



Activity Report 2015

Project-Team PARIETAL

Modelling brain structure, function and variability based on high-field MRI data.

RESEARCH CENTER
Saclay - Île-de-France

THEME
Computational Neuroscience and
Medicine

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Project-Team PARIETAL

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Keywords:

Computer Science and Digital Science:

- 3.3. - Data and knowledge analysis
- 3.4. - Machine learning and statistics
- 5.3.2. - Sparse modeling and image representation
- 5.3.3. - Pattern recognition
- 5.9.1. - Sampling, acquisition
- 5.9.2. - Estimation, modeling
- 6.2.4. - Statistical methods
- 6.2.6. - Optimization

Other Research Topics and Application Domains:

- 1.3. - Neuroscience and cognitive science
 - 1.3.1. - Understanding and simulation of the brain and the nervous system
 - 1.3.2. - Cognitive science
- 2.2.6. - Neurodegenerative diseases
- 2.6.1. - Brain imaging

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2. Overall Objectives

2.1. Overall Objectives

The Parietal team focuses on mathematical methods for statistical inference based on neuroimaging data, with a particular reliance on machine learning techniques and applications of human functional imaging. This general theme splits into four research axes: Mathematical methods for multi-modal brain atlases, Statistical methods for high-dimensional data, Modeling brain function through neuroimaging and Parallel reconstruction and high-resolution MRI. Parietal is also strongly involved in open-source software development in scientific Python (machine learning) and for neuroimaging applications.

3. Research Program

3.1. Inverse problems in Neuroimaging

Many problems in neuroimaging can be framed as forward and inverse problems. For instance, the neuroimaging *inverse problem* consists in predicting individual information (behavior, phenotype) from neuroimaging data, while the *forward problem* consists in fitting neuroimaging data with high-dimensional (e.g. genetic) variables. Solving these problems entails the definition of two terms: a loss that quantifies the goodness of fit of the solution (does the model explain the data reasonably well ?), and a regularization schemes that represents a prior on the expected solution of the problem. In particular some priors enforce some properties of the solutions, such as sparsity, smoothness or being piece-wise constant.

Let us detail the model used in the inverse problem: Let \mathbf{X} be a neuroimaging dataset as an (n_{subj}, n_{voxels}) matrix, where n_{subj} and n_{voxels} are the number of subjects under study, and the image size respectively, \mathbf{Y} an array of values that represent characteristics of interest in the observed population, written as (n_{subj}, n_f) matrix, where n_f is the number of characteristics that are tested, and β an array of shape (n_{voxels}, n_f) that represents a set of pattern-specific maps. In the first place, we may consider the columns $\mathbf{Y}_1, \dots, \mathbf{Y}_{n_f}$ of \mathbf{Y} independently, yielding n_f problems to be solved in parallel:

$$\mathbf{Y}_i = \mathbf{X}\beta_i + \epsilon_i, \forall i \in \{1, \dots, n_f\},$$

where the vector contains β_i is the i^{th} row of β . As the problem is clearly ill-posed, it is naturally handled in a regularized regression framework:

$$\hat{\beta}_i = \operatorname{argmin}_{\beta_i} \|\mathbf{Y}_i - \mathbf{X}\beta_i\|^2 + \Psi(\beta_i), \quad (1)$$

where Ψ is an adequate penalization used to regularize the solution:

$$\Psi(\beta; \lambda_1, \lambda_2, \eta_1, \eta_2) = \lambda_1 \|\beta\|_1 + \lambda_2 \|\beta\|_2 + \eta_1 \|\nabla\beta\|_1 + \eta_2 \|\nabla\beta\|_2 \quad (2)$$

with $\lambda_1, \lambda_2, \eta_1, \eta_2 \geq 0$ (this formulation particularly highlights the fact that convex regularizers are norms or quasi-norms). In general, only one or two of these constraints is considered (hence is enforced with a non-zero coefficient):

- When $\lambda_1 > 0$ only (LASSO), and to some extent, when $\lambda_1, \lambda_2 > 0$ only (elastic net), the optimal solution β is (possibly very) sparse, but may not exhibit a proper image structure; it does not fit well with the intuitive concept of a brain map.
- Total Variation regularization (see Fig. 1) is obtained for ($\eta_1 > 0$ only), and typically yields a piecewise constant solution. It can be associated with Lasso to enforce both sparsity and sparse variations.
- Smooth lasso is obtained with ($\eta_2 > 0$ and $\lambda_1 > 0$ only), and yields smooth, compactly supported spatial basis functions.

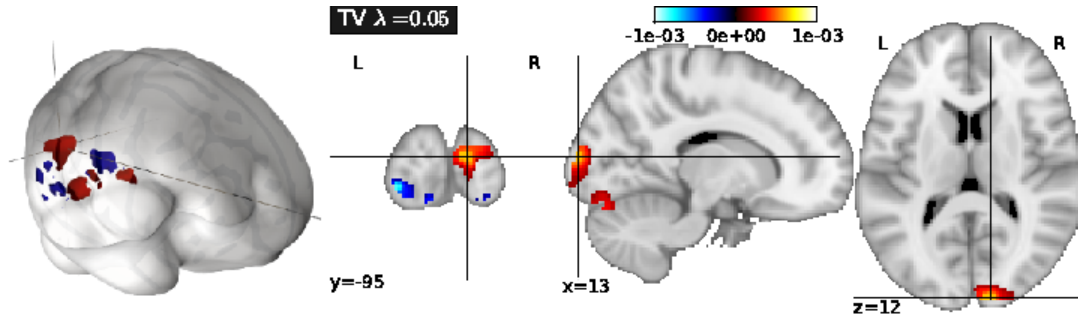


Figure 1. Example of the regularization of a brain map with total variation in an inverse problem. The problem here consists in predicting the spatial scale of an object presented as a stimulus, given functional neuroimaging data acquired during the observation of an image. Learning and test are performed across individuals. Unlike other approaches, Total Variation regularization yields a sparse and well-localized solution that enjoys particularly high accuracy.

The performance of the predictive model can simply be evaluated as the amount of variance in \mathbf{Y}_i fitted by the model, for each $i \in \{1, \dots, n_f\}$. This can be computed through cross-validation, by *learning* $\hat{\beta}_i$ on some part of the dataset, and then estimating $(Y_i - X\hat{\beta}_i)$ using the remainder of the dataset.

This framework is easily extended by considering

- *Grouped penalization*, where the penalization explicitly includes a prior clustering of the features, i.e. voxel-related signals, into given groups. This is particularly important to include external anatomical priors on the relevant solution.
- *Combined penalizations*, i.e. a mixture of simple and group-wise penalizations, that allow some variability to fit the data in different populations of subjects, while keeping some common constraints.
- *Logistic regression*, where a logistic non-linearity is applied to the linear model so that it yields a probability of classification in a binary classification problem.
- *Robustness to between-subject variability* is an important question, as it makes little sense that a learned model depends dramatically on the particular observations used for learning. This is an important issue, as this kind of robustness is somewhat opposite to sparsity requirements.
- *Multi-task learning*: if several target variables are thought to be related, it might be useful to constrain the estimated parameter vector β to have a shared support across all these variables. For instance, when one of the variables \mathbf{Y}_i is not well fitted by the model, the estimation of other variables $\mathbf{Y}_j, j \neq i$ may provide constraints on the support of β_i and thus, improve the prediction of \mathbf{Y}_i . Yet this does not impose constraints on the non-zero parameters of the parameters β_i .

$$\mathbf{Y} = \mathbf{X}\beta + \epsilon, \quad (3)$$

then

$$\hat{\beta} = \operatorname{argmin}_{\beta=(\beta_i), i=1..n_f} \sum_{i=1}^{n_f} \|\mathbf{Y}_i - \mathbf{X}\beta_i\|^2 + \lambda \sum_{j=1}^{n_{voxels}} \sqrt{\sum_{i=1}^{n_f} \beta_{i,j}^2} \quad (4)$$

3.2. Multivariate decompositions

Multivariate decompositions are an important tool to model complex data such as brain activation images: for instance, one might be interested in extracting an *atlas of brain regions* from a given dataset, such as regions depicting similar activities during a protocol, across multiple protocols, or even in the absence of protocol (during resting-state). These data can often be factorized into spatial-temporal components, and thus can be estimated through *regularized Principal Components Analysis* (PCA) algorithms, which share some common steps with regularized regression.

Let \mathbf{X} be a neuroimaging dataset written as an (n_{subj}, n_{voxels}) matrix, after proper centering; the model reads

$$\mathbf{X} = \mathbf{A}\mathbf{D} + \epsilon, \quad (5)$$

where \mathbf{D} represents a set of n_{comp} spatial maps, hence a matrix of shape (n_{comp}, n_{voxels}) , and \mathbf{A} the associated subject-wise loadings. While traditional PCA and independent components analysis are limited to reconstruct components \mathbf{D} within the space spanned by the column of \mathbf{X} , it seems desirable to add some constraints on the rows of \mathbf{D} , that represent spatial maps, such as sparsity, and/or smoothness, as it makes the interpretation of these maps clearer in the context of neuroimaging.

This yields the following estimation problem:

$$\min_{\mathbf{D}, \mathbf{A}} \|\mathbf{X} - \mathbf{A}\mathbf{D}\|^2 + \Psi(\mathbf{D}) \text{ s.t. } \|\mathbf{A}_i\| = 1 \forall i \in \{1..n_f\}, \quad (6)$$

where $(\mathbf{A}_i), i \in \{1..n_f\}$ represents the columns of \mathbf{A} . Ψ can be chosen such as in Eq. (2) in order to enforce smoothness and/or sparsity constraints.

The problem is not jointly convex in all the variables but each penalization given in Eq (2) yields a convex problem on \mathbf{D} for \mathbf{A} fixed, and conversely. This readily suggests an alternate optimization scheme, where \mathbf{D} and \mathbf{A} are estimated in turn, until convergence to a local optimum of the criterion. As in PCA, the extracted components can be ranked according to the amount of fitted variance. Importantly, also, estimated PCA models can be interpreted as a probabilistic model of the data, assuming a high-dimensional Gaussian distribution (probabilistic PCA).

3.3. Covariance estimation

Another important estimation problem stems from the general issue of learning the relationship between sets of variables, in particular their covariance. Covariance learning is essential to model the dependence of these variables when they are used in a multivariate model, for instance to assess whether an observation is aberrant or not or in classification problems. Covariance learning is necessary to model latent interactions in high-dimensional observation spaces, e.g. when considering multiple contrasts or functional connectivity data.

The difficulties are two-fold: on the one hand, there is a shortage of data to learn a good covariance model from an individual subject, and on the other hand, subject-to-subject variability poses a serious challenge to the use of multi-subject data. While the covariance structure may vary from population to population, or depending on the input data (activation versus spontaneous activity), assuming some shared structure across problems, such as their sparsity pattern, is important in order to obtain correct estimates from noisy data. Some of the most important models are:

- **Sparse Gaussian graphical models**, as they express meaningful conditional independence relationships between regions, and do improve conditioning/avoid overfit.
- **Decomposable models**, as they enjoy good computational properties and enable intuitive interpretations of the network structure. Whether they can faithfully or not represent brain networks is an important question that needs to be addressed.
- **PCA-based regularization of covariance** which is powerful when modes of variation are more important than conditional independence relationships.

Adequate model selection procedures are necessary to achieve the right level of sparsity or regularization in covariance estimation; the natural evaluation metric here is the out-of-samples likelihood of the associated Gaussian model. Another essential remaining issue is to develop an adequate statistical framework to test differences between covariance models in different populations. To do so, we consider different means of parametrizing covariance distributions and how these parametrizations impact the test of statistical differences across individuals.

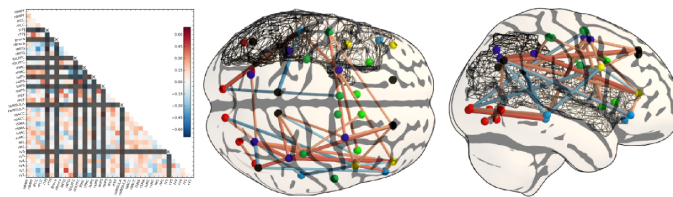


Figure 2. Example of functional connectivity analysis: The correlation matrix describing brain functional connectivity in a post-stroke patient (lesion volume outlined as a mesh) is compared to a group of control subjects. Some edges of the graphical model show a significant difference, but the statistical detection of the difference requires a sophisticated statistical framework for the comparison of graphical models.

4. Application Domains

4.1. Human neuroimaging data and their use

Human neuroimaging consists in acquiring non-invasively image data from normal and diseased human populations. Magnetic Resonance Imaging (MRI) can be used to acquire information on brain structure and function at high spatial resolution.

- T1-weighted MRI is used to obtain a segmentation of the brain into different different tissues, such as gray matter, white matter, deep nuclei, cerebro-spinal fluid, at the millimeter or sub-millimeter resolution. This can then be used to derive geometric and anatomical information on the brain, e.g. cortical thickness.
- Diffusion-weighted MRI measures the local diffusion of water molecules in the brain at the resolution of 1 to 2mm, in a set of directions (60 typically). Local anisotropy, observed in white matter, yields a local model of fiber orientation that can be integrated into a geometric model of fiber tracts along which water diffusion occurs, and thus provides information on the connectivity structure of the brain.
- Functional MRI measures the blood-oxygen-level-dependent (BOLD) contrast that reflects neural activity in the brain, at a spatial resolution of 1.5 to 3mm, and a temporal resolution of about 2s. This yields a spatially resolved image of brain functional networks that can be modulated either by specific cognitive tasks or exhibit spontaneous co-activations.
- Electro- and Magneto-encephalography (MEEG) are two additional modalities that complement functional MRI, as they directly measure the electric and magnetic signals elicited by neural activity, at the millisecond scale. These modalities rely on surface measurements and do not localize brain activity very accurately in the spatial domain.

4.2. High-field MRI

High field MRI as performed at NeuroSpin (7T on humans, 11.7T in 2017, 17.6T on rats) brings an improvement over traditional MRI acquisitions at 1.5T or 3T, related to a higher signal-to-noise ratio in the data. Depending on the data and applicative context, this gain in SNR can be traded against spatial resolution improvements, thus helping in getting more detailed views of brain structure and function. This comes at the risk of higher susceptibility distortions of the MRI scans and signal inhomogeneities, that need to be corrected for. Improvements at the acquisition level may come from the use of new coils (such as the 32 channels coil on the 7T at NeuroSpin), as well as the use of multi-band sequences [62].

4.3. Technical challenges for the analysis of neuroimaging data

The first limitation of Neuroimaging-based brain analysis is the limited Signal-to-Noise Ratio of the data. A particularly striking case is functional MRI, where only a fraction of the data is actually understood, and from which it is impossible to observe by eye the effect of neural activation on the raw data. Moreover, far from traditional i.i.d. Gaussian models, the noise in MRI typically exhibits local and long-distance correlations (e.g. motion-related signal) and has potentially large amplitude, which can make it hard to distinguish from true signal on a purely statistical basis. A related difficulty is the *lack of salient structure* in the data: it is hard to infer meaningful patterns (either through segmentation or factorization procedures) based on the data only. A typical case is the inference of brain networks from resting-state functional connectivity data.

Regarding statistical methodology, neuroimaging problems also suffer from the relative paucity of the data, i.e. the relatively small number of images available to learn brain features or models, e.g. with respect to the size of the images or the number of potential structures of interest. This leads to several kinds of difficulties, known either as *multiple comparison problems* or *curse of dimensionality*. One possibility to overcome this challenge is to increase the amount of data by using images from multiple acquisition centers, at the risk of introducing scanner-related variability, thus challenging the homogeneity of the data. This becomes an important concern with the advent of cross-modal neuroimaging-genetics studies.

5. Highlights of the Year

5.1. Highlights of the Year

Michael Eickenberg got an oral presentation at the OHBM 2015 conference(success rate < 1%). Elvis Dohmatob got an oral presentation at the OHBM 2015 conference(success rate < 1%).

6. New Software and Platforms

6.1. Scikit-learn

KEYWORDS: Classification - Learning - Clustering - Regression - Medical imaging

SCIENTIFIC DESCRIPTION

Scikit-learn is a Python module integrating classic machine learning algorithms in the tightly-knit scientific Python world. It aims to provide simple and efficient solutions to learning problems, accessible to everybody and reusable in various contexts: machine-learning as a versatile tool for science and engineering.

FUNCTIONAL DESCRIPTION

Scikit-learn can be used as a middleware for prediction tasks. For example, many web startups adapt Scikitlearn to predict buying behavior of users, provide product recommendations, detect trends or abusive behavior (fraud, spam). Scikit-learn is used to extract the structure of complex data (text, images) and classify such data with techniques relevant to the state of the art.

Easy to use, efficient and accessible to non datascience experts, Scikit-learn is an increasingly popular machine learning library in Python. In a data exploration step, the user can enter a few lines on an interactive (but non-graphical) interface and immediately sees the results of his request. Scikitlearn is a prediction engine . Scikit-learn is developed in open source, and available under the BSD license.

- Participants: Olivier Grisel, Gaël Varoquaux, Bertrand Thirion, Michael Eickenberg, Loïc Estève, Alexandre Gramfort and Fabian Pedregosa Izquierdo
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- Contact: Olivier Grisel
- URL: <http://scikit-learn.org>

6.2. Nilearn

KEYWORDS: Health - Neuroimaging - Medical imaging

FUNCTIONAL DESCRIPTION

NiLearn is the neuroimaging library that adapts the concepts and tools of scikit-learn to neuroimaging problems. As a pure Python library, it depends on scikit-learn and nibabel, the main Python library for neuroimaging I/O. It is an open-source project, available under BSD license. The two key components of NiLearn are i) the analysis of functional connectivity (spatial decompositions and covariance learning) and ii) the most common tools for multivariate pattern analysis. A great deal of efforts has been put on the efficiency of the procedures both in terms of memory cost and computation time.

- Participants: Gaël Varoquaux, Bertrand Thirion, Loïc Estève, Alexandre Abraham, Michael Eickenberg, Alexandre Gramfort, Fabian Pedregosa Izquierdo, Elvis Dohmatob.
- Contact: Bertrand Thirion
- URL: <http://nilearn.github.io>

6.3. Mayavi

FUNCTIONAL DESCRIPTION

Mayavi is the most used scientific 3D visualization Python software. Mayavi can be used as a visualization tool, through interactive command line or as a library. It is distributed under Linux through Ubuntu, Debian, Fedora and Mandriva, as well as in PythonXY and EPD Python scientific distributions. Mayavi is used by several software platforms, such as PDE solvers (fipy, sfepy), molecule visualization tools and brain connectivity analysis tools (connectomeViewer).

- Contact: Gaël Varoquaux
- URL: <http://mayavi.sourceforge.net/>

6.4. PyHRF

KEYWORDS: fMRI - Statistic analysis - Neurosciences - IRM - Brain - Health - Medical imaging

FUNCTIONAL DESCRIPTION

As part of fMRI data analysis, PyHRF provides a set of tools for addressing the two main issues involved in intra-subject fMRI data analysis : (i) the localization of cerebral regions that elicit evoked activity and (ii) the estimation of the activation dynamics also referenced to as the recovery of the Hemodynamic Response Function (HRF). To tackle these two problems, PyHRF implements the Joint Detection-Estimation framework (JDE) which recovers parcel-level HRFs and embeds an adaptive spatio-temporal regularization scheme of activation maps.

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7. New Results

7.1. Semi-Supervised Factored Logistic Regression for High-Dimensional Neuroimaging Data

Imaging neuroscience links human behavior to aspects of brain biology in ever-increasing datasets. Existing neuroimaging methods typically perform either discovery of unknown neural structure or testing of neural structure associated with mental tasks. However, testing hypotheses on the neural correlates underlying larger sets of mental tasks necessitates adequate representations for the observations. We therefore propose to blend representation modelling and task classification into a unified statistical learning problem. A multinomial logistic regression is introduced that is constrained by factored coefficients and coupled with an autoencoder. We show that this approach yields more accurate and interpretable neural models of psychological tasks in a reference dataset, as well as better generalization to other datasets.

More information can be found in [50].

7.2. NeuroVault.org: a web-based repository for collecting and sharing unthresholded statistical maps of the human brain

Here we present NeuroVault — a web based repository that allows researchers to store, share, visualize, and decode statistical maps of the human brain. NeuroVault is easy to use and employs modern web technologies to provide informative visualization of data without the need to install additional software. In addition, it leverages the power of the Neurosynth database to provide cognitive decoding of deposited maps. The data are exposed through a public REST API enabling other services and tools to take advantage of it. NeuroVault is a new resource for researchers interested in conducting meta- and coactivation analyses.

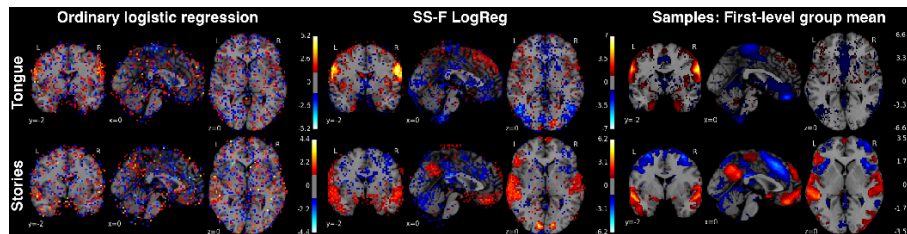


Figure 3. Classification weight maps. The voxel predictors corresponding to 2 exemplary (of 18 total) psychological tasks (rows) from the Human Connectome Project dataset. Left column: multinomial logistic regression (same implementation but without bottleneck or autoencoder), middle column: Semi-Supervised Factored Logistic Regression (SSFLogReg), right column: voxel-wise average across all samples of whole-brain activity maps from each task. SSFLogReg puts higher absolute weights on relevant structure, lowers ones on irrelevant structure, and yields BOLD-typical local contiguity (without enforcing an explicit spatial prior). More information can be found in [50].

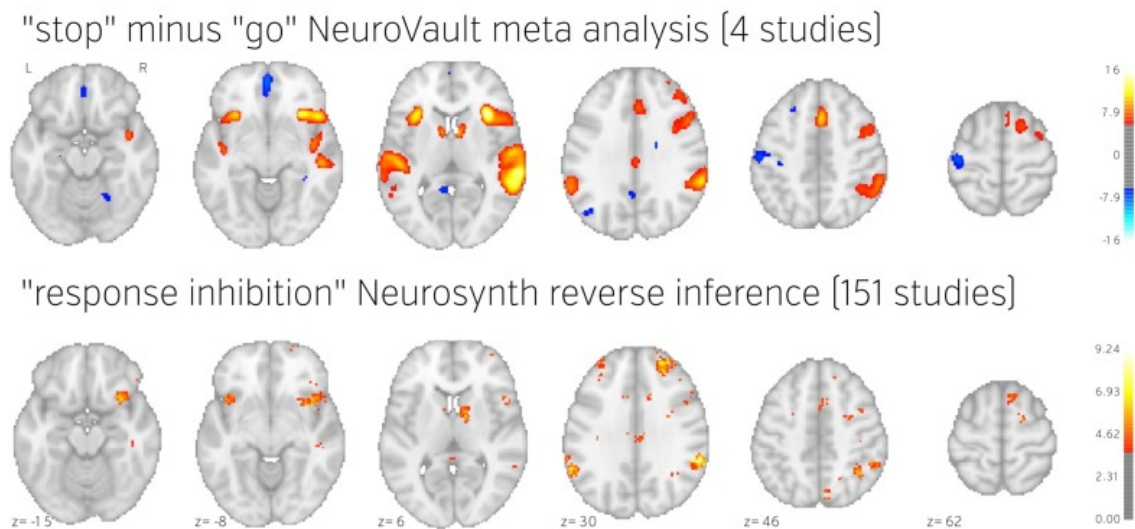


Figure 4.

Comparison of image based and coordinate based meta analysis of response inhibition. Meta analysis based on unthresholded statistical maps obtained from NeuroVault (top row) managed to recover the pattern of activation obtained using traditional methods despite including much fewer studies. NeuroVault map has been thresholded at $z = 6$, response inhibition map has been thresholded at $z = 1.77$ (the threshold values were chosen for visualization purposes only, but both are statistically significant at $p < 0.05$). Unthresholded versions of these maps are available at <http://neurovault.org/collections/439/>

More information can be found in [18] and [17].

7.3. FAASTA: A fast solver for total-variation regularization of ill-conditioned problems with application to brain imaging

The total variation (TV) penalty, as many other analysis-sparsity problems, does not lead to separable factors or a proximal operator with a closed-form expression, such as soft thresholding for the ℓ_1 penalty. As a result, in a variational formulation of an inverse problem or statistical learning estimation, it leads to challenging non-smooth optimization problems that are often solved with elaborate single-step first-order methods. When the data-fit term arises from empirical measurements, as in brain imaging, it is often very ill-conditioned and without simple structure. In this situation, in proximal splitting methods, the computation cost of the gradient step can easily dominate each iteration. Thus it is beneficial to minimize the number of gradient steps. We present FAASTA, a variant of FISTA, that relies on an internal solver for the TV proximal operator, and refines its tolerance to balance computational cost of the gradient and the proximal steps. We give benchmarks and illustrations on “brain decoding”: recovering brain maps from noisy measurements to predict observed behavior. The algorithm as well as the empirical study of convergence speed are valuable for any non-exact proximal operator, in particular analysis-sparsity problems.

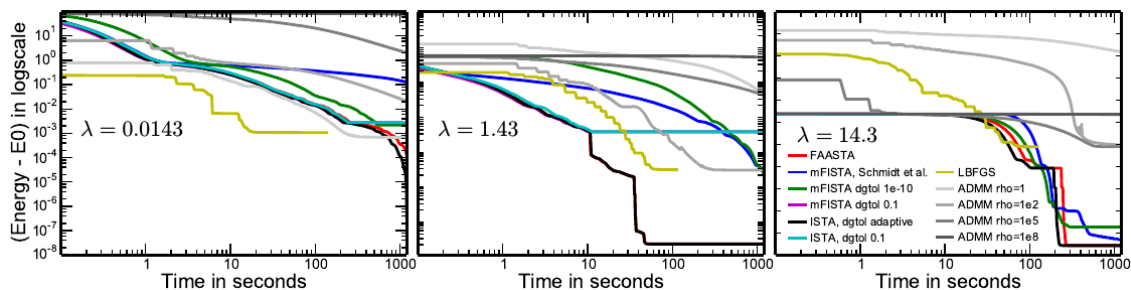


Figure 5.

Convergence of currently available optimization algorithms, for 3 scenarios, with weak, medium and strong regularization, where medium regularization corresponds to the value chosen by cross-validation. These are log-log plots with the 0 defined as the lowest energy value reached across all algorithms.

More information can be found in [47].

7.4. Bootstrapped Permutation Test for Multiresponse Inference on Brain Behavior Associations.

Despite that diagnosis of neurological disorders commonly involves a collection of behavioral assessments, most neuroimaging studies investigating the associations between brain and behavior largely analyze each behavioral measure in isolation. To jointly model multiple behavioral scores, sparse multi-response regression (SMR) is often used. However, directly applying SMR without statistically controlling for false positives

could result in many spurious findings. For models, such as SMR, where the distribution of the model parameters is unknown, permutation test and stability selection are typically used to control for false positives. In this paper, we present another technique for inferring statistically significant features from models with unknown parameter distribution. We refer to this technique as bootstrapped permutation test (BPT), which uses Studentized statistics to exploit the intuition that the variability in parameter estimates associated with relevant features would likely be higher with responses permuted. On synthetic data, we show that BPT provides higher sensitivity in identifying relevant features from the SMR model than permutation test and stability selection, while retaining strong control on the false positive rate. We further apply BPT to study the associations between brain connectivity estimated from pseudo-rest fMRI data of 1139 fourteen year olds and behavioral measures related to ADHD. Significant connections are found between brain networks known to be implicated in the behavioral tasks involved. Moreover, we validate the identified connections by fitting a regression model on pseudo-rest data with only those connections and applying this model on resting state fMRI data of 337 left out subjects to predict their behavioral scores. The predicted scores are shown to significantly correlate with the actual scores of the subjects, hence verifying the behavioral relevance of the found connections.

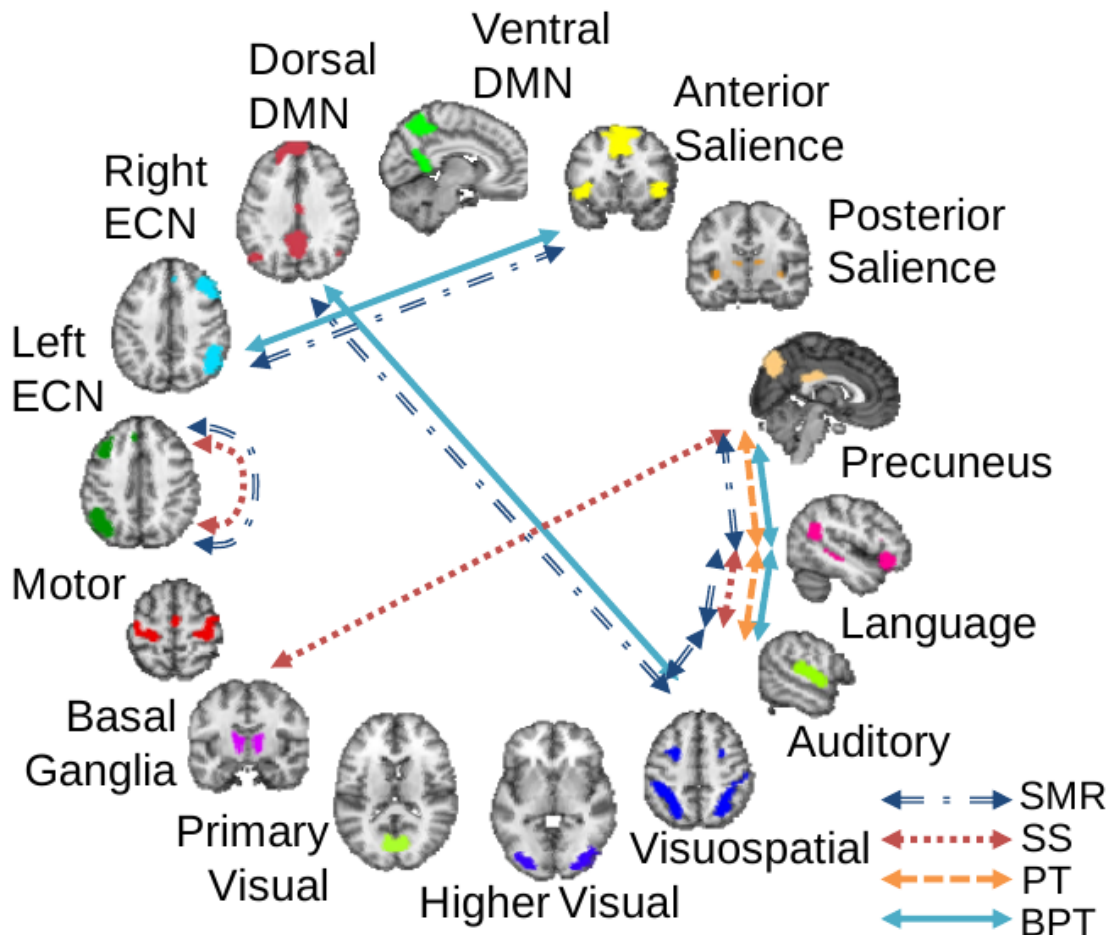


Figure 6.

Real data results: Statistically significant connectivity differences between populations (a) Significant network connections found on pseudo-rest fMRI data. (b) Pearson's correlation between predicted and actual scores with p-values noted. Each set of three bars (top to bottom) correspond to spatial working memory strategy, spatial working memory between errors, and rapid visual information processing accuracy scores. Significance is declared at $p < 0.05$.

More information can be found in [43].

7.5. Total Variation meets Sparsity: statistical learning with segmenting penalties

Prediction from medical images is a valuable aid to diagnosis. For instance, anatomical MR images can reveal certain disease conditions, while their functional counterparts can predict neuropsychiatric phenotypes. However, a physician will not rely on predictions by black-box models: understanding the anatomical or functional features that underpin decision is critical. Generally, the weight vectors of classifiers are not easily amenable to such an examination: Often there is no apparent structure. Indeed, this is not only a prediction task, but also an inverse problem that calls for adequate regularization. We address this challenge by introducing a convex region-selecting penalty. Our penalty combines total-variation regularization, enforcing spatial contiguity, and l_1 regularization, enforcing sparsity, into one group: Voxels are either active with non-zero spatial derivative or zero with inactive spatial derivative. This leads to segmenting contiguous spatial regions (inside which the signal can vary freely) against a background of zeros. Such segmentation of medical images in a target-informed manner is an important analysis tool. On several prediction problems from brain MRI, the penalty shows good segmentation. Given the size of medical images, computational efficiency is key. Keeping this in mind, we contribute an efficient optimization scheme that brings significant computational gains.

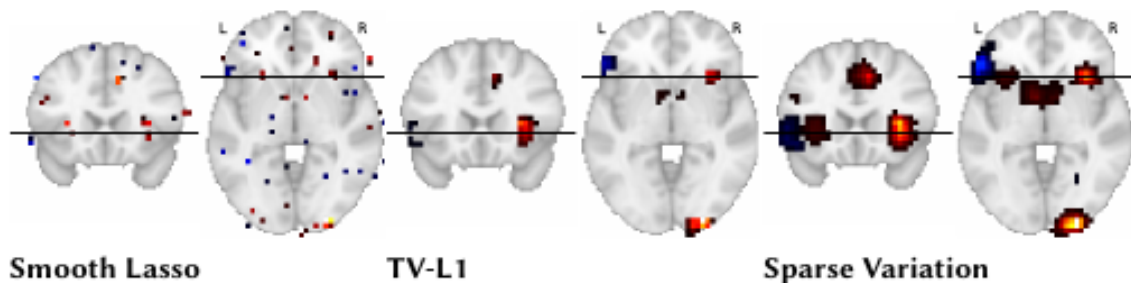


Figure 7.

Weight vectors from estimating gain on the mixed gambles task for three sparse methods: Graphnet, TV-11 and Sparse Variation. This inter- subject analysis shows broader regions of activation. Mean correlation scores on held out data: Graphnet: 0.128, TV-11 : 0.147, Sparse Variation: 0.149. One can see that both TV-11 and Sparse Variation regularizations yield more interpretable patterns than Graphnet.

More information can be found in [40].

7.6. Improving sparse recovery on structured images with bagged clustering

The identification of image regions associated with external variables through discriminative approaches yields ill-posed estimation problems. This estimation challenge can be tackled by imposing sparse solutions. However, the sensitivity of sparse estimators to correlated variables leads to non-reproducible results, and

only a subset of the important variables are selected. In this paper, we explore an approach based on bagging clustering-based data compression in order to alleviate the instability of sparse models. Specifically, we design a new framework in which the estimator is built by averaging multiple models estimated after feature clustering, to improve the conditioning of the model. We show that this combination of model averaging with spatially consistent compression can have the virtuous effect of increasing the stability of the weight maps, allowing a better interpretation of the results. Finally, we demonstrate the benefit of our approach on several predictive modeling problems.

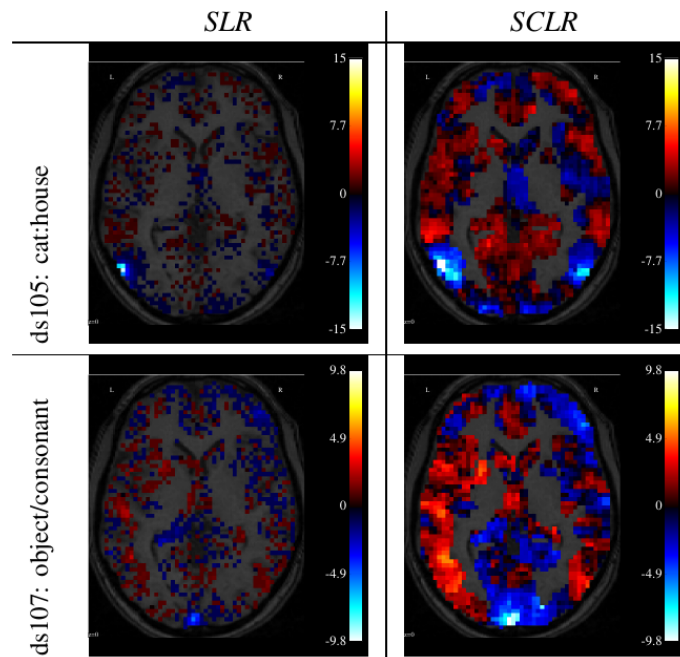


Figure 8.

Z-score obtained across bootstraps for two discriminative tasks, using the candidate approaches. Higher values hint at lower variability across bootstrap replications. SCLR decreases the variability and yields larger standardized effects.

More information can be found in [42].

7.7. Integrating Multimodal Priors in Predictive Models for the Functional Characterization of Alzheimer’s Disease

Functional brain imaging provides key information to characterize neurodegenerative diseases, such as Alzheimer’s disease (AD). Specifically, the metabolic activity measured through fluorodeoxyglucose positron emission tomography (FDG-PET) and the connectivity extracted from resting-state functional magnetic resonance imaging (fMRI), are promising biomarkers that can be used for early assessment and prognosis of the disease and to understand its mechanisms. FDG-PET is the best suited functional marker so far, as it gives a reliable quantitative measure, but is invasive. On the other hand, non-invasive fMRI acquisitions do not provide a straightforward quantification of brain functional activity. To analyze populations solely based on resting-state fMRI, we propose an approach that leverages a metabolic prior learned from FDG-PET. More formally, our classification framework embeds population priors learned from

another modality at the voxel-level, which can be seen as a regularization term in the analysis. Experimental results show that our PET-informed approach increases classification accuracy compared to pure fMRI approaches and highlights regions known to be impacted by the disease.

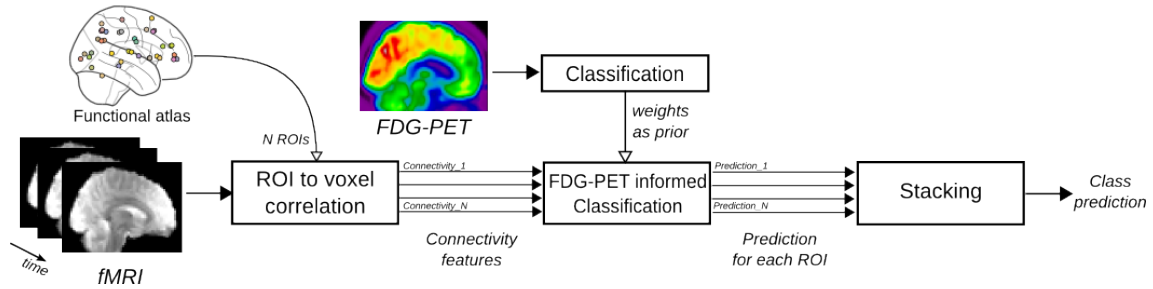


Figure 9.

Overview of the proposed classification pipeline: The inputs are ROI-to-voxel connectivities computed from the rs-fMRI time-series. FDG-PET model weights are integrated as prior for the classification. Then, predictions of all ROIs are the inputs of a stacking model to predict the clinical group.

More information can be found in [44].

7.8. Inverse problems with time-frequency dictionaries and Gaussian non-white noise

Sparse regressions to solve ill-posed inverse problems have been massively investigated over the last decade. Yet, when noise is present in the model, it is almost exclusively considered as Gaussian and white. While this assumption can hold in practice it rarely holds when observations are time series as they are corrupted by auto-correlated and colored noise. In this work we study sparse regression under the assumption of non white Gaussian noise and explain how to run the inference using proximal gradient methods. We investigate an application in brain imaging: the problem of source localization using magneto- and electroencephalography (M/EEG) which allow functional brain imaging with high temporal resolution. We use a time-frequency representation of the source waveforms and a sparse regularization which promotes focal sources with smooth and transient activations. Our approach is evaluated using simulations comparing it to strategies that assume the noise is white or to simple prewhitening.

More information can be found in [30].

7.9. Variable density sampling based on physically plausible gradient waveform. Application to 3D MRI angiography

Performing k-space variable density sampling is a popular way of reducing scanning time in Magnetic Resonance Imaging (MRI). Unfortunately, given a sampling trajectory, it is not clear how to traverse it using gradient waveforms. In this paper, we actually show that existing methods can yield large traversal time if the trajectory contains high curvature areas. Therefore, we consider here a new method for gradient waveform design which is based on the projection of unrealistic initial trajectory onto the set of hardware constraints. Next, we show on realistic simulations that this algorithm allows implementing variable density trajectories resulting from the piecewise linear solution of the Travelling Salesman Problem in a reasonable time. Finally, we demonstrate the application of this approach to 2D MRI reconstruction and 3D angiography in the mouse brain.

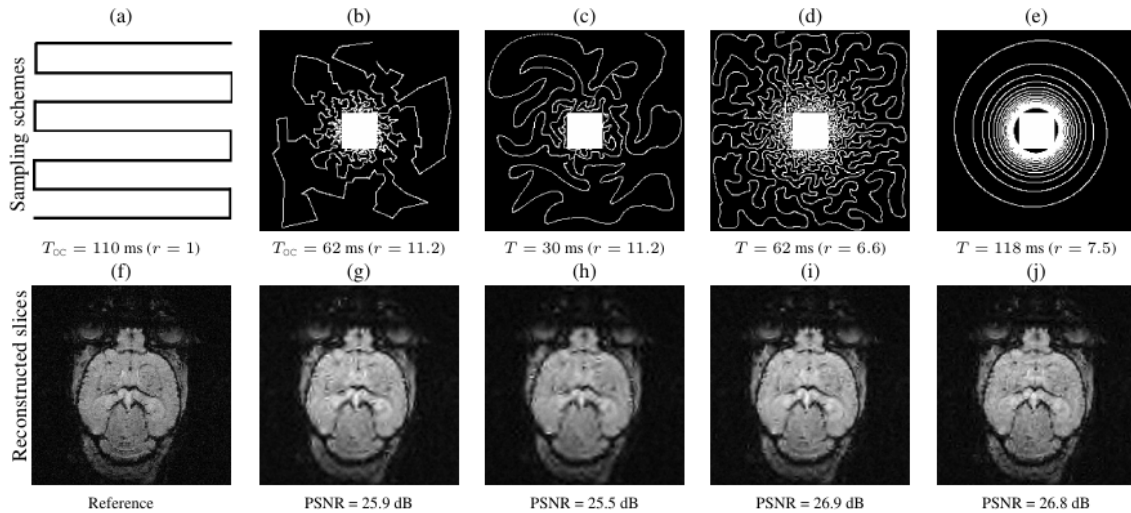


Figure 10.

Full k-space acquisition with an EPI sequence (a) and corresponding reference image (f). Comparison between an exact parameterization of the TSP trajectory (b) and projection from Travelling Salesman Problem trajectory onto the set of constraints (c),(d). In experiments (b,c), the number of measured locations is fixed to 9% ($r = 11.2$), whereas in (b,d), the time to traverse the curve is fixed to 62 ms. (e): Spiral trajectory with acquisition of the k-space center. (g-j): Reconstructed images corresponding to sampling strategies (b-e). More information can be found in [38].

7.10. A projection method on measures sets.

We consider the problem of projecting a probability measure π on a set \mathcal{M}_N of Radon measures. The projection is defined as a solution of the following variational problem:

$$\inf_{\mu \in \mathcal{M}_N} \|h(\mu - \pi)\|_2^2,$$

where $h \in L^2(\Omega)$ is a kernel, $\Omega \subset \mathbb{R}^d$ and denotes the convolution operator. To motivate and illustrate our study, we show that this problem arises naturally in various practical image rendering problems such as stippling (representing an image with N dots) or continuous line drawing (representing an image with a continuous line). We provide a necessary and sufficient condition on the sequence $(\mathcal{M}_N)_{N \in \mathbb{N}}$ that ensures weak convergence of the projections $(\mu_N^*)_{N \in \mathbb{N}}$ to π . We then provide a numerical algorithm to solve a discretized version of the problem and show several illustrations related to computer-assisted synthesis of artistic paintings/drawings.

Projection of a lion image onto $P_N^{1,\infty}$ with $N = 8,000$. The figure depicts the resulting line with several values of the iterates of our Algorithm.

More information can be found in [55].

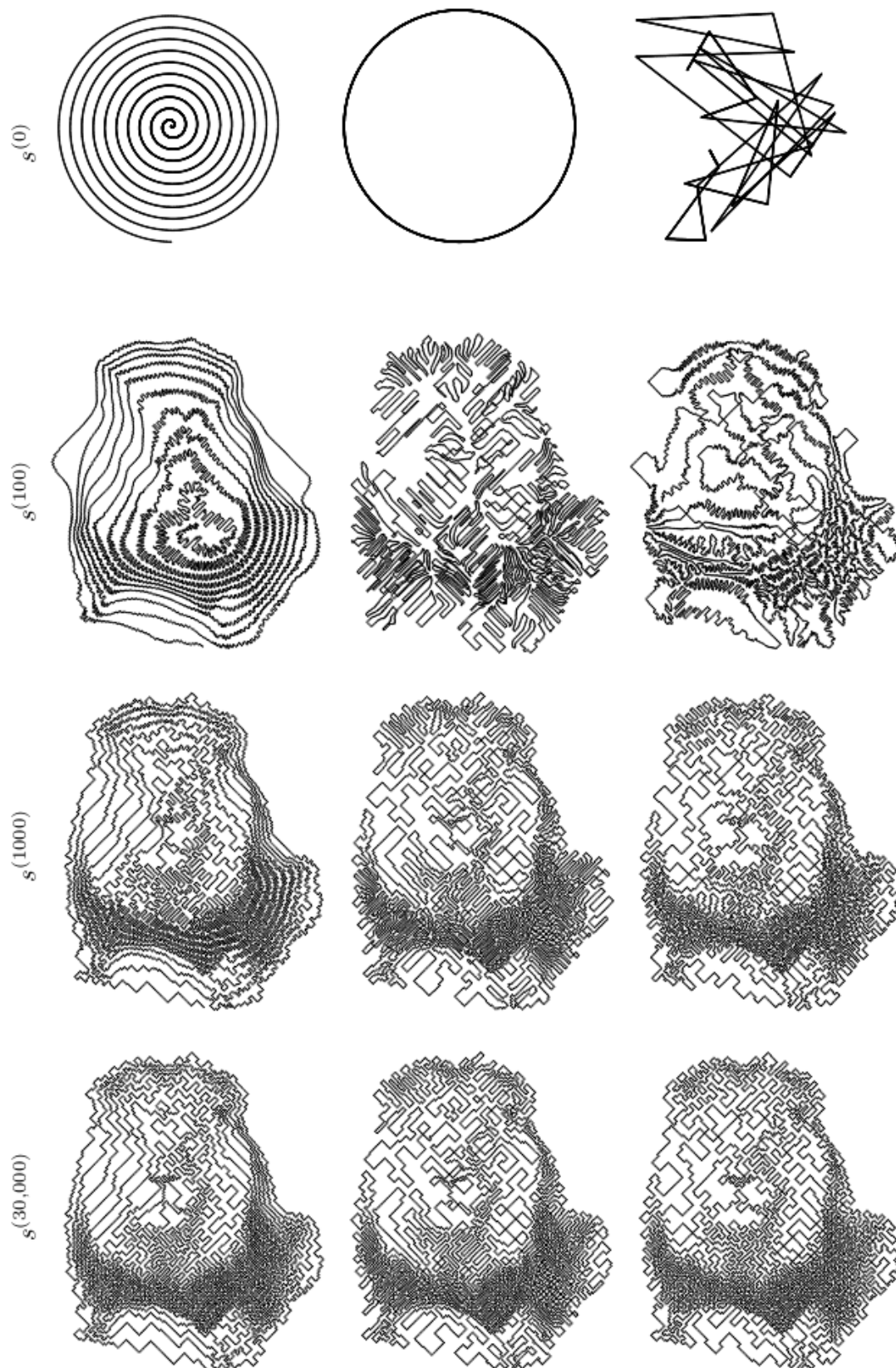


Figure 11.

8. Bilateral Contracts and Grants with Industry

8.1. The LearnClues Labcomm

The LearnClues LabComm has been granted in Oct, 2014, and the agreement was signed in Dec. 2015.

Statistical learning is a field of mathematics and computer science that enables the extraction of predictive models from data with weak signal to noise ratio. These techniques are behind the successes of Google or the progresses of automatic medical diagnostic. Combined with a knowledge of the field of application, they open the door to optimal decisions. Tinyclues is a start-up that applies statistical learning to e-commerce, adapting the marketing practice from customer databases. Parietal is an Inria research group that develops statistical learning for neurosciences and is the driving force behind the software tool "scikit-learn", that is a standard in statistical learning.

The goal of this proposed common lab is to transfer the expertise of Parietal on big data and to improve statistical learning techniques and implementation on distributed systems to open the door to faster analysis of very large datasets. Indeed, processing more data implies detecting smaller effects in the signals. Tinyclues already uses the tools developed par Parietal on the "cloud", and thus in distributed computing environments. The practical experience of Parietal enables us to plan substantial improvements to computational performance as well as to the amount of information extracted from big data.

From a strategical standpoint for Tinyclues, such progress are important to vary the number of domain scenarios that it can address, by analyzing jointly more data of a wider type, and to render fully automatic the data analysis platform that it is offering to its customers, replacing challenging tasks currently performed by experts. These developments are particularly important given that Tinyclues is developing at a very fast rate and is processing bigger and bigger datasets and an increasing number of different problems.

The project partners are:

- Parietal, Inria
- Tiny Clues

8.2. The Wendelin FUI project

The Wendelin project has been granted on December 3rd, 2014. It has been selected at the *Programme d'Investissements d'Avenir (PIA)* that supports "cloud computing et Big Data". It gives visibility and fosters the French technological big data sector, and in particular the scikit-learn library, the NoSQL "NEO" et the decentralized "SlapOS" cloud, three open-source software supported by the Systematic *pôle de compétitivité*.

Scikit-learn is a worldwide reference library for machine learning. Gaël Varoquaux, Olivier Grisel and Alexandre Gramfort have been major players in the design of the library and Scikit-learn has then been supported by the growing scientific Python community. It is currently used by major internet companies as well as dynamic start-ups, including Google, Airbnb, Spotify, Evernote, AWeber, TinyClues; it wins more than half of the data science "Kaggle" competitions. Scikit-learn makes it possible to predict future outcomes given a training data, and thus to optimize company decisions. Almost 1 million euros will be invested to improve the algorithmic core of scikit-learn through the Wendelin project thanks to the Inria, ENS and Institut Mines Télécom teams. In particular, scikit-learn will be extended in order to ease online prediction and to include recent stochastic gradient algorithms.

NEO is the native NoSQL base of the Python language. It was initially designed by Nexedi and is currently used and embedded in the main software of company information systems. More than one million euros will be invested into NEO, so that scikit-learn can process within 10 years (out-of-core) data of 1 exabyte size.

Paris13 university and the Mines Télécom institute will extend the SlapOS distributed mesh cloud to deploy Wendelin in *Big Data as a Service (BDaaS)* mode, to achieve the interoperability between the Grid5000 and Teralab infrastructures and to extend the cloud toward smart sensor systems.

The combination of scikit-learn, NEO and SlapOS will improve the predictive maintenance of industrial plants with two major use cases: connected windmills (GDF SUEZ, Woelfel) and customer satisfaction in car sale systems (MMC Rus). In both cases it is about non-personal, yet profitable big data. The Wendelin project actually demonstrates that Big data can improve infrastructure and everyday-life equipment without intrusive data collection. For more information, please see www.wendelin.io.

The project partners are:

- Nexedi (leader)
- GDF SUEZ
- Abilian
- 2ndQuadrant
- Institut Mines Télécom
- Inria
- Université Paris 13

9. Partnerships and Cooperations

9.1. Regional Initiatives

9.1.1. *iConnectom project*

Participants: Bertrand Thirion [Correspondant], Gaël Varoquaux, Elvis Dohmatob.

This is a Digiteo project (2014-2017).

Mapping brain functional connectivity from functional Magnetic Resonance Imaging (MRI) data has become a very active field of research. However, analysis tools are limited and many important tasks, such as the empirical definition of brain networks, remain difficult due to the lack of a good framework for the statistical modeling of these networks. We propose to develop population models of anatomical and functional connectivity data to improve the alignment of subjects brain structures of interest while inferring an average template of these structures. Based on this essential contribution, we will design new statistical inference procedures to compare the functional connections between conditions or populations and improve the sensitivity of connectivity analysis performed on noisy data. Finally, we will test and validate the methods on multiple datasets and distribute them to the brain imaging community.

9.1.2. *SUBSAMPLE Digiteo chair*

Participants: Bertrand Thirion [Correspondant], Gaël Varoquaux, Alexandre Abraham.

Parietal is associated with this Digiteo Chair by Dimitris Samaras, in which we will address the probabilistic structure learning of salient brain states (PhD of Alexandre Abraham, 2012-2015).

Cognitive tasks systematically involve several brain regions, and exploratory approaches are generally necessary given the lack of knowledge of the complex mechanisms that are observed. The goal of the project is to understand the neurobiological mechanisms that are involved in complex neuro-psychological disorders. A crucial and poorly understood component in this regard refers to the interaction patterns between different regions in the brain. In this project we will develop machine learning methods to capture and study complex functional network characteristics. We hypothesize that these characteristics not only offer insights into brain function but also can be used as concise features that can be used instead of the full dataset for tasks like classification of healthy versus diseased populations or for clustering subjects that might exhibit similarities in brain function. In general, the amount of correlation between distant brain regions may be a more reliable feature than the region-based signals to discriminate between two populations e.g. in schizophrenia. For such exploratory methods to be successful, close interaction with neuroscientists is necessary, as the salience of the features depends on the population and the observed effects of psychopathology. For this aim we propose to develop a number of important methodological advances in the context of prediction of treatment outcomes for drug addicted populations, e.g. for relapse prediction.

9.1.3. Medilearn/braincodes Inria-MSR project

Participants: Bertrand Thirion [Correspondant], Gaël Varoquaux, Andrés Hoyos Idrobo.

Neuroimaging is accumulating large functional MRI datasets that display –among artefacts and noise– brain activation patterns giving access to a meaningful representation of brain spatial organization. This ongoing accumulation is intensified via new large-scale international initiatives such as the *Human Connectome Project* (www.humanconnectomeproject.org), but also to existing open repositories of functional neuroimaging datasets (<https://openfmri.org/>) or <http://www.fmridc.org/>. These datasets represent a very significant resource for the community, but require new analytic approaches in order to be fully exploited. The MediLearn/BrainCodes project strives to provide a synthetic picture of the brain substrate of human cognition and its pathologies. In practice, this can be achieved by learning from large-scale datasets a brain atlas that summarizes adequately these functional activation maps drawing from a large number of protocols and subjects. Once learned, such an atlas is extremely useful to understand the large-scale functional organization of the brain: it is a tool for understanding *brain segregation*, the different encoding of many cognitive parameters into different brain regions, as well as *brain integration*, *i.e.* how remote brain regions co-activate across subjects and experiments.

9.2. National Initiatives

9.2.1. ANR

9.2.1.1. BrainPedia project

Participants: Bertrand Thirion [Correspondant], Gaël Varoquaux, Yannick Schwartz.

BrainPedia is an ANR JCJC (2011-2015) which addresses the following question: Neuroimaging produces huge amounts of complex data that are used to better understand the relations between brain structure and function. While the acquisition and analysis of this data is getting standardized in some aspects, the neuroimaging community is still largely missing appropriate tools to store and organize the knowledge related to the data. Taking advantage of common coordinate systems to represent the results of group studies, coordinate-based meta-analysis approaches associated with repositories of neuroimaging publications provide a crude solution to this problem, that does not yield reliable outputs and loses most of the data-related information. In this project, we propose to tackle the problem in a statistically rigorous framework, thus providing usable information to drive neuroscientific knowledge and questions.

9.2.1.2. NiConnect project

Participants: Bertrand Thirion, Gaël Varoquaux [Correspondant], Alexandre Abraham.

- **Context:** The NiConnect project (2012-2016) arises from an increasing need of medical imaging tools to diagnose efficiently brain pathologies, such as neuro-degenerative and psychiatric diseases or lesions related to stroke. Brain imaging provides a non-invasive and widespread probe of various features of brain organization, that are then used to make an accurate diagnosis, assess brain rehabilitation, or make a prognostic on the chance of recovery of a patient. Among different measures extracted from brain imaging, functional connectivity is particularly attractive, as it readily probes the integrity of brain networks, considered as providing the most complete view on brain functional organization.
- **Challenges:** To turn methods research into popular tool widely usable by non specialists, the NiConnect project puts specific emphasis on producing high-quality open-source software. NiConnect addresses the many data analysis tasks that extract relevant information from resting-state fMRI datasets. Specifically, the scientific difficulties are *i)* conducting proper validation of the models and tools, and *ii)* providing statistically controlled information to neuroscientists or medical doctors. More importantly, these procedures should be robust enough to perform analysis on limited quality data, as acquiring data on diseased populations is challenging and artifacts can hardly be controlled in clinical settings.

- **Outcome of the project:** In the scope of computer science and statistics, NiConnect pushes forward algorithms and statistical models for brain functional connectivity. In particular, we are investigating structured and multi-task graphical models to learn high-dimensional multi-subject brain connectivity models, as well as spatially-informed sparse decompositions for segmenting structures from brain imaging. With regards to neuroimaging methods development, NiConnect provides systematic comparisons and evaluations of connectivity biomarkers and a software library embedding best-performing state-of-the-art approaches. Finally, with regards to medical applications, the NiConnect project also plays a support role in on going medical studies and clinical trials on neurodegenerative diseases.
- **Consortium**
 - Parietal Inria research team: applied mathematics and computer science to model the brain from MRI
 - LIF INSERM research team: medical image data analysis and modeling for clinical applications
 - CATI center: medical image processing center for large scale brain imaging studies
 - Henri-Mondor hospital neurosurgery and neuroradiology: clinical teams conducting research on treatments for neurodegenerative diseases, in particular Huntington and Parkinson diseases
 - Logilab: consulting in scientific computing

9.3. European Initiatives

9.3.1. FP7 & H2020 Projects

9.3.1.1. HBP

Title: The Human Brain Project

Programm: FP7

Duration: October 2013 - April 2016

Coordinator: EPFL

Partners: See <https://www.humanbrainproject.eu/fr/discover/the-community/partners>

Inria contact: Olivier Faugeras

Understanding the human brain is one of the greatest challenges facing 21st century science. If we can rise to the challenge, we can gain profound insights into what makes us human, develop new treatments for brain diseases and build revolutionary new computing technologies. Today, for the first time, modern ICT has brought these goals within sight. The goal of the Human Brain Project, part of the FET Flagship Programme, is to translate this vision into reality, using ICT as a catalyst for a global collaborative effort to understand the human brain and its diseases and ultimately to emulate its computational capabilities. The Human Brain Project will last ten years and will consist of a ramp-up phase (from month 1 to month 36) and subsequent operational phases.

This Grant Agreement covers the ramp-up phase. During this phase the strategic goals of the project will be to design, develop and deploy the first versions of six ICT platforms dedicated to Neuroinformatics, Brain Simulation, High Performance Computing, Medical Informatics, Neuromorphic Computing and Neurorobotics, and create a user community of research groups from within and outside the HBP, set up a European Institute for Theoretical Neuroscience, complete a set of pilot projects providing a first demonstration of the scientific value of the platforms and the Institute, develop the scientific and technological capabilities required by future versions of the platforms, implement a policy of Responsible Innovation, and a programme of transdisciplinary education, and develop a framework for collaboration that links the partners under strong scientific leadership and professional project management, providing a coherent European approach and ensuring effective

alignment of regional, national and European research and programmes. The project work plan is organized in the form of thirteen subprojects, each dedicated to a specific area of activity. A significant part of the budget will be used for competitive calls to complement the collective skills of the Consortium with additional expertise.

9.4. International Initiatives

9.4.1. Inria International Labs

Inria@SiliconValley

Associate Team involved in the International Lab:

9.4.1.1. *MetaMRI*

Title: Machine learning for meta-analysis of functional neuroimaging data

International Partner (Institution - Laboratory - Researcher):

Stanford (United States) - Department of Psychology - Russ Poldrack

Start year: 2015

See also: <https://team.inria.fr/metamri>

Neuroimaging produces huge amounts of complex data that are used to better understand the relations between brain structure and function. Observing that the neuroimaging community is still largely missing appropriate tools to store and organize the knowledge related to the data, Parietal team and Poldrack's lab, have decided to join forces to set up a framework for functional brain image meta-analysis, i.e. a framework in which several datasets can be jointly analyzed in order to accumulate information on the functional specialization of brain regions. MetaMRI will build upon Poldrack's lab expertise in handling, sharing and analyzing multi-protocol data and Parietal's recent developments of machine learning libraries to develop a new generation of meta-analytic tools.

9.5. International Research Visitors

9.5.1. *Visits of International Scientists*

Danilo Bzdok (Forschungszentrum Jülich and University of Aachen) visited Parietal several months in 2015 (January- December), to develop collaborations on the use of machine learning techniques to model behavioral variables and find data-driven characterization of brain diseases.

9.5.1.1. *Internships*

- Jacob Schreiber (Univ. Washington), went for an internship (June-September) to develop fas methods for three-based regression with Scikit-Learn.
- Giorgio Patrini (Australian National University) developed some tools for online learning during his internship (July-November) in Scikit-Learn.
- Daniel Alcala Lopez (Univ. Aachen) joined us for a three month internship to discover the use of machine learning for neuroimaging in psychiatry (June-September 2015).

10. Dissemination

10.1. Promoting Scientific Activities

10.1.1. *Scientific events organisation*

10.1.1.1. *Member of the organizing committees*

- **Bertrand Thirion**: STAMLINS workshop (ICML 2015)
- **Gaël Varoquaux**: MLOSS workshop (ICML 2015)

10.1.2. Scientific events selection

10.1.2.1. Member of the conference program committees

- **Philippe Ciuciu:** Member of the programm committe for the GRETSI 2015 conference located in Lyon.
- **Philippe Ciuciu:** Organizer of the special session dedicated to Signal processing for Neurosciences
- **Bertrand Thirion:** Organization for Human Brain Mapping.

10.1.2.2. Reviewer

- **Bertrand Thirion:** IPMI, MICCAI, NIPS, ISBI, PRNI
- **Gaël Varoquaux:** IPMI, MICCAI, NIPS, ICASSP, Scipy
- **Philippe Ciuciu:** IEEE ICASSP, IEEE ISBI, IEEE ICIP, PRNI.

10.1.3. Journal

10.1.3.1. Member of the editorial boards

- **Bertrand Thirion:** Medical Image Analysis, Frontiers in brain imaging
- **Gaël Varoquaux:** Frontiers in NeuroInformatics, Frontiers in brain imaging methods, NeuroImage

10.1.3.2. Reviewer - Reviewing activities

- **Bertrand Thirion:** Human Brian Mapping, IEEE TMI, MedIA, NeuroImage, PNAS
- **Gaël Varoquaux:** NeuroImage, JSTSP, PNAS
- **Philippe Ciuciu:** IEEE Signal Processing letters, IEEE Trans on Medical Imaging, IEEE Trans on Selected Topics in Signal Processing, NeuroImage, Human Brain Mapp, The Journal of Neuroscience, Frontiers in Neuroscience - Brain Imaging Section, The Journal of Neuroscience Methods. Reviewer for the following international conferences in 2015: The first three are commitments due to my involvement to the IEEE BioImaging Signal Processing committee since 2013. Reviewer for the following national conference: GRETSI

10.1.4. Invited talks

10.1.4.1. Bertrand Thirion

- Seminar QBIN, Montreal (Jan 30th)
- Invited talk MILM workshop, ICML, Lille (July 11th)
- Seminar Lear, Inria GRA (Sept 3rd)
- Seminar Univ. Lièges (Sept 23rd)
- Seminar INT, Marseille (Sept 24th)
- Invited talk, Big Data Convention, Saclay (Nov 30th)
- Invited Talk, Seminar 'Horizon Math', FSMP (Dec 15th)

10.1.4.2. Gaël Varoquaux

- Seminar Max Planck Institute Tuebingen (Oct 8th)
- Seminar fMRIB Oxford (Sept 24th)
- Invited talk MLOSS workshop, ICML, Lille (July 7th)
- Seminar OECD Paris, (July 1st)
- Invited talk ODSC (Boston May 30th)
- Keynote: workshop on machine learning at Society for Affective Neuroscience (Oakland, April 9th)
- Invited talk IRT Système X, (Palaiseau, May 19th)
- Keynote Pycon Russia (Yekaterinburg, Sept 18th)
- Keynote Pydata Paris (Paris, April 4th)

- Invited talk, Feindel Brain Imaging Lecture (McGill, Montreal): <http://www.mcgill.ca/bic/channels/event/feindel-brain-imaging-lecture-methods-resting-state-connectome-biomarkers-dr-gael-varoquaux-256587>
- Invited speaker BioImage Informatics GDR, Paris <http://gdr-miv.fr/en/events/bioimageinformatics2015/>
- Invited speaker, workshop LHCb, Paris <https://indico.cern.ch/event/337568/session/1/contribution/32>

10.1.4.3. Philippe Ciuciu

- European Institute of Theoretical Neuroscience: March, 13 2015: Convergence to Asymptotic Multifractal Dynamics Predicts Learning
- IXXI Rhône Alpes, Grenoble Dec, 8 2015: Complexity Measures in Brain Activity: The functional Role of Scale-Free Brain Dynamics

10.1.4.4. Loïc Estève

- Scipy 2015 (July 9th), <http://scipy2015.scipy.org/ehome/115969/297898/>
- Open Software Initiative (October 26th), <https://indico.lal.in2p3.fr/event/2987/other-view?view=standard>

10.1.5. Leadership within the scientific community

- Gaël Varoquaux: Chair of the steering committee, IEEE PRNI
- Philippe Ciuciu: Member of the newly founded Biomedical Image & Signal Analytics Special Area Teams in the EURASIP society. Chairman: Dimitri Van De Ville.
- Bertrand Thirion: member of the *Committee on Best Practices in Data Analysis and Sharing* for the OHBM community.

10.1.6. Scientific expertise

Gaël Varoquaux:

- Member of the working group on big data for the Paris-Saclay university
- Member of the working group on smart data in the "TIC & Santé" commission

Philippe Ciuciu:

- Expert for funding agencies: 1st round for ANR, annual call of FWO (Flanders universities), Fond National Suisse de la Recherche, Wellcome Trust (UK), NSERC (Canada).
- Participation to the CEA scientific council on Nov/Dec 2015 on High Performance Computing.

10.1.7. Research administration

Bertrand Thirion:

- Comex Labex Digicosme
- Comex Lidex PIM
- Comex department STIC Paris-Saclay University
- DSA Saclay.

Gaël Varoquaux:

- Member of "Comité de suivi doctoral", Inria Saclay
- Member of "Comité cluster", Inria Saclay

10.2. Teaching - Supervision - Juries

10.2.1. Teaching

Master : Bertrand Thirion, Brain Computer interface and Functional Neuroimaging, 12 heures équivalent TD, niveau M2, ENS Cachan

Master : Bertrand Thirion, Analysis of functional connectivity, 3 heures équivalent TD, niveau M2, Université Paris 5

Master : Gaël Varoquaux, Advanced Neuroimaging Data Analysis, 7.5 heures équivalent TD, niveau M2, Télécom ParisTech, Paris

Master : Gaël Varoquaux, Python for data science, 3 heures équivalent TD, niveau M2, ENSAE, Paris

Master : Michael Eickenberg, Loïc Estève, Practical sessions on scikit-learn, 6 hours, M2, Paris-Saclay University, France

Doctorat : Gaël Varoquaux, nilearn: machine learning for neuroimaging, 12 heures équivalent TD, Max Planck Institute Leipzig, Allemagne

Doctorat : Gaël Varoquaux, nilearn: machine learning for neuroimaging, 12 heures équivalent TD, Stanford, Etats Unis

Doctorat : Gaël Varoquaux, pattern recognition for neuroimaging, 1 heures équivalent TD, OHBM, Honolulu, Etats Unis

Doctorat : Gaël Varoquaux, statistics in Python, 3 heures équivalent TD, Euroscipy, Cambridge, Angleterre

Doctorat : Loïc Estève (helper), Software Carpentry Bootcamp, 12 hours, European Institute for Theoretical Neuroscience, France <https://btel.github.io/2015-11-19-eitn/>

E-learning

Pedagogical resources : Gaël Varoquaux, Scipy lecture notes, ebook, niveau master ou plus, <http://www.scipy-lectures.org>

10.2.2. Supervision

PhD : Nicolas Chauffert, "Physically plausible k-space trajectories for compressed sensing in MRI", Université de Paris-Sud, ED EOBÉ, 28/9/2015, Philippe Ciuciu (Directeur) & Pierre Weiss

PhD : Yannick Schwartz, "Large-scale functional MRI analysis to accumulate knowledge on brain functions" Université de Paris-Sud, ED STIC, 21/4/2015, Bertrand Thirion (Directeur) & Gaël Varoquaux

PhD : Fabian Pedregosa, "Feature extraction and supervised learning on fMRI: from practice to theory" Université de Paris-Sud, ED STIC, 21/4/2015, Bertrand Thirion (Directeur) & Alexandre Gramfort

PhD : Michael Eickenberg," Université de Paris-Sud, ED STIC, 21/4/2015, Bertrand Thirion (Directeur) & Alexandre Gramfort

PhD : Alexandre Abraham," " Université de Paris-Sud, ED STIC, 21/4/2015, Bertrand Thirion (Directeur) & Gaël Varoquaux

10.2.3. Juries

Bertrand Thirion:

- Rapporteur de la thèse de Raphael Liégeois (Liège University, Belgium)
- Rapporteur de la thèse de Loïc Le Folgoc (Université Nice Sophia-Antipolis)
- Directeur du jury de thèse de Sylvain Takerkart (Université Aix-Marseille)

Gaël Varoquaux:

- Rapporteur de la thèse de Siina Pamila (Aalto University, Finlande)
- Examineur de la thèse de Yoann Isaac (Université Paris Sud, directrice de thèse Michèle Sébag)

10.3. Popularization

Gaël Varoquaux: La tête au carré, on Junarury 13th, 2015: <http://www.franceinter.fr/emission-la-tete-au-carre-big-data-quand-les-donnees-servent-a-predire>

Stand à la Fete de la science CRI Saclay, 9 octobre (Alexandre Abraham, Arthur Mensch, Bertrand Thirion).

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