INRIA

INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

Project-Team parietal

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

Saclay - Île-de-France

THEME BIO

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1. Team

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2. Overall Objectives

2.1. Parietal@Neuropsin

Bertrand Thirion joined INRIA Futurs/Saclay on November 1st, 2005, where he started to work with J.B.Poline (CEA, DSV, SHFJ) and two students, A. Tucholka and C. Damon. All of them moved to the novel Neurospin research Centre on January 1st, 2007. The activities of PARIETAL started on January 1st, 2008. As an INRIA team, the originality of PARIETAL is that it is situated within the CEA/DSV high-field neuroimaging platform, Neurospin.

Neurospin is a leading neuroimaging centre that aims at producing high quality data through novel high field MRI scanners (http://www-dsv.cea.fr/neurospin/): 3T for humans (with a 32 channels antenna), 7T for humans (the only one in France), a 7T MRI scanner for rats (17.6T in 2009), EEG EEG-MRI compatible and MEG equipment. By 2013, Neurospin should have the first 11.7T MRI scanner for humans in the world.

These formidable equipment will produce better quality and/or higher resolution images. While most current analysis solutions might not allow neuroscientists to take advantage of it, PARIETAL commits itself to developing original methods to analyse this data in order to better capture the informative content of anatomical and functional brain images. This goal includes the use of modelling tools (mathematical morphology, shape analysis, surface charting), various statistical techniques (descriptive statistics, data mining, inference, model selection), and the use of intensive computations to analyse the large volumes of data. PARIETAL also shares its tools with various developers of neuroscientific applications and neuroscientists (functional toolbox of Brainvisa, fff/nipy project).

2.2. Highlights of the year

Parietal officially started its existence as an INRIA team on January 1st, 2008. The team *texte fondateur* is currently under review.

3. Scientific Foundations

3.1. Neuroimaging data analysis: state of the art

PARIETAL aims at proposing innovative techniques to study brain function through the analysis of anatomical and functional brain images. Although much work has been performed in this field since the mid 90's, and standard solutions have been proposed - in particular a procedure called statistical parametric mapping (SPM), which has been progressively elaborated from 1995 to ca 2005 and implemented in several software packages- some important issues still need to be addressed:

- First, quite surprisingly, the SPM framework does not fit with the way neuroscientists think of their data, which is driven by prior knowledge about functional anatomy and the understanding of the brain as a modular functional network.
- Second, in spite of the intuitive evidence -blood oxygen-level dependent (BOLD) activity seen in fMRI originates mainly from the cortex- analysis on the cortical surface is not a standard yet. Spatial models are thus quite coarse and not informed by the anatomy.
- Third, a crucial problem within the mass univariate approach is that the SPM framework still relies on poor approximations and invalid assumptions to deal with multiple comparison problems. More work is needed in inter-subject modelling and reproducibility assessment.
- Finally, it is still necessary to understand and characterize the informative content of neuroimaging activation maps, beyond the traditional maps of activity. In particular, the neuroimaging community should benefit from the current advances in machine learning and computational neuroscience.

3.2. Parietal research axes

In order to address these questions, PARIETAL currently develops three main research axes:

1. Create some tools to understand brain functional architecture, i.e. the relationship between anatomy and function, e.g. the relationships between cortical maps and cortical folding. In particular, our aim is to extract the main salient brain structures that can be observed in neuroimaging datasets from several subjects. The final aim of this axis is to build atlases of the brain that will be based on multi-modal information (anatomical, functional and diffusion MRI).
2. The second axis is more classically related to the methodology for group analysis of neuroimaging data based on regression and classification techniques, thus trying to quantify and explain inter-subject differences, in particular when behavioral or genetic information are available to characterize the patients.
3. The third axis consists in finding some *coding schemes* that express how the brain processes some particular information, either in perception or action context. A very promising approach, called *inverse inference*, proceeds by predicting mental state from functional neuroimaging data.

An important motivation for these developments is that the advent of high-field Magnetic Resonance Imaging (MRI) will allow an increase of image resolution and quality which should be used to enhance image understanding and analysis. As a member of Neurospin platform, PARIETAL aims at proposing novel analyzing techniques that will take advantage of the high-quality data.

4. Software

4.1. Nipy/fff

Keywords: *General Linear Model*, *clustering*, *graphical-model based analysis*.

Participants: Bertrand Thirion [Correspondant], Merlin Keller, Vincent Michel, Gaël Varoquaux, Alan Tucholka.

NIPY/FFF is a development framework in python for the neuroimaging community (publicly available at https://code.launchpad.net/nipy), developed mainly at Berkeley, Stanford, Cambridge and Neurospin (fff). An important point is that nipy is open to any contributors and aims at developing code and tools sharing.
While the nipy part is more devoted to a global analysis framework, the other part (fff), which is completely developed by Parietal and LNAO (CEA, DSV, Neurospin) is devoted to algorithmic solutions for various issues in neuroimaging data analysis. fff has been registered at APP. As all the nipy project, fff is freely available, under BSD licence since last summer.

4.2. Brainvisa software

Keywords: *neuroimaging analysis pipeline*, *neuroimaging databases*.

Participants: Bertrand Thirion [Correspondant], Lise Favre, Alan Tucholka.

PARIETAL is involved in the development of a functional neuroimaging analysis toolbox in *Brainvisa*: this project includes the implementation of standard toolkit for the analysis of fMRI data, which is an important building block of Neurospin software platform, but it is an interface for the diffusion of the methods developed in our team. It benefits from the general infrastructure of *Brainvisa*, which has been set since 2001 by the LNAO laboratory (CEA, DSV, Neurospin) and several other teams from IFR 49 (http://www.ifr49.org/, http://brainvisa.info/).

5. New Results

5.1. Joint modelling of anatomical and functional features

Participants: Bertrand Thirion, Alan Tucholka.

5.1.1. Understanding and modelling the anatomy

PARIETAL is involved in the development of analysis tools to extract informative features from various anatomical data.

- T1 MRI data provides a segmentation of the sulci, whose shape can be further characterized in order to assess how well the shape intrinsically characterizes the sulci [13].
- Diffusion MRI provides a local model of water diffusion in the brain which can then be integrated into trajectories to yield the main fiber tracts of the brain and finally yield a model of the connectivity between brain regions. The connectivity information can be used to parcel the brain into pieces with homogeneous connectivity information [3].

This research is performed in the LNAO team (CEA, DSV, Neurospin), with some contributions of PARIETAL.

5.1.2. Comparison of anatomical and functional features observed in neuroimaging data

One of the ultimate goals in neuroimaging is to match functional and anatomical regions across subjects in order to better understand and characterize brain regions. In that perspective, we have performed a comparison of the position of brain functional landmarks, as defined in [14], with the position of the main anatomical landmarks, i.e. labelled brain sulci (inner parts of the cortical surface), and found that in some cases, these would provide finer position information than standard coregistration to a brain template [16]: see Fig. 1 for an illustration related to the frontal eye field region.

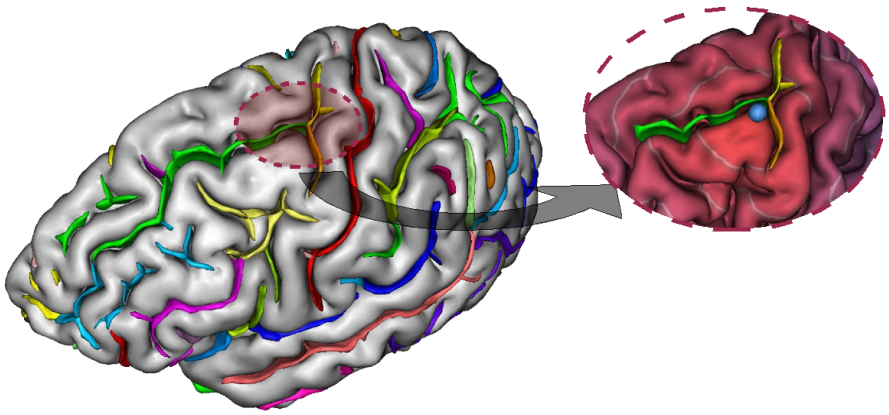

Figure 1. Given a sulci labelling, the activation focus (blue ball on the picture) in the pre-frontal lobe (frontal eye field region) is localized near the intersection of the three sulci: PreCentral Superior, PreCentral Marginal and Frontal Superior. More precisely, the local coordinate system implied by the three sulci yields a more accurate definition of the position of the functional focus than standard three-dimensional coordinates.

A practical way to study functional anatomy is to define brain regions using both anatomical and functional information, in a consistent manner across individuals. This segmentation process is called *parcellation*. Anatomical parcellations are generally related to a coordinate system on the cortical surface that represents the position of the main anatomical features (identified sulci, curvature), and maps the cortex to a sphere. Then the cortical maps are further segmented into gyri (outer regions of the cortical surface), which are defined with respect to the main sulci of the brain, or directly in the sulci-based coordinate system. Although the nomenclature of the gyri may vary across publications and softwares, the advantage of these approaches is that they provide a relatively standard division of the cortex into regions; still this description is quite coarse (30 to 60 regions), which limits its usefulness for cortical surface mapping.

In order to more finely delineate cortical regions, functional information, obtained using e.g. fMRI data, provides further insights, and can easily be compared across subjects. A few approaches had been proposed in the literature to identify reproducible functional activity areas among a group of subjects, using various clustering techniques. These approaches usually do not consider the anatomical information related to the data or simply reduce it to the three-dimensional coordinate systems. By contrast, it is important for interpretation purposes to relate functional information to anatomical structures. Moreover, these previous approaches have not addressed the question of model selection. Specifically they do not perform a probabilistic comparison of different parcellation techniques.

We have thus proposed in [16] a novel approach that combines anatomical parcellation of the data into gyri and functional information that further refine the parcellation. The final parcellation procedure is cast into a probabilistic framework and the parameters of the model are identified using a Variational Bayes approach. Finally, cross-validation procedures are used to optimize the number of components. Starting from 47 initial anatomical parcels (gyri), 254 and 229 anatomo-functional parcels are found in the left and right hemisphere respectively. For instance, as shown in Fig. 2, Broca's gyrus, delineated from the anatomical (sulci-based) information, was further sub-divided into four parcels using functional information.

5.1.3. Use of parcellation techniques to study various parameters of brain functional responses

The parcellations techniques implemented by PARIETAL have also been successfully used to analyse the temporal characteristics of the brain activity seen in fMRI in particular regions of the brain, as demonstrated by [2]: dividing the brain into small homogeneous entities is in fact extremely useful to launch expensive

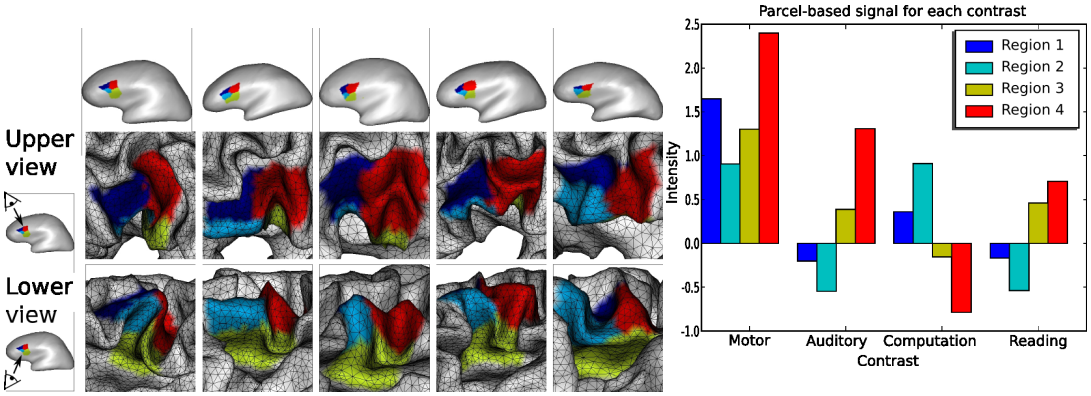

Figure 2. Parcellation of the opercular section of the Broca's area based on functional information. (Left) In these five representative subjects, the relative position of the parcels on the cortical surface is remarkably stable. (Right) The functional information related to the different parcels of this Parcellation can be used to further understanding the sensitivity of these parcel maps for several cognitive activities of interest.

whole brain analyses of haemodynamic parameters. The impact of the parcellation procedure on the analysis was investigated in [17].

5.2. Group inference and comparison of neuroimaging data with behavioural data

Participants: Bertrand Thirion, Cécilia Damon, Merlin Keller.

5.2.1. Improving activation detection in standard Group analyses

We have performed some theoretical and empirical analysis of standard group-level analyses procedures: In neuroimaging, it is a general aim to decide which brain regions show a positive effect for a certain functional combination or contrast of experimental conditions in a small group of subjects (10 to 20). The standard technique to do that is the so-called random effects analysis which consists in a t-test in each voxel of the image. We have generalized this by introducing several decision statistics for mass univariate mixed effects models which can be modelled as likelihood ratios. We have also proposed to use non-parametric extensions of these statistics, when the assumption of normality is not fulfilled [5]. The assessment of these statistics is unbiased through the use of permutation procedures.

We have also performed an in-depth study of the empirically observed inter-subject variability (variance and normality of multi-subject data) and of its impact on group studies; in particular we have quantified the effect of this variability on the reproducibility of the results of standard mixed effects analyses [6]. We have also discussed the impact of several parameters on these analyses (cohort size, threshold, contrast strength, inference technique). This was done using statistical resampling techniques on a uniquely large database of subjects, the *localizer* dataset.

We have contributed to increasing the sensitivity of group studies using *spatially relaxed models*:

Inter-subject brain registration is prone to errors (even assuming the existence of point-to-point correspondences between different brains), hence it does not seem reasonable to assume that homologous points are aligned across subjects. To date however, most methods for group analysis compare individual images on a voxelwise basis, thus making an implicit assumption that each subject is in perfect match with the template. Consequently, they tend to produce a stretching effect on group activity patterns due to the *jitter* induced by

inaccurate registration. This effect can only be reinforced by preliminary linear spatial smoothing of the data, as is the traditional heuristic. We have contributed a *low-level*, as opposed to feature-based, approach that generalizes existing voxel-based methods while relaxing the assumption that the effects are well localized in the standard space. The method is developed extends standard hierarchical formulation of the general linear model commonly used in fMRI by incorporating a simple model of spatial uncertainty [11]. We then derive a Bayes factor to test for the mean population effect's sign in a given voxel, and justify a Metropolis-within-Gibbs sampling scheme to effectively compute this Bayes factor. We have shown in [1] that this approach yields more accurate results in synthetic data and behaves well on real datasets.

Another solution for that problem is to escape from mass univariate modelling, thus making inference on spatially extended objects, such as clusters or parcels. Cluster-level inference consists in declaring active the connected components of supra-threshold volume elements (voxels) that are larger than expected by chance; this approach has been shown to be effective in standard group studies and it benefits to the reproducibility of the analysis [6]. However, a more radical solution consists in shifting from a voxel-based approach to a feature-based approach, which is exemplified by the introduction of brain functional landmarks.

Definition of Brain Functional Landmarks (BFLs) and their use in group studies: when a particular functional contrast is studied, it may be more interesting to concentrate the analysis on a few regions that show a reproducible pattern of activity across subjects. These activity foci have been called *functional brain landmarks*. Defining them properly raises several challenges:

- What objects/structures should be extracted from the individual data to build a group model ? In the case of functional MRI (fMRI) data, most of the information of interest is coded in the maxima of activity maps, e.g. large supra-threshold clusters, scale-space blobs or activity peaks. Some of these approaches might be somewhat coarse for a fine description of activated areas. In recent works, we have introduced watershed segmentations of supra-threshold areas [7], and blob models [14], which present an acceptable compromise between robustness and precision.
- How to associate such regions across subjects ? This point is more challenging, because there exists clearly no isomorphism between individual active regions. While the position in a common space is an important information, anatomical variability introduces ambiguities in straightforward position matching procedures. In fact, the global activity pattern should be matched. We have thus introduced novel solutions based on Bayesian Networks models [7], [14] that perform a probabilistic coregistration of the activated areas.
- How to validate, i.e. declare as active, the sets of regions that have been associated across subjects? We have proposed two solutions: the first one keeps only the spatial regions where there are significantly more cross-subjects maxima than expected by chance [7], and the second one, based on a Bayesian approach, validates the individual regions based on their signal and their position [14]. Unlike previous solution, our approach provides explicit significance indexes.

These approaches have proved to be quite sensitive in group studies [7], [14]; moreover, they have a noticeably positive impact on the between-group reproducibility of the results. Finally, the definition of such functional landmarks can also be viewed as automated region selection procedures, in which the landmark regions that can be further used as regions of interest for future analyses, e.g. population comparison.

5.2.2. Comparing the neuroimaging information with behavioural data

Inter-subject anatomical and functional variability represents a difficulty for the interpretation of neuroimaging data. It manifests itself either by mis-alignments of datasets that remain after spatial normalization, by an important residual variance in between-subjects analyses, and has rarely been explored. However, variability can be an informative element that has to be explicitly taken into account to interpret group studies. Our work aims at establishing a relationship between functional neuroimaging variability with binary individual information (e.g. behavioural data), called henceforth *targets*. The difficulties of this study are related to the high dimension and weak contrast-to-noise ratio of fMRI data. Moreover, fMRI signals are uncalibrated, which makes quantitative inter-subject comparison difficult in general. Anatomical variability results in shifts in the

location of corresponding regions; nevertheless, stereotactic normalization is the most widely used technique and therefore the one we choose for this study.

In order to capture the relationship between fMRI data with targets of interest, we take advantage of the power of recent supervised classification techniques that fit the target with the set of available information (here voxel-based signals). However, given the large size of the data (about 65000 voxels at 3mm resolution), which is much larger than the number of samples (about 200 subjects), the classifiers tend to overfit, because they use non-specific information to make predictions. To make sure that the classification rule will generalize to unobserved data, we need to base the classification on a restricted number of features/voxels.

We have compare the standard analysis of variance (Anova) procedure and two different multivariate features selection techniques, Manova and Mutual Information, with a technique that takes into account the image structure: the Local Maxima (LM) of features saliency map. We have also compared standard classifiers, support vector machines (SVM) and relevance vector machines (RVM), which are known to be effective on high-dimensional data, with the SRDA classifier, an extension of the LDA classifier for high dimensional space, that operates in the feature space and not in the dual. We have shown that the SRDA classifier especially used in conjunction with a selection of local maxima of the features saliency map outperforms other combinations of features selection (Anova, Manova and Mutual Information) and classifiers (Linear SVM and RVM); see [9] and Fig. 3 and [9] for more details .

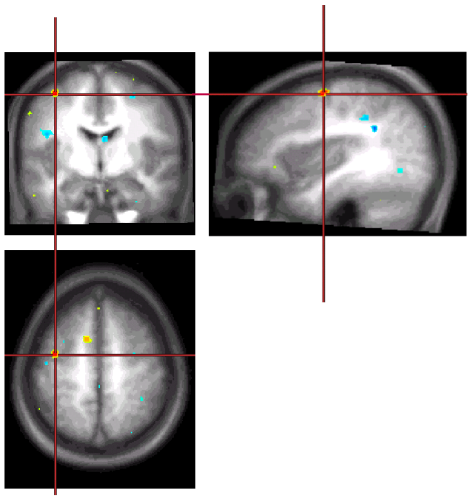

Figure 3. Map of the final feature weights of the LMSRDA classifier for the prediction of an index of the difficulty of the subjects to identify right and left, given functional maps related to the contrast of a subtraction task minus sentence reading. The peak weight belongs to the prefrontal cortex (the coordinates in MNI space are(-24, -18, 65)mm) . See [9] for more details.

5.3. Brain decoding techniques

Participants: Bertrand Thirion, Vincent Michel, Gaël Varoquaux.

Traditional inference in neuroimaging consists in describing the fluctuations of brain activity related to the modification of a stimulation parameter (a functional contrast). There might exist a relationship that relates functional contrasts and brain states. Inferring functional contrasts from a certain dataset is known as *inverse inference*. The quality of this inference is easily characterized by a correct classification rate if the target variable belongs to some finite set. Such estimation of is usually carried out using classifiers.

5.3.1. Feature selection and classification approach

We have used several classification (Support Vector Machines, Relevant Vector Machines, Linear Discriminant Analysis, Elsaticnet) and feature selection methods (Anova, Manova, Mutual information) to perform the classification of task-related activation images. Feature selection is of primary interest in this problem, because of the huge number of voxels (about 10^5) that are potential predictors of the particular brain state or percept, especially compared t the few sample images that are available to characterize these brain states ($10^1 - 10^2$). This induces classically an overfit issue, that can be solved through data reduction approaches. We have developed a multivariate approach based on a mutual information criterion, estimated by nearest neighbors techniques, which can handle a large number of dimensions and is able to detect the non-linear statistical relationships between the features and the label [12]. Our research now focuses on clustering techniques that can take into account spatial information (parcellation), i.e. account for the three-dimensional structure of the data to reduce it, while discarding a minimal amount of information. We have applied this to three different datasets: object identification in the visual cortex (see [12] and Fig. 4), but also encoding of the preference of one image over another and numerotopy (see Fig. 5).

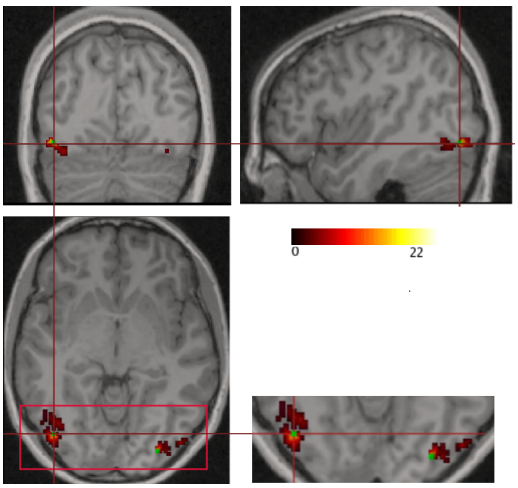

Figure 4. One of the main objective of functional MRI is to detect areas of the brain which are implied in different cognitive tasks. Here study some regions implied in objects identification tasks (discrimination between the 3 different sizes of objects). This is the representation of the voxels selected by two different algorithms: the reference method (Anova, with values of the F-score in hot colors) and our Mutual Information (MI) based algorithm (green). The main activity found by MI is at the (42,-75,-5) mm position in the lateral occipital cortex. The localization of the activity is much sparser with the MI selection than the reference method, and allows a more straightforward interpretation of the results.

5.3.2. Retinotopic mapping

In parallel, we have continued our work on retinotopy by analysing conjointly MEG and fMRI data on the same subject (see [10] for preliminary results). This collaborative work with INRIA Sophia-Antipolis/Odyssée and La Pitié-Salpètrière/LENA has been funded this year as an ANR project, which will allow us to continue this work using high-field MRI in the next years. We have performed one of the first using the 32 channels antenna on the 3T scanner at Neurospin in order to make a high resolution (1.5mm) retinotopy study.

6. Other Grants and Activities

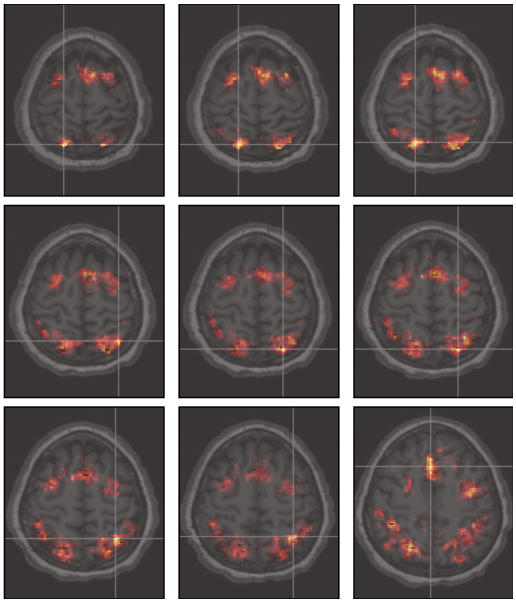

Figure 5. This figure shows different slices of the brain maps related to the coding of quantities (the functional images were acquired while the subjects were presented different clouds of 4,8,16 or 32 dots which they had to recall; this data is from E. Eger, INSERM U562, Neurospin). Those results are found by using regression techniques in a greedy search in the brain: here it is a searchlight approach, in which we analyse brain activity locally, by investigating whether the information around each brain site can be used to reliably predict the number of dots presented to the subject.

6.1. National Actions

Participants: Bertrand Thirion, Vincent Michel.

- Vimagine is an accepted ANR blanc project (2008-2012), which aims at building a novel view on the retinotopic organization of the visual cortex, based on MEG and MRI. Vimagine should open the way to understanding the dynamics of brain processes for low-level vision, with an emphasis on neuropathologies. This project is leaded by S. Baillet (MMiXT, CNRS UPR640 LENA, Pitié-Salpêtrière), in collaboration with M.Clerc, O. Faugeras (INRIA Sophia-Antipolis, Odyssée) and J. Lorenceau(LPPA, CNRS, Collège de France). The fMRI part of the project will be done by PARIETAL, and will consist in a study of spatially resolved retinotopic maps at the mm scale, the decoding of retinotopic information and the comparison of retinotopy with sulco-gyral anatomy.
- The Resting-State project is a joint INRIA-INSERM research project (2008-2010), leaded by B. Thirion, and dedicated to the study of the connectivity of the brain during resting state based on fMRI data. It is a collaborative project with INSERM U562, U678, the Alchemy INRIA Saclay team and LNAO (CEA,DSV Neurospin).
  It was launched in February 2008 in an INRIA-INSERM joint *young researchers* seminary. The first meeting of this project took place at Neurospin on November 5th. The post-doc of Gaël Varoquaux is funded by this project, and will consist in inferring the structure of the main resting-state networks of the brain and the modulation of this spontaneous activity in various experimental contexts.
- Brainvar is an INRIA ARC (2006-2008), whose purpose is to model the anatomical structure of the brain and its variability based on recent computational neuro-anatomy approaches. It especially aims at sharing databases and tools to enhance comparison of the best approaches to model the anatomy. This is an INRIA ARC (http://www-sop.inria.fr/asclepios/projects/ARCBrainVar/) leaded by X.Pennec (INRIA/Asclepios).
- PARIETAL is animating a working group on Classification, Statistics and fMRI imaging with Select and the LNAO team (CEA, DSV, Neurospin). One meeting per month took place in 2008 at Neurospin.
- J.B Poline leads a Neurospin research program on the study of genetics and neuroimaging data (Genim) at Neurospin. This group includes researchers from LNAO (CEA, DSV, Neurospin), Parietal, INSERM U562, INSERM U797, Supelec and CNG (Evry), with two meetings per month.

6.2. European actions

IMAGEN is an Integrated Project funded by the European Commission in the 6th Framework Program LSH-2005-2.1.3-1: Neuroimaging (2007-2012): "Bridging genetics and neural function". J.B. Poline is involved as the responsible for the bio-informatics and bio-statistics work package, and directly fits with PARIETAL's research axes. Half of the PhD theses of M.Keller and C.Damon are funded by IMAGEN, given that their work will contribute to Imagen data analysis part.
Imagen consists in acquiring in 8 centers across Europe, neuroimaging (anatomical, functional and diffusion-weighted), genetic and behavioral data from teenagers, in order to find risk factors of addiction for this population. The database (2000 subjects) is stored and analysed at Neurospin, and handled by a team with three engineers (CEA, DSV, Neurospin) headed by J.B. Poline. In 2008, the databasing system was released and data from about 300 subjects have been received, and are currently being analysed.

7. Dissemination

7.1. Scientific Community animation

7.1.1. Invited conferences

Participants: Bertrand Thirion, Jean-Baptiste Poline.

- ABIM conference, January 2008: B. Thirion gave a conference at the Alpine Brain Imaging meeting on resting-state fMRI data analysis techniques.
- FENS Forum, July 2008: B.Thirion was invited to give a presentation on the analysis of mental images in the brain through the use of neuroimaging techniques, where he presented his results on the inference on visual percepts in mental imagery.
- NIPS 2008: B. Thirion was invited to present the state of the art in functional neuroimaging data modelling at the functional neuroimaging workshop of the NIPS conference (December 2008).
- B. Thirion was invited speaker at Forum de la théorie 2008, CEA Saclay (http://ipht.cea.fr/Meetings/ForumTheory2008/), where his contribution was related to the various aspects of brain complexity as observed in neuroimaging data and the means to model it.
- J.-B. Poline was invited to UCLA institute for pure and applied mathematics IPAM at the neuroimaging summer school (http://www.ipam.ucla.edu/programs/mbi2008/).
- J.-B. Poline was invited to teach at the advanced fMRI course at HBM 2008 in Melbourne.
- J.-B. Poline was invited at the Institute of Psychiatry, London, UK, to give a lecture on neuroimaging and its computational aspects.
- J.-B. Poline was invited to a talk at the JFR 2008 on Bold imaging analysis (http://www.sfrnet.org/).
- J.-B. Poline was invited to teach to the 2008 SPM course.

7.1.2. Scientific animation

Participants: Bertrand Thirion, Jean-Baptiste Poline.

- Nipy meeting at Paris (April 2008): the last meeting of the nipy/fff developers tool place at Paris (at the risc institute) under the organization of Jean-Baptiste Poline, and with the participation of Gaël Varoquaux, Vincent Michel and Bertrand Thirion. This was the opportunity to launch the new bazaar system for control version system of these libraries, while fff changed from GPL to BSD licence by droping the GSL dependence of the previous release.
- Jirfni 2008: Lise Favre and B. Thirion leaded the first tutorial on the functional toolbox of Brainvisa at the Journées Inter-Régionales de Formation à la Neuroimagerie within INSERM institute, 17-19 November.
- JB Poline organised a meeting between the XNAT team in St Louis USA (26-29 May) to work on databasing systems for Neuroimaging.

7.2. Teaching

Participants: Bertrand Thirion, Jean-Baptiste Poline.

- B. Thirion taught in the functional Neuroimaging course (EEG, MEG, fMRI) of MVA master2 (ENS Cachan), conjointly with T. Papadopoulos and M. Clerc (INRIA Odyssée).
- J.B. Poline is reponsible for the master neuroimaging modules for Cogmaster (http://lumiere.ens.fr/~cogmaster/www/) and Paris XI medical physics mater.
- J.B. Poline teaches regularly the basis of functional neuroimaging (ENSEA, BMS).

8. Bibliography

Year Publications

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