convolutional Transform Learning. Our approach has the advantage that it does not require an additional decoder network during the training phase. This makes our model less prone to overfitting in data-constrained scenarios, as opposed to several recent studies based on the encoder-decoder framework. Furthermore, our method incorporates a loss function inspired by K-Means, which enables it to learn more effective representations for the clustering task.

8.14 Deep learning method for accessible eccentric photorefraction

Participants: Nguyen Vu, Emilie Chouzenoux, Jean-Christophe Pesquet (Collaboration: ESSILOR R&D)

In this work [59], we introduce an end-to-end eccentric photorefraction pipeline, merging an innovative capture device with an original refraction parameters regression method based on deep learning. Our approach infers refraction indexes from a patient eye picture to determine its refraction error. The proposed capture device is designed with the purpose of being a portable and affordable device, without sacrificing its effectiveness. Its design, incorporating infrared LEDs, allows for a measurable range that covers most vision impairments. Our deep-learning based regression model shows accurate results evaluated on both synthetic and real images, and an assessed robustness, increasing confidence in its prediction ability.

8.15 Deep learning for bowel-obstruction identification

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Maxence Gélard (Collaboration: Q. Vanderbecq, M. Zins, Hôpital Saint Antoine, AP-HP)

Automated evaluation of abdominal computed tomography (CT) scans should help radiologists manage their massive workloads, thereby leading to earlier diagnoses and better patient outcomes. In

the work [33], we develop a machine-learning model capable of reliably identifying suspected bowel obstruction (BO) on abdominal CT, based on a 3D mixed convolutional neural network. The method shows great potential for the automated binary classification (BO yes/no) of abdominal CT scans from patients with suspected BO.

8.16 Mapping photogenerated carrier lifetime from noisy photoluminescence images

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Gabriele Scrivanti (Collaboration: S. Caco-vich, E. Soret, G. Vidon, IPVF)

Halide perovskite materials offer significant promise for solar energy and optoelectronics yet understanding and enhancing their efficiency and stability require addressing lateral inhomogeneity challenges. While photoluminescence imaging techniques are employed for the measurement of their opto-electronic and transport properties, going further in terms of precision requires longer acquisition times. In the paper [34], a method to extract high-quality lifetime images from rapidly acquired, noisy time-resolved photoluminescence images is proposed. This method leverages concepts of the field of constrained reconstruction and includes the Huber loss function and a specific form of total variation regularization.

8.17 Iterative optimization for independent vector analysis

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Clement Cosserat (Collaboration: T. Adali, Univ. Baltimore)

Independent vector analysis (IVA) is an attractive solution to address the problem of joint blind source separation (JBSS), that is, the simultaneous extraction of latent sources from several datasets implicitly sharing some information. Among IVA approaches, we focus in [65] on the celebrated IVA-G model, that describes observed data through the mixing of independent Gaussian source vectors across the datasets. We formulate a cost function whose mathematical properties enable the use of a proximal alternating algorithm based on closed form operators with proved convergence to a critical point.

8.18 Convex estimation of regularized MGGDS and robust few-shot learning

Participants: Nora Ouzir, Jean-Christophe Pesquet (collaboration: Frédéric Pascal, L2S, CentraleSupélec)

In [29], we propose a novel convex formulation for the robust estimation of parameters of the multivariate Generalized Gaussian distribution (MGGD) in the presence of multiplicative perturbations. This family of distributions is essential for various tasks in image and signal processing, as well as in machine learning. We demonstrate in [29] that this traditionally challenging and non-convex problem can be transformed into a convex formulation, and we show that this property is maintained for several useful regularization functions.

8.19 Primary liver cancer classification from routine tumour biopsy using weakly supervised deep learning

Participants: Nora Ouzir, Jean-Christophe Pesquet (Collaboration: Beaujon Hospital AP-HP)

The diagnosis of primary liver cancers can be challenging, especially on biopsies and for combined hepatocellular-cholangiocarcinoma (cHCC-CCA). In [5], we automatically classified primary liver cancers on routine-stained biopsies using a weakly supervised learning method. Our model identified specific features of hepatocellular carcinoma and intrahepatic cholangiocarcinoma. Despite no specific features of cHCC-CCA being recognized, the identification of hepatocellular carcinoma and intrahepatic cholangiocarcinoma tiles within a slide could facilitate the diagnosis of primary liver cancers, and particularly cHCC-CCA.

8.20 Realtime flow estimation for interventional doppler ultrafast ultrasound

Participants: Nora Ouzir, Jean-Christophe Pesquet (Collaboration: IRIT, Toulouse)

Assessing blood flow and vascular structures is crucial for the treatment of various conditions, including brain tumours and cardiovascular disorders. During surgical procedures, the successful removal of a tumour relies on accurately defining the boundary between the tumour and the surrounding vital brain tissues. Traditional methods for separating blood flow from tissues typically employ filtering techniques, often utilizing SVD. More recent approaches, like DRPCA, tackle an inverse problem that incorporates blood sparsity along with the low-rank structure of tissues. In our recent work [76], we expanded this method to account for tissue motion, developing an algorithm that jointly estimates blood flow, tissues, and their movements. This advancement results in more accurate blood flow estimations and significantly reduces sensitivity to motion.

8.21 Robust neural networks for EMG-based Automatic Gesture Recognition

Participants: Ana Neacsu, Jean-Christophe Pesquet (collaboration: C. Burileanu, University Politehnica of Bucarest)

We introduce in [31] a novel approach for building a robust Automatic Gesture Recognition system based on Surface Electromyographic (sEMG) signals, acquired at the forearm level. Our main contribution is to propose new constrained learning strategies that ensure robustness against adversarial perturbations by controlling the Lipschitz constant of the classifier. We focus on positive neural networks for which accurate Lipschitz bounds can be derived, and we propose different spectral norm constraints offering robustness guarantees from a theoretical viewpoint. Experimental results on two distinct datasets highlight that a good trade-off in terms of accuracy and performance is achieved. We then demonstrate the robustness of our models, compared to standard trained classifiers in three scenarios, considering both white-box and black-box attacks.

8.22 Coping with positivity, expressivity, and robustness in neural networks

Participants: Ana Neacsu, Jean-Christophe Pesquet (collaboration: C. Burileanu and V. Vasilescu, University Politehnica of Bucarest)

We introduce in [27], ABBA networks, a novel class of (almost) non-negative neural networks, which are shown to possess a series of appealing properties. In particular, we demonstrate that these networks are universal approximators while enjoying the advantages of non-negative weighted networks. We derive tight Lipschitz bounds both in the fully connected and convolutional cases. We propose a strategy for designing ABBA nets that are robust against adversarial attacks, by finely controlling the Lipschitz constant of the network during the training phase. We show that our method outperforms other state-of-the-art defenses against adversarial white-box attackers. Experiments are performed on image classification tasks on four benchmark datasets.

8.23 Training robust Graph Neural Networks

Participants: Simona Juvina, Ana Neacsu, Jean-Christophe Pesquet (collaboration: C. Burileanu, University Politehnica of Bucarest ; I. Ben Ayed and J. Rony, ETS Montréal)

We propose in [23], a strategy for training a wide range of graph neural networks (GNNs) under tight Lipschitz bound constraints. Specifically, by leveraging graph spectral theory, we derive computationally tractable expressions of a tight Lipschitz constant. This allows us to propose a constrained-optimization approach to control the constant, ensuring robustness to adversarial perturbations. Unlike the existing methods for controlling the Lipschitz constant, our approach reduces the size of the handled matrices by a factor equal to the square of the number of nodes in the graph. We employ a stochastic projected subgradient algorithm, which operates in a block-coordinate manner, with the projection step performed

via an accelerated iterative proximal algorithm. We focus on defending against attacks that perturb features while keeping the topology of the graph constant. This contrasts with most of the existing defenses, which tackle perturbations of the graph structure. We report experiments on various datasets in the context of node classification tasks, showing the effectiveness of our constrained GNN model.

8.24 A primal-dual data-driven method for computational optical imaging

Participant: Jean-Christophe Pesquet (Collaboration: A. Repetti and 5 Master students, Heriot-Watt University, Edinburgh, UK)

Optical fibres aim to image in-vivo biological processes. In this context, high spatial resolution and stability to fibre movements are key to enable decision-making processes (e.g., for microendoscopy). In our work [32], a single-pixel imaging technique based on a multicore fibre photonic lantern has been designed, named computational optical imaging using a lantern (COIL). A proximal algorithm based on a sparsity prior, dubbed SARA-COIL, has been further proposed to solve the associated inverse problem, to enable image reconstructions for high resolution COIL microendoscopy. In this work, we develop a data-driven approach for COIL. We replace the sparsity prior in the proximal algorithm by a learned denoiser, leading to a plug-and-play (PnP) algorithm. The resulting PnP method, based on a proximal primal-dual algorithm, enables to solve the Morozov formulation of the inverse problem. We use recent results in learning theory to train a network with desirable Lipschitz properties, and we show that the resulting primal-dual PnP algorithm converges to a solution to a monotone inclusion problem. Our simulations highlight that the proposed data-driven approach improves the reconstruction quality over variational SARA-COIL method on both simulated and real data.

8.25 Learning truly monotone operators

Participants: Younes Belkouchi, Jean-Christophe Pesquet, Hugues Talbot (Collaboration: A. Repetti, Heriot Watt University)

We introduce in [6], a novel approach to learning monotone neural networks through a newly defined penalization loss. The proposed method is particularly effective in solving classes of variational problems, specifically monotone inclusion problems, commonly encountered in image processing tasks. The Forward-Backward-Forward (FBF) algorithm is employed to address these problems, offering a solution even when the Lipschitz constant of the neural network is unknown. Notably, the FBF algorithm provides convergence guarantees under the condition that the learned operator is monotone. Building on plug-and-play methodologies, our objective is to apply these newly learned operators to solving non-linear inverse problems. To achieve this, we initially formulate the problem as a variational inclusion problem. Subsequently, we train a monotone neural network to approximate an operator that may not inherently be monotone. Leveraging the FBF algorithm, we then show simulation examples where the non-linear inverse problem is successfully solved.

8.26 Deep learning classification and quantification of architectures in hepatocellular carcinoma from digital histopathologic images

Participants: Aymen Sadraoui, Jean-Christophe Pesquet (Collaboration: J. Calderaro, D. Cherqui, L. Claude, C. Guettier, A. Laurent-Bellue, M. Lewin, K. Posseme, E. Vibert, O. Rosmorduc, APHP)

Liver resection is one of the best treatments for small hepatocellular carcinoma (HCC), but post-resection recurrence is frequent. Biotherapies have emerged as an efficient adjuvant treatment, making the identification of patients at high risk of recurrence critical. Microvascular invasion (mVI), poor differentiation, pejorative macrotrabecular architectures, and vessels encapsulating tumor clusters architectures are the most accurate histologic predictors of recurrence, but their evaluation is time-consuming and imperfect. In the work [24], a supervised deep learning-based approach with ResNet34 on 680 whole slide images (WSIs) from 107 liver resection specimens was used to build an algorithm for the identification and quantification of these pejorative architectures. This model achieved an accuracy of

0.864 at patch level and 0.823 at WSI level. To assess its robustness, it was validated on an external cohort of 29 HCCs from another hospital, with an accuracy of 0.787 at WSI level, affirming its generalization capabilities. Moreover, the largest connected areas of the pejorative architectures extracted from the model were positively correlated to the presence of mVI and the number of tumor emboli. These results suggest that the identification of pejorative architectures could be an efficient surrogate of mVI and have a strong predictive value for the risk of recurrence. This study is the first step in the construction of a composite predictive algorithm for early post-resection recurrence of HCC, including artificial intelligence-based features.

8.27 Transductive few-shot for vision-language models

Participants: Ségolène Martin and Jean-Christophe Pesquet (Collaboration: Y. Huang, F. Shakeri, I Ben Ayed, ETS Montréal)

Transductive inference has been widely investigated in few-shot image classification, but completely overlooked in the recent, fast growing literature on adapting vision-language models like CLIP. This paper [49] addresses the transductive zero-shot and few-shot CLIP classification challenge, in which inference is performed jointly across a mini-batch of unlabeled query samples, rather than treating each instance independently. We initially construct informative vision-text probability features, leading to a classification problem on the unit simplex set. Inspired by Expectation-Maximization (EM), our optimization-based classification objective models the data probability distribution for each class using a Dirichlet law. The minimization problem is then tackled with a novel block Majorization-Minimization algorithm, which simultaneously estimates the distribution parameters and class assignments. Extensive numerical experiments underscore the benefits and efficacy of our batch inference approach.

8.28 A foundation for binary neural networks

Participants: Theodore Aouad, Hugues Talbot

Whereas there has been a lot of progress in deep learning over the last decade or so, theoretical and computing aspects of this body of techniques can still be improved. On the one hand, it has been observed that many layers in deep learning networks can be interpreted as mathematical morphology operators, and on the other hand, thanks to this observation, many deep learning networks can be simplified as layers with binary weights, utilizing a fraction of the memory required for standard networks, with little loss in performance and sometimes significant gains in interpretability.

However, binary networks are notoriously difficult to train, requiring specialized techniques, which are not well founded theoretically. In this work we defined a notion of binary morphological neuron and we build neural networks to use these as their building blocks instead of convolutions. This can be justified, as using morphological operators can be thought as combining linear filters with activations, which is a basic construction mechanism in most CNNs. In this manner, training can be performed naturally using existing frameworks (e.g. pytorch), then when training is completed, the weights can be binarized with a simple method without loss of performance. This is a promising avenue of research, and we are currently working on extending this work to more complex networks and to other types of morphological operators. This work corresponds to Theodore Aouad's PhD work, which was completed in June 2024.

Most of these results were reported in [36], including experiments showing that these networks can indeed learn sequences of operators as well as perform classification tasks with good results.

8.29 Transductive few-shot learning approach for classification of digital histopathological slides

Participants: Elliot Barbot, Ségolène Martin, Jean-Christophe Pesquet, and Aymen Sadraoui (Collaboration: A. Laurent-Bellue, C. Guettier, APHP, I Ben Ayed, ETS Montréal)

This paper [54] presents a new approach for classifying 2D histopathology patches using few-shot learning. The method is designed to tackle a significant challenge in histopathology, which is the limited

availability of labeled data. By applying a sliding window technique to histopathology slides, we illustrate the practical benefits of transductive learning (i.e., making joint predictions on patches) to achieve consistent and accurate classification. Our approach involves an optimization-based strategy that actively penalizes the prediction of a large number of distinct classes within each window. We conducted experiments on histopathological data to classify tissue classes in digital slides of liver cancer, specifically hepatocellular carcinoma. The initial results show the effectiveness of our method and its potential to enhance the process of automated cancer diagnosis and treatment, all while reducing the time and effort required for expert annotation.

8.30 Data augmentation in self supervised learning

Participant: Maria Vakalopoulou (Collaboration: MICS CentraleSupélec, FAIR Meta)

Self-Supervised learning (SSL) with Joint-Embedding Architectures (JEA) has led to outstanding performances. All instantiations of this paradigm were trained using strong and well-established hand-crafted data augmentations, leading to the general belief that they are required for the proper training and performance of such models. On the other hand, generative reconstruction-based models such as BEIT and MAE or Joint-Embedding Predictive Architectures such as I-JEPA have shown strong performance without using data augmentations except masking. In [51], we challenge the importance of invariance and data-augmentation in JEAs at scale. By running a case-study on a recent SSL foundation model – DINOv2 – we show that strong image representations can be obtained with JEAs and only cropping without resizing provided the training data is large enough, reaching state-of-the-art results and using the least amount of augmentation in the literature. Through this study, we also discuss the impact of compute constraints on the outcomes of experimental deep learning research, showing that they can lead to very different conclusions.

8.31 Detection and classification of pulmonary embolisms

Participants: Theodore Aouad, Hugues Talbot (Collaboration: BIOMAPS).

Pulmonary embolisms are a major health issue, associated, like many cardio-vascular accident, with a poor prognosis if not treated correctly and on time. However, classifying embolisms is difficult, and the various clinical scores that have been developed are in practice difficult to compute even by specialists. The purpose of this study was to propose a deep learning-based approach to detect pulmonary embolism and quantify its severity using the Qanadli score and the right-to-left ventricle diameter (RV/LV) ratio on three-dimensional (3D) computed tomography pulmonary angiography (CTPA) examinations with limited annotations.

This study was the topic of the 2022 challenge of the Société Française de Radiologie (SFRadio). Our role was to help collect the data, run the challenge smoothly and assess the results, including designing fair and relevant metrics with the help of expert radiologists. The scientific results of this challenge were reported in XXX

8.32 Analysis of pathology Whole Slide Images with spatial context

Participants: Loïc Le Bescond, Hugues Talbot (Collaboration: Marvin Lrousseau, Institut Curie ; Fabrice André, Institut Gustave-Roussy)

The computer analysis of Whole Slide Images (WSI) is becoming increasingly prevalent in pathology-based diagnosis, although it presents considerable challenges due to the voluminous nature of the data. To address this issue, Multiple Instance Learning (MIL) has emerged as a viable approach that involves partitioning WSI into tiles for processing. Nevertheless, conventional MIL methodologies inadequately capture the essential spatial context between tiles, which is imperative for accurate diagnosis across various diseases. In this work [73], we present a novel framework, SparseXceptionMIL (SparseXMIL), aiming to enhance the modeling of spatial interactions within WSI data by introducing a multi-dimensional sparse image representation and a novel pooling operator. This operator integrates

sparse convolutions within the Xception architecture. It enables effective spatial information processing across multiple scales. Empirical evaluations conducted on various classification tasks, encompassing subtyping for breast and lung carcinomas and predicting abnormalities in the DNA damage response in breast cancer WSI, consistently demonstrate the superiority of our approach over benchmark methods. These results underscore the potential of sparse convolutional architectures to improve WSI classification.

8.33 Optimizing Binary-tree based transport networks

Participants: Hugues Talbot, Raoul Sallé de Chou (Collaboration: Laurent Najman, Université Gustave-Eiffel ; Irène Vignon-Clementel, Inria SimbiotX)

Optimizing transport networks is a well-known class of problems that have been extensively studied, with application in many domains. In this work [56], we are interested in a generalization of the well-studied Steiner problem, which entails finding a graph minimizing a cost function associated with connecting a given set of points, for which the topology is not given. In this paper, we focus on a specific formulation of this problem which is applied to the generation of synthetic vascular trees. More precisely, we study the Constrained Constructive Optimization (CCO) tree algorithm, which constructs a vascular network iteratively, optimizing a blood transport energy efficiency. We show that the classical incremental construction method often leads to sub-optimal results, and that a significantly better global solution can be reached.

8.34 Combotherapy vs monotherapy in the case of colorectal cancer

Participants: Younes Belkouchi, Hugues Talbot (Collaboration: Nathalie Lassau, Institut Gustave Roussy ; Paul-Henry Cournède, MICS)

In this retrospective study [4], using classical Machine Learning methods and statistical analysis, we determined survival responses to immune checkpoint inhibitors (ICIs), comparing mono- (mono) and combo-immunotherapy (combo) in patients with microsatellite instability-high (MSI-H) metastatic colorectal cancer (mCRC) by analyzing quantitative imaging data and clinical factors. Radiologists manually annotated chest-abdomen-pelvis computed tomography and calculated tumor burden. Progression-free survival (PFS) was assessed, and variables were selected through Recursive Feature Elimination. Cutoff values were determined using maximally selected rank statistics to binarize features, forming a risk score with hazard ratio-derived weights. In total, 2258 lesions were annotated with excellent reproducibility. In the validation set, low-score patients exhibited no significant difference in overall survival and PFS with mono or combo. However, patients with a high-score had worse PFS with mono ($P = 0.046$). The importance and usefulness of this study is not so much the end result as the fact that obtaining solid and verified data in sufficient amounts is indeed necessary to obtain verifiable conclusions, together with the fact that obtaining this data was made possible thanks to semi-automated tools developed in partnership with Gustave Roussy.

8.35 Myocardial perfusion simulation with a physics-informed GNN

Participants: Raoul Sallé de Chou, Hugues Talbot (Collaboration: Laurent Najman, Université Gustave-Eiffel ; Irène Vignon-Clementel, Inria SimbiotX ; Matthew Sinclair, Heartflow Inc)

Medical imaging and numerical simulation of partial differential equations (PDEs) representing biophysical processes have been combined in the past few decades to provide noninvasive diagnostic and treatment prediction tools for various diseases. Most approaches involve solving computationally expensive PDEs, which can hinder their effective deployment in clinical settings. To overcome this limitation, deep learning has emerged as a promising method to accelerate numerical solvers. However, the generalization abilities of these models is often put into question, given the wide variety of patient morphologies. This study [55] addresses this challenge by introducing a physics-informed graph neural network designed to solve Darcy equations for the simulation of myocardial perfusion. Leveraging a finite volume discretization of the equations as a “physics-informed” loss, our model was successfully trained and tested on a 3D synthetic dataset, namely meshes representing simplified myocardium

shapes. Subsequent evaluation on genuine myocardium meshes, extracted from patients Computed Tomography images, demonstrated promising results, and generalized capabilities. Such a fast solver, within a differentiable learning framework, will enable to tackle inverse problems based on H2O-PET perfusion imaging data.

8.36 Detection and characterisation of pancreatic lesions with AI methods

Participants: Theodore Aouad, Hugues Talbot (Collaboration: Nathalie Lassau, Institut Gustave Roussy)

In this study [3], which corresponds to the 2023 AI challenge of the SFRadio, anonymized abdominal CT examinations acquired from 18 French centers. They were divided into three groups including CT examinations with no lesion, CT examinations with benign pancreatic mass, or CT examinations with malignant pancreatic mass. Each team included at least one radiologist, one data scientist, and one engineer. Pancreatic lesions were annotated by expert radiologists. CT examinations were distributed in balanced batches via a Health Data Hosting certified platform. Data were distributed into four batches, two for training, one for internal evaluation, and one for the external evaluation. Training used 83 % of the data from 14 centers and external evaluation used data from the other four centers. The metric (i.e., final score) used to rank the participants was a weighted average of mean sensitivity, mean precision and mean area under the curve. A total of 1037 abdominal CT examinations were divided into two training sets (including 500 and 232 CT examinations), an internal evaluation set (including 139 CT examinations), and an external evaluation set (including 166 CT examinations). The training sets were distributed on September 7 and October 13, 2023, and evaluation sets on October 15, 2023. Ten teams with a total of 93 members participated to the data challenge, with the best final score being 0.72.

In this work, we managed the data acquisition, the labeling, the interaction with radiologists and oncologists as well as all the participants, the running of the challenge itself, the development of the result metrics, and the ranking. This was another demonstration that acquiring and labeling data on a large scale is possible, yielding interesting and useful results in a relatively short amount of time.

8.37 Bone surface reconstruction in 3D from a single X-ray radiography

Participant: Hugues Talbot (Collaboration: Yi Gu, Yoshito Otake, Yoshinobu Sato, NAIST, Japan)

Radiography is widely used in orthopedics for its affordability and low radiation exposure. 3D reconstruction from a single radiograph, so-called 2D-3D reconstruction, offers the possibility of various clinical applications, but achieving clinically viable accuracy and computational efficiency is still an unsolved challenge. Unlike other areas in computer vision, X-ray imaging's unique properties, such as ray penetration and standard geometry, have not been fully exploited. In this study [41], we propose a novel approach that simultaneously learns multiple depth maps (front and back surfaces of multiple bones) derived from the X-ray image to computed tomography (CT) registration. The proposed method, based on deep-learning approach combining segmentation, monocular vision and a statistical shape model not only leverages the standard geometry characteristic of X-ray imaging but also enhances the precision of the reconstruction of the whole surface. Our study involved 600 CT and 2651 X-ray images (4 to 5 posed X-ray images per patient), demonstrating our method's superiority over traditional approaches with a surface reconstruction error reduction from 4.78 mm to 1.96 mm and further to 1.76 mm using higher resolution and pretraining. This significant accuracy improvement and enhanced computational efficiency suggest our approach's potential for clinical application.

8.38 Automated segmentation of sperm cell parts for in-vitro fertilization

Participant: Hugues Talbot (Collaboration: Daniel Wesierski, Anna Jezierska, Gdansk University of Technology)

Infertility affects around 15% of couples worldwide. Male fertility problems include poor sperm quality and low sperm count. Advanced fertility treatment methods like ICSI are nowadays supported by vision systems to assist embryologists in selecting good quality sperm. Computer-Assisted Semen

Analysis (CASA) provides quantitative and qualitative sperm analysis concerning concentration, motility, morphology, vitality, and fragmentation. However, fertility assessment algorithms often neglect individual spermatozoon tail and its beating patterns because recognizing the tails in blurry microscopic images reliably is challenging. In this work [44], we propose that models trained with head and tail part classes can better localize parts and segment the whole spermatozoon. Usually, the training of segmentation sperm models is supported by image-level augmentation. We argue that models guided by class-specific data augmentation attend to less discriminative sperm parts. To demonstrate this, we decouple the augmentation into object-level and background augmentation for the sperm part segmentation problem. Our proposed method outperforms state-of-the-art methods on the SegSperm dataset. Moreover, our ablation studies confirm the effectiveness of the proposed part-based object representation and augmentation. The deep learning architecture for this project used specifically designed morphological layers to compensate the thinness of the sperm cell tails.

8.39 Pretraining for quantitative image synthesis

Participant: Hugues Talbot (Collaboration: Yi Gu, Yoshito Otake, Yoshinobu Sato, NAIST, Japan)

While most vision tasks are essentially visual in nature, some important tasks, especially in the medical field, also require quantitative analysis. For these tasks, pixel values in quantitative images correspond to physical metrics measured by specific devices (e.g., a depth image). However, recent work has shown that it is sometimes possible to synthesize accurate quantitative values from visual ones (e.g., depth from visual cues or defocus). With this research [42] we aim to improve quantitative image synthesis (QIS) by exploring pretraining and image resolution scaling. We propose a benchmark for evaluating pretraining performance using the task of QIS-based bone mineral density (BMD) estimation from plain X-ray images, where the synthesized quantitative image is used to derive BMD. Our results show that appropriate pretraining can improve QIS performance, significantly raising the correlation of BMD estimation from 0.820 to 0.898, while others do not help or even hinder it. Scaling-up the resolution can further boost the correlation up to 0.923, a significant enhancement over conventional methods.

8.40 Fraud detection in ID photographs

Participant: Hugues Talbot (Collaboration: Manel Ben Youssef, Sylvain Lempereur, SmartphoneID)

Today many industrial and government sign-on systems (e.g when taking the written exam to obtain a driving license) require users to take or provide a photograph of themselves to prove that they correspond to their ID document (passport, national identity card, etc). Current systems are relatively difficult to use, requiring users to assume various poses to also prove "liveliness", i.e. the fact that the photograph being taken is really that of a real person, and not for example the photograph of a printed photograph. This patented work [80] makes the point that a very fast system consisting of taking a limited number of independent photographs in rapid succession is sufficient and more effective in a majority of the cases.

8.41 Can Liquid biopsy provide an alternative to a CT scan in some cancer care situations?

Participants: Younes Belkouchi, Hugues Talbot (Collaboration: Nathalie Lassau, Institut Gustave Roussy)

Liquid biopsy is a simple and non-invasive alternative to surgical biopsies which enables doctors to discover a range of information about a tumour through a simple blood sample. Traces of the cancer's DNA in the blood can give clues about which treatments are most likely to work for that patient. In this study [15], we sought to ascertain whether such biopsies can be considered a suitable alternative to a CT scan, e.g. when estimating the tumor burden of a patient. For this a retrospective cohort of 1065 patients was considered, with a total of 56288 lesions which were all annotated. A total of 763 liquid biopsies were considered. A range of models predicting Tumor Fraction at CT was built from the liquid biopsy data. Unfortunately, the correlation was not found to be strong enough to offer a replacement for the costlier exam. However the cheaper exam could still prove useful in developing countries for example.

8.42 Performance analysis of a deep-learning model to detect inflammation in MRI of the sacro-iliac joint

Participants: Theodore Aouad, Hugues Talbot (Collaboration: Antoine Feydy, Maxime Dougados, APHP, Cochin hospital)

It is often difficult and costly to validate results obtained with a deep-learning method in medical imaging. In this study [28], we confirmed the performance of such a network in the context of the assessment of a relatively rare auto-immune disease that affects the pelvis, and more specifically the sacro-iliac joint, i.e. the joint between the spine and the pelvis. This disease, axial spondyloarthritis (axSpA), affects relatively young people and can be debilitating if not diagnosed early enough. We essentially provided a trained network to the company UCB pharma, which ran the software on an internal cohort of patients suspected of suffering from axSpA. The data was never available to us, we only knew that it had been acquired according to the accepted guidelines for the diagnosis of this illness. Analysis of the results showed that our network still performed at the level of a specialist radiologist for this disease.

8.43 Robust automatic crater detection at all latitudes on Mars with Deep-learning

Participant: Hugues Talbot (Collaboration: Leonard Martinez, François Andrieu, Frédéric Schmidt, Geoscience Paris-Saclay)

Understanding the distribution and characteristics of impact craters on planetary surfaces allows researchers to unravel geological processes and the evolution of celestial bodies. Several machine learning and AI-based approaches have been proposed to detect craters on planetary surface images automatically. However, designing a robust tool for an entire complex planet such as Mars, is still an open problem. Our work [26] presents a novel approach using the Faster Region-based Convolutional Neural Network (Faster R-CNN) for such a detection. The proposed method involves the pre-processing, training and crater detection steps, which are especially designed for robustness regarding latitude and complex geomorphological features. The objectives of this studies are to (i) be robust at all latitudes and (ii) for ≥ 1 km diameter crater sizes. (iii) To propose an open-source and re-usable algorithm that (iv) only needs an image to run. Extensive experiments on high-resolution planetary imagery demonstrate excellent performances with an average precision mAP > 0.82 with an intersection over union criterion IoU ≥ 0.5 , irrespective of crater scale. For mid and high latitudes (higher than 48° north and south), performance decreases down to mAP 0.7 , which is still better than the current state of the art. Loss of performance is mostly due to strong shadowing effects. Our results also highlight the versatility and potential of our robust model for automating the analysis of craters across different celestial bodies. The automated crater detection tool presented in this article is publicly available as open-source and holds great promise for future scientific research of space exploration missions.

8.44 Computational pathology and foundation models

Participant: Maria Vakalopoulou (Collaboration: MICS CentraleSupélec ; Stony Brook University)

Introducing interpretability and reasoning into Multiple Instance Learning (MIL) methods for Whole Slide Image (WSI) analysis is challenging, given the complexity of gigapixel slides. Traditionally, MIL interpretability is limited to identifying salient regions deemed pertinent for downstream tasks, offering little insight to the end-user (pathologist) regarding the rationale behind these selections. To address this, in [45], we propose Self-Interpretable MIL (SI-MIL), a method intrinsically designed for interpretability from the very outset. SI-MIL employs a deep MIL framework to guide an interpretable branch grounded on handcrafted pathological features, facilitating linear predictions. Beyond identifying salient regions, SI-MIL uniquely provides feature-level interpretations rooted in pathological insights for WSIs. Notably, SI-MIL, with its linear prediction constraints, challenges the prevalent myth of an inevitable trade-off between model interpretability and performance, demonstrating competitive results compared to state-of-the-art methods on WSI-level prediction tasks across three cancer types. In addition, we thoroughly

benchmark the local- and global-interpretability of SI-MIL in terms of statistical analysis, a domain expert study, and desiderata of interpretability, namely, user-friendliness and faithfulness.

8.45 Deep learning models for the prediction of interstitial lung disease

Participant: Maria Vakalopoulou (Collaboration: Hôpital Cochin, AP-HP)

Stratifying the risk of death in SSc-related interstitial lung disease (SSc-ILD) is a challenging issue. The extent of lung fibrosis on high-resolution CT (HRCT) is often assessed by a visual semiquantitative method that lacks reliability. We aimed to assess the potential prognostic value of a deep-learning-based algorithm enabling automated quantification of ILD on HRCT in patients with SSc. In [25], we propose a deep-learning-based, computer-aided quantification of ILD extent on HRCT that provides an effective tool for risk stratification in SSc. It might help identify patients at short-term risk of death.

8.46 Learning graph representations for influence maximization

Participant: Fragkiskos Malliaros (Collaboration: Jellyfish ; Université du Luxembourg ; Ecole Polytechnique)

Finding the seed set that maximizes the influence spread over a network is a wellknown NP-hard problem. Though a greedy algorithm can provide near-optimal solutions, the subproblem of influence estimation renders the solutions inefficient. In this work [30], we propose Glie, a graph neural network that learns how to estimate the influence spread of the independent cascade. Glie relies on a theoretical upper bound that is tightened through supervised training. Experiments indicate that it provides accurate influence estimation for real graphs up to 10 times larger than the train set.

8.47 Gegenbauer Graph Neural Networks for time-varying signal reconstruction

Participant: Fragkiskos Malliaros (Collaboration: Jhon Castro-Correa, Mohsen Badiey, Univ. of Delaware ; Jhony H. Giraldo, Télécom Paris)

Reconstructing time-varying graph signals is a critical problem in machine learning and signal processing with broad applications, ranging from missing data imputation in sensor networks to time-series forecasting. However, existing approaches relying on smoothness assumptions of temporal differences and simple convex optimization techniques that have inherent limitations. To address these challenges, we have proposed an approach that incorporates a learning module to enhance the accuracy of the downstream task [8]. To this end, we have introduced the Gegenbauer-based graph convolutional (GegenConv) operator, which is a generalization of the conventional Chebyshev graph convolution by leveraging the theory of Gegenbauer polynomials. Building upon GegenConv, we have designed the Gegenbauer-based time graph neural network (GegenGNN) architecture, which adopts an encoder decoder structure. This combination enables GegenGNN to capture both the fidelity to ground truth and the underlying smoothness properties of the signals, enhancing the reconstruction performance.

8.48 Estimation of a causal directed acyclic graph process using non-gaussianity

Participant: Fragkiskos Malliaros (Collaboration: Aref Einizade and Jhony H. Giraldo, Télécom Paris)

In machine learning and data mining, causal relationship discovery is a critical task. While the state-of-the-art Vector Auto-Regressive Linear Non-Gaussian Acyclic Model (VAR-LiNGAM) method excels in uncovering both instantaneous and time-lagged connections, it entails analyzing multiple VAR matrices, leading to heightened parameter complexity. To address this challenge, we introduce in [17], the Causal Graph Process-LiNGAM (CGP-LiNGAM), a novel approach that significantly reduces parameter load by focusing on a single causal graph, a Directed Acyclic Graph (DAG). Leveraging Graph Signal Processing (GSP) techniques, our method interprets causal relations with graph shift invariance and uniqueness. Our

experimental results demonstrate the superiority and robustness of CGP-LiNGAM, particularly in high-noise environments. Moreover, we showcase its real-world applicability in studying brain connectivity during sleep, underlining its compatibility with previous sleep-related neuroscientific research

8.49 Continuous Product Graph Neural Networks

Participant: Fragkiskos Malliaros (Collaboration: Aref Einizade and Jhony H. Giraldo, Télécom Paris)

Processing multidomain data defined on multiple graphs holds significant potential in various practical applications in computer science. However, current methods are mostly limited to discrete graph filtering operations. Tensorial partial differential equations on graphs (TPDEGs) provide a principled framework for modeling structured data across multiple interacting graphs, addressing the limitations of the existing discrete methodologies. In our recent work [38], we have introduced Continuous Product Graph Neural Networks (CITRUS) that emerge as a natural solution to the TPDEG. CITRUS leverages the separability of continuous heat kernels from Cartesian graph products to efficiently implement graph spectral decomposition. We have further conducted a thorough theoretical analyses of the stability and over-smoothing properties of CITRUS in response to domain-specific graph perturbations and graph spectra effects on the performance.

8.50 Sparse Sobolev Graph Neural Networks

Participant: Fragkiskos Malliaros (Collaboration: Jhony H. Giraldo, Aref Einizade, Andjela Todorovic, Télécom Paris ; Jhon Castro-Correa, Mohsen Badiey, Univ. of Delaware ; Thierry Bouwmans, La Rochelle Univ.)

Graph Neural Networks (GNNs) have shown great promise in modeling relationships between nodes in a graph, but capturing higher-order relationships remains a challenge for large-scale networks. Previous studies have primarily attempted to utilize the information from higher-order neighbors in the graph, involving the incorporation of powers of the shift operator, such as the graph Laplacian or adjacency matrix. In our recent work [giraldo:hal-04801077], relying on the observation that the spectrum of the regular and the Hadamard power of the Laplacian matrix behave similarly, we have proposed a novel graph convolutional operator based on the sparse Sobolev norm of graph signals. Our approach, known as Sparse Sobolev GNN (S2-GNN), employs Hadamard products between matrices to maintain the sparsity level in graph representations, achieving competitive performance compared to state-of-the-art GNNs in terms of accuracy on downstream tasks and running time.

8.51 Uplift modeling under limited supervision

Participants: Fragkiskos Malliaros, Daniele Malitesta (Collaboration: George Panagopoulos and J. Pung, Univ. of Luxembourg)

Estimating causal effects in e-commerce tends to involve costly treatment assignments which can be impractical in large-scale settings. Leveraging machine learning to predict such treatment effects without actual intervention is a standard practice to diminish the risk. However, existing methods for treatment effect prediction tend to rely on training sets of substantial size, which are built from real experiments and are thus inherently risky to create. In our work [52], we proposed a graph neural network to diminish the required training set size, relying on graphs that are common in e-commerce data. Specifically, we view the problem as node regression with a restricted number of labeled instances, develop a two-model neural architecture akin to previous causal effect estimators, and test varying message-passing layers for encoding. Furthermore, as an extra step, we combine the model with an acquisition function to guide the creation of the training set in settings with extremely low experimental budget. The framework is flexible since each step can be used separately with other models or treatment policies.

8.52 Missing modalities in multimodal recommendation

Participants: Fragkiskos Malliaros, Daniele Malitesta (Collaboration: Emanuele Rossi, VantAI ; Claudio Pomo, Tommaso Di Noia, Politecnico di Bari)

Generally, items with missing modalities are dropped in multimodal recommendation systems. In our recent work [47], we have questioned this procedure, highlighting that it would further damage the pipeline of any multimodal recommender system. We have proposed a pipeline that imputes missing multimodal features in recommendation by leveraging traditional imputation strategies in machine learning. Then, given the graph structure of the recommendation data, we have also introduced several effective imputation solutions that leverage the item-item co-purchase graph and the multimodal similarities of co-interacted items. Our method can be plugged into any multimodal recommender system in the literature working as an untrained pre-processing phase, showing (through extensive experiments) that any data pre-filtering is not only unnecessary but also harmful to the performance.

8.53 Measuring factual correctness of large language models

Participant: Fragkiskos Malliaros (Collaboration: Rajaa El Hamdani, Thomas Bonald, Nils Holzenberger, and Fabian Suchanek, Télécom Paris)

In our recent work [39], we have investigated the factuality of large language models (LLMs) as knowledge bases in the legal domain, in a realistic usage scenario: we allow for acceptable variations in the answer, and let the model abstain from answering when uncertain. First, we designed a dataset of diverse factual questions about case law and legislation. We then used the dataset to evaluate several LLMs under different evaluation methods, including exact, alias, and fuzzy matching. Our results have demonstrated that the performance improves significantly under the alias and fuzzy matching methods. Further, we explored the impact of abstaining and in-context examples, finding that both strategies enhance precision.

8.54 Unrolled algorithm for stain separation in histopathological images

Participants: Aymen Sadraoui, Mounir Kaaniche, Jean-Christophe Pesquet (Collaboration: Astrid Laurent-Bellue & Catherine Guettier, Department of Pathology, AP-HP, hôpital Bicêtre)

Stain separation is a crucial step in histopathological image analysis and aims to identify each stain in the original image. In this respect, we proposed in [53] a new approach for stain separation of HES-stained images. The proposed method takes advantage of the projected gradient algorithm and the unrolling paradigm. More precisely, starting from the standard problem formulation used in NMF based methods, we include a total-variation based regularization to impose the smoothness of the separated images. The regularized problem is then solved by a projected gradient algorithm. Finally, the algorithm is unrolled into layers of a neural network. Our experiments, carried out on data acquired at the Kremlin-Bicêtre hospital, demonstrate the efficiency of the proposed method, yielding significant objective and subjective gains compared to state-of-the-art methods.

8.55 A dynamic squeeze network for real-time weld seam image segmentation

Participant: Mounir Kaaniche (Collaboration: Tianjin University of Technology, China)

The image noise generated by the welding process, such as arc light, splash, and smoke, brings significant challenges for the laser vision sensor-based welding robot to locate the weld seam and accurately conduct automatic welding. Currently, deep learning-based approaches surpass traditional methods in flexibility and robustness. However, their significant computational cost leads to a mismatch with the real-time requirement of automated welding. In this paper [9], we propose an efficient hybrid architecture of Convolutional Neural Network (CNN) and transformer, referred to as Dynamic Squeeze Network (DSNet), for real-time weld seam segmentation.

8.56 Multi-task neural networks for lifting-based image coders

Participants: Tassnim Dardouri, Mounir Kaaniche, Jean-Christophe Pesquet (Collaboration: Amel Benazza-Benyahia, SUP'COM-Tunis)

Motivated by the several advantages of lifting-based representations and the promising results shown by our recent FCNN-LS-based coding methods, the use of neural networks in lifting-based image coding systems has been further investigated in [14]. While considering a popular non-separable lifting structure that relies on three prediction stages and an update stage, we propose to perform the different involved lifting steps by using CNN models to better capture the local structure of the input image. Most importantly, unlike previous works where different neural network models are employed to carry out the LS-based decomposition at a given resolution level, a new multi-task CNN architecture is developed. The proposed architecture aims to exploit the similarities between the second and third prediction steps and perform their learning in a joint manner. The experimental results, obtained with different standard image datasets, have shown the good performance of the proposed approach compared to the state-of-the-art methods, and more specifically, the recent neural networks-based lifting schemes.

8.57 Differentiating nonsmooth solutions to parametric monotone inclusion problems

Participant: Antonio Silveti-Falls (Collaboration: J. Bolte, TSE ; E. Pauwels, IRIT)

We leverage in [7] path differentiability and a recent result on nonsmooth implicit differentiation calculus to give sufficient conditions ensuring that the solution to a monotone inclusion problem will be path differentiable, with formulas for computing its generalized gradient. A direct consequence of our result is that these solutions happen to be differentiable almost everywhere. Our approach is fully compatible with automatic differentiation and comes with assumptions which are easy to check, roughly speaking: semialgebraicity and strong monotonicity. We illustrate the scope of our results by considering three fundamental composite problem settings: strongly convex problems, dual solutions to convex minimization problems and primal-dual solutions to min-max problems.

9 Bilateral contracts and grants with industry

9.1 Bilateral contracts with industry

- PhD Contract with Nokia Bell Labs
 - Project title: Graph Neural Networks for Causal Inference for Wireless Network Management
 - Duration: 2024-2027
 - Leader: Fragkiskos Malliaros
- PhD Contract with Heartflow Inc
 - Project title: Estimating heart perfusion based on physics-aware machine-learning methods
 - Duration: 2022-2025
 - Leaders: Hugues Talbot and I. Vignon-Clementel (Inria REO).
- PhD Contract with SAFRAN (CIFRE)
 - Project title: Safran fibres composites
 - Duration: 2023-2026
 - Leaders: Hugues Talbot
- Contract with Schneider Electric
 - Project title: AI for electrical motor diagnosis and control

- Duration: 2022-2024
- Leaders: Marc Castella (Télécom ParisTech) and Jean-Christophe Pesquet
- Contract with Schneider Electric
 - Project title: Detection of pump cavitation using artificial intelligence algorithms
 - Duration: 2024-2025
 - Leaders: Jean-Christophe Pesquet
- Contract with ESSILOR
 - Project title: Software development for photo-refraction analysis
 - Duration: 2020-2024
 - Leaders: Emilie Chouzenoux and Jean-Christophe Pesquet
- Contract with AIRBUS (Plan de Relance - mesure de préservation de l'emploi en R&D)
 - Project title: AI for composite quality
 - Duration: 2022-2024
 - Leaders: Nora Ouzir and Jean-Christophe Pesquet

10 Partnerships and cooperations

10.1 International initiatives

10.1.1 STIC/MATH/CLIMAT AmSud projects

CGLFRVE

Title: Context-guided future liver remnant volume estimation using artificial intelligence models

Program: STIC-AmSud

Duration: January 1, 2024 – December 31, 2025

Local supervisor: Maria Vakalopoulou

Partners:

- Chang (Chili)
- Ferrante (Argentine)
- Universidad de los Andes

Inria contact: Maria Vakalopoulou

Summary: Automatic Liver-Segmentation is an essential task in the medical context. Current AI-based models are focused on liver and tumor segmentation, that is not enough for surgical planning, especially for liver metastases. An automatic liver and tumor segmentation method can greatly relieve physicians of the heavy workload of examining CT images. However, for surgery, a more challenging task is required. In this context, it is critical to estimate accurately the remnant liver volume after resection; for instance, in patients with liver metastases. Estimating the future liver remnant is a challenging task because the type of surgery to be performed depends on each patient's clinical setting, the center's experience, number and location of liver lesions, among others. This means that future liver remnant segmentation depends on the patient's clinical context. Therefore, the goal of this project is to design, implement and evaluate fine-grained liver segmentation guided by the context that allows us to precisely estimate remnant liver volume. Our work is guided

by five objectives: (1) evaluate SOTA liver segmentation models, including the recent published architecture HybridGNet; (2) design and evaluate models for fine-grained liver segmentation models taking into account models like SAM and HybridGNet; (3) estimate remnant liver volume using the fine-grained liver segmentation model; (4) Integrate contextual information by prompts for liver segmentation. Finally, we present results on public and private datasets. For the private case, we collaborate with a local health center, which provides us access to data. To accomplish the proposed objectives, we have formed a multidisciplinary team, including physicians with specialization in radiology and experts on computer vision applied to medical images.

10.2 International research visitors

10.2.1 Visits of international scientists

Other international visits to the team

Luis Manuel Briceno Arias

Status: Associate Professor

Institution of origin: Universidad Técnica Federico Santa María

Country: Chile

Dates: 15th June to 19 July 2024

Context of the visit: Collaboration with E. Chouzenoux and J.-C. Pesquet.

Mobility program/type of mobility: Research stay funded by ERC MAJORIS.

Giorgia Franchini

Status: Associate Professor

Institution of origin: UNIMORE

Country: Italy

Dates: 29 Sep. to 11st Oct. 2024

Context of the visit: Collaboration with E. Chouzenoux and J.-C. Pesquet.

Mobility program/type of mobility: Research stay funded by ERC MAJORIS.

Filippo Camellini

Status: PhD student

Institution of origin: UNIMORE

Country: Italy

Dates: 29 Sep. to 4th Oct. 2024

Context of the visit: Collaboration with E. Chouzenoux and J.-C. Pesquet.

Mobility program/type of mobility: Research stay funded by ERC MAJORIS.

Marian Negru

Status: PhD student

Institution of origin: University of Bucharest

Country: Romania

Dates: 01 Feb. 2024 to 31 May 2025

Context of the visit: Collaboration with J.-C. Pesquet.

Mobility program/type of mobility: Research stay funded by ERASMUS

Nontokozo Mpofo

Status: PhD Student

Institution of Origin: University of Witwatersrand

Country: South Africa

Dates: Mar. to Aug. 2024

Context of the visit: Collaboration with Nora Ouzir and Jean-Christophe Pesquet

Mobility program/type of mobility: Research stay funded by DATAIA mobility grant

Wang Xinjue

Status: PhD Student

Institution of Origin: Aalto University

Country: Finland

Dates: Nov. 2024

Context of the visit: Collaboration with Nora Ouzir and Jean-Christophe Pesquet

Mobility program/type of mobility: Research stay

10.2.2 Visits to international teams**Research stays abroad****Thomas Guilmeau**

Visited institution: University of Edinburgh

Country: UK

Dates: 26 Feb. to 6 April 2024

Context of the visit: Collaboration with V. Elvira

Mobility program/type of mobility: Research stay funded by Inria International Program

Clément Cosserat

Visited institution: University of Baltimore

Country: USA

Dates: 21 Nov. to 23 Dec. 2024

Context of the visit: Collaboration with T. Adali

Mobility program/type of mobility: Research stay funded by DATAIA mobility grant

10.3 European initiatives

10.3.1 H2020 projects

MAJORIS [MAJORIS project on cordis.europa.eu](https://cordis.europa.eu/project/MAJORIS)

Title: Majorization-Minimization algorithms for Image Processing

Duration: From January 1, 2020 to June 30, 2025

Partners:

- INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET AUTOMATIQUE (INRIA), France

Inria contact: Emilie CHOUZENOUX

Coordinator:

Summary: Mathematical optimization is the key to solving many problems in science, based on the observation that physical systems obey a general principle of least action. While some problems can be solved analytically, many more can only be solved via numerical algorithms. Research in this domain has proved essential over many years. In addition, science in general is changing. Increasingly, in biology, medicine, astronomy, chemistry, physics, large amounts of data are collected by constantly improving signal and image acquisition devices, that must be analyzed by sophisticated optimization tools. In this proposal, we consider handling optimization problems with large datasets. This means minimizing a cost function with a complex structure and many variables. The computational load for solving these problems is too great for even state-of-the-art algorithms. Thus, only relatively rudimentary data processing techniques are employed, reducing the quality of the results and limiting the outcomes that can be achieved via these novel instruments. New algorithms must be designed with computational scalability, robustness and versatility in mind.

In this context, Majorization-Minimization (MM) approaches have a crucial role to play. They consist of a class of efficient and effective optimization algorithms that benefit from solid theoretical foundations. The MAJORIS project aims at proposing a breakthrough in MM algorithms, so that they remain efficient when dealing with big data. I propose to tackle several challenging questions concerning algorithm design. These include acceleration strategies, convergence analysis with complex costs and inexact schemes. I will also tackle practical, massively parallel and distributed architecture implementations. Three specific applications are targeted: super-resolution in multi-photon microscopy in biology; on-the-fly reconstruction for 3D breast tomosynthesis in medical imaging; and mass spectrometry data processing in chemistry.

10.4 National initiatives

10.4.1 ANR

- Program: Chaire IA - ANR
 - Project acronym: [Bridgeable](#)

- Project title: BRIDinG the gAp Between iterative proximal methods and nEural networks
- Duration: 2020-2024
- Coordinator: Jean-Christophe Pesquet
- Program: ANR PRCE
 - Project acronym: **R-Vessel-X**
 - Project title: Extraction et interprétation robustes des réseaux vasculaires dans les images biomédicales hépatiques
 - Duration: 2018-2022
 - Coordinator: A. Vacavant (Univ. Clermont Auvergne), local: Hugues Talbot
- Program: ANR RHU
 - Project acronym: **Innov4-ePiK**
 - Project title: Innovative diagnostic and therapeutic approaches in epileptic and developmental encephalopathies linked to potassium channel genes using the 4P framework for medicine.
 - Duration: 2024-2028
 - Coordinator: Rima Nabbout, Université Paris Cité / AP-HP, local: Fragkiskos Malliaros
- Program: ANR JCJC
 - Project acronym: **Hagnodice**
 - Project title: Holistic explainable artificial intelligence schemes for lung cancer prognosis
 - Duration: 2022-2026
 - Coordinator: Maria Vakalopoulou
- Program: ANR JCJC
 - Project acronym: **GraphIA**
 - Project title: Scalable and robust representation learning on graphs
 - Duration: 2021-2025
 - Coordinator: Fragkiskos Malliaros

10.4.2 Others

PRISM Participants: Hugues Talbot, Loïc Le Bescond, Maria Vakalopoulou (Collaboration: S. Christodoulidis, P.-H. Cournède, MICS, CentraleSupélec ; F. André, Gustave-Roussy)

The **PRISM** program at Gustave-Roussy, which is a major research program on precision medicine, has been funded by the ANR since 2018 by a grant of €5 millions. This was considered a major achievement for the team, as it has allowed us to continue our research on the use of AI for precision medicine.

It has now received Institut Hospitalo-Universitaire (IHU) label. The vision of the project is transformative in its approach for cancer treatment. It aims to better understand the biology of each patient's cancer and to identify, from diagnosis, those with the most aggressive tumours in order to offer them the most appropriate treatment. This IHU label is part of the perspective of making Gustave Roussy the largest campus in Europe dedicated to cancer.

The PRISM program has become one of the 5 IHU endowed with 30 to 40 million euros announced by the Government as part of the 3rd call for projects of the France 2030 plan. The objective of the IHUs is to strengthen French medical research capacity by developing world-class research (clinical and translational) skills involving university, health establishment, research organizations and companies.

PRISM is the result of several years of research conducted by the teams of Gustave Roussy in partnership with CentraleSupélec, Université Paris-Saclay, Inserm and Unicancer.

FMJH

- Project title: Fast Optimization and Computational Understanding of Systems
- Duration: 01/09/2023 - 31/08/2024
- Coordinator: Antonio Silveti-Falls
- Organization: Fondation Mathématique Jacques Hadamard

11 Dissemination**11.1 Promoting scientific activities****11.1.1 Scientific events: organisation****General chair, scientific chair**

- Maria Vakalopoulou (together with N. Burgos and C. Petitjean) served as general chair for the organization of the international conference **MIDL 2024** in Paris.
- Maria Vakalopoulou: Tutorial chair at IGARSS 2024.

Member of the organizing committees

- Emilie Chouzenoux. Co-organizer of the recurrent workshop Mathematical Foundations of AI (DATAIA and SCAI), 31 Jan. 2024, 17 June, and 12 Sep. 2024, Paris.
- Emilie Chouzenoux: Co-organizer of a special session at IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP), April 2024.
- Mounir Kaaniche: Tutorial Co-Chair at the European Workshop on Visual Information Processing (EUVIP), Sept. 2024, Geneva, Switzerland.

11.1.2 Scientific events: selection**Chair of conference program committees**

- Emilie Chouzenoux: Technical program co-chair at MLSP conference 2024, London, UK.
- Fragkiskos Malliaros: Co-organizer, Learning on Graphs (LoG) Paris meet up, 2024.
- Fragkiskos Malliaros: Co-organizer of a special session at the European Symposium on Artificial Neural Networks, Computational Intelligence and Machine Learning (ESANN), Bruges, Belgium, 2024.
- Fragkiskos Malliaros: Journal track co-chair, 11th IEEE International Conference on Data Science and Advanced Analytics (DSAA 2024), San Diego, CA, 2024.
- Fragkiskos Malliaros: Sponsor co-chair, 24th International Conference on Web Engineering (ICWE 2024), Tampere, Finland, 2024.
- Fragkiskos Malliaros: Senior Program Committee and Area Chair at eural Information Processing Systems (NeurIPS), European Conference on Machine Learning (ECML PKDD).
- Hugues Talbot: Member of the steering committee, 3rd conference on Discrete Geometry and Mathematical Morphology, Florence, Italy, April 15-18 2024.
- Maria Vakalopoulou: Member of the award committee at ISBI 2024.
- Maria Vakalopoulou: Coordination of invited sessions "Precision Medicine, AI and Longitudinal Monitoring" in IABM 2024 (March 2024), "Deep Learning in Medical Imaging: The era of foundation models", in the 9e Journée Statistique et Informatique pour la Science des Données à Paris-Saclay (April 2024), and "Precision Medicine, AI and Longitudinal Monitoring" in Archimedes 2024 (May 2024).

Member of the conference program committees

- Maria Vakalopoulou: Area Chair at Computer Vision and Pattern Recognition (CVPR) 2024, International Computer Vision and Pattern Recognition (ICCV) 2024.

Reviewing activity

The members of the team reviewed numerous papers for several international conferences, such as for the annual conferences on Computer Vision and Pattern Recognition (CVPR), Medical Image Computing and Computer Assisted Intervention (MICCAI), Neural Information Processing Systems (NeurIPS), IEEE International Workshop on Machine Learning for Signal Processing (MLSP), International Conference on Learning Representations (ICLR), IEEE International Conference and Acoustics Speech and Signal Processing (ICASSP), IEEE International Conference on Image Processing (ICIP), IEEE Statistical Signal Processing workshop (SSP), European Signal Processing Conference (EUSIPCO), AAAI Conference on Artificial Intelligence (AAAI), The Web Conference (WWW), Annual Conference of the North American Chapter of the Association for Computational Linguistics (NAACL), International Conference on Web and Social Media (ICWSM), International Conference on Machine Learning (ICML), Conference on Neural Information Processing Systems (NeurIPS), International Conference on Complex Networks and Their Applications (Complex Networks), International Workshop on Graph-Based Natural Language Processing (TextGraphs), Artificial Intelligence and Statistics Conference (AISTAT), British Machine Vision Conference, Montreal AI Symposium, ACM SIGKDD Conference on Knowledge Discovery and Data Mining (KDD), IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM), and Learning on Graphs Conference (LoG).

11.1.3 Journal

Member of the editorial boards

- Emilie Chouzenoux: Associate Editor of the SIAM Journal on Imaging Sciences.
- Emilie Chouzenoux: Associate Editor of the SIAM Journal on Mathematics of Data Sciences.
- Fragkiskos Malliaros: Associate Editor, Big Data Research, Elsevier.
- Fragkiskos Malliaros: Guest Editor, International Journal of Data Science and Analytics (JDSA), Springer.
- Jean-Christophe Pesquet: Associate Editor for SIAM Journal on Imaging Sciences.
- Hugues Talbot: Editor in Chief for the journal Mathematical Morphology - Theory and Applications.
- Hugues Talbot: Review Editor for the journal Frontiers in Computer Science.
- Maria Vakalopoulou: Editor at Computer Vision and Image Understanding (CVIU) Journal.
- Maria Vakalopoulou: Editor at IEEE Medical Image Analysis Journal.

Reviewing activity

The members of the team reviewed numerous papers for several international journals, such as Inverse Problems, IEEE Transactions on Signal Processing, IEEE Transactions on Computational Imaging, IEEE Signal Processing Letters, Signal Processing (Elsevier), International Journal of Data Science and Analytics, Digital Signal Processing, Siam Journal of Optimization, and Computational Optimization and Application.

11.1.4 Invited talks

- Emilie Chouzenoux: Keynote talk, journées des doctorants de l'université Paris Saclay, June 2024, Gif-sur-Yvette.
- Emilie Chouzenoux: Invited talk, workshop Approximate Inference in Theory and Practice, June 2024, Paris.
- Fragkiskos Malliaros: Kenote speaker, Graduate School of Translational Bioinformatics, Université Paris-Cite, France, 2024.
- Fragkiskos Malliaros: Invited talk, LIPN, Université Sorbonne Paris Nord, France, 2024.
- Antonio Silveti-Falls: Invited talk at the workshop Fondements Mathématiques de l'IA, 2024, Paris.
- Antonio Silveti-Falls: Invited talk at the European Conference on Operational Research, 2024, Copenhagen, Denmark.
- Antonio Silveti-Falls: Invited talk at the conference Optimization Techniques for Inverse Problems, 2024, Modena, Italy.
- Antonio Silveti-Falls: Invited talk at the TraDE-OPT Final Conference, 2024, Sestri Levante, Italy.
- Antonio Silveti-Falls: Invited talk at the workshop ISMP, 2024, Montreal, Canada.
- Jean-Christophe Pesquet: Invited speaker at the workshop Imaging inverse problems and generating models at the International Center for Mathematical Sciences, Edinburgh, April 2024.
- Jean-Christophe Pesquet: Invited lecturer at Ph.D international school in Mathematics and Machine Learning for Image Processing, Bologna, June 2024.
- Hugues Talbot: Invited talk on Non-linearly constrained neural-networks for inverse problems, NAIST, Nara, Japan, February 2024
- Hugues Talbot: Invited talk on AI for computer vision and medical imaging, Joint Robotics Lab, Tsukuba, Japan, February 2024
- Hugues Talbot: Invited talk on Digital Twin of the Left Ventricle, MICS seminar, CentraleSupélec, May 2024
- Thomas Guilmeau: Invited talk, 21st EUROPT Conference on Advances in Continuous Optimization (EUROPT 2024), June, Lund, Sweden.
- Loïc Le Bescond: Invited talk, Breast and Gynecological Cancer Conference (PGCC), Kinshasa, July 2024.

11.1.5 Leadership within the scientific community

- Emilie Chouzenoux: Senior member of the IEEE. Elected member of the EURASIP Signal and Data Analytics for Machine Learning TAC. Elected member of the Signal Processing Theory and Methods IEEE Technical Committee.
- Mounir Kaaniche: Elected member of the EURASIP Technical Area Committee (TAC) on Signal and Data Analytics for Machine Learning (SiG-DML)
- Mounir Kaaniche: Senior member of the IEEE.
- Nora Ouzir: Elected member of the EURASIP Biomedical Image and Signals Analytics TAC.
- Jean-Christophe Pesquet: Senior honorary member of the Institut Universitaire de France and Fellow of IEEE and EURASIP.

11.1.6 Scientific expertise

The members of the team participated to numerous PhD Thesis Committees, PhD “comité de suivi individuel”, Hdr Committees, recruiting Committees, and served as Grant Reviewers.

- Emilie Chouzenoux is member of the scientific committee of PIQ program of Inria.
- Emilie Chouzenoux is member of the executive committee of DataIA institute of University Paris Saclay.
- Emilie Chouzenoux is member of the scientific committee of the programme Mathématiques du Calcul Scientifique et de l'Ingénierie of the Labex Mathématiques Hadamard (Maths CSI LJH).
- Alix Chazottes is a student member of the ANR jury, for the section "Compétences and Métiers d'Avenir, plan de relance France2030".
- Mounir Kaaniche: Elected member of the expert committee of the national board of universities (CE61) at USPN.
- Nora Ouzir is an elected member of CCUPS, Consultative Commission of Paris-Saclay University.
- Maria Vakalopoulou served as a monitor-expert for EU research grants.

11.1.7 Research administration

- Jean-Christophe Pesquet is the head of the laboratoire Centre pour la Vision Numérique (CVN), CentraleSupélec.

11.1.8 Teaching administration

- Emilie Chouzenoux: attached professor in AI in CentraleSupélec, since sep. 2022.
- Nora Ouzir: Co-coordinator of the Bachelor in Artificial Intelligence, Data and Management Sciences, AIDAMS, with ESSEC Business School and CentraleSupélec.
- Nora Ouzir: Co-coordinator of the Thematic Sequence 2 (ST2) Viral Propagation, 1st year of CentraleSupélec.
- Nora Ouzir: Head for the Machine Learning Elective course in 2nd year of CentraleSupélec (210 students).
- Fragkiskos Malliaros: co-director of the Master in Data Sciences and Business Analytics (DSBA).
- Fragkiskos Malliaros: head of the Data and Information Sciences (SDI) specialization at Centrale-Supélec.
- Jean-Christophe Pesquet: local head for the Optimization M.Sc. at CentraleSupélec.
- Jean-Christophe Pesquet: head for the main Optimization course in 2nd year of CentraleSupélec (600 students).
- Hugues Talbot: head of the Mastère Spécialisé in "Trustworthy AI". It was in development since 2022 with IRT SystemX and CentraleSupélec Exed. This Master is designed for professionals who want to retrain in AI and focuses on the explainability and trustworthiness of models. It represents 400h of teaching and opened its first batch this year.
- Hugues Talbot: local head for CentraleSupélec the Mathématiques, Vision Apprentissage (MVA) Master of Ecole Normale Supérieure Paris-Saclay

11.2 Teaching - Supervision - Juries

11.2.1 Teaching

Several permanent members of OPIS were involved as lecturer (lec.) or lab instructors (lab), in the following courses.

- Master: Emilie Chouzenoux. Foundations of Distributed and Large Scale Computing, 26h (lec.), 3rd year CentraleSupélec and M.Sc. MVA Paris Saclay.
- Master: Emilie Chouzenoux. Advanced Machine Learning, 18h (lec.), 3rd year CentraleSupélec.
- Bachelor: Emilie Chouzenoux. Optimization, 24h (lec.), 1st year Bachelor AIDAMS, Univ. Paris Saclay.
- Master: Nora Ouzir. Machine Learning, 30h (lec.), 2nd year course, CentraleSupélec, EN
- Master: Nora Ouzir. Advanced Machine Learning, 24h (lec.), Msc DSBA, CentraleSupélec/ESSEC.
- Master: Nora Ouzir. Optimization, 15h (lab.), 2nd year course, CentraleSupélec.
- Bachelor: Nora Ouzir. Signal Processing, 10h (lab.), 1st year course, CentraleSupélec.
- Master: Nora Ouzir. Medical Image Processing 3h (lec.), AI and Global Health program of the European University Alliance for Global Health (EUGLOH).
- Master: Fragkiskos Malliaros. Machine Learning in Network Science, 27h (lec.), Master in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School, M.Sc. in Artificial Intelligence, CentraleSupélec, 3rd year data science mention, CentraleSupélec.
- Master: Fragkiskos Malliaros. Foundations of Machine Learning, 48h (lec.), Master in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School.
- Master: Jean-Christophe Pesquet. Introductory course on Optimization, 33h (lec.), 2nd year CentraleSupélec.
- Master: Jean-Christophe Pesquet. Introduction to Optimization, 6h (lec.), M.Sc. MVA Paris Saclay.
- Master: Jean-Christophe Pesquet. Advanced course on Optimization, 10h (lec.), M.Sc. in Signal Processing and Automatic Control, Univ. Paris-Saclay.
- Master: Jean-Christophe Pesquet. Convex Optimization Algorithms, 15h (lec.), M.Sc. in Optimization, Univ. Paris-Saclay.
- Master: Antonio Silveti-Falls. Convergence, Integration, and Probability, 18h (lec.) + 18h (lab), 1st year course, CentraleSupélec.
- Master: Antonio Silveti-Falls. Optimization for Computer Vision, 21h (lec. + lab), 3rd year course, CentraleSupélec.
- Master: Antonio Silveti-Falls. Partial Differential Equations, 13.5h (lab), 1st year course, CentraleSupélec.
- Master: Antonio Silveti-Falls. Optimization, 12.5h (lab), 2nd year course, CentraleSupélec.
- Bachelor: Antonio Silveti-Falls. Analysis I, 18h (lab), First year Bachelors of Global Engineering students, Univ. Paris Saclay.
- Bachelor: Antonio Silveti-Falls. Analysis II, 18h (lab), First year Bachelors of Global Engineering students, Univ. Paris Saclay.
- Bachelor: Antonio Silveti-Falls. Analysis III, 18h (lab), First year Bachelors of Global Engineering students, Univ. Paris Saclay.

- Bachelor: Antonio Silveti-Falls. Probability, 18h (lab), First year Bachelors of Global Engineering students, Univ. Paris Saclay.
- Bachelor: Antonio Silveti-Falls. Topology and Functional Analysis, 18h (lab), Second year Bachelors of Global Engineering students, Univ. Paris Saclay.
- Master: Hugues Talbot. Convergence Integration Probabilité, 18h (lab), 1st year course, Centrale-Supélec.
- Master: Hugues Talbot. High-performance computing, 12h (lab), 2nd year CentraleSupélec.
- Master: Hugues Talbot. Introduction à la morphologie mathématique: 12h (lab), 3rd year Centrale-Supélec.
- Master: Hugues Talbot. Modern mathematical morphology (20h lec. + 8h lab), 3rd Year Centrale-Supélec and MVA (ENS Paris-Saclay).
- Master: Hugues Talbot. Optimisation for AI, (20h lec + 8h lab) M.Sc in AI, CentraleSupélec.
- Master: Hugues Talbot. Introduction to Machine Learning, MS Management of Technogy, 30h (lec.).
- Master: Maria Vakalopoulou. Introduction to Visual Computing, CentraleSupélec, 25h (lec).
- Master: Maria Vakalopoulou. Introduction to Deep Learning, M.Sc. in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School, 24h (lec).
- Master: Maria Vakalopoulou. Introduction to Deep Learning, M.Sc. in Artificial Intelligence, CentraleSupélec, 24h (lec).
- Master: Maria Vakalopoulou. Deep Learning, M.Sc. in Vision and Machine Learning, ENS Paris-Saclay, 25h (lec).
- Master: Maria Vakalopoulou. Deep Learning in Medical Imaging, M.Sc. in Vision and Machine Learning, ENS Paris-Saclay, 25h (lec).

Several students members of OPIS have teaching assistant activities, in the following cursus of the Univ. Paris Saclay campus:

- Bachelor AIDAMS, CentraleSupélec and ESSEC
- ENSTA ParisTech
- CentraleSupélec
- M.Sc. DSBA, Univ. Paris Saclay
- M.Sc. MVA, Univ. Paris Saclay

11.2.2 PhD supervision

- PhD (completed): Gabriele Scrivanti. New algorithms for large scale problems exploiting geometric problem structure and convex relaxation, 2020-2024, supervised by Jean-Christophe Pesquet and E. Bednarczuk (Polish Academy of Sciences, Warsaw).
- PhD (completed): Ségolène Martin. Majorization-Minimization methods for constrained optimization, 2020-2024, supervised by Jean-Christophe Pesquet and I. Ben Ayed (ETS Montréal, Canada).
- PhD (completed): Theodore Aouad. Geometric semi-supervised machine-learning methods in medical imaging, 2020-2024, supervised by Hugues Talbot.
- PhD (completed): Younes Belkouchi. Graph neural network generative methods in oncology, 2020-2024, supervised by N. Lassau (IGR), Fragkiskos Malliaros, and Hugues Talbot.

- PhD (completed): Mouna Gharbi. Unfolded Majorization-Minimization algorithms, 2020-2023, supervised by Emilie Chouzenoux and L. Duval (IFPEN).
- PhD (completed): Nguyen Vu. Algorithmes d'assemblage pour l'apprentissage en imagerie médicale, 2021-2024, supervised by Emilie Chouzenoux and P. Pinault (ESSILOR).
- PhD (completed): Alexandre Duval. Algorithmes d'apprentissage automatique sur des graphes: explicabilité, évolutivité et applications, 2020-2023, supervised by Fragkiskos Malliaros and Hugues Talbot
- PhD (in progress): Loïc Le Bescond. Precision medicine, Histology and Deep learning, 2021-2024, supervised by F. André (IGR) and Hugues Talbot.
- PhD (in progress): Thomas Guilmeau. Algorithmes stochastiques pour l'optimisation non convexe, 2021-2024, supervised by Emilie Chouzenoux and V. Elvira (Univ. Edinburgh).
- PhD (in progress): Raaja El Hamdani. Robust graph representation learning and applications in misinformation detection, 2021-2024, supervised by Fragkiskos Malliaros and T. Bonald (Télécom-Paris).
- PhD (in progress): Othmane Laousy. Graph-based artificial intelligence methods for medical image diagnosis, 2019-2024, supervised by Maria Vakalopoulou and M.-P. Revel (AP-HP Hospital Cochin).
- PhD (in progress): Clement Cosserat. Algorithmes de majoration-minimisation pour le traitement du signal statistique, 2022-2025, supervised by Emilie Chouzenoux and T. Adali (Univ. Baltimore, USA).
- PhD (in progress): Alix Chazottes. Algorithmes d'optimisation dépliés pour la reconstruction d'images à partir de données TEP dynamique, 2023-2026, supervised by Emilie Chouzenoux and F. Sureau (CEA, Biomaps).
- PhD (in progress): Aymen Sardroui. Histopathological image analysis, 2022-2025, supervised by Mounir Kaaniche and Jean-Christophe Pesquet.
- PhD (in progress): Arsene Amoya. Neural networks-based stereo image retrieval, supervised by Mounir Kaaniche and A. Benazza-Benyahia (SUP'COM-Tunis).
- PhD (in progress): Nabil Mouadden. Deep Learning methods for lung applications, 2023-2026, supervised by Maria Vakalopoulou and G. Chassagnon (Hôpital Cochin).
- PhD (in progress): Jinqwei Zhang. Deep Learning methods on Digital Pathology, 2020-2024, supervised by Maria Vakalopoulou, and D. Samaras (Stony Brook University).
- PhD (in progress): Yassine Abbahaddou. Topics in Geometric Deep Learning, 2022-2025, supervised by Fragkiskos Malliaros, J. Lutzeyer, and M. Vazirgiannis (École Polytechnique).
- PhD (in progress): Vahan Martirosyan. Deep Graph Neural Networks (GNNs) and Applications in Biomedicine, 2023-2026, supervised by Fragkiskos Malliaros, Hugues Talbot, and J. Giraldo (Télécom Paris).
- PhD (in progress): Nicolas Salvy. Génération d'images cérébrales fonctionnelles à grande échelle pour améliorer la cartographie cérébrale, 2023-2026, supervised by Hugues Talbot, and Bertrand Thirion (Inria Saclay, MIND).
- PhD (in progress): Hafsa El Herichi. Extraction du tissage 3D des pièces composites de grandes dimensions à partir d'images tomographiques, 2023-2026, supervised by Hugues Talbot, and Stéphane Roux (Laboratoire de Mécanique de Paris-Saclay, ENS Paris-Saclay).
- PhD (in progress): David Restrepo. Bias Analysis on vision and language models 2024-2027, supervised by Maria Vakalopoulou, Stergios Christodoulidis, Enzo Ferrante and Gilles Fay, MICS, CentraleSupélec.

- PhD (in progress): Adam Ghalem. Graph Neural Networks for Causal Inference for Wireless Network Management, 2024-2027, supervised by Fragkiskos Malliaros.
- PhD (in progress): Vuk Ignjatovic. Generative Models for Motion Correction in Computed Tomography, 2024-2027, supervised by Nora Ouzir, Jean-Christophe Pesquet, and Cyril Riddell (GE Healthcare).
- PhD (in progress): Raoul Sallé de Chou, Machine-learning based Prediction of heart perfusion maps, 2021-2025, supervised by Laurent Najman (UGE), Hugues Talbot, Irene Vignon-Clémentel (Inria SimbotX)
- PhD (in progress): Francesco Songia, Reduced order modelling of hemodynamics for liver surgery procedure, 2025-2028, supervised by Nicolas Golse (APHP), Irene Vignon-Clementel (Inria SimbiotX), Hugues Talbot.

11.2.3 Intern/Engineers/Apprentices supervision

- Maxence Adly, Sep. 2024-Feb. 2025, supervised by Emilie Chouzenoux
- Hugo Pham, Jan-June 2024, supervised by Emilie Chouzenoux and Quentin Vanderbecq
- Gaspard Blaise, Apr.-July 2024, supervised by Clement Cosserat
- Miguel Amorim, Feb.-July 2024, supervised by Antonio Silveti-Falls
- Idriss Benkirane, Sep. 2024-Feb. 2025, supervised by Hugues Talbot
- Benjamin Clene, Nov. 2024-Jan. 2025, supervised by Hugues Talbot
- Mohammad Mehdi Kalla, Sep. 2024-Aug. 2025, supervised by Emilie Chouzenoux,
- Quentin Mace, May-Oct. 2024, supervised by Nora Ouzir
- Solal Martin, Apr.-Aug. 2024, supervised by Emilie Chouzenoux
- Gabriel Pirlogeanu, Feb.-June 2024, supervised by Jean-Christophe Pesquet
- Soukaina Tichirra, Mar.-Aug. 2024, supervised by Jean-Christophe Pesquet
- Ludovic Trautmann, Dec. 2024-June 2025, supervised by Emilie Chouzenoux
- Clement Lavaud, Mar.-Oct. 2024, supervised by Nguyen Vu
- Caglayan Tuna, May-Oct. 2024, supervised by Nora Ouzir
- Long Zhou, March-June 2024, supervised by Mounir Kaaniche and Jean-Christophe Pesquet.

11.2.4 Juries

The faculty members of the team serve regularly as a jury Member to Final Engineering Internship and the Research Innovation Project for students of CentraleSupélec, and to Research Internship for students of Ms.C. MVA, ENS Paris Saclay.

11.3 Popularization

11.3.1 Participation in Live events

- Alix Chazottes: Group supervision at Rendez-vous des Jeunes Mathématiciennes et Informatiennes, Inria Saclay, February 2024.
- Alix Chazottes: Intervention at Science en Baskets (in the context of the Paris-Saclay Summit 2024), Inria Saclay, February 2024.
- Alix Chazottes: Animation at Fête de la Science, Inria Saclay, October 2024.

12 Scientific production

12.1 Publications of the year

International journals

- [1] J. Ajdenbaum, E. Chouzenoux, C. Lefort, S. Martin and J.-C. Pesquet. ‘A Novel Variational Approach for Multiphoton Microscopy Image Restoration: from PSF Estimation to 3D Deconvolution’. In: *Inverse Problems* 40.6 (24th Apr. 2024). DOI: [10.1088/1361-6420/ad3c67](https://doi.org/10.1088/1361-6420/ad3c67). URL: <https://hal.science/hal-04296247> (cit. on pp. 9, 19).
- [2] S. Ammari, A. Quillent, V. Elvira, F. Bidault, G. Garcia, D. Hartl, C. Balleyguier, N. Lassau and É. Chouzenoux. ‘Using Machine Learning on MRI Radiomics to Diagnose Parotid Tumours Before Comparing Performance with Radiologists: A Pilot Study’. In: *Journal of Imaging Informatics in Medicine* (10th Oct. 2024), Online ahead of print. DOI: [10.1007/s10278-024-01255-y](https://doi.org/10.1007/s10278-024-01255-y). URL: <https://hal.science/hal-04734195> (cit. on p. 21).
- [3] T. Aouad, V. Laurent, P. Levant, A. Rode, N. Brillat-Savarin, P. Gaillot, C. Hoeffel, E. Frampas, M. Barat, R. Russo, M. Wagner, M. Zappa, O. Ernst, A. Delagnes, Q. Fillias, L. Dawi, C. Savoye-Collet, P. Copin, P. Calame, E. Reizine, A. Luciani, M.-F. Bellin, H. Talbot and N. Lassau. ‘Detection and characterization of pancreatic lesion with artificial intelligence: The SFR 2023 artificial intelligence data challenge’. In: *Diagnostic and Interventional Imaging* 105.10 (2024), pp. 395–399. DOI: [10.1016/j.diii.2024.07.002](https://doi.org/10.1016/j.diii.2024.07.002). URL: <https://hal.science/hal-04670352> (cit. on p. 28).
- [4] R. Barbe, Y. Belkouchi, Y. Menu, R. Cohen, C. David, M. Kind, S. Harguem, L. Dawi, J. Hadchiti, F. Selhane, N. Billet, S. Ammari, A. Bertin, L. Lawrance, B. Cervantes, A. Hollebecque, C. Balleyguier, P.-H. Courneade, H. Talbot, N. Lassau and T. Andre. ‘Imaging-guided prognostic score-based approach to assess the benefits of combotherapy versus monotherapy with immune checkpoint inhibitors in metastatic MSI-H colorectal cancer patients’. In: *European Journal of Cancer* 202 (May 2024), p. 114020. DOI: [10.1016/j.ejca.2024.114020](https://doi.org/10.1016/j.ejca.2024.114020). URL: <https://hal.science/hal-04907203> (cit. on p. 27).
- [5] A. Beaufrère, N. Ouzir, P. E. Zafar, A. Laurent-Bellue, M. Albuquerque, G. Lubuela, J. Grégory, C. Guettier, K. Mondet, J.-C. Pesquet and V. Paradis. ‘Primary liver cancer classification from routine tumour biopsy using weakly supervised deep learning’. In: *JHEP Reports Innovation in Hepatology* 6.3 (2024), p. 101008. DOI: [10.1016/j.jhepr.2024.101008](https://doi.org/10.1016/j.jhepr.2024.101008). URL: <https://hal.science/hal-04534805> (cit. on p. 22).
- [6] Y. Belkouchi, J.-C. Pesquet, A. Repetti and H. Talbot. ‘Learning truly monotone operators with applications to nonlinear inverse problems: LEARNING TRULY MONOTONE OPERATORS’. In: *SIAM Journal on Imaging Sciences* (30th Mar. 2024). URL: <https://hal.science/hal-04530164>. In press (cit. on p. 24).
- [7] J. Bolte, E. Pauwels and A. J. Silveti-Falls. ‘Differentiating Nonsmooth Solutions to Parametric Monotone Inclusion Problems’. In: *SIAM Journal on Optimization* 34.1 (4th Jan. 2024), 27 p. DOI: [10.1137/22M1541630](https://doi.org/10.1137/22M1541630). URL: <https://hal.science/hal-03900339> (cit. on p. 34).
- [8] J. Castro-Correa, J. Giraldo, M. Badiéy and F. D. Malliaros. ‘Gegenbauer Graph Neural Networks for Time-Varying Signal Reconstruction’. In: *IEEE Transactions on Neural Networks and Learning Systems* (10th Apr. 2024). DOI: [10.1109/TNNLS.2024.3381069](https://doi.org/10.1109/TNNLS.2024.3381069). URL: <https://hal.science/hal-04541700> (cit. on pp. 17, 31).
- [9] J. Chen, C. Wang, F. Shi, M. Kaaniche, M. Zhao, Y. Jing and S. Chen. ‘DSNet: A Dynamic Squeeze Network for Real-time Weld Seam Image Segmentation’. In: *Engineering Applications of Artificial Intelligence* (15th Mar. 2024). URL: <https://hal.science/hal-04505581> (cit. on p. 33).
- [10] E. Chouzenoux, M.-C. Corbineau, J.-C. Pesquet and G. Scrivanti. ‘A variational approach for joint image recovery and feature extraction based on spatially varying generalised Gaussian models’. In: *Journal of Mathematical Imaging and Vision* (2024). URL: <https://hal.science/hal-03591742>. In press (cit. on p. 20).

- [11] E. Chouzenoux and V. Elvira. ‘Sparse Graphical Linear Dynamical Systems’. In: *Journal of Machine Learning Research* 25.223 (2024), pp. 1–53. URL: <https://inria.hal.science/hal-04358490> (cit. on pp. 10, 15, 20).
- [12] E. Chouzenoux and J.-B. Frest. ‘Convergence Analysis of Block Majorize-Minimize Subspace Approach’. In: *Optimization Letters* 18 (2024), pp. 1111–1130. DOI: 10.1007/s11590-023-02055-z. URL: <https://inria.hal.science/hal-04202728> (cit. on p. 18).
- [13] E. Chouzenoux, J.-C. Pesquet and F. Roldán. ‘Solution of Mismatched Monotone+Lipschitz Inclusion Problems’. In: *SIAM Journal on Optimization* (2024). DOI: 10.48550/arXiv.2310.06402. URL: <https://inria.hal.science/hal-04237154>. In press (cit. on p. 18).
- [14] T. Dardouri, M. Kaaniche, A. Benazza-Benyahia and G. Dauphin. ‘Multi-Task Convolution Neural Network-Based Lifting Scheme for Image Compression’. In: *Pattern Recognition Letters* (2025). URL: <https://hal.science/hal-04464338> (cit. on p. 34).
- [15] L. Dawi, Y. Belkouchi, L. Lawrance, O. Gautier, S. Ammari, D. Vasseur, F. Wirth, J. Hadchiti, S. Morer, C. David, F. Bidault, C. Balleyguier, M. Kind, A. Bayle, L. Belcaid, M. Aldea, C. Nicotra, A. Geraud, M. Sakkal, F. Blanc-Durand, S. Moog, M. F. Mosele, M. Tagliamento, A. Bernard-Tessier, B. Verret, C. Smolenschi, N. Auger, A. Gazzah, J.-B. Micol, O. Caron, A. Hollebecque, Y. Lorient, B. Besse, L. Lacroix, E. Rouleau, S. Ponce, F. André, J.-C. Soria, F. Barlesi, S. Muller, P.-H. Courneade, H. Talbot, A. Italiano and N. Lassau. ‘Liquid Biopsy versus CT: Comparison of Tumor Burden Quantification in 1065 Patients with Metastases’. In: *Radiology* 313.2 (1st Nov. 2024). DOI: 10.1148/radiol.232674. URL: <https://hal.science/hal-04905199> (cit. on p. 29).
- [16] A. Djahnine, C. Lazarus, M. Lederlin, S. Mulé, R. Wiemker, S. Si-Mohamed, E. Jupin-Delevaux, O. Nempont, Y. Skandarani, M. de Craene, S. Goubalan, C. Raynaud, Y. Belkouchi, A. B. Afia, C. Fabre, G. Ferretti, C. de Margerie, P. Berge, R. Liberge, N. Elbaz, M. Blain, P.-Y. Brilllet, G. Chassagnon, F. Cadour, C. Caramella, M. E. Hajjam, S. Boussouar, J. Hadchiti, X. Fablet, A. Khalil, H. Talbot, A. Luciani, N. Lassau and L. Bousset. ‘Detection and severity quantification of pulmonary embolism with 3D CT data using an automated deep learning-based artificial solution’. In: *Diagnostic and Interventional Imaging* (Mar. 2024). DOI: 10.1016/j.diii.2023.09.006. URL: <https://hal.science/hal-04396326>.
- [17] A. Einizade, J. H. Giraldo, F. D. Malliaros and S. Hajipour Sardouie. ‘Estimation of a causal directed acyclic graph process using non-gaussianity’. In: *Digital Signal Processing* 146 (Mar. 2024), p. 104400. DOI: 10.1016/j.dsp.2024.104400. URL: <https://hal.science/hal-04541701> (cit. on p. 31).
- [18] M. Gharbi, E. Chouzenoux and J.-C. Pesquet. ‘An Unrolled Half-Quadratic Approach for Sparse Signal Recovery in Spectroscopy’. In: *Signal Processing* 218 (May 2024). DOI: 10.1016/j.sigpro.2023.109369. URL: <https://inria.hal.science/hal-04229774> (cit. on pp. 8, 16, 18).
- [19] T. Guilmeau, E. Chouzenoux and V. Elvira. ‘A Divergence-Based Condition to Ensure Quantile Improvement in Black-Box Global Optimization’. In: *IEEE Transactions on Evolutionary Computation* (2nd Sept. 2024), pp. 1–1. DOI: 10.1109/TEVC.2024.3452420. URL: <https://hal.science/hal-04711649> (cit. on p. 19).
- [20] T. Guilmeau, E. Chouzenoux and V. Elvira. ‘On variational inference and maximum likelihood estimation with the λ -exponential family’. In: *Foundations of Data Science* 6.1 (2024), pp. 85–123. DOI: 10.3934/fods.2024011. URL: <https://inria.hal.science/hal-04616759> (cit. on p. 19).
- [21] T. Guilmeau and A. Rapaport. ‘Multiplicity of neutrally stable periodic orbits with coexistence in the chemostat subject to periodic removal rate’. In: *SIAM Journal on Applied Mathematics* 84.1 (16th Jan. 2024), pp. 39–59. DOI: 10.1137/23M1552450. URL: <https://hal.inrae.fr/hal-04248438>.
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