RESEARCH CENTRE

**Saclay - Île-de-France**

**IN PARTNERSHIP WITH:**

**CentraleSupélec**

2021

ACTIVITY REPORT

Project-Team

# OPIS

## OPtImization for large Scale biomedical data

**DOMAIN**

**Digital Health, Biology and Earth**

**THEME**

**Computational Neuroscience and Medicine**

# Contents

# Project-Team OPIS

*Creation of the Project-Team: 2019 May 01*

## 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

# 1 Team members, visitors, external collaborators

## Research Scientist

- Emilie Chouzenoux [Inria, Researcher, HDR]

## Faculty Members

- Jean-Christophe Pesquet [Team leader, CentraleSupélec, Professor, HDR]
- Fragkiskos Malliaros [CentraleSupélec, Associate Professor]
- Nora Ouzir [CentraleSupélec, Associate Professor]
- Hugues Talbot [CentraleSupélec, Professor, HDR]
- Maria Vakalopoulou [CentraleSupélec, Associate Professor]

## Post-Doctoral Fellow

- Andres Antonio Contreras Tavarez [Inria]

## PhD Students

- Samy Ammari [Université Paris-Saclay]
- Theodore Aouad [CentraleSupélec]
- Enzo Battistella [CentraleSupélec, until Aug 2021]
- Younes Belkouchi [CentraleSupélec]
- Abdulkadir Celikkanat [CentraleSupélec, until Feb 2021]
- Tassnim Dardouri [Université Paris-Nord]
- Alexandre Duval [CentraleSupélec, from Mar 2021]
- Theo Estienne [CentraleSupélec, until Apr 2021]
- Jean Baptiste Fest [Inria]
- Mouna Gharbi [CentraleSupélec]
- Thomas Guilmeau [Inria]
- Kavya Gupta [Thalès, CIFRE]
- Yunshi Huang [Université Paris Est Marne-la-Vallée]
- Surabhi Jagtap [IFPEN]
- Othmane Laousy [CentraleSupélec]
- Marvin Lerousseau [CentraleSupélec, until Sep 2021]
- Segolene Martin [CentraleSupélec]
- Leo Milecki [CentraleSupélec]
- Ana Neacsu [CentraleSupélec]
- Marion Savanier [GE Healthcare, CIFRE]

- Gabriele Scrivanti [CentraleSupélec]
- Matthieu Terris [Université Heriot-Watt Edimbourg - Ecosse, until Jun 2022]
- Sagar Verma [Schneider Electrics, CIFRE]
- Mario Viti [CentraleSupélec, CIFRE]
- Mathieu Vu [Inria, from Feb 2021]

## Technical Staff

- Alexandre Duval [CentraleSupélec, Engineer, until Feb 2021]
- Stuti Jain [Inria, Engineer, from Nov 2021]
- Benjamin Maheu [Inria, Engineer, from Feb 2021 to Oct 2021]
- Arnaud Quillent [Inria, Engineer, from Feb 2021 to Jan 2022]
- Claire Rossignol [Inria, Engineer, from Mar 2021]
- Mathieu Vu [Inria, Engineer, Jan 2021]

## Interns and Apprentices

- Victor Bennini [CentraleSupélec, Intern, until Mar 2021]
- David Boudin [CentraleSupélec, Intern, From Apr 2021 to Sep 2021]
- Pierre Antoine Comby [CentraleSupélec, Intern, from Apr 2021 until Aug 2021]
- Clara Donnart [Inria, Intern, from May 2021 until Aug 2021]
- Sidi Mohamed El Kharchi [CentraleSupélec, Intern, until Apr 2021]
- Emmanuel Kahanam [CentraleSupélec, Intern, From Jun 2021 to Sep 2021]
- Garance Martin [CentraleSupélec, Intern, From May 2021 to Oct 2021]
- Aymen Sadraoui [CentraleSupélec, Intern, from Feb 2021 until Aug 2021]
- Marin Stamm [CentraleSupélec, Intern, From May 2021 to Aug 2021]
- Yannick Sun [Inria, Intern, from May 2021 until Oct 2021]
- Vlad Vasilescu [CentraleSupélec, Intern, From Jul 2021 to Sep 2021]

## Administrative Assistants

- Jana Dutrey [CentraleSupélec]
- Irina Lahaye [Inria]

## Visiting Scientists

- Tulay Adali [University of Maryland, Baltimore County, from Oct 2021]
- Ismail Ben Ayed [ETS Montréal, From Oct 2021 to Sep 2022]

## 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 medecine 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 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** will be major outcomes of this research project. We will 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 will be grounded on nonsmooth functional analysis, fixed point theory, parallel/distributed strategies, and neural networks. The new optimization tools that will be developed will be 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 will be explored, namely:

1. proposing novel algorithms able to encompass high-dimensional continuous optimization problems, with established convergence guarantees, and that are well-suited to parallel implementation;

2. designing efficient optimization approaches for the resolution of graph signal processing and graph mining problems;

3. developing a new generation of deep learning strategies, characterized by robustness guarantees, fast training and suitable account for prior information.

Our research program is detailed in the next subsections. We also indicate applications in the medical and biomedical areas on which our program is expected to have a significant impact.

# 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 fufill some physical constraints. In such a challenging context, there is a strong need for developing fast parallelized optimization agorithms 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 [2]. 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 aim in [3, 1] 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.

In our work [71], in collaboration with University of Bucharest, we introduce an automatic lesion segmentation tool, MASC-Net, based on a novel neural network architecture that automatically detects COVID-19 related infected lung regions from chest CT scans. The proposed architecture consists of a multi-input encoder-decoder that aggregates high-level features extracted with variable-size receptive fields.

Our works [29, 30], in collaboration with IIIT Delhi, build 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 Neacsu, 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 [34]. 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 [44, 60].

### 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 recruted with PRISM funding and has started working on automated analyses of breast cancer biopsies. Publishable results are expected in 2022.

## 4.4 Sparse inverse problems

### 4.4.1 Sparse signal processing in chemistry

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

Mass Spectrometry (MS) is a powerful tool used for robust, accurate, and sensitive detection and quantification of molecules of interest. Thanks to its sensibility and selectivity, MS is widely used in proteomics such anti-doping, metabolomics, medicine or structural biology. In particular, it has applications in clinical research, personalized medicine, diagnosis process and tumours profiling and pharmaceutical quality control. In an MS experiment, the raw signal arising from the molecule ionization in an ion beam is measured as a function of time via Fourier Transform-based measures such as Ion Cyclotron Resonance (FT-ICR) and Orbitrap. A spectral analysis step is then performed to improve the quality of data. The goal is then to determine from this observed pattern distribution the most probable chemical composition of the sample, through the determination of the monoisotopic mass, charge state and abundance of each present molecule. We develop new methodological tools combining recent advances in optimization and artificial intelligence to solve large scale signal estimation problem under specific sparsity constraints, with fast processing on GPU [50]. 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 [23, 21].

### 4.4.3 Reconstruction approaches in medical imaging

**Participants:** Emilie Chouzenoux, Jean-Christophe Pesquet, Marion Savanier, Maissa Sghaier (Collaboration: S. Muller, C. Riddel, Y. Trousset, 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 [38] 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 [37], so that the adjoint property is no longer fulfilled. In the works [68, 14], we investigate the proximal gradient algorithm stability properties when such an adjoint mismatch arises.

## 4.5 Graph mining applications

**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 [56].

## 4.6 Other biomedical applications

### 4.6.1 Imaging biomarkers and characterization for chronic lung diseases

**Participants**: Guillaume Chassagnon, Maria Vakalopoulou (Collaboration: Marie-Pierre Revel, AP-HP - Hopital Cochin Broca Hotel Dieu ; Nikos Paragios, Therapanacea)

Diagnosis and staging of chronic 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 parenchyma currently offering the highest spatial resolution in chronic 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 develop quantitative imaging biomarkers that allow (i)severity assessment (based on the correlation to functional and clinical data) and (ii) monitoring the disease progression. In the current analysis we focus on scleroderma and cystic fibrosis as models for restrictive and obstructive lung disease, respectively. Two different approaches are investigated: disease assessment by deep convolutional neural networks and assessment of the regional lung elasticity through deformable registration. This work is in collaboration with the Department of Radiology, Cochin Hospital, Paris.

#### 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.

This work was published in [33].

# 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, ...). In addition, OPIS has active collaborations with several hospitals, particularly Institut Gustave Roussy and 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, microscopy images,...) OPIS is also currently involved in several projects for helping to better diagnose and cure COVID-19 infection.

# 6 Highlights of the year

2021 has been a fruitful year, but still strongly impacted by the covid outbreak. OPIS has contributed to the fight against this plague by publishing two highly cited studies in medical journals [1, 3], resulting from collaborations with several teams of medical doctors in Paris hospitals. In the meantime, research efforts have still continued towards more traditional topics in precision medicine. In parallel, the COMPASS Inria associate team has been created with purpose to bring AI in the arena of pharmacology. This project also allows us to strengthen a solid existing collaboration with IIIT Dehli. It is also worth emphasizing the recent successes of Maria Vakalopoulou and Fragkiskos Malliaros in their two applications to ANR young researcher grants.

## 6.1 Awards

### 6.1.1 Publication awards

- Marvin Lerousseau and Maria Vakalopoulou received the best paper award on the COMPAY workshop of MICCAI 2021 [61].
- Maria Vakalopoulou received the best paper award on the CVMI workshop of CVPR 2021 [74].
- Maria Vakalopoulou received the second best paper award on the CDPath workshop of ICCV 2021 [44].
- The article [52] was shortlisted as a finalist of the best paper award at the *AISafety* workshop collocated with IJCAI 2021.

### 6.1.2 Other awards

- Théo Estienne received *the second price of the Foundation CentraleSupélec in the category impact innovation* for his PhD thesis.
- Fragkiskos Malliaros received an *outstanding reviewer award* from the Conference on Neural Information Processing Systems (NeurIPS), 2021.
- Our Master program in Data Sciences and Business Analytics (with ESSEC Business School) was ranked $4^{th}$ worldwide in the *QS World University Rankings*.

# 7 New software and platforms

## 7.1 New platforms

### 7.1.1 The Proximity Operator Repository

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with Giovanni Chierchia, Univ. Paris Est, and Patrick Combettes, North Carolina State University).
**link:** Proximity Repository
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.

### 7.1.2 Computational tools for multiphotonic microscopy

**Participants:** Emilie Chouzenoux, Claire Lefort (XLIM), and Jean-Christophe Pesquet
**links:** FIGARO ; BD3MG

- The plugin **FIGARO**, for ImageJ software, helps tracking resolution of microscope systems by extracting dimensions and orientation of standardized microbeads images, acquired from test samples. In the development of optical microscopes for biomedical imaging, the evaluation of resolution is a fundamental parameter achieved by Point Spread Function (PSF) measurements. Sometimes, PSF measurement procedure is not easy or impossible in case of microspheres images presenting a high noise level. The current method proposed into the plugin FIGARO is based on a variational approach for PSF modeling through multivariate Gaussian fitting, adapted to images acquired in a high noise context.

- **BD3MG** (block distributed Majorize-Minorize Memory Gradient) implements an optimization algorithm for solving large scale non-convex differentiable optimization problems. Assuming a distributed memory environment, the algorithm casts the efficient 3MG scheme into smaller dimension subproblems where blocks of variables are addressed in an asynchronous manner. The code, in Python, is dedicated to an application to the restoration of 3D images degraded by a depth-variant blur.

Both FIGARO and BD3MG serve as key computational tools for deploying the pipeline FAMOUS for in-vivo muscle imaging with multiphotonic microscopy [23].

### 7.1.3 BiasedWalk: Learning latent node features with biased random walks

**Participants:** Fragkiskos Malliaros and Duong Nguyen (UC San Diego)
**link:** BiasedWalk
The BiasedWalk network representation learning algorithm, computes latent node features on graphs based on biased random walks. The framework has been implemented in Python and has been built upon widely used modules, including `networkx`, `numpy`, `gensim` and `scikit-learn`.

### 7.1.4 DiffuGreedy: Influence maximization in complex networks based on diffusion cascades

**Participants:** Fragkiskos Malliaros, Georgios Panagopoulos and Michalis Vazirgiannis (École Polytechnique)
**link:** DiffuGreedy
The DiffuGreedy is an algorithm for influence maximization in complex networks, that is based on diffusion cascades. It has been implemented in Python and has been built upon widely used modules, including `networkx`, `igraph`, `numpy` and `pandas`.

### 7.1.5 Graph-based text categorization

**Participants:** Fragkiskos Malliaros, Konstantinos Skianis and Michalis Vazirgiannis (École Polytechnique)
**link:** GraphBasedTC
Graph-based TC is a framework for text categorization that relies on a graph representation of documents. The framework uses various graph centrality criteria to determine the importance of a term within a document. It also makes use of word embeddings to further boost the performance of graph-based methods. It has been implemented in Python and has been built upon widely used modules, including `networkx`, `igraph`, `numpy` and `scikit-learn`.

### 7.1.6 KernelNE - Topical Node Embeddings

**Participants:** Abdulkadir Çelikkanat, Fragkiskos Malliaros
**link:** KernelNE
KernelNE learns node representations on graphs based on a weighted matrix factorization model which encodes random walk-based information about the nodes.

### 7.1.7 EFGE - Exponential Family Graph Embeddings

**Participants:** Abdulkadir Çelikkanat, Fragkiskos Malliaros
**link:** EFGE
EFGE learns node embeddings generalizing random walk-based network representation learning techniques to exponential family conditional distributions.

### 7.1.8 Semi-supervised Fake News Detection

**Participants:** Adrien Benamira, Benjamin Devillers, Etienne Lesot, Ayush K. Ray, Manal Saadi, and Fragkiskos Malliaros
**link:** FakeNews
We propose a graph-based semi-supervised fake news detection method, based on graph neural networks.

### 7.1.9 Graph-based models for multiomics data integration

**Participants:** Surabhi Jagtap, Abdulkadir Çelikkanat, Fragkiskos Malliaros, Aurélie Pirayre (IFPEN), Frederique Bidard (IFPEN), and Laurent Duval (IFPEN)
**links:** Brane-Exp ; BRANet

- **Brane-Exp** is a network fusion model that learns embeddings of biological entities with exponential family distributions. The model has primarily been used as a multiomics data integration tool for gene regulatory network inference [55].
- **BraNet** integrates heterogeneous biological networks for miRNA-mRNA regulatory network inference. Methodologically, it performs matrix factorization on a multilayer network represented by a random walk proximity matrix [56].

### 7.1.10 GraphSVX: Shapley Value Explanations for Graph Neural Networks

**Participants:** Alexandre Duval and Fragkiskos Malliaros
**link:** GraphSVX
GraphSVX is a model-agnostic explanation method for Graph Neural Networks. It is a decomposition technique that captures the contribution of each feature and node towards the explained prediction by constructing a surrogate model on a perturbed dataset [47].

### 7.1.11 The PINK image library

**Participant:** Hugues Talbot
**link:** PINK
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.

### 7.1.12 The Vivabrain AngioTK toolkit

**Participant:** Hugues Talbot
**link:** AngioTK
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.

### 7.1.13 The PET/CT FIJI Viewer

**Participant:** Hugues Talbot
**link:** PET/CT Viewer
Quantitive Positron Emission Tomography is a new area for which software is not readily availble. With our partners from Toulouse and Beth Israel hospitals, we have proposed a free open-source plugin allowing clinicians to view, interact and perform automated and interactive lesion segmentation in the context of PET/CT.

### 7.1.14 A scientific image viewer

**Participant:** Hugues Talbot
**link:** IMVIEW
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.

# 8 New results

## 8.1 Severity prediction of hospitalized COVID-19 patients

**Participants:** Samy Ammari, Emilie Chouzenoux, Kavya Gupta, Yingping Li, Ana Neascu, Jean-Christophe Pesquet, Hugues Talbot, Matthieu Terris, Sagar Verma (Collaboration: Nathalie Lassau, Institut Gustave Roussy ; Marie-France Bellin, Kremlin-Bicetre APHP ; Mickaël Blum, Owkin France)

The SARS-COV-2 pandemic has put pressure on intensive care units, so that identifying predictors of disease severity is a priority that we address in the work [3]. We collect 58 clinical and biological variables, and chest CT scan data, from 1003 coronavirus-infected patients from two French hospitals. We train a deep learning model based on CT scans to predict severity. We then construct the multimodal AI-severity score that includes 5 clinical and biological variables (age, sex, oxygenation, urea, platelet) in addition to the deep learning model. We show that neural network analysis of CT-scans brings unique prognosis information, although it is correlated with other markers of severity (oxygenation, LDH, and CRP) explaining the measurable but limited 0.03 increase of AUC obtained when adding CT-scan information to clinical variables. Here, we show that when comparing AI-severity with 11 existing severity scores, we find significantly improved prognosis performance; AI-severity can therefore rapidly become a reference scoring approach.

## 8.2 Blind Kalman filtering for time series modeling and inference

**Participants:** Emilie Chouzenoux (Collaboration: Shalini Sharma, Angshul Majumdar, IIIT 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 the work [39], we address the problem of short-term load forecasting. We propose a blind Kalman filter algorithm associated to mini-batch processing strategy to allow on-the-fly forecasting. The experimental results show that the proposed method outperforms the state-of-the-art techniques, both on load profile estimation and peak load forecast problems. In the work [45], we consider the application of our approach to the problem of predicting hate content in tweets.

## 8.3 Theoretical and practical advances for majorize-minimize algorithms

**Participants**: Emilie Chouzenoux, Jean-Baptiste Fest, Mouna Gharbi, Jean-Christophe Pesquet, Ségolène Martin (Collaboration: Laurent Duval, IFPEN)

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 [49] 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 [64], a new MM method for solving largescale 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 [50], we propose unfolded Majorization-Minimization (MM) algorithms with the aim to reach fast and accurate methods for sparse spectroscopy signal restoration. Two state-of-the-art iterative MM algorithms are unfolded onto deep network architectures. This allows both the deployment of GPU-friendly tools for accelerated implementation, as well as the introduction of a supervised learning strategy for tuning automatically the regularization parameter. The effectiveness of our approach is demonstrated on the restoration of a large dataset of realistic mass spectrometry data.

## 8.4 Fundamental problems in image reconstruction

**Participants**: Emilie Chouzenoux, Jean.-Christophe Pesquet, Marion Savanier, (Collaboration: Cyril Riddell, Yves Trousset, GE Heathcare, Buc)

In [68, 14], we consider the proximal gradient algorithm for solving penalized least-squares minimization problems arising in data science. This first-order algorithm is attractive due to its 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 this paper, we propose to analyze the effect of such an adjoint mismatch on the convergence of the proximal gradient algorithm in an infinite-dimensional setting, thus generalizing the existing results on PGA. We derive conditions on the step-size and on the gradient of the smooth part of the objective function under which convergence of the algorithm 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 with two image reconstruction tasks in computed tomography.

Discretizing tomographic forward and backward operations is a crucial step in the design of model-based reconstruction algorithms. Standard projectors rely on linear interpolation, whose adjoint introduces discretization errors during backprojection. More advanced techniques are obtained through geometric footprint models that may present a high computational cost and an inner logic that is not suitable for implementation on massively parallel computing architectures. In [37], we take a fresh look at the discretization of resampling transforms and focus on the issue of magnification-induced local sampling variations by introducing a new magnification-driven interpolation approach for tomography. We provide a mathematical formulation for discretizing a one-dimensional homography. We then extend our approach to two-dimensional representations in order to account for the geometry of cone-beam computed tomography with a at panel detector. Our new method relies on the decomposition of signals onto a space generated by non-uniform B-splines so as to capture the spatially varying magnification that locally affects sampling. We propose various degrees of approximations for a rapid implementation of the proposed approach. Our framework allows us to define a novel family of projector/backprojector pairs parameterized by the order of the employed B-splines. Results on both synthetic data and real data using a quality assurance phantom, were performed to validate our approach.

## 8.5 Computational approaches for multiphotonic image restoration

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

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 [21]. 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 [23].

## 8.6 Parallel MRI image reconstruction with sparsity-based priors

**Participants:** Emilie Chouzenoux (Collaboration: Philippe Ciuciu, Inria Parietal and CEA Neuropsin)

Over the last decade, the combination of compressed sensing (CS) with acquisition over multiple receiver coils in magnetic resonance imaging (MRI) has allowed the emergence of faster scans while maintaining a good signal-to-noise ratio (SNR). Self-calibrating techniques, such as ESPiRIT, have become the standard approach to estimating the coil sensitivity maps prior to the reconstruction stage. In this work, we proceed differently and introduce a new calibration-less multi-coil CS reconstruction method. Calibration-less techniques no longer require the prior extraction of sensitivity maps to perform multi-coil image reconstruction but usually alternate estimation sensitivity map estimation and image reconstruction. In the work [18], to get rid of the nonconvexity of the latter approach we reconstruct as many MR images as the number of coils. To compensate for the ill-posedness of this inverse problem, we leverage structured sparsity of the multi-coil images in a wavelet transform domain while adapting to variations in SNR across coils owing to the OSCAR (octagonal shrinkage and clustering algorithm for regression) regularization. Coil-specific complex-valued MR images are thus obtained by minimizing a convex but nonsmooth objective function using the proximal primal-dual Condat-Vù algorithm. Comparison and validation on retrospective Cartesian and non-Cartesian studies based on the Brain fastMRI data set demonstrate that the proposed reconstruction method outperforms the state-of-the-art (L1-ESPIRiT, calibration-less AC-LORAKS and CaLM methods) significantly on magnitude images for the T1 and FLAIR contrasts. Additionally, further validation operated on 8 to 20-fold prospectively accelerated high-resolution ex vivo human brain MRI data collected at 7 Tesla confirms the retrospective results. Overall, OSCAR-based regularization preserves phase information more accurately (both visually and quantitatively) compared to other approaches, an asset that can only be assessed on real prospective experiments.

## 8.7 Probabilistic modeling and inference for sequential space-varying blur identification

**Participants:** Emilie Chouzenoux and Yunshi Huang (Collaboration: Victor Elvira, University of Edinburg)

The identification of parameters of spatially variant blurs given a clean image and its blurry noisy version is a challenging inverse problem of interest in many application fields, such as biological microscopy and astronomical imaging. In the work [22], we consider a parametric model of the blur and introduce an 1D state-space model to describe the statistical dependence among the neighboring kernels. We apply a Bayesian approach to estimate the posterior distribution of the kernel parameters given the available data. Since this posterior is intractable for most realistic models, we propose to approximate it through a sequential Monte Carlo approach by processing all data in a sequential and efficient manner. Additionally, we propose a new sampling method to alleviate the particle degeneracy problem, which is present in approximate Bayesian filtering, particularly in challenging concentrated posterior distributions. The considered method allows us to process sequentially image patches at a reasonable computational and memory costs. Moreover, the probabilistic approach we adopt provides uncertainty quantification which is useful for image restoration. The practical experimental results illustrate the improved estimation performance of our novel approach, demonstrating also the benefits of exploiting the spatial structure the parametric blurs in the considered models.

## 8.8 Monte-Carlo approaches for global optimization

**Participants:** Emilie Chouzenoux and Thomas Guilmeau (Collaboration: Victor Elvira, University of Edinburg)

Finding the global minimum of a nonconvex optimization problem is a notoriously hard task appearing in numerous applications, from signal processing to machine learning. Simulated annealing (SA) is a family of stochastic optimization methods where an artificial temperature controls the exploration of the search space while preserving convergence to the global minima. SA is efficient, easy to implement, and theoretically sound, but suffers from a slow convergence rate. The purpose of [51] is twofold. First, we provide a comprehensive overview on SA and its accelerated variants. Second, we propose a novel SA scheme called curious simulated annealing, combining the assets of two recent acceleration strategies. Theoretical guarantees of this algorithm are provided. Its performance with respect to existing methods is illustrated on practical examples.

In [77], we propose a novel sampling algorithm for multi-modal target exploration, that exploits the benefits of the population Monte-Carlo framework and includes more efficient adaptive mechanisms, exploiting geometric information of the target distribution. In particular, the novel algorithm adapts the location and scale parameters of a set of importance densities (proposals). At each iteration, the location parameters are adapted by combining a versatile resampling strategy (i.e., using the information of previous weighted samples) with an advanced optimization-based scheme. Local second-order information of the target distribution is incorporated through a preconditioning matrix acting as a scaling metric onto a gradient direction. A damped Newton approach is adopted to ensure robustness of the scheme. The resulting metric is also used to update the scale parameters of the proposals. We discuss several key theoretical foundations for the proposed approach. Finally, we show the successful performance of the proposed method in three numerical examples, involving challenging distributions.

## 8.9 Deep transform and metric learning networks

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (Collaboration: Wen Tang and Hamid Krim, North Carolina State University)

Based on its great successes in inference and denosing 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 [69] 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.

## 8.10 Computational approaches for drug-disease associations

**Participant:** Emilie Chouzenoux (Collaboration: Angshul Majumdar, IIIT Delhi)

Investigation of existing drugs is an effective alternative to the discovery of new drugs for treating diseases. This task of drug re-positioning can be assisted by various kinds of computational methods to predict the best indication for a drug given the open-source biological datasets. Owing to the fact that similar drugs tend to have common pathways and disease indications, the association matrix is assumed to be of low-rank structure. Hence, the problem of drug-disease association prediction can be modeled as a low-rank matrix completion problem. In [29], we propose a novel matrix completion framework that makes use of the side-information associated with drugs/diseases for the prediction of drug-disease indications modeled as neighborhood graph, in line with our previous methodological work [41]. The usage of the method is also evaluated through a case study where top 5 indications are predicted for novel drugs, which then are verified with the CTD database. In [30], we build computational models using matrix completion techniques to predict drug-virus association for drug re-positioning. The main contribution of this work is a manually curated database publicly shared, comprising of existing associations between viruses and their corresponding antivirals. The database gathers similarity information using the chemical structure of drugs and the genomic structure of viruses. Along with this database, we make available a set of state-of-the-art computational drug re-positioning tools based on matrix completion. The tools are first analysed on a standard set of experimental protocols for drug target interactions. The best performing ones are applied for the task of re-positioning antivirals for COVID-19.

## 8.11 Task-based reconstruction approach for digital breast tomosynthesis

**Participants:** Emilie Chouzenoux, Jean-Christophe Pesquet, Maissa Sghaier (Collaboration: Serge Muller, GE Healthcare)

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 [38], 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. Our contribution is threefold. First, we introduce an original task-based reconstruction framework through the proposition of a detectability function inspired from mathematical model observers. Second, we propose a novel total-variation regularizer where the gradient field accounts for the different morphological contents of the imaged breast. Third, we integrate the two developed measures into a cost function, minimized thanks to a new form of the Majorize Minimize Memory Gradient (3MG) algorithm. We conduct a numerical comparison of the convergence speed of the proposed method with those of standard convex optimization algorithms. Experimental results show the interest of our DBT reconstruction approach, qualitatively and quantitatively.

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

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

The objective of [40] 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.

## 8.13 Machine-learning-based radiomics models for lesion identification in MRI

**Participants:** Emilie Chouzenoux, Samy Ammari, Arnaud Quillent, Hugues Talbot (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 aim of [5] was to assess the impact of magnetic field strength on magnetic resonance imaging (MRI) radiomics features in neuroradiology clinical practice. The paper [24] 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 study [4] proposes and evaluates a deep learning method that predicts surrogate images for contrast-enhanced T1 from multiparametric magnetic resonance imaging (MRI) acquired using only a quarter of the standard 0.1 mmol/kg dose of gadolinium-based contrast agent. In particular, the predicted images are quantitatively evaluated in terms of lesion detection performance.

The objective of [7] was to develop machine learning (ML) algorithms for survival prediction of Glioblastoma (GBM) patient. The objective of [6] was to identify novel biomarkers, extracted from MRI and clinical data, which could predict overall survival (OS) and progression-free survival (PFS) in GBM patients treated with bevacizumab using machine-learning algorithms.

## 8.14 A 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 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.

## 8.15 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.

## 8.16 Robustness of neural networks

**Participants**: Ana Neacsu, Kavya Gupta, Fragkiskos Malliaros, Jean-Christophe Pesquet (Collaboration: Patrick Combettes, North Caroline State University, Corneliu Burileanu, Polithenica University of Bucharest, Fateh Kaakai, Béatrice Pesquet-Popescu, Thalès LAS)

In [53], we present a quantitative approach to demonstrate the robustness of neural networks for tabular data. We analyse the effect of various widely used techniques we encounter in neural network practice, such as regularization of weights, addition of noise to the data, and positivity constraints. We provide mathematical proofs of robustness in terms of Lipschitz constant for feed-forward networks. In [52], we present an adversarial attacker for regression tasks, derived from the algebraic properties of the Jacobian of the network. We show that our attacker successfully fools the neural network. Our analysis relies on the quantification of the fooling error as well as various error metrics. A noteworthy feature of our attacker is that it allows us to optimally attack a subset of inputs, which may be helpful to analyse the sensitivity of some specific inputs.

## 8.17 Compression of neural networks

**Participants**: Jean-Christophe Pesquet, Sagar Verma

Sparsifying deep neural networks is of paramount interest in many areas, especially when those networks have to be implemented on low-memory devices. In [73], we propose a new formulation of the problem of generating sparse weights for a pre-trained neural network. By leveraging the properties of standard nonlinear activation functions, we show that the problem is equivalent to an approximate subdifferential inclusion problem. The accuracy of the approximation controls the sparsity. We show that the proposed approach is valid for a broad class of activation functions (ReLU, sigmoid, softmax). We propose an iterative optimization algorithm to induce sparsity whose convergence is guaranteed. Because of the algorithm flexibility, the sparsity can be ensured from partial training data in a minibatch manner. To demonstrate the effectiveness of our method, we perform experiments on various networks in different applicative contexts: image classification, speech recognition, natural language processing, and time-series forecasting.

## 8.18 Learning maximally monotone operators for image recovery

**Participant**: Jean-Christophe Pesquet (Collaboration: Audrey Repetti, Matthieu Terris, Yves Wiaux, Heriot Watt University, UK)

In [34] a new paradigm is introduced for solving regularized variational problems. These are typically formulated to address ill-posed inverse problems encountered in signal and image processing. The objective function is traditionally defined by adding a regularization function to a data fit term, which is subsequently minimized by using iterative optimization algorithms. Recently, several works have proposed to replace the operator related to the regularization by a more sophisticated de- noiser. These approaches, known as plug-and-play (PnP) methods, have shown excellent performance. Although it has been noticed that, under nonexpansiveness assumptions on the denoisers, the convergence of the resulting algorithm is guaranteed, little is known about characterizing the asymptotically delivered solution. In the current article, we propose to address this limitation. More specifically, in- stead of employing a functional regularization, we perform an operator regularization, where a maximally monotone operator (MMO) is learned in a supervised manner. This formulation is flexible as it allows the solution to be characterized through a broad range of variational inequalities, and it includes convex regularizations as special cases. From an algorithmic standpoint, the proposed approach con- sists in replacing the resolvent of the MMO by a neural network (NN). We provide a universal approx- imation theorem proving that nonexpansive NNs provide suitable models for the resolvent of a wide class of MMOs. The proposed approach thus provides a sound theoretical framework for analyzing the asymptotic behavior of first-order PnP algorithms. In addition, we propose a numerical strategy to train NNs corresponding to resolvents of MMOs. We apply our approach to image restoration problems and demonstrate its validity in terms of both convergence and quality.

### 8.19 New generation of image coders

**Participants**: Tasnim Dardouri, Jean-Christophe Pesquet (Collaboration: Mounir Kaaniche, Université Sorbonne Paris Nord ; Amel Benazza-Benyahia, Sup'Com Tunis)

Lifting-based wavelet transform has been extensively used for efficient compression of various types of visual data. Generally, the performance of such coding schemes strongly depends on the lifting operators used, namely the prediction and update filters. Unlike conventional schemes based on linear filters, we propose, in [17], to learn these operators by exploiting neural networks. More precisely, a classical Fully Connected Neural Network (FCNN) architecture is firstly employed to perform the prediction and update. Then, we propose to improve this FCNN-based Lifting Scheme (LS) in order to better take into account the input image to be encoded. Thus, a novel dynamical FCNN model is developed, making the learning process adaptive to the input image contents for which two adaptive learning techniques are proposed. While the first one resorts to an iterative algorithm where the computation of two kinds of variables is performed in an alternating manner, the second learning method aims to learn the model parameters directly through a reformulation of the loss function. Experimental results carried out on various test images show the benefits of the proposed approaches in the context of lossy and lossless image compression. Extensions are discussed in [46].

### 8.20 Artificial intelligence for histopathology

**Participants:** Marvin Lerousseau, Maria Vakalopoulou (Collaboration: Stergios Christodoulidis, MICS CentraleSupélec ; Eric Deutsch, Institute Gustave Roussy ; Dimitris Samaras, StonyBrook University ; Nikos Paragios, Therapanacea)

The examination of histopathology images is considered to be the gold standard for the diagnosis and stratification of cancer patients. A key challenge in the analysis of such images is their size, which can run into the gigapixels and can require tedious screening by clinicians. In [74], we propose a novel spatial and magnification based attention sampling strategy. First, we use a down-sampled large size image to estimate an attention map that represents a spatial probability distribution of informative patches at different magnifications. Then a small number of patches are cropped from the large size medical image at certain magnifications based on the obtained attention. The final label of the large size image is predicted solely by these patches using an end-to-end training strategy.

In [61], we propose a novel MIL approach that exploits the spatial relationship of tiles for classifying whole slide images. To do so, a sparse map is built from tiles embeddings, and is then classified by a sparse-input CNN. It obtained state-of-the-art performance over popular MIL approaches on the classification of cancer subtype involving 10000 whole slide images. Our results suggest that the proposed approach might (i) improve the representation learning of instances and (ii) exploit the context of instance embeddings to enhance the classification performance.

In [60], we propose a novel weakly supervised multi-instance learning approach that deciphers quantitative slide-level annotations which are fast to obtain and regularly present in clinical routine. The extreme potentials of the proposed approach are demonstrated for tumor segmentation of solid cancer subtypes. The proposed approach achieves superior performance in out-of-distribution, out-of-location, and out-of-domain testing sets.

In [44] we propose a novel generative framework that can learn powerful representations for such tiles by learning to plausibly expand their visual field. In particular, we developed a progressively grown generative model with the objective of visual field expansion. Thus trained, our model learns to generate different tissue types with fine details, while simultaneously learning powerful representations that can be used for different clinical endpoints, all in a self-supervised way. To evaluate the performance of our model, we conducted classification experiments on CAMELYON17 and CRC benchmark datasets, comparing favorably to other self-supervised and pre-trained strategies that are commonly used in digital pathology.

## 8.21 Artificial intelligence for thoracic imaging

**Participant:** Maria Vakalopoulou (Collaboration: Stergios Christodoulidis, MICS CentraleSupélec ; Marie-Pierre Revel, AP-HP - Hopital Cochin Broca Hotel Dieu; Nikos Paragios, Therapanacea)

In [11] we aimed to assess lung structural changes after one year of lumacaftor-ivacaftor treatment, and to use unsupervised machine learning to identify morphological phenotypes of lung disease that are associated with response to lumacaftor-ivacaftor. Methods Adolescents and adults with CF from the French multicenter real-world prospective observational study evaluating the first year of treatment with lumacaftor-ivacaftor were included if they had pretherapeutic and follow-up chest computed tomography (CT)-scans available. CT scans were visually scored using a modified Bhalla score. A k-mean clustering method was performed based on 120 radiomics features extracted from unenhanced pretherapeutic chest CT scans.

The study in [20] was to determine whether a single reconstruction kernel or both high and low frequency kernels should be used for training deep learning models for the segmentation of diffuse lung disease on chest computed tomography (CT). Two annotated datasets of COVID-19 pneumonia (323,960 slices) and interstitial lung disease (ILD) (4,284 slices) were used. Annotated CT images were used to train a U-Net architecture to segment disease. All CT slices were reconstructed using both a lung kernel (LK) and a mediastinal kernel (MK). Three different trainings, resulting in three different models were compared for each disease: training on LK only, MK only or LK+MK images. Dice similarity scores (DSC) were compared using the Wilcoxon signed-rank test.

In [13], we develop a deep learning–based method to depict worsening of ILD based on lung shrinkage detection from elastic registration of chest CT scans in patients with systemic sclerosis (SSc). Patients with SSc evaluated between January 2009 and October 2017 who had undergone at least two unenhanced supine CT scans of the chest and pulmonary function tests (PFTs) performed within 3 months were retrospectively included. Morphologic changes on CT scans were visually assessed by two observers and categorized as showing improvement, stability, or worsening of ILD. Elastic registration between baseline and follow-up CT images was performed to obtain deformation maps of the whole lung. Jacobian determinants calculated from the deformation maps were given as input to a deep learning–based classifier to depict morphologic and functional worsening. For this purpose, the set was randomly split into training, validation, and test sets. Correlations between mean Jacobian values and changes in PFT measurements were evaluated with the Spearman correlation.

In [59], we propose a deep reinforcement learning method for accurate localization of the L3 CT slice. Our method trains a reinforcement learning agent by incentivizing it to discover the right position. Specifically, a Deep Q-Network is trained to find the best policy to follow for this problem. Visualizing the training process shows that the agent mimics the scrolling of an experienced radiologist. Extensive experiments against other state-of-the-art deep learning based methods for L3 localization prove the superiority of our technique which performs well even with a limited amount of data and annotations.

## 8.22 Learning-based registration of medical imaging and remote sensing.

**Participants:** Théo Estienne and Maria Vakalopoulou (Collaboration: Stergios Christodoulidis, MICS CentraleSupélec ; Konstantinos Karantzalos, NTUA ; Eric Deutsch, Institute Gustave Roussy ; Nikos Paragios, Therapanacea)

In [48], we investigate the topic focusing on the interpretability of deep learning-based registration methods. In particular, with the appropriate model architecture and using a simple linear projection, we decompose the encoding space, generating a new basis, and we empirically show that this basis captures various decomposed anatomically aware geometrical transformations. We perform experiments using two different datasets focusing on lungs and hippocampus MRI. We show that such an approach can decompose the highly convoluted latent spaces of registration pipelines in an orthogonal space with several interesting properties. We hope that this work could shed some light on a better understanding of deep learning based registration methods.

In [32] we propose a fully unsupervised, deep learning based multistep deformable registration scheme for aligning pairs of satellite imagery. The presented method is based on the expression power of deep fully convolutional networks, regressing directly the spatial gradients of the deformation and employing a 2D transformer layer to efficiently warp one image to the other, in an end-to-end fashion. The displacements are calculated with an iterative way, utilizing different time steps to refine and regress them. Our formulation can be integrated into any kind of fully convolutional architecture, providing at the same time fast inference performances. The developed methodology has been evaluated in two different datasets depicting urban and peri urban areas; i.e., the very high-resolution dataset of the East Prefecture of Attica, Greece, as well as the high resolution ISPRS Ikonos dataset. Quantitative and qualitative results demonstrated the high potentials of our method.

In the chapter [75], a comprehensive survey of recent advances in image matching and registration is presented. The analysis is structured around the main components of these algorithms, presenting some recent works for both supervised and unsupervised settings, focusing mainly within Earth observation applications. Experimental results from a recently proposed deep learning-based method are presented. Based on the current status, the recent works, and the special challenges of these algorithms, the present study highlights certain limitations and insights that may be applicable for future research and development in the field of Earth observation with high-dimensional, multi-temporal, and multimodal datasets.

## 8.23 Genomics using advance machine learning approaches

**Participants:** Enzo Battistella and Maria Vakalopoulou (Collaboration: Eric Deutsch, Gustave Roussy; Nikos Paragios, Therapanacea)

Precision medicine is a paradigm shift in healthcare relying heavily on genomics data. However, the complexity of biological interactions, the large number of genes and the lack of comparisons on the analysis of data, remain a tremendous bottleneck regarding clinical adoption. In [9], we introduce a novel, automatic and unsupervised framework to discover low-dimensional gene biomarkers. Our method is based on the center-based LP-Stability clustering algorithm. Our evaluation includes both mathematical and biological criteria. The recovered signature is applied to several biological tasks, including screening of biological pathways and functions, and tumor types and subtypes characterization. Quantitative comparisons among different distance metrics, commonly used clustering methods and a referential gene signature from literature, confirm the high performance of our approach. In particular, our signature, based on 27 genes, reports at least 30 times better mathematical significance (Dunn's Index) and 25% better biological significance (Enrichment in Protein-Protein Interaction) than those produced by other referential clustering methods. Our signature reports promising results on distinguishing immune-inflammatory and immune desert tumors, while reporting a high balanced accuracy of 92% on tumor types classification and averaged balanced accuracy of 68% on tumor subtypes, which represents 7% and 9% higher performance compared to the referential signature.

## 8.24 Deep learning for kidney graft segmentation

**Participants:** Leo Milecki and Maria Vakalopoulou (Collaboration: Jean-Michel Correas Paris University; Marc-Olivier Timsit Hopital Européen Georges-Pompidou)

Image segmentation is one of the most popular problems in medical image analysis. Recently, with the success of deep neural networks, these powerful methods provide state of the art performance on various segmentation tasks. However, one of the main challenges relies on the high number of annotations that they need to be trained, which is crucial in medical applications. In [65], we propose an unsupervised method based on deep learning for the segmentation of kidney grafts. Our method is composed of two different stages, the detection of the area of interest and the segmentation model that is able, through an iterative process, to provide accurate kidney draft segmentation without the need for annotations. The proposed framework works in the 3D space to explore all the available information and extract meaningful representations from Dynamic Contrast-Enhanced and T2 MRI sequences.

## 8.25 Explanation models for graph neural networks

**Participants:** Alexandre Duval and Fragkiskos Malliaros

Graph Neural Networks (GNNs) achieve significant performance for various learning tasks on geometric data due to the incorporation of graph structure into the learning of node representations, which renders their comprehension challenging. In this work, we have first proposed a unified framework satisfied by most existing GNN explainers [47]. Then, we have introduced GraphSVX, a post hoc local model-agnostic explanation method specifically designed for GNNs. GraphSVX is a decomposition technique that captures the "fair" contribution of each feature and node towards the explained prediction by constructing a surrogate model on a perturbed dataset. It extends to graphs and ultimately provides as explanation the Shapley Values from game theory. Experiments on real-world and synthetic datasets have demonstrated that GraphSVX achieves state-of-the-art performance compared to baseline models while presenting core theoretical and human-centric properties.*

## 8.26 Topic-aware latent models for graph representation learning

**Participants:** Abdulkadir Çelikkanat and Fragkiskos Malliaros

Graph representation learning (GRL) methods aim to map each vertex of the graph into a low dimensional space in a way that the structural information of the network is preserved. Of particular interest are methods based on random walks; such methods transform the network into a collection of node sequences, aiming to learn node representations by predicting the context of each node within the sequence. In this work, we have introduced TNE, a generic framework to enhance the embeddings of nodes acquired by means of random walk-based approaches with topic-based information [12]. The proposed model first assigns each node to a latent community with the favor of various statistical graph models and community detection methods, and then learns the enhanced topic-aware representations. We have evaluated the model in two downstream tasks: node classification and link prediction. The experimental results have demonstrated that by incorporating node and community embeddings, we are able to outperform widely-known baseline GRL models.

## 8.27 Multiomics data integration via graph representation learning

**Participants:** Surabhi Jagtap, Abdulkadir Çelikkanat, Fragkiskos Malliaros (Collaboration: Aurélie Pirayre, Frederique Bidard, and Laurent Duval, IFPEN)

The advent of omics technologies have enabled the generation of huge, complex, heterogeneous, and high-dimensional omics data. Imposing numerous challenges in data integration, these data could lead to a better understanding of the organism's cellular system. Omics data are typically represented as networks to study relations between biological entities, such as protein-protein interaction, gene regulation, and signal transduction. To this end, network embedding approaches allow us to learn latent feature representations for nodes of a graph structure. In this line of research, we have proposed two new methodologies to learn embeddings from multiomics data by modeling the underlying interactions among biological entities. The first one is based on the concept of exponential family embeddings [55], while the second one relies on the factorization of a random walk transition matrix [56]. Both models have been evaluated on the gene regulatory network (GRN) inference problem, focusing on data from well-known model organisms.

## 8.28 Myocardial perfusion simulation for coronary artery disease

**Participant:** Hugues Talbot (Collaboration: Lazaros Papamanolis and Irene Vignon-Clementel, Inria SIMBIOTX ; Charles Taylor, Heartflow Inc, USA ; Laurent Najman, ESIEE Paris)

Patient-specific models of blood flow are being used clinically to diagnose and plan treatment for coronary artery disease. A remaining challenge is bridging scales from flow in arteries to the micro-circulation supplying the myocardium. Previously proposed models are descriptive rather than predictive and have not been applied to human data. In this article [33], we develop a multiscale patient-specific model enabling blood flow simulation from large coronary arteries to myocardial tissue. Patient vasculatures are segmented from coronary computed tomography angiography data and extended from the image-based model down to the arteriole level using a space-filling forest of synthetic trees. Blood flow is modeled by coupling a 1D model of the coronary arteries to a single-compartment Darcy myocardium model. Simulated results on five patients with non-obstructive coronary artery disease compare overall well to $H_2^{15}O$ PET exam data for both resting and hyperemic conditions. Results on a patient with severe obstructive disease link coronary artery narrowing with impaired myocardial blood flow, demonstrating the model's ability to predict myocardial regions with perfusion deficit. This is the first report of a computational model for simulating blood flow from the epicardial coronary arteries to the left ventricle myocardium applied to and validated on human data.

## 8.29 In-vivo quantification of skin ageing

**Participant:** Hugues Talbot (Collaboration: Kattell Vie, Laboratoires Clarins)

Reflectance confocal microscopy (RCM) is a powerful tool to visualize the skin layers at cellular resolution up to a depth of 200$\mu$m. A semi-quantitative score of skin aging from RCM images has been previously published, requiring visual assessment of the images by experienced dermatologists. In this new article [35], we propose new computer-based methods to automatically quantify the skin aging process on RCM image. The method uses a 3D graphical model, which behaves in 3D like a Hidden Markov Model, which makes sense since layers of the skin are ordered. To quantify aging, we segment the Dermis-Epidermal Junction (DEJ), which is traditionally difficult to do even for trained clinicians. Then we assess the regularity of this junction with image and shape-based radiomic features. We were able to validate the relationship of radiomic features to ageing with about 80% accuracy.

## 8.30 Flow cytometry and micro-organisms classification

**Participant:** Hugues Talbot

Flow cytometry is a high-speed optical modality for micro-organism classification and counting, widely used for blood tests for examples. It does not rely on imaging for decision making and counting. With the advent of fast hardware and GPU computing together with deep-learning techniques, imaging has become a feasible technique in the flow cytometry domain. We have conducted a review [26] of existing techniques in this domain, and proposed a very efficient method for water-quality estimation [25]. We detect the two most common water pollutant micro-organisms with very high accuracy (> 99%).

## 8.31 An Elastica-driven digital curve evolution model for image segmentation

**Participant:** Hugues Talbot (Collaboration: Daniel Antunes and Jacques-Olivier Lachaud, University Grenoble-Alpes Savoie Mont-Blanc)

Geometric priors have been shown to be useful in image segmentation to regularize the results. For example, the classical Mumford-Shah functional uses region perimeter as prior. This has inspired much research in the last few decades, with classical approaches like the Rudin-Osher-Fatemi and most graph-cut formulations, which all use a weighted or binary perimeter prior. It has been observed that this prior is not suitable in many applications, for example for segmenting thin objects or some textures, which may have high perimeter/surface ratio.Mumford observed that an interesting prior for natural objects is the Euler elastical model, which involves the squared curvature. In other areas of science, researchers have noticed that some physical binarization processes, like emulsion unmixing, can be well-approximated by curvature-related flow like the Willmore flow. However, curvature-related flows are not easy to compute because curvature is difficult to estimate accurately, and the underlying optimization processes are not convex. In this article [8], we propose to formulate a digital flow that approximates an Elastica-related flow using a multigrid-convergent curvature estimator, within a discrete variational framework. We also present an application of this model as a post-processing step to a segmentation framework.

### 8.32 Multiband astronomical source detection

**Participant:** Hugues Talbot (ERC SUNDIAL ITN Grant, collaboration with 7 other institutes in Europe)

In the context of mathematical morphology, component-graphs are complex but powerful structures for multi-band image modeling, processing, and analysis. In this work [31], we propose a novel multiband object detection method relying on the component-graphs and statistical hypothesis tests. Our analysis shows that component-graphs are better at capturing image structures compared to the classical component-trees, with significantly higher detection capacity. Besides, we introduce two filtering algorithms to identify duplicated and partial nodes in the component-graphs. The proposed method, applied to the detection of sources on astronomical images, demonstrates a significant improvement in detecting faint objects on both multi-band simulated and real astronomical images compared to the state of the art.

### 8.33 Fine-grained classification in computer vision

**Participant:** Hugues Talbot (Collaboration: Charles Kantor, MILA, Montreal, Canada ; Léonard Boussioux, MIT, Cambridge, USA.)

Fine-grained classification is the problem of distinguishing objects that look very much alike, based on few, sometimes subtle but important features. The problem is classical in taxonomy, e.g. differences between an edible and a poisonous mushroom sometimes are very slight. In this work, we have proposed methods for focusing on important features based on self-attention approaches, as well as dealing with class imbalance. Indeed, visually similar objects can appear with widely different densities. We applied this work on the detection of populations of butterflies in North America [58].

### 8.34 Plaque detection and classification in coronary trees

**Participants: Mario Viti, Hugues Talbot** (Collaboration: Nicolas Gogin, GE Healthcare)

Plaque deposition in coronary arteries is the principal cause of Major Adverse Cardio-Vascular Events (MACE). To predict MACE and avoid them, multiple exams might be necessary. It is important to subject patient to as little invasive procedures as possible. One problem we studied was the detection of calcified plaque, which is highly visible in X-ray CT, but difficult to associate with vessels in the absence of contrast agent [19]. Exploiting our work on self-attention mechanisms in deep networks, we've worked on the segmentation of such plaque using Graphical CNN exploiting the tree-like structure of coronary blood vessels [81].

# 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
    - Responsible: J.-C. Pesquet and F. Malliaros

- PhD Contract with General Electric Healthcare
    - Project title: Minimally invasive assessement of coronary disease
    - Duration: 2018-2021
    - Leader: Hugues Talbot
- PhD Contract with General Electric Healthcare
    - Project title: Reconstruction 3D interventionnelle
    - Duration: 2019-2022
    - Leader: 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
    - Leader: H. Talbot, 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
    - Leader: E. Chouzenoux, J.-C. Pesquet
- Contract with Caerus Medical
    - Project title: Aide au diagnostic des pathologies rachidiennes dégénératives
    - Duration: 2020-2021
    - Leader: E. Chouzenoux, 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 ->

**Coordinators:** Emilie Chouzenoux (emilie.chouzenoux@inria.fr) and Angshul Majumdar (angshul@iiitd.ac.in)

**Partner:**

- Indraprastha Institute of Information Technology

**Summary:** The COMPASS 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.

**Webpage:** COMPASS

### 10.1.2 Inria international partners

**Informal international partners**

- Sup'Com Tunis - Prof. Amel Benazza-Benhayia. Collaboration Topic: Multispectral imaging and image compression.
- North Carolina State University - Prof. Patrick Louis Combettes. Collaboration Topic: Fixed point theory.
- Heriot-Watt University, UK - Prof. Audrey Repetti and Prof. Yves Wiaux. Collaboration Topic: Large-scale image restoration.
- University of Edinburgh, UK - Prof. Victor Elvira. Collaboration Topic: Bayesian signal processing.
- Indraprastha Information Institute Technology, Delhi, India - Prof. Angshul Majumdar. Collaboration Topic: Dictionary learning.
- Universidad Técnica Federico Santa María, Valparaíso, Chile - Prof. Luis M. Briceño-Arias. Collaboration Topic: Stochastic optimization.
- Aristotle University of Thessaloniki, Greece - Prof. Apostolos N. Papadopoulos, Prof. Grigorios Tsoumakas. Collaboration Topic: Drug-target interaction prection.
- University of California, Irvine – Prof. Yanning Shen. Collaboration Topic: graph rerepsentation learning.
- Aalto University, Finland - Profs. Sergiy Vorobyov and Esa Ollila. Collaboration topic: Robust Dictionary Learning for Medical Imaging.

## 10.2 International research visitors

### 10.2.1 Visits of international scientists

**Tulay Adali**

**Status** Professor

**Institution of origin:** University of Maryland

**Country:** USA

**Dates:** From Oct 2021 to May 2022

**Context of the visit:** Visiting scientist

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

**Ismail Ben Ayed**

**Status** Professor

**Institution of origin:** ETS Montréal

**Country:** Canada

**Dates:** From Oct 2021 to Sep 2022

**Context of the visit:** Visiting scientist

**Mobility program/type of mobility:** Sabbatical year funded by CentraleSupélec

### 10.2.2 Visits to international teams

**Gabriele Scrivanti**

**Visited institution:** IBSPAN – System Research Institute Polish Academy of Science

**Country:** Poland

**Dates:** From Nov 2021 to Apr 2022

**Context of the visit:** Visiting researcher

**Mobility program/type of mobility:** Secondment for the MSCA TraDe-OPT ITN project

## 10.3 European initiatives

### 10.3.1 FP7 & H2020 projects

- Program: H2020 ITN Marie Sklodowska-Curie
    - Project acronym: Trade-Opt
    - Project title: Training Data-Drive Experts in Optimization
    - Duration: 2020-2024
    - Coordinator: S. Villa (Univ. Genova, Italy), Local: J.-C. Pesquet
- Program: H2020 ITN Marie Sklodowska-Curie
    - Projet acronym: SUNDIAL
    - Project Title: SUrvey Network for Deep Imaging Analysis and Learning
    - Duration: 2017-2021
    - Coordinator: Reynier Peletier (U. Groningen, NL), local: H. Talbot
- Program: ERC StG
    - Project acronym: MAJORIS
    - Project title: Majoration-Minimization algorithms for image processing
    - Duration: 2020-2024
    - Coordinator: E. Chouzenoux

## 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 PRC
  - Project acronym: CoMeDIC
  - Project title: Convergent Metrics for DIscrete Calculus
  - Duration: 2016-2021
  - Coordinator: J.-O. Lachaud (Univ. Rhones Alpes Savoie Mont-Blanc), Local: H. Talbot
- 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: 2017-2021
  - 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**

- E. Chouzenoux, M. Gharbi, J.-C. Pesquet and G. Scrivanti. Organizers of the First Summer School on "Optimization Methods for Machine Learning and Inverse Problems", ITN TradeOpt, CentraleSupélec, Online, 5-9 July 2021.
- F. Malliaros. Organizer of the Summer School on Artificial Intelligence, CentraleSupélec, Online, 28 June - 2 July 2021.

**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. Member of the organizing committee of the 15th International Workshop on Graph-Based Natural Language Processing (TextGraphs), Annual Conference of the North American Chapter of the Association for Computational Linguistics (NAACL), Online, 2021.
- H. Talbot. Member of the organizing committee for ICCV 2023 in Paris.
- H. Talbot. Member of the board and program committee for the conference Discrete Geometry and Mathematical Morphology, which took place in Uppsala, Sweden, in April 2021.

### 11.1.2 Scientific events: selection

**Chair of conference program committees**

- E. Chouzenoux. Tutorial chair of European Signal Processing Conference (EUSIPCO), 2022.
- S. Verma. Area Chair of International Conference on Artificial Neural Networks (ICANN), 2021.

**Member of the conference program committees**

- E. Chouzenoux. Elected member of the EURASIP Signal and Data Analytics for Machine Learning technical committee (since 2018), and of the IEEE Signal Processing Theory and Methods technical committee (since 2017).
- H. Talbot. Member of the board and program committee for the conference Discrete Geometry and Mathematical Morphology, Uppsala, Sweden, April 2021.
- E. Chouzenoux. Session chair of EUSIPCO 2021 and ISBI 2021.
- M. Vakalopoulou. Area chair of the Medical Imaging with Deep Learning (MIDL) 2021 and the Computer Vision and Pattern Recognition (CVPR) 2021.

**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 (NIPS) and 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).

### 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
- 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**

- A. Contreras: Optimization - A Journal of Mathematical Programming and Operations Research.
- E. Chouzenoux: IEEE Trans. on Image Processing, SIAM Journal on Imaging Science, Journal of Optimization Theory and Applications, Journal of Mathematical Imaging and Vision, Inverse Problems.
- J.-C. Pesquet: IEEE Trans. on Signal Processing, IEEE Trans. on Image Processing, IEEE Trans. on Information Theory (IEEE-TI), Signal Processing, SIAM Journal on Optimization, SIAM Journal on Imaging Sciences, Journal of Mathematical Imaging and Vision, Journal of Optimization Theory and Applications, Mathematical Programming.
- F. Malliaros: IEEE Transactions on Knowledge and Data Engineering (TKDE), Data Mining and Knowledge Discovery, World Wide Web Journal, Marchine Learning.
- N. Ouzir: IEEE Trans. Biomedical Engineering, Elsevier Digital Signal Processing, Computer Vision and Image Understanding, Elsevier Signal Processing.
- M. Savanier: IEEE Open Journal of Signal Processing.
- G. Scrivanti: SIAM Journal on Mathematics of Data Science; SIAM Journal on Imaging Science; Transactions on Pattern Analysis and Machine Intelligence.
- H. Talbot: IEEE Pattern Analysis and Machine Intelligence, IEEE Transaction on Image Processing, Computer Vision and Image Understanding, J. on Mathematical Imaging and Vision, Signal Processing Letters, Transactions on Signal Processing.
- M. Vakalopoulou: International Journal of Computer Assisted Radiology and Surgery (IJCARS), IEEE Trans. on Geoscience and Remote Sensing (TGRS), Journal of Selected Topics in Applied Earth Observations and Remote Sensing (JSTARS), ISPRS Journal of Photogrammetry and Remote Sensing, Computer Methods and Programs in Biomedicine (CMPB), Pattern Recognition Letters, Computer Vision and Image Understanding (CVIU), SPIE Optical Engineering (OE), Remote Sensing MDPI, AAAI Conference on Artificial Intelligence 2021.

### 11.1.4 Invited talks

- E. Chouzenoux. January 2021. Invited talk (online) at "Présentation GENCI et projets de santé avec Medicen".
- E. Chouzenoux. February 2021. Invited webinar at "séminaire Palaisien", University Paris Saclay.
- E. Chouzenoux. February 2021. Invited talk (online) at "Journée statistique et Informatique pour la science des données à Paris Saclay",IHES.
- E. Chouzenoux. May 2021. Invited talk (online) at "Covid-19 and AI" organized by Inria UK.
- E. Chouzenoux. June 2021. Invited talk (online) at "IA et santé" organized by GENCI.
- E. Chouzenoux. June 2021. Invited talk (online) at "Journées scientifiques de Inria".
- E. Chouzenoux. September 2021. Invited talk (online) at "Neural networks for Inverse Problems in Satellite Imaging" organized by GdR MIA.
- E. Chouzenoux. October 2021. Invited talk at "Séminaire Parisien d'Optimisation", Jussieu, Paris.
- E. Chouzenoux. November 2021. Invited webinar, University of Bordeaux.
- F. Malliaros. April 2021, Invited webinar, Aristotle Univiversity of Thessaloniki, Greece.
- F. Malliaros. June 2021. Invited webinar, Nokia Bell Labs.
- J.-C. Pesquet. October 2021, keynote speaker, SpeD conference, Bucharest.
- M. Savanier. July 2021, invited talk (online), SIAM Conference on Optimization.
- M. Savanier. September 2021. Invited talk (online), IFIP TC7 Conference on System Modelling and Optimization.
- H. Talbot. October 2021. Invited talk, Université Pierre-et-Marie-Curie.
- H. Talbot. October 2021 . Invited talk, Institut Gustave-Roussy.
- H. Talbot. October 2021. Invited talk, Journées Françaises de Radiologie.
- S. Verma. January 2021. Presentation at Cambridge Innovation Center, Boston, MA, USA.
- S. Verma. November 2021. Presentation at US SpaceForce.
- S. Verma. June 2021. Presentation at National Geospatial Agency (NGA) and Defense Advanced Research Project Agency (DARPA).
- S. Verma. February 2021. Presentation at Techstars Boston Demo Day.

### 11.1.5 Leadership within the scientific community

J.-C. Pesquet is senior member of the Institut Universitaire de France and a Fellow of 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.

#### 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 $\beta$iomathematics teams of the MICS CentraleSupélec.

### 11.2 Teaching - Supervision - Juries

#### 11.2.1 Teaching administration

- F. Malliaros: co-director of the Master DSBA.
- F. Malliaros: responsible of the Data and Information Science (SDI) specialization at CentraleSupélec.
- H. Talbot: local responsible of the Master MVA (ENS Paris-Saclay) at CentraleSupélec.
- J.-C. Pesquet: local responsible of the Master Optimization (Univ. Orsay) at CentraleSupélec.

#### 11.2.2 Teaching

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

- Master: E. Chouzenoux. Foundations of Distributed and Large Scale Computing, 26h, M.Sc. in Data Sciences and Business Analytics, 3rd year course, CentraleSupélec, M.Sc. MVA, ENS Paris-Saclay, and ESSEC Business School, FR
- Master: E. Chouzenoux. Advanced Machine Learning, 18h, 3rd year course, CentraleSupélec, FR
- Master: F. Malliaros. Foundations of Machine Learning, 27h, Master in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School, FR
- 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, FR
- Master: F. Malliaros. 2EL1730: Machine Learning, 33h, 2nd year CentraleSupélec, FR
- Master: N. Ouzir. Advanced Machine Learning, 24h, M.Sc. in Data Sciences and Business Analytics, EN
- Master: J.-C. Pesquet. Introductory course on Optimization, 33h, 2nd year course, CentraleSupélec, FR
- Master: J.-C. Pesquet. Advanced course on Optimization, 10h, M.Sc. in Signal Processing and Automatic Control, Univ. Paris- Saclay, FR
- Master: J.-C. Pesquet. Introduction to Optimization, 6h, M.Sc. MVA, ENS Paris-Saclay, FR
- Master: J.-C. Pesquet. Convex Optimization Algorithms, 15h, M.Sc. in Optimization, Univ. Paris-Saclay , FR
- Master: H. Talbot. High-performance computing, 2nd year course, CentraleSupélec, 12h, EN
- Master: H. Talbot. Optimisation for AI, M.Sc in AI, CentraleSupélec and ESSEC Business School, 30h, EN
- Master: H. Talbot. Introduction to Machine Learning, MS Management of Technology, 30h, EN
- Master: H. Talbot. Introduction à la morphologie mathématique, 3rd year course, CentraleSupélec, 12h, FR

- Master: M. Vakalopoulou. Introduction to Visual Computing, 25h, 3rd year course, CentraleSupélec, FR
- Master: M. Vakalopoulou. Deep Learning, 25h, M.Sc. in Vision and Machine Learning, ENS Paris-Saclay, FR
- Master: M. Vakalopoulou. Introduction to Machine Learning, 33h, 2nd year course, CentraleSupélec, FR
- 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, CentraleSupélec, FR
- Master: M. Vakalopoulou. Deep Learning in Medical Imaging, 25h, M.Sc. in Vision and Machine Learning, ENS Paris-Saclay, FR
- PhD: E. Chouzenoux and J.-C. Pesquet. Convex Analysis and Convex Optimization Algorithms, 18h, ITN TradeOpt Winter School, 15-19 February 2021.

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

- T. Aouad
  Optimization, 11h, tutorials, 2nd year CentraleSupélec
  AI in Computer Vision, 12h, labs, ESIB, Liban
- J.-B. Fest
  Optimisation quadratique, 12h, tutorials, 1st year ENSTA Paristech
  Large scale distributed Optimiziation, 10h, labs, 3rd year CentraleSupélec
- A. Contreras
  Optimization and Proximal Methods, 21h, tutorials, 3rd year ENSTA
- T. Guilmeau
  Optimization, 11h, tutorials, 2nd year CentraleSupélec
- H. Huang
  Machine Learning, 18h, tutorials, 2nd year CentraleSupélec
  Optimization, 11h, tutorials, 2nd year CentraleSupélec
- S. Jain
  Machine Learning, 18h, tutorials, 2nd year CentraleSupélec
- S. Martin
  Signal processing, 18h, labs, 2nd year IUT
  Informatics, 30h, labs, 1st year BUT
  Introductory course in optimization, 5h, tutorials, M.Sc. MVA, ENS Paris-Saclay
- G. Scrivanti
  Optimization, 11h, tutorials, 2nd year CentraleSupélec
- S. Verma
  Foundation of Deep Learning, tutorials, 21h, 1st year CentraleSupelec

### 11.2.3 Supervision

- PhD (completed): Thank Xuan Nguyen. Détection et étude morphologique des sources extragalactiques par analyse variationnelle, 2018-2021, Supervised by H. Talbot and L. Najman (ESIEE PARIS).
- PhD (completed): Shaobo Luo. Deep learning-enabled imaging flow cytometry for micro organisms and micro-particle sizing, 2018-2021. Supervised by H. Talbot and T. Bourouina (ESIEE Paris)

- PhD (completed): Samy Ammari, Imagerie médicale computationnelle en neuro oncologie, 2019-2022, supervised by C. Balleyguier (Institut Gustave Roussy) and E. Chouzenoux.
- PhD (completed): Abdulkadir Çelikkanat, Graph representation learning with random walk diffusions, Dec. 2017 - April 2021, supervised by F. Malliaros and N. Paragios (TheraPanacea).
- PhD (completed): Théo Estienne, Improving anticancer therapies efficacy through Machine Learning on Medical Imaging & Genomic Data, 2017-2021, supervised by M. Vakalopoulou, N. Paragios (TheraPanacea) and E. Deutsch (Institut Gustave Roussy).
- PhD (completed): Enzo Battistella, Development of novel imaging approaches for tumour phenotype assessment by noninvasive imaging, 2017-2021, supervised by M. Vakalopoulou , N. Paragios (TheraPanacea) and E. Deutsch (Institut Gustave Roussy).
- 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): 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): Théodore Aouad. Geometric semi-supervised lachine-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): Mario Viti. Low-dose assessment of coronal vessel health on CT. 2019-2022, supervised by H. Talbot.
- PhD (in progress) : Yingping Li, Deep learning for medical imaging, 2018-2022, supervised by E. Chouzenoux and N. Lassau (Institut Gustave Roussy)
- PhD (in progress): Yunshi Huang, Majorization-Minimization approaches for large scale problems in image processing, 2018-2022, supervised by E. Chouzenoux and V. Elvira (Univ. Edinburgh).

- 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 Bucarest).
- 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): Marion Savanier, Reconstruction 3D interventionnelle, 2019-2022, supervised by E. Chouzenoux and C. Riddell (GE Healthcare).
- PhD (in progress): 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 (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): Georgios Panagopoulos, Influence maximization in social networks, 2018-2022, supervised by F. Malliaros and M. Vazirgiannis (Ècole Polytechnique).
- PhD (in progress): Surabhi Jagtap, Graph-based learning from multi-omics data, 2019-2022, 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. Karantzalos (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).

### 11.2.4 Juries

The faculty members of the team serve regularly as a jury Member to Final Engineering Internship and the Research Innovation Project for students of CentraleSupélec, 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

- E. Chouzenoux:
  Participation to the "Rendez-vous des Jeunes Mathématiciennes et Informaticiennes", 25 February 2021, Saclay (online event).
- M. Vakalopoulou:
  Coordinating a Study Group on MIDL2O21, 08 July 2021.
  Mentoring Session for the Women in Computer Vision Workshop at CVPR2021 (20 June 2021).
  Coordinating a working group on "How to write an outstanding review?" for the MIDL Winter Workshop 2021 (1st Dec. 2021).

# 12 Scientific production

## 12.1 Major publications

[1] G. Chassagnon, M. Vakalopoulou, E. Battistella, S. Christodoulidis, T.-N. Hoang-Thi, S. Dangeard, E. Deutsch, F. Andre, E. Guillo, N. Halm, S. El Hajj, F. Bompard, S. Neveu, C. Hani, I. Saab, A. Campredon, H. Koulakian, S. Bennani, G. Freche, M. Barat, A. Lombard, L. Fournier, H. Monnier, T. Grand, J. Gregory, Y. Nguyen, A. Khalil, E. Mahdjoub, P.-Y. Brillet, S. Tran Ba, V. Bousson, A. Mekki, R.-Y. Carlier, M.-P. Revel and N. Paragios. 'AI-driven quantification, staging and outcome prediction of COVID-19 pneumonia'. In: *Medical Image Analysis* 67 (Jan. 2021), p. 101860. DOI: 10.1016/j.media.2020.101860. URL: https://hal.archives-ouvertes.fr/hal-03133234.

[2] P. Combettes and J.-C. Pesquet. 'Fixed Point Strategies in Data Science'. In: *IEEE Transactions on Signal Processing* 69 (2021), pp. 3878–3905. DOI: 10.1109/TSP.2021.3069677. URL: https://hal.archives-ouvertes.fr/hal-03495546.

[3] N. Lassau, S. Ammari, E. Chouzenoux, H. Gortais, P. Herent, M. Devilder, S. Soliman, O. Meyrignac, M.-P. Talabard, J.-P. Lamarque, R. Dubois, N. Loiseau, P. Trichelair, E. Bendjebbar, G. Garcia, C. Balleyguier, M. Merad, A. Stoclin, S. Jegou, F. Griscelli, N. Tetelboum, Y. Li, S. Verma, M. Terris, T. Dardouri, K. Gupta, A. Neacsu, F. Chemouni, M. Sefta, P. Jehanno, I. Bousaid, Y. Boursin, E. Planchet, M. Azoulay, J. Dachary, F. Brulport, A. Gonzalez, O. Dehaene, J.-B. Schiratti, K. Schutte, J.-C. Pesquet, H. Talbot, E. Pronier, G. Wainrib, T. Clozel, F. Barlesi, M.-F. Bellin and M. Blum. 'Integrating deep learning CT-scan model, biological and clinical variables to predict severity of COVID-19 patients'. In: *Nature Communications* 12.634 (Jan. 2021). DOI: 10.1038/s41467-020-20657-4. URL: https://hal.archives-ouvertes.fr/hal-03136018.

## 12.2 Publications of the year

### International journals

[4] S. Ammari, A. Bône, C. Balleyguier, E. Moulton, É. Chouzenoux, A. Volk, Y. Menu, F. Bidault, F. Nicolas, P. Robert, M.-M. Rohé and N. Lassau. 'Can deep learning replace gadolinium in neuro-oncology?' In: *Investigative Radiology* 57 (29th July 2021), pp. 99–107. DOI: 10.1097/rli.0000000000000811. URL: https://hal.inria.fr/hal-03527628.

[5] S. Ammari, S. Pitre-Champagnat, L. Dercle, E. Chouzenoux, S. Moalla, S. Reuze, H. Talbot, T. Mokoyoko, J. Hadchiti, S. Diffetocq, A. Volk, M. El Haik, S. Lakiss, C. Balleyguier, N. Lassau and F. Bidault. 'Influence of magnetic field strength on magnetic resonance imaging radiomics features in brain imaging, an in vitro and in vivo study'. In: *Frontiers in Oncology* 10 (2021), p. 541663. DOI: 10.3389/fonc.2020.541663. URL: https://hal.archives-ouvertes.fr/hal-03117688.

[6] S. Ammari, R. Sallé de Chou, T. Assi, M. Touat, E. Chouzenoux, A. Quillent, E. Limkin, L. Dercle, J. Hadchiti, M. Elhaik, S. Moalla, M. Khettab, C. Balleyguier, N. Lassau, S. Dumont and C. Smolenschi. 'Machine-Learning-Based Radiomics MRI Model for Survival Prediction of Recurrent Glioblastomas Treated with Bevacizumab'. In: *Diagnostics* 11.7 (2021), p. 1263. DOI: 10.3390/diagnostics11071263. URL: https://hal.sorbonne-universite.fr/hal-03292019.

[7] S. Ammari, R. Sallé de Chou, C. Balleyguier, E. Chouzenoux, M. Touat, A. Quillent, S. Dumont, S. Bockel, G. C. T. E. Garcia, M. Elhaik, B. Francois, V. Borget, N. Lassau, M. Khettab and T. Assi. 'A Predictive Clinical-Radiomics Nomogram for Survival Prediction of Glioblastoma Using MRI'. In: *Diagnostics* 11.11 (4th Nov. 2021), p. 2043. DOI: 10.3390/diagnostics11112043. URL: https://hal.sorbonne-universite.fr/hal-03424507.

[8] D. Antunes, J.-O. Lachaud and H. Talbot. 'An Elastica-driven Digital Curve Evolution Model for Image Segmentation'. In: *Journal of Mathematical Imaging and Vision* 63.1 (Jan. 2021), pp. 1–17. DOI: 10.1007/s10851-020-00983-4. URL: https://hal.archives-ouvertes.fr/hal-03144926.

[9] E. Battistella, M. Vakalopoulou, R. Sun, T. Estienne, M. Lerousseau, S. Nikolaev, É. A. Andres, A. Carré, S. Niyoteka, C. Robert, N. Paragios, E. Alvarez Andres and E. Deutsch. 'COMBING: Clustering in Oncology for Mathematical and Biological Identification of Novel Gene Signatures'. In: *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (1st Nov. 2021), pp. 1–1. DOI: 10.1109/TCBB.2021.3123910. URL: https://hal-centralesupelec.archives-ouvertes.fr/hal-03530265.

[10] A. Bône, S. Ammari, Y. Menu, C. Balleyguier, E. Moulton, E. Chouzenoux, A. Volk, G. C. Garcia, F. Nicolas, P. Robert, M.-M. Rohé and N. Lassau. 'From dose reduction to contrast maximization: can deep learning amplify the impact of contrast media on brain MR image quality? A reader study'. In: *Investigative Radiology* (2022). URL: https://hal.inria.fr/hal-03535186.

[11] A. Campredon, E. Battistella, C. Martin, I. Durieu, L. Mely, C. Marguet, C. Belleguic, M. Murris-Espin, R. Chiron, A. Fanton, S. Bui, M. Reynaud-Gaubert, P. Reix, T.-N. Hoang-Thi, M. Vakalopoulou, M.-P. Revel, J. Da Silva, P.-R. Burgel and G. Chassagnon. 'Using chest CT scan and unsupervised machine learning for predicting and evaluating response to lumacaftor-ivacaftor in people with cystic fibrosis'. In: *European Respiratory Journal* (12th Oct. 2021), p. 2101344. DOI: 10.1183/13993003.01344-2021. URL: https://hal.archives-ouvertes.fr/hal-03539118.

[12] A. Çelikkanat and F. D. Malliaros. 'Topic-aware latent models for representation learning on networks'. In: *Pattern Recognition Letters* (14th Jan. 2021). URL: https://hal.archives-ouvertes.fr/hal-03420690.

[13] G. Chassagnon, M. Vakalopoulou, A. Régent, M. Sahasrabudhe, R. Marini, T.-N. Hoang-Thi, A.-T. Dinh-Xuan, B. Dunogué, L. Mouthon, N. Paragios and M.-P. Revel. 'Elastic Registration–driven Deep Learning for Longitudinal Assessment of Systemic Sclerosis Interstitial Lung Disease at CT'. In: *Radiology* 298.1 (Jan. 2021), pp. 189–198. DOI: 10.1148/radiol.2020200319. URL: https://hal.archives-ouvertes.fr/hal-03134510.

[14] E. Chouzenoux, J.-C. Pesquet, C. Riddell, M. Savanier and Y. Trousset. 'Convergence of Proximal Gradient Algorithm in the Presence of Adjoint Mismatch'. In: *Inverse Problems* 37.6 (Jan. 2021), p. 065009. URL: https://hal.archives-ouvertes.fr/hal-03136110.

[15] P. Combettes and J.-C. Pesquet. 'Fixed Point Strategies in Data Science'. In: *IEEE Transactions on Signal Processing* 69 (2021), pp. 3878–3905. DOI: 10.1109/TSP.2021.3069677. URL: https://hal.archives-ouvertes.fr/hal-03495546.

[16] A. Contreras and J. Peypouquet. 'Forward-backward approximation of nonlinear semigroups in finite and infinite horizon'. In: *Communications on Pure & Applied Analysis* 20.5 (May 2021), pp. 1893–1906. DOI: 10.3934/cpaa.2021051. URL: https://hal.archives-ouvertes.fr/hal-03528849.

[17] T. Dardouri, M. Kaaniche, A. Benazza-Benyahia and J.-C. Pesquet. 'Dynamic Neural Network for Lossy-to-Lossless Image Coding'. In: *IEEE Transactions on Image Processing* 31 (17th Dec. 2021), pp. 569–584. DOI: 10.1109/TIP.2021.3132825. URL: https://hal.archives-ouvertes.fr/hal-03526618.

[18] L. El Gueddari, C. Giliyar Radhakrishna, E. Chouzenoux and P. Ciuciu. 'Calibration-Less Multi-Coil Compressed Sensing Magnetic Resonance Image Reconstruction Based on OSCAR Regularization'. In: *Journal of Imaging* 7.3 (Mar. 2021), p. 58. DOI: 10.3390/jimaging7030058. URL: https://hal.inria.fr/hal-03366158.

[19] N. Gogin, M. Viti, L. Nicodème, M. Ohana, H. Talbot, U. Gencer, M. Mekukosokeng, T. Caramella, Y. Diascorn, J.-Y. Airaud, M.-S. Guillot, Z. Bensalah, C. Dam Hieu, B. Abdallah, I. Bousaid, N. Lassau and E. Mousseaux. 'Automatic coronary artery calcium scoring from unenhanced-ECG-gated CT using deep learning'. In: *Diagnostic and Interventional Imaging* 102.11 (Nov. 2021), pp. 683–690. DOI: 10.1016/j.diii.2021.05.004. URL: https://hal.archives-ouvertes.fr/hal-03500506.

[20] T.-N. Hoang-Thi, M. Vakalopoulou, S. Christodoulidis, N. Paragios, M.-P. Revel and G. Chassagnon. 'Deep learning for lung disease segmentation on CT: Which reconstruction kernel should be used?' In: *Diagnostic and Interventional Imaging* 102.11 (Nov. 2021), pp. 691–695. DOI: 10.1016/j.diii.2021.10.001. URL: https://hal.archives-ouvertes.fr/hal-03539082.

[21] T. Hortholary, C. Carrion, E. Chouzenoux, J.-C. Pesquet and C. Lefort. 'Multiplex-multiphoton microscopy and computational strategy for biomedical imaging'. In: *Microscopy Research and Technique* (2021). DOI: 10.1002/jemt.23712. URL: https://hal.archives-ouvertes.fr/hal-03126396.

[22] Y. Huang, E. Chouzenoux and V. Elvira. 'Probabilistic modeling and inference for sequential space-varying blur identification'. In: *IEEE Transactions on Computational Imaging* 7 (2021), pp. 531–546. URL: https://hal.archives-ouvertes.fr/hal-03225842.

[23] C. Lefort, M. Chalvidal, A. Parenté, V. Blanquet, H. Massias, L. Magnol and E. Chouzenoux. 'FAMOUS: a fast instrumental and computational pipeline for multiphoton microscopy applied to 3D imaging of muscle ultrastructure'. In: *Journal of Physics D: Applied Physics* 54.27 (30th Apr. 2021), p. 274005. DOI: 10.1088/1361-6463/abf8f2. URL: https://hal.archives-ouvertes.fr/hal-03225997.

[24] Y. Li, S. Ammari, C. Balleyguier, N. Lassau and E. Chouzenoux. 'Impact of Preprocessing and Harmonization Methods on the Removal of Scanner Effects in Brain MRI Radiomic Features'. In: *Cancers* 13 (15th June 2021). DOI: 10.3390/cancers13123000. URL: https://hal.archives-ouvertes.fr/hal-03261617.

[25] S. Luo, T. Bourouina, G. Chierchia, H. Talbot, A.-Q. Liu, Y. Shi, K. T. Nguyen, S. Feng and A. Elsayed. 'Deep learning-enabled imaging flow cytometry for high-speed Cryptosporidium and Giardia detection'. In: *Cytometry Part A* (3rd Feb. 2021). DOI: 10.1002/cyto.a.24321. URL: https://hal-upec-upem.archives-ouvertes.fr/hal-03161362.

[26] S. Luo, Y. Shi, L. K. Chin, P. E. Hutchinson, Y. Zhang, G. Chierchia, H. Talbot, X. Jiang, T. Bourouina and A.-Q. Liu. 'Machine-Learning-Assisted Intelligent Imaging Flow Cytometry: A Review'. In: *Advanced Intelligent Systems* 3.11 (Nov. 2021), p. 2100073. DOI: 10.1002/aisy.202100073. URL: https://hal.archives-ouvertes.fr/hal-03540960.

[27] S. Luo, Y. Shi, L. K. Chin, Y. Zhang, B. Wen, Y. Sun, B. T. T. Nguyen, G. Chierchia, H. Talbot, T. Bourouina, X. Jiang and A.-Q. Liu. 'Rare bioparticle detection via deep metric learning'. In: *RSC Advances* 11.29 (2021), pp. 17603–17610. DOI: 10.1039/D1RA02869C. URL: https://hal.archives-ouvertes.fr/hal-03541059.

[28] A. Marmin, M. Castella, J.-C. Pesquet and L. Duval. 'Sparse signal reconstruction for nonlinear models via piecewise rational optimization'. In: *Signal Processing* 179 (Feb. 2021), 107835:1–107835:13. DOI: 10.1016/j.sigpro.2020.107835. URL: https://hal.archives-ouvertes.fr/hal-02972442.

[29] A. Mongia, E. Chouzenoux and A. Majumdar. 'Computational prediction of Drug-Disease association based on Graph-regularized one bit Matrix completion'. In: *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (2021). URL: https://hal.archives-ouvertes.fr/hal-03465955.

[30] A. Mongia, S. K. Saha, E. Chouzenoux and A. Majumdar. 'A computational approach to aid clinicians in selecting anti-viral drugs for COVID-19 trials'. In: *Scientific Reports* 11.9047 (27th Apr. 2021). DOI: 10.1038/s41598-021-88153-3. URL: https://hal.archives-ouvertes.fr/hal-02888874.

[31] T. X. Nguyen, G. Chierchia, O. Razim, R. Peletier, L. Najman, H. Talbot and B. Perret. 'Object Detection with Component-Graphs in Multi-band Images: Application to Source Detection in Astronomical Images'. In: *IEEE Access* 9 (16th Nov. 2021), pp. 156482–156491. DOI: 10.1109/ACCESS.2021.3128519. URL: https://hal.archives-ouvertes.fr/hal-03429058.

[32] M. Papadomanolaki, S. Christodoulidis, K. Karantzalos and M. Vakalopoulou. 'Unsupervised Multistep Deformable Registration of Remote Sensing Imagery Based on Deep Learning'. In: *Remote Sensing* 13.7 (29th Mar. 2021). DOI: 10.3390/rs13071294. URL: https://hal.inria.fr/hal-03538150.

[33] L. Papamanolis, H. J. Kim, C. Jaquet, M. Sinclair, M. Schaap, I. Danad, P. Van Diemen, P. Knaapen, L. Najman, H. Talbot, C. A. Taylor and I. Vignon-Clementel. 'Myocardial Perfusion Simulation for Coronary Artery Disease: A Coupled Patient-Specific Multiscale Model'. In: *Annals of Biomedical Engineering* 49 (May 2021), pp. 1432–1447. DOI: 10.1007/s10439-020-02681-z. URL: https://hal.archives-ouvertes.fr/hal-03036457.

[34] J.-C. Pesquet, A. Repetti, M. Terris and Y. Wiaux. 'Learning Maximally Monotone Operators for Image Recovery'. In: *SIAM Journal on Imaging Sciences* 14.3 (19th Aug. 2021), pp. 1206–1237. URL: https://hal.archives-ouvertes.fr/hal-03087515.

[35] J. Robic, A. Nkengne, B. Perret, M. Couprie, H. Talbot, G. Pellacani and K. Vie. 'Clinical validation of a computer-based approach for the quantification of the skin ageing process of women using in vivo confocal microscopy'. In: *Journal of the European Academy of Dermatology and Venereology* 35.1 (Jan. 2021). DOI: 10.1111/jdv.16810. URL: https://hal.archives-ouvertes.fr/hal-03144931.

[36] T. Routtenberg, A. Carini, E. Chouzenoux, P. Pal, J. C. M. Bermudez and L. Marcenaro. 'Fight the Pandemic: Highlights From the 2020 IEEE 5-Minute Video Clip Contest'. In: *IEEE Signal Processing Magazine*. 38th ser. 2 (Feb. 2021), pp. 138–143. DOI: 10.1109/MSP.2020.3046230. URL: https://hal.archives-ouvertes.fr/hal-03161830.

[37] M. Savanier, C. Riddell, Y. Trousset, E. Chouzenoux and J.-C. Pesquet. 'Magnification-driven B-spline Interpolation for Cone Beam Projection and Backprojection'. In: *Medical Physics* 48.10 (Dec. 2021). DOI: 10.1002/mp.15179. URL: https://hal.archives-ouvertes.fr/hal-03464469.

[38] M. Sghaier, E. Chouzenoux, J.-C. Pesquet and S. Muller. 'A Novel Task-Based Reconstruction Approach for Digital Breast Tomosynthesis'. In: *Medical Image Analysis* (2021). URL: https://hal.archives-ouvertes.fr/hal-02972386.

[39] S. Sharma, V. Elvira, E. Chouzenoux and A. Majumdar. 'Recurrent Dictionary Learning for State-Space Models with an Application in Stock Forecasting'. In: *Neurocomputing* (2021). URL: https://hal.archives-ouvertes.fr/hal-03184841.

[40] S. Singh, E. Chouzenoux, G. Chierchia and A. Majumdar. 'Multi-label Deep Convolutional Transform Learning for Non-intrusive Load Monitoring'. In: *ACM Transactions on Knowledge Discovery from Data (TKDD)* (Dec. 2021). URL: https://hal.archives-ouvertes.fr/hal-03463403.

[41] D. Talwar, A. Mongia, E. Chouzenoux and A. Majumdar. 'Binary Matrix Completion on Graphs: Application to Collaborative Filtering'. In: *Digital Signal Processing* (2021). URL: https://hal.archives-ouvertes.fr/hal-03500279.

[42] S. Verma, S. Singh and A. Majumdar. 'Multi-label LSTM autoencoder for non-intrusive appliance load monitoring'. In: *Electric Power Systems Research* 199 (Oct. 2021), p. 107414. DOI: 10.1016/j.epsr.2021.107414. URL: https://hal.archives-ouvertes.fr/hal-03294549.

### International peer-reviewed conferences

[43] A. Bône, S. Ammari, J.-P. Lamarque, M. Elhaik, É. Chouzenoux, F. Nicolas, P. Robert, C. Balleyguier, N. Lassau and M.-M. Rohé. 'Contrast-enhanced brain MRI synthesis with deep learning: key input modalities and asymptotic performance'. In: *Proceedings ISBI 2021*. ISBI 2021 - International Symposium on Biomedical Imaging. Nice / Virtual, France, 13th Apr. 2021. URL: https://hal.archives-ouvertes.fr/hal-03128023.

[44] J. Boyd, M. Liashuha, E. Deutsch, N. Paragios, S. Christodoulidis and M. Vakalopoulou. 'Self-Supervised Representation Learning using Visual Field Expansion on Digital Pathology'. In: 2021 IEEE/CVF International Conference on Computer Vision Workshops (ICCVW). Montreal, Canada: IEEE, 11th Oct. 2021, pp. 639–647. DOI: 10.1109/ICCVW54120.2021.00077. URL: https://hal-centralesupelec.archives-ouvertes.fr/hal-03448192.

[45] S. Dahiya, S. Sharma, D. Sahnan, V. Goel, E. Chouzenoux, V. Elvira, A. Majumdar, A. Bandhakavi and T. Chakraborty. 'Would Your Tweet Invoke Hate on the Fly? Forecasting Hate Intensity of Reply Threads on Twitter'. In: SIGKDD 2021 - 27th Conference on Knowledge Discovery and Data Mining. Proceedings of the 27th SIGKDD Conference on Knowledge Discovery and Data Mining (KDD 2021). Singapore, Singapore, Aug. 2021. DOI: 10.1145/3447548.3467150. URL: https://hal.archives-ouvertes.fr/hal-03281567.

[46] T. Dardouri, M. Kaaniche, A. Benazza-Benyahia, J.-C. Pesquet and G. Dauphin. 'A Neural Network Approach For Joint Optimization Of Predictors In Lifting-Based Image Coders'. In: 2021 IEEE International Conference on Image Processing (ICIP). Anchorage / Virtual, United States: IEEE, 19th Sept. 2021, pp. 3747–3751. DOI: 10.1109/ICIP42928.2021.9506737. URL: https://hal.archives-ouvertes.fr/hal-03526467.

[47] A. Duval and F. D. Malliaros. 'GraphSVX: Shapley Value Explanations for Graph Neural Networks'. In: European Conference on Machine Learning and Knowledge Discovery in Databases (ECML PKDD). Bilbao, Spain, 13th Sept. 2021. URL: https://hal.archives-ouvertes.fr/hal-03539183.

[48] T. Estienne, M. Vakalopoulou, S. Christodoulidis, E. Battistella, T. Henry, M. Lerousseau, A. Leroy, G. Chassagnon, M.-P. Revel, N. Paragios and E. Deutsch. 'Exploring Deep Registration Latent Spaces'. In: *Domain Adaptation and Representation Transfer, and Affordable Healthcare and AI for Resource Diverse Global Health.* DART in MICCAI 2021, the 24th International Conference on Medical Image Computing and Computer Assisted Intervention. Vol. 12968. Lecture Notes in Computer Science. Strasbourg, France: Springer International Publishing, 21st Sept. 2021, pp. 112–122. DOI: 10.1007/978-3-030-87722-4_11. URL: https://hal.archives-ouvertes.fr/hal-03524105.

[49] J.-B. Fest and E. Chouzenoux. 'Stochastic Majorize-Minimize Subspace Algorithm with Application to Binary Classification'. In: EUSIPCO 2021 - 29th European Signal Processing Conference. Proceedings of the 29th European Signal Processing Conference (EUSIPCO 2021). Dublin / Virtual, Ireland, Aug. 2021. URL: https://hal.inria.fr/hal-03275377.

[50] M. Gharbi, E. Chouzenoux, J.-C. Pesquet and L. Duval. 'GPU-based Implementations of MM Algorithms. Application to Spectroscopy Signal Restoration'. In: EUSIPCO 2021 - 29th European Signal Processing Conference. Dublin / Virtual, Ireland, 23rd Aug. 2021. URL: https://hal.inria.fr/hal-03275427.

[51] T. Guilmeau, E. Chouzenoux and V. Elvira. 'Simulated annealing: a review and a new scheme'. In: SSP 2021 - IEEE Statistical Signal Processing Workshop. Proceedings of the IEEE Statistical Signal Processing Workshop (SSP 2021). Rio de Janeiro, Brazil, July 2021. URL: https://hal.inria.fr/hal-03275401.

[52] K. Gupta, J.-C. Pesquet, B. Pesquet-Popescu, F. D. Malliaros and F. Kaakai. 'An Adversarial Attacker for Neural Networks in Regression Problems'. In: IJCAI Workshop on Artificial Intelligence Safety (AI Safety). Montreal/Virtual, Canada, 19th Aug. 2021. URL: https://hal-centralesupelec.archives-ouvertes.fr/hal-03527640.

[53] K. Gupta, B. Pesquet-Popescu, F. Kaakai and J.-C. Pesquet. 'A Quantitative Analysis Of The Robustness Of Neural Networks For Tabular Data'. In: ICASSP 2021 - 2021 IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP). Toronto, Canada: IEEE, 6th June 2021, pp. 8057–8061. DOI: 10.1109/ICASSP39728.2021.9413858. URL: https://hal-centralesupelec.archives-ouvertes.fr/hal-03527634.

[54] P. Gupta, J. Maggu, A. Majumdar, E. Chouzenoux and G. Chierchia. 'ConFuse: Convolutional Transform Learning Fusion Framework For Multi-Channel Data Analysis'. In: EUSIPCO 2020 - 28th European Signal Processing Conference. Proceedings of the 28th European Signal Processing Conference (EUSIPCO 2020). Amsterdam / Virtual, Netherlands, 18th Jan. 2021. URL: https://hal.archives-ouvertes.fr/hal-02943658.

[55] S. Jagtap, A. Çelikkanat, A. Pirayre, F. Bidard, L. Duval and F. D. Malliaros. 'Multiomics Data Integration for Gene Regulatory Network Inference with Exponential Family Embeddings'. In: EUSIPCO - 29th European Signal Processing Conference. Dublin / Online, Ireland, 23rd Aug. 2021. URL: https://hal.archives-ouvertes.fr/hal-03336884.

[56] S. Jagtap, A. Pirayre, F. Bidard, L. Duval and F. D. Malliaros. ‘BRANet: Graph-based Integration of Multi-omics Data with Biological a priori for Regulatory Network Inference’. In: 17th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB). Online, Italy, 15th Nov. 2021. URL: https://hal.archives-ouvertes.fr/hal-03425420.

[57] C. A. Kantor, L. Boussioux, B. Rauby and H. Talbot. ‘Over-MAP: Structural Attention Mechanism and Automated Semantic Segmentation Ensembled for Uncertainty Prediction’. In: AAAI 2021 - 35th AAAI Conference on Artificial Intelligence. Vol. 35. Proceedings of the AAAI Conference on Artificial Intelligence 17. Virtual, China, 2nd Feb. 2021, pp. 15316–15322. URL: https://hal.archives-ouvertes.fr/hal-03541009.

[58] C. A. Kantor, M. Skreta, B. Rauby, L. Boussioux, E. Jehanno, A. Luccioni, D. Rolnick and H. Talbot. ‘Geo-Spatiotemporal Features and Shape-Based Prior Knowledge for Fine-grained Imbalanced Data Classification’. In: *Proc. IJCAI 2021 Workshop on AI for Social Good (2021)*. IJCAI 2021 - Workshop on AI for Social Good. Tokyo, Japan, Jan. 2021. URL: https://hal.archives-ouvertes.fr/hal-03150686.

[59] O. Laousy, G. Chassagnon, E. Oyallon, N. Paragios, M.-P. Revel and M. Vakalopoulou. ‘Deep Reinforcement Learning for L3 Slice Localization in Sarcopenia Assessment’. In: Machine Learning in Medical Imaging @MICCAI. Strasbourg, France, 27th Sept. 2021. URL: https://hal.archives-ouvertes.fr/hal-03532954.

[60] M. Lerousseau, M. Classe, E. Battistella, T. Estienne, T. Henry, A. Leroy, R. Sun, M. Vakalopoulou, J.-Y. Scoazec, E. Deutsch and N. Paragios. ‘Weakly Supervised Pan-Cancer Segmentation Tool’. In: *Medical Image Computing and Computer Assisted Intervention – MICCAI 2021*. Medical Image Computing and Computer Assisted Intervention. Vol. 12908. Lecture Notes in Computer Science. Stansbroug, France: Springer International Publishing, 21st Sept. 2021, pp. 248–256. DOI: 10.1007/978-3-030-87237-3_24. URL: https://hal.archives-ouvertes.fr/hal-03539272.

[61] M. Lerousseau, M. Vakalopoulou, E. Deutsch and N. Paragios. ‘SparseConvMIL: Sparse Convolutional Context-Aware Multiple Instance Learning for Whole Slide Image Classification’. In: Machine Learning Research 156. Strasbourg, France, 27th Sept. 2021. URL: https://hal.archives-ouvertes.fr/hal-03539261.

[62] E. Leroy, A. Marmin, M. Castella and L. Duval. ‘Weight identification through global optimization in a new hysteretic neural network model’. In: *2021 IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*. ICASSP 2021 - 46th International Conference on Acoustics, Speech and Signal Processing. Toronto (online), Canada: IEEE, 2021, pp. 5315–5319. DOI: 10.1109/ICASSP39728.2021.9413383. URL: https://hal.archives-ouvertes.fr/hal-03227078.

[63] Y. Li, E. Chouzenoux, B. Charmettant, B. Benatsou, J.-P. Lamarque and N. Lassau. ‘Lightweight U-Net for Lesion Segmentation in Ultrasound Images’. In: ISBI 2021 - IEEE International Symposium on Biomedical Imaging. Proceedings of the IEEE International Symposium on Biomedical Imaging (ISBI 2021). Nice / Virtual, France, 13th Apr. 2021. URL: https://hal.archives-ouvertes.fr/hal-03140737.

[64] S. Martin, E. Chouzenoux and J.-C. Pesquet. ‘A Penalized Subspace Strategy for Solving Large-Scale Constrained Optimization Problems’. In: EUSIPCO 2021 - 29th European Signal Processing Conference. Proceedings of the 29th European Signal Processing Conference (EUSIPCO 2021). Dublin / Virtual, Ireland, 23rd Aug. 2021. URL: https://hal.archives-ouvertes.fr/hal-03275387.

[65] L. Milecki, S. Bodard, J.-M. Correas, M.-O. Timsit and M. Vakalopoulou. ‘3D Unsupervised Kidney Graft Segmentation Based on Deep Learning and Multi-Sequence MRI’. In: IEEE ISBI 2021 - International Symposium on Biomedical Imaging. Nice / Virtual, France, 13th Apr. 2021. URL: https://hal.archives-ouvertes.fr/hal-03141528.

[66] A. Neacsu, K. Gupta, J.-C. Pesquet and C. Burileanu. ‘Signal Denoising Using a New Class of Robust Neural Networks’. In: EUSIPCO 2020 - 28th European Signal Processing Conference. Amsterdam, Netherlands: IEEE, 18th Jan. 2021, pp. 1492–1496. DOI: 10.23919/Eusipco47968.2020.9287630. URL: https://hal-centralesupelec.archives-ouvertes.fr/hal-03115064.

[67] G. Panagopoulos and F. D. Malliaros. ‘Influence Learning and Maximization’. In: 21st International Conference on Web Engineering (ICWE). Biarritz, France, 18th May 2021. URL: https://hal.archives-ouvertes.fr/hal-03539200.

[68] M. Savanier, E. Chouzenoux, J.-C. Pesquet, C. Riddell and Y. Trousset. ‘Proximal Gradient Algorithm in the Presence of Adjoint Mismatch’. In: EUSIPCO 2020 - 28th European Signal Processing Conference. Proceedings of the 28th European Signal Processing Conference (EUSIPCO 2020). Amsterdam (virtual), Netherlands, 18th Jan. 2021. URL: https://hal.archives-ouvertes.fr/hal-02943659.

[69] W. Tang, E. Chouzenoux, J.-C. Pesquet and H. Krim. ‘Deep transform and metric learning networks’. In: ICASSP 2021 - IEEE International Conference on Acoustics, Speech and Signal Processing. Proceedings of the IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP 2021). Toronto Virtual, Canada, June 2021. URL: https://hal.archives-ouvertes.fr/hal-03281571.

[70] M. Terris, A. Repetti, J.-C. Pesquet and Y. Wiaux. ‘Enhanced convergent PnP agorithms for image restoration’. In: 2021 IEEE International Conference on Image Processing (ICIP). Proceedings of the 2021 IEEE International Conference on Image Processing (ICIP). Anchorage, United States, 2021, pp. 1684–1688. URL: https://hal.archives-ouvertes.fr/hal-03497818.

[71] V. Vasilescu, A. Neacsu, E. Chouzenoux, J.-C. Pesquet and C. Burileanu. ‘A Deep Learning Approach for Improved Segmentation of Lesions Related to Covid-19 Chest CT Scans’. In: ISBI 2021 - IEEE International Symposium on Biomedical Imaging. Nice / Virtual, France, 13th Apr. 2021. URL: https://hal.archives-ouvertes.fr/hal-03188444.

[72] S. Verma, A. Panigrahi and S. Gupta. ‘QFabric: Multi-Task Change Detection Dataset’. In: EARTHVISION 2021 Workshops - Large Scale Computer Vision for Remote Sensing Imagery: in conjunction with the Conference on Computer Vision and Pattern Recognition (CVPR 2021). Virtual, France, 19th June 2021. URL: https://hal.archives-ouvertes.fr/hal-03294534.

[73] S. Verma and J.-C. Pesquet. ‘Sparsifying Networks via Subdifferential Inclusion’. In: ICML 2021 - Thirty-eighth International Conference on Machine Learning. Virtual, France, 18th July 2022. URL: https://hal.archives-ouvertes.fr/hal-03294543.

[74] J. Zhang, K. Ma, J. Van Arman, R. Gupta, J. Saltz, M. Vakalopoulou and D. Samaras. ‘A Joint Spatial and Magnification Based Attention Framework for Large Scale Histopathology Classification’. In: CVMI. Nashville, United States, 25th June 2021. URL: https://hal.archives-ouvertes.fr/hal-03539240.

### Scientific book chapters

[75] M. Vakalopoulou, S. Christodoulidis, M. Sahasrabudhe and N. Paragios. ‘Deep Learning for the Earth Sciences’. In: *Deep Learning for the Earth Sciences: A Comprehensive Approach to Remote Sensing, Climate Science, and Geosciences*. 1. Wiley, 27th Sept. 2021. DOI: 10.1002/9781119646181.ch9. URL: https://hal.archives-ouvertes.fr/hal-03539417.

### Reports & preprints

[76] E. Chouzenoux, C. Della Valle and J.-C. Pesquet. *Inversion of Integral Models: a Neural Network Approach*. 31st May 2021. URL: https://hal.archives-ouvertes.fr/hal-03243257.

[77] V. Elvira and E. Chouzenoux. *Optimized Population Monte Carlo*. 2nd Mar. 2021. URL: https://hal.archives-ouvertes.fr/hal-03136318.

[78] J.-Y. Tourneret, A. Basarab, N. L. Ouzir and Q. Wei. *Sparse representations and dictionary learning: from image fusion to motion estimation*. 4th Jan. 2021. URL: https://hal.inria.fr/hal-03130465.

[79] S. Verma. *A Survey on Machine Learning Applied to Dynamic Physical Systems*. 25th Jan. 2021. URL: https://hal.archives-ouvertes.fr/hal-03120225.

[80] F. G. Veshki, N. L. Ouzir, S. A. Vorobyov and E. Ollila. *Coupled Feature Learning for Multimodal Medical Image Fusion*. 3rd Feb. 2021. URL: `https://hal.inria.fr/hal-03130475`.

[81] M. Viti, H. Talbot and N. Gogin. *Coronary Plaque Localization and Characterization using Self-Attention Tree-Graph embeddings*. 22nd Dec. 2021. URL: `https://hal.archives-ouvertes.fr/hal-03500460`.

### Other scientific publications

[82] C. Lefort, M. Chalvidal, A. Parente, V. Blanquet, H. Massias, L. Magnol and E. Chouzenoux. 'Deep-3D-multiphoton imaging of whole biological structures with a computational assistance and the pipeline FAMOUS'. In: Physics and Biological Systems 2021. Grenoble, France, 22nd June 2021. URL: `https://hal.archives-ouvertes.fr/hal-03274262`.