
Activity Report 2013

# 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 Medecine**

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## Project-Team PARIETAL

**Keywords:** Medical Images, Image Processing, Biological Images, Brain Computer Interface, Machine Learning

*Creation of the Project-Team:* 2009 July 01.

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# 2. Overall Objectives

## 2.1. Highlights of the Year

- The **Therapixel** start-up was created by Pierre Fillard (effective on July 1st, 2013) http://www.therapixel.com/company/. Therapixel is designing a device to look at and interact with images without any contact to a screen or a keyboard. This technical solution is very handy for surgeons who have to avoid any contact while in the operating room, and yet need pre-operative images. The technologies developed at Therapixel are based on those of the medInria software. Therapixel got an OSEO 2013 grant.
- The **Human Brain Project** European flagship project has been accepted in 2013 for a ten years duration (see section 7.3.1). Parietal is part of it and took part to the kick-off in October 2013.

# 3. Research Program

## 3.1. Human neuroimaging data and its 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 2mm, in a set of directions (30 to 60 typically). Local anisotropy, observed in white matter, yields a local model of fiber orientation that can be integrated nito 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 2 to 3mm, and a temporal resolution of 2-3s. This yields a spatially resolved image of brain functional networks that can be modulated either by specific cognitive tasks or appear as networks of correlated activity.
- 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.

## 3.2. 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 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 [77].

## 3.3. 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 if 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 correlations and long-distance correlation properties (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.

# 4. Application Domains

## 4.1. 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 an important 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 piecewise 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 $\beta$ 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 $\mathbf{Y}_1, .., \mathbf{Y}_{n_f}$ of $Y$ independently, yielding $n_f$ problems to be solved in parallel:

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

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

$$\widehat{\beta}_i = \text{argmin}_{\beta_i} \|\mathbf{Y}_i - \mathbf{X}\beta_i\|^2 + \Psi(\beta_i), \tag{1}$$

where $\Psi$ is an adequate penalization used to regularize the solution:

$$\Psi(\beta; \lambda_1, \lambda_2, \eta_1, \eta_2) = \lambda_1 \|\beta\|_1 + \lambda_2 \|\beta\|_2^2 + \eta_1 \|\nabla\beta\|_1 + \eta_2 \|\nabla\beta\|_2^2 \tag{2}$$

with $\lambda_1,\ \lambda_2,\ \eta_1,\ \eta_2 \geq 0$. 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 $\beta$ 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.
- Smooth lasso is obtained with ($\eta_2 > 0$ and $\lambda_1 > 0$ only), and yields smooth, compactly supported spatial basis functions.

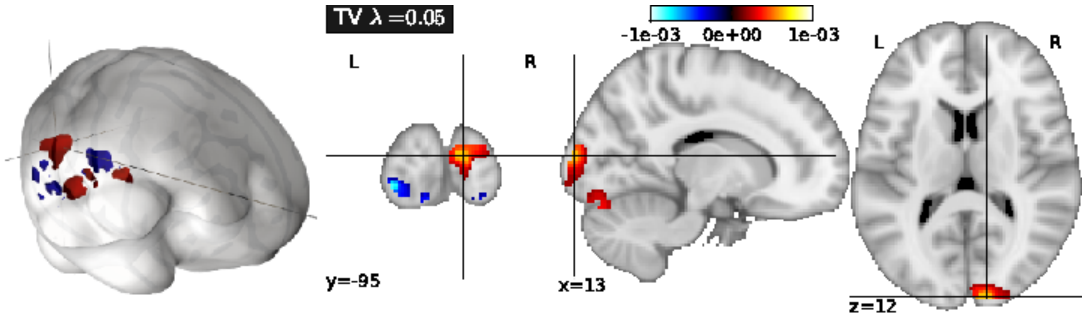


*Figure 1. Example of the regularization of a brain map with total variation in an inverse problem. The problems here consists in predicting the spatial scale of an object presented as a stimulus, given functional neuroimaging data acquired during the observation of an image. Learning and test are performed 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 $i \in \{1, .., n_f\}$. This can be computed through cross-validation, by *learning* $\widehat{\beta}_i$ on some part of the dataset, and then estimating $(Y_i - X\widehat{\beta}_i)$ 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 $\beta$ 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 $\beta_i$ and thus, improve the prediction of $\mathbf{Y}_i$. Yet this does not impose constraints on the non-zero parameters of the parameters $\beta_i$.

$$\mathbf{Y} = \mathbf{X}\beta + \epsilon, \tag{3}$$

then

$$\widehat{\beta} = \text{argmin}_{\beta=(\beta_i), i=1..n_f} \sum_{i=1}^{n_f} \|\mathbf{Y_i} - \mathbf{X}\beta_\mathbf{i}\|^2 + \lambda \sum_{j=1}^{n_{voxels}} \sqrt{\sum_{i=1}^{n_f} \beta^2_{\mathbf{i,j}}} \tag{4}$$

## 4.2. 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

$$\mathbf{X} = \mathbf{AD} + \epsilon, \tag{5}$$

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:

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

where $(\mathbf{A}_i),\ i \in \{1..n_f\}$ represents the columns of $\mathbf{A}$. $\Psi$ 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).

## 4.3. 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. Our current work on post-stroke patients (see e.g. Fig. 2) suggests indeed that modeling may prove essential to perform sensitive inference.

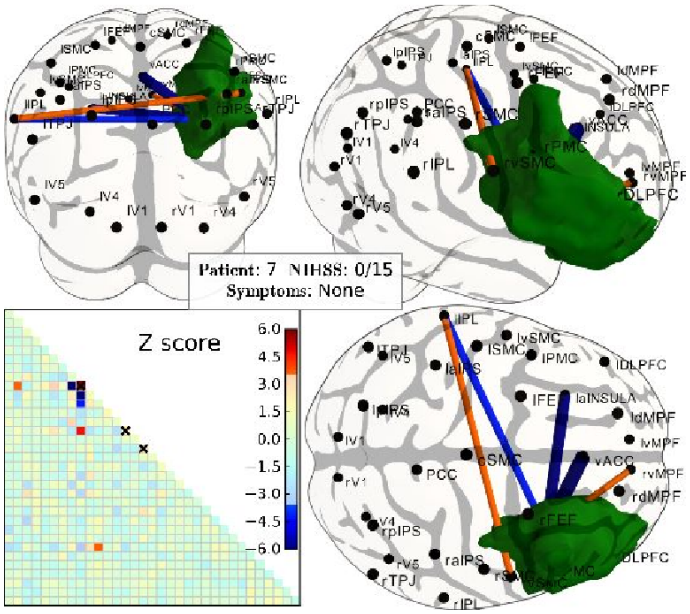


*Figure 2. Example of functional connectivity analysis: The correlation matrix describing brain functional connectivity in a post-stroke patient (lesion outlined in green) is compared to a group of control subjects. Some edges of the graphical model show a significant difference, but the statistical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

# 5. Software and Platforms

## 5.1. Scikit learn

**Participants:** Bertrand Thirion, Gaël Varoquaux, Olivier Grisel [correspondant], Jaques Grobler, Alexandre Gramfort, Fabian Pedregosa, Virgile Fritsch.

Scikit-learn is an open-source machine learning toolkit written in Python/C that provides generic tools to learn information for the classification of various kinds of data, such as images or texts. It is tightly associated to the scientific Python software suite (numpy/scipy) for which it aims at providing a complementary toolkit for machine learning (classification, clustering, dimension reduction, regression). There is an important focus on code quality (API consistency, code readability, tests, documentation and examples), and on efficiency, as the scikit-learn compares favorably to state-of-the-art modules developed in R in terms of computation time or memory requirements. Scikit-learn is currently developed by more than 60 contributors, but the core developer team has been with the Parietal Inria team at Saclay-Île-de-France since January 2010. The scikit-learn has recently become the reference machine learning library in Python.

- Version: 0.14
- Programming language: Python, C/Cython

## 5.2. Nilearn

**Participants:** Bertrand Thirion, Gaël Varoquaux [correspondant], Philippe Gervais, Jaques Grobler, Alexandre Gramfort, Fabian Pedregosa, Alexandre Abraham, Michael Eickenberg.

NiLearn is the neuroimaging library that adapts the concepts and tools of the 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. NiLearn is maintained both through the help of Inria: (a developer funded by Saclay CRI in 2012-2013, a 2013-2014 ADT, and through the NiConnect project (P. Gervais).

- Version: 0.1
- Programming language: Python

## 5.3. Mayavi

**Participant:** Gaël Varoquaux [Correspondant].

Mayavi is the most used scientific 3D visualization Python software (http://mayavi.sourceforge.net/). It has been developed by Prabhu Ramachandran (IIT Bombay) and Gaël Varoquaux (PARIETAL, Inria Saclay). 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 (http://pyrx.scripps.edu) and brain connectivity analysis tools (connectomeViewer).

See also the web page http://mayavi.sourceforge.net/ and the following paper http://hal.inria.fr/inria-00528985/en.

- Version: 3.4.0

## 5.4. Nipy

**Participants:** Bertrand Thirion [correspondant], Virgile Fritsch, Elvis Dohmatob, Gaël Varoquaux.

Nipy is an open-source Python library for neuroimaging data analysis, developed mainly at Berkeley, Stanford, MIT and Neurospin. It is open to any contributors and aims at developing code and tools sharing. Some parts of the library are completely developed by Parietal and LNAO (CEA, DSV, Neurospin). It is devoted to algorithmic solutions for various issues in neuroimaging data analysis. All the nipy project is freely available, under BSD license. It is available in NeuroDebian.

See also the web page http://nipy.org.

- Version: 0.3

## 5.5. MedInria

**Participants:** Pierre Fillard [correspondant], Sergio Medina, Viviana Siless.

MedInria is a free collection of softwares developed within the ASCLEPIOS, ATHENA and VISAGES research projects. It aims at providing to clinicians state-of-the-art algorithms dedicated to medical image processing and visualization. Efforts have been made to simplify the user interface, while keeping high-level algorithms. MedInria is available for Microsoft windows XP/Vista, Linux Fedora Core, MacOSX, and is fully multi-threaded.
See also the web page http://med.inria.fr/.

- Version: 2.0

## 5.6. PyHRF

**Participants:** Philippe Ciuciu [correspondant], Solveig Badillo, Aina Frau Pascual.

PyHRF is a set of tools for within-subject fMRI data analysis, focused on the characterization of the hemodynamics. Within the chain of fMRI data processing, these tools provide alternatives to the classical within-subject GLM estimation step. The inputs are preprocessed within-subject data and the outputs are statistical maps and/or fitted HRFs. The package is mainly written in Python and provides the implementation of the two following methods:

- The joint-detection estimation (JDE) approach, that divides the brain into functionally homogeneous regions and provides one HRF estimate per region as well as response levels specific to each voxel and each experimental condition. This method embeds a temporal regularization on the estimated HRFs and an adaptive spatial regularization on the response levels.
- The Regularized Finite Impulse Response (RFIR) approach, that provides HRF estimates for each voxel and experimental conditions. This method embeds a temporal regularization on the HRF shapes, but proceeds independently across voxels (no spatial model).

The development of PyHRF is now funded by an Inria ADT, in collaboration with MISTIS.

- Version: 0.1
- Keywords: Hemodynamic response function; estimation; detection; fMRI
- License: BSD 4
- Multiplatform: Windows - Linux - MacOSX
- Programming language: Python

# 6. New Results

## 6.1. Deformable Template estimation for joint anatomical and functional brain images

**Participants:** Bertrand Thirion [Correspondant], Hao Xu, Stéphanie Allassonnière.

Traditional analyses of Functional Magnetic Resonance Imaging (fMRI) use little anatomical information. The registration of the images to a template is based on the individual anatomy and ignores functional information; subsequently detected activations are not confined to gray matter (GM). In this work, we propose a statistical model to estimate a probabilistic atlas from functional and T1 MRIs that summarizes both anatomical and functional information and the geometric variability of the population. Registration and Segmentation are performed jointly along the atlas estimation and the functional activity is constrained to the GM, increasing the accuracy of the atlas.

More details can be found in [69].

## 6.2. Randomized parcellation-based inference

**Participants:** Gaël Varoquaux, Bertrand Thirion, Benoit Da Mota, Virgile Fritsch.

Neuroimaging group analyses are used to relate inter-subject signal differences observed in brain imaging with behavioral or genetic variables and to assess risks factors of brain diseases. The lack of stability and of sensitivity of current voxel-based analysis schemes may however lead to non-reproducible results. We introduce a new approach to overcome the limitations of standard methods, in which active voxels are detected according to a consensus on several random parcellations of the brain images, while a permutation test controls the false positive risk (see Fig. 3). Both on synthetic and real data, this approach shows higher sensitivity, better accuracy and higher reproducibility than state-of-the-art methods. In a neuroimaging-genetic application, we find that it succeeds in detecting a significant association between a genetic variant next to the COMT gene and the BOLD signal in the left thalamus for a functional Magnetic Resonance Imaging contrast associated with incorrect responses of the subjects from a Stop Signal Task protocol.

More details can be found in [55].

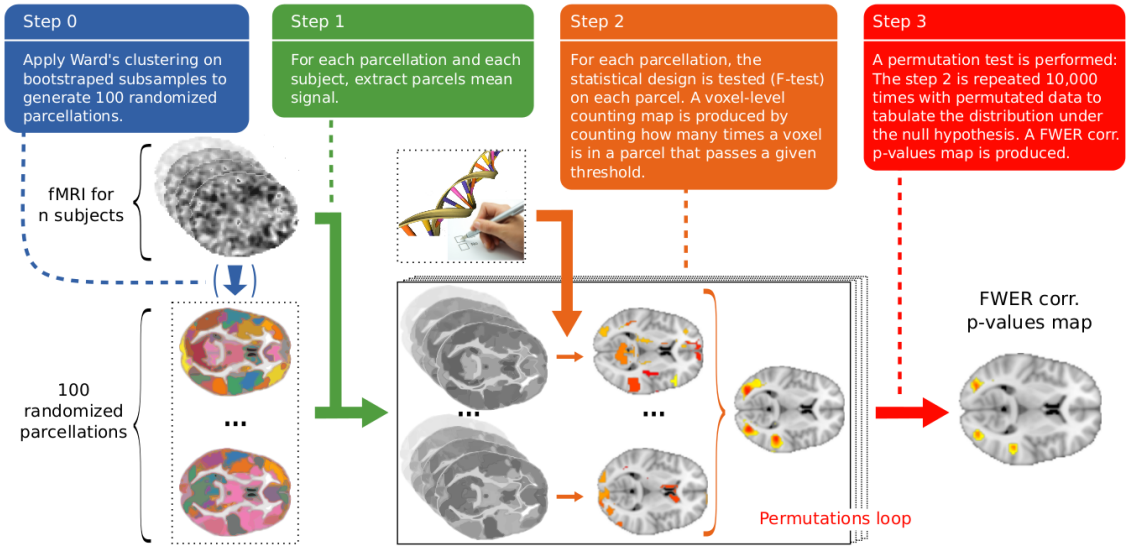


*Figure 3. Overview of the randomized parcellation based inference framework on an example with few parcels. The variability of the parcels definition is used to obtain voxel-level statistics.*

## 6.3. Group-level impacts of within- and between-subject hemodynamic variability in fMRI

**Participants:** Gaël Varoquaux, Solveig Badillo, Philippe Ciuciu [Correspondant].

Inter-subject fMRI analyses have specific issues regarding the reliability of the results concerning both the detection of brain activation patterns and the estimation of the underlying dynamics. Among these issues lies the variability of the hemodynamic response function (HRF), that is usually accounted for using functional basis sets in the general linear model context. Here, we use the joint detection-estimation approach (JDE) [76], [78], which combines regional nonparametric HRF inference with spatially adaptive regularization of activation clusters to avoid global smoothing of fMRI images (see Fig. 4). We show that the JDE-based inference brings a significant improvement in statistical sensitivity for detecting evoked activity in parietal regions. In contrast, the canonical HRF associated with spatially adaptive regularization is more sensitive in other regions, such as motor cortex. This different regional behavior is shown to reflect a larger discrepancy of HRF with the canonical model. By varying parallel imaging acceleration factor, SNR-specific region-based hemodynamic parameters (activation delay and duration) were extracted from the JDE inference. Complementary analyses highlighted their significant departure from the canonical parameters and the strongest between-subject variability that occurs in the parietal region, irrespective of the SNR value. Finally, statistical evidence that the fluctuation of the HRF shape is responsible for the significant change in activation detection performance is demonstrated using paired t-tests between hemodynamic parameters inferred by GLM and JDE.

More details can be found in [49].

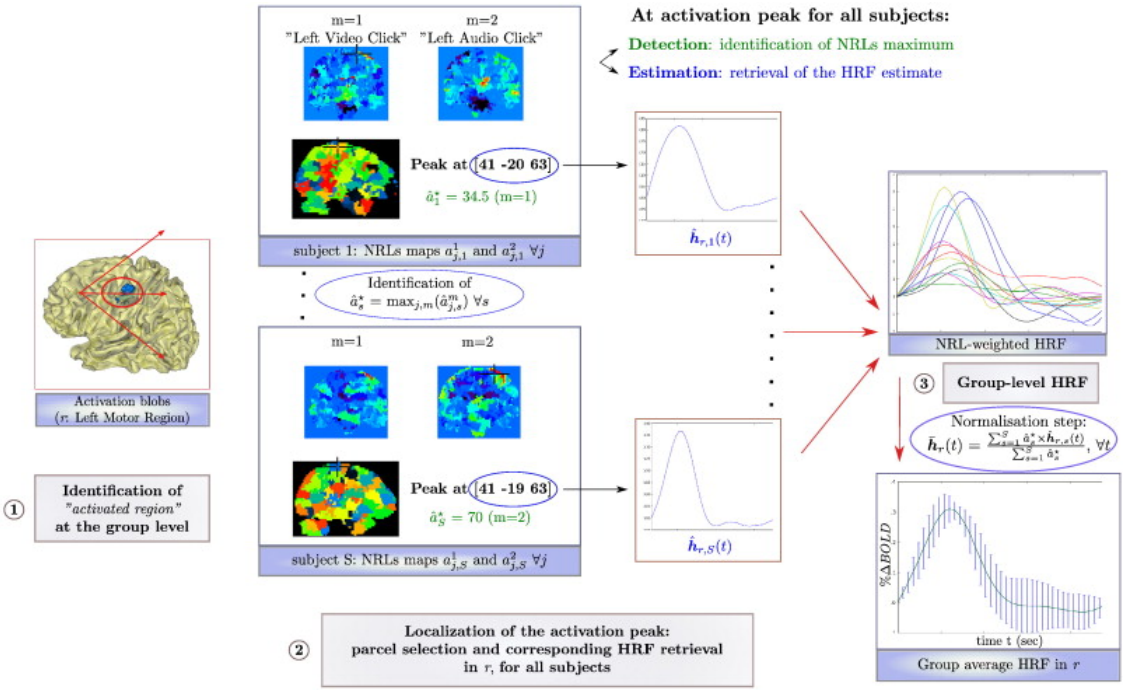


*Figure 4. General sketch summarizing the HRF computation at the subject and group-levels in activated regions r. Left: Position of the activation peak in r (here left motor cortex) given in mm in the Talairach space. Center: Individual weighted HRF time course extraction. Right: Computation of the group average normalized HRF time course with corresponding error bars ($\pm\sigma$).*

## 6.4. Mapping cognitive ontologies to and from the brain

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

Imaging neuroscience links brain activation maps to behavior and cognition via correlational studies. Due to the nature of the individual experiments, based on eliciting neural response from a small number of stimuli, this link is incomplete, and unidirectional from the causal point of view. To come to conclusions on the function implied by the activation of brain regions, it is necessary to combine a wide exploration of the various brain functions and some inversion of the statistical inference. Here we introduce a methodology for accumulating knowledge towards a bidirectional link between observed brain activity and the corresponding function. We rely on a large corpus of imaging studies and a predictive engine. Technically, the challenges are to find commonality between the studies without denaturing the richness of the corpus. The key elements that we contribute are labeling the tasks performed with a cognitive ontology, and modeling the long tail of rare paradigms in the corpus. To our knowledge, our approach is the first demonstration of predicting the cognitive content of completely new brain images. To that end, we propose a method that predicts the experimental paradigms across different studies (see Fig. 5).

More details can be found in [63].

## 6.5. Implications of Inconsistencies between fMRI and dMRI on Multimodal Connectivity Estimation

**Participants:** Gaël Varoquaux [Correspondant], Bertrand Thirion, Bernard Ng.

There is a recent trend towards integrating resting state functional magnetic resonance imaging (RS-fMRI) and diffusion MRI (dMRI) for brain connectivity estimation, as motivated by how estimates from these modalities are presumably two views reflecting the same underlying brain circuitry. In this work, we show on a cohort of 60 subjects that conventional functional connectivity (FC) estimates based on Pearson's correlation and anatomical connectivity (AC) estimates based on fiber counts are actually not that highly correlated for typical RS-fMRI ( 7 min) and dMRI ( 32 gradient directions) data. The FC-AC correlation can be significantly increased by considering sparse partial correlation and modeling fiber endpoint uncertainty, but the resulting FC-AC correlation is still rather low in absolute terms. We further exemplify the inconsistencies between FC and AC estimates by integrating them as priors into activation detection and demonstrating significant differences in their detection sensitivity. Importantly, we illustrate that these inconsistencies can be useful in fMRI-dMRI integration for improving brain connectivity estimation.

More details can be found in [61]. See also [60].

## 6.6. Extracting brain regions from rest fMRI with Total-Variation constrained dictionary learning

**Participants:** Gaël Varoquaux [Correspondant], Alexandre Abraham.

Spontaneous brain activity reveals mechanisms of brain function and dysfunction. Its population-level statistical analysis based on functional images often relies on the de nition of brain regions that must summarize e ciently the covariance structure between the multiple brain networks. In this paper, we extend a network-discovery approach, namely dictionary learning, to readily extract brain regions. To do so, we intro duce a new tool drawing from clustering and linear decomposition methods by carefully crafting a penalty. Our approach automatically extracts regions from rest fMRI that better explain the data and are more stable across subjects than reference decomposition or clustering methods (see FIg. 6).

More details can be found in [47].

## 6.7. Cohort-level brain mapping: learning cognitive atoms to single out specialized regions

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

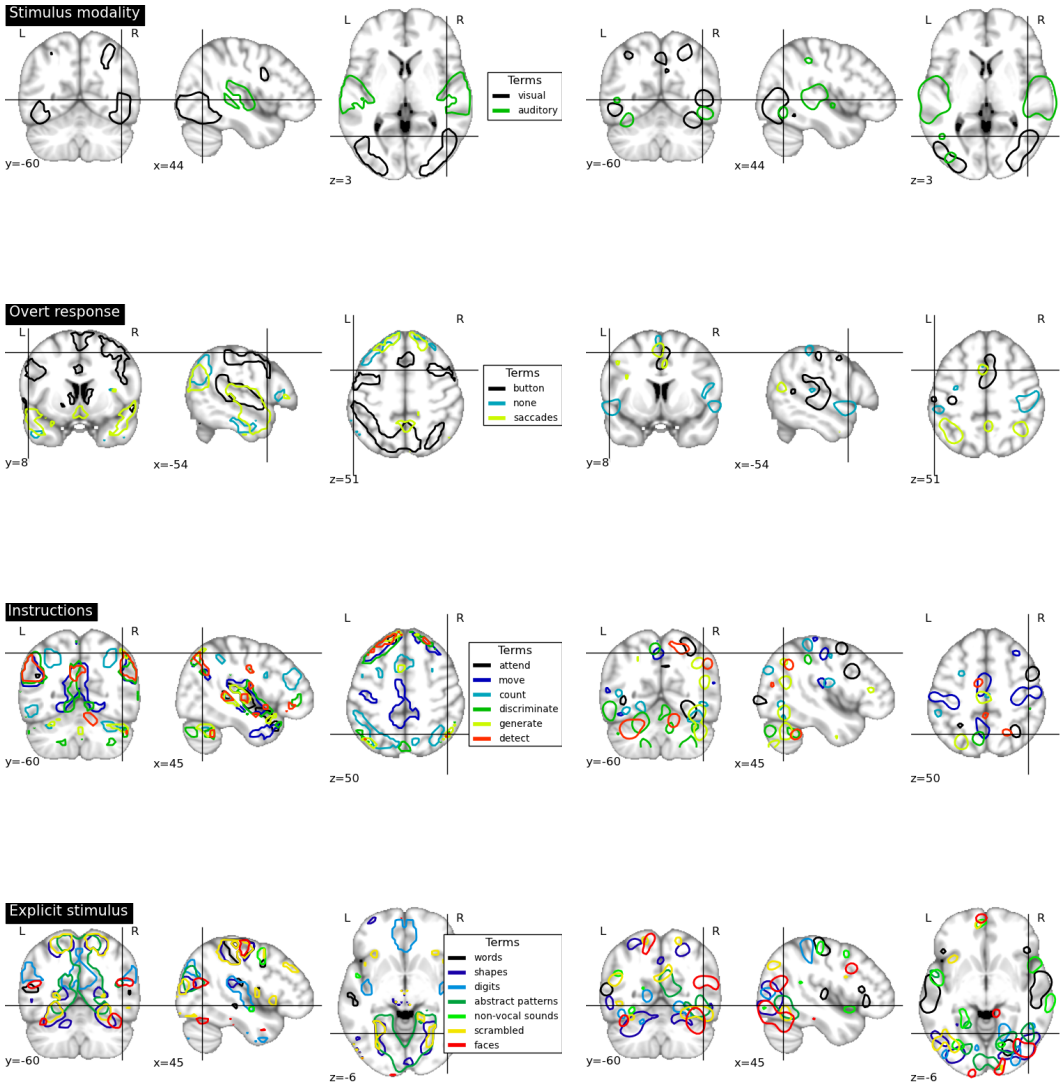


*Figure 5. Maps for the forward inference (left) and the reverse inference (right) for each term category. To minimize clutter, we set the outline so as to encompass 5% of the voxels in the brain on each figure, thus highlighting only the salient features of the maps. In reverse inference, to reduce the visual effect of the parcellation, maps were smoothed using a $\sigma$ of 1.5 voxel.*

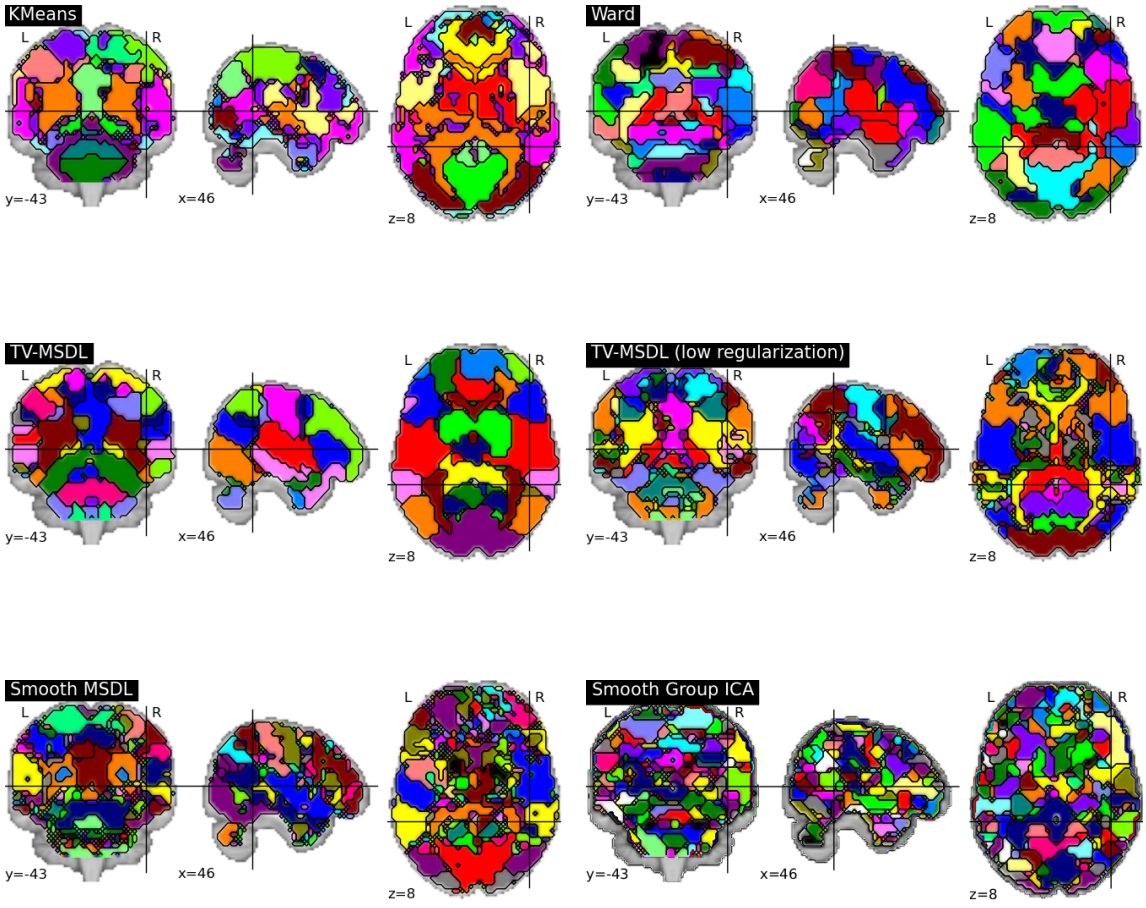


*Figure 6. Regions extracted with the different strategies (colors are random). Please note that a 6mm smoothing has been applied to data before ICA to enhance region extraction.*

Functional Magnetic Resonance Imaging (fMRI) studies map the human brain by testing the response of groups of individuals to carefully-crafted and contrasted tasks in order to delineate specialized brain regions and networks. The number of functional networks extracted is limited by the number of subject-level contrasts and does not grow with the cohort. Here, we introduce a new group-level brain mapping strategy to differentiate many regions reflecting the variety of brain network configurations observed in the population. Based on the principle of functional segregation, our approach singles out functionally-specialized brain regions by learning group-level functional profiles on which the response of brain regions can be represented sparsely. We use a dictionary-learning formulation that can be solved efficiently with on-line algorithms, scaling to arbitrary large datasets. Importantly, we model inter-subject correspondence as structure imposed in the estimated functional profiles, integrating a structure-inducing regularization with no additional computational cost. On a large multi-subject study, our approach extracts a large number of brain networks with meaningful functional profiles (see Fig. 7).

More details can be found in [66].

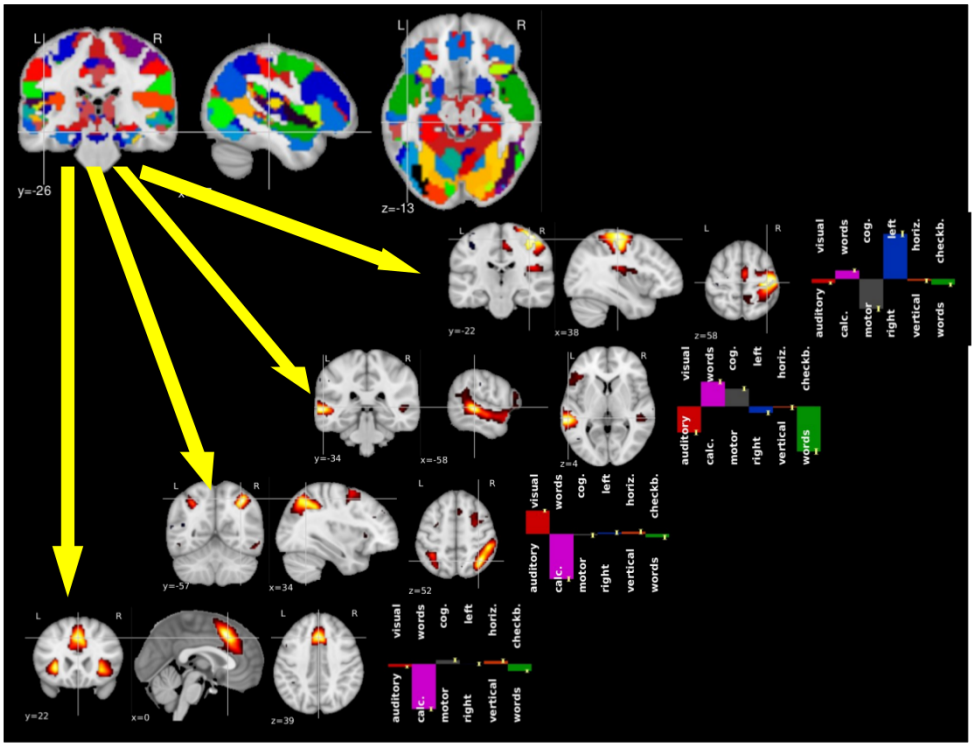


*Figure 7. (Left) A brain functional atlas can be conceptualized as a parcellation of the brain volume into overlapping networks, where each functional network is characterized by a profile of activation for a set of functional contrasts. (Right) Such an atlas can be learned by applying an adapted dictionary learning to a set of images that display the activation observed in different subjects for a (very large) set of cognitive tasks.*

## 6.8. Identifying predictive regions from fMRI with TV-$\ell 1$ prior

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

Decoding, i.e. predicting stimulus related quantities from functional brain images, is a powerful tool to demonstrate differences between brain activity across conditions. However, unlike standard brain mapping, it offers no guaranties on the localization of this information. Here, we consider decoding as a statistical estimation problem and show that injecting a spatial segmentation prior leads to unmatched performance in recovering predictive regions. Specifically, we use $\ell 1$ penalization to set voxels to zero and Total-Variation (TV) penalization to segment regions. Our contribution is two-fold. On the one hand, we show via extensive experiments that, amongst a large selection of decoding and brain-mapping strategies, TV+$\ell 1$ leads to best region recovery (see Fig. 8). On the other hand, we consider implementation issues related to this estimator. To tackle efficiently this joint prediction-segmentation problem we introduce a fast optimization algorithm based on a primal-dual approach. We also tackle automatic setting of hyper-parameters and fast computation of image operation on the irregular masks that arise in brain imaging.

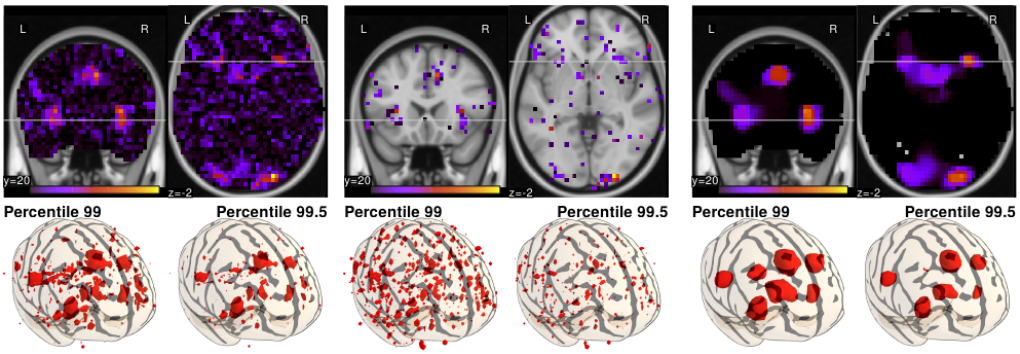


*Figure 8. Results on fMRI data from (from left to right F-test, ElasticNet and TV-$\ell_1$ ). The TV-$\ell_1$ regularized model segments neuroscientificly meaningful predictive regions in agreement with univariate statistics while the ElasticNet yields sparse although very scattered non-zero weights.*

More details can be found in [59].

## 6.9. Second order scattering descriptors predict fMRI activity due to visual textures

**Participants:** Michael Eickenberg, Bertrand Thirion [Correspondant], Alexandre Gramfort.

Second layer scattering descriptors are known to provide good classification performance on natural quasi-stationary processes such as visual textures due to their sensitivity to higher order moments and continuity with respect to small deformations. In a functional Magnetic Resonance Imaging (fMRI) experiment we present visual textures to subjects and evaluate the predictive power of these descriptors with respect to the predictive power of simple contour energy - the first scattering layer. We are able to conclude not only that invariant second layer scattering coefficients better encode voxel activity, but also that well predicted voxels need not necessarily lie in known retinotopic regions (see Fig. 9).

More details can be found in [56].

## 6.10. Bayesian Joint Detection-Estimation of cerebral vasoreactivity from ASL fMRI data

**Participants:** Thomas Vincent, Philippe Ciuciu [Correspondant].

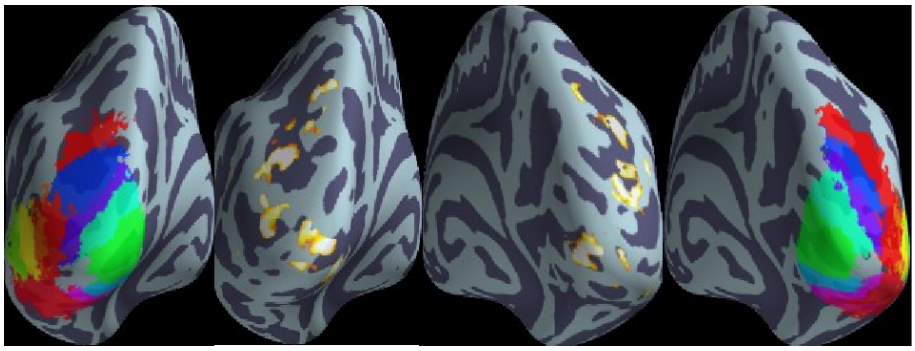

*Figure 9. Some brain regions are better explained by using two scattering layers rather than one (middle). These regions are symetric across hemispheres, and are observed mostly in the dorsal stream of the visual cortex. An atlas of the visual areas (left and right) shows that the mai foci are found in the V1, V2, V3AB and IPS0 regions.*

Although the study of cerebral vasoreactivity using fMRI is mainly conducted through the BOLD fMRI modality, owing to its relatively high signal-to-noise ratio (SNR), ASL fMRI provides a more interpretable measure of cerebral vasoreactivity than BOLD fMRI. Still, ASL suffers from a low SNR and is hampered by a large amount of physiological noise. The current contribution aims at improving the recovery of the vasoreactive component from the ASL signal. To this end, a Bayesian hierarchical model is proposed, enabling the recovery of perfusion levels as well as fitting their dynamics. On a single-subject ASL real data set involving perfusion changes induced by hypercapnia, the approach is compared with a classical GLM-based analysis. A better goodness-of-fit is achieved, especially in the transitions between baseline and hypercapnia periods. Also, perfusion levels are recovered with higher sensitivity and show a better contrast between gray- and white matter.

More details can be found in [68].

# 7. Partnerships and Cooperations

## 7.1. Regional Initiatives

### *7.1.1. Digiteo/DIM*

*7.1.1.1. HIDINIM Digiteo project*

**Participants:** Bertrand Thirion [Correspondant], Virgile Fritsch.

High-dimensional Neuroimaging– Statistical Models of Brain Variability observed in Neuroimaging

This is a joint project with Select project team and with SUPELEC Sciences des Systèmes (E3S), Département Signaux & Systèmes Électroniques (A. Tennenhaus), 2010-2013.

Statistical inference in a group of subjects is fundamental to draw valid neuroscientific conclusions that generalize to the whole population, based on a finite number of experimental observations. Crucially, this generalization holds under the hypothesis that the population-level distribution of effects is estimated accurately. However, there is growing evidence that standard models, based on Gaussian distributions, do not fit well empirical data in neuroimaging studies.

In particular, Hidinim is motivated by the analysis of new databases hosted and analyzed at Neurospin that contain neuroimaging data from hundreds of subjects, in addition to genetic and behavioral data. We propose to investigate the statistical structure of large populations observed in neuroimaging. In particular, we investigate the use of region-level averages of brain activity, that we plan to co-analyse with genetic and behavioral information, in order to understand the sources of the observed variability. This entails a series of modeling problems that we address in this project: *i)* Distribution normality assessment and variables covariance estimation, *ii)* model selection for mixture models and *iii)* setting of classification models for heterogeneous data, in particular for mixed continuous/discrete distributions.

*7.1.1.2. ICOGEN Digiteo project*

**Participants:** Bertrand Thirion [Correspondant], Benoit Da Mota.

**ICOGEN : Intensive COmputing for GEnetic-Neuroimaging studies**

Project supported by a Digiteo grant in collaboration with Inria's KerData Team, MSR-Inria joint centre, Supélec Engineer School, Imagen project and CEA/Neurospin, 2012-2014.

In this project, we design and deploy some computational tools to perform neuroimaging-genetics association studies at a large scale.

Unveiling the relationships between genetic variability and brain structure and function is one of the main challenges in neuroscience, which can be partly addressed through the information conveyed by high-throughput genotyping on the one hand, and neuroimaging data on the other hand. Finding statistical associations between these different variables is important in order to find relevant biomarkers for various brain diseases and improve patient handling. Due to the huge size of the datasets involved and the requirement for tight bounds on statistical significance, such statistical analysis are particularly demanding and cannot be performed easily at a large scale with standard software and computational tools. In ICOGEN, we design and deploy some computational tools to perform neuroimaging-genetics association studies at a large scale. We implement and assess on real data the use of novel statistical methodologies and run the statistical analysis on various architectures (grids, clouds), in a unified environment.

*7.1.1.3. 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 thesis 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, i.e. for relapse prediction.

*7.1.1.4. MMoVNI Digiteo project*

**Participants:** Bertrand Thirion [Correspondant], Pierre Fillard, Viviana Siless, Stéphanie Allassonnière, Hao Xu.

This is a joint project with CMAP http://www.cmapx.polytechnique.fr/~allassonniere/, 2010-2013.

Modeling and understanding brain structure is a great challenge, given the anatomical and functional complexity of the brain. In addition to this, there is a large variability of these characteristics among the population. To give a possible answer to these issues, medical imaging researchers proposed to construct a template image. Most of the time, these analysis only focus on one category of signals (called modality), in particular, the anatomical one was the main focus of research these past years. Moreover, these techniques are often dedicated to a particular problem and raise the question of their mathematical foundations. The MMoVNI project aims at building atlases based on multi-modal images (anatomy, diffusion and functional) data bases for given populations. An atlas is not only a template image but also a set of admissible deformations which characterize the observed population of images. The estimation of these atlases will be based on a new generation of deformation and template estimation procedures that build an explicit statistical generative model of the observed data. Moreover, they make it possible to infer all the relevant variables (parameters of the atlases) thanks to stochastic algorithms. Lastly, this modeling allows also to prove the convergence of both the estimator and the algorithms which provides a theoretical guarantee to the results. The models will first be proposed independently for each modality and then merged together to take into account, in a correlated way, the anatomy, the local connectivity through the cortical fibers and the functional response to a given cognitive task. This model will then be generalized to enable the non-supervised clustering of a population. This leads therefore to a finer representation of the population and a better comparison for classification purposes for example. The Neurospin center, partner of this project, will allow us to have access to databases of images of high-quality and high-resolution for the three modalities: anatomical, diffusion and functional imaging. This project is expected to contribute to making neuroimaging a more reliable tool for understanding inter-subject differences, which will eventually benefit to the understanding and diagnosis of various brain diseases like Alzheimer's disease, autism or schizophrenia.

## 7.2. National Initiatives

### *7.2.1. ANR*

#### *7.2.1.1. BrainPedia project*

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

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 looses 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.

#### *7.2.1.2. IRMgroup project*

**Participants:** Bertrand Thirion [Correspondant], Alexandre Gramfort, Michael Eickenberg.

This is a joint project with Polytechnique/CMAP http://www.cmap.polytechnique.fr/: Stéphanie Allassonnière and Stéphane Mallat (2010-2013).

Much of the visual cortex is organized into visual field maps, which means that nearby neurons have receptive fields at nearby locations in the image. The introduction of functional magnetic resonance imaging (fMRI) has made it possible to identify visual field maps in human cortex, the most important one being the medial occipital cortex (V1,V2,V3). It is also possible to relate directly the activity of simple cells to an fMRI activation pattern and Parietal developed some of the most effective methods. However, the simple cell model is not sufficient to account for high-level information on visual scenes, which requires the introduction of specific semantic features. While the brain regions related to semantic information processing are now well understood, little is known on the flow of visual information processing between the primary visual cortex and the specialized regions in the infero-temporal cortex. A central issue is to better understand the behavior of intermediate cortex layers.

Our proposition is to use our mathematical approach to formulate explicitly some generative model of information processing, such as those that characterize complex cells in the visual cortex, and then to identify the brain substrate of the corresponding processing units from fMRI data. While fMRI resolution is still too coarse for a very detailed mapping of detailed cortical functional organization, we conjecture that some of the functional mechanisms that characterize biological vision processes can be captured through fMRI; in parallel we will push the fMRI resolution to increase our chance to obtain a detailed mapping of visual cortical regions.

*7.2.1.3. 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 structured 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

## 7.3. European Initiatives

### *7.3.1. HBP*

Type: COOPERATION

Instrument: Collaborative Project with Coordination and Support Action

Objectif: NC

Duration: October 2013 - March 2016

Coordinator: EPFL, Lausanne

Partner: 86 partners, https://www.humanbrainproject.eu/fr/discover/the-community/partners;jsessionid=10vokilfkjcyhhgmfxu609p40

Inria contact: Olivier Faugeras

Abstract:

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 disease and build revolutionary new computing technologies. Today, for the first time, modern ICT has brought these goals within sight.

**Convergence of ICT and Biology** The convergence between biology and ICT has reached a point at which it can turn the goal of understanding the human brain into a reality. This realisation motivates the Human Brain Project – an EU Flagship initiative in which over 80 partners will work together to realise a new "ICT-accelerated" vision for brain research and its applications.

One of the major obstacles to understanding the human brain is the fragmentation of brain research and the data it produces. Our most urgent need is thus a concerted international effort that uses emerging emerging ICT technologies to integrate this data in a unified picture of the brain as a single multi-level system.

**Research Areas** The HBP will make fundamental contributions to neuroscience, to medicine and to future computing technology.

In *neuroscience*, the project will use neuroinformatics and brain simulation to collect and integrate experimental data, identifying and filling gaps in our knowledge, and prioritising future experiments.

In *medicine*, the HBP will use medical informatics to identify biological signatures of brain disease, allowing diagnosis at an early stage, before the disease has done irreversible damage, and enabling personalized treatment, adapted to the needs of individual patients. Better diagnosis, combined with disease and drug simulation, will accelerate the discovery of new treatments, drastically lowering the cost of drug discovery.

In *computing*, new techniques of interactive supercomputing, driven by the needs of brain simulation, will impact a vast range of industries. Devices and systems, modelled after the brain, will overcome fundamental limits on the energy-efficiency, reliability and programmability of current technologies, clearing the road for systems with brain-like intelligence.

**The Future of Brain Research**

Applying ICT to brain research and its applications promises huge economic and social benefits. But to realise these benefits, the technology needs to be made accessible to scientists – in the form of research platforms they can use for basic and clinical research, drug discovery and technology development. As a foundation for this effort, the HBP will build an integrated system of ICT-based research platforms, building and operating the platforms will require a clear vision, strong, flexible leadership, long-term investment in research and engineering, and a strategy that leverages the diversity and strength of European research. It will also require continuous dialogue with civil society, creating consensus and ensuring the project has a strong grounding in ethical standards.

The Human Brain Project will last ten years and will consist of a ramp-up phase and a partially overlapping operational phase.

## 7.4. International Initiatives

### *7.4.1. Inria Associate Teams*

Title: Analysis of structural MR and DTI in neonates

Inria principal investigator: Pierre Fillard

International Partner:

Institution: University of Southern California (United States)

Laboratory: Image Lab at Children Hospital at Los Angeles

Researcher: Natasha Lepore

International Partner:

Institution: University of Pennsylvania (United States)

Laboratory: Penn Image Computing and Science Laboratory

Researcher: Caroline Brun

Duration: 2011 - 2013

See also: http://www.capneonates.org/

While survival is possible at increasingly lower gestational ages at birth, premature babies are at higher risk of developing mental disorders or learning disabilities than babies born at term. A precise identification of the developmental differences between premature and control neonates is consequently of utmost importance. Nowadays, the continuously improving quality and availability of MR systems makes it possible to precisely determine, characterize and compare brain structures such as cortical regions, or white matter fiber bundles. The objective of this project is to understand the developmental differences of premature versus normal neonates, using structural and diffusion MRI. This work will consist in identifying, characterizing and meticulously studying the brain structures that are different between the two groups. To do so, we propose to join forces between the Parietal team at Inria and the University of Southern California. Parietal has a recognized expertise in medical image registration and in statistical analyses of groups of individuals. USC has a broad knowledge in MR image processing. In particular, the Children's Hospital at Los Angeles (CHLA), which is part of USC, is in the process of collecting a unique database of several hundreds of premature and normal neonates MR scans. This joint collaboration is consequently a unique chance of addressing key questions pertaining to neonatal and premature development. It will make it possible to elaborate new tools to analyze neonate MR images while tremendously increasing our knowledge of neuroanatomy at such an early stage in life.

### *7.4.2. Inria International Labs*

Parietal has taken part to the program Inria@SiliconValley, and had a 18-months post-doc funded to work on the comparison of anatomical and functional connectivity (18 months, 2011-2013):

In this project, we build probabilistic models that relates quantitatively the observations in anatomical and functional connectivity. For instance given a set of brain regions, the level of functional integration might be predicted by the anatomical connectivity measurement derived from the fibers in a given population of subjects. More generally, we seek to extract latent factors explaining both connectivity measures across the population. Such models require specifically that a generative model is proposed to explain the observations in either domain, so that a meaningful and testable link is built between the two modalities. The inference problem can then be formulated as learning the coupling parameters that are necessary to model the association between modalities, and tested e.g. by assessing the ability of the learned model to generalize to new subjects. The aim is then to provide the mathematical and algorithmic tools necessary to build a standardized model of brain connectivity informed by both modalities, associated with confidence intervals to take into account between subject variability. Such an atlas is a long-term project, that requires adequate validation on high-resolution data, but it is tightly linked to this project.

## 7.5. International Research Visitors

### 7.5.1. Visits of International Scientists

#### 7.5.1.1. Internships

Felipe Yanez made a three months internship (January-March 2013), funded by Inria Chile and Conycit. His research topic was *Improving the fit of functional MRI data through the use of sparse linear models*.

#### 7.5.1.2. Other visitors

Danilo Bzdok (Forschungszentrum Jülich, institue of neuroscience and medicine) visited Parietal in September 2013, to develop collaborations on the use of machine learning techniques to model behavioral variables and find data-driven characterization of brain diseases.

### 7.5.2. Visits to International Teams

- Yannick Schwartz spent one month in University of Texas at Austin, in Poldrack's lab http://www.poldracklab.org/. This stay was an opportunity to improve our understanding of the main challenges in functional brain imaging modalities.
- Philippe Ciuciu spent two months in the Paul Sabatier University (Toulouse, france), as part of the CIMI labex, where he runs a collaboration on compressed sensing for MRI.

# 8. Dissemination

## 8.1. Scientific Animation

- B. Thirion acts as reviewers for Medical Image Analysis, IEEE Transactions on Medical Imaging, NeuroImage, ISBI, IPMI, as associate editor for Frontiers in Neuroscience Methods, as program committee for the MICCAI 2012 conference and as expert for ANR, NWO.
- B.Thirion set up the following workshop at the OHBM 2013 conference: *Functional Data-Driven Atlases of the Brain* http://www.humanbrainmapping.org/i4a/pages/index.cfm?pageid=3526 and took part to the morning workshop entitled *Big Data in Neuroimaging: Big Opportunities or Just a Big Hassle - The Skeptical Neuroimagers View*.
- Bertrand Thirion organized a national workshop on Brain-Computer Interfaces at ICM, paris, on June 4th https://itneuro.aviesan.fr/Local/itneuro/dir/documents/newsletter/Newsletteroctobre2013.pdf.
- B. Thirion and G. Varoquaux organized the MMBC workshop at MICCAI 2013 http://groups.csail.mit.edu/vision/mmbc2013/.
- G. Varoquaux was program chair for PRNI 2013 and committee for Euroscipy 2013.
- G. Varoquaux acts as reviewer for NeuroImage, HBM, MedIA, TMI, Frontiers in NeuroInformatics, Frontiers in Brain Imaging methods and Trends in cognitive science Review editor for Frontiers in NeuroInformatics and Frontiers in Brain Imaging methods and as expert for ANR and Agoranov.
- Gael Varoquaux presented scikit-learn and machine learning tools and concepts at the Microsoft Spark incubator, and at Cap Digital.
- Philippe Ciuciu is IEEE senior member, member of the BioImaging Signal Processing (BISP) committee of the IEEE ISBI conference for 3 years (2013-15). He will be BISP area chair of the 2014 IEEE ICASSP conference in Florence.
- Philippe Ciuciu was the main organizer with JM Lina of a symposium in Montreal in Oct 2013: *Scale-free Dynamics and Networks in Neurosciences*, financially supported by the Centre de recherche mathématique de l'université de Montreal. http://www.crm.umontreal.ca/2013/Neuro13/.

- Philippe Ciuciu is an international expert and reviewer for the *Biotechnology and Biological Sciences Research Council*: http://www.bbsrc.ac.uk and the *Technology Foundation STW, Netherlands*. He also serves as **reviewer** for the French research funding agency (ANR) in the field of biomedical engineering and life science research calls. He is also reviewer for 16 peer-reviewing journals including IEEE TMI/BME/SP/IP/PAMI, Medical Image Analysis, NeuroImage, Human Brain Mapping, Plos One, MAGMA, JMRI, Journal of Neuroscience Methods, Signal Processing. He regularly serves as reviewer for the MICCAI, IEEE (ICASSP, ISBI, ICIP, EMBC, PRNI), EUSIPCO, HBM, SampTA, conferences.
- Alexandre Gramfort is Program committee PRNI, Associate editor IEEE EMBC conference and Associate editor Frontiers in brain imaging methods.
- Alexandre Gramfort acts as reviewer for Neuroimage, IEEE TMI, brain topography, HBM journal, PLOS ONE, brain connectivity, journal of clinical neurophysiology, MICCAI, physics in medicine and biology.

## 8.2. Teaching - Supervision - Juries

### *8.2.1. Teaching*

Gael Varoquaux

- Stat Course cogmaster (3 $\times$ 3H)
- Python course Inria Rocquencourt et Rennes: 8Hrs each time
- Optimization tutoral at Euroscipy: 2H
- Scikit-learn tutorial at Scipy: 4H
- Functional connectivity course at OHBM: 30mn, ISMRM 30mn

Bertrand Thirion

- Master MVA, Imagerie fonctionnelle cérébrale et interface cerveau machine, 12h + 3h, M2, ENS Cachan, France.

### *8.2.2. Supervision*

PhD : Solveig Badillo, Study of hemodynamic variability in sane adults and children in fMRI, Paris XI, 18/11/2013, supervised by Philippe Ciuciu

PhD : Virgile Fritsch, High-dimensional statistical methods for inter-subject neuroimaging studies, Paris XI, 18/12/2013, supervised by J.-B. Poline and B. Thirion

### *8.2.3. Juries*

- B. Thirion was reviewer for the PhD thesis of A.C. Philippe (Inria Sophia-Antipolis); the defense took place at Sophia-Antipolis on Dec. 19th, 2013.
- G. Varoquaux was examinator for the PhD defense of Katerina Gkirtzou at Centrale Paris, in Dec. 2013.
- P.Ciuciu took part to three PhD committees in 2013, one as reviewer (F. Karahonuglu, EPFL, Lausanne, Switzerland).

## 8.3. Popularization

PARIETAL presented a game designed by Virgile Fritsch to illustrate our research activities on brain activity decoding, at the Salon de jeux et culture mathématique (May 30$^{\text{th}}$-June 2$^{\text{nd}}$, 2013).

# 9. Bibliography

## Major publications by the team in recent years

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