

Enhancement of functional brain connectome analysis by the use of deformable models in the estimation of spatial decompositions of the brain images.

Scientific Context

Introduction: In human brain imaging, the inaccuracy of cross-subject registration is a well-identified bottleneck for data analysis. Registration is an important field of research in which many groups are investing resources; these efforts are almost entirely based on the information carried by anatomical images. Yet, there is rich and relevant information in functional connectivity data that might be used to improve cross-subject registration in regions where the anatomical information is poorly informative or unreliable. Such an effect has been shown for functional data [1] and is expected to play a major impact in connectome mapping. Our proposition to revisit cross-subject registration by taking into account functional connectivity data addresses a central technical issue for multi-subject connectome mapping.

Brain image registration: Most modern registration algorithms (see [2] for a user-oriented review, [3] for a technical review) impose diffeomorphic registration models to warp a given image to a template by matching some contrast, and rely on alternate template and warping estimation. While the use of functional connectivity information is a priori well suited to inform the correspondence between subjects [1], it is still unclear how a computationally tractable representation of such data can be constructed, given their lack of salient features. Our hope is that Dictionary Learning [4] will provide potentially useful contrasts to match multisubject datasets, as these analytic tools have a denoising effect: i) through the regularizing prior commonly used in these settings ii) and by enforcing cross-subject consistency that tends to regularize the information observed in some subjects based on group-level information. This makes the low SNR data obtained from functional acquisitions usable to drive registration.

Brain atlas: A brain atlas is a reference image or template that represents the spatial organization of some structures of interest of brain images together with a distribution of the deformations that are used in a reference population to map individual data to the template [6]. This is typically the result of a learning procedure that estimates in parallel a family of deformations that are used for cross-subject registration and an average of the samples. Brain atlases can thus be used to sample new data from the learned model.

Project

The project consists in blending functional information into brain image registration algorithms. We will inject functional information by coupling a deformation framework with a set of contrasts, that comprise spatial maps obtained from multi-subject dictionary learning procedures [4], in order to jointly estimate functional regions and coregister individual data. Regarding the registration problem, we will consider different standard alternative models, the cost and merit of which (in terms of cost and accuracy) will be assessed carefully:

- The diffeomorphic log-daemons framework, which is efficient, has proven to be effective in many contexts and is well-mastered by our lab (PhD thesis of V. Siless).
- Several avatars of the LDDMM framework [5], that is considered as the state-of-the art approach
- Discrete optimization approaches [3] for multi-modal cross-subject registrations, that has particular strengths, such as a lesser sensitivity to initialization or bypassing the need of gradient estimation.

- Generative formulations of image deformation [6], as these are three state-of-the-art solutions to multi-modal matching.

Our aim is to provide public open-source implementations of the methods developed as part of this thesis. The functions developed to solve functional data analysis problems, after a thorough assessment, will be made available with a homogeneous Application Program Interface (API); these libraries, in particular Nilearn <http://nilearn.github.io> or Nipy <http://nipy.org/nipy>, rely as much as possible on existing functions of the Python ecosystem, to read images (nibabel, <http://nipy.org/nibabel>), filter signals (scipy, <http://scipy.org>), perform statistical inference (statsmodel <http://statsmodels.sourceforge.net>), classification/regression problems, clustering, sparse covariance estimation (scikit-learn, <http://scikit-learn.org>).

We will evaluate the tools on the various databases available as open resources. We will take advantage of the many existing public datasets, such as those available from the ABIDE project http://fcon_1000.projects.nitrc.org/indi/abide and the Human Connectome Project <http://www.humanconnectome.org>.

Required skills

- Fluency in English
- Some prior experience with medical imaging
- Knowledge of the open-source world
- Statistics and machine learning
- Computer skills: Linux systems, scientific Python

Contact

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