



Activity Report 2018

Team GALEN-POST

Organ Modeling through Extraction, Representation and Understanding of Medical Image Content

Inria teams are typically groups of researchers working on the definition of a common project, and objectives, with the goal to arrive at the creation of a project-team. Such project-teams may include other partners (universities or research institutions).

RESEARCH CENTER
Saclay - Île-de-France

THEME
Computational Neuroscience and
Medicine

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Team GALEN-POST

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Computer Science and Digital Science:

- A5.3. - Image processing and analysis
- A5.4. - Computer vision
- A5.9. - Signal processing
- A8. - Mathematics of computing
- A8.2. - Optimization
- A8.7. - Graph theory
- A9. - Artificial intelligence
- A9.2. - Machine learning
- A9.3. - Signal analysis

Other Research Topics and Application Domains:

- B1. - Life sciences
- B2. - Health
- B2.6. - Biological and medical imaging

1. Team, Visitors, External Collaborators

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2. Overall Objectives

2.1. GALEN-POST Centrale-Supélec

Computational vision is one of the most challenging research domains in engineering sciences. The aim is to reproduce human visual perception through intelligent processing of visual data. The application domains span from computer aided diagnosis to industrial automation & robotics. The most common mathematical formulation to address such a challenge is through mathematical modeling. In such a context, first the solution of the desired vision task is expressed in the form of a parameterized mathematical model. Given such a model, the next task consists of associating the model parameters with the available observations, which is often called the model-to-data association. The aim of this task is to determine the impact of a parameter choice to the observations and eventually maximize/minimize the adequacy of these parameters with the visual observations. In simple words, the better the solution is, the better it will be able to express and fit the data. This is often achieved through the definition of an objective function on the parametric space of the model. Last, but not least given the definition of the objective function, visual perception is addressed through its optimization with respect to the model parameters. To summarize, computation visual perception involves three aspects, a task-specific definition of a parametric model, a data-specific association of this model with the available observations and last the optimization of the model parameters given the objective and the observations.

Such a chain processing inherits important shortcomings. The curse of dimensionality is often used to express the importance of the model complexity. In simple words, the higher the complexity of the model is, the better its expressive power will be with counter effect the increase of the difficulty of the inference process. Non-linearity is another issue to be addressed which simply states that the association between the model and the data is a (highly) non-linear function and therefore direct inference is almost infeasible. The impact of this aspect is enforced from the curse of non-convexity that characterizes the objective function. Often it lives in high-dimensional spaces and is ill posed making exact inference problematic (in many cases not possible) and computationally expensive. Last, but not least modularity and scalability is another important concern to be addressed in the context of computational vision. The use of task-specific modeling and algorithmic solutions make their portability infeasible and therefore transfer of knowledge from one task to another is not straightforward while the methods do not always scale well with respect either to the dimensionality of the representation or the data.

GALEN aims at proposing innovative techniques towards automatic structuring, interpretation and longitudinal modeling of visual data. In order to address these fundamental problems of computational perception, GALEN investigates the use of discrete models of varying complexity. These methods exhibit an important number of strengths such as their ability to be modular with respect to the input measurements (clinical data), the nature of the model (certain constraints are imposed from computational perspective in terms of the level of interactions), and the model-to-data association while being computationally efficient.

3. Research Program

3.1. Shape, Grouping and Recognition

A general framework for the fundamental problems of image segmentation, object recognition and scene analysis is the interpretation of an image in terms of a set of symbols and relations among them. Abstractly stated, image interpretation amounts to mapping an observed image, X to a set of symbols Y . Of particular interest are the symbols Y^* that *optimally explain the underlying image*, as measured by a scoring function s that aims at distinguishing correct (consistent with human labellings) from incorrect interpretations:

$$Y^* = \operatorname{argmax}_Y s(X, Y) \quad (1)$$

Applying this framework requires (a) identifying which symbols and relations to use (b) learning a scoring function s from training data and (c) optimizing over Y in Eq.1.

One of the main themes of our work is the development of methods that jointly address (a,b,c) in a shape-grouping framework in order to reliably extract, describe, model and detect shape information from natural and medical images. A principal motivation for using a shape-based framework is the understanding that shape- and more generally, grouping- based representations can go all the way from image features to objects. Regarding aspect (a), image representation, we cater for the extraction of image features that respect the shape properties of image structures. Such features are typically constructed to be purely geometric (e.g. boundaries, symmetry axes, image segments), or appearance-based, such as image descriptors. The use of machine learning has been shown to facilitate the robust and efficient extraction of such features, while the grouping of local evidence is known to be necessary to disambiguate the potentially noisy local measurements. In our research we have worked on improving feature extraction, proposing novel blends of invariant geometric- and appearance- based features, as well as grouping algorithms that allow for the efficient construction of optimal assemblies of local features.

Regarding aspect (b) we have worked on learning scoring functions for detection with deformable models that can exploit the developed low-level representations, while also being amenable to efficient optimization. Our works in this direction build on the graph-based framework to construct models that reflect the shape properties of the structure being modeled. We have used discriminative learning to exploit boundary- and symmetry-based representations for the construction of hierarchical models for shape detection, while for medical images we have developed methods for the end-to-end discriminative training of deformable contour models that combine low-level descriptors with contour-based organ boundary representations.

Regarding aspect (c) we have developed algorithms which implement top-down/bottom-up computation both in deterministic and stochastic optimization. The main idea is that ‘bottom-up’, image-based guidance is necessary for efficient detection, while ‘top-down’, object-based knowledge can disambiguate and help reliably interpret a given image; a combination of both modes of operation is necessary to combine accuracy with efficiency. In particular we have developed novel techniques for object detection that employ combinatorial optimization tools (A* and Branch-and-Bound) to tame the combinatorial complexity, achieving a best-case performance that is logarithmic in the number of pixels.

In the long run we aim at scaling up shape-based methods to 3D detection and pose estimation and large-scale object detection. One aspect which seems central to this is the development of appropriate mid-level representations. This is a problem that has received increased interest lately in the 2D case and is relatively mature, but in 3D it has been pursued primarily through ad-hoc schemes. We anticipate that questions pertaining to part sharing in 3D will be addressed most successfully by relying on explicit 3D representations. On the one hand depth sensors, such as Microsoft’s Kinect, are now cheap enough to bring surface modeling and matching into the mainstream of computer vision - so these advances may be directly exploitable at test time for detection. On the other hand, even if we do not use depth information at test time, having 3D information can simplify the modeling task during training. In on-going work with collaborators we

have started exploring combinations of such aspects, namely (i) the use of surface analysis tools to match surfaces from depth sensors (ii) using branch-and-bound for efficient inference in 3D space and (iii) groupwise-registration to build statistical 3D surface models. In the coming years we intend to pursue a tighter integration of these different directions for scalable 3D object recognition.

3.2. Machine Learning & Structured Prediction

The foundation of statistical inference is to learn a function that minimizes the expected loss of a prediction with respect to some unknown distribution

$$\mathcal{R}(f) = \int \ell(f, x, y) dP(x, y), \quad (2)$$

where $\ell(f, x, y)$ is a problem specific loss function that encodes a penalty for predicting $f(x)$ when the correct prediction is y . In our case, we consider x to be a medical image, and y to be some prediction, e.g. the segmentation of a tumor, or a kinematic model of the skeleton. The loss function, ℓ , is informed by the costs associated with making a specific misprediction. As a concrete example, if the true spatial extent of a tumor is encoded in y , $f(x)$ may make mistakes in classifying healthy tissue as a tumor, and mistakes in classifying diseased tissue as healthy. The loss function should encode the potential physiological damage resulting from erroneously targeting healthy tissue for irradiation, as well as the risk from missing a portion of the tumor.

A key problem is that the distribution P is unknown, and any algorithm that is to estimate f from labeled training examples must additionally make an implicit estimate of P . A central technology of empirical inference is to approximate $\mathcal{R}(f)$ with the empirical risk,

$$\mathcal{R}(f) \approx \widehat{\mathcal{R}}(f) = \frac{1}{n} \sum_{i=1}^n \ell(f, x_i, y_i), \quad (3)$$

which makes an implicit assumption that the training samples (x_i, y_i) are drawn i.i.d. from P . Direct minimization of $\widehat{\mathcal{R}}(f)$ leads to overfitting when the function class $f \in \mathcal{F}$ is too rich, and regularization is required:

$$\min_{f \in \mathcal{F}} \lambda \Omega(\|f\|) + \widehat{\mathcal{R}}(f), \quad (4)$$

where Ω is a monotonically increasing function that penalizes complex functions.

Equation Eq. 4 is very well studied in classical statistics for the case that the output, $y \in \mathcal{Y}$, is a binary or scalar prediction, but this is not the case in most medical imaging prediction tasks of interest. Instead, complex interdependencies in the output space leads to difficulties in modeling inference as a binary prediction problem. One may attempt to model e.g. tumor segmentation as a series of binary predictions at each voxel in a medical image, but this violates the i.i.d. sampling assumption implicit in Equation Eq. 3. Furthermore, we typically gain performance by appropriately modeling the inter-relationships between voxel predictions, e.g. by incorporating pairwise and higher order potentials that encode prior knowledge about the problem domain. It is in this context that we develop statistical methods appropriate to structured prediction in the medical imaging setting.

3.3. Self-Paced Learning with Missing Information

Many tasks in artificial intelligence are solved by building a model whose parameters encode the prior domain knowledge and the likelihood of the observed data. In order to use such models in practice, we need to estimate its parameters automatically using training data. The most prevalent paradigm of parameter estimation is supervised learning, which requires the collection of the inputs x_i and the desired outputs y_i . However, such an approach has two main disadvantages. First, obtaining the ground-truth annotation of high-level applications, such as a tight bounding box around all the objects present in an image, is often expensive. This prohibits the use of a large training dataset, which is essential for learning the existing complex models. Second, in many applications, particularly in the field of medical image analysis, obtaining the ground-truth annotation may not be feasible. For example, even the experts may disagree on the correct segmentation of a microscopical image due to the similarities between the appearance of the foreground and background.

In order to address the deficiencies of supervised learning, researchers have started to focus on the problem of parameter estimation with data that contains hidden variables. The hidden variables model the missing information in the annotations. Obtaining such data is practically more feasible: image-level labels ('contains car', 'does not contain person') instead of tight bounding boxes; partial segmentation of medical images. Formally, the parameters \mathbf{w} of the model are learned by minimizing the following objective:

$$\min_{\mathbf{w} \in \mathcal{W}} R(\mathbf{w}) + \sum_{i=1}^n \Delta(y_i, y_i(\mathbf{w}), h_i(\mathbf{w})). \quad (5)$$

Here, \mathcal{W} represents the space of all parameters, n is the number of training samples, $R(\cdot)$ is a regularization function, and $\Delta(\cdot)$ is a measure of the difference between the ground-truth output y_i and the predicted output and hidden variable pair $(y_i(\mathbf{w}), h_i(\mathbf{w}))$.

Previous attempts at minimizing the above objective function treat all the training samples equally. This is in stark contrast to how a child learns: first focus on easy samples ('learn to add two natural numbers') before moving on to more complex samples ('learn to add two complex numbers'). In our work, we capture this intuition using a novel, iterative algorithm called self-paced learning (SPL). At an iteration t , SPL minimizes the following objective function:

$$\min_{\mathbf{w} \in \mathcal{W}, \mathbf{v} \in \{0,1\}^n} R(\mathbf{w}) + \sum_{i=1}^n v_i \Delta(y_i, y_i(\mathbf{w}), h_i(\mathbf{w})) - \mu_t \sum_{i=1}^n v_i. \quad (6)$$

Here, samples with $v_i = 0$ are discarded during the iteration t , since the corresponding loss is multiplied by 0. The term μ_t is a threshold that governs how many samples are discarded. It is annealed at each iteration, allowing the learner to estimate the parameters using more and more samples, until all samples are used. Our results already demonstrate that SPL estimates accurate parameters for various applications such as image classification, discriminative motif finding, handwritten digit recognition and semantic segmentation. We will investigate the use of SPL to estimate the parameters of the models of medical imaging applications, such as segmentation and registration, that are being developed in the GALEN team. The ability to handle missing information is extremely important in this domain due to the similarities between foreground and background appearances (which results in ambiguities in annotations). We will also develop methods that are capable of minimizing more general loss functions that depend on the (unknown) value of the hidden variables, that is,

$$\min_{\mathbf{w} \in \mathcal{W}, \theta \in \Theta} R(\mathbf{w}) + \sum_{i=1}^n \sum_{h_i \in \mathcal{H}} \Pr(h_i | x_i, y_i; \theta) \Delta(y_i, h_i, y_i(\mathbf{w}), h_i(\mathbf{w})). \quad (7)$$

Here, θ is the parameter vector of the distribution of the hidden variables h_i given the input x_i and output y_i , and needs to be estimated together with the model parameters \mathbf{w} . The use of a more general loss function will allow us to better exploit the freely available data with missing information. For example, consider the case where y_i is a binary indicator for the presence of a type of cell in a microscopical image, and h_i is a tight bounding box around the cell. While the loss function $\Delta(y_i, y_i(\mathbf{w}), h_i(\mathbf{w}))$ can be used to learn to classify an image as containing a particular cell or not, the more general loss function $\Delta(y_i, h_i, y_i(\mathbf{w}), h_i(\mathbf{w}))$ can be used to learn to detect the cell as well (since h_i models its location)

3.4. Discrete Biomedical Image Perception

A wide variety of tasks in medical image analysis can be formulated as discrete labeling problems. In very simple terms, a discrete optimization problem can be stated as follows: we are given a discrete set of variables \mathcal{V} , all of which are vertices in a graph \mathcal{G} . The edges of this graph (denoted by \mathcal{E}) encode the variables' relationships. We are also given as input a discrete set of labels \mathcal{L} . We must then assign one label from \mathcal{L} to each variable in \mathcal{V} . However, each time we choose to assign a label, say, x_{p_1} to a variable p_1 , we are forced to pay a price according to the so-called *singleton* potential function $g_p(x_p)$, while each time we choose to assign a pair of labels, say, x_{p_1} and x_{p_2} to two interrelated variables p_1 and p_2 (two nodes that are connected by an edge in the graph \mathcal{G}), we are also forced to pay another price, which is now determined by the so called *pairwise* potential function $f_{p_1 p_2}(x_{p_1}, x_{p_2})$. Both the singleton and pairwise potential functions are problem specific and are thus assumed to be provided as input.

Our goal is then to choose a labeling which will allow us to pay the smallest total price. In other words, based on what we have mentioned above, we want to choose a labeling that minimizes the sum of all the MRF potentials, or equivalently the MRF energy. This amounts to solving the following optimization problem:

$$\arg \min_{\{x_p\}} \mathcal{P}(g, f) = \sum_{p \in \mathcal{V}} g_p(x_p) + \sum_{(p_1, p_2) \in \mathcal{E}} f_{p_1 p_2}(x_{p_1}, x_{p_2}). \quad (8)$$

The use of such a model can describe a number of challenging problems in medical image analysis. However these simplistic models can only account for simple interactions between variables, a rather constrained scenario for high-level medical imaging perception tasks. One can augment the expression power of this model through higher order interactions between variables, or a number of cliques $\{C_i, i \in [1, n] = \{p_{i1}, \dots, p_{i|C_i|}\}\}$ of order $|C_i|$ that will augment the definition of \mathcal{V} and will introduce hyper-vertices:

$$\arg \min_{\{x_p\}} \mathcal{P}(g, f) = \sum_{p \in \mathcal{V}} g_p(x_p) + \sum_{(p_1, p_2) \in \mathcal{E}} f_{p_1 p_2}(x_{p_1}, x_{p_2}) + \sum_{C_i \in \mathcal{E}} f_{p_1 \dots p_n}(x_{p_{i1}}, \dots, p_{x_{i|C_i|}}). \quad (9)$$

where $f_{p_1 \dots p_n}$ is the price to pay for associating the labels $(x_{p_{i1}}, \dots, p_{x_{i|C_i|}})$ to the nodes $(p_1 \dots p_{i|C_i|})$. Parameter inference, addressed by minimizing the problem above, is the most critical aspect in computational medicine and efficient optimization algorithms are to be evaluated both in terms of computational complexity as well as of inference performance. State of the art methods include deterministic and non-deterministic annealing, genetic algorithms, max-flow/min-cut techniques and relaxation. These methods offer certain strengths while exhibiting certain limitations, mostly related to the amount of interactions which can be tolerated among neighborhood nodes. In the area of medical imaging where domain knowledge is quite strong, one would expect that such interactions should be enforced at the largest scale possible.

4. Application Domains

4.1. Representation Learning for Network Biology

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.

4.2. 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 will be modeled.

4.3. Inference of gene regulatory networks

Participants: 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 different living conditions. From these data, gene regulation mechanisms can be recovered by revealing topological links encoded in graphs. In regulatory graphs, nodes correspond to genes. A link between two nodes is identified if a regulation relationship exists between the two corresponding genes. In our work, we propose to address this network inference problem with recently developed techniques pertaining to graph optimization. Given all the pairwise gene regulation information available, we propose to determine the presence of edges in the considered GRN by adopting an energy optimization formulation integrating additional constraints. Either biological (information about gene interactions) or structural (information about node connectivity) a priori are considered to restrict the space of possible solutions. Different priors lead to different properties of the global cost function, for which various optimization strategies, either discrete and continuous, can be applied.

4.4. Imaging biomarkers and characterization for chronic lung diseases

Participants: Guillaume Chassagnon, Maria Vakalopoulou (in collaboration with Evangelia Zacharaki and Nikos Paragios: University of Patras; 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.

4.5. Imaging radiomics and genes to assess immunotherapy

Participants: Roger Sun, Théo Estienne, Enzo Batistella, Maria Vakalopoulou (in collaboration with Éric Deutsch and Nikos Paragios: Institut de Cancérologie Gustave Roussy, Therapanacea)

Because responses of patients with cancer to immunotherapy can vary in success, innovative predictors of response to treatment are urgently needed to improve treatment outcomes. We aimed to develop and independently validate a radiomics-based biomarker of tumour-infiltrating CD8 cells in patients included in phase I trials of 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. This work is in collaboration with the Institut de Cancérologie Gustave Roussy Paris.

4.6. Restoration of old video archives

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet (collaboration F. Abboud, WITBE, J.-H. Chenot and L. Laborelli, INA)

The last century has witnessed an explosion in the amount of video data stored with holders such as the National Audiovisual Institute whose mission is to preserve and promote the content of French broadcast programs. The cultural impact of these records, their value is increased due to commercial reexploitation through recent visual media. However, the perceived quality of the old data fails to satisfy the current public demand. The purpose of our work is to propose new methods for restoring video sequences supplied from television archive documents, using modern optimization techniques with proven convergence properties [21], [50], [3].

4.7. 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, Inria, Leo Grady, Heartflow Inc.)

Cardio-vascular diseases are the leading cause of mortality in the world. Understanding these diseases is still 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 allow to assess coronary diseases but are typically invasive, requiring catheterization and relatively toxic contrast agents injection. With 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. 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.

With heartflow and with the REO team of Inria, 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 solve the inverse problem of locating and assessing coronary diseases even though the affected vessels are too small to be imaged directly.

5. Highlights of the Year

5.1. Highlights of the Year

5.1.1. Awards

The work on graph-based text categorization by F. Malliaros et al. [39] has received the best paper award at the 12th NAACL-HLT Workshop on Graph-Based Natural Language Processing (TextGraphs), held in New Orleans, Louisiana in June 2018.

Riza Alp Güler obtained the 2nd place at Prix du Doctorant for the Doctoral School STIC of Univ. Paris Saclay.

M. Papadomanolaki and M. Vakalopoulou got the 2nd place at the Earth Observation Challenge organised by Digital Globe and ESA for the project UrbanMonitor: Mapping Changes in Urban Environments towards Resilient Cities and Urban Sustainability. <http://blog.digitalglobe.com/news/earth-observation-challenge-the-three-winners/>

A. Pirayre whose PhD thesis was advised by J.-C. Pesquet received the Yves Chauvin PhD award (IFPEN).

Our M.Sc. program in Data Sciences and Business Analytics (with ESSEC Business School) was ranked 4th worldwide in the QS World University Rankings.

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. Kymatio

Participant: Edouard Oyallon.

link: <http://www.kymatio.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`.

6.1.3. Topical Node Embeddings

Participant: Abdulkadir Çelikkanat

link: <https://abdcelikkanat.github.io/projects/TNE/>

TNE learns node representations on graphs combining node and topic information, as described in [45]. The framework has been implemented in Python and has been built upon widely used modules, including `networkx`, `scipy`, `gensim` and `scikit-learn`.

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 [33]. 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. The algorithm implements the methodology described in [35]. 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. The algorithm implements the methodology described in [39]. It has been implemented in Python and has been built upon widely used modules, including `networkx`, `igraph`, `numpy` and `scikit-learn`.

6.1.7. *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.

6.1.8. *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.

7. New Results

7.1. Invertible Deep Networks

Participant: Edouard Oyallon (in collaboration with J.H. Jacobsen and A. Smeulders, Instituut voor Informatica)

It is widely believed that the success of deep convolutional networks is based on progressively discarding uninformative variability about the input with respect to the problem at hand. This is supported empirically by the difficulty of recovering images from their hidden representations, in most commonly used network architectures. In this paper we show via a one-to-one mapping that this loss of information is not a necessary condition to learn representations that generalize well on complicated problems, such as ImageNet. Via a cascade of homeomorphic layers, we build the *i*-RevNet, a network that can be fully inverted up to the final projection onto the classes, i.e. no information is discarded. Building an invertible architecture is difficult, for one, because the local inversion is ill-conditioned, we overcome this by providing an explicit inverse. An analysis of *i*-RevNet’s learned representations suggests an alternative explanation for the success of deep networks by a progressive contraction and linear separation with depth. To shed light on the nature of the model learned by the *i*-RevNet we reconstruct linear interpolations between natural image representations [28].

7.2. Compression of CNNs inputs

Participant: Edouard Oyallon (in collaboration with E. Belilovsky, DIRO, Montréal, S. Zagoruyko, WILLOW, Inria Paris and M. Valko, SEQUEL, Inria Lille)

Typical inputs of CNNs are highly redundant and could be potentially reduced. We study the first-order scattering transform as a candidate for reducing the signal processed by a convolutional neural network (CNN). We study this transformation and show theoretical and empirical evidence that in the case of natural images and sufficiently small translation invariance, this transform preserves most of the signal information needed for classification while substantially reducing the spatial resolution and total signal size. We show that cascading a CNN with this representation performs on par with ImageNet classification models commonly used in downstream tasks such as the ResNet-50. We subsequently apply our trained hybrid ImageNet model as a base model on a detection system, which has typically larger image inputs. On Pascal VOC and COCO detection tasks we deliver substantial improvements in the inference speed and training memory consumption compared to models trained directly on the input image [34].

7.3. Interstitial lung disease segmentation

Participants: Guillaume Chassagnon, Norbert Bus, Rafael Marini Silva, Evangelia Zacharaki, Maria Vakalopoulou (in collaboration with Marie-Pierre Revel and Nikos Paragios: AP-HP - Hopital Cochin Broca Hotel Dieu; Therapanacea)

Interstitial lung diseases (ILD) encompass a large spectrum of diseases sharing similarities in their physiopathology and computed tomography (CT) appearance. In the work [42], we propose the adaption of a deep convolutional encoder-decoder (CED) that has shown high accuracy for image segmentation. Such architectures require annotation of the total region with pathological findings. This is difficult to acquire, due to uncertainty in the definition and extent of disease patterns and the need of significant human effort, especially for large datasets. Therefore, often current methods use patch-based implementations of convolutional neural networks, which however tend to produce spatially inhomogeneous segmentations due to their local contextual view. We exploit the advantages of both architectures by using the output of a patch-based classifier as a prior to a CED.

Moreover, in order to deal with the limited available datasets that are available, in [41], we introduce a novel multi-network architecture that exploits domain knowledge to address those challenges. The proposed architecture consists of multiple deep neural networks that are trained after co-aligning multiple anatomies through multi-metric deformable registration. This multi-network architecture can be trained with fewer examples and leads to better performance, robustness and generalization through consensus. Comparable to human accuracy, highly promising results on the challenging task of interstitial lung disease segmentation demonstrate the potential of our approach.

7.4. Image Registration with 3D Convolutional Neural Networks

Participants: Stergios Christodoulidis, Mihir Sahasrabudhe, Guillaume Chassagnon, Maria Vakalopoulou (in collaboration with Stavroula Mougiakakou and Marie-Pierre Revel and Nikos Paragios: University of Bern; AP-HP - Hopital Cochin Broca Hotel Dieu; Therapanacea)

Image registration and in particular deformable registration methods are pillars of medical imaging. Inspired by the recent advances in deep learning, we propose in this paper, [25] we proposed a new deep learning based and unsupervised method for image registration. In particular, a novel convolutional neural network architecture that couples linear and deformable registration within a unified architecture endowed with near real-time performance. Our framework is modular with respect to the global transformation component, as well as with respect to the similarity function while it guarantees smooth displacement fields. We evaluate the performance of our network on the challenging problem of MRI lung registration, and demonstrate superior performance with respect to state of the art elastic registration methods. The proposed deformation (between inspiration & expiration) was considered within a clinically relevant task of interstitial lung disease (ILD) classification and showed promising results.

7.5. Radiomics for response to immunotherapy

Participants: Roger Sun, Maria Vakalopoulou (in collaboration with Elaine Johanna Limkin, Laurent Derclé, Stéphane Champiat, Shan Rong Han, Loic Verlingue, David Brandao, Andrea Lancia, Samy Ammari, Antoine Hollebecque, Jean-Yves Scoazec, Aurélien Marabelle, Christophe Massard, Jean-Charles Soria, Charlotte Robert, Nikos Paragios, Eric Deutsch, Charles Ferté: Institute Gustave Roussy; Therapanacea)

Because responses of patients with cancer to immunotherapy can vary in success, innovative predictors of response to treatment are urgently needed to improve treatment outcomes. In this retrospective multicohort work [17], we used four independent cohorts of patients with advanced solid tumours to develop and validate a radiomic signature predictive of immunotherapy response by combining contrast-enhanced CT images and RNA-seq genomic data from tumour biopsies to assess CD8 cell tumour infiltration. To develop the radiomic signature of CD8 cells, we used the CT images and RNA sequencing data of 135 patients with advanced solid malignant tumours who had been enrolled into the MOSCATO trial between May 1, 2012, and March 31, 2016, in France (training set). The genomic data, which are based on the CD8B gene, were used to estimate the abundance of CD8 cells in the samples and data were then aligned with the images to generate the radiomic signatures. The concordance of the radiomic signature (primary endpoint) was validated in a Cancer Genome Atlas [TCGA] database dataset including 119 patients who had available baseline preoperative imaging data and corresponding transcriptomic data on June 30, 2017. From 84 input variables used for the machine-learning method (78 radiomic features, five location variables, and one technical variable), a radiomics-based predictor of the CD8 cell expression signature was built by use of machine learning (elastic-net regularised regression method). Two other independent cohorts of patients with advanced solid tumours were used to evaluate this predictor. The immune phenotype internal cohort (n=100), were randomly selected from the Gustave Roussy Cancer Campus database of patient medical records based on previously described, extreme tumour-immune phenotypes: immune-inflamed (with dense CD8 cell infiltration) or immune-desert (with low CD8 cell infiltration), irrespective of treatment delivered; these data were used to analyse the correlation of the immune phenotype with this biomarker. Finally, the immunotherapy-treated dataset (n=137) of patients recruited from Dec 1, 2011, to Jan 31, 2014, at the Gustave Roussy Cancer Campus, who had been treated with anti-PD-1 and anti-PD-L1 monotherapy in phase 1 trials, was used to assess the predictive value of this biomarker in terms of clinical outcome.

7.6. Semantic Segmentation Techniques for Brain Tumor Patients

Participants: Siddhartha Chandra, Théo Estienne, Roger Sun, Enzo Battistella, Maria Vakalopoulou (in collaboration with Charlotte Robert, Nikos Paragios, Eric Deutsch: Institute Gustave Roussy; Therapanacea)

In this work [23] we propose a novel deep learning based pipeline for the task of brain tumor segmentation. Our pipeline consists of three primary components: (i) a preprocessing stage that exploits histogram standardization to mitigate inaccuracies in measured brain modalities, (ii) a first prediction stage that uses the V-Net deep learning architecture to output dense, per voxel class probabilities, and (iii) a prediction refinement stage that uses a Conditional Random Field (CRF) with a bilateral filtering objective for better context awareness. Additionally, we compare the V-Net architecture with a custom 3D Residual Network architecture, trained on a multi-view strategy, and our ablation experiments indicate that V-Net outperforms the 3D ResNet-18 with all bells and whistles, while fully connected CRFs as post processing, boost the performance of both networks. We report competitive results on the BraTS 2018 validation and test set as also summarized on [52].

7.7. Demystification of AI-driven medical image interpretation

Participants: Maria Vakalopoulou (in collaboration with P. Savadjiev, J. Chong, A. Dohan, C. Reinhold, B. Gallix; McGill University; Therapanacea)

The recent explosion of 'big data' has ushered in a new era of artificial intelligence (AI) algorithms in every sphere of technological activity, including medicine, and in particular radiology. However, the recent success of AI in certain flagship applications has, to some extent, masked decades-long advances in computational technology development for medical image analysis. In this work [16], we provide an overview of the history of AI methods for radiological image analysis in order to provide a context for the latest developments. We review the functioning, strengths and limitations of more classical methods as well as of the more recent deep learning techniques. We discuss the unique characteristics of medical data and medical science that set medicine apart from other technological domains in order to highlight not only the potential of AI in radiology but also the very real and often overlooked constraints that may limit the applicability of certain AI methods. Finally, we provide a comprehensive perspective on the potential impact of AI on radiology and on how to evaluate it not only from a technical point of view but also from a clinical one, so that patients can ultimately benefit from it.

7.8. Semantic Segmentation for Remote Sensing Data

Participants: Maria Papadomanolaki, Maria Vakalopoulou (in collaboration with Christina Karakizi, Georgia Antoniou, Konstantinos Karantzas, Nikos Paragios; National Technical University of Athens, Therapanacea)

Detailed, accurate and frequent land cover mapping is a prerequisite for several important geospatial applications and the fulfilment of current sustainable development goals. This work [9] introduces a methodology for the classification of annual high-resolution satellite data into several detailed land cover classes. In particular, a nomenclature with 27 different classes was introduced based on CORINE Land Cover (CLC) Level-3 categories and further analysing various crop types. Without employing cloud masks and/or interpolation procedures, we formed experimental datasets of Landsat-8 (L8) images with gradually increased cloud cover in order to assess the influence of cloud presence on the reference data and the resulting classification accuracy. The performance of shallow kernel-based and deep patch-based machine learning classification frameworks was evaluated. Quantitatively, the resulting overall accuracy rates differed within a range of less than 3%; however, maps produced based on Support Vector Machines (SVM) were more accurate across class boundaries and the respective framework was less computationally expensive compared to the applied patch-based deep Convolutional Neural Network (CNN). Further experimental results and analysis indicated that employing all multitemporal images with up to 30% cloud cover delivered relatively higher overall accuracy rates as well as the highest per-class accuracy rates. Moreover, by selecting 70% of the top-ranked features after applying a feature selection strategy, slightly higher accuracy rates were achieved. A detailed discussion of the quantitative and qualitative evaluation outcomes further elaborates on the performance of all considered classes and highlights different aspects of their spectral behaviour and separability.

Moreover, semantic segmentation is a mainstream method in several remote sensing applications based on very-high-resolution data, achieving recently remarkable performance by the use of deep learning and more specifically, pixel-wise dense classification models. In this work [36], we exploit the use of a relatively deep architecture based on repetitive downscale upscale processes that had been previously employed for human pose estimation. By integrating such a model, we are aiming to capture low-level details, such as small objects, object boundaries and edges. Experimental results and quantitative evaluation has been performed on the publicly available ISPRS (WGIII/4) benchmark dataset indicating the potential of the proposed approach.

7.9. BRANE Clust: Cluster-Assisted Gene Regulatory Network Inference Refinement

Participants: Jean-Christophe Pesquet (in collaboration with Aurélie Pirayre, IFP Energies nouvelles, Camille Couprie, Facebook Research, Laurent Duval, IFP Energies nouvelles)

Discovering meaningful gene interactions is crucial for the identification of novel regulatory processes in cells. Building accurately the related graphs remains challenging due to the large number of possible solutions from available data. Nonetheless, enforcing a priori on the graph structure, such as modularity, may reduce network indeterminacy issues. BRANE Clust (Biologically-Related A priori Network Enhancement with Clustering) refines gene regulatory network (GRN) inference thanks to cluster information. It works as a post-processing tool for inference methods (i.e. CLR, GENIE3). In BRANE Clust, the clustering is based on the inversion of a system of linear equations involving a graph-Laplacian matrix promoting a modular structure. Our approach [14] is validated on DREAM4 and DREAM5 datasets with objective measures, showing significant comparative improvements. We provide additional insights on the discovery of novel regulatory or co-expressed links in the inferred *Escherichia coli* network evaluated using the STRING database. The comparative pertinence of clustering is discussed computationally (SIMoNe, WGCNA, X-means) and biologically (RegulonDB).

7.10. Proximity Operators of Discrete Information Divergences

Participants: Jean-Christophe Pesquet (in collaboration with Mireille El Gheche, EPFL, Giovanni Chierchia, ESIEE Paris)

Information divergences allow one to assess how close two distributions are from each other. Among the large panel of available measures, a special attention has been paid to convex ϕ -divergences, such as Kullback-Leibler, Jeffreys-Kullback, Hellinger, Chi-Square, Renyi, and I_α divergences. While ϕ -divergences have been extensively studied in convex analysis, their use in optimization problems often remains challenging. In this regard, one of the main shortcomings of existing methods is that the minimization of ϕ -divergences is usually performed with respect to one of their arguments, possibly within alternating optimization techniques. In this paper, we overcome this limitation by deriving new closed-form expressions for the proximity operator of such two-variable functions. This makes it possible to employ standard proximal methods for efficiently solving a wide range of convex optimization problems involving ϕ -divergences. In addition, we show that these proximity operators are useful to compute the epigraphical projection of several functions of practical interest. The proposed proximal tools are numerically validated in the context of optimal query execution within database management systems, where the problem of selectivity estimation plays a central role. Experiments are carried out on small to large scale scenarios [6].

7.11. Stochastic quasi-Fejèr block-coordinate fixed point iterations with random sweeping

Participants: Jean-Christophe Pesquet (in collaboration with Patrick Combettes, North Caroline State University)

Our previous work 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 present paper establishes results on the mean-square and linear convergence of the iterates. Applications to monotone operator splitting and proximal optimization algorithms are presented.

7.12. Rational optimization for nonlinear 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 [53].

7.13. Representation Learning on Real-World Graphs

Participants: Fragkiskos Malliaros, Abdulkadir Çelikkanat (in collaboration with Duong Nguyen, UC San Diego)

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 BiasedWalk, an unsupervised Skip-gram-based network embedding algorithm which can preserve higher-order proximity information, as well as capture both the homophily and role equivalence relationships between nodes [33]. BiasedWalk relies on a novel node sampling procedure based on biased random walks, that can behave as actual depth-first-search and breath-first-search explorations – thus, forcing the sampling scheme to capture both role equivalence and homophily relations between nodes. Furthermore, BiasedWalk is scalable on large scale graphs, and is able to handle different types of networks structures, including (un)weighted and (un)directed ones.

Furthermore, we have introduced TNE (Topical Node Embeddings), a general framework to enhance node embeddings acquired by means of the random walk-based approaches [45]. Similar to the notion of *topical word embeddings* in the domain of Natural Language Processing, the proposed framework assigns each vertex to a topic with the favor of various statistical models and community detection methods, and then generates enhanced community representations.

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 the biased random walks as well as the incorporation of vertex and topic embeddings outperform widely-known baseline NRL methods.

7.14. Anonymity on Directed Networks

Participants: Fragkiskos Malliaros (in collaboration with Jordi Casas-Roma and Julián Salas, Universitat Oberta de Catalunya; Michalis Vazirgiannis, École Polytechnique)

In recent years, a huge amount of social and human interaction networks have been made publicly available. Embedded within this data, there is user's private information that must be preserved before releasing the data to third parties and researchers. In this work, we have considered the problem of anonymization on directed networks. Although there are several anonymization methods for networks, most of them have explicitly been designed to work with undirected networks and they can not be straightforwardly applied when they are directed. Moreover, ignoring the direction of the edges causes important information loss on the anonymized networks in the best case. In the worst case, the direction of the edges may be used for reidentification, if it is not considered in the anonymization process. Here, we have proposed two different models for k -degree anonymity on directed networks, and we also present algorithms to fulfill these k -degree anonymity models [4]. Given a network G , we construct a k -degree anonymous network by the minimum number of edge additions. Our algorithms use multivariate micro-aggregation to anonymize the degree sequence, and then they modify the graph structure to meet the k -degree anonymous sequence. We apply our algorithms to several real datasets and demonstrate their efficiency and practical utility.

7.15. Influence Maximization in Complex Networks

Participants: Fragkiskos Malliaros (in collaboration with Michalis Vazirgiannis, George Panagopoulos, Maria-Evgenia Rossi, Bowen Shi, Christos Giatsidis, École Polytechnique; Nikolaos Tziortziotis, Université Paris-Sud)

Influence maximization in complex networks has attracted a lot of attention due to its numerous applications, including diffusion of social movements, the spread of news, viral marketing and outbreak of diseases. The objective is to discover a group of users that are able to maximize the spread of influence across a network. The seminal *greedy* algorithm developed by Kempe, Kleinberg and Tardos progressively adds new nodes to the seed set, maximizing the expected influence spread; the algorithm gives a solution to the influence maximization problem while having a good approximation ratio.

Nevertheless, one of the bottlenecks of the greedy algorithm is that it does not scale well on large scale datasets. In our work, we have proposed Matrix Influence (MATI), an efficient algorithm that can be used under both the Linear Threshold and Independent Cascade diffusion models [15]. MATI is based on the precalculation of the influence by taking advantage of the simple paths in the node's neighborhood. An extensive empirical analysis has been performed on multiple real-world datasets showing that MATI has competitive performance when compared to other well-known algorithms with regards to running time and expected influence spread.

Furthermore, the previously described greedy algorithm focuses solely on static networks. However, with the emergence of several complementary data, such as the network's temporal changes and the diffusion cascades taking place over it, novel methods have been proposed with promising results. In our work, we have introduced a simple yet effective algorithm (called DiffuGreedy) that combines the algorithmic methodology of the greedy approach with diffusion cascades [35]. We have compared it with four different prevalent influence maximization approaches, on a large scale Chinese microblogging dataset. More specifically, for comparison, we have employed methods that derive the seed set using the static network, the temporal network, the diffusion cascades, and their combination. A set of diffusion cascades from the latter part of the dataset is set aside for evaluation. The experimental evaluation has shown that the proposed DiffuGreedy outperforms widely used baseline methods in both quality of the seed set and computational efficiency.

7.16. Graph-based Text Analytics

Participants: Fragkiskos Malliaros (in collaboration with Konstantinos Skianis and Michalis Vazirgiannis, École Polytechnique)

Text categorization is a core task in a plethora of text mining applications. In our work, contrary to the traditional *Bag-of-Words* approach, we have considered the *Graph-of-Words* model in which each document is represented by a graph that encodes relationships between the different terms. Based on this formulation, we treat the term weighting task as a node ranking problem; the importance of a term is determined by the importance of the corresponding node in the graph, using node centrality criteria. We have also introduced novel graph-based weighting schemes by enriching graphs with word-embedding distances, in order to reward or penalize the importance of semantically close terms [39]. Our methods produce more discriminative feature weights for text categorization, outperforming existing frequency-based criteria – highlighting also the importance of graph-based methods in text analytics and natural language processing in general.

7.17. Auxiliary Variable Method for MCMC Algorithms in High Dimension

Participants: Emilie Chouzenoux, Jean-Christophe Pesquet (Collaboration: Yosra Marnissi, SAFRAN TECH, and Amel Benazza-Benyahia, SUP'COM Tunis)

In this work, we are interested in Bayesian inverse problems where either the data fidelity term or the prior distribution is Gaussian or driven from a hierarchical Gaussian model. Generally, Markov chain Monte Carlo (MCMC) algorithms allow us to generate sets of samples that are employed to infer some relevant parameters of the underlying distributions. However, when the parameter space is high-dimensional, the performance of stochastic sampling algorithms is very sensitive to existing dependencies between parameters. In particular, this problem arises when one aims to sample from a high-dimensional Gaussian distribution whose covariance matrix does not present a simple structure. Another challenge is the design of Metropolis–Hastings proposals that make use of information about the local geometry of the target density in order to speed up the convergence and improve mixing properties in the parameter space, while not being too computationally expensive. These two contexts are mainly related to the presence of two heterogeneous sources of dependencies stemming either from the prior or the likelihood in the sense that the related covariance matrices cannot be diagonalized in the same basis. In this work, we address these two issues. Our contribution consists of adding auxiliary variables to the model in order to dissociate the two sources of dependencies. In the new augmented space, only one source of correlation remains directly related to the target parameters, the other sources of correlations being captured by the auxiliary variables. Experimental results conducted on two practical image restoration problems indicate that adding the proposed auxiliary variables makes the sampling problem simpler, and thus the computational cost of each iteration of the Gibbs sampler is significantly reduced while ensuring good mixing properties [11].

7.18. Generation of patient-specific cardiac vascular networks

Participant: Hugues Talbot (in collaboration with C. Jaquet, L. Najman, ESIEE Paris; L. Grady, M. Schaap, B. Spain, H. Kim, C. Taylor, HeartFlow; I. Vignon-Clementel, REO)

In this work, we have proposed a blood-vessel generation procedure for extending known patient vasculature over and within the heart ventricle [8]. It is patient-specific, in the sense that it extends 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 solve the associated inverse problem of finding the cause of observed perfusion deficits associated with coronary diseases that cannot be imaged directly.

7.19. Curvilinear structure analysis using path operators

Participant: Hugues Talbot (in collaboration with O. Merveille, N. Passat, CRESTIC, and L. Najman, ESIEE Paris)

In this work, we propose mathematical morphology based operators that use paths as families of structuring elements [12]. Structuring elements are like the windows of linear operators, they define the extent of the related operators (convolutions in the linear case, openings and closings in the morphology case). When dealing with thin objects (e.g. fibres, blood vessels, textures, etc), a compact, isotropic window is usually inappropriate because no such window can fit in these objects. This is more critical for morphology, which is concerned with preserving shapes, than with linear operators. Thin windows must therefore be devised, but there are a large number of potentially interesting thin windows at each point in an image. In this article, we leverage the definition of noise-resistant, path operators to define a non-linear notion of vesselness, that can be used for thin object detection, filtering and segmentation in 2D and 3D.

7.20. High throughput automated detection of axial malformations in fish embryo

Participant: Hugues Talbot (in collaboration with D. Genest, M. Léonard, N. De Crozé, L'Oréal, and E. Puybureau, J. Cousty, LIGM)

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 tail malformation in fish embryo, based on image analysis and machine learning [5]. 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 partnership 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.

8. Bilateral Contracts and Grants with Industry

8.1. Bilateral Contracts with Industry

PhD Contract with General Electric Healthcare
 Project title: Minimally invasive assesement 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

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

GPU grant from NVIDIA
 NVIDIA's Academic Programs Team is dedicated to empowering and collaborating with professors and researchers at universities worldwide. For a research project on compressing CNNs input, Edouard Oyallon received a TitanXP from NVIDIA.

9. Partnerships and Cooperations

9.1. National Initiatives

9.1.1. ANR

Program: ANR PRC

Project acronym: CoMeDIC

Project title: Convergent Metrics for DIcrete 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: LearnCost

Project title: Learning Model Constraints for Structured Prediction

Duration: 2014-2018

Coordinator: M. Blaschko

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.

9.1.2. Others

Program: CNRS MASTODONS

Project acronym: TABASCO

Project title: Traitement du bruit non Gaussien en spectroscopie

Duration: 2016-2018

Coordinator: E. Chouzenoux

Program: CNRS-CEFIPRA

Project acronym: NextGenBP

Project title: Looking Beyond Backpropagation in Deep Learning

Duration : 2017-2019

Coordinator: E. Chouzenoux

Program: CNRS MI

Project acronym: SUPREMA

Project title: Super-résolution en microscopie biphotonique

Duration: 2018

Coordinator: E. Chouzenoux

Program: PHC - Campus France
Project acronym: POLONIUM
Project title: When Poisson and Gauss meet in imaging
Duration: 2018-2020
Coordinator: E. Chouzenoux

9.2. European Initiatives

9.2.1. H2020 Projects

Program: H2020 ITN Marie Skłodowska-Curie
Project acronym: SUNDIAL
Project title: SURvey Network for Deep Imaging Analysis and Learning
Duration: 2017-2021
Coordinator: R. Peletier (Univ. Groningen, NL), local: H. Talbot

9.3. International Initiatives

9.3.1. Informal International Partners

Sup'Com Tunis - Pr. Amel Benazza-Benhayia. Collaboration Topic: Multispectral imaging.
University of Patras, Greece - Dr. V. Megalooikonomou. Collaboration Topic: Biosignal analysis.
University of Pennsylvania - Prof. Aristeidis Sotiras. Collaboration Topic: Higher Order Graphs in biomedical image analysis.
University of Montréal, MILA - Dr. Eugene Belilovsky, Pr. Simon Lacoste-Julien. Collaboration Topic : Deep learning, scattering transform.
Berkeley University - Dr. Michael Eickenberg and Dr. Damien Scieur. Collaboration Topic : Deep learning.
KU Leuven - Pr. Matthew Blashcko. Collaboration Topic : Scattering transform.
University of Amsterdam - Dr. Jörn Jacobsen. Collaboration Topic : Deep learning.
Aristotle University of Thessaloniki, Greece - Prof. Apostolos N. Papadopoulos. Collaboration Topic: Graph mining and learning.
Indraprastha Information Institute Technology, Delhi, India - Dr. Angshul Majumdar. Collaboration Topic: Dictionary learning.
Universidad Técnica Federico Santa María, Valparaíso, Chile - Dr. Luis M. Briceño-Arias. Collaboration Topic: Stochastic optimization.
North Carolina State University - Prof. Patrick Louis Combettes. Collaboration Topic: Stochastic optimization.

9.4. International Research Visitors

9.4.1. Visits of International Scientists

Dr. Luis M. Briceño-Arias, Universidad Técnica Federico Santa María, Valparaíso, Chile, 1 Jun. - 1 Jul. 2018, 21 Nov. - 21 Dec. 2018
Jyoti Maggu (PhD student), IIIT New Delhi, India, 05 Mar.-28 May 2018
Vanika Singhal (PhD student), IIIT New Delhi, India, 05 Mar.-20 Apr. 2018
Georgios Panagopoulos (PhD student), Ecole Polytechnique, 15 Jun. - 31 Jul. 2018

9.4.2. Visits to International Teams

9.4.2.1. Research Stays Abroad

M.C. Corbineau, Department of Physics, Informatics and Mathematics, Università degli studi di Modena e Reggio Emilia, Modena, Italy, 20 Sep. - 20 Oct. 2018.

10. Dissemination

10.1. Promoting Scientific Activities

10.1.1. Scientific Events Organisation

10.1.1.1. Member of the Organizing Committees

R. Güler organized the Workshop “COCO + Mapillary Joint Recognition Challenge” at ECCV 2018, September 2018, Munich, Germany.

R. Güler organized the Workshop “Posetrack Challenge Articulated People Tracking in the Wild”, at ECCV 2018, September 2018, Munich, Germany.

F. Malliaros was a member of the organizing committee of the 3rd International Workshop on Learning Representations for Big Networks (BigNet), The Web Conference (WWW), Lyon, France, 2018.

10.1.2. Scientific Events Selection

10.1.2.1. Chair of Conference Program Committees

H. Talbot chaired the 2nd Workshop on Reproducible Research in Pattern Recognition organized at ICPR 2018, Beijing, China.

10.1.2.2. Member of the Conference Program Committees

H. Talbot. Member of the board and program committee for the International Symposium in Mathematical Morphology, to take place in Saarbrücken, Germany, May 2019.

E. Chouzenoux. Member of the technical committees “Signal Processing Theory and Methods” of the IEEE Signal Processing Society and “SAT Signal and Data Analytics for Machine Learning” of EURASIP.

F. Malliaros. Member of the program committee at: AAAI Conference on Artificial Intelligence (AAAI), The Web Conference (WWW), Annual Conference of the North American Chapter of the Association for Computational Linguistics (NAACL), Conference on Neural Information Processing Systems (NeurIPS), International Conference on Complex Networks and Their Applications (Complex Networks)

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), Joint Urban Remote Sensing Event (JURSE).

10.1.3. Journal

10.1.3.1. Member of the Editorial Boards

Hugues Talbot: Senior Area Editor for IEEE Signal Processing Letters

Maria Vakalopoulou: Lead Guest Editor for the special issue on Remote Sensing, in Computer Vision and Image Understanding (CVIU)

Emilie Chouzenoux: Associate Editor of the IEEE Transactions on Signal Processing

Jean-Christophe Pesquet: Associate Editor of the SIAM Journal on Imaging Sciences

10.1.3.2. Reviewer - Reviewing Activities

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.

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.

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: Data Mining and Knowledge Discovery (DAMI), ACM Transactions on Knowledge Discovery from Data (TKDD).

M. C. Corbineau: Signal Processing: Image Communication (SPIC), Computer Vision and Image Understanding (CVIU).

M. Papadomanolaki: Computer Vision and Image Understanding (CVIU), Journal of Basic and Applied Research International, Journal of Geography, Environment and Earth Science International.

M. Sahasrabudhe: Computer Vision and Image Understanding (CVIU).

D. Khuê Lê-Huu: IEEE Transactions on Pattern Analysis and Machine Intelligence (TPAMI), International Journal of Computer Vision (IJCV).

10.1.4. Invited Talks

J.-C. Pesquet:

SAMSI workshop on Operator Splitting Methods in Data Analysis, Raleigh, March 2018,

New York University, March 2018,

Entropy workshop, Barcelona, May 2018,

SIAM Conference on Imaging Science, Bologna, Italy, June 2018,

Aalto University, Helsinki, October 2018,

Polish Science Academy, Warsaw, December 2018.

H. Talbot:

Heartflow, Redwood City, California, April 2018,

Imperial College, London, October 2018,

Institut Henri Poincaré, Paris, December 2018.

E. Chouzenoux:

CRIStAL, Lille, February 2018,
Ann Arbor University, USA, April 2018,
International Conference Inverse Problems: Modeling and Simulation (IPMS 2018), Malta, 21st-25th May 2018,
Heriot Watt University, Edimburg, UK, June 2018,
SIAM Conference on Imaging Science, Bologna, Italy, June 2018.

F. Malliaros:

The Web Conference, Lyon, France, April 2018,
Paris Descartes University, Paris, France, May 2018,
ACM International Conference on Information and Knowledge Management (CIKM), Turin, Italy, October 2018.

E. Oyallon:

SONY CSL, Paris, January 2018,
DeepMind CSML Seminar Series, January 2018,
Imaging in Paris Seminar, IHP, January 2018,
Criteo, Paris, May 2018,
SequeL, Lille, May 2018,
GE Healthcare, Bures-sur-Yvette, June 2018,
NAVER LABS, Grenoble, June 2018,
GT DeepNet, LRI/TAO, Gif-sur-Yvette, December 2018,
GREYC, Caen, December 2018.

M. Vakalapolou:

ONERA, March 2018,
Telecom ParisTech - LTCI, May 2018,
CNRS Workshop on Artificial Intelligence and its Applications, CentraleSupélec, July 2018.

A. Celikkanat:

Paris-Saclay Junior Conference on Data Science and Engineering (JDSE2018) (Poster), Orsay, France, 13-14th September 2018.

M. C. Corbineau:

SIAM Conference on Imaging Science, Bologna, Italy, June 2018.

R. A. Guler:

Inria Paris, March 2018,
University of Amsterdam, April 2018
Max Planck Institute for Intelligent Systems, Tübingen, July 2018.

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 : Corbineau, Marie-Caroline and Pesquet, Jean-Christophe. Advanced course on Optimization, 33h, M1, CentraleSupélec, FR

Master : Chouzenoux, Emilie and Pesquet, Jean-Christophe and Corbineau, Marie-Caroline. Foundations of Distributed and Large Scale Computing, 26h, M.Sc. in Data Sciences and Business Analytics, CentraleSupélec, MVA ENS Cachan, Master Optimization Paris Sud and ESSEC Business School, FR

Master: Pesquet, Jean-Christophe. Introduction to Optimization, 6h, MVA ENS Cachan, FR

Master: Malliaros, Fragkiskos. Machine Learning, 27h, M.Sc. in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School, FR

Master: Malliaros, Fragkiskos. Network Science Analytics, 27h, M.Sc. in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School and M.Sc. in Artificial Intelligence, CentraleSupélec, FR

Master: Malliaros, Fragkiskos. Introduction to Machine Learning, 33h, 2nd year course at Centrale-Supélec, FR

Master: Malliaros, Fragkiskos. Mathematical Modeling of Propagation Phenomena – Propagation on Graphs, 15h, 1st year course at CentraleSupélec, FR

Master: Sahasrabudhe, Mihir: Programming and Languages, 24h, M.Sc. in Data Science and Business Analytics, CentraleSupélec and ESSEC Business School, FR

Master: Sahasrabudhe, Mihir and Battistella, Enzo: Introduction to Machine Learning, 28h, 2nd year CentraleSupélec, FR

Master: Chouzenoux, Emilie. Advanced Machine Learning, 24h, 3rd year CentraleSupélec, FR

Master: Papadomanolaki, Maria. Deep Learning, 3rd year CentraleSupélec and MVA ENS Cachan, FR

Master: Marmin, Arthur, Cours de soutien de mathématiques, 28h, 2nd year CentraleSupélec, FR

Master: Celikkanat, Abdulkadir. Network Science Analytics, 20h, M.Sc. in Data Sciences and Business Analytics, ESSEC and 3rd year CentraleSupélec, FR

Master: Celikkanat, Abdulkadir. Mathematical Modeling of Propagation Phenomena - Propagation on Graphs, 12h, 3rd year CentraleSupélec, FR

Master: Estienne, Théo. Deep Learning, 7h30, 3rd year CentraleSupélec, FR

Master: Papadomanolaki, Maria. Deep Learning, 7h30, 3rd year CentraleSupélec, FR

Master: Oyallon, Edouard. Deep Learning, 12h, 3rd year CentraleSupélec, FR

Master: Oyallon, Edouard. Deep Learning, 1h, MVA ENS Cachan, FR

Master: Vakalopoulou, Maria. Deep Learning, 12h, 3rd year CentraleSupélec, FR

Master: Vakalopoulou, Maria. Introduction to Machine Learning, 12h, 2nd year CentraleSupélec, FR

Master: Talbot, Hugues. Discrete Optimisation, 2nd year course, CentraleSupélec, 30h, FR

Master: Talbot, Hugues. Big Data, Techniques and Platforms, M.Sc in Data Science and Business Analytics, CentraleSupélec and ESSEC Business School, 30h, FR

10.2.2. Lecturing activities

Chouzenoux, Emilie and Talbot, Hugues. Enjeux et technologies de l'intelligence artificielle. CentraleSupélec Exed, 2 days (×2), FR.

Oyallon, Edouard. Introduction to Deep Learning. Ateliers Statistiques de la Société Française de Statistique, 2 days, IHP, Paris, FR.

Oyallon, Edouard. Advanced Deep Learning. Mathematical Coffees, 3 hours, Huawei, Paris, FR.

Chouzenoux, Emilie. Parallel Stochastic Computing. Mathematical Coffees, 3 hours, Huawei, Paris, FR.

Vakalopoulou, Maria. Introduction to Computer Vision, Applications to Medical Images. Summer School on Artificial Intelligence, 5 hours, CentraleSupélec, FR.

Pesquet, Jean-Christophe. Proximal Splitting Methods in Image Processing, Lake Como School of Advanced Studies on Computational Methods for Inverse Problems in Imaging, 12 hours, May 2018, Italy.

10.2.3. Supervision

PhD (defended) : Siddhartha Chandra, Deep Structured Prediction for Dense Labeling Tasks in Computer Vision, 2014-2018, supervised by Iasonas Kokkinos. Defended on 11st May 2018.

PhD (defended) : Stefan Kinauer, Représentations à base de parties pour la vision 3D de haut niveau, 2014-2018, supervised by Iasonas Kokkinos. Defended on 31st August 2018.

PhD (defended) : Afef Cherni, Méthodes modernes d'analyse de données en biophysique analytique, 2015-2018, supervised by Emilie Chouzenoux and Marc-André Delsuc (IGBMC, Strasbourg). Defended on 20th September 2018.

PhD (defended): Clara Jaquet. Vers la simulation de perfusion du myocarde à partir d'image tomographique scanner. 2014-2018. Supervised by Hugues Talbot and Laurent Najman (ESIEE). Defended on 13 December 2018.

PhD in progress : Mihir Sahasrabudhe, Understanding Correlations in High-Dimensional Spaces and their Applications in Medical Imaging and Computer Vision, 2015-2019, supervised by Nikos Paragios

PhD in progress : Marie-Caroline Corbineau, Fast online optimization algorithms for machine learning and medical imaging, 2016-2019, supervised by Emilie Chouzenoux and J.-C. Pesquet

PhD in progress : 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: Diane Genest. Imagerie du Modele alevin de poisson / Application a la toxicologie du developpement. 2016-2019. Supervised by Hugues Talbot and Jean Cousty (ESIEE).

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: Guillaume Chassagnon, Development of new quantitative imaging biomarkers for obstructive and interstitial lung diseases, 2016-2019, supervised by N. Paragios

PhD in progress: Maïssa Sghaier, clinical Task-Based Reconstruction in tomosynthesis, 2017-2020, supervised by E. Chouzenoux, J.-C. Pesquet and G. Palma (GE Healthcare)

PhD in progress: Arthur Marmin, Rational models optimized exactly for chemical processes improvement, 2017-2020, supervised by Marc Castella (Telecom Paristech) and J.-C. Pesquet

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 N. Paragios

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: Théo Estienne, Improving anticancer therapies efficacy through Machine Learning on Medical Imaging & Genomic Data, 2017-2020, supervised by N. Paragios

PhD in progress: Abdulkadir Celikkanat, Representation learning methods on graphs, 2017-2020, supervised by N. Paragios (TheraPanacea, Paris) and F. Malliaros

PhD in progress: Maria Papadomanolaki, Change Detection from Multitemporal High Resolution Data with Deep Learning, 2017-2021, supervised by M. Vakalopoulou and K. Karantzas (National Technical University of Athens).

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: 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: Yunshi Huang, Majorization-Minimization approaches for large scale problems in image processing, 2018-2021, supervised by E. Chouzenoux.

PhD in progress: Georgios Panagopoulos, Influence maximization in social networks, 2018-2021, supervised by F. Malliaros and M. Vazirgiannis (École Polytechnique).

10.2.4. Juries

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

Emilie Chouzenoux, Marie-Caroline Corbineau, Fragkiskos Malliaros, Edouard Oyallon, Jean-Christophe Pesquet, Mihir Sahasrabudhe and Hugues Talbot were part of the jury committee for several end-of-course internship presentations in CentraleSupélec.

10.3. Popularization

10.3.1. Interventions

Enzo Battistella, Marie-Caroline Corbineau, Théo Estienne and Maria Vakalopoulou have participated at the 'Demi-journée Recherche' organised by CentraleSupélec for the first year students of the school.

11. Bibliography

Publications of the year

Doctoral Dissertations and Habilitation Theses

- [1] S. CHANDRA. *Efficient Deep Structured Prediction for Dense Labeling Tasks in Computer Vision*, Université Paris-Saclay, May 2018, <https://tel.archives-ouvertes.fr/tel-01812763>
- [2] S. KINAUER. *Part-Based Representations for High-Level 3D Vision*, Université Paris-Saclay, August 2018, <https://tel.archives-ouvertes.fr/tel-01885958>

Articles in International Peer-Reviewed Journals

- [3] F. ABOUD, E. CHOUZENOUX, J.-C. PESQUET, J.-H. CHENOT, L. LABORELLI. *An Alternating Proximal Approach for Blind Video Deconvolution*, in "Signal Processing: Image Communication", 2018, vol. 70, pp. 21-36, <https://hal.archives-ouvertes.fr/hal-01668437>

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- [4] J. CASAS-ROMA, J. SALAS, F. MALLIAROS, M. VAZIRGIANNIS. *k-Degree anonymity on directed networks*, in "Knowledge and Information Systems (KAIS)", September 2018 [DOI : 10.1007/s10115-018-1251-5], <https://hal-centralesupelec.archives-ouvertes.fr/hal-01950285>
- [5] D. GENEST, É. PUYBAREAU, M. LÉONARD, N. DE CROZÉ, J. COUSTY, H. TALBOT. *High throughput automated detection of axial malformations in Medaka fish embryo*, in "Computers in Biology and Medicine", 2019, <https://hal.archives-ouvertes.fr/hal-01971148>
- [6] M. E. GHECHE, G. CHERCHIA, J.-C. PESQUET. *Proximity Operators of Discrete Information Divergences*, in "IEEE Transactions on Information Theory", February 2018, vol. 64, n^o 2, pp. 1092-1104, <https://hal.archives-ouvertes.fr/hal-01672646>
- [7] E. GROSSIORD, B. NAEGEL, H. TALBOT, L. NAJMAN, N. PASSAT. *Shape-based analysis on component-graphs for multivalued image processing*, in "Mathematical Morphology - Theory and Applications", 2019, <https://hal.univ-reims.fr/hal-01695384>
- [8] C. JAQUET, L. NAJMAN, H. TALBOT, L. GRADY, M. SCHAAP, B. SPAIN, H. J. KIM, I. VIGNON-CLEMENTEL, C. A. TAYLOR. *Generation of patient-specific cardiac vascular networks: a hybrid image-based and synthetic geometric model*, in "IEEE Transactions on Biomedical Engineering", 2018 [DOI : 10.1109/TBME.2018.2865667], <https://hal.archives-ouvertes.fr/hal-01869264>
- [9] C. KARAKIZI, K. KARANTZALOS, M. VAKALOPOULOU, G. ANTONIOU. *Detailed Land Cover Mapping from Multitemporal Landsat-8 Data of Different Cloud Cover*, in "Remote Sensing", August 2018, <https://hal.inria.fr/hal-01959065>
- [10] P. KONDAXAKIS, K. GULZAR, S. KINAUER, I. KOKKINOS, V. KYRKI. *Robot–Robot Gesturing for Anchoring Representations*, in "IEEE Transactions on Robotics", October 2018, pp. 1-15, <https://hal.archives-ouvertes.fr/hal-01961433>
- [11] Y. MARNISSI, E. CHOUZENOUX, A. BENAZZA-BENYAHIA, J.-C. PESQUET. *An Auxiliary Variable Method for Markov Chain Monte Carlo Algorithms in High Dimension*, in "Entropy", 2018, vol. 20, n^o 2 [DOI : 10.3390/E20020110], <https://hal.archives-ouvertes.fr/hal-01797093>
- [12] O. MERVEILLE, H. TALBOT, L. NAJMAN, N. PASSAT. *Curvilinear structure analysis by ranking the orientation responses of path operators*, in "IEEE Transactions on Pattern Analysis and Machine Intelligence", 2018, vol. 40, n^o 2, pp. 304-317 [DOI : 10.1109/TPAMI.2017.2672972], <https://hal.archives-ouvertes.fr/hal-01262728>
- [13] E. OYALLON, S. ZAGORUYKO, G. HUANG, N. KOMODAKIS, S. LACOSTE-JULIEN, M. BLASCHKO, E. BELILOVSKY. *Scattering Networks for Hybrid Representation Learning*, in "IEEE Transactions on Pattern Analysis and Machine Intelligence", September 2018, 11 p. , <https://arxiv.org/abs/1809.06367> [DOI : 10.1109/TPAMI.2018.2855738], <https://hal.inria.fr/hal-01837587>
- [14] A. PIRAYRE, C. COUPRIE, L. DUVAL, J.-C. PESQUET. *BRANE Clust: Cluster-Assisted Gene Regulatory Network Inference Refinement*, in "IEEE/ACM Transactions on Computational Biology and Bioinformatics", June 2018, vol. 15, n^o 3, pp. 850-860, <https://hal-ifp.archives-ouvertes.fr/hal-01330638>

- [15] M.-E. ROSSI, B. SHI, N. TZIORTZIOTIS, F. MALLIAROS, C. GIATSIDIS, M. VAZIRGIANNIS. *MATI: An efficient algorithm for influence maximization in social networks*, in "PLoS ONE", October 2018, <https://hal-centralesupelec.archives-ouvertes.fr/hal-01950273>
- [16] P. SAVADJIEV, J. CHONG, A. DOHAN, M. VAKALOPOULOU, C. REINHOLD, N. PARAGIOS, B. GALLIX. *Demystification of AI-driven medical image interpretation: past, present and future*, in "European Radiology", August 2018, <https://hal.inria.fr/hal-01958231>
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Invited Conferences

- [18] P. L. COMBETTES, J.-C. PESQUET. *Linear convergence of stochastic block-coordinate fixed point algorithms*, in "European Signal and Image Processing Conference (EUSIPCO 2018)", Rome, Italy, September 2018, <https://hal.archives-ouvertes.fr/hal-01964580>
- [19] M.-C. CORBINEAU, E. CHOUZENOUX, J.-C. PESQUET. *Geometry-Texture Decomposition/Reconstruction Using a Proximal Interior Point Algorithm*, in "10th IEEE Sensor Array and Multichannel Signal Processing Workshop (SAM 2018)", Sheffield, United Kingdom, Proceedings of the 10th IEEE Sensor Array and Multichannel Signal Processing Workshop (SAM 2018), July 2018, <https://hal.archives-ouvertes.fr/hal-01863408>
- [20] J. MAGGU, A. MAJUMDAR, E. CHOUZENOUX. *Transformed Locally Linear Manifold Clustering*, in "26th European Signal Processing Conference", Rome, Italy, Proceedings of the 26th European Signal Processing Conference (EUSIPCO 2018), September 2018, <https://hal.archives-ouvertes.fr/hal-01862192>

International Conferences with Proceedings

- [21] F. ABBOUD, E. CHOUZENOUX, J.-C. PESQUET, H. TALBOT. *A Multicore Convex Optimization Algorithm with Applications to Video Restoration*, in "IEEE International Conference on Image Processing", Athens, Greece, Proceedings of the IEEE International Conference on Image Processing (ICIP 2018), October 2018, <https://hal.archives-ouvertes.fr/hal-01862210>
- [22] A. BENFENATI, E. CHOUZENOUX, J.-C. PESQUET. *A Nonconvex Variational Approach for Robust Graphical Lasso.*, in "IEEE International Conference on Acoustics, Speech, and Signal Processing (ICASSP 2018)", Calgary, Canada, Proceedings of the IEEE International Conference on Acoustics, Speech, and Signal Processing (ICASSP 2018), April 2018, <https://hal.archives-ouvertes.fr/hal-01803424>
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