

RESEARCH CENTRE

**Inria Saclay Center
at Université Paris-Saclay**

IN PARTNERSHIP WITH:

Université Paris-Saclay

2022

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 we work on, a wide range of applications in image recovery are considered: parallel MRI, breast tomosynthesis, 3D ultrasound imaging, and two-photon microscopy. For example, in breast tomosynthesis (collaboration with GE Healthcare), 3D breast images have to be reconstructed from a small number of X-ray projections with limited view angles. Our objective is to facilitate the clinical task by developing advanced reconstruction methods allowing micro-calcifications to be highlighted. 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 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 Artificial intelligence fighting against COVID-19

Participants: Guillaume Chassagnon, Emilie Chouzenoux, Kavya Gupta, Yingping Li, Ana Neascu, Jean-Christophe Pesquet, Hugues Talbot, Matthieu Terris, Maria Vakalopoulou, Sagar Verma (Collaboration: Institut Gustave Roussy ; Kremlin-Bicetre APHP ; Owkin France ; Hopital Cochin Broca Hotel Dieu ; Therapanacea ; IIIT Delhi, India ; University Politehnica of Bucharest, Romania)

Coronavirus disease 2019 (COVID-19) emerged in 2019 and disseminated around the world rapidly. Computed tomography (CT) imaging has been proven to be an important tool for screening, disease quantification and staging. The latter is of extreme importance for organizational anticipation (availability of intensive care unit beds, patient management planning) as well as to accelerate drug development through rapid, reproducible and quantified assessment of treatment response. Even if currently there are no specific guidelines for the staging of the patients, CT together with some clinical and biological biomarkers are used. Through two collaborative projects with medical partners and French start-ups, we aimed to investigate and propose artificial intelligence tools that could help on the clinical practice. The proposed methodologies have been validated on multicentric cohorts of patients, whose data has been collected in 2020 during the first wave of the pandemia.

Our work [22], in collaboration with IIIT Delhi, builds computational models for drug re-positioning for COVID-19 treatment. The aim is to assist clinicians with a tool for selecting prospective antiviral treatments. The main contributions are (i) a manually curated database publicly shared, comprising of existing associations between viruses and their corresponding antivirals along with a set of state-of-the-art computational drug re-positioning tools based on matrix completion, (ii) a novel multiple graph regularized matrix completion approach with assessed performance on antiviral repositioning.

4.2 Design of robust neural networks in safety critical industrial domains

Participants: Ana Neascu, Kavya Gupta, Fragkiskos Malliaros, Jean-Christophe Pesquet (collaboration: Patrick Combettes, North Caroline State University, Corneliu 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 [73]. 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.

4.3 Radiology, hyper-progressive disease and immunotherapy

In recent years, novel treatments for a variety of cancers have emerged, as a “fourth way”, beyond the well-established chemotherapy, surgery and radiotherapy. These treatments have been in development for decades under the heading of “immunotherapy” but have finally met with considerable success.

One defining feature of cancer cells is that they are considered as host cells by the patient’s immune system, even when they are malignant, and so they are allowed to grow unchecked, whereas normally abnormal mutant cells are recognized and destroyed by the host.

Successful immunotherapy has focused on programmed cell death, also known as apoptosis. These approaches against some forms of cancer aim to block the ability of tumor cells to resist patient immune response by acting on the checkpoints of immune cells. These drugs are able to either block the PD-1 receptor present on the surface of the lymphocytes, or the PD-L1 and PD-L2 ligands expressed by the cancer cells. This can prevent the binding of both, blocking the immunomodulatory signal and allowing the killer T cells continue to be active against the tumor.

However, no therapy is yet universal. One aspect of these approaches is that some patient will respond (and their tumor will therefore not “progress”) and some not. “Progressor” patient, in oncology, are those who continue to see their tumor grow. It is important to use all available data as early as possible in the treatment to decide quickly if the patient is responding positively. One of our projects in this sections aims at doing this.

4.3.1 Imaging radiomics and pathomics to assess response to treatment

Participants: Roger Sun, Théo Estienne, Enzo Batistella, Marvin Lerousseau, Maria Vakalopoulou, Mihir Sahasrabudhe, Hugues Talbot (Collaboration: E. Deutsch, Institut Gustave Roussy ; Nikos 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 [42].

4.3.2 Vision, machine learning and precision medicine

Participants: Younes Belkouchi, Loïc Le Bescond, Hugues Talbot (Collaboration: Nathalie 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.

This year, PhD student Loïc Le Bescond was recruited with PRISM funding and has started working on automated analyses of breast cancer biopsies. Publishable results are expected in 2022.

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

Participants: Raoul Salle de Chou, Hugues Talbot, in collaboration with Irène Vignon-Clementel, SIM-BIOTX Team Inria, Laurent Najman, Université Gustave-Eiffel.

Coronary arteries feed the heart muscles with nutrients and oxygen and as such 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, blood perfusion imaging is invasive, requiring continuous injection of a radioactive tracer: $[^{15}\text{O}]\text{H}_2\text{O}$, or water molecules with radioactive oxygen isotope. In turn, this tracer is difficult to produce because it has a very short half-life, requiring a particle accelerator to continuously produce the radioisotope as the medical exam is conducted. This makes this type of imaging very challenging and expensive. The aim of this project is to replace the actual exam with a numerical twin and conduct it via simulations.

A previous model was developed for myocardial perfusion simulation for coronary artery disease in [\[link\]](#). The model aims at reproducing $[^{15}\text{O}]\text{H}_2\text{O}$ PET imaging exam using only CT scans as input. However, in addition to a high computational cost, the simulation fails to accurately reproduce some diseases, particularly those that affect medium-size coronary branches. One of the main challenges is the low resolution of the CT scans which complexifies the inference of the micro-vascular parameters necessary for tuning the simulation. We developed a graph neural network in order to solve the Darcy equations on irregular shapes in order to replace the myocardium part of the simulation, modeled as a porous medium. This model reduces the computational burden at the cost of some inaccuracies, and facilitates the tuning of the simulation parameters. In parallel, sensitivity analysis on micro-vascular artery resistance computed from $[^{15}\text{O}]\text{H}_2\text{O}$ PET exams were conducted. Based on these analyses, a machine learning model aiming to predict the biological parameter using only CT scans is being developed.

4.4 Sparse inverse problems

4.4.1 Sparse signal processing in chemistry

Participants: Emilie Chouzenoux (Collaboration: Laurent 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 the problem of joint trend removal and blind deconvolution of sparse peaklike signals. The trend accounts for mere offsets to slowly-varying amplitude

shifts (seasonality, calibration distortion, sensor decline), making its automated removal challenging. We proposed the method PENDANTSS [77] that handles smooth trend removal by exploiting their low-pass property and simplifies the problem into a blind deconvolution problem. The proposed approach implements a convergent and efficient tool, with a novel Trust-Region block alternating variable metric forward-backward approach. Simulation results confirm that PENDANTSS outperforms comparable methods on typical sparse analytical signals. Collaboration with Dr. L. Duval, Research Engineer at IFP Energies Nouvelles, France is on-going in this applicative context.

4.4.2 Image restoration for two-photon microscopy

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet (Collaboration: Claire Lefort, XLIM, CNRS, Limoges)

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 is 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 [43], and to visualize bacteria and viral structures [38, 44].

4.4.3 Reconstruction approaches in medical imaging

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Marion Savanier, Maissa Sghaier (Collaboration: S. Muller, C. Riddell, Y. Troussset, GE Healthcare)

The objective of these works, in collaboration with researchers from GE Healthcare, is to develop high quality reconstruction methodologies, for two modalities of medical imaging, namely digital breast tomosynthesis (DBT) and CT for interventional surgery.

The reconstruction of a volumetric image from DBT measurements is an ill-posed inverse problem, for which existing iterative regularized approaches can provide a good solution. However, the clinical task is somehow omitted in the derivation of those techniques, although it plays a primary role in the radiologist diagnosis. In the CIFRE PhD thesis of Maissa Sghaier, we addressed this issue by introducing a novel variational formulation for DBT reconstruction, tailored for a specific clinical task, namely the detection of microcalcifications. Our method [27] aims at simultaneously enhancing the detectability performance and enabling a high-quality restoration of the background breast tissues.

Discretizing and implementing tomographic forward and backward operations is a crucial step in the design of model-based iterative reconstruction algorithms in interventional CT, that we investigate in the CIFRE PhD thesis of Marion Savanier. The mathematical constraint of symmetry on the projector/backprojector pair prevents linear interpolation, which is a standard method in analytical reconstruction, to be used. Consequently, it often happens that these operators are approximated numerically, so that the adjoint property is no longer fulfilled. In the works [63, 26], we investigate fixed point algorithms stability properties when such an adjoint mismatch arises.

4.5 Graph mining applications

4.5.1 Graph inference for gene regulation analysis

Participants: Surabhi Jagtap, Fragkiskos Malliaros (Collaboration: Aurélie Pirayre, Frédérique Bidard and Laurent 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 [17].

4.5.2 Graph representation learning for computational medicine

Participants: Emilie Chouzenoux, Stuti Jain (Collaboration: Angshul Majumdar, IIT Delhi)

Through the Associate International Inria Team COMPASS, we 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 for Covid19 [22] and Monkey-Pox [72].

4.6 Other biomedical applications

4.6.1 Imaging biomarkers and characterization for chronic lung diseases

Participants: Othmane Laoussy, Maria Vakalopoulou (in collaboration with Stergions Christodoulidis, Guillaume Chassagnon and Marie-Pierre Revel and Nikos Paragios: MICS CentraleSupélec, CNRS, AP-HP - Hopital Cochin Broca Hotel Dieu; 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 is to provide automatic and accurate tools that could help clinicians with their everyday practice. In [7], we discuss different artificial intelligence approaches and the new directions of thoracic imaging. Moreover, in [8] we provide a comprehensive review of the current applications and perspectives of AI in thoracic oncology. In particular, we discuss classical machine learning and deep learning methods for pulmonary nodule segmentation allowing nodule volumetry and pulmonary nodule characterization. Moreover, we discuss radiomics and deep-learning approaches to characterize pulmonary nodules. In a similar topic, in [33], we appraise the impact of functional and nutritional status and skeletal muscle mass as a prognostic factor for solid cancer patients.

4.6.2 A generative model for heart left ventricle perfusion analysis

Participant: Hugues Talbot (Collaboration: Laurent Najman ESIEE Paris ; Irene Vignon-Clementel, REO Team leader, Inria ; Charles 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 Electric, 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

J.-C. Pesquet was one of the three EURASIP Fellows elected in 2022.

6.1 Awards

- The Master program DSBA is ranked 4th worldwide in the QSWorld Business Master Rankings in 2022.
- E. Chouzenoux got the best oral presentation award at International Conference on Machine Learning and Intelligent Science (MLIS 2022) Workshop.
- K. Gupta was Runner up to Best Award for her paper co-authored with J.-C. Pesquet presented at Workshop on Artificial Intelligence Safety Engineering (WAISE), International Conference on Computer Safety, Reliability and Security (SAFECOMP 2022).
- T. Silveti-Falls got the Outstanding Reviewer Award at ICLR 2022 and NeurIPS 2022.
- A. Duval received the Mitacs Globalink Scholarship award in 2022, to reward and support my research work at MILA on accelerated catalysis design.
- L. Milecki had a honorable mention as a reviewer in MICCAI 2023.

7 New software and platforms

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 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.

7.1.8 iRestNet

Web site: [iRestNet](#)

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

7.1.9 PnP-MMO-imaging

Web site: [PnP-MMO-imaging](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: This code is produced by the OPIS PhD student M. Terris.
- Duration of the Development: This software is developed during the PhD thesis of M. Terris, mostly during 2021-2022.
- This is a Python/Pytorch code allowing to reproduce the results of the paper [\[link\]](#).
- The codes provided are distributed under a GNU General Public License v3.0.

7.1.10 UNetLSTM

Web site: [UNetLSTM](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Context/Role of OPIS: This code has been produced by the PhD student M. Papadomanaloki during her stay in OPIS lab.
- Duration of the Development: This software has been developed during the PhD thesis of M. Papadomanaloki, mostly during 2019
- This is a Python/Pytorch code allowing to reproduce the results of the paper [\[link\]](#).
- The codes provided are distributed under a GNU General Public License v3.0.

7.1.11 GraphSVX

Web site: [GraphSVX](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: This software is developed during the PhD thesis of A. Duval in 2021.
- This is a Python/Pytorch code allowing to reproduce the results of the paper [\[link\]](#).
- The codes provided are distributed under a GNU General Public License v3.0.

7.1.12 BraneMF

Web site: [BraneMF](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: This software is developed during the PhD thesis of S. Jagtap in 2022.
- This is a Python code allowing to reproduce the results of the paper [\[16\]](#).
- The codes provided are distributed under the licence GNU General Public License v3.0.

7.1.13 BRANENet

Web site: [BRANENet](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: This software is developed during the PhD thesis of S. Jagtap in 2022.
- This is a Python code allowing to reproduce the results of the paper [\[17\]](#).
- The codes provided are distributed under the licence GNU General Public License v3.0.

7.1.14 HoscPool

Web site: [HoscPool](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: This software is developed during the PhD thesis of A. Duval in 2022.
- This is a Python code allowing to reproduce the results of the paper [\[39\]](#).
- The codes provided are distributed under the licence GNU General Public License v3.0.

7.1.15 NodeSig

Web site: [NodeSig](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: The development started during the PhD thesis of A. Çelikkanat in 2021, and was completed in 2022.
- This is a Python code allowing to reproduce the results of the paper [37].
- The codes provided are distributed under the licence GNU General Public License v3.0.

7.1.16 kernelNE

Web site: [kernelNE](#)

- Software Family: `vehicle`
- Audience: `community`
- Evolution and maintenance: `basic`
- Duration of the Development: The development started during the PhD thesis of A. Çelikkanat in 2021, and was completed in 2022.
- This is a Python code allowing to reproduce the results of the paper [6].
- The codes provided are distributed under the licence GNU General Public License v3.0.

8 New results

8.1 Theoretical and practical advances for majorize-minimize algorithms

Participants: Emilie Chouzenoux, Jean-Baptiste Fest, Jean-Christophe Pesquet, Ségolène Martin.

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. The work [9] introduces novel theoretical convergence guarantees for MM algorithms when approximate gradient terms are employed, generalizing some recent work to a wider class of functions and algorithms. We illustrate our theoretical results with a binary classification problem. In [10], a new MM method for solving large scale constrained differentiable optimization problems is proposed. To account efficiently for a wide range of constraints, our approach embeds a subspace algorithm into an exterior penalty framework. The subspace strategy, combined with the MM step search, takes great advantage of the smoothness of the penalized cost function. Assuming that the latter is convex, the convergence of our algorithm to a solution of the constrained optimization problem is proved. In [49], we provide a unified view of MM-based methods for image reconstruction in the presence of Poisson noise, by introducing the concept of Bregman majorization. From this general approach, we exhibit three algorithmic solutions and compare their computational efficiency on a problem of dynamic PET image reconstruction, either using GPU or CPU processing.

8.2 Fundamental problems in image reconstruction

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Marion Savanier, Maissa Sghaier (Collaboration: Serge Muller, Cyril Riddell, Yves Troussset, GE Healthcare, Buc)

In [63, 26], we consider fixed point proximal algorithms for solving penalized least-squares minimization problems arising in data science. These first-order schemes are attractive due to their flexibility and minimal memory requirements allowing to tackle large-scale minimization problems involving non-smooth penalties. However, for 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 these papers, we propose to analyze the effect of such an adjoint mismatch on the convergence of preconditioned proximal gradient algorithm [26] and primal-dual proximal algorithms [63]. 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.

In interventional radiology, 3D reconstruction of devices such as needles can increase the precision of procedures. Doing so with CBCT is time-consuming and increases the X-ray dose. In [50], we investigate the benefits of directional total variation as an adequate prior for anisotropic devices. We introduce a decomposition method that allows several a priori directions to be considered at once as well as excludes the anatomical background that is not sparse. The capacity of the method is illustrated in simulations of limited-angle acquisitions.

The reconstruction of a volumetric image from Digital Breast Tomosynthesis (DBT) measurements is an ill-posed inverse problem, for which existing iterative regularized approaches can provide a good solution. However, the clinical task is somehow omitted in the derivation of those techniques, although it plays a primary role in the radiologist diagnosis. In the work [27], we address this issue by introducing a novel variational formulation for DBT reconstruction, tailored for a specific clinical task, namely the detection of microcalcifications. Our method aims at simultaneously enhancing the detectability performance and enabling a high-quality restoration of the background breast tissues. Experimental results show the interest of our DBT reconstruction approach, qualitatively and quantitatively.

8.3 Deep unrolled algorithms for inverse problems in image processing

Participants: Emilie Chouzenoux, Yunshi Huang, Marion Savanier, Jean-Christophe Pesquet

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 [74], we address the problem of image reconstruction for region-of-interest (ROI) computed tomography (CT). We introduced a novel, unfolded deep learning approach called U-RDBFB designed for ROI CT reconstruction from limited data. Few-view truncated data are efficiently handled thanks to a robust non-convex data fidelity function combined with sparsity inducing regularization functions. Iterations of a block dual forward-backward algorithm, embedded in an iterative reweighted scheme, are then unrolled over a neural network architecture, allowing the learning of various parameters in a supervised manner. Our experiments show an improvement over various state-of-the-art methods, including model-based iterative schemes, deep learning architectures, and deep unfolding methods. In [15], we introduce the deep unfolding of a variational Bayesian algorithm (VBA) for image blind deconvolution. Our VBA generic framework incorporates smoothness priors on the unknown blur/image and possible affine constraints

(e.g., sum to one) on the blur kernel, integrating the VBA within a neural network paradigm following an unrolling methodology. The proposed architecture is trained in a supervised fashion, which allows us to optimally set two key hyperparameters of the VBA model and leads to further improvements in terms of resulting visual quality. Various experiments involving grayscale/color images and diverse kernel shapes, are performed. The numerical examples illustrate the high performance of our approach when compared to state-of-the-art techniques based on optimization, Bayesian estimation, or deep learning.

8.4 Computational approaches for multiphotonic image restoration

Participants: Emilie Chouzenoux and Jean-Christophe Pesquet (Collaboration: Claire Lefort, XLIM, CNRS ; Mathieu Chalvidal, ANITI Toulouse)

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 [62]. This allows to deduce a new instrumental and computational pipeline for MPM of biomedical structures. When applied to the visualization of the axial information of myosin structure, our pipeline allows to decipher, for the first time, the 3D organization of the myosin in skeletal muscle is visually shown from an unsliced whole muscle, starting with a solution of optical microscopy [43]. We demonstrate in [38][11] the interest of our pipeline for imaging bacteria without any labelling process. In [44], we are presenting the application of an optical and computational pipeline FAMOUS for revealing the presence of bacteria and viral particles.

8.5 Monte-Carlo approaches for global optimization

Participants: Emilie Chouzenoux, Thomas Guilmeau (Collaboration: Victor 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 [41], we introduce a new simulated annealing approach that selects the cooling schedule on the fly. Starting from a variational formulation of the problem of joint temperature and proposal adaptation, we derive an alternating Bregman proximal algorithm to minimize the resulting cost, obtaining the sequence of Boltzmann distributions and proposals. We recently explore the convergence of the scheme in [69].

8.6 Fast schemes for adaptive importance sampling

Participants: Emilie Chouzenoux, Yunshi Huang, Jean-Christophe Pesquet (Collaboration: Victor Elvira, University of Edinburgh)

Adaptive importance sampling (AIS) methods are increasingly used for the approximation of distributions and related intractable integrals in the context of Bayesian inference. In [13], we propose a novel sampling algorithm for multi-modal target exploration, that exploits the benefits of AIS framework and includes more efficient adaptive mechanisms, exploiting geometric information of the target distribution. In [71], we propose a novel algorithm PMCnet that includes an efficient AIS mechanism, to efficiently explore the highly multimodal posterior distribution involved in the training of Bayesian Neural Networks. Numerical results illustrate the excellent performance and the improved exploration capabilities of PMCnet for the training of both shallow and deep neural networks. In [67], we propose an AIS method, called GRAMIS, that iteratively improves the set of proposals by exploiting geometric information of the target to adapt the location and scale parameters of those proposals. A repulsion term is introduced that favors a coordinated exploration of the state space. We provide a theoretical justification of the repulsion term and show the good performance of GRAMIS in problems where the target cannot be easily approximated by a standard uni-modal proposal.

8.7 Deep transform and metric learning approaches

Participants: Emilie Chouzenoux and Jean-Christophe Pesquet (Collaboration: Wen Tang and Hamid Krim, North Carolina State University ; Angshul Majumdar, IIIT Delhi, India ; Giovanni Chierchia, ESIEE Paris)

Based on its great successes in inference and denoising tasks, Dictionary Learning (DL) and its related sparse optimization formulations have garnered a lot of research interest. While most solutions have focused on single layer dictionaries, the recently improved Deep DL methods have also fallen short on a number of issues. We hence propose a novel Deep DL approach where each DL layer can be formulated and solved as a combination of one linear layer and a Recurrent Neural Network, where the RNN is flexibly regraded as a layer-associated learned metric. Our work [30] unveils new insights between the Neural Networks and Deep DL, and provides a novel, efficient and competitive approach to jointly learn the deep transforms and metrics. Extensive experiments are carried out to demonstrate that the proposed method can not only outperform existing Deep DL, but also state-of-the-art generic Convolutional Neural Networks. In [40], we introduce a Deep Convolutional Transform Learning (DCTL) based clustering framework. The advantage of our proposed formulation is that we do not require learning the additional decoder network. Therefore our formulation is less prone to over-fitting. Comparison with state-of-the-art deep learning based clustering solutions on benchmark image datasets shows that our proposed method improves over the rest in challenging scenarios where there are many clusters with limited samples. In [52], we address the problem of hyperspectral image classification when the number of labeled samples is very small (few shot learning). We propose a semisupervised version of DCTL, that compares favorably with four recent methods tailored for solving the few-shot learning problem in hyperspectral classification.

8.8 Computational approaches for drug discovery

Participant: Emilie Chouzenoux, Stuti Jain, Fragkiskos Malliaros (Collaborations: Angshul Majumdar, IIIT Delhi ; Bin Liu, Dimitrios Papadopoulos, Grigorios Tsoumakas, Apostolos Papadopoulos, Aristotle Univ. of Thessaloniki)

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.

In [22], we formulate antiviral repositioning as a matrix completion problem wherein the antiviral drugs are along the rows and the viruses are along the columns. The input matrix is partially filled, with ones in positions where the antiviral drug has been known to be effective against a virus. The curated metadata for antivirals (chemical structure and pathways) and viruses (genomic structure and symptoms) are encoded into our matrix completion framework as graph Laplacian regularization. We then frame the resulting multiple graph regularized matrix completion (GRMC) problem as deep matrix factorization solved by using a novel optimization method called HyPALM (Hybrid Proximal Alternating Linearized Minimization). Results of our curated RNA drug-virus association data set show that the proposed approach excels over state-of-the-art GRMC techniques. When applied to in silico prediction of antivirals for COVID-19, our approach returns antivirals that are either used for treating patients or are under trials for the same. In [72], we extend the previous approach by incorporating expert knowledge metadata and deep factorization term in our formulation. Our algorithm is applied to in silico predictions of anti-virals for monkeypox. In [70], we propose a Siamese-like architecture with two processing channels' networks based on deep convolutional transform learning for drug-drug interaction prediction.

In the work [21], we take a multi-layered network approach to handle diverse drug and target similarities, and propose a novel optimization framework, called Multiple similarity DeepWalk-based Matrix Factorization (MDMF), for DTI prediction. The framework unifies embedding generation and interaction prediction, learning vector representations of drugs and targets that not only retain higher-order proximity across all hyper-layers and layer-specific local invariance, but also approximate the interactions with their inner product. Furthermore, we develop an ensemble method (MDMF2A) that integrates

two instantiations of the MDMF model, optimizing the area under the precision-recall curve (AUPR) and the area under the receiver operating characteristic curve (AUC) respectively. The empirical study on real-world DTI datasets shows that our method achieves statistically significant improvement over current state-of-the-art approaches in four different settings. Moreover, the validation of highly ranked non-interacting pairs also demonstrates the potential of MDMF2A to discover novel DTIs.

8.9 Multi-label deep convolutional transform learning for non-intrusive load monitoring

Participant: Emilie Chouzenoux (Collaboration: Giovanni Chierchia, ESIEE Paris ; Angshul Majumdar, IIT Delhi)

The objective of [28] is to propose a novel computational method to learn the state of an appliance (ON / OFF) given the aggregate power consumption recorded by the smart-meter. We formulate a multi-label classification problem where the classes correspond to the appliances. The proposed approach is based on our recently introduced framework of convolutional transform learning. We propose a deep supervised version of it relying on an original multi-label cost. Comparisons with state-of-the-art techniques show that our proposed method improves over the benchmarks on popular non-intrusive load monitoring datasets.

8.10 Binary matrix completion on graphs

Participant: Emilie Chouzenoux (Collaboration: Angshul Majumdar, IIT Delhi)

The work [29] addresses the problem of completing a partially observed matrix where the entries are either ones or zeroes. This is typically called one-bit matrix completion or binary matrix completion. In this problem, the association among the rows and among the columns can be modeled through graph Laplacians. Since the Laplacians cannot be computed from the incomplete matrix, they must be simultaneously estimated while completing the matrix. We model the problem as graph regularized binary matrix completion where the graphs need to be learnt from the data. We proposed an algorithm based on an alternating minimization scheme, taking advantage of an efficient proximity-based inner solver. The algorithm is applied to the problem of collaborative filtering. Experiments on benchmark datasets with state-of-the-art techniques in collaborative filtering show that the proposed method improves over the rest by a considerable margin.

8.11 Machine-learning-based radiomics models for lesion identification in MRI

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

The development and clinical adoption of quantitative imaging biomarkers (radiomics) has established the need for the identification of parameters altering radiomics reproducibility. The paper [20] assesses how the preprocessing methods (including N4 bias field correction and image resampling) and the harmonization methods (either the six intensity normalization methods working on brain MRI images or the ComBat method working on radiomic features) help to remove the scanner effects and improve the radiomic feature reproducibility in brain MRI radiomics. The paper [5] evaluates a deep learning method designed to increase the contrast-to-noise ratio in contrast-enhanced gradient echo T1-weighted brain MRI acquisitions. The processed images are quantitatively evaluated in terms of lesion detection performance. The proposed deep learning method successfully amplified the beneficial effects of contrast agent injection on gradient echo T1 image quality, contrast level, and lesion detection performance. In particular, the sensitivity of the MRI sequence was improved by up to 16%, whereas the false detection rate remained similar.

8.12 Blind Kalman filtering for time series modeling and inference

Participants: Emilie Chouzenoux (Collaboration: Shalini Sharma, Angshul Majumdar, IIT Delhi, India ; Victor 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.

In [12], we introduce 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 a new method called GraphEM based on the well sounded expectation-maximization (EM) methodology for inferring the transition matrix jointly with the smoothing/filtering of the observed data. We propose an advanced convex optimization solver relying on a consensus-based implementation of a proximal splitting strategy for solving the M-step. This approach enables an efficient and versatile processing of various sophisticated priors on the graph structure, such as parsimony constraints, while benefiting from convergence guarantees. We demonstrate the good performance and the interpretable results of GraphEM by means of two sets of numerical examples. In [75], we specialize the proposed methodology to the problem of stock forecasting, by proposing an online training strategy and a probabilistic assessment of the trading decision. Numerical experiments on a problem of stock market data inference shows its superiority among several state-of-the art dynamic modeling tools.

8.13 Distributed optimization for large scale image processing

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Hugues Talbot, Jean-Baptiste Fesl, Marin Stamm (Collaboration: Ferial Abboud, Witbe ; Mathieu Chalvidal, ANITI Toulouse)

Optimization problems arising in signal and image processing involve an increasingly large number of variables. 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, which are non-necessarily smooth and possibly composed with large-size linear operators. Distributed algorithms are fundamental tools to address such problems, with demonstrated efficiency in many applicative fields. The implementation of distributed algorithms requires to pay careful attention to the cost of communication, which can be reduced and controlled by resorting to an asynchronous implementation. However, asynchronous implementation raises challenging questions, in terms of convergence analysis, as the communication delays may introduce instabilities in the algorithm behavior. In [1], we present a new distributed algorithm for computing the proximity operator of a sum of non-necessarily smooth convex functions composed with arbitrary linear operators. Our algorithm relies on a primal-dual splitting strategy, and benefits from established convergence guaranties. Each involved function is associated with a node of a hypergraph, with the ability to communicate with neighboring nodes sharing the same hyperedge. Thanks to this structure, our method can be efficiently implemented on modern parallel computing architectures, distributing the computations on multiple nodes or machines, with controlled requirements for synchronization steps. Good numerical performance and scalability properties are demonstrated on a problem of video sequence denoising. In [62], we propose an asynchronous majoration-minimization algorithm for solving large scale differentiable non-convex optimization problems. The proposed algorithm runs efficient MM memory gradient updates on block of coordinates, in a parallel and possibly asynchronous manner. We establish the convergence of the resulting sequence of iterates under mild assumptions. The performance of the algorithm is illustrated on the restoration of 3D images degraded by depth-variant 3D blur, arising in multiphoton microscopy.

8.14 Optimization for few-shot learning

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Ségolène Martin (Collaboration: Ismail Ben Ayed, ETS Montréal)

Standard few-shot benchmarks are often built upon simplifying assumptions on the query sets, which may not always hold in practice. In particular, for each task at testing time, the classes effectively present in the unlabeled query set are known a priori, and correspond exactly to the set of classes represented in the labeled support set. In [45], we relax these assumptions and extend current benchmarks, so that the query-set classes of a given task are unknown, but just belong to a much larger set of possible classes. Our setting could be viewed as an instance of the challenging yet practical problem of extremely imbalanced K -way classification, K being much larger than the values typically used in standard benchmarks, and with potentially irrelevant supervision from the support set. Expectedly, our setting incurs drops in the performances of state-of-the-art methods. Motivated by these observations, we introduce a PrimAl Dual Minimum Description LEngth (PADDLE) formulation, which balances data-fitting accuracy and model complexity for a given few-shot task, under supervision constraints from the support set. Our constrained MDL-like objective promotes competition among a large set of possible classes, preserving only effective classes that fit better the data of a few-shot task. It is hyperparameter free, and could be applied on top of any base-class training. Furthermore, we derive a fast block coordinate descent algorithm for optimizing our objective, with convergence guarantee, and a linear computational complexity at each iteration. Comprehensive experiments over the standard few-shot datasets and the more realistic and challenging i-Nat dataset show highly competitive performances of our method, more so when the numbers of possible classes in the tasks increase.

8.15 Advanced nonconvex priors for image restoration

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Gabriele Scrivanti

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 [2], we propose an adaptive, smooth, nonconvex and sparsity-promoting variational model for singleimage super-resolution of real murine Optical Coherence Tomography data. We follow a sparse-representation approach where sparsity is modelled with respect to a suitable dictionary generated from high-resolution OCT data. As a regulariser, we employ a smooth, nonconvex and separable Cauchy-type penalty. Our numerical results show that the combination of a space-variant modelling with a fast optimisation strategy improves reconstruction results, maintaining tissue texture and suppressing background noise to a desirable amount at the same time. In [51], we propose a new variational formulation to implement the recently introduced convex-nonconvex approach in the context of image denoising. By suitably exploiting duality properties, our formulation allows to encompass sophisticated directional total variation priors. We additionally propose an efficient optimisation strategy for the resulting convex minimisation problem. We illustrate on numerical examples the good performance of the resulting method, when compared to the standard convex total variation denoiser. In [64], we propose a novel non-smooth 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.

8.16 Multivariate Lipschitz analysis of the stability of neural networks

Participants: Kavya Gupta, Jean-Christophe Pesquet and Fragkiskos Malliaros (Collaboration: Fateh Kaakai and Béatrice Pesquet-Popescu, Thales)

The stability of neural networks with respect to adversarial perturbations has been extensively studied. One of the main strategies consist of quantifying the Lipschitz regularity of neural networks. In this work [14], we introduce a multivariate Lipschitz constant-based stability analysis of fully connected neural networks allowing us to capture the influence of each input or group of inputs on the neural network stability. Our approach relies on a suitable re-normalization of the input space, with the objective to perform a more precise analysis than the one provided by a global Lipschitz constant. We investigate the mathematical properties of the proposed multivariate Lipschitz analysis and show its usefulness in better understanding the sensitivity of the neural network with regard to groups of inputs. We display the results of this analysis by a new representation designed for machine learning practitioners and safety engineers termed as a Lipschitz star. The Lipschitz star is a graphical and practical tool to analyze the sensitivity of a neural network model during its development, with regard to different combinations of inputs. By leveraging this tool, we show that it is possible to build robust-by-design models using spectral normalization techniques for controlling the stability of a neural network, given a safety Lipschitz target. Thanks to our multivariate Lipschitz analysis, we can also measure the efficiency of adversarial training in inference tasks. We perform experiments on various open access tabular datasets, and also on a real Thales Air Mobility industrial application subject to certification requirements.

8.17 Safe design of stable neural networks for fault detection in small UAVs

Participants: Kavya Gupta and Jean-Christophe Pesquet (Collaboration: Fateh Kaakai and Béatrice Pesquet-Popescu, Thales)

Stability of a machine learning model is the extent to which a model can continue to operate correctly despite small perturbations in its inputs. A formal method to measure stability is the Lipschitz constant of the model which allows to evaluate how small perturbations in the inputs impact the output variations. Variations in the outputs may lead to high errors for regression tasks or unintended changes in the classes for classification tasks. Verification of the stability of ML models is crucial in many industrial domains such as aeronautics, space, automotive etc. It has been recognized that data-driven models are intrinsically extremely sensitive to small perturbation of the inputs. Therefore, the need to design methods for verifying the stability of ML models is of importance for manufacturers developing safety critical products. In this work [58], we focus on Small Unmanned Aerial Vehicles (UAVs) which are in the frontage of new technology solutions for intelligent systems. However, real-time fault detection/diagnosis in such UAVs remains a challenge from data collection to prediction tasks. This work presents application of neural networks to detect in real-time elevation positioning faults. We show the efficiency of a formal method based on the Lipschitz constant for quantifying the stability of neural network models. We also present how this method can be coupled with spectral normalization constraints at the design phase to control the internal parameters of the model and make it more stable while keeping a high level of performance (accuracy-stability trade-off).

8.18 Design of robust complex-valued feed-forward neural networks

Participants: Ana Neacsu and Jean-Christophe Pesquet (Collaboration: Ravzan Ciubotaru and Corneliu Burileanu, Polithenica Bucurest)

This work [47] addresses the problem of designing robust complex-valued neural networks in order to reduce their sensitivity to adversarial perturbations. The robustness is guaranteed by imposing a bound on the Lipschitz constant of the network. We present a new architecture (RCFF-Net), for which we derive tight Lipschitz constant bounds. A constrained learning strategy is then developed to train the proposed structure, while controlling its global Lipschitz constant. The proposed approach is evaluated in an audio signal denoising task. The achieved results demonstrate the effectiveness of the aforementioned design method.

8.19 Differentiation tools for non-smooth functions

Participant: Tony Silveti-Falls (Collaboration: Jérôme Bolte, Toulouse School of Economics ; Edouard Pauwels, Université Toulouse III Paul Sabatier)

Many problems in data science and machine learning, ranging from meta-learning to dataset distillation and adversarial examples and beyond, can be posed as bilevel optimization problems. A key hurdle in solving these problems is the often-present lack of differentiability of the solution to the lower level problem with respect to the problem data. Our past work on a novel implicit function theorem has paved the way to address such hurdles in a rigorous way, compatible with automatic differentiation. As a key step in this direction, we have studied sufficient conditions to ensure generalized differentiability of the solution to a broad class of monotone inclusion problems, and characterized the formulas for computing the generalized derivatives as well. Our work [61] provides intuition for the design of neural network architectures with implicit layers, discretization problems in imaging and dictionary learning, among others.

8.20 Automatic optic nerve sheath assesement from ultrasound images using weakly supervised approaches

Participants: Nora Ouzir, Jean-Christophe Pesquet (Collaborations: Clément Dubost, Centre Borelli, CNRS, Université de Paris, ENS Paris-Saclay, SSA, INSERM, Anesthesia-Intensive Care Unit of Hôpital Bégin)

Precise quantification of the nerve sheath diameter plays a crucial role in intracranial blood pressure monitoring, which is vital for surgical interventions and a key indicator of diseases such as preeclampsia. Despite the need for a precise measurement, there is currently a significant variability between human operators when using ultrasonic images. This project seeks to address this problem by developing an automatic method for optic nerve sheath diameter assessment adapted to ultrasound imaging. Although several deep learning based detection and segmentation methods have been proposed in the literature, key challenges remain in the specific context of optic nerve imaging using ultrasound. First, the extremely poor quality of the images is to be taken into account. Secondly, the variability in image acquisition of the optic nerve due, for example, to the positioning of the ultrasound probe is particularly high. Finally, there is no labelled database that would enable training and testing of deep learning approaches in this context. In this project, we develop a learning-based approach for the segmentation and measurement of the optic nerve sheath diameter adapted to ultrasound imaging. The main objective is to investigate the potential of weakly supervised approaches in dealing with the lack of labelled images. This is achieved by combining deep neural networks (e.g., ResNet, Unet) and traditional model-based machine learning strategies. Particular attention is paid to robust strategies that can handle noisy and varying input images.

8.21 Blood flow estimation in moving tissues using ultrasound imaging

Participants: Nora Ouzir, Jean-Christophe Pesquet (Collaboration: Denis Kouamé, University of Toulouse)

Quantification of blood flow, and more generally vascular structures, plays a key role in the treatment of various diseases, such as brain tumors or cardiovascular diseases. Classical approaches rely on filtering techniques and are typically based on singular value decomposition (SVD). More realistic alternatives formulate the blood-tissue separation as an inverse problem, where a priori knowledge about both tissue and blood structures can be incorporated. Specifically, sparsity of the blood and low-rank structure of the tissues can be considered. In this work, we address the key challenge of considering tissue motions which have a significant impact on the quality of the blood estimation, especially, at the boundaries of the flow. In addition, an appropriate alternating proximal-forward-backward algorithm is developed to deal with several possible blood and tissue motion regularizations.

8.22 Convex formulation for the robust estimation of multivariate exponential power models

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

The multivariate power exponential (MEP) distribution can model a broad range of signals. In noisy scenarios, the robust estimation of the MEP parameters has been traditionally addressed by a fixed-point approach associated with a nonconvex optimization problem. Establishing convergence properties for this approach when the distribution mean is unknown is still an open problem. As an alternative, we present in [48] a novel convex formulation for robustly estimating MEP parameters in the presence of multiplicative perturbations. The proposed approach is grounded on a re-parametrization of the original likelihood function in a way that ensures convexity. We also show that this property is preserved for several typical regularization functions. Compared with the robust Tyler's estimator, the proposed method shows a more accurate precision matrix estimation, with similar mean and covariance estimation performance. Currently, we are developing robust clustering approaches based on this framework.

8.23 Integration of biological networks for functional analysis of proteins

Participants: Surabhi Jagtap, Fragkiskos Malliaros (Collaborations: Abdulkadir Çelikkanat, Technical Univ. of Denmark; Aurélie Pirayre, Frédérique Bidard, Laurent Duval, IFP Energies Nouvelles)

The cellular system of a living organism is composed of interacting bio-molecules that control cellular processes at multiple levels. Their correspondences are represented by tightly regulated molecular networks. The increase of omics technologies has favored the generation of large-scale disparate data and the consequent demand for simultaneously using molecular and functional interaction networks: gene co-expression, protein-protein interaction (PPI), genetic interaction and metabolic networks. They are rich sources of information at different molecular levels, and their effective integration is essential to understand cell functioning and their building blocks (proteins). Therefore, it is necessary to obtain informative representations of proteins and their proximity, that are not fully captured by features extracted directly from a single informational level.

We have proposed BraneMF [16], a novel random walk-based matrix factorization method for learning node representation in a multilayer network, with application to omics data integration. We test BraneMF with PPI networks of *Saccharomyces cerevisiae*, a well-studied yeast model organism. We demonstrate the applicability of the learned features for essential multi-omics inference tasks: clustering, function and PPI prediction. We have also introduced BRANENet [17], an expressive, scalable, and versatile method to learn node embeddings across multilayer heterogeneous graphs. We have tested BRANENet on transcriptomics (RNA-seq) and targeted metabolomics (NMR) data for wild-type yeast strain. Our framework learns features for differentially expressed bio-molecules showing heat stress response. We demonstrate the applicability of the learned features for targeted omics inference tasks: transcription factor (TF)-target prediction, integrated omics network (ION) inference, and module identification.

8.24 Multiple kernel graph representation learning

Participants: Fragkiskos Malliaros (Collaborations: Abdulkadir Çelikkanat, Technical Univ. of Denmark ; Yanning Shen, University of California, Irvine)

Learning representations of nodes in a low dimensional space is a crucial task with numerous interesting applications in network analysis, including link prediction, node classification, and visualization. Two popular approaches for this problem are matrix factorization and random walk-based models. In the work [6], we aim to bring together the best of both worlds, towards learning node representations. In particular, we propose a weighted matrix factorization model that encodes random walk-based information about nodes of the network. The benefit of this novel formulation is that it enables us to utilize kernel functions without realizing the exact proximity matrix so that it enhances the expressiveness of existing matrix decomposition methods with kernels and alleviates their computational complexities. We extend the approach with a multiple kernel learning formulation that provides the flexibility of learning

the kernel as the linear combination of a dictionary of kernels in data-driven fashion. We perform an empirical evaluation on real-world networks, showing that the proposed model outperforms baseline node embedding algorithms in downstream machine learning tasks.

8.25 Clustering and pooling for graph neural networks

Participants: Alexandre Duval, Fragkiskos Malliaros

Graph Neural Networks achieve state-of-the-art performance on a plethora of graph classification tasks, especially due to pooling operators, which aggregate learned node embeddings hierarchically into a final graph representation. However, they are not only questioned by recent work showing on par performance with random pooling, but also ignore completely higher-order connectivity patterns. To tackle this issue, we have proposed HoscPool [39], a clustering-based graph pooling operator that captures higher-order information hierarchically, leading to richer graph representations. In fact, we learn a probabilistic cluster assignment matrix end-to-end by minimising relaxed formulations of motif spectral clustering in our objective function, and we then extend it to a pooling operator. We evaluate HoscPool on graph classification tasks and its clustering component on graphs with ground-truth community structure, achieving best performance. Lastly, we provide a deep empirical analysis of pooling operators' inner functioning.

8.26 Scalable graph representation learning

Participants: Fragkiskos Malliaros (Collaborations: Abdulkadir Çelikkanat, Technical Univ. of Denmark ; Apostolos Papadopoulos, Aristotle Univ. of Thessaloniki)

As the scale of networks increases, most of the widely used learning-based graph representation models also face computational challenges. While there is a recent effort toward designing algorithms that solely deal with scalability issues, most of them behave poorly in terms of accuracy on downstream tasks. In the work [37], we aim to study models that balance the trade-off between efficiency and accuracy. In particular, we have proposed NodeSig, a scalable model that computes binary node representations. NodeSig exploits random walk diffusion probabilities via stable random projections towards efficiently computing embeddings in the Hamming space. Our extensive experimental evaluation on various networks has demonstrated that the proposed model achieves a good balance between accuracy and efficiency compared to well-known baseline models on the node classification and link prediction tasks.

8.27 Artificial Intelligence for Radiology and Medicine

Participants: Theodore Aouad, Younes Belkouchi, Mario Viti, Hugues Talbot (Collaborations: Samy Amari, Nathalie Lassau, Gustave-Roussy ; Antoine Feydy, Hôpital Cochin and Nicolas Gogin, GE Health-care).

Radiology in medicine is a major domaine of research and applications in Artificial Intelligence. This year, we contributed in proposing a validated set of measures to assess the effect of immunotherapy on oncology patients. Particularly, it is important to detect as early as possible whether patients undergoing immunotherapy in oncology are responding favorably to the treatment. Some patient do not respond at all and still other respond negatively, making matters worse. We have proposed a set of easily available clinical and radiological measures, which when combined make such an assessment much more rapid than before, sometimes only after only a week [78, 3].

When the use of ultrasound imaging is possible, which is often the case, then an even faster and more accurate approach can be used, by looking at the way blood circulation varies in the tumors as the treatment is ongoing [24]. The use of tumor volume variation is more classical but was validated in a comprehensive study [4].

In terms of applications, we successfully applied deep-learning methods in musculo-skeletal imaging to help diagnose a relatively rare disease: axial spondylo-arthritis. This is an auto-immune disease, which is difficult to diagnose [35]. The use of AI provides an additional opinion and also an ability to diagnose the illness by non-specialist clinicians, alleviating the need for rare expertise in this type of imaging. We

are currently endeavouring to extend the work to clinical practice through the use of the AP-HP datacenter for medical exams.

Radiological imaging of heart vessel is an essential application of AI. We proposed a new way to segment coronaries taking into account connectivity, with significantly improved results [citeviti:hal-03724882](#). We used this work to help detect plaque within coronary vessels with improved accuracy with respect to the state of the art [\[55\]](#).

AI challenges are a major way by which AI results can be publicized and become visible. We participated in organizing, validating and evaluating the results during the 2022 Société Francophone de Radiology challenge in September 2022 [\[23\]](#).

8.28 Explainable deep learning via binary morphological neural networks

Participants: Theodore Aouad, Hugues Talbot

Deep learning has enabled a lot of progress in computer vision tasks in the last 10 years. However, a widely acknowledge element is that deep network results are not always stable or easy to interpret. Also deep network require significant computing resources in both computation and memory, often requiring graphical processing units (GPUs) for both training and inference. A recent popular topic of interest is to study whether neural networks can be drastically simplified using only binary weights. By construction this would also regularize networks. There can also be a benefit in interpretability because complex networks would essentially be learning compositions of mathematical morphology operators, which are often subject to expected mathematical behaviour.

However, binary networks are difficult to train. 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 makes scientific sense since using morphological operators can be thought as using activated linear filters, 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.

We have shown in [\[34\]](#) that these networks can indeed learn basic morphological operators correctly. In more recent, ongoing work [\[59\]](#), we have shown that we can learn sequences of operators as well as perform classification tasks with good results.

8.29 Generative methods in image computing, application to whole-slide pathology analysis

Participants: Loïc Le Bescond, Hugues Talbot

A major challenge in supervised machine learning is the necessity to use annotations, typically performed by humans. This is always demanding, sometimes extremely so. In the problem of segmenting cell nuclei in pathology slides, this is very difficult due to the very large number of such cells. Only semi-supervised methods can be used at best. In this article, we have proposed a totally unsupervised method for this problem that uses the shape of the segmented nuclei only as prior, learned on a different problem, and reused in a generative context by comparing achieved segmentation with the expected results. The outcome is a general cell nuclei segmenter that can work across a large number of stainings and modalities [\[42\]](#).

8.30 Discrete optimisation for gamma-knife treatment planning

Participants: Hugues Talbot (Collaborations: Thomas Klinge, Ian Paddick, Sebastien Ourselin, Jamie McClelland and Mark Modal, University City London and King's College London)

For some brain tumors, traditional surgery is too invasive. Instead, gamma-ray irradiation can be used instead. This type of radiotherapy can be very precise, but 3D dosage must be very precisely determined so as to minimize dosage to the healthy part of the brain. In this study, we proposed an exact,

computationally intensive discrete optimisation method to determine the bounds on a much faster, less precise but still acceptable method for such treatment planning.

8.31 Discrete optimisation for homotopic affine transformation in the 2D grid

Participants: Hugues Talbot (Collaborations: Nicolas Passat, Université de Reims ; Phuc Ngo, LORIA, Nancy ; Yukiko Kenmochi, GREYC, Caen)

Affine transforms of binary or labelled objects is a challenge to perform correctly, in particular when the preservation of topology is essential. In this article we propose a discrete optimisation framework to perform such transforms with tight topological constraints [25].

8.32 Artificial intelligence applications on histopathology

Participants: M. Vakalopoulou (Collaborations: MICS CentraleSupélec, Institute Gustave Roussy, Stony-Brook University, Therapanacea)

The examination of histopathology images is considered to be the gold standard for the diagnosis and stratification of cancer patients. However, generating automatic tools for processing WSIs is challenging due to their enormous sizes. Currently, to deal with this issue, conventional methods rely on a multiple instance learning (MIL) strategies to process a WSI at the patch level. Although effective, such methods are computationally expensive, because tiling a WSI into patches takes time and does not explore the spatial relations between these tiles. In [56], we propose a locally supervised learning framework that processes the entire slide by exploring the entire local and global information that it contains. This framework divides a pre-trained network into several modules and optimizes each module locally using an auxiliary model. We also introduce a random feature reconstruction unit (RFR) to preserve distinguishing features during training and improve the performance of our method.

In whole slide imaging, commonly used staining techniques based on hematoxylin and eosin (H-E) and immunohistochemistry (IHC) stains accentuate different aspects of the tissue landscape. In the case of detecting metastases, IHC provides a distinct readout that is readily interpretable by pathologists. In [36], we propose an extension to CycleGANs in the form of a region of interest discriminator. This allows the CycleGAN to learn from unpaired datasets where, in addition, there is a partial annotation of objects for which one wishes to enforce consistency. We present a use case on whole slide images, where an IHC stain provides an experimentally generated signal for metastatic cells. We demonstrate the superiority of our approach over the prior art in stain transfer on histopathology tiles over two datasets

8.33 Artificial intelligence applications for thoracic imaging

Participant: Maria Vakalopoulou (Collaborations: MICS CentraleSupélec, AP-HP - Hôpital Cochin Broca Hotel Dieu, Therapanacea)

In [33], we appraise the impact of functional and nutritional status and skeletal muscle mass in this population. We conducted a retrospective (2007-2020) single-center study by enrolling adult patients with solid cancers requiring unplanned ICU admission. Performance status, body weight, and albumin level were collected at ICU admission and over six months. Skeletal muscle mass was assessed at ICU admission by measuring muscle areas normalized by height (SMI).

8.34 Contrastive masked transformers for forecasting renal transplant function

Participants: Leo Milecki, Maria Vakalopoulou (Collaborations: Paris University, Hôpital Européen Georges-Pompidou, Ecole Polytechnique)

In [57], we propose a sequential architecture based on transformer encoders to predict the renal function 2-years post-transplantation. Our method uses features generated from Dynamic Contrast-Enhanced Magnetic Resonance Imaging from 4 follow-ups during the first year after the transplant

surgery. To deal with missing data, a key mask tensor exploiting the dot product attention mechanism of the transformers is used. Moreover, different contrastive schemes based on cosine similarity distance are proposed to handle the limited amount of available data. Our experiments highlight the relevance of considering sequential imaging data for this task and therefore in the study of chronic dysfunction mechanisms in renal transplantation, setting the path for future research in this area.

9 Bilateral contracts and grants with industry

9.1 Bilateral contracts with industry

- PhD Contract with IFP Energies Nouvelles
 - Project title: Seismic signal analysis by using neural networks
 - Duration: 2019-2022
 - Leaders: A. Fraysse and J.-C. Pesquet
- PhD Contract with Thales Group
 - Project title: Neural network solutions for safety of complex systems
 - Duration: 2019-2022
 - Leaders: J.-C. Pesquet and F. Malliaros
- PhD Contract with General Electric Healthcare
 - Project title: Reconstruction 3D interventionnelle
 - Duration: 2019-2022
 - Leaders: J.-C. Pesquet and E. Chouzenoux
- PhD Contract with IFP Energies nouvelles
 - Project title: Graph-based learning from integrated multi-omics and multi-species data
 - Duration: 2019-2022
 - Leader: F. Malliaros and J.-C. Pesquet
- PhD Contract with Heartflow Inc
 - Project title: Estimating heart perfusion based on physics-aware machine-learning methods
 - Duration: 2022-2025
 - Leaders: H. Talbot and I. Vignon-Clementel (Inria REO).
- Contract with Schneider Electric
 - Project title: Neural network modeling of electrical motors
 - Duration: 2019-2022
 - Leader: J.-C. Pesquet
- Contract with ESSILOR
 - Project title: Software development for photo-refraction analysis
 - Duration: 2020-2024
 - Leaders: E. Chouzenoux and J.-C. 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: N. Ouzir and J.-C. Pesquet

10 Partnerships and cooperations

10.1 International initiatives

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

COMPASS

Title: Computational medicine for optimal drug association

Duration: 2021 ->

Coordinator: Angshul Majumdar (Indian partner) and Emilie Chouzenoux (French partner)

Partners:

- Indraprastha Institute of Information Technology New Delhi, Inde,
- Inria Saclay, OPIS, France.

Summary: The associate team intends to foster a collaboration between the Inria project-team OPIS, and the SALSA laboratory in IIIT Delhi, India. The team will investigate new models and inference tools to understand and predict optimal drug association, so as to tackle real-life problems of computational drug discovery. Expected contributions lie in the curation of open access databases and in methodological developments within the fields of data mining, graphical modeling, representation learning and optimization/game theory.

Funding: We receive 6kE per year for covering traveling expenses in between French-Indo teams.

Website: [COMPASS](#)

10.2 International research visitors

10.2.1 Visits of international scientists

Tulay Adali

Status Professor

Institution of origin: University of Baltimore

Country: USA

Dates: Oct. 2021 to Jan. 2022, Oct. 2022 to Nov. 2022

Context of the visit: Research collaboration with E. Chouzenoux, J.-C. Pesquet and C. Cosserat.

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

Ismail Ben Ayed

Status Professor

Institution of origin: ETS Montréal

Country: Canada

Dates: Sep. 2021 to Aug. 2022

Context of the visit: Research collaboration with E. Chouzenoux, J.-C. Pesquet, S. Martin, M. Vu and R. Nouaji.

Mobility program/type of mobility: Sabbatical stay funded by Data IA program.

Audrey Repetti

Status Associate Professor

Institution of origin: Heriot-Watt University, Edinburg

Country: Scotland

Dates: Apr. 2022 to July 2022

Context of the visit: Research collaboration with E. Chouzenoux, J.-C. Pesquet, M. Terris and J.-B. Fést.

Mobility program/type of mobility: Research stay funded by Data IA program and ERC STG MAJORIS.

Jhony Heribereto Giraldo Zuluaga

Status PhD student

Institution of origin: Université de La Rochelle

Country: France

Dates: Jan. 2022 to June 2022

Context of the visit: Research collaboration with F. Malliaros.

Mobility program/type of mobility: Research stay funded by Data IA program.

Anchalee Sripattanet

Status PhD student

Institution of origin: King Montut's Institut of Technology, Bangkok

Country: Thailand

Dates: Nov. 2022 to Apr. 2023

Context of the visit: Research collaboration with F. Malliaros.

Mobility program/type of mobility: Research stay funded by National Research Council of Thailand and CVN.

Flavia Chorobura

Status PhD student

Institution of origin: University Politehnica of Bucharest

Country: Romania

Dates: 6 Oct. 2022 to 31st Dec. 2022

Context of the visit: ITN TradeOpt secondment visit.

Mobility program/type of mobility: Research stay funded by ITN TradeOpt.

Giovanni Bruccola

Status PhD student

Institution of origin: IBS-PAN, Warsaw

Country: Poland

Dates: 1st Sep. 2022 to 31st Jan 2023.

Context of the visit: ITN TradeOpt secondment visit.

Mobility program/type of mobility: Research stay funded by ITN TradeOpt.

10.2.2 Visits to international teams**Research stays abroad****Fragkiskos Malliaros**

Visited institution: Sapienza University of Rome

Country: Italy

Dates: 25th April - 6th May 2022

Context of the visit: Collaboration with Pr. Ioannis Chatzigiannakis at the Department of Computer, Control and Management Engineering.

Mobility program/type of mobility: Research stay funded by the visiting professor mobility grant program of Sapienza University of Rome and CVN.

Alexandre Duval

Visited institution: Montreal Institute of Learning Algorithms, Quebec AI Institute

Country: Canada

Dates: 1st Feb - 1st Aug. 2022

Context of the visit: Collaboration with Pr. Yoshua Bengio and Pr. David Rolnick.

Mobility program/type of mobility: Research stay funded by Globalink Mitacs - Inria grant, and mobility grant from ED STIC.

Mouna Gharbi

Visited institution: University of Genoa

Country: Italy

Dates: 1st Apr. - 31st July. 2022, 1st Sep.-30th Nov. 2022

Context of the visit: ITN TradeOpt secondment visit.

Mobility program/type of mobility: Research stay funded by ITN TradeOpt.

Gabriele Scrivanti

Visited institution: Designers company, Warsaw

Country: Poland

Dates: 1st Nov. - 30th Apr. 2022

Context of the visit: ITN TradeOpt secondment visit.

Mobility program/type of mobility: Research stay funded by ITN TradeOpt.

Visited institution: IBS-PAN, Systems Research Institute, Polish Academy of Science, Warsaw

Country: Poland

Dates: 1st May - 31st July 2022

Context of the visit: ITN TradeOpt secondment visit.

Mobility program/type of mobility: Research stay funded by ITN TradeOpt.

Sékolène Martin

Visited institution: LIVIA laboratory, École de Technologie Supérieure, Montréal

Country: Canada

Dates: 1st Sep.- 19th Dec. 2022

Context of the visit: Collaboration with Ismail Ben Ayed.

Mobility program/type of mobility: Research stay funded by Data IA call for international mobility.

Jean-Baptiste Fest

Visited institution: Heriott-Watt University, Edimbourg

Country: UK

Dates: 5th Sep.-15th Oct. 2022

Context of the visit: Collaboration with Audrey Repetti.

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

Leo Milecki

Visited institution: Provost Ultrasound Lab, Polytechnique Montreal

Country: Canada

Dates: 29th Sep.-21st Dec. 2022

Context of the visit: Collaboration on the topic of kidney transplant forecasting.

Mobility program/type of mobility: Research stay funded by DATAIA call for international mobility.

Othmane Laoussy

Visited institution: Computer Vision Lab, Computer Science Department at StonyBrook University

Country: USA

Dates: 3rd Oct.-1st Nov. 2022

Context of the visit: Collaboration with Dimitri Samaras.

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

10.3 European initiatives

10.3.1 H2020 projects

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

Title: Majorization-Minimization algorithms for Image Processing

Duration: 2020 - 2025

Coordinator: E. Chouzenoux

Partners:

- Inria Saclay, OPIS, France.

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.

H2020 ITN Marie Skłodowska-Curie Trade-Opt [Trade-Opt](#)

Title: Training Data-Drive Experts in Optimization

Duration: 2020 - 2024

Partners:

- CentraleSupélec, France,
- TU Braunschweig, Germany,

- Univ. Graz, Austria,
- Univ. Bucharest, Romania,
- IBS PAN, Poland,
- Univ. Louvain, Belgium.

Coordinator: S. Villa (Univ. Genova, Italy), local: J.-C. Pesquet

Summary: The main scientific objective of the TraDE-OPT is to derive and analyse efficient optimization algorithms for solving data-driven problems. Applications to a broad range of social, economic, health and urban problems are expected. Nowadays, data production explodes: data are produced by a variety of sensors in industry, vehicles, scanners, internet and mobile devices. One of the emerging challenges is to extract interpretable information from these data. Currently, optimization, and especially, convex optimization, is at the core of many theoretical and algorithmic methods underpinning solver technologies for a myriad of data driven problems.

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: J.-C. 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: H. Talbot
- Program: ANR JCJC
 - Project acronym: Hagnodice
 - Project title: Holistic explainable artificial intelligence schemes for lung cancer prognosis
 - Duration: 2022-2026
 - Coordinator: M. Vakalopoulou
- Program: ANR JCJC
 - Project acronym: GraphIA
 - Project title: Scalable and robust representation learning on graphs
 - Duration: 2021-2025
 - Coordinator: F. Malliaros
- Program: ANR JCJC
 - Project acronym: MajIC
 - Project title: Majorization-Minimization Algorithms for Image Computing
 - Duration: 2017-2022

- Coordinator: E. Chouzenoux
- Program: ANR JCJC
 - Project acronym: AVENUE
 - Project title: A Visual memory network for scene understanding
 - Duration: 2018-2022
 - Coordinator: Dr. Karteek Alahari (Inria Grenoble - Rhône-Alpes). Local: F. Malliaros.

10.5 Regional initiatives

- Labex DigiCosme, PhD grant
 - Project acronym: GratifAI
 - Project title: Graph enhancement for robust representation learning and applications
 - Duration: 2021-2024
 - Coordinators: F. Malliaros, T. Bonald (Télécom Paris)

11 Dissemination

11.1 Promoting scientific activities

11.1.1 Scientific events: organisation

General chair, scientific chair

- J.-C. Pesquet. Technical Chair of the IEEE International Conference on Image Processing (ICIP) in Bordeaux, France, 2022.
- E. Chouzenoux. Tutorial Chair of the 30th European Signal Processing Conference, EUSIPCO 2022, in Belgrade, Serbia, 2022.

Member of the organizing committees

- F. Malliaros. Member of the organizing committee of the 33rd European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML PKDD), Grenoble, France, 2022.
- F. Malliaros. Organizer of the Summer School in Artificial Intelligence, CentraleSupélec.
- H. Talbot. Member of the organizing committee for ICCV 2023 in Paris.
- E. Chouzenoux. Co-organising a mini-symposium at SIAM Conference on Data Science, San Diego, CA, 2022.
- E. Chouzenoux. Co-organising a special session at IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP 2023), Rhodes, Greece, 2023.
- E. Chouzenoux. Member of the organizing committee for the 5-Minute Video Clip Contest at IEEE International Conference on Acoustics, Speech, and Signal Processing (ICASSP 2022) (online).
- Y. Belkouchi. Member of the organizing committee of the JFR Data Challenge, Paris, 9-10 Oct. 2022.
- M. Vakalopoulou. Co-organization of the the Machine Learning for Medical Imaging workshop at ACML conference 2022.
- M. Vakalopoulou. Co-organising the CVPR Demo 2022 session, CVPR 2022 in New Orleans, USA.

11.1.2 Scientific events: selection

Chair of conference program committees

- E. Malliaros. Area chair at the European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML PKDD), 2021, 2022.
- N. Ouzir. Students activities co-chair, European Signal Processing Conference (EUSIPCO 2023), Helsinki, Finland.
- H. Talbot. Program Committee (PC) member on the Discrete Geometry and Mathematical Morphology conference 2022.
- M. Vakalopoulou. Area Chair at Computer Vision and Pattern Recognition (CVPR) 2022 and Medical Image Computing and Computer Assisted Intervention - MICCAI 2022.

Member of the conference program committees

- E. Chouzenoux. Technical program co-chair at MLSP conference 2024, London, UK.

Reviewer 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), 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), Learning on Graphs Conference (LoG).

11.1.3 Journal

Member of the editorial boards

- Emilie Chouzenoux: Associate Editor at IEEE Transactions on Signal Processing
- Emilie Chouzenoux: Associate Editor of the SIAM Journal on Mathematics of Data Sciences
- Emilie Chouzenoux: Associate Editor of the SIAM Journal on Imaging Sciences
- Jean-Christophe Pesquet: Associate Editor of the SIAM Journal on Imaging Sciences
- Hugues Talbot: Editor in Chief, Mathematical Morphology, Theory and Applications (De Gruyter)
- Hugues Talbot: Review Editor for Frontiers in Computer Vision, Nature group.
- Maria Vakalopoulou: Editor at Computer Vision and Image Understanding (CVIU) Journal.

Reviewer - reviewing activities

- E. Chouzenoux: Journal of Optimization Theory and Applications, Journal of Mathematical Imaging and Vision.
- H. Talbot: Computer Methods and Programs in Biomedicine, Pattern Recognition Letters, Computer Vision and Image Understanding.
- T. Silveti-Falls: Journal of Scientific Computing, SIAM Journal on Mathematics of Data Science, SIAM Journal on Optimization.
- J.-B. Frest. IEEE Transactions on Signal Processing.
- A. Contreras. IEEE Transactions on Signal Processing.
- F. Malliaros: IEEE Transactions on Knowledge and Data Engineering (TKDE), ACM Transactions on Knowledge Discovery from Data (TKDD), Transactions on Machine Learning Research (TMLR).

11.1.4 Invited talks

- E. Chouzenoux. Keynote talk, AI4FA Workshop, Bilbao, Spain, 7 Apr. 2022.
- E. Chouzenoux. Seminar, Café de la fédération de mathématiques, CentraleSupélec, 13 Sep. 2022.
- E. Chouzenoux. Invited talk, HUST-UPSaclay Joint Workshop on "Math for Data Science", 23 Sep. 2022 (online).
- E. Chouzenoux. Invited talk, SIAM Conference on Mathematics of Data Science (MDS22), 26 Sep. 2022 (online).
- E. Chouzenoux. Invited talk, International Conference on Machine Learning and Intelligent Science (MLIS 2022) Workshop, 10 Nov. 2022 (online).
- E. Chouzenoux. Keynote talk, Advanced Techniques in Optimization for Machine learning and Imaging (ATOMI) Workshop, Roma, 21 June 2022.
- Y. Huang. Seminar, CVN, CentraleSupélec, 28 Jan. 2022.
- Y. Huang. Seminar, CRISTAL lab, Lille, 21st Feb. 2022.
- Y. Belkouchi. Oral presentation, Clinical Trials Methodology (RSNA 2022) Workshop, Chicago, USA, 27 Nov. 2022.
- T. Aouad. Oral presentation, Journées de Géométrie Discrète et Morphologie Mathématique (GDMM 2022), Bordeaux, 22 Nov. 2022.
- T. Guilmeau. Oral presentation, PGMODays 2022, EDF Lab Paris-Saclay, Palaiseau, 29 Nov. 2022.
- F. Malliaros. Invited talk, HEALTH and THERAPEUTIC INNOVATION (HEALTHI) consortium, Univ. Paris-Saclay, 18 March 2022 (online).
- F. Malliaros. Invited talk, Sapienza University of Rome, 4 May 2022.
- F. Malliaros. Invited talk, Graph Representation Learning summer school, Technical University of Denmark, 22 Aug. 2022.
- J.-C. Pesquet. Invited talk, EURASIP Journal on Image and Video Processing Webinar, 5 May 2022 (online).
- J.-C. Pesquet. Introductory talk, Advanced Techniques in Optimization for Machine learning and Imaging (ATOMI) Workshop, Roma, 20 June 2022.
- J.-C. Pesquet. EURASIP Fellow plenary talk, EUSIPCO, Belgrade, 30 Aug. 2022.

- G. Scrivanti. Invited talk, 10th International Conference Inverse Problems: Modelling and Simulation (IPMS 2022), 22-28 May 2022, Malta.
- G. Scrivanti. Invited talk, SIAM Conference on Imaging Science (IS22), 21-25 March 2022, Berlin, Germany (online).
- G. Scrivanti. Invited talk, workshop on Modern Techniques of Very Large Scale Optimisation, University of Edinburgh, UK, May 19-20 2022.
- H. Talbot. Invited talk, Biomarkers in Oncology, Kremlin-Bicetre hospital, Jan. 2022.
- H. Talbot. Invited talk, Vascular Imaging, Université Paris-Est Créteil, Feb. 2022.
- H. Talbot. Invited talk, Artificial Intelligence in medicine: Gustave-roussey hospital, Dec. 2022.
- S. Martin. Invited talk, 10th International Conference Inverse Problems: Modelling and Simulation (IPMS 2022), 22-28 May 2022, Malta.
- S. Martin. Oral presentation, Advanced Techniques in Optimization for Machine learning and Imaging (ATOMI) Workshop, 20 June 2022, Roma, Italy.
- S. Martin. Invited talk, SIAM Conference on Imaging Science (IS22), 21-25 March 2022, Berlin, Germany (online).
- M. Gharbi. Invited talk, International conference on optimization and decision science (ODS2022), 30 Aug. 2022, Florence, Italy.
- T. Silveti-Falls. Oral presentation, Curves and Surfaces, 20th June 20th 2022, Arcachon, France.
- T. Silveti-Falls. Invited talk, Inauguration de la Fédération de Mathématiques, CentraleSupélec, 4th Nov. 4th 2022.
- T. Silveti-Falls. Seminar, Mathematical Optimization Group, 8th. Sep. 2022, Tübingen, Germany.
- T. Silveti-Falls. Seminar, GREYC Lab, 1st Dec. 2022, Caen, France.
- J.-B. Fest. Invited talk, SIAM Conference on Imaging Science (IS22), 21-25 March 2022, Berlin, Germany (online).
- J.-B. Fest. Oral presentation, Advanced Techniques in Optimization for Machine learning and Imaging (ATOMI) Workshop, 20 June 2022, Roma, Italy.
- J.-B. Fest. Seminar, MINDS Group Meeting, 9th Sep. 2022, Heriot-Watt University Edimbourg, UK.
- A. Contreras. Invited talk, 15th Viennese Conference on Optimal Control and Dynamic Games (ORCOS22), 11th-15th July, Vienna, Austria.
- A. Duval. Seminar, CRUNCH group of Brown University, 6th Jan. 2022, Brown, USA .
- A. Duval. Seminar, Gauthier Gidel group at MILA, 23 June 2022, Montreal, Canada.
- A. Duval. Keynote talk, 31st ACM International Conference on Information and Knowledge Management (CIKM), 20 Oct. 2022, Baltimore, USA.
- M. Vakalopoulou. Invited talk, Journées d'Onco-Urologie Médicale (JOURM), 17 June 2022, Toulouse, France.
- M. Vakalopoulou. Keynote talk, Workshop on Biomedical Image Registration (WBIR), 12 July 2022, Munich, Germany.
- M. Vakalopoulou. Invited talk, Summer School Archimedes, 26 July 2022, Athens, Greece.
- M. Vakalopoulou. Webinar, SystemX, 13 Oct. 2022 (online).

- M. Vakalopoulou. Invited talk, 3rd Athenian Oncology Congress, 22 Oct. 2022, Athens, Greece.
- M. Vakalopoulou. Invited talk, Conference of Head and Neck Cancer, 17 Dec. 2022, Athens, Greece.
- M. Vakalopoulou. Invited talk, 2nd edition of the annual UDOPIA PhD students' day DATAIA institute of the University of Paris-Saclay, 5Dec. 2022, Saclay, France.

11.1.5 Leadership within the scientific community

J.-C. Pesquet was senior member of the Institut Universitaire de France.

J.-C. Pesquet is a Fellow of the IEEE.

E. Chouzenoux is a senior member of the IEEE.

11.1.6 Scientific expertise

The members of the team participated to numerous PhD Thesis Committees, HDR Committees, recruiting Committees, and served as Grant Reviewers.

- E. Chouzenoux is member of the scientific committee of Inria Saclay.
- M. Vakalopoulou served as a panel member for ANR in 2022.
- M. Vakalopoulou served as a monitor-expert for EU research grants.

11.1.7 Research administration

- J.-C. Pesquet is the head of the laboratoire Centre pour la Vision Numérique (CVN), CentraleSupélec.
- M. Vakalopoulou is the group leader of the β iomathematics teams of the MICS CentraleSupélec.
- N. Ouzir is an elected member of the consultative commission of Paris-Saclay University.
- M. Gharbi is the student representative in the TraDE-OPT ITN network.
- A. Duval is "Expert" at AI for tomorrow, a non-profit association aiming to promote beneficial uses of AI.

11.1.8 Teaching administration

- E. Chouzenoux: attached professor in AI in CentraleSupélec, since sep. 2022.
- F. Malliaros: co-director of the DSBA M.Sc.
- F. Malliaros: head for the Data and Information Science (SDI) specialization at CentraleSupélec.
- H. Talbot: local head of the MVA M.Sc. at CentraleSupélec.
- N. Ouzir: co-responsible of the AIDAMS Bachelor with ESSEC (Artificial Intelligence, Data and Management Sciences), at CentraleSupélec.
- J.-C. Pesquet: local head for the Optimization M.Sc. at CentraleSupélec.
- J.-C. Pesquet: head for the main Optimization course in 2nd year of CentraleSupélec (600 students).

11.2 Teaching - Supervision - Juries

11.2.1 Teaching

Several permanent members of OPIS were lecturers of the following courses.

- Master: E. Chouzenoux. Foundations of Distributed and Large Scale Computing, 26h, 3rd year CentraleSupélec and M.Sc. MVA Paris Saclay.
- Master: E. Chouzenoux. Advanced Machine Learning, 18h, 3rd year CentraleSupélec.
- Master: F. Malliaros. Foundations of Machine Learning, 27h, Master in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School.
- Master: F. Malliaros. Machine Learning in Network Science, 27h, 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: N. Ouzir. Machine Learning, 33h, 2nd year CentraleSupélec.
- Master: N. Ouzir. Advanced Machine Learning, 24h, M.Sc. in Data Sciences and Business Analytics.
- Master: N. Ouzir. Processing of Medical Image Sequences with Applications in Ultrasound Imaging, 3h, AI and Global Health program, European University Alliance for Global Health (EUGLOH).
- Master: J.-C. Pesquet. Introductory course on Optimization, 33h, 2nd year CentraleSupélec.
- Master: J.-C. Pesquet. Advanced course on Optimization, 10h, M.Sc. in Signal Processing and Automatic Control, Univ. Paris- Saclay.
- Master: J.-C. Pesquet. Introduction to Optimization, 6h, M.Sc. MVA, ENS Paris-Saclay.
- Master: J.-C. Pesquet. Convex Optimization Algorithms, 15h, M.Sc. in Optimization, Univ. Paris-Saclay.
- Master: H. Talbot. High-performance computing, 2nd year CentraleSupélec, 12h.
- Master: H. Talbot. Parallel computing, 2nd year CentraleSupélec, 20h.
- Master: H. Talbot. Optimization for AI, M.Sc in AI, CentraleSupélec and ESSEC Business School, 30h.
- Master: H. Talbot. Introduction to Machine Learning, MS Management of Technology, 30h.
- Master: H. Talbot. Introduction à la morphologie mathématique, 3rd year CentraleSupélec, 12h.
- Master: M. Vakalopoulou. Introduction to Visual Computing, 25h, 3rd year CentraleSupélec.
- Master: M. Vakalopoulou. Deep Learning, 25h, M.Sc. in Vision and Machine Learning, ENS Paris-Saclay.
- Master: M. Vakalopoulou. Introduction to Machine Learning, 33h, 2nd year CentraleSupélec.
- Master: M. Vakalopoulou. Introduction to Deep Learning, 24h, M.Sc. in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School and M.Sc. in Artificial Intelligence.
- Master: M. Vakalopoulou. Deep Learning in Medical Imaging, 25h, M.Sc. in Vision and Machine Learning, ENS Paris-Saclay.
- Master: M. Vakalopoulou. Deep Learning, 25h, M.Sc. in Vision and Machine Learning, ENS Paris-Saclay.
- Master: T. Silveti-Falls. Optimization for Big Data, 12h, Toulouse School of Economics.

- Bachelor: T. Silveti-Falls. Convergence, Integration, and Probability, 18h, 1st year CentraleSupélec.
- Bachelor: T. Silveti-Falls. Partial Differential Equations, 15h, 1st year CentraleSupélec.

Several students members of OPIS have teaching assistant activities, that we list herebelow.

- Master: A. Contreras. Optimization and Proximal Methods, 21h, 2nd year ENSTA, lecturer.
- Bachelor: Y. Belkouchi. Introduction to SQL, 48h, 1st year IUT Paris Saclay, lab instructor.
- Bachelor: Y. Belkouchi. Introduction to Computer Hardware, 16h, 1st year IUT Paris Saclay, lab instructor.
- Master: Y. Belkouchi. Project Innovation, 16h, 2nd year CentraleSupélec, project monitor.
- Master: T. Aouad. Machine Learning, 2nd year CentraleSupélec, 15h, lab instructor.
- Master: T. Aouad. Optimization, 2nd year CentraleSupélec, 10.5h, lab instructor.
- Master: T. Aouad. AI for Computer Vision, Master IA ESIB, Université Saint Joseph, Beyrouth, 15h, lecturer.
- Master: T. Guilmeau. Optimization, 2nd year CentraleSupélec, 10.5h, lab instructor.
- Master: M. Gharbi. Optimization, 2nd year CentraleSupélec, 10.5h, lab instructor.
- Master: R. El Hamdani, Machine Learning in Network Science, 7.5h, 3rd year CentraleSupélec, M.Sc. DSBA, lab instructor
- Master: A. Duval, Machine Learning in Network Science, 1.5h, 3rd year CentraleSupélec, M.Sc. DSBA, lab instructeur.
- Master: Y. Huang. Optimization, 2nd year CentraleSupélec, 10.5h, lab instructor.
- Bachelor: S. Martin. Informatics, 16h, 1st year BUT of physical measurements, Orsay, lecturer.
- Master: S. Martin. Catch-up course in optimization, 5h, 2nd year of master MVA, Univ. Paris Saclay, lecturer.
- Master: J.-B. Fest. Foundations of Distributed and Large Scale Computing, 12h, 3rd year Centrale-Supélec and M.Sc. MVA Paris Saclay, lab instructor.
- Bachelor: J.-B. Fest. Optimisation Quadratique, 16h, 1st year ENSTA ParisTech, lab instructor.

11.2.2 Supervision

- PhD (completed): Mario Viti. Low-dose assessment of coronal vessel health on CT. 2019-2022, supervised by H. Talbot.
- PhD (completed) : Yingping Li, Deep learning for medical imaging, 2018-2022, supervised by E. Chouzenoux and N. Lassau (Institut Gustave Roussy)
- PhD (completed): Yunshi Huang, Majorization-Minimization approaches for large scale problems in image processing, 2018-2022, supervised by E. Chouzenoux and V. Elvira (Univ. Edinburgh).
- PhD (completed): Marion Savanier, Reconstruction 3D interventionnelle, 2019-2022, supervised by E. Chouzenoux and C. Riddell (GE Healthcare).
- PhD (completed): Matthieu Terris, Learning priors for scalable robust and precise image reconstruction algorithms, 2018-2022, supervised by Y. Wiaux (Univ. Heriot-Watt) and J.-C. Pesquet.
- PhD (completed): Georgios Panagopoulos, Influence maximization in social networks, 2018-2022, supervised by F. Malliaros and M. Vazirgiannis (École Polytechnique).

- PhD (completed): Marvin Lerousseau. Apprentissage statistique en imagerie médicale et en génomique pour prédire l'efficacité des thérapies anti-tumorales, 2018-2022, supervised by N. Paragios (Therapanacea), E. Deutsch (IGR) and H. Talbot.
- PhD (in progress): Jean-Baptiste Fest, Stochastic Majorization-Minimization algorithms, 2020-2023, supervised by E. Chouzenoux.
- PhD (in progress): Gabriele Scrivanti, New algorithms for large scale problems exploiting geometric problem structure and convex relaxation, 2020-2023, supervised by J.-C. Pesquet and E. Bednarczuk (Polish Academy of Sciences, Warsaw).
- PhD (in progress): Segolène Martin, Majorization-Minimization methods for constrained optimization, 2020-2023, supervised by J.-C. Pesquet and I. Ben Ayed (ETS Montréal, Canada).
- PhD (in progress): Marie-Charlotte Poilpre: Méthode de comparaison faciale morphologique, adaptée aux expertise judiciaires, basée sur la modélisation 3D, 2017-2022, supervised by H. Talbot and V. Nozick (Univ. Paris-Est).
- PhD (in progress): Théodore Aouad. Geometric semi-supervised machine-learning methods in medical imaging, 2020-2023, supervised by H. Talbot.
- PhD (in progress): Younes Belkouchi. Graph neural network generative methods in oncology, 2020-2023, supervised by N. Lassau (IGR), F. Malliaros, and H. Talbot.
- PhD (in progress): Thomas Guilmeau, Algorithmes stochastiques pour l'optimisation non convexe, 2021-2024, supervised by E. Chouzenoux and V. Elvira (Univ. Edinburgh).
- PhD (in progress): Mouna Gharbi, Unfolded Majorization-Minimization algorithms, 2020-2023, supervised by E. Chouzenoux and L. Duval (IFPEN).
- PhD (in progress): Mathieu Vu, Algorithmes d'assemblage pour l'apprentissage en imagerie médicale, 2021-2024, supervised by E. Chouzenoux and P. Pinault (ESSILOR).
- PhD (in progress): Alexandre Duval. Algorithmes d'apprentissage automatique sur des graphes: explicabilité, évolutivité et applications, 2020-2023, supervised by F. Malliaros and H. Talbot.
- PhD (in progress): Loïc Le Bescond. Precision medicine, Histology and Deep learning, 2021-2024, supervised by F. André (IGR) and H. Talbot.
- PhD (in progress): Ana Neacsu, Méthodes d'apprentissage profond inspirées d'algorithmes de traitement du signal, 2019-2022, supervised by J.-C. Pesquet and C. Burileanu (Politehnica Bucurest).
- PhD (in progress): Sagar Verma, Modélisation, contrôle et supervision de moteurs électriques par réseaux de neurones profonds, 2019-2022, supervised by M. Castella and J.-C. Pesquet.
- PhD (in progress): Rajaa El Hamdani, Robust graph representation learning and applications in misinformation detection, 2021-2024, supervised by F. Malliaros and T. Bonald (Télécom-Paris).
- PhD (in progress): Surabhi Jagtap, Graph-based learning from multi-omics data, 2019-2023, supervised by F. Malliaros, J.-C. Pesquet, and L. Duval (IFP Energies Nouvelles).
- PhD (in progress): Kavya Gupta, Neural network solutions for safety of complex systems, 2019-2022, supervised by J.-C. Pesquet, F. Malliaros, and F. Kaakai (Thales Group).
- PhD (in progress): Maria Papadomanolaki, Change Detection from Multitemporal High Resolution Data with Deep Learning, 2017-2022, supervised by M. Vakalopoulou and K. Karantzas (National Technical University of Athens).
- PhD (in progress): Leo Milescki, Domain adaptation and self supervised methods for kidney transplantation, 2019-2022, supervised by M. Vakalopoulou and M.O. Timsit (Hôpital Européen Georges-Pompidou).

- PhD (in progress): Othmane Laousy, Graph-based artificial intelligence methods for medical image diagnosis, 2019-2022, supervised by M. Vakalopoulou and M.-P. Revel (AP-HP Hospital Cochin).
- PhD (in progress): Clément Cosserat, Algorithmes de majoration-minimisation pour le traitement du signal statistique, 2022-2025, supervised by E. Chouzenoux and T. Adali (Univ. Baltimore, USA).
- PhD (in progress): Yassine Abbahaddou, Graph Machine Learning and Applications, 2022-2025, supervised by F. Malliaros and M. Vazirgiannis (École Polytechnique).
- PhD (in progress): Raoul Sallé De Chou, Prédiction de cartes de perfusion du cœur par apprentissage automatique, 2022-2025, supervised by I. Vignon-Clémentel (Inria) and H. Talbot.
- PhD (in progress): Jinqwei Zhang, Deep Learning methods on Digital Pathology, 2020-2023, supervised by M. Vakalopoulou and D. Samaras (Stony Brook University).

11.2.3 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, FR.

11.3 Popularization

11.3.1 Internal or external Inria responsibilities

Thomas Guilmeau performs a “mission de médiation scientifique” at Inria Saclay, during his PhD thesis.

11.3.2 Interventions

- T. Guilmeau. Coaching session at Rendez-vous des Jeunes Mathématiciennes et Informaticiennes, 21-22 Oct. 2022, Saclay.
- T. Guilmeau. Vulgarisation talks in several high schools of Créteil academy, France, during Semaine des Mathématiques, 7-14 March 2022.
- T. Guilmeau. Animation during Fête de la Science 2022, Saclay, 7-17 Oct. 2022.
- T. Guilmeau. Organization of filmed interviews of OPIS members (Y. Belkouchi, E. Chouzenoux, G. Scrivanti, Y. Huang), by students of BUT MMI Vélizy, CVN, Saclay, 12 Oct. 2022.

12 Scientific production

12.1 Publications of the year

International journals

- [1] F. Abboud, M. Stamm, E. Chouzenoux, J.-C. Pesquet and H. Talbot. ‘Distributed Algorithms for Scalable Proximity Operator Computation and Application to Video Denoising’. In: *Digital Signal Processing* 128 (Aug. 2022), p. 103610. DOI: [10.1016/j.dsp.2022.103610](https://doi.org/10.1016/j.dsp.2022.103610). URL: <https://hal.science/hal-03684063>.
- [2] A. Achim, L. Calatroni, S. Morigi and G. Scrivanti. ‘Space-Variant Image Reconstruction via Cauchy Regularisation: Application to Optical Coherence Tomography’. In: *Signal Processing* 205 (1st Apr. 2023). DOI: [10.1016/j.sigpro.2022.108866](https://doi.org/10.1016/j.sigpro.2022.108866). URL: <https://hal.science/hal-03594202>.
- [3] Y. Belkouchi, H. Talbot, N. Lassau, L. Lawrance, S. Farhane, R. Feki-Mkaouar, J. Vibert, P.-H. P.-H. Cournède, A. Marabelle, S. Ammari and S. Champiat. ‘Better than RECIST and faster than iRECIST: Defining the immunotherapy progression decision score to better manage progressive tumors on immunotherapy’. In: *Annals of Oncology* 33 (Sept. 2022), S595–S596. DOI: [10.1016/j.annonc.2022.07.159](https://doi.org/10.1016/j.annonc.2022.07.159). URL: <https://hal.science/hal-03940635>.

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International peer-reviewed conferences

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