



IN PARTNERSHIP WITH:  
**Ecole Centrale Paris**

Activity Report 2017

## **Project-Team GALEN**

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

RESEARCH CENTER  
**Saclay - Île-de-France**

THEME  
**Computational Neuroscience and  
Medicine**



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## Project-Team GALEN

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### **Keywords:**

#### **Computer Science and Digital Science:**

- A3.4. - Machine learning and statistics
  - A3.4.1. - Supervised learning
  - A3.4.2. - Unsupervised learning
  - A3.4.3. - Reinforcement learning
  - A3.4.4. - Optimization and learning
  - A3.4.5. - Bayesian methods
  - A3.4.6. - Neural networks
  - A3.4.7. - Kernel methods
  - A3.4.8. - Deep learning
- A5.3.1. - Compression
- A5.3.2. - Sparse modeling and image representation
- A5.3.3. - Pattern recognition
- A5.3.4. - Registration
- A5.4.1. - Object recognition
- A5.4.2. - Activity recognition
- A5.4.4. - 3D and spatio-temporal reconstruction
- A5.9. - Signal processing
  - A5.9.1. - Sampling, acquisition
  - A5.9.2. - Estimation, modeling
  - A5.9.3. - Reconstruction, enhancement
  - A5.9.4. - Signal processing over graphs
  - A5.9.5. - Sparsity-aware processing
  - A5.9.6. - Optimization tools
- A6.2.3. - Probabilistic methods
- A6.2.4. - Statistical methods
- A6.2.6. - Optimization
- A6.2.7. - High performance computing
- A6.3.1. - Inverse problems
- A8.1. - Discrete mathematics, combinatorics
- A8.2. - Optimization
- A8.6. - Information theory
- A8.7. - Graph theory
- A9.2. - Machine learning
- A9.3. - Signal analysis
- A9.5. - Robotics

**Other Research Topics and Application Domains:**

- B2.2.3. - Cancer
- B2.6.1. - Brain imaging
- B2.6.2. - Cardiac imaging
- B2.6.3. - Biological Imaging
- B9.4.2. - Mathematics
- B9.4.5. - Data science

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## 2. Overall Objectives

### 2.1. GALEN@Centrale-Paris

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 computational 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,  $\ell$ , 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  $\Omega$  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  $\mu_t$  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,  $\theta$  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  $\{C_i, i \in [1, n] = \{\{p_{i^1}, \dots, p_{i^{|C_i|}}\}\}$  of order  $|C_i|$  that will augment the definition of  $\mathcal{V}$  and will introduce hyper-vertices:

$$\arg \min_{\{x_p\}} \mathcal{P}(g, f) = \sum_{p \in \mathcal{V}} g_p(x_p) + \sum_{(p_1, p_2) \in \mathcal{E}} f_{p_1 p_2}(x_{p_1}, x_{p_2}) + \sum_{C_i \in \mathcal{E}} f_{p_1 \dots p_n}(x_{p_{i^1}}, \dots, x_{p_{i^{|C_i|}}}). \quad (9)$$

where  $f_{p_1 \dots p_n}$  is the price to pay for associating the labels  $(x_{p_{i^1}}, \dots, x_{p_{i^{|C_i|}}})$  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. 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.

### 4.2. 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.

### 4.3. Lung Tumor Detection and Characterization

**Participants:** Evgenios Kornaropoulos, Evangelia Zacharaki, Nikos Paragios

The use of Diffusion Weighted MR Imaging (DWI) is investigated as an alternative tool to radiologists for tumor detection, tumor characterization, distinguishing tumor tissue from non-tumor tissue, and monitoring and predicting treatment response. In collaboration with Hôpitaux Universitaires Henri-Mondor in Paris, France and Chang Gung Memorial Hospital – Linkou in Taipei, Taiwan we investigate the use of modelbased methods of 3D image registration, clustering and segmentation towards the development of a framework for automatic interpretation of images, and in particular extraction of meaningful biomarkers in aggressive lymphomas.

### 4.4. Protein function prediction

**Participants:** Evangelia Zacharaki, Nikos Paragios (in collaboration with D. Vlachakis, University of Patras, Greece)

The massive expansion of the worldwide Protein Data Bank (PDB) provides new opportunities for computational approaches which can learn from available data and extrapolate the knowledge into new coming instances. The aim of our work was to exploit experimentally acquired structural information of enzymes through machine learning techniques in order to produce models that predict enzymatic function.

### 4.5. Imaging biomarkers for chronic lung diseases

**Participants:** Guillaume Chassagnon, Evangelia Zacharaki, Maria Vakalopoulou, Nikos Paragios

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 histogram or texture analysis and assessment of the regional lung elasticity through deformable registration. This work is in collaboration with the Department of Radiology, Cochin Hospital, Paris.

### 4.6. Co-segmentation and Co-registration of Subcortical Brain Structures

**Participants:** Enzo Ferrante, Nikos Paragios, Iasonas Kokkinos

New algorithms to perform co-segmentation and co-registration of subcortical brain structures on MRI images were investigated in collaboration with Ecole Polytechnique de Montreal and the Sainte-Justine Hospital Research Center from Montreal. Brain subcortical structures are involved in different neurodegenerative and neuropsychiatric disorders, including schizophrenia, Alzheimers disease, attention deficit, and subtypes of epilepsy. Segmenting these parts of the brain enables a physician to extract indicators, facilitating their quantitative analysis and characterization. We are investigating how estimated maps of semantic labels (obtained using machine learning techniques) can be used as a surrogate for unlabelled data. We are exploring how to combine them with multi-population deformable registration to improve both alignment and segmentation of these challenging brain structures.

## 4.7. 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.

# 5. Highlights of the Year

## 5.1. Highlights of the Year

### 5.1.1. Awards

The work on dense registration of faces [22] was selected as demo at the IEEE Conference on Computer Vision and Pattern Recognition.

The work [26] received the best poster award at the BASP workshop 2017.

### 5.1.2. Others

Emilie Chouzenoux received an ANR JCJC grant, for her project MajJC:Majorization-Minimization algorithms for Image Computing.

Evangelia Zacharaki has defended her 'Habilitation à Diriger des Recherches' [3].

Emilie Chouzenoux has defended her 'Habilitation à Diriger des Recherches' [1].

# 6. New Software and Platforms

## 6.1. DISD

### *Dense Image and Surface Descriptors*

FUNCTIONAL DESCRIPTION: Scale-Invariant Descriptor, Scale-Invariant Heat Kernel Signatures DISD implements the SID, SI-HKS and ISC descriptors. SID (Scale-Invariant Descriptor) is a densely computable, scale- and rotation- invariant descriptor. We use a log-polar grid around every point to turn rotation/scalings into translation, and then use the Fourier Transform Modulus (FTM) to achieve invariance. SI-HKS (Scale-Invariant Heat Kernel Signatures) extract scale-invariant shape signatures by exploiting the fact that surface scaling amounts to multiplication and scaling of a properly sampled HKS descriptor. We apply the FTM trick on HKS to achieve invariance to scale changes. ISC (Intrinsic Shape Context) constructs a net-like grid around every surface point by shooting outwards and tracking geodesics. This allows us to build a meta-descriptor on top of HKS/SI-HKS that takes neighborhood into account, while being invariant to surface isometries.

- Participants: Eduard Trulls and Iasonas Kokkinos
- Contact: Iasonas Kokkinos
- URL: <http://vision.mas.ecp.fr/Personnel/iasonas/descriptors.html>

## 6.2. DPMS

FUNCTIONAL DESCRIPTION: Dpms implements branch-and-bound object detection, cutting down the complexity of detection from linear in the number of pixels to logarithmic.

- Participant: Iasonas Kokkinos
- Contact: Iasonas Kokkinos

## 6.3. DROP

KEYWORDS: Health - Merging - Registration of 2D and 3D multimodal images - Medical imaging

FUNCTIONAL DESCRIPTION: Drop is a software programme that registers images originating from one or more modes by quickly and efficiently calculating a non-rigid / deformable field of deformation. Drop is a new, quick and effective registration tool based on new algorithms that do not require a cost function derivative.

- Partner: Centrale Paris
- Contact: Nikolaos Paragyios
- URL: <http://campar.in.tum.de/Main/Drop>

## 6.4. FastPD

KEYWORD: Medical imaging

FUNCTIONAL DESCRIPTION: FastPD is an optimization platform in C++ for the computer vision and medical imaging community.

- Contact: Nikolaos Paragyios
- URL: <http://www.csd.uoc.gr/~komod/FastPD/>

## 6.5. GraPeS

*Grammar Parser for Shapes*

FUNCTIONAL DESCRIPTION: It is a software for parsing facade images using shape grammars. Grapes implement a parsing methods based on Reinforcement Learning principles. It optimizes simultaneously the topology of the parse tree as well as the associated parameters. GraPeS comes along with predefined shape grammars as XML files and defines three kinds of rewards. However, it also offers the possibility to create new grammars and to provide custom rewards in text files, widening the scope of potential applications. The name of the software comes from the aspect of the parse tree of the binary split grammars involved in the process.

RELEASE FUNCTIONAL DESCRIPTION: Supports jpg and gif file formats.

- Participant: Iasonas Kokkinos
- Contact: Iasonas Kokkinos

## 6.6. HOAP-SVM

*High-Order Average Precision SVM*

SCIENTIFIC DESCRIPTION: We consider the problem of using high-order information (for example, persons in the same image tend to perform the same action) to improve the accuracy of ranking (specifically, average precision). We develop two learning frameworks. The high-order binary SVM (HOB-SVM) optimizes a convex upper bound of the surrogate 0-1 loss function. The high-order average precision SVM (HOAP-SVM) optimizes a difference-of-convex upper bound on the average precision loss function.

Authors of the research paper: Puneet K. Dokania, A. Behl, C. V. Jawahar and M. Pawan Kumar

**FUNCTIONAL DESCRIPTION:** The software provides a convenient API for learning to rank with high-order information. The samples are ranked according to a score that is proportional to the difference of max-marginals of the positive and the negative class. The parameters of the score function are computed by minimizing an upper bound on the average precision loss. The software also provides an instantiation of the API for ranking samples according to their relevance to an action, using the poselet features. The following learning algorithms are included in the API:

(1) Multiclass-SVM (2) AP-SVM (3) High Order Binary SVM (HOB-SVM) (4) High Order AP-SVM (HOAP-SVM) (5) M4 Learning (unpublished work)

The API is developed in C/C++ by Puneet K. Dokania.

- Participants: Pawan Kumar and Puneet Dokania
- Contact: Puneet Dokania
- URL: <http://puneetkdokania.github.io/projects/ranking-highorder/ranking-highorder.html>

## 6.7. LBSD

*Learning-Based Symmetry Detection*

**FUNCTIONAL DESCRIPTION:** LBSD implements the learning-based approach to symmetry detection. It includes the code for running a detector, alongside with the ground-truth symmetry annotations that we have introduced for the Berkeley Segmentation Dataset (BSD) benchmark.

- Participant: Stavros Tsogkas
- Contact: Stavros Tsogkas
- URL: [https://github.com/tsogkas/oid\\_1.0](https://github.com/tsogkas/oid_1.0)

## 6.8. mrf-registration

**KEYWORDS:** Health - Medical imaging

**FUNCTIONAL DESCRIPTION:** Deformable image and volume registration, is a deformable registration platform in C++ for the medical imaging community. This is the first publicly available platform which contains most of the existing metrics to perform registration under the same concept. The platform is used for clinical research from approximately 3,000 users worldwide.

**RELEASE FUNCTIONAL DESCRIPTION:** Bugfix in image resampling Resampling of binary mask is now w.r.t. to target image Added adjustable sigma for Gaussian image pyramid Added level dependent scaling of maximum displacement when linkMax is disabled Changed approximation method for computation of the inverse displacement field (less memory demanding) Bugfix in grid and quiver visualization Added support for compressed MHD Bugfix in 3D thin-plate splines in landmark-based registration

- Participant: Nikolaos Paragios
- Contact: Nikolaos Paragios
- URL: <http://www.mrf-registration.net/>

## 6.9. TeXMeG

**FUNCTIONAL DESCRIPTION:** Texture, modulation, generative models, segmentation, TeXMeG is a front-end for texture analysis and edge detection platform in Matlab that relies on Gabor filtering and image demodulation. Includes frequency- and time- based definition of Gabor- and other Quadrature-pair filterbanks, demodulation with the Regularized Energy Separation Algorithm and Texture/Edge/Smooth classification based on MDL criterion.

- Participant: Iasonas Kokkinos
- Contact: Iasonas Kokkinos
- URL: <http://cvsp.cs.ntua.gr/software/texture/>

## 6.10. Platforms

### 6.10.1. 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.

## 7. New Results

### 7.1. Graph Based Slice-to-Volume Deformable Registration

**Participants:** Enzo Ferrante, Nikos Paragios

Deformable image registration is a fundamental problem in computer vision and medical image computing. In this contribution [9], we investigate the use of graphical models in the context of a particular type of image registration problem, known as slice-to-volume registration, while we introduced the first comprehensive survey [10] of the literature about slice-to-volume registration, presenting a categorical study of the algorithms according to an ad-hoc taxonomy and analyzing advantages and disadvantages of every category. We introduce a scalable, modular and flexible formulation that can accommodate low-rank and high order terms, that simultaneously selects the plane and estimates the in-plane deformation through a single shot optimization approach. The proposed framework is instantiated into different variants seeking either a compromise between computational efficiency (soft plane selection constraints and approximate definition of the data similarity terms through pair-wise components) or exact definition of the data terms and the constraints on the plane selection. Simulated and real-data in the context of ultrasound and magnetic resonance registration (where both framework instantiations as well as different optimization strategies are considered) demonstrate the potentials of our method.

### 7.2. Deformable Registration Through Learning of Context-Specific Metric Aggregation

**Participants:** Enzo Ferrante, Rafael Marini, Punnet K. Dokania, Nikos Paragios

We propose a novel weakly supervised discriminative algorithm [21] for learning context specific registration metrics as a linear combination of conventional similarity measures. Conventional metrics have been extensively used over the past two decades and therefore both their strengths and limitations are known. The challenge is to find the optimal relative weighting (or parameters) of different metrics forming the similarity measure of the registration algorithm. Hand-tuning these parameters would result in sub optimal solutions and quickly become infeasible as the number of metrics increases. Furthermore, such hand-crafted combination can only happen at global scale (entire volume) and therefore will not be able to account for the different tissue properties. We propose a learning algorithm for estimating these parameters locally, conditioned to the data semantic classes. The objective function of our formulation is a special case of non-convex function, difference of convex function, which we optimize using the concave convex procedure. As a proof of concept, we show the impact of our approach on three challenging datasets for different anatomical structures and modalities.

### 7.3. Promises and challenges for the implementation of computational medical imaging (radiomics) in oncology

**Participants:** Roger Sun, Evangelia I. Zacharaki, Nikos Paragios (in collaboration with Gustave Roussy and Paris Sud University)



Computational medical imaging (also known as radiomics) is a promising and rapidly growing discipline that consists in the analysis of high-dimensional data extracted from medical imaging, to further describe tumour phenotypes. The end goal of radiomics is to determine imaging biomarkers as decision support tools for clinical practice and to facilitate better understanding of cancer biology, allowing the assessment of the changes throughout the evolution of the disease and the therapeutic sequence. We have reviewed [12], [17] the critical issues necessary for proper development of radiomics as a biomarker and for its implementation in clinical practice.

## 7.4. Multi-atlas segmentation in medical imagery

**Participants:** Stavros Alchatzidis, Evangelia I. Zacharaki, Nikos Paragios (in collaboration with University of Pennsylvania)

Multi-atlas segmentation has emerged in recent years as a simple yet powerful approach in medical image segmentation. It commonly comprises two steps: (1) a series of pairwise registrations that establish correspondences between a query image and a number of atlases, and (2) the fusion of the available segmentation hypotheses towards labeling objects of interest. In [5], we introduce a novel approach that solves simultaneously for the underlying segmentation labels and the multi-atlas registration. We propose a pairwise Markov Random Field approach, where registration and segmentation nodes are coupled towards simultaneously recovering all atlas deformations and labeling the query image.

## 7.5. Protein function prediction

**Participants:** Evangelia I. Zacharaki, Nikos Paragios (in collaboration with University of Patras)

The massive expansion of the worldwide Protein Data Bank (PDB) provides new opportunities for computational approaches which can learn from available data and extrapolate the knowledge into new coming instances. The aim of our work in [6], [18] was to exploit experimentally acquired structural information of enzymes through machine learning techniques in order to produce models that predict enzymatic function.

## 7.6. Deformable group-wise registration using a physiological model: Application to diffusion-weighted MRI

**Participants:** Evgenios Kornaropoulos, Evangelia I. Zacharaki, Nikos Paragios (in collaboration with Centre Hospitalier Universitaire Henri-Mondor and Chang Gung Memorial Hospital)

In this contribution [2] we develop a novel group-wise deformable registration method for motion correction in Diffusion-Weighted MRI towards computing a more accurate Apparent Diffusion Coefficient parametric map (ADC map). Calculation of the ADC has been performed without motion correction in the previous studies. It is reported though that ADC is a parameter susceptible to artifacts, the most frequent of all being patient's motion and breathing, resulting in misregistration of the images obtained with different b-values. Being group-wise designed, the image registration method we propose has no need of choosing a reference template while in the same time it is computationally efficient. We aim at finding the optimal deformation fields of the diffusion-weighted (DW) images using a temporal constraint, related to the diffusion process, as well as a smoothness penalty on the deformations. To this end, we address the deformation fields estimation problem with an Markov Random Fields formulation, in which the latent variables are the deformations (B-spline polynomials) of the images. The latent variables are connected with the observations towards ensuring meaningful temporal correspondence among the DW images. They are also inter-connected in order to decrease the cost of pairwise comparisons between individual images. Linear programming and duality are used to determine the optimal solution of the problem. Finally, as an image similarity criterion in the MRF framework, we used a metric that was based on a physiological model describing the image acquisition process. Quantitative evaluation of the method was performed, in which it was compared against two state-of-the-art methods that use other modelling criteria. It outperformed both of them, while the ADC map derived by our method appeared to preserve structure, that was not observable by the other methods.

## 7.7. Variational Bayesian Approach for Image Restoration

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with Y. Marnissi, SAFRAN TECH and Y. Zheng, IBM Research China)

In the work [13], a methodology is investigated for signal recovery in the presence of non-Gaussian noise. In contrast with regularized minimization approaches often adopted in the literature, in our algorithm the regularization parameter is reliably estimated from the observations. As the posterior density of the unknown parameters is analytically intractable, the estimation problem is derived in a variational Bayesian framework where the goal is to provide a good approximation to the posterior distribution in order to compute posterior mean estimates. Moreover, a majorization technique is employed to circumvent the difficulties raised by the intricate forms of the non-Gaussian likelihood and of the prior density. We demonstrate the potential of the proposed approach through comparisons with state-of-the-art techniques that are specifically tailored to signal recovery in the presence of mixed Poisson-Gaussian noise. Results show that the proposed approach is efficient and achieves performance comparable with other methods where the regularization parameter is manually tuned from an available ground truth.

## 7.8. Non-Modular Loss Functions

**Participant:** Jiaqian Yu

Defining Non-modular loss functions and their optimization procedure present an interesting direction for many classes of problems. Jiaqian Yu has completed her PhD Thesis on Non-Modular Loss Functions this year. The PhD Thesis has included several yet unpublished results regarding approximate losses for Jaccard index and DICE coefficients commonly used in evaluating segmentation algorithms.

## 7.9. Graph Structure Discovery

**Participant:** Eugene Belilovsky

Discovering the interaction structure amongst variables, particularly from few observations, has important implications in many fields including neuroimaging, genetics and finance. Eugene Belilovsky in collaboration with Gael Varoquaux (Inria Parietal), Kyle Kastner (University of Montreal) and Matthew Blaschko has published a new approach for graph structure discovery in high dimensional gaussian markov random fields. The work has been presented in [19].

## 7.10. Structured and Efficient Convolutional Networks

**Participant:** Eugene Belilovsky

Convolutional Neural Networks have revolutionized the computer vision field. Yet, they are not well understood and do not well leverage basic geometric structures known by the computer vision community. In recent work in collaboration with the Ecole Normale Superier and the École des Ponts ParisTech we have tried to address some of these issues. We use as a starting point the recently introduced Scattering Transform and show that we can use this to build Convolutional Networks that are more interpretable and can generalize faster in the few sample regime. This work has been presented in [25].

## 7.11. Stochastic Majorize-Minimize Subspace Algorithm

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet

Stochastic optimization plays an important role in solving many problems encountered in machine learning or adaptive processing. In this context, the second-order statistics of the data are often unknown a priori or their direct computation is too intensive, and they have to be estimated on-line from the related signals. In the context of batch optimization of an objective function being the sum of a data fidelity term and a penalization (e.g. a sparsity promoting function), Majorize-Minimize (MM) subspace methods have recently attracted much interest since they are fast, highly flexible and effective in ensuring convergence. The goal of the work [8] is to show how these methods can be successfully extended to the case when the cost function is replaced by a sequence of stochastic approximations of it. Simulation results illustrate the good practical performance of the proposed MM Memory Gradient (3MG) algorithm when applied to 2D filter identification

## 7.12. Deconvolution and Deinterlacing of Video Sequences

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with F. Abboud, PhD student, J.-H. Chenot and L. Laborelli, research engineers, Institut National de l'Audiovisuel)

Optimization methods play a central role in the solution of a wide array of problems encountered in various application fields, such as signal and image processing. Especially when the problems are highly dimensional, proximal methods have shown their efficiency through their capability to deal with composite, possibly non smooth objective functions. The cornerstone of these approaches is the proximity operator, which has become a quite popular tool in optimization. In the work [31], we propose new dual forward-backward formulations for computing the proximity operator of a sum of convex functions involving linear operators. The proposed algorithms are accelerated thanks to the introduction of a block coordinate strategy combined with a preconditioning technique. Numerical simulations emphasize the good performance of our approach for the problem of jointly deconvoluting and deinterlacing video sequences.

## 7.13. PALMA, an improved algorithm for DOSY signal processing

**Participants:** Emilie Chouzenoux (in collaboration with M.-A. Delsuc, IGBMC, Strasbourg, and A. Cherni, PhD student, Univ. Strasbourg)

NMR is a tool of choice for the measure of diffusion coefficients of species in solution. The DOSY experiment, a 2D implementation of this measure, has proven to be particularly useful for the study of complex mixtures, molecular interactions, polymers, etc. However, DOSY data analysis requires to resort to inverse Laplace transform, in particular for polydisperse samples. This is a known difficult numerical task, for which we present here a novel approach. A new algorithm based on a splitting scheme and on the use of proximity operators is introduced in [7]. Used in conjunction with a Maximum Entropy and  $\ell_1$  hybrid regularisation, this algorithm converges rapidly and produces results robust against experimental noise. This method has been called PALMA. It is able to reproduce faithfully monodisperse as well as polydisperse systems, and numerous simulated and experimental examples are presented. It has been implemented on the server <http://palma.labo.igbmc.fr> where users can have their datasets processed automatically.

## 7.14. Proximal Approaches for Solving Matrix Optimization Problems

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with A. Benfenati, Univ. Paris Est)

In recent years, there has been a growing interest in problems where the underlining mathematical model involves the minimization in a matrix space of a Bregman divergence function coupled with a regularization term. We consider a general framework where the regularization term is decoupled in two parts, one acting only on the eigenvalues of the matrix and the other on the whole matrix. We propose in [26], [32] a new minimization approach to address problem of this type, by providing a list of proximity operators allowing us to consider various choices for the fit-to-data functional and for the regularization term. The numerical experience show that this approach gives better results in term of computational time with respect to some state of the arts algorithms.

## 7.15. Fast Algorithm for Least-Squares Regression with GMRF Prior

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with J.Y. Tourneret, IRIT, Toulouse, and Q. Wei, Duke Univ.)

The paper [29] presents a fast approach for penalized least squares (LS) regression problems using a 2D Gaussian Markov random field (GMRF) prior. More precisely, the computation of the proximity operator of the LS criterion regularized by different GMRF potentials is formulated as solving a Sylvester-like matrix equation. By exploiting the structural properties of GMRFs, this matrix equation is solved column-wise in an analytical way. The proposed algorithm can be embedded into a wide range of proximal algorithms to solve LS regression problems including a convex penalty. Experiments carried out in the case of a constrained

LS regression problem arising in a multichannel image processing application, provide evidence that an alternating direction method of multipliers performs quite efficiently in this context.

## 7.16. Optimization Approach for Deep Neural Network Training

**Participants:** Emilie Chouzenoux, Jean-Christophe Pesquet, Vyacheslav Dudar (in collaboration with G. Chierchia, Univ. Paris Est and V. Semenov, Univ. of Kiev)

In paper [28], we develop a novel second-order method for training feed-forward neural nets. At each iteration, we construct a quadratic approximation to the cost function in a low-dimensional subspace. We minimize this approximation inside a trust region through a two-stage procedure: first inside the embedded positive curvature subspace, followed by a gradient descent step. This approach leads to a fast objective function decay, prevents convergence to saddle points, and alleviates the need for manually tuning parameters. We show the good performance of the proposed algorithm on benchmark datasets.

## 7.17. Auxiliary Variable Method for MCMC Algorithms in High Dimension

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with Y. Marnissi, SAFRAN TECH and A. Benazza-Benhayia, SUP'COM, COSIM, Tunis)

When the parameter space is high dimensional, the performance of stochastic sampling algorithms is very sensitive to existing dependencies between parameters. For instance, this problem arises when one aims to sample from a high dimensional Gaussian distribution whose covariance matrix does not present a simple structure. Then, one often resorts to sampling algorithms based on a perturbation-optimization technique that requires to minimize a cost function using an iterative algorithm. This makes the sampling process time consuming, especially when used within a Gibbs sampler. 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 being not 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 covariances matrices cannot be diagonalized in the same basis. In paper [34], we are interested in inverse problems where either the data fidelity term or the prior distribution is Gaussian or driven from a hierarchical Gaussian model. We propose to add 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. Experiments conducted on two image restoration problems show the good performance of the proposed strategy.

## 7.18. Block Coordinate Approach for Sparse Logistic Regression

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with G. Chierchia, Univ. Paris Est, L. M. Briceno-Arias, CMM - Univ. Chile, and A. Cherni, PhD student, Univ. Strasbourg)

We propose in [20], [33] stochastic optimization algorithms for logistic regression based on a randomized version of Douglas-Rachford splitting method. Our approach sweeps the training set by randomly selecting a mini-batch of data at each iteration, and it performs the update step by leveraging the proximity operator of the logistic loss, for which a closed-form expression is derived. Experiments carried out on standard datasets compare the efficiency of our algorithm to stochastic gradient-like methods.

## 7.19. An Alternating Proximal Approach for Blind Video Deconvolution

**Participants:** Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with Feriel Abboud, WITBE, Jean-Hugues Chenot, Louis Laborelli, INA)

Blurring occurs frequently in video sequences captured by consumer devices, as a result of various factors such as lens aberrations, defocus, relative camera scene motion, and camera shake. When it comes to the contents of archive documents such as old films and television shows, the degradations are even more serious due to several physical phenomena happening during the sensing, transmission, recording, and storing processes. We propose in [31] a versatile formulation of blind video deconvolution problems that seeks to estimate both the sharp unknown video sequence and the underlying blur kernel from an observed video. This inverse problem is severely ill-posed, and an appropriate solution can be obtained by modeling it as a nonconvex minimization problem. We provide a novel iterative algorithm to solve it, grounded on the use of recent advances in convex and nonconvex optimization techniques, and having the ability of including numerous well-known regularization strategies

## 7.20. 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 [16] 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).

## 7.21. 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  $\phi$ -divergences, such as Kullback-Leibler, Jeffreys-Kullback, Hellinger, Chi-Square, Renyi, and  $I_\alpha$  divergences. While  $\phi$ -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  $\phi$ -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  $\phi$ -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.

## 7.22. Stochastic Quasi-Fejér Block-Coordinate Fixed Point Iterations With Random Sweeping: Mean-Square and Linear Convergence

**Participants:** Jean-Christophe Pesquet (in collaboration with Patrick L. Combettes, North Carolina State University)

In one of our previous works, we investigated the almost sure weak convergence of a block-coordinate fixed point algorithm and discussed its application to nonlinear analysis and optimization. This algorithm 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.

### 7.23. Human Joint Angle Estimation and Gesture Recognition for Assistive Robotic Vision

**Participants:** Riza Alp Guler, Siddhartha Chandra, Iasonas Kokkinos (in collaboration with National Technical University of Athens)

In this work, we explore new directions for automatic human gesture recognition and human joint angle estimation as applied for human-robot interaction in the context of an actual challenging task of assistive living for real-life elderly subjects. Our contributions include state-of-the-art approaches for both low- and mid-level vision, as well as for higher level action and gesture recognition. The first direction investigates a deep learning based framework for the challenging task of human joint angle estimation on noisy real world RGB-D images. The second direction includes the employment of dense trajectory features for online processing of videos for automatic gesture recognition with real-time performance. Our approaches are evaluated both qualitatively and quantitatively on a newly acquired dataset that is constructed on a challenging real-life scenario on assistive living for elderly subjects.

### 7.24. Fast, Exact and Multi-Scale Inference for Semantic Image Segmentation with Deep Gaussian CRFs

**Participants:** Siddhartha Chandra, Iasonas Kokkinos

In this work we propose a structured prediction technique that combines the virtues of Gaussian Conditional Random Fields (G-CRF) with Deep Learning: (a) our structured prediction task has a unique global optimum that is obtained exactly from the solution of a linear system (b) the gradients of our model parameters are analytically computed using closed form expressions, in contrast to the memory-demanding contemporary deep structured prediction approaches that rely on back-propagation-through-time, (c) our pairwise terms do not have to be simple hand-crafted expressions, as in the line of works building on the DenseCRF, but can rather be ‘discovered’ from data through deep architectures, and (d) our system can be trained in an end-to-end manner. Building on standard tools from numerical analysis we develop very efficient algorithms for inference and learning, as well as a customized technique adapted to the semantic segmentation task. This efficiency allows us to explore more sophisticated architectures for structured prediction in deep learning: we introduce multi-resolution architectures to couple information across scales in a joint optimization framework, yielding systematic improvements. We demonstrate the utility of our approach on the challenging VOC PASCAL 2012 image segmentation benchmark, showing substantial improvements over strong baselines.

### 7.25. Dense and Low-Rank Gaussian CRFs Using Deep Embeddings

**Participants:** Siddhartha Chandra, Iasonas Kokkinos

In this work we introduce a structured prediction model that endows the Deep Gaussian Conditional Random Field (G-CRF) with a densely connected graph structure. We keep memory and computational complexity under control by expressing the pairwise interactions as inner products of low-dimensional, learnable embeddings. The G-CRF system matrix is therefore low-rank, allowing us to solve the resulting system in a few milliseconds on the GPU by using conjugate gradient. As in G-CRF, inference is exact, the unary and pairwise terms are jointly trained end-to-end by using analytic expressions for the gradients, while we also develop even faster, Potts-type variants of our embeddings. We show that the learned embeddings capture pixel-to-pixel affinities in a task-specific manner, while our approach achieves state of the art results on three challenging benchmarks, namely semantic segmentation, human part segmentation, and saliency estimation. This work was published in [30].

## 7.26. DenseReg: Fully Convolutional Dense Shape Regression In-the-Wild

**Participants:** Riza Alp Guler, Iasonas Kokkinos (in collaboration with Imperial College London)

In this work we propose to learn a mapping from image pixels into a dense template grid through a fully convolutional network. We formulate this task as a regression problem and train our network by leveraging upon manually annotated facial landmarks “in-the-wild”. We use such landmarks to establish a dense correspondence field between a three-dimensional object template and the input image, which then serves as the ground-truth for training our regression system. We show that we can combine ideas from semantic segmentation with regression networks, yielding a highly-accurate ‘quantized regression’ architecture.

Our system, called DenseReg allows us to estimate dense image-to-template correspondences in a fully convolutional manner. As such our network can provide useful correspondence information as a stand-alone system, while when used as an initialization for Statistical Deformable Models we obtain landmark localization results that largely outperform the current state-of-the-art on the challenging 300W benchmark. We thoroughly evaluate our method on a host of facial analysis tasks, and also demonstrate its use for other correspondence estimation tasks, such as modelling of the human ear. This work was published in [22].

## 7.27. Structured Output Prediction and Learning for Deep Monocular 3D Human Pose Estimation

**Participants:** Stefan Kinauer, Riza Alp Guler, Siddhartha Chandra, Iasonas Kokkinos

In this work we address the problem of estimating 3D human pose from a single RGB image by blending a feed-forward Convolutional Neural Network (CNN) with a graphical model that couples the 3D positions of parts. The CNN populates a volumetric output space that represents the possible positions of 3D human joints, and also regresses the estimated displacements between pairs of parts. These constitute the ‘unary’ and ‘pairwise’ terms of the energy of a graphical model that resides in a 3D label space and delivers an optimal 3D pose configuration at its output. The CNN is trained on the 3D human pose dataset 3.6M, the graphical model is trained jointly with the CNN in an end-to-end manner, allowing us to exploit both the discriminative power of CNNs and the top-down information pertaining to human pose. We introduce (a) memory efficient methods for getting accurate voxel estimates for parts by blending quantization with regression (b) employ efficient structured prediction algorithms for 3D pose estimation using branch-and-bound and (c) develop a framework for qualitative and quantitative comparison of competing graphical models. We evaluate our work on the Human 3.6M dataset, demonstrating that exploiting the structure of the human pose in 3D yields systematic gains.

## 7.28. Newton-type Methods for Inference in Higher-Order Markov Random Fields

**Participants:** Hariprasad Kannan, Nikos Paragios

Linear programming relaxations are central to MAP inference in discrete Markov Random Fields. The ability to properly solve the Lagrangian dual is a critical component of such methods. In this paper, we study the benefit of using Newton-type methods to solve the Lagrangian dual of a smooth version of the problem. We investigate their ability to achieve superior convergence behavior and to better handle the ill-conditioned nature of the formulation, as compared to first order methods. We show that it is indeed possible to efficiently apply a trust region Newton method for a broad range of MAP inference problems. In this paper we propose a provably convergent and efficient framework that includes (i) excellent compromise between computational complexity and precision concerning the Hessian matrix construction, (ii) a damping strategy that aids efficient optimization, (iii) a truncation strategy coupled with a generic pre-conditioner for Conjugate Gradients, (iv) efficient sum-product computation for sparse clique potentials. Results for higher-order Markov Random Fields demonstrate the potential of this approach. This work was published in [23].

## 7.29. Alternating Direction Graph Matching

**Participants:** D. Khuê Lê-Huu, Nikos Paragios

In this work, we introduce a graph matching method that can account for constraints of arbitrary order, with arbitrary potential functions. Unlike previous decomposition approaches that rely on the graph structures, we introduce a decomposition of the matching constraints. Graph matching is then reformulated as a non-convex non-separable optimization problem that can be split into smaller and much-easier-to-solve subproblems, by means of the alternating direction method of multipliers. The proposed framework is modular, scalable, and can be instantiated into different variants. Two instantiations are studied exploring pairwise and higher-order constraints. Experimental results on widely adopted benchmarks involving synthetic and real examples demonstrate that the proposed solutions outperform existing pairwise graph matching methods, and competitive with the state of the art in higher-order settings. This work was published in [24].

### 7.30. Prediction and classification in biological and information networks

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

We investigate how network representation learning algorithms can be applied to deal with the problem of link prediction and classification in protein-protein interaction networks as well as in social and information networks. In particular, we have proposed BiasedWalk, a scalable, unsupervised feature learning algorithm that is based on biased random walks to sample context information about each node in the network.

## 8. Bilateral Contracts and Grants with Industry

### 8.1. Bilateral Contracts with Industry

Contract with General Electric Healthcare  
Project title: Optimization methods for breast tomosynthesis  
Duration: 2017-2020  
Responsible: J.-C. Pesquet

## 9. Partnerships and Cooperations

### 9.1. National Initiatives

#### 9.1.1. ANR

Program: ANR Blanc International  
Project acronym: ADAMANTIUS  
Project title: Automatic Detection And characterization of residual Masses in pAtients with lymphomas through fusioN of whole-body diffusion-weighTed mri on 3T and 18F-flUorodeoxyglucoSe pet/ct  
Duration: 9/2012-8/2015  
Coordinator: CHU Henri Mondor - FR

Program: ANR JCJC  
Project acronym: HICORE  
Project title: HIerarchical COmpositional REpresentations for Computer Vision  
Duration: 10/2010-9/2014  
Coordinator: ECP - FR

Program: ANR JCJC  
Project acronym: LearnCost  
Project title: Learning Model Constraints for Structured Prediction



Duration: 2014-2018

Coordinator: Inria Saclay - FR

Program: ANR JCJC

Project acronym: MajIC

Project title: Majorization-Minimization Algorithms for Image Computing

Duration: 2017-2021

Coordinator: E. Chouzenoux

Program: ITMOs Cancer & Technologies pour la santé d'Aviesan / INCa

Project acronym: CURATOR

Project title: Slice-to-Image Deformable Registration towards Image-based Surgery Navigation & Guidance

Duration: 12/2013-11/2015

Coordinator: ECP - FR

### 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

## 9.2. European Initiatives

### 9.2.1. FP7 & H2020 Projects

#### 9.2.1.1. MOBOT

Title: Intelligent Active MObility Aid RoBOT integrating Multimodal Communication

Programm: FP7

Duration: February 2013 - January 2016

Coordinator: Technische Universität München

Partners:

Bartłomiej Marcin Stanczyk (Poland)

Athena Research and Innovation Center in Information Communication & Knowledge Technologies (Greece)

Bethanien Krankenhaus - Geriatrisches Zentrum - Gemeinnützige (Germany)

Diaplasia Rehabilitation Center (Greece)

Ecole Centrale des Arts et Manufactures (France)

Institute of Communication and Computer Systems (Greece)

Technische Universitaet Muenchen (Germany)

Ruprecht-Karls-Universitaet Heidelberg (Germany)

Inria contact: Iasonas Kokkinos

Mobility disabilities are prevalent in our ageing society and impede activities important for the independent living of elderly people and their quality of life. The MOBOT project aims at supporting mobility and thus enforcing fitness and vitality by developing intelligent active mobility assistance robots for indoor environments that provide user-centred, context-adaptive and natural support. Our driving concept envisions cognitive robotic assistants that act (a) proactively by realizing an autonomous and context-specific monitoring of human activities and by subsequently reasoning on meaningful user behavioural patterns, as well as (b) adaptively and interactively, by analysing multi-sensory and physiological signals related to gait and postural stability, and by performing adaptive compliance control for optimal physical support and active fall prevention. Towards these targets, a multimodal action recognition system will be developed to monitor, analyse and predict user actions with a high level of accuracy and detail. The main thrust of our approach will be the enhancement of computer vision techniques with modalities such as range sensor images, haptic information as well as command-level speech and gesture recognition. Data-driven multimodal human behaviour analysis will be conducted and behavioural patterns will be extracted. Findings will be imported into a multimodal human-robot communication system, involving both verbal and nonverbal communication and will be conceptually and systemically synthesised into mobility assistance models taking into consideration safety critical requirements. All these modules will be incorporated in a behaviour-based and context-aware robot control framework. Direct involvement of end-user groups will ensure that actual user needs are addressed. Finally, user trials will be conducted to evaluate and benchmark the overall system and to demonstrate the vital role of MOBOT technologies for Europe's service robotics.

#### 9.2.1.2. *Strategie*

Title: Statistically Efficient Structured Prediction for Computer Vision and Medical Imaging

Programm: FP7

Duration: January 2014 - December 2017

Coordinator: Inria

Inria contact: Matthew Blaschko

'Inference in medical imaging is an important step for disease diagnosis, tissue segmentation, alignment with an anatomical atlas, and a wide range of other applications. However, imperfections in imaging sensors, physical limitations of imaging technologies, and variation in the human population mean that statistical methods are essential for high performance. Statistical learning makes use of human provided ground truth to enable computers to automatically make predictions on future examples without human intervention. At the heart of statistical learning methods is risk minimization - the minimization of the expected loss on a previously unseen image. Textbook methods in statistical learning are not generally designed to minimize the expected loss for loss functions appropriate to medical imaging, which may be asymmetric and non-modular. Furthermore, these methods often do not have the capacity to model interdependencies in the prediction space, such as those arising from spatial priors, and constraints arising from the volumetric layout of human anatomy. We aim to develop new statistical learning methods that have these capabilities, to develop efficient learning algorithms, to apply them to a key task in medical imaging (tumor segmentation), and to prove their convergence to optimal predictors. To achieve this, we will leverage the structured prediction framework, which has shown impressive empirical results on a wide range of learning tasks. While theoretical results giving learning rates are available for some algorithms, necessary and sufficient conditions for consistency are not known for structured prediction. We will consequently address this issue, which is of key importance for algorithms that will be applied to life critical applications, e.g. segmentation of brain tumors that will subsequently be targeted by radiation therapy or removed by surgery. Project components will address both theoretical and practical issues.'

#### 9.2.2. **I-SUPPORT**

Title: ICT-Supported Bath Robots

Project-Team GALEN 17

Program: FP7

Duration: March 2015 - March 2018

Coordinator: Robotnik Automation S.L.L.

Partners:

Bethanien Krankenhaus - Geriatisches Zentrum - Gemeinnutzige GMBH (Germany)

Fondazione Santa Lucia (Italy)

Institute of Communication and Computer Systems (Greece)

Karlsruher Institut für Technologie (Germany)

Theofanis Alexandridis Kai Sia Ee (OMEGATECH) (Greece)

Robotnik Automation Sll (Spain)

Scuola Superiore di Studi Universitari E di Perfezionamento Sant'Anna (Italy)

Frankfurt University of Applied Sciences (Germany)

Inria contact: Iasonas Kokkinos

The I-SUPPORT project envisions the development and integration of an innovative, modular, ICTsupported service robotics system that supports and enhances older adults' motion and force abilities and assists them in successfully, safely and independently completing the entire sequence of bathing tasks, such as properly washing their back, their upper parts, their lower limbs, their buttocks and groin, and to effectively use the towel for drying purposes. Advanced modules of cognition, sensing, context awareness and actuation will be developed and seamlessly integrated into the service robotics system to enable the robotic bathing system to adapt to the frail elderly population' capabilities and the frail elderly to interact in a master-slave mode, thus, performing bathing activities in an intuitive and safe way. Adaptation and integration of state-of-the-art, cost-effective, soft-robotic manipulators will provide the hardware constituents, which, together with advanced human-robot force/compliance control that will be developed within the proposed project, will form the basis for a safe physical human-robot interaction that complies with the most up-to-date safety standards. Human behavioural, sociological, safety, ethical and acceptability aspects, as well as financial factors related to the proposed service robotic infrastructure will be thoroughly investigated and evaluated so that the I-SUPPORT end result is a close-to-market prototype, applicable to realistic living settings.

## 9.3. International Initiatives

### 9.3.1. Inria International Partners

#### 9.3.1.1. Informal International Partners

Sup'Com Tunis - Collaborative research with Amel Benazza-Benhayia. Collaboration Topic: Multi-spectral imaging.

Universidad Tecnica Federico Santa Maria - Collaborative research with Luis M. Briceno Arias. Collaboration Topics: Variational approaches for monotone inclusions.

University of Patras, Greece - Collaborative research with V. Megalooikonomou. Collaboration Topic: Biosignal analysis.

University of Pennsylvania - Collaborative research with Aristeidis Sotiras. Collaboration Topic: Higher Order Graphs in biomedical image analysis.

## 9.4. International Research Visitors

### 9.4.1. Visits of International Scientists

#### 9.4.1.1. Internships

The following international students did an internship at CVN in the past year:

Huidong Liu, Stony Brook University, NY (may 2017)  
Zhixin Shu, Stony Brook University, NY (may 2017)  
Vu Nguyen, Stony Brook University, NY (jul. 2017)  
Han Anh Vu Le, Houston University (jul. 2017)  
Anisia Florescu, University of Galati Romania (feb. 2017)  
Vyacheslav Dudar, Taras Sheuchenko National University of Kyiv (nov. 2017)  
Carla Bertolocchi, Universita degli studi di Modena e Reggio Emilia (dec. 2017)  
Yana Vedel, Taras Sheuchenko National University of Kyiv (dec. 2017)

## 10. Dissemination

### 10.1. Promoting Scientific Activities

#### 10.1.1. Scientific Events Organisation

##### 10.1.1.1. Member of the Organizing Committees

E. Chouzenoux (co-organizer). Organization of the special session “Interactions entre méthodes d’optimisation et algorithmes de simulation stochastique” in the conference GRETSI 2017, Juan-les-Pins, 5-8 sep. 2017.

E. Chouzenoux and J.C. Pesquet. Organization of the special session “Advanced optimization methods for solving inverse problems at a large scale” in the International Biomedical and Astronomical Signal Processing Frontiers workshop (BASP 2017), Villars-sur-Ollon, Suisse, 29 jan.- 3 feb. 2017.

E. Belilovsky. Co-Organizer of Learning with Limited Labeled Data Workshop, in conjunction with Conference on Neural Information Processing Systems (NIPS).

#### 10.1.2. Scientific Events Selection

##### 10.1.2.1. Member of the Conference Program Committees

E. Chouzenoux. Member of the technical committee “Signal Processing Theory and Methods” of the IEEE Signal Processing Society.

F. Malliaros. Member of the program committee at: International Conference on World Wide Web (WWW), Conference on Artificial Intelligence (AAAI), International Joint Conference on Artificial Intelligence (IJCAI).

##### 10.1.2.2. 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).

### **10.1.3. Journal**

#### *10.1.3.1. Member of the Editorial Boards*

Zacharaki, Evangelia I.: Medical Physics (guest editor), International Journal of Radiology, Dataset Papers in Science (Radiology), International Journal of Biostatistics & Computational Biology

#### *10.1.3.2. Reviewer - Reviewing Activities*

E. I. Zacharaki: IEEE Trans. on Medical Imaging (T-MI), Medical Image Analysis (MedIA), Trans. on Biomedical Engineering, Neuroimage, Artificial Intelligence in Medicine, Expert Systems with Applications, Bioinformatics, European Radiology

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

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.

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

### **10.1.4. Invited Talks**

J.-C. Pesquet:

Villars sur Oulon (International Biomedical and Astronomical Signal Processing Frontiers workshop, Feb. 2017)

Taras Shevchenko National University of Kiev (Feb. 2017)

Politecnico di Milano (Apr. 2017)

Gdansk University (Mar. 2017)

Juans-les-Pins (Colloque GRETSI, Sep. 2017)

Polytechnic University of Warsaw (Oct. 2017)

Université Libre de Bruxelles (Nov. 2017)

E. Chouzenoux:

Invited seminar, LCS, Saclay, 8 décembre 2017.

Invited seminar, IFPEN, Rueil Malmaison, 6 décembre 2017.

Invited seminar, S3, CentraleSupélec, 24 novembre 2017.

Invited seminar, IIIT Delhi, 8 novembre 2017.

Journées annuelles 2017 des GdR MOA et MIA, Talence, 18 octobre 2017.

Journées Franco-Chiliennes d'Optimisation, Toulouse, 6 juillet 2017

Ecole d'été "Structured Regularization for High-Dimensional Data Analysis", IHP, 21 juin 2017.

Invited seminar, Université de Modène, 3 avril 2017.

Journée GDR ISIS, Inversion et problèmes multi-\*, IAP, Paris, 20 mars 2017.

### **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. Foundations of Distributed and Large Scale Computing, 26h, M.Sc. in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School, FR

Master: Zacharaki, Evangelia I. Foundations in Machine Learning, 36, M2 DataScience, Centrale-Supélec , FR

Master: Malliaros, Fragkiskos. Machine Learning, 30h, M.Sc. in Data Sciences and Business Analytics, CentraleSupélec and ESSEC Business School, FR

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

### 10.2.2. Supervision

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

PhD in progress : Siddhartha Chandra, Deep Structured Prediction for Dense Labeling Tasks in Computer Vision, 2014-2018, Iasonas Kokkinos

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

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

PhD in progress : Evgenios Kornaropoulos, Diffusion Coefficient: a novel computer aided biomarker, 2013-2017, N. Paragios

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

PhD in progress: Roger Sun, Deep learning and computer vision approaches on medical imaging and genomic data to improve the prediction of anticancer therapies' efficacy, 2017-2020, N. Paragios

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

PhD in progress: Abdulkadir Celikkanat, Representation learning methods on graphs, 2017-2020, N. Paragios and F. Malliaros

### 10.2.3. Juries

The faculty members of the team (N. Paragios, J.-C. Pesquet, E. Chouzenoux and F. Malliaros) participated to numerous PhD Thesis Committees, HDR Committees and served as Grant Reviewers.

Emilie Chouzenoux, Mihir Sahasrabudhe, Jean-Christophe Pesquet, Marie-Caroline Corbineau and Nikos Paragios were part of the jury committee for several end-of-course internship presentations in CentraleSupélec.

# 11. Bibliography

## Publications of the year

### Doctoral Dissertations and Habilitation Theses

- [1] E. CHOUZENOUX. *Algorithmes de majoration-minimisation. Application aux problèmes inverses de grande taille en signal/image*, Université Paris Est - Marne-la-Vallée, December 2017, Habilitation à diriger des recherches, <https://hal.archives-ouvertes.fr/tel-01661236>
- [2] E. N. KORNAPOULOS. *Deformable Group-wise Image Registration for Motion Estimation in 4D Medical Imaging*, Ecole Centrale Paris, June 2017, <https://hal.inria.fr/tel-01577683>
- [3] E. I. ZACHARAKI. *Computational methods towards image-based biomarkers and beyond*, Université Paris-Est, March 2017, Habilitation à diriger des recherches, <https://hal.inria.fr/tel-01648583>

### Articles in International Peer-Reviewed Journals

- [4] F. ABBOUD, E. CHOUZENOUX, J.-C. PESQUET, J.-H. CHENOT, L. LABORELLI. *Dual Block Coordinate Forward-Backward Algorithm with Application to Deconvolution and Deinterlacing of Video Sequences*, in "Journal of Mathematical Imaging and Vision", November 2017, vol. 59, n<sup>o</sup> 3, pp. 415-431 [DOI : 10.1007/s10851-016-0696-Y], <https://hal.archives-ouvertes.fr/hal-01418393>
- [5] S. ALCHATZIDIS, A. SOTIRAS, E. I. ZACHARAKI, N. PARAGIOS. *A Discrete MRF Framework for Integrated Multi-Atlas Registration and Segmentation*, in "International Journal of Computer Vision", January 2017 [DOI : 10.1007/s11263-016-0925-2], <https://hal.archives-ouvertes.fr/hal-01359094>
- [6] S. AMIDI, A. AMIDI, D. VLACHAKIS, N. PARAGIOS, E. I. ZACHARAKI. *Automatic single- and multi-label enzymatic function prediction by machine learning*, in "PeerJ", 2017, vol. 5, pp. 1-16 [DOI : 10.7717/PEERJ.3095], <https://hal.inria.fr/hal-01648529>
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- [9] E. FERRANTE, N. PARAGIOS. *Graph-Based Slice-to-Volume Deformable Registration*, in "International Journal of Computer Vision", 2017 [DOI : 10.1007/s11263-017-1040-8], <https://hal.inria.fr/hal-01576314>
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