The Aramis Lab brings together methodological researchers (computer scientists, applied mathematics) and medical experts (neurology, medical imaging) to build numerical models of brain diseases from multimodal patient data: medical imaging, clinical data and genomic data.

The Aramis Lab is a joint research team between CNRS, Inria, Inserm and Sorbonne University and belongs to the Paris Brain Institute (ICM), which is a neuroscience center based in the Pitié-Salpêtrière hospital in Paris, the largest adult hospital in Europe.

The team develops new data representations and statistical learning approaches that can integrate multiple types of data acquired in the living patient, including medical imaging, clinical and genomic data. In turn, these models shall allow for a better understanding of disease progression, and the development of new decision support systems for diagnosis, prognosis and design of clinical trials.

We are financially supported by these institutions.

Key methododological domains

- **Machine Learning**
  - Statistical learning, Deep learning, Generative models, Bayesian models
- **Medical image processing**
- **Morphometry and shape analysis**
- **Complex network theory**
- **Longitudinal analysis**

Main applications

- **Alzheimer's disease**
  - Clinical decision support systems, Disease progression models, Network alterations
- **Fronto-temporal dementia**
- **Multiple sclerosis**
- **Parkinson's disease**
- **Brain computer interfaces**

Team retreat at the villa Finaly, Florence, Italy

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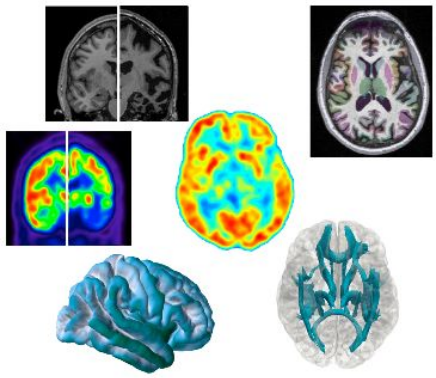
Context and general aim

The tremendous progress of neuroimaging, genomic and biomarker technologies has allowed capturing various characteristics of brain diseases in living patients. Collection of multimodal data in large patient databases provides a comprehensive view of brain alterations biological processes, genetic risk factors and symptoms. The team aims to build numerical models of brain diseases from multimodal patien based on appropriate data-driven approaches. To this end, we develop new data representations and statistical learning approaches that car integrate multiple types of data: neuroimaging, peripheral biomarkers, clinical and omics data (genetics, transcriptomics).

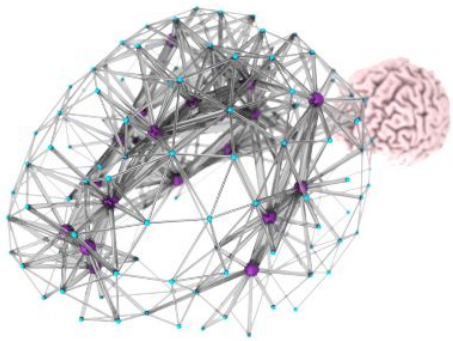
In particular, we develop methods to highlight networks of interactions among multiple sources of data, to track data changes during disease progression, and to automatically predict current or future clinical outcomes from these data. We apply these models to neurodegenerative diseases (Alzheimer's disease and other dementias, multiple sclerosis, Parkinson's disease…). They shall allow deepening our understanding of neurological diseases and developing new decision support systems for diagnosis, prognosis and design of clinical trials.

New representations from multimodal medical images

Combining multiple neuroimaging modalities is necessary to obtain a comprehensive picture of alterations in brain diseases (atrophy, anatomical disconnections, functional connectivity alterations, metabolic alterations, abnormal protein deposits…). Such a combination is a non-trivial task because different types of information are conveyed by the different modalities, which in turns leads to different natural data representations (meshes and curves for geometrical information, signals, networks). We propose to build new integrated data representations from multiple modalities. Such representations will be subsequently entered into statistical models and decision support systems. Specifically, we will introduce representations that can integrate geometrical information (anatomical surfaces extracted from anatomical MRI, white matter tracts extracted from diffusion MRI) together with functional (PET, ASL, EEG/MEG) and microstructural information.



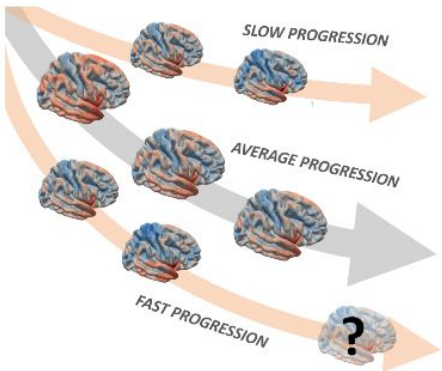
Network theoretic approaches to integrate heterogeneous brain networks



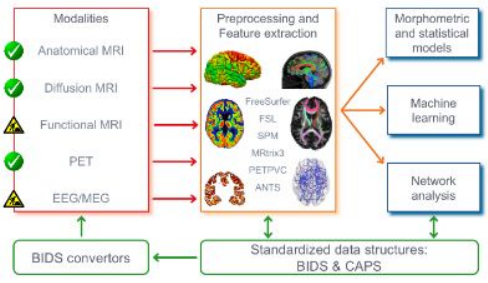
The complexity of biological systems often emerges from interactions between components at multiple spatial and temporal scales. Neglecting this information, and analyzing separately the levels of such scales, is an oversimplification of the real phenomenon. We propose a methodological framework that aims, on the one hand, to integrate information from networks describing different modes of connectivity (e.g. multi-modal, cross-frequency) and, on the other hand, to statistically model the organizational mechanisms of temporally dynamic networks (e.g. nonstationary, longitudinal). Target applications include: i) human learning in brain-computer interface, ii) prediction of neurodegenerative disease progression, and iii) identification of driving nodes in biological pathways (gene expression networks).

Spatio-temporal models to build trajectories of disease progression from longitudinal data

Longitudinal data sets are collected to capture variable temporal phenomena, which may be due to ageing or disease progression for instance. They consist in the observation of several individuals, each of them being observed at multiple points in time. The statistical exploitation of such data sets is notably difficult since data of each individual follow a different trajectory of changes and at its own pace. Our team has contributed to the definition of a generic theoretical and algorithmic framework for learning typical trajectories from longitudinal data sets. This framework is built on tools from Riemannian geometry and the inference is based on a stochastic Expectation Maximization (EM) algorithm coupled with Markov Chain Monte Carlo methods.



Decision support systems for diagnosis, prognosis and design of clinical trials



Based on the new representations and statistical models, we design decision support systems for diagnosis, prognosis and design of clinical trials. These systems are based on: i) personalization of statistical models to predict evolution at the patient level; ii) new machine learning approches for classification and regression on high-dimensional and structured data; iii) content-based retrieval techniques.