

Activity Report 2019

Project-Team OPIS

OPtImization for large Scale biomedical data

RESEARCH CENTER Saclay - Île-de-France

THEME

Computational Neuroscience and Medicine

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Keywords:

Computer Science and Digital Science:

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

Other Research Topics and Application Domains:

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

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2. Overall Objectives

2.1. OPIS

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. Because of the versatility of the methods that will be proposed, 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. Sparse signal processing in chemistry

Participants: Marc Castella, Emilie Chouzenoux, Arthur Marmin, 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 antidoping, 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. This amounts to solve a large scale signal estimation problem under specific sparsity constraints [35], [55]. Collaboration with Dr. L. Duval, Research Engineer at IFP Energies Nouvelles, France is on-going in this applicative context.

4.2. Image restoration for two-photon microscopy

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Mathieu Chalvidal (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 [12] 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.

4.3. Representation Learning for Biological Networks

Participants: Fragkiskos Malliaros, Abdulkadir Çelikkanat (Collaboration: Duong Nguyen, UC San Diego) Networks (or graphs) are ubiquitous in the domain of biology, as many biological systems can naturally be mapped to graph structures. Characteristic examples include protein-protein interaction and gene regulatory networks. To this extend, machine learning on graphs is an important task with many practical applications in network biology. For example, in the case on protein-protein interaction networks, predicting the function of a protein is a key task that assigns biochemical roles to proteins. The main challenge here is to find appropriate representations of the graph structure, in order to be easily exploited by machine learning models. The traditional approach to the problem was relying on the extraction of "hand-crafted" discriminating features that encode information about the graph, based on user-defined heuristics. Nevertheless, this approach has demonstrated severe limitations, as the learning process heavily depends on the manually extracted features. To this end, feature (or representation) learning techniques can be used to automatically learn to encode the graph structure into low-dimensional feature vectors – which can later be used in learning tasks. Our goal here is to develop a systematic framework for large-scale representation learning on biological graphs. Our approach takes advantage of the clustering structure of these networks, to further enhance the ability of the learned features to capture intrinsic structural properties.

4.4. Breast tomosynthesis

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet, Maissa Sghaier (collaboration G. Palma, GE Healthcare)

Breast cancer is the most frequently diagnosed cancer for women. Mammography is the most used imagery tool for detecting and diagnosing this type of cancer. Since it consists of a 2D projection method, this technique is sensitive to geometrical limitations such as the superimposition of tissues which may reduce the visibility of lesions or make even appear false structures which are interpreted by radiologists as suspicious signs. Digital breast tomosynthesis allows these limitations to be circumvented. This technique is grounded on the acquisition of a set of projections with a limited angle view. Then, a 3D estimation of the sensed object is performed from this set of projections, so reducing the overlap of structures and improving the visibility and detectability of lesions possibly present in the breast. The objective of our work is to develop a high quality reconstruction methodology where the full pipeline of data processing is modeled [50].

4.5. Inference of gene regulatory networks

Participants: Surabhi Jagtap, Fragkiskos Malliaros, Jean-Christophe Pesquet (collaboration A. Pirayre and L. Duval, IFPEN)

The discovery of novel gene regulatory processes improves the understanding of cell phenotypic responses to external stimuli for many biological applications, such as medicine, environment or biotechnologies. To this purpose, transcriptomic data are generated and analyzed from DNA microarrays or more recently RNAseq experiments. They consist in genetic expression level sequences obtained for all genes of a studied organism placed in dierent living conditions. From these data, gene regulation mechanisms can be recovered by revealing topological links encoded in graphs. In regulatory graphs, nodes correspond to genes. A link between two nodes is identified if a regulation relationship exists between the two corresponding genes. In our work, we propose to address this network inference problem with recently developed techniques pertaining to graph optimization. Given all the pairwise gene regulation information available, we propose to determine the presence of edges in the considered GRN by adopting an energy optimization formulation integrating additional constraints. Either biological (information about gene interactions) or structural (information about node connectivity) a priori are considered to restrict the space of possible solutions. Different priors lead to different properties of the global cost function, for which various optimization strategies, either discrete and continuous, can be applied.

4.6. Imaging biomarkers and characterization for chronic lung diseases

Participants: Guillaume Chassagnon, Maria Vakalopoulou (in collaboration with Marie-Pierre Revel and Nikos Paragios: AP-HP - Hopital Cochin Broca Hotel Dieu; 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.

4.7. Imaging radiomics and genes to assess immunotherapy

Participants: Samy Ammari, Enzo Batistella, Emilie Chouzenoux, Théo Estienne, Marvin Lerousseau, Hugues Talbot, Roger Sun, Maria Vakalopoulou (in collaboration with Corinne Balleyguier, Caroline Caramella, Éric Deutsch, Nathalie Lassau, Institut de Cancérologie Gustave Roussy, Nikos Paragios, Therapanacea)

Because responses of cancer patients to immunotherapy can vary considerably, innovative predictors of response to treatment are urgently needed to improve patients outcomes.

We have aimed to develop and independently validate a radiomics-based biomarkers of tumour-infiltrating CD8 cells in patients included in phase 1 trials of anti-programmed cell death protein (PD)-1 or anti-programmed cell death ligand 1 (PD-L1) mono-therapy. We also aimed to evaluate the association between the biomarker, tumour immune phenotype and clinical outcomes of these patients.

Concurrently, we have evaluated various ways of estimating patient response to treatment based on well-established radiomics such as estimated tumour count and volumes. Among published metrics, we have select those that shown good predictive power and proposed a new one, which is particularly effective for patient with a poor response [63].

Furthermore, we have developed and validated a novel imaging-based decision-making algorithm for use by the clinician that helps differentiate pituitary metastasis from autoimmune hypophysitis in patients undergoing immune checkpoint blockade therapy [21].

These works are in collaboration with the Institut de Cance rologie Gustave Roussy Paris.

4.8. Development of a heart ventricle vessel generation model for perfusion analysis

Participant: Hugues Talbot (collaboration with L. Najman ESIEE Paris, I. Vignon-Clementel, REO Team leader, Inria, Charles Taylor, Heartflow Inc.)

Cardio-vascular diseases are 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 catheterization and relatively 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 worked to use image-based exams only, limiting the use of contrast agents and in many cases eliminating catheterisation. Heartflow is current the market leader in non-invasive coronary exams.

Unfortunately, current imaging technology is unable to assess 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. Blood perfusion throughout the heart muscle can provide insight regarding coronary health in areas that CT or MRI cannot assess. Perfusion imaging with PET or a Gamma camera, the current gold standard, is an invasive technology requiring the use of radioactive tracers.

We have investigated patient-specific vessel generation models together with porous model simulations in order to propose a forward 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 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.

In 2019, we have produced 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 have produced a CFD code capable of simulating blood flow in all three coupled compartments, which allows us to simulate perfusion realistically.

5. Highlights of the Year

5.1. Highlights of the Year

• Our M.Sc. program in Data Sciences and Business Analytics (with ESSEC Business School) was ranked 3rd worldwide in the OS World University Rankings.

- E. Chouzenoux was laureate of the ERC Starting Grant MAJORIS (starting date: 01-01-2020).
- M.C. Corbineau received the best poster award at "Journée de rencontre entre entreprises, doctorants et jeunes docteurs" (J-RED) in 2019.

6. New Software and Platforms

6.1. Platforms

6.1.1. 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: http://proximity-operator.net/

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.

6.1.2. FIGARO

Participants: Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with Claire Lefort, XLIM, Limoges).

link: https://imagejdocu.tudor.lu/plugin/analysis/figaro_psf_3d_optical_microscopy/start

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 [12].

6.1.3. Kymatio

Participant: Edouard Oyallon. **link:** http://www.kymat.io

The website shares the software Kymatio for Scattering Transform, that computes cascade of wavelets and modulus non-linearity. The codes have been optimized for GPUs and work on the open-source framework *PyTorch*.

6.1.4. BiasedWalk: Learning latent node features with biased random walks

Participants: Fragkiskos Malliaros and Duong Nguyen (UC San Diego)

link: https://github.com/duong18/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.

6.1.5. DiffuGreedy: Influence maximization in complex networks based on diffusion cascades

Participants: Fragkiskos Malliaros, Georgios Panagopoulos and Michalis Vazirgiannis (École Polytechnique) **link:** https://goo.gl/GpfCVZ

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.

6.1.6. Graph-based text categorization

Participants: Fragkiskos Malliaros, Konstantinos Skianis and Michalis Vazirgiannis (École Polytechnique) **link:** https://github.com/y3nk0/Graph-Based-TC/

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.

6.1.7. KernelNE - Topical Node Embeddings

Participants: Abdulkadir Çelikkanat, Fragkiskos Malliaros

link: https://abdcelikkanat.github.io/projects/kernelNE/

KernelNE learns node representations on graphs based on a weighted matrix factorization model which encodes random walk-based information about the nodes, as described in [53].

6.1.8. EFGE - Exponential Family Graph Embeddings

Participants: Abdulkadir Çelikkanat, Fragkiskos Malliaros

link: https://abdcelikkanat.github.io/projects/EFGE/

EFGE learns node embeddings generalizing random walk-based network representation learning techniques to exponential family conditional distributions, as described in [54].

6.1.9. Semi-supervised Fake News Detection

Participants: Adrien Benamira, Benjamin Devillers, Etienne Lesot, Ayush K. Ray, Manal Saadi, and Fragkiskos Malliaros

link: https://github.com/bdvllrs/misinformation-detection-tensor-embeddings

We propose a graph-based semi-supervised fake news detection method, based on graph neural networks, as described in [34].

6.1.10. The PINK image library

Participant: Hugues Talbot **link:** http://ibipio.hu/joomla/

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.

6.1.11. The Vivabrain AngioTK toolkit

Participant: Hugues Talbot

link: https://github.com/vivabrain/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.

6.1.12. The PET/CT FIJI Viewer

Participant: Hugues Talbot
link: http://petctviewer.org/

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. New Results

7.1. General risk measures for robust machine learning

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet (Collaboration: Henri Gérard, ENPC, Paris) A wide array of machine learning problems are formulated as the minimization of the expectation of a convex loss function on some parameter space. Since the probability distribution of the data of interest is usually unknown, it is is often estimated from training sets, which may lead to poor out-of-sample performance. In the work [11], we bring new insights in this problem by using the framework which has been developed in quantitative finance for risk measures. We show that the original min-max problem can be recast as a convex minimization problem under suitable assumptions. We discuss several important examples of robust formulations, in particular by defining ambiguity sets based on φ -divergences and the Wasserstein metric. We also propose an efficient algorithm for solving the corresponding convex optimization problems involving complex convex constraints. Through simulation examples, we demonstrate that this algorithm scales well on real data sets.

7.2. Deep Latent Factor Model for Collaborative Filtering

Participants: Emilie Chouzenoux (Collaboration: Aanchal Mongia, Neha Jhamb, Angshul Majumdar, IIIT Delhi, India)

Latent factor models have been used widely in collaborative filtering based recommender systems. In recent years, deep learning has been successful in solving a wide variety of machine learning problems. Motivated by the success of deep learning, we propose in [44], [23] a deeper version of latent factor model. Experiments on benchmark datasets shows that our proposed technique significantly outperforms all stateof-the-art collaborative filtering techniques.

7.3. A Proximal Interior Point Algorithm with Applications to Image Processing

Participants: Emilie Chouzenoux, Marie-Caroline Corbineau, Jean-Christophe Pesquet
In the work [10], we introduce a new proximal interior point algorithm (PIPA). This algorithm is able to handle convex optimization problems involving various constraints where the objective function is the sum of a Lipschitz differentiable term and a possibly nonsmooth one. Each iteration of PIPA involves the minimization of a merit function evaluated for decaying values of a logarithmic barrier parameter. This inner minimization is performed thanks to a finite number of subiterations of a variable metric forward-backward method employing a line search strategy. The convergence of this latter step as well as the convergence the global method itself are analyzed. The numerical efficiency of the proposed approach is demonstrated in two image processing applications.

7.4. Deep Unfolding of a Proximal Interior Point Method for Image Restoration

Participants: Emilie Chouzenoux, Marie-Caroline Corbineau, Jean-Christophe Pesquet (Collaboration: Carla Bertocchi, Marco Prato, Universita di Modena, Italy)

Variational methods are widely applied to ill-posed inverse problems for they have the ability to embed prior knowledge about the solution. However, the level of performance of these methods significantly depends on a set of parameters, which can be estimated through computationally expensive and time consuming methods. In contrast, deep learning offers very generic and efficient architectures, at the expense of explainability, since it is often used as a black-box, without any fine control over its output. Deep unfolding provides a convenient approach to combine variational-based and deep learning approaches. Starting from a variational formulation for image restoration, we developped in [36], [5], iRestNet, a neural network architecture obtained by unfolding a proximal interior point algorithm. Hard constraints, encoding desirable properties for the restored image, are incorporated into the network thanks to a logarithmic barrier, while the barrier parameter, the stepsize, and the penalization weight are learned by the network. We derive explicit expressions for the gradient of the proximity operator for various choices of constraints, which allows training iRestNet with gradient descent and backpropagation. In addition, we provide theoretical results regarding the stability of the network for a common inverse problem example. Numerical experiments on image deblurring problems show that the proposed approach compares favorably with both state-of-the-art variational and machine learning methods in terms of image quality.

7.5. Preconditioned P-ULA for Joint Deconvolution-Segmentation of Ultrasound Images

Participants: Emilie Chouzenoux, Marie-Caroline Corbineau, Jean-Christophe Pesquet (Collaboration: Denis Kouamé, Jean-Yves Tourneret, IRIT, Toulouse)

Joint deconvolution and segmentation of ultrasound images is a challenging problem in medical imaging. By adopting a hierarchical Bayesian model, we propose in [15] an accelerated Markov chain Monte Carlo scheme where the tissue reflectivity function is sampled thanks to a recently introduced proximal unadjusted Langevin algorithm. This new approach is combined with a forward-backward step and a preconditioning strategy to accelerate the convergence, and with a method based on the majorization-minimization principle to solve the inner nonconvex minimization problems. As demonstrated in numerical experiments conducted on both simulated and in vivo ultrasound images, the proposed method provides high-quality restoration and segmentation results and is up to six times faster than an existing Hamiltonian Monte Carlo method.

7.6. A Random Block-Coordinate Douglas-Rachford Splitting Method with Low Computational Complexity for Binary Logistic Regression

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet (Collaboration: Giovanni Chierchia, ESIEE Paris, Luis Bricenos Arias, Universidad Técnica Federico Santa Maria, Valparaiso, Chile)

In the paper [6], we proposed a new optimization algorithm for sparse logistic regression based on a stochastic version of the Douglas-Rachford splitting method. Our algorithm sweeps the training set by randomly selecting a mini-batch of data at each iteration, and it allows us to update the variables in a block coordinate manner. Our approach leverages the proximity operator of the logistic loss, which is expressed with the generalized Lambert W function. Experiments carried out on standard datasets demonstrate the efficiency of our approach w.r.t. stochastic gradient-like methods.

7.7. A probabilistic incremental proximal gradient method

Participant: Emilie Chouzenoux (Collaboration: Omer Deniz Akyildiz, Alan Turing Institute, London, UK, Victor Elvira, University of Edinburgh, Joaquin Miguez, Universidad Carlos III de Madrid, Spain)

In the paper [3], we proposed a probabilistic optimization method, named probabilistic incremental proximal gradient (PIPG) method, by developing a probabilistic interpretation of the incremental proximal gradient algorithm. We explicitly model the update rules of the incremental proximal gradient method and develop a systematic approach to propagate the uncertainty of the solution estimate over iterations. The PIPG algorithm takes the form of Bayesian filtering updates for a state-space model constructed by using the cost function. Our framework makes it possible to utilize well-known exact or approximate Bayesian filters, such as Kalman or extended Kalman filters, to solve large scale regularized optimization problems.

7.8. Optimal Multivariate Gaussian Fitting with Applications to PSF Modeling in Two-Photon Microscopy Imaging

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet (Collaboration: Claire Lefort, XLIM, Limoges, Tim Tsz-Kit Lau, Northwestern University, USA)

Fitting Gaussian functions to empirical data is a crucial task in a variety of scientific applications, especially in image processing. However, most of the existing approaches for performing such fitting are restricted to two dimensions and they cannot be easily extended to higher dimensions. Moreover, they are usually based on alternating minimization schemes which benefit from few theoretical guarantees in the underlying nonconvex setting. In the paper [12], we provided a novel variational formulation of the multivariate Gaussian fitting problem, which is applicable to any dimension and accounts for possible non-zero background and noise in the input data. The block multiconvexity of our objective function leads us to propose a proximal alternating method to minimize it in order to estimate the Gaussian shape parameters. The resulting FIGARO algorithm is shown to converge to a critical point under mild assumptions. The algorithm shows a good robustness when tested on synthetic datasets. To demonstrate the versatility of FIGARO, we also illustrate its excellent performance in the fitting of the Point Spread Functions of experimental raw data from a two-photon fluorescence microscope.

7.9. Calibration-less parallel imaging compressed sensing reconstruction based on OSCAR regularization

Participants: Emilie Chouzenoux, Loubna El Gueddari (Collaboration: Philippe Ciuciu, Alexandre Vignaut, Inria Saclay, Parietal)

Over the last decade, the combination of parallel imaging (PI) and compressed sensing (CS) in magnetic resonance imaging (MRI) has allowed to speed up acquisition while maintaining a good signal-to-noise ratio (SNR) for millimetric resolution. Self-calibrating techniques such as L1-ESPiRIT have emerged as a standard approach to estimate the coil sensitivity maps that are required at the reconstruction stage. Although straightforward in Cartesian acquisitions, these approaches become more computationally demanding in non-Cartesian scenarios especially for high resolution imaging (e.g. 500 μm in plane). Instead, calibrationless techniques no longer require this prior knowledge to perform multi-channel image reconstruction from undersampled k-space data. In this work, we introduce a new calibration-less PI-CS reconstruction method that is particularly suited to non-Cartesian data. It leverages structure sparsity of the multi-channel images in a wavelet transform domain while adapting to SNR inhomogeneities across receivers thanks to the OSCAR-norm regularization. Comparison and validation on 8 to 20-fold prospectively accelerated highresolution ex-vivo human brain MRI data collected at 7 Tesla shows that the subbandwise OSCAR-norm regularization achieves the best trade-off between image quality and computational cost at the reconstructions stage compared to other tested versions (global, scalewise and pixelwise). This approach provides slight to moderate improvement over its state-of-the-art competitors (self-calibrating '1-ESPIRiT method and calibration-less AC-LORAKS and CaLM methods) in terms of closeness to the Cartesian reference magnitude image. Importantly, it also preserves much better phase information compared to other approaches [37], [57],

7.10. Proximal approaches for matrix optimization problems: Application to robust precision matrix estimation

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet (Collaboration: Alessandro Benfenati, Universita di Milano)

In recent years, there has been a growing interest in mathematical models leading to the minimization, in a symmetric matrix space, of a Bregman divergence coupled with a regularization term. We address problems of this type within a general framework where the regularization term is split into two parts, one being a spectral function while the other is arbitrary. A Douglas–Rachford approach is proposed to address such problems, and a list of proximity operators is provided allowing us to consider various choices for the fit–to–data functional and for the regularization term. Based on our theoretical results, two novel approaches are proposed for the noisy graphical lasso problem, where a covariance or precision matrix has to be statistically estimated in presence of noise. The Douglas–Rachford approach directly applies to the estimation of the covariance matrix. When the precision matrix is sought, we solve a nonconvex optimization problem. More precisely, we propose a majorization–minimization approach building a sequence of convex surrogates and solving the inner optimization subproblems via the aforementioned Douglas–Rachford procedure. We establish conditions for the convergence of this iterative scheme. We illustrate the good numerical performance of the proposed approaches with respect to state–of–the–art approaches on synthetic and real-world datasets [4].

7.11. Representation Learning on Real-World Graphs

Participants: Fragkiskos Malliaros, Abdulkadir Çelikkanat

Network representation learning (NRL) methods aim to map each vertex into a low dimensional space by preserving both local and global structure of a given network. In recent years, various approaches based on random walks have been proposed to learn node embeddings – thanks to their success in several challenging problems. In this work, we have introduced two methodologies to compute latent representations of nodes based on random walks.

In particular, we have proposed *Kernel Node Embeddings* (KernelNE) [53], a model that aims to bring together two popular approaches for NRL, namely matrix factorization and random walk-based models. KernelNE is a weighted matrix factorization model which encodes random walk-based information about the nodes of the graph. The main benefit of this formulation is that it allows to utilize kernel functions on the computation of the embeddings.

Our second approach is motivated by the fact that the popular Skip-Gram algorithm models the conditional distribution of nodes within a random walk based on the softmax function, which might prohibit to capture richer types of interaction patterns among nodes that co-occur within a random walk. Here we argue that considering more expressive conditional probability models to relate nodes within a random walk sequence, might lead to more informative representations. That way, we have introduced the *Exponential Family Graph Embedding* (EFGE) model [54], that capitalizes on exponential family distribution models to capture interactions between nodes.

We have evaluated our methods on two downstream tasks: node classification and link prediction in social, information and biological networks. The experimental results demonstrate that random walk-based models accompanied with kernels as well as exponential family distributions outperform widely-known baseline NRL methods.

7.12. Semi-supervised Learning for Misinformation Detection

Participants: Fragkiskos Malliaros (Collaboration: Adrien Benamira, Benjamin Devillers, Etienne Lesot, Ayush K. Ray, Manal Saadi, CentraleSupélec)

Social networks have become the main platforms for information dissemination. Nevertheless, due to the increasing number of users, social media platforms tend to be highly vulnerable to the propagation of disinformation – making the detection of fake news a challenging task. In our work, we have focused on content-based methods for detecting fake news – casting the problem to a binary text classification one (an article corresponds to either fake news or not). The main challenge here stems from the fact that the number of labeled data is limited; very few articles can be examined and annotated as fake. To this extend, we opted for semi-supervised learning approaches. In particular, we have proposed a graph-based semi-supervised fake news detection method, based on graph neural networks [34]. Our intuition is that, graphs are expressive

models that are able to capture contextual dependencies among articles, alleviating the label scarcity constraint. On a high level, our framework is composed of three components: *i*) embedding of articles in the Euclidean space; *ii*) construction of an article similarity graph; *iii*) inference of missing labels using graph learning techniques. The experimental results indicate that the proposed methodology achieves better performance compared to traditional classification techniques, especially when trained on limited number of labeled articles.

7.13. A Perturb and Combine Approach to Analyze Real-World Graphs

Participants: Fragkiskos Malliaros (Collaboration: Antoine J.-P. Tixier, Maria Evgenia G. Rossi, Jesse Read, Michalis Vazirgiannis, École Polytechnique)

Influential spreaders are nodes that can diffuse information to the largest part of the network in a minimum amount of time. Detecting influential spreaders is an important task with numerous real-world applications. Nevertheless, some of the most effective influential spreader detection algorithms (e.g., the k-core decomposition) are unstable to small perturbations of the network structure. Inspired by bagging in Machine Learning, we have proposed the first Perturb and Combine (P&C) procedure for networks [51]. It (1) creates many perturbed versions of a given graph, (2) applies a node scoring function separately to each graph, and (3) combines the results. Experiments conducted on real-world networks of various sizes with the k-core, generalized k-core, and PageRank algorithms reveal that P&C brings substantial improvements. Moreover, this performance boost can be obtained at almost no extra cost through parallelization. Finally, a bias-variance analysis suggests that P&C works mainly by reducing bias, and that therefore, it should be capable of improving the performance of all vertex scoring functions, including stable ones.

7.14. Stochastic quasi-Fejér block-coordinate fixed point iterations with random sweeping: Mean-square and linear convergence

Participant: Jean-Christophe Pesquet (Collaboration: Patrick Louis Combettes, North Carolina University, USA)

In our previous work, we investigated the almost sure weak convergence of block-coordinate fixed point algorithms and discussed their applications to nonlinear analysis and optimization. This algorithmic framework features random sweeping rules to select arbitrarily the blocks of variables that are activated over the course of the iterations and it allows for stochastic errors in the evaluation of the operators. The paper [14] establishes results on the mean-square and linear convergence of the iterates. Applications to monotone operator splitting and proximal optimization algorithms are presented.

7.15. Rational optimization for non-linear reconstruction with approximate ℓ_0 penalization

Participants: Marc Castella, Arthur Marmin, Jean-Christophe Pesquet

Recovering nonlinearly degraded signal in the presence of noise is a challenging problem. In this work, this problem is tackled by minimizing the sum of a non convex least-squares fit criterion and a penalty term. We assume that the nonlinearity of the model can be accounted for by a rational function. In addition, we suppose that the signal to be sought is sparse and a rational approximation of the ℓ_0 pseudo-norm thus constitutes a suitable penalization. The resulting composite cost function belongs to the broad class of semi-algebraic functions. To find a globally optimal solution to such an optimization problem, it can be transformed into a generalized moment problem, for which a hierarchy of semidefinite programming relaxations can be built. Global optimality comes at the expense of an increased dimension and, to overcome computational limitations concerning the number of involved variables, the structure of the problem has to be carefully addressed. A situation of practical interest is when the nonlinear model consists of a convolutive transform followed by a componentwise nonlinear rational saturation. We then propose to use a sparse relaxation able to deal with up to several hundreds of optimized variables. In contrast with the naive approach consisting of linearizing the model, our experiments show that the proposed approach offers good performance [7].

7.16. Deep neural network structures solving variational inequalities

Participant: Jean-Christophe Pesquet (Collaboration: Patrick Louis Combettes, North Carolina University, USA)

Motivated by structures that appear in deep neural networks, we investigate nonlinear composite models alternating proximity and affine operators defined on different spaces. We first show that a wide range of activation operators used in neural networks are actually proximity operators. We then establish conditions for the averagedness of the proposed composite constructs and investigate their asymptotic properties. It is shown that the limit of the resulting process solves a variational inequality which, in general, does not derive from a minimization problem [13].

7.17. Generation of patient-specific cardiac vascular networks: a hybrid image-based and synthetic geometric model

Participant: Hugues Talbot (Collaboration: Clara Jaquet, Laurent Najman, ESIEE Paris, Leo Grady, Michiel Schaap, Buzzy Spain, Hyun Kim, Charles Taylor, HeartFlow Inc, Irene Vignon-Clementel, Inria Paris) In this work, we have proposed a blood-vessel generation procedure for extending known patient vasculature over and within the heart ventricle [19]. It is patient-specific, in the sense that it extend the known, segmented patient vasculature, and it is consistent with physics-based blood vessels characteristics (i.e. derived from CFD) and known vessel physiology. The generated vascular network bridges the gap between the vasculature that can be imaged and assessed via classical means (CT or MRI) and perfusion maps that can be imaged with specific modalities (radiotracer injected scintigraphy or PET). One objective of this work is to eventually propose a forward model for perfusion map generation, that can be used to solved the associated inverse problem of finding the cause of observed perfusion deficits associated with coronary diseases that cannot be imaged directly.

7.18. High throughput automated detection of axial malformations in Medaka fish embryo

Participant: Hugues Talbot (Collaboration: Diane Genest, Élodie Puybareau, Jean Cousty, ESIEE Paris, Marc Léonard, Noémie de Crozé, L'Oréal Recherche)

Fish embryos are used throughout the cosmetics industry to assess the toxicity of the components of their products, as well as more generally in waterways pollution measurements. Indeed pollution is often detectable in trace amounts when they hinder, stop or cause malformations during fish embryo development. In this work, we propose a high-throughput procedure for detecting most important malformations in fish embryo. For examples those affecting the tail or the eyes, based on image analysis and machine learning [16]. We have also proposed an atlas-based automated procedure for detecting swim bladder malformations, which are very difficult to assess manually [39].

These malformation are among the most difficult to assess but very common in various degrees of severity. Our procedure provide similar error rate as trained and careful humans operators, as assessed on thousands of images acquired in partneship with L'Oréal. We also show that our procedure is much faster and more consistent than human operators. It is now used in production by our partner.

7.19. Quantitative PET in the context of lymphoma

Participant: Hugues Talbot (Collaboration: Eloïse Grossiord, Laurent Najman, ESIEE Paris, Benoît Naegel, iCube, Strasbourg, Nicolas Passat, CRESTIC, Reims)

Lymphoma is type of cancer affecting the lymph system. Similar to blood disorders, these cancers can be difficult to cure because they affect a large portion of the body and metastasize easily. In contrast to leukemia, lymphoma also affects organs: the lymph nodes. Assessing the effectiveness of therapies implies to follow the impact of treatment on lymph nodes. This requires segmenting a large number of lesion, often several dozens. In [17], we have proposed an automated procedure based on hierarchical mathematical morphology, which has been extensively validated, and is now available as a plug-in for ImageJ/FIJI.

7.20. nD variational restoration of curvilinear structures with prior-based directional regularization

Participant: Hugues Talbot (Collaboration: Odyssée Merveille, Benoît Naegel, iCube, Strasbourg, Nicolas Passat, CRESTIC, Reims)

Curvilinear structure restoration in image processing procedures is a difficult task, which can be compounded when these structures are thin, i.e., when their smallest dimension is close to the resolution of the sensor. Many recent restoration methods involve considering a local gradient-based regularization term as prior, assuming gradient sparsity. An isotropic gradient operator is typically not suitable for thin curvilinear structures, since gradients are not sparse for these. In this paper [22], we propose a mixed gradient operator that combines a standard gradient in the isotropic image regions, and a directional gradient in the regions where specific orientations are likely. In particular, such information can be provided by curvilinear structure detectors (e.g., RORPO or Frangi filters). Our proposed mixed gradient operator, that can be viewed as a companion tool of such detectors, is proposed in a discrete framework and its formulation/computation holds in any dimension; in other words, it is valid in Z^n , $n \ge 1$. We show how this mixed gradient can be used to construct image priors that take edge orientation, as well as intensity, into account, and then involved in various image processing tasks while preserving curvilinear structures. The experiments carried out on 2D, 3D, real, and synthetic images illustrate the relevance of the proposed gradient, and its use in variational frameworks for both denoising and segmentation tasks.

7.21. Skin aging automated assessment

Participant: Hugues Talbot (Collaboration: Julie Robic, Alex Nkengne, Clarins laboratories, Benjamin Perret, Michel Couprie, ESIEE Paris)

With aging, human skin becomes drier, thinner and more irregular, but these characteristics are highly persondependent, and can be brought about via exposure to heat, cold or Sun. It is important to the cosmetics industry to assess objectively the effect of their products on skin aging. With our partner Clarins laboratory, we have proposed a series of automated procedures based on graph-based image analysis. We have in particular proposed to detect the surface that correspond to the dermal-epidermal junction [25], and a series or procedures to link the appearance of this surfact to aging characteristics [48]. Both have been validated by dermatologists specialized in skin aging.

7.22. Particle tracking

Participant: Hugues Talbot (Collaboration: Alessandro Benfenati, Universita di Milano, Francesco Bonacci, Laboratoire Navier, Tarik Bourouina, ESIEE Paris)

Fluorescent bead tracking is important in biomedical application related to biomechanics, rheology and fluid dynamics. We have made several contributions for the detection and tracking of micrometer-scale fluorescent bead in 3D confocal microscopy [47], [61]. Many software packages exist for 2D tracking but almost none exist for 3D. It is a harder problem because in general beads are not fixed and move between plane acquisitions, due to the relatively slow scanning characteristics of confocal microscopy.

7.23. Artificial Intelligence Applications for Thoracic imaging

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

Relevance and penetration of machine learning in clinical practice is a recent phenomenon with multiple applications being currently under development. Deep learning –and especially convolutional neural networks (CNNs)— is a subset of machine learning, which has recently entered the field of thoracic imaging. The structure of neural networks, organized in multiple layers, allows them to address complex tasks. For several clinical situations, CNNs have demonstrated superior performance as compared with classical machine learning algorithms and in some cases achieved comparable or better performance than clinical experts. Chest radiography, a high-volume procedure, is a natural application domain because of the large amount of stored images and reports facilitating the training of deep learning algorithms. Several algorithms for automated reporting have been developed. The training of deep learning algorithm CT images is more complex due to the dimension, variability, and complexity of the 3D signal. The role of these methods is likely to increase in clinical practice as a complement of the radiologist's expertise. The objective of these two reviews [9], [26] is to provide definitions for understanding the methods and their potential applications for thoracic imaging.

7.24. Use of Elastic Registration in Pulmonary MRI for the Assessment of Pulmonary Fibrosis in Patients with Systemic Sclerosis

Participants: Guillaume Chassagnon, Maria Vakalopoulou (Collaboration: Charlotte Martin, Rafael Marini Silva, Alexis Régent, Luc Mouthon, Nikos Paragios and Marie-Pierre Revel, AP-HP - Hopital Cochin Broca Hotel Dieu, Therapanacea)

Elastic registration of inspiratory and expiratory MRI revealed qualitative and quantitative differences in lung deformation in study participants with systemic sclerosis compared with healthy volunteers. Current imaging methods are not sensitive to changes in pulmonary function resulting from fibrosis. MRI with ultrashort echo time can be used to image the lung parenchyma and lung motion. To evaluate elastic registration of inspiratory to expiratory lung MRI for the assessment of pulmonary fibrosis in study participants with systemic sclerosis (SSc). This prospective study [8] was performed from September 2017 to March 2018 and recruited healthy volunteers and participants with SSc and high-resolution CT (within the previous 3 months) of the chest for lung MRI. Two breath-hold, coronal, three-dimensional, ultrashort-echo-time, gradient-echo sequences of the lungs were acquired after full inspiration and expiration with a 3.0-T unit. Images were registered from inspiration to expiration by using an elastic registration algorithm. Jacobian determinants were calculated from deformation fields and represented on color maps. Similarity between areas with marked shrinkage and logarithm of Jacobian determinants were compared between healthy volunteers and study participants with SSc. Receiver operating characteristic curve analysis was performed to determine the best Dice similarity coefficient threshold for diagnosis of fibrosis. Sixteen participants with SSc (seven with pulmonary fibrosis at high-resolution CT) and 11 healthy volunteers were evaluated. Areas of marked shrinkage during expiration with logarithm of Jacobian determinants less than -0.15 were found in the posterior lung bases of healthy volunteers and in participants with SSc without fibrosis, but not in participants with fibrosis. The sensitivity and specificity of MRI for presence of fibrosis at high-resolution CT were 86% and 75%, respectively (area under the curve, 0.81; P = .04) by using a threshold of 0.36 for Dice similarity coefficient. Elastic registration of inspiratory to expiratory MRI shows less lung base respiratory deformation in study participants with systemic sclerosis related pulmonary fibrosis compared with participants without fibrosis.

7.25. U-ReSNet: Ultimate Coupling of Registration and Segmentation with Deep Nets

Participants: Théo Estienne, Enzo Battistella, Marvin Lerousseau, Roger Sun, Maria Vakalopoulou (Collaboration: Stergios Christodoulidis, Alexandre Carre, Guillaume Klausner, Stavroula Mougiakakou, Charlotte Robert, Nikos Paragios and Eric Deutsch, Institute Gustave Roussy, University of Bern, Therapanacea)

We proposed in [58] a 3D deep neural network called U-ReSNet, a joint framework that can accurately register and segment medical volumes. The proposed network learns to automatically generate linear and elastic deformation models, trained by minimizing the mean square error and the local cross correlation similarity metrics. In parallel, a coupled architecture is integrated, seeking to provide segmentation maps for anatomies or tissue patterns using an additional decoder part trained with the dice coefficient metric. U-ReSNet is trained in an end to end fashion, while due to this joint optimization the generated network features are more informative leading to promising results compared to other deep learning-based methods existing in the literature. We evaluated the proposed architecture using the publicly available OASIS 3 dataset, measuring the dice coefficient metric for both registration and segmentation tasks. Our promising results indicate the potentials of our method which is composed from a convolutional architecture that is extremely simple and light in terms of parameters.

7.26. Gene Expression High-Dimensional Clustering Towards a Novel, Robust, Clinically Relevant and Highly Compact Cancer Signature

Participants: Enzo Battistella, Théo Estienne, Marvin Lerousseau, Roger Sun, Maria Vakalopoulou (Collaboration: Charlotte Robert, Nikos Paragios and Eric Deutsch, Institute Gustave Roussy, Therapanacea) Precision medicine, a highly disruptive paradigm shift in healthcare targeting the personalizing treatment, heavily relies on genomic data. However, the complexity of the biological interactions, the important number of genes as well as the lack of substantial patient's clinical data consist a tremendous bottleneck on the clinical implementation of precision medicine. In this work [32], we introduce a generic, low dimensional gene signature that represents adequately the tumor type. Our gene signature is produced using LP-stability algorithm, a high dimensional center-based unsupervised clustering algorithm working in the dual domain, and is very versatile as it can consider any arbitrary distance metric between genes. The gene signature produced by LP-stability reports at least 10 times better statistical significance and 35% better biological significance than the ones produced by two referential unsupervised clustering methods. Moreover, our experiments demonstrate that our low dimensional biomarker (27 genes) surpass significantly existing state of the art methods both in terms of qualitative and quantitative assessment while providing better associations to tumor types than methods widely used in the literature that rely on several omics data.

7.27. A Novel Object-Based Deep Learning Framework for Semantic Segmentation of Very High-Resolution Remote Sensing Data: Comparison with Convolutional and Fully Convolutional Networks

Participants: Maria Papadomanolaki and Maria Vakalopoulou (Collaboration: Konstantinos Karantzalos, National Technical University of Athens)

Deep learning architectures have received much attention in recent years demonstrating state-of-the-art performance in several segmentation, classification and other computer vision tasks. Most of these deep networks are based on either convolutional or fully convolutional architectures. In this study [24], we propose a novel object-based deep-learning framework for semantic segmentation in very high-resolution satellite data. In particular, we exploit object-based priors integrated into a fully convolutional neural network by incorporating an anisotropic diffusion data preprocessing step and an additional loss term during the training process. Under this constrained framework, the goal is to enforce pixels that belong to the same object to be classified at the same semantic category. We compared thoroughly the novel object-based framework with the currently dominating convolutional and fully convolutional deep networks. In particular, numerous experiments were conducted on the publicly available ISPRS WGII/4 benchmark datasets, namely Vaihingen and Potsdam, for validation and inter-comparison based on a variety of metrics. Quantitatively, experimental results indicate that, overall, the proposed object-based framework slightly outperformed the current stateof-the-art fully convolutional networks by more than 1% in terms of overall accuracy, while intersection over union results are improved for all semantic categories. Qualitatively, man-made classes with more strict geometry such as buildings were the ones that benefit most from our method, especially along object boundaries, highlighting the great potential of the developed approach.

7.28. A multi-task deep learning framework coupling semantic segmentation and image reconstruction for very high resolution imagery

Participants: Maria Papadomanolaki and Maria Vakalopoulou (Collaboration: Konstantinos Karantzalos, National Technical University of Athens)

Semantic segmentation, especially for very high-resolution satellite data, is one of the pillar problems in the remote sensing community. Lately, deep learning techniques are the ones that set the state-of-the-art for a number of benchmark datasets, however, there are still a lot of challenges that need to be addressed, especially in the case of limited annotations. To this end, in this study [45], we propose a novel framework based on deep neural networks that is able to address concurrently semantic segmentation and image reconstruction in an end to end training. Under the proposed formulation, the image reconstruction acts as a regularization, constraining efficiently the solution in the entire image domain. This self-supervised component helps significantly the generalization of the network for the semantic segmentation, especially in cases of a low number of annotations. Experimental results and the performed quantitative evaluation on the publicly available ISPRS (WGIII/4) dataset indicate the great potential of the developed approach.

7.29. Detecting Urban Changes with Recurrent Neural Networks from Multitemporal Sentinel-2 Data

Participants: Maria Papadomanolaki, Sagar Verma and Maria Vakalopoulou (Collaboration: Siddharth Gupta and Konstantinos Karantzalos, Granular AI and National Technical University of Athens)

The advent of multitemporal high resolution data, like the Copernicus Sentinel-2, has enhanced significantly the potential of monitoring the earth's surface and environmental dynamics. In this study [45], we present a novel deep learning framework for urban change detection which combines state-of-the-art fully convolutional networks (similar to U-Net) for feature representation and powerful recurrent networks (such as LSTMs) for temporal modeling. We report our results on the recently publicly available bi-temporal Onera Satellite Change Detection (OSCD) Sentinel-2 dataset, enhancing the temporal information with additional images of the same region on different dates. Moreover, we evaluate the performance of the recurrent networks as well as the use of the additional dates on the unseen test-set using an ensemble cross-validation strategy. All the developed models during the validation phase have scored an overall accuracy of more than 95%, while the use of LSTMs and further temporal information, boost the F1 rate of the change class by an additional 1.5%.

7.30. Image Registration of Satellite Imagery with Deep Convolutional Neural Networks

Participants: Maria Vakalopoulou and Mihir Sahasrabudhe (Collaboration: Stergios Christodoulidis, Stavroula Mougiakakou and Nikos Paragios, University of Bern and Therapanacea)

Image registration in multimodal, multitemporal satellite imagery is one of the most important problems in remote sensing and essential for a number of other tasks such as change detection and image fusion. In this study [52], inspired by the recent success of deep learning approaches we propose a novel convolutional neural network architecture that couples linear and deformable approaches for accurate alignment of remote sensing imagery. The proposed method is completely unsupervised, ensures smooth displacement fields and provides real time registration on a pair of images. We evaluate the performance of our method using a challenging multitemporal dataset of very high resolution satellite images and compare its performance with a state of the art elastic registration method based on graphical models. Both quantitative and qualitative results prove the high potentials of our method.

7.31. Lifting AutoEncoders: Unsupervised Learning of a Fully-Disentangled 3D Morphable Model Using Deep Non-Rigid Structure From Motion

Participants: Mihir Sahasrabudhe (Collaboration: Eqward Bartrum, Riza Alp Guler, Dimitris Samaras and Iasonas Kokkinos, Stony Brook, UCL and Ariel AI)

We introduced, in [49], Lifting Autoencoders, a generative 3D surface-based model of object categories. We bring together ideas from non-rigid structure from motion, image formation, and morphable models to learn a controllable, geometric model of 3D categories in an entirely unsupervised manner from an unstructured set of images. We exploit the 3D geometric nature of our model and use normal information to disentangle appearance into illumination, shading, and albedo. We further use weak supervision to disentangle the non-rigid shape variability of human faces into identity and expression. We combine the 3D representation with a differentiable renderer to generate RGB images and append an adversarially trained refinement network to obtain sharp, photorealistic image reconstruction results. The learned generative model can be controlled in terms of interpretable geometry and appearance factors, allowing us to perform photorealistic image manipulation of identity, expression, 3D pose, and illumination properties.

8. Bilateral Contracts and Grants with Industry

8.1. Bilateral Contracts with Industry

• PhD Contract with IFP Energies Nouvelles

Project title: Polynomial optimization for sparse signal recovery

Duration: 2018-2020

Leaders: M. Castella and J.-C. Pesquet

• 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: Optimization methods for breast tomosynthesis

Duration: 2017-2020

Leader: J.-C. Pesquet and E. Chouzenoux

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

• Contract with Schneider Electric

Project title: Neural network modeling of electrical motors

Duration: 2019 Leader: J.-C. Pesquet

Contract with SNCF

Project title: SIARA project: Developing an automatic system based on deep learning which monitors different types of defects in the current railway network of France.

Duration: 2018-2019 Leader: M. Vakalopoulou

Contract with SNCF

Project title: SNCF Platipus: Examining the potential of machine learning algorithms in the analysis of scouring reports of aquatic foundations.

Duration: 2019-2020

Leader: F. Malliaros, M. Vakalopoulou.

9. Partnerships and Cooperations

9.1. Regional Initiatives

• DATAIA UltraBioLearn (2019-2022). The project aims to research machine learning approaches for medical applications, in particular by leveraging semi-supervised learning using generative, graph-based and certifiable networks, in the context of predicting patient response to cancer treatments. Responsible: H. Talbot, F. Malliaros (N. Lassau, Institut Gustave Roussy).

9.2. National Initiatives

9.2.1. ANR

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: 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.

9.2.2. Others

Program: CNRS-CEFIPRA

Project acronym: NextGenBP

Project title: Looking Beyond Backpropagation in Deep Learning

Duration : 2017-2019 Coordinator: E. Chouzenoux

• Program: PHC - Campus France

Projet acronym: POLONIUM

Project title: When Poisson and Gauss meet in imaging

Duration: 2018-2020 Coordinator: J.C. Pesquet

9.3. European Initiatives

9.3.1. FP7 & H2020 Projects

• 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: Hugues Talbot

9.4. International Initiatives

9.4.1. Inria International Partners

9.4.1.1. 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.

9.5. International Research Visitors

9.5.1. Visits of International Scientists

- Prof. Angshul Majumdar, IIIT Delhi, India, June 2019 and December 2019
- Prof. Apostolos N. Papadopoulos, Aristotle University of Thessaloniki, June 2019 to July 2019

- Prof. Patrick L. Combettes, North Carolina State University, US, 18-22 February 2019
- W. Tang (PhD student), North Carolina State University, US, 2-29 May 2019
- S. Sharma (PhD student), IIIT Delhi, India, June 2019 to August 2019

9.5.2. Visits to International Teams

9.5.2.1. Research Stays Abroad

- M. Vakalopoulou, visiting researcher for 1 month (June-July 2019): Stony Brook University, research team of D. Samaras.
- T. Estienne, 4 months internship (May-August 2019): Center for Biomedical Image Computing and Analytics (CBICA) of University of Pennsylvania.
- E. Battistella, 4 months internship (August-December 2019): Computational Robotics, AI & Biomedicine Lab of RICE University.
- M. Sahasrabudhe, 2 months intership (November-December 2019): Boston Children's Hospital & Harvard Medical School.

10. Dissemination

10.1. Promoting Scientific Activities

10.1.1. Scientific Events: Organisation

10.1.1.1. General Chair, Scientific Chair

 F. Malliaros. Organizer of the Summer School in Artificial Intelligence, CentraleSupélec, France, 2019.

10.1.1.2. Member of the Organizing Committees

- H. Talbot. Member of the organizing committee for ICCV 2023 in Paris.
- F. Malliaros. Member of the organizing committee of the International Workshop of Deep Learning for Graphs and Structured Data Embedding (DL4G-SDE), The Web Conference (WWW), San Francisco, California, 2019.
- F. Malliaros. Member of the organizing committee for the special session on Machine Learning with Graphs: Algorithms and Applications, 28th International Conference on Artificial Neural Networks (ICANN), Munich, Germany, 2019.

10.1.2. Scientific Events: Selection

10.1.2.1. Chair of 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).

10.1.2.2. Member of the Conference Program Committees

- E. Chouzenoux. Organization of a special session at the 45th International Conference on Acoustics, Speech, and Signal Processing, ICASSP 2020.
- M. Castella. Organization of a special session at the 27th European Signal Processing Conference, EUSIPCO 2019.
- F. Malliaros. Member of the program committee at International Conference on Artificial Neural Networks, ICANN 2019.
- J.C. Pesquet. Member of the program committee at GRETSI 2019.

- H. Talbot. Member of the board and program committee at the International Symposium in Mathematical Morphology, which took place in Saarbrücken, Germany, July 2019.
- H. Talbot. Member of the program committee at the conference Discrete Geometry for Computer Imagery, which took place in Noisy-le-Grand, France, March 2019.
- M. Vakalopoulou. Member of the program committee at the Joint Urban Remote Sensing Event (JURSE), 2019.

10.1.2.3. 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).

10.1.3. Journal

10.1.3.1. Member of the Editorial Boards

- Emilie Chouzenoux: Associate Editor at IEEE Transactions on Signal Processing
- 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: Senior area editor for IEEE Signal Processing Letters.

10.1.3.2. Reviewer - Reviewing Activities

- E. Chouzenoux: IEEE Trans. on Image Processing, IEEE Trans. Signal Processing, SIAM Journal on Imaging Science, Journal of Optimization Theory and Applications, Journal of Global Optimization, 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), Applied Network Science, International Journal on Artificial Intelligence Tools (IJAIT).
- 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. Reviewer for the conferences ACCV, BMVC, CVPR, ICIP, ICML, ISBI, and NeurIPS (ex-NIPS),.
- 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.

10.1.4. Invited Talks

• E. Chouzenoux:

Polish academy of science, Warsaw, Poland, November 2019

University of Edinburgh, UK, October 2019

AIP 2019, Grenoble, France, July 2019

SPARS 2019, Toulouse, France, 4 July 2019

Inria Rennes PANAMA, April 2019

Imagine ENPC, Champs-sur-Marne, April 2019

Univ. Paris-Dauphine, Paris, March 2019

Imaging in Paris, IHP, Paris, February 2019

• J.C. Pesquet:

BASP Frontiers Workshop, Villars-sur-Ollon, Suisse, February 2019

Modern Maximal Monotone Operator Theory workshop, Vienna, February 2019

Workshop on Operator Splitting Methods in Data Analysis, New York, US, March 2019

Marseille Université, Juin 2019

International Conference on Optimisation, Berlin, August 2019

EUSIPCO, A Coruña, Spain, September 2019

French-German-Swiss Conference on Optimization, Nice, September 2019

Wavelet and Applications workshop, Brussels, November 2019

• H. Talbot:

CentraleSupélec: March 2019, November 2019

Institut Henri Poincaré, Paris, February 2019

• M. Vakalopoulou:

ARTORG Center for Biomedical Engineering Research, University of Bern, March 2019

European Society of Thoracic Imaging 2019, May 2019

Department of Computer Science, Stony Brook University, June 2019

Electrical & Computer Engineering, University of Houston, June 2019

France is AI, October 2019

Intelligence Artificielle et Santé, Faculté de Médicine Paris-Sud, November 2019

Annual Symposium of Belgian Association for Neuro-Oncology, December 2019

10.1.5. Leadership within the Scientific Community

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

10.2. Teaching - Supervision - Juries

10.2.1. Teaching

- Master: E. Chouzenoux. Foundations of Distributed and Large Scale Computing, 26h, M.Sc. in Data Sciences and Business Analytics, 3rd year CentraleSupélec, MVA ENS Cachan, Master Optimization Paris Sud and ESSEC Business School, FR
- Master: E. Chouzenoux. Advanced Machine Learning, 18h, 3rd year CentraleSupélec, FR
- Master: F. Malliaros. Machine Learning, 27h, M.Sc. in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School and M.Sc. in Artificial Intelligence, CentraleSupélec, FR.
- Master: F. Malliaros. Introduction to Machine Learning, 33h, 2nd year course at CentraleSupélec, FR.
- Master: F. Malliaros. Mathematical Modeling of Propagation Phenomena Propagation on Graphs, 15h, 1st year course at CentraleSupélec, FR.
- Master: Oyallon, Edouard. Deep Learning, 24h, 3rd year CentraleSupélec, FR
- Master: Oyallon, Edouard. Reinforcement Learning, 24h, 3rd year CentraleSupélec, FR
- Master: J.C. Pesquet. Advanced course on Optimization, 33h, M1, CentraleSupélec, FR
- Master: J.C. Pesquet. Introduction to Optimization, 6h, MVA ENS Cachan, FR
- Master: Talbot, Hugues. Discrete Optimisation, 2nd year course, CentraleSupelec, 30h, EN
- Master: Talbot, Hugues. Big Data, Techniques and Platforms, M.Sc in Data Science and Business Analytics, CentraleSupelec and ESSEC Business School, 30h, EN
- Master: Talbot, Hugues. Optimisation for AI, M.Sc in AI, CentraleSupelec and ESSEC Business School. 30h. EN
- Master: M. Vakalopoulou. Introduction to Visual Computing, 25h, 3rd year CentraleSupélec, FR
- Master: M. Vakalopoulou. Deep Learning, 25h, 3rd year CentraleSupélec, FR
- Master: M. Vakalopoulou. Introduction to Machine Learning, 33h, 2nd year CentraleSupélec, FR

10.2.2. Lecturing activities

- F. Malliaros. Summer School Artificial Intelligence, July 1-12, 2019, CentraleSupélec.
- J.C. Pesquet. Erwin Schrödinger Institute for Mathematics and Physics in Vienna, 4-6 March 2019, Austria.
- M. Vakalopoulou. Summer School on Artificial Intelligence, July 1-12n 2019, CentraleSupélec.
- E. Chouzenoux. Summer School Sparsity for Physics, Signal and Learning, June 24-27, 2019, Inria Paris.

10.2.3. Supervision

- PhD (defended): Huu Dien Khue Le, Algorithme des directions alternées non convexe pour graphes: inférence et apprentissage, 2016-2019, supervised by N. Paragios.
- PhD (defended): Riza Alp Guler, Apprentissage de Correspondances Image-Surface, 2016-2019, supervised by I. Kokkinos and N. Paragios.
- PhD (defended): Marie-Caroline Corbineau, Fast online optimization algorithms for machine learning and medical imaging, 2016-2019, supervised by E. Chouzenoux and J.-C. Pesquet.
- PhD (defended): Loubna El Gueddari, Parallel proximal algorithms for compressed sensing MRI reconstruction - Applications to ultra-high magnetic field imaging, 2016-2019, supervised by J.-C. Pesquet and Ph. Ciuciu (Inria PARIETAL).
- PhD (in progress): Abdulkadir Çelikkanat, Representation learning methods on graphs, 2017-2020, supervised by F. Malliaros and N. Paragios.

• PhD (in progress): Yunshi Huang, Majorization-Minimization approaches for large scale problems in image processing, 2018-2021, supervised by E. Chouzenoux and V. Elvira (Univ. Edinburgh).

- PhD (in progress): Samy Ammari, Imagerie médicale computationnelle en neuro oncologie, 2019-2022, supervised by C. Balleyguier (Institut Gustave Roussy) and E. Chouzenoux.
- PhD (in progress): Georgios Panagopoulos, Influence maximization in social networks, 2018-2021, supervised by F. Malliaros and M. Vazirgiannis (École 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 F. Malliaros, J.-C. Pesquet and F. Kaakai (Thales Group).
- PhD (in progress): Maria Papadomanolaki, Change Detection from Multitemporal High Resolution Data with Deep Learning, 2017-2021, supervised by M. Vakalopoulou and with K. Karantzalos.
- PhD (in progress): Mihir Sahasrabudhe, Unsupervised ans Weakly Supervised Deep Learning Methods for Computer Vision and Medical Imaging, 2016-2020, supervised by N. Paragios.
- PhD (in progress): Théo Estienne, Improving anticancer therapies efficacy through Machine Learning on Medical Imaging & Genomic Data, 2017-2020, supervised by M. Vakalopoulou and N. Paragios.
- PhD (in progress): Enzo Battistella, Development of novel imaging approaches for tumour phenotype assessment by noninvasive imaging 2017-2020, supervised by M. Vakalopoulou and N. Paragios.
- PhD (in progress): Roger Sun, Deep learning and computer vision approaches on medical imaging and genomic data to improve the prediction of anticancer therapies' efficacy, 2017-2020, supervised by M. Vakalopoulou and N. Paragios.
- 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): Maïssa Sghaier, clinical Task-Based Reconstruction in tomosynthesis, 2017-2020, supervised by J.-C. Pesquet and S. Muller (GE Healthcare).
- PhD (in progress): Marion Savanier, Reconstruction 3D interventionnelle, 2019-2022, supervised by E. Chouzenoux and C. Riddell (GE Healthcare).
- PhD (in progress): Arthur Marmin, Rational models optimized exactly for chemical processes improvement, 2017-2020, supervised by M. Castella (Telecom Paristech) and J.-C. Pesquet.
- PhD (in progress): Sylvain Lempereur. Analyse quantitative de la morphologie de poissons aux stades larvaire et juvénile. 2017-2020. Supervised by Hugues Talbot and Jean-Stéphane Joly (CNRS).
- PhD (in progress): Daniel Antunes: Contraintes géométriques et approches variationnelles pour l'analyse d'image. 2016-2019. Supervised by Hugues Talbot and Jacques-Olivier Lachaud (U. Savoie-Mont Blanc)
- PhD (in progress): Marie-Charlotte Poilpre: Méthode de comparaison faciale morphologique, adaptée aux expertise judiciaires, basée sur la modélisation 3D. 2017-2020. Supervised by Hugues Talbot and Vincent Nozick (U. Paris-Est)
- PhD (in progress): Thank Xuan Nguyen. Détection et étude morphologique des sources extragalactiques par analyse variationnelle. 2018-2021. Supervised by Hugues Talbot and Laurent Najman (ESIEE)
- PhD (in progress): Marvin Lerousseau. Apprentissage statistique en imagerie médicale et en génomique pour prédire l'efficacité des thérapies anti-tumorales. 2018-2021. Supervised by Nikos Paragios (Therapanacea), Eric Deutch (IGR) and Hugues Talbot.

PhD (in progress): Mario Viti. Low-dose assessment of coronal vessel health on CT. 2019-2022.
 Supervised by Hugues Talbot.

10.2.4. Juries

The faculty members of the team participated to numerous PhD Thesis Committees, HDR Committees and served as Grant Reviewers. Moreover, they serve regularly as a jury Member to Final Engineering Internship and the Research Innovation Project for students of CentraleSupélec, FR.

11. Bibliography

Publications of the year

Doctoral Dissertations and Habilitation Theses

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