RESEARCH CENTRE

Sophia Antipolis - Méditerranée

2021 ACTIVITY REPORT

Project-Team ATHENA

Computational Imaging of the Central Nervous System

DOMAIN

Digital Health, Biology and Earth

THEME

Computational Neuroscience and Medicine

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Project-Team ATHENA

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Computer sciences and digital sciences

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1 Team members, visitors, external collaborators

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2 Overall objectives

2.1 Presentation

The main objective of ATHENA is to develop rigorous mathematical models and computational tools for analyzing and modeling the complex Central Nervous System structure and function. These models and tools will help to better understand the structure and the functioning of the human brain and address pressing and challenging clinical and neuroscience questions. Exploring new directions to solve these challenging problems will push forward the state-of-the-art in Structural and Functional Computational Brain Connectivity Mapping.

The relationship between brain structure and function is fundamental in neuroscience. Developing computational models and techniques that recover the structural and functional connectivities of the brain in vivo is thus of utmost importance: it will definitely improve the understanding of the brain and its mechanisms. On the basis of our expertise and contributions to the field of computational neuroimaging and in order to have an impact on this field, our research focusses mainly on the structural and functional Imaging of the brain with a particular emphasis on signal and image recording from diffusion Magnetic Resonance Imaging (dMRI), Magneto-Encephalography (MEG) and Electro-Encephalography (EEG).

In order to further increase the impact of our research, we also aim to push our contributions towards some applications related to brain diseases with characteristic abnormalities in the micro-structure of brain tissues that are not apparent and cannot be revealed reliably by standard imaging techniques. Diffusion MRI, a non invasive imaging modality based on the measurement of the random thermal movement (diffusion) of water molecules within samples can make visible these co-lateral damages to the fibers of the brain white matter and can also help in the development of new biomarkers related to the progression of certain types of neurodegenerative disease. Diffusion MRI is the imaging modality that we will primarly consider to recover the structural brain connectivity.

Connectivity represents the network infrastructure of the brain. Electric activity corresponds to communications over this network. MEG and EEG (jointly as M/EEG), two non-invasive techniques, reveal part of the cortical electric activity and are instrumental in better understanding the brain functional connectivity and in diagnosing diseases linked to anomalous brain function - that in some cases structural or other functional MR images do not reveal. MEG and EEG are the imaging modalities that we will primarly consider to recover the functional brain connectivity.

In some CNS injuries (medullar injuries, strokes, AMS), the peripheral nervous system may not be able to execute commands that are issued by the brain. Brain Computer Interfaces (BCI) use brain signals such as measured through EEG, and translate in real-time the electrical activity of the brain in commands to control external devices. While BCI is advocated as a means to communicate and help restore mobility or autonomy for very severe cases of disabled patients, it is also a new tool for interactively probing and training the human brain.

These considerations support the need to do research on new models and computational tools to analyse brain signals and imaging data. Our main objective is to push forward the state-of-the-art in Structural and Functional Computational Brain Connectivity Mapping to better understand the structure and function of the brain.

In order to tackle these long term and challenging objectives, our strategy is based on the following road map:

- Develop rigorous mathematical and computational tools for the analysis and interpretation of Diffusion MRI and M/EEG data.
- Improve acquisition and processing techniques and push forward the state-of-the-art in Computational brain imaging.
- Use our expertise to address with collaborators clinical and neuroscience questions.

This is implemented through:

- Publications in international conferences and journals dedicated to promoting advances in computational methods for Diffusion MRI and M/EEG analysis and/or use of Diffusion MRI and M/EEG in clinical and neuroscience applications.

- A dense network of collaborations with national as well as international neuroimaging laboratories through which we have access equipment and data and with whom we will jointly contribute to solve common crucial problems of interest.

- Software packages developed to be used in a first stage by our national and international collaborators and then made available to other partners.

3 Research program

3.1 Computational diffusion MRI

Diffusion MRI (dMRI) provides a non-invasive way of estimating in-vivo CNS fiber structures using the average random thermal movement (diffusion) of water molecules as a probe. It's a relatively recent field of research with a history of roughly three decades. It was introduced in the mid 80's by Le Bihan et al [61], Merboldt et al [66] and Taylor et al [80]. As of today, it is the unique non-invasive technique capable of describing the neural connectivity in vivo by quantifying the anisotropic diffusion of water molecules in biological tissues.

Diffusion Tensor Imaging & High Angular Resolution Diffusion Imaging In dMRI, the acquisition and reconstruction of the diffusion signal allows for the reconstruction of the water molecules displacement probability, known as the Ensemble Average Propagator (EAP) [79, 42]. Historically, the first model in dMRI is the 2nd order diffusion tensor (DTI) [39, 38] which assumes the EAP to be Gaussian centered at the origin. DTI (Diffusion Tensor Imaging) has now proved to be extremely useful to study the normal and pathological human brain [62, 51]. It has led to many applications in clinical diagnosis of neurological diseases and disorder, neurosciences applications in assessing connectivity of different brain regions, and more recently, therapeutic applications, primarily in neurosurgical planning. An important and very successful application of diffusion MRI has been brain ischemia, following the discovery that water diffusion drops immediately after the onset of an ischemic event, when brain cells undergo swelling through cytotoxic edema.

The increasing clinical importance of diffusion imaging has driven our interest to develop new processing tools for Diffusion Tensor MRI. Because of the complexity of the data, this imaging modality raises a large amount of mathematical and computational challenges. We have therefore developed original and efficient algorithms relying on Riemannian geometry, differential geometry, partial differential equations and front propagation techniques to correctly and efficiently estimate, regularize, segment and process Diffusion Tensor MRI (DT-MRI) (see [64] and [63]).

In DTI, the Gaussian assumption over-simplifies the diffusion of water molecules. While it is adequate for voxels in which there is only a single fiber orientation (or none), it breaks for voxels in which there are more complex internal structures and limitates the ability of the DTI to describe complex, singular and intricate fiber configurations (U-shape, kissing or crossing fibers). To overcome this limitation, so-called Diffusion Spectrum Imaging (DSI) [83] and High Angular Resolution Diffusion Imaging (HARDI) methods such as Q-ball imaging [81] and other multi-tensors and compartment models [76, 78, 59, 58, 73] were developed to resolve the orientationnality of more complicated fiber bundle configurations.

Q-Ball imaging (QBI) has been proven very successful in resolving multiple intravoxel fiber orientations in MR images, thanks to its ability to reconstruct the Orientation Distribution Function (ODF, the probability of diffusion in a given direction). These tools play a central role in our work related to the development of a robust and linear spherical harmonic estimation of the HARDI signal and to our development of a regularized, fast and robust analytical QBI solution that outperforms the state-of-the-art ODF numerical technique developed by Tuch [81]. Those contributions are fundamental and have already started to impact on the Diffusion MRI, HARDI and Q-Ball Imaging community [46]. They are at the core of our probabilistic and deterministic tractography algorithms devised to best exploit the full distribution of the fiber ODF (see [47, 4, 48, 5]).

Beyond DTI with high order tensors High Order Tensors (HOT) models to estimate the diffusion function while overcoming the shortcomings of the 2nd order tensor model have also been proposed such as the Generalized Diffusion Tensor Imaging (G-DTI) model developed by Ozarslan et al [71, 72] or 4th order Tensor Model [37]. For more details, we refer the reader to our articles in [56, 76] where we review HOT models and to our articles in [63], co-authored with some of our close collaborators, where we review recent mathematical models and computational methods for the processing of Diffusion Magnetic Resonance Images, including state-of-the-art reconstruction of diffusion models, cerebral white matter connectivity analysis, and segmentation techniques. We also worked on Diffusion Kurtosis Imaging (DKI), of great interest for the company OLEA MEDICAL. Indeed, DKI is fastly gaining popularity in the domain for characterizing the diffusion propagator or EAP by its deviation from Gaussianity. Hence it is an important clinical tool for characterizing the white-matter's integrity with biomarkers derived from the 3D 4th order kurtosis tensor (KT) [57].

All these powerful techniques are of utmost importance to acquire a better understanding of the CNS mechanisms and have helped to efficiently tackle and solve a number of important and challenging problems [58, 59]. They have also opened up a landscape of extremely exciting research fields for medicine and neuroscience. Hence, due to the complexity of the CNS data and as the magnetic field strength of scanners increases, as the strength and speed of gradients increase and as new acquisition techniques appear [3], these imaging modalities raise a large amount of mathematical and computational challenges at the core of the research we develop at ATHENA [54, 76].

Improving dMRI acquisitions One of the most important challenges in diffusion imaging is to improve acquisition schemes and analyse approaches to optimally acquire and accurately represent diffusion profiles in a clinically feasible scanning time. Indeed, a very important and open problem in Diffusion MRI is related to the fact that HARDI scans generally require many times more diffusion gradient than traditional diffusion MRI scan times. This comes at the price of longer scans, which can be problematic for children and people with certain diseases. Patients are usually unable to tolerate long scans and excessive motion of the patient during the acquisition process can force a scan to be aborted or produce useless diffusion MRI images. We have developed novel methods for the acquisition and the processing of diffusion magnetic resonance images, to efficiently provide, with just few measurements, new insights into the structure and anatomy of the brain white matter in vivo.

First, we contributed developing real-time Q-Ball Imaging reconstruction algorithm based on the Kalman filter [45]. Then, we started to explore the utility of Compressive Sensing methods to enable faster acquisition of dMRI data by reducing the number of measurements, while maintaining a high quality for the results. Compressed Sensing (CS) is a relatively recent technique which has been proved to accurately reconstruct sparse signals from undersampled measurements acquired below the Shannon-Nyquist rate [67].

We have also contributed to the reconstruction important features of the diffusion signal as the orientation distribution function and the ensemble average propagator, with a special focus on clinical setting in particular for single and multiple Q-shell experiments. Compressive sensing as well as the parametric reconstruction of the diffusion signal in a continuous basis of functions such as the Spherical Polar Fourier basis, have been proved through our contributions to be very useful for deriving simple and analytical closed formulae for many important dMRI features, which can be estimated via a reduced number of measurements [67, 43, 44].

We have also contributed to design optimal acquisition schemes for single and multiple Q-shell experiments. In particular, the method proposed in [3] helps generate sampling schemes with optimal angular coverage for multi-shell acquisitions. The cost function we proposed is an extension of the electrostatic repulsion to multi-shell and can be used to create acquisition schemes with incremental angular distribution, compatible with prematurely stopped scans. Compared to more commonly used radial sampling, our method improves the angular resolution, as well as fiber crossing discrimination. The optimal sampling schemes, freely available for download, have been selected for use in the HCP (Human Connectome Project).

We think that such kind of contributions open new perspectives for dMRI applications including, for example, tractography where the improved characterization of the fiber orientations is likely to greatly and quickly help tracking through regions with and/or without crossing fibers [55].

dMRI modelling, tissue microstructures features recovery & applications The dMRI signal is highly complex, hence, the mathematical tools required for processing it have to be commensurate in their complexity. Overall, these last years have seen an explosion of intensive scientific research which has vastly improved and literally changed the face of dMRI. In terms of dMRI models, two trends are clearly visible today: the parametric approaches which attempt to build models of the tissue to explain the signal based on model-parameters such as CHARMED [33], AxCaliber [34] and NODDI [84] to cite but a few, and the non-parametric approaches, which attempt to describe the signal in useful but generic functional bases such as the Spherical Polar Fourier (SPF) basis [35, 36], the Solid Harmonic (SoH) basis [49], the Simple Harmonic Oscillator based Reconstruction and Estimation (SHORE) basis [69] and more recent Mean Apparent Propagator or MAP-MRI basis [70].

We propose to investigate the feasibility of using our new models and methods to measure extremely important biological tissue microstructure quantities such as axonal radius and density in white matter. These parameters could indeed provide new insight to better understand the brain's architecture and more importantly could also provide new imaging bio-markers to characterize certain neurodegenerative diseases. This challenging scientific problem, when solved, will lead to direct measurements of important microstructural features that will be integrated in our analysis to provide much greater insight into disease mechanisms, recovery and development. These new microstructural parameters will open the road to go far beyond the limitations of the more simple bio-markers derived from DTI that are clinically used to this date – such as MD (Mean Diffusivity) and FA (Fractional Anisotropy) which are known to be extremely sensitive to confounding factors such as partial volume and axonal dispersion, non-specific and not able to capture any subtle effects that might be early indicators of diseases [8].

Towards microstructural based tractography In order to go far beyond traditional fiber-tracking techniques, we believe that first order information, i.e. fiber orientations, has to be superseeded by second and third order information, such as microstructure details, to improve tractography. However, many of these higher order information methods are relatively new or unexplored and tractography algorithms based on these high order based methods have to be conceived and designed. In this aim, we propose to work with multiple-shells to reconstruct the Ensemble Average Propagator (EAP), which represents the whole 3D diffusion process and use the possibility it offers to deduce valuable insights on the microstructural properties of the white matter. Indeed, from a reconstructed EAP one can compute the angular features of the diffusion in an diffusion Orientation Distribution Function (ODF), providing insight in axon orientation, calculate properties of the entire diffusion in a voxel such as the Mean Squared Diffusivity (MSD) and Return-To-Origin Probability (RTOP), or come forth with bio-markers detailing diffusion along a particular white matter bundle direction such as the Return-to-Axis or Return-to-Plane Probability (RTAP or RTPP). This opens the way to a ground-breaking computational and unified framework for tractography based on EAP and microstructure features [10]. Using additional a priori anatomical and/or functional information, we could also constrain the tractography algorithm to start and terminate the streamlines only at valid processing areas of the brain.

This development of a computational and unified framework for tractography, based on EAP, microstructure and a priori anatomical and/or functional features, will open new perspectives in tractography, paving the way to a new generation of realistic and biologically plausible algorithms able to deal with intricate configurations of white matter fibers and to provide an exquisite and intrinsic brain connectivity quantification.

Going beyond the state-of-the-art dMRI Although great improvements in dMRI modelling have been made during the last years, major problems are still unsolved and improvements are still required to better acquire dMRI data, better understand the biophysics of the signal formation, go beyond classical second order tensors invariants and recover high order invariants, recover robust and intrinsic microstructure features, identify bio-physically important bio-markers, improve tractography and in fine contribute to reconstruct the complete map of the cerebral connections, the connectome, as well as to better understand brain structure and function.

Therefore, there is still considerable room for improvement when it comes to the concepts and tools able to efficiently acquire, process and analyze the complex structure of dMRI data. Develop ground-

breaking dMRI tools and models for brain connectomics is one of the major objective we would like to achieve in order to take dMRI from the benchside to the bedside and lead to a decisive advance and breakthrough in this field.

3.2 MEG and EEG

Electroencephalography (EEG) and Magnetoencephalography (MEG) are two non-invasive techniques for measuring (part of) the electrical activity of the brain. While EEG is an old technique (Hans Berger, a German neuropsychiatrist, measured the first human EEG in 1929), MEG is a rather new one: the first measurements of the magnetic field generated by the electrophysiological activity of the brain were made in 1968 at MIT by D. Cohen. Nowadays, EEG is relatively inexpensive and is routinely used to detect and qualify neural activities (epilepsy detection and characterisation, neural disorder qualification, BCI, ...). MEG is, comparatively, much more expensive as SQUIDS (Superconducting QUantum Interference Device) only operate under very challenging conditions (at liquid helium temperature) and as a specially shielded room must be used to separate the signal of interest from the ambient noise. However, as it reveals a complementary vision to that of EEG and as it is less sensitive to the head structure, it also bears great hopes and an increasing number of MEG machines are being installed throughout the world. Inria and ODYSSÉE/ATHENA have participated in the acquisition of one such machine installed in the hospital "La Timone" in Marseille.

MEG and EEG can be measured simultaneously (M/EEG) and reveal complementary properties of the electrical fields. The two techniques have temporal resolutions of about the millisecond, which is the typical granularity of the measurable electrical phenomena that arise within the brain. This high temporal resolution makes MEG and EEG attractive for the functional study of the brain. The spatial resolution, on the contrary, is somewhat poor as only a few hundred data points can be acquired simultaneously (about 300-400 for MEG and up to 256 for EEG). MEG and EEG are somewhat complementary with fMRI (Functional MRI) and SPECT (Single-Photon Emission Computed Tomography) in that those provide a very good spatial resolution but a rather poor temporal resolution (of the order of a second for fMRI and a minute for SPECT). Also, contrarily to fMRI, which “only” measures an haemodynamic response linked to the metabolic demand, MEG and EEG measure a direct consequence of the electrical activity of the brain: it is acknowledged that the signals measured by MEG and EEG correspond to the variations of the post-synaptic potentials of the pyramidal cells in the cortex. Pyramidal neurons compose approximately 80% of the neurons of the cortex, and it requires at least about 50,000 active such neurons to generate some measurable signal.

While the few hundred temporal curves obtained using M/EEG have a clear clinical interest, they only provide partial information on the localisation of the sources of the activity (as the measurements are made on or outside of the head). Thus the practical use of M/EEG data raises various problems that are at the core of the ATHENA research in this topic:

- First, as acquisition is continuous and is run at a rate up to 1kHz, the amount of data generated by each experiment is huge. Data selection and reduction (finding relevant time blocks or frequency bands) and pre-processing (removing artifacts, enhancing the signal to noise ratio, ...) are largely done manually at present. Making a better and more systematic use of the measurements is an important step to optimally exploit the M/EEG data [2].

- With a proper model of the head and of the sources of brain electromagnetic activity, it is possible to simulate the electrical propagation and reconstruct sources that can explain the measured signal. Proposing better models [60, 12] and means to calibrate them [82] so as to have better reconstructions are other important aims of our work.

- Finally, we wish to exploit the temporal resolution of M/EEG and to apply the various methods we have developed to better understand some aspects of the brain functioning, and/or to extract more subtle information out of the measurements. This is of interest not only as a cognitive goal, but it also serves the purpose of validating our algorithms and can lead to the use of such methods in the field of Brain Computer Interfaces. To be able to conduct such kind of experiments, an EEG lab has been set up at ATHENA.

3.3 Combined M/EEG and dMRI

dMRI provides a global and systematic view of the long-range structural connectivity within the whole brain. In particular, it allows the recovery of the fiber structure of the white matter which can be considered as the wiring connections between distant cortical areas. These white matter based tractograms are analyzed, e.g. to explore the differences in structural connectivity between pathological and normal populations. Moreover, as a by-product, the tractograms can be processed to reveal the nodes of the brain networks, i.e. by segregating together gray matter that share similar connections to the rest of the white matter. But dMRI does not provide information on:

- the cortico-cortical pathways (not passing through white matter) and to some extent, on the short-range connections in the white matter,
- the actual use of connections over time during a given brain activity.

On the opposite, M/EEG measures brain activation over time and provides, after source reconstruction (solving the so-called inverse problem of source reconstruction), time courses of the activity of the cortical areas. Unfortunately, deep brain structures have very little contribution to M/EEG measurements and are thus difficult to analyze. Consequently, M/EEG reveals information about the nodes of the network, but in a more blurry (because of the inverse problem) and fragmented view than dMRI (since it can only reveal brain areas measurable in M/EEG whose activity varies during the experimental protocol). Given its very high temporal resolution, the signal of reconstructed sources can be processed to reveal the functional connectivity between the nodes [77].

While dMRI and M/EEG have been the object of considerable research separately, there have been very few studies on combining the information they provide. Some existing studies deal with the localization of abnormal MEG signals, particularly in the case of epilepsy, and on studying the white matter fibers near the detected abnormal source [65, 68], but to our knowledge there are very few studies merging data coming both from M/EEG and dMRI at the analysis level [75, 52, 40, 74].

Combining the structural and functional information provided by dMRI and M/EEG is a difficult problem as the spatial and temporal resolutions of the two types of measures are extremely different. Still, combining the measurements obtained by these two types of techniques has the great potential of providing a detailed view both in space and time of the functioning brain at a macroscopic level. Consequently, it is a timely and extremely important objective to develop innovative computational tools and models that advance the dMRI and M/EEG state-of-the-art and combine these imaging modalities to build a comprehensive dynamical structural-functional brain connectivity network to be exploited in brain connectivities diseases.

The CoBCoM ERC project aims to develop a joint dynamical structural-functional brain connectivity network built on advanced and integrated dMRI and M/EEG ground-breaking methods. To this end, CoBCoM develops new generation of computational dMRI and M/EEG models and methods for identifying and characterizing the connectivities on which the joint network is built [6, 7, 18, 17, 13, 50, 1, 16, 9]. The CoBCoM URL summarizes the contributions and publications, some of which given also via Videos Lectures.

The 3IA UCA Chair AI-based Computational Brain Connectomics project aims to reconstruct and analyse the network of neural connections of the brain, called the connectome via a computational brain connectomics framework based on ground-breaking AI algorithms and machine learning tools to gain insight into brain architecture, functioning and neurodegenerative diseases. The avalanche of big data required to reconstruct the connectome and the study of the high complexity of structural and functional interactions within the connectome clearly position brain connectomics as a big data problem where AI & machine learning in particular, represent a very promising trend, as recently demonstrated in computer vision and in some biomedical image data-driven analysis. Partly related to the ERC Advanced Grant CoBCoM, this project aims to construct networks specifically built on new generation of AI algorithms and machine learning tools to reconstruct structural and functional connectomes using advanced and integrated diffusion MRI, Electro and Magneto-Encephalography (EEG & MEG) methods [13, 21, 24, 25, 23, 26, 31].

Capitalizing on the strengths of dMRI & M/EEG and building on the bio-physical and mathematical foundations of our models, CoBCoM and the 3IA UCA Chair AI-based Computational Brain Connectomics contribute to create a joint and solid network which will be exploited to identify and characterize

white matter abnormalities in some high-impact brain diseases such as Multiple Sclerosis (MS), Epilepsy and mild Traumatic Brain Injury (mTBI) [15, 53].

4 Application domains

4.1 Applications of diffusion MRI

Clinical domain: Diagnosis of neurological disorder

Various examples of CNS diseases as Alzheimer's and Parkinson's diseases and others like multiple sclerosis, traumatic brain injury and schizophrenia have characteristic abnormalities in the microstructure of brain tissues that are not apparent and cannot be revealed reliably by standard imaging techniques. Diffusion MRI can make visible these co-lateral damages to the fibers of the CNS white matter that connect different brain regions.

4.2 Applications of M/EEG

Clinical domain: Diagnosis of neurological disorders

The dream of all M/EEG researchers is to alleviate the need for invasive recordings (electrocorticograms or intracerebral electrodes), which are often necessary prior to brain surgery, in order to precisely locate both pathological and vital functional areas. We are involved in this quest, particularly through our collaborations with the La Timone hospital in Marseille.
Subtopics include:

- Diagnosis of neurological disorders such as epilepsy, schizophrenia, tinnitus, ...
- Presurgical planning of brain surgery.
- Collaboration with the *Institut de Neurosciences des Systèmes* in Marseille on these topics.

Cognitive research

- Aims at better understanding the brain spatio-temporal organisation.
- Collaboration with laboratories of cognitive neuroscience in order to develop methods that suit their needs for sophisticated data analysis.

Brain Computer Interfaces (BCI) aim to allow direct control of external devices using brain signals such as measured through EEG. In our project, BCI can be seen as an application of EEG processing techniques, but also as an object of fundamental and applied research as they open the way for more dynamical and active brain cognitive protocols.

We develop a research collaboration with the eemagine/ANT-Neuro company. We collaborate with Nice University Hospital on the usage of BCI-based communication for ALS[1] patients.

5 New software and platforms

Here are the softwares that evolved significantly in 2021 in which the Athena team has participated.

5.1 New software

5.1.1 OpenMEEG

Keywords: Health, Neuroimaging, Medical imaging

[1] Nice University Hospital hosts a regional reference center for patients suffering from Amyotrophic Lateral Sclerosis

Scientific Description: OpenMEEG provides a symmetric boundary element method (BEM) implementation for solving the forward problem of electromagnetic propagation over heterogeneous media made of several domains of homogeneous and isotropic conductivities. OpenMEEG works for the quasistatic regime (frequencies < 100Hz and medium diameter < 1m).

Functional Description: OpenMEEG provides state-of-the art tools for modelling bio-electromagnetic propagation in the quasi-static regime. It is based on the symmetric BEM for the EEG/MEG forward problem, with a distributed source model. OpenMEEG has also been used to model the forward problem of ECoG, for modelling nerves or the cochlea. OpenMEEG is a free, open software written in C++ with python bindings. OpenMEEG is used through a command line interface, but is also interfaced in graphical interfaces such as BrainStorm, FieldTrip or SPM.

Release Contributions: OpenMEEG has had a large update including notably the parallelisation of some operators and bug corrections. The new version allows in addition the use of non-nested domains.

News of the Year: The python interface of OpenMEEG has been improved and now allows to pass python data structures (meshes, conductivities) to characterize the gain matrices to be calculated without going through files. This is done to ease a future integration of OpenMEEG in MNE-python. A code factorization also took place to allow in the long term to facilitate the integration in OpenMEEG of the work of K. Maksymenko on the efficient calculation of gain matrices for several conductivity values. This work has not yet been released.

URL: http://openmeeg.github.io/

Publications: inria-00467061v2, inria-00584205v1, hal-01278377v1

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5.1.2 Dmipy

Name: Diffusion MRI Multi-Compartment Modeling and Microstructure Recovery Made Easy

Keywords: Diffusion MRI, Multi-Compartment Modeling, Microstructure Recovery

Functional Description: Non-invasive estimation of brain microstructure features using diffusion MRI (dMRI) – known as Microstructure Imaging – has become an increasingly diverse and complicated field over the last decades. Multi-compartment (MC)-models, representing the measured diffusion signal as a linear combination of signal models of distinct tissue types, have been developed in many forms to estimate these features. However, a generalized implementation of MC-modeling as a whole, providing deeper insights in its capabilities, remains missing. To address this fact, we present Diffusion Microstructure Imaging in Python (Dmipy), an open-source toolbox implementing PGSE-based MC-modeling in its most general form. Dmipy allows on-the-fly implementation, signal modeling, and optimization of any user-defined MC-model, for any PGSE acquisition scheme. Dmipy follows a "building block"-based philosophy to Microstructure Imaging, meaning MC-models are modularly constructed to include any number and type of tissue models, allowing simultaneous representation of a tissue's diffusivity, orientation, volume fractions, axon orientation dispersion, and axon diameter distribution. In particular, Dmipy is geared toward facilitating reproducible, reliable MC-modeling pipelines, often allowing the whole process from model construction to parameter map recovery in fewer than 10 lines of code. To demonstrate Dmipy's ease of use and potential, we implement a wide range of well-known MC-models, including IVIM, AxCaliber, NODDI(x), Bingham-NODDI, the spherical mean-based SMT and MC-MDI, and spherical convolution-based single- and multi-tissue CSD. By allowing parameter cascading between MC-models, Dmipy also facilitates implementation of advanced approaches like CSD with voxel-varying kernels and single-shell 3-tissue CSD. By providing a well-tested, user-friendly toolbox that simplifies the interaction with the otherwise complicated field of dMRI-based Microstructure Imaging, Dmipy contributes to more reproducible, high-quality research.

Release Contributions: The current version features stability updates and bug fixes.

News of the Year: The current version features stability updates and bug fixes.

URL: https://github.com/AthenaEPI/dmipy

Publication: hal-02400877

Authors: Rutger Fick, Demian Wassermann, Rachid Deriche, Samuel Deslauriers-Gauthier

Contact: Rachid Deriche

5.1.3 Talon

Name: Tractograms As Linear Operators in Neuroimaging

Keywords: Diffusion imaging, Diffusion MRI, Brain MRI, Brain

Scientific Description: Talon is a Python package that implements Tractograms As Linear Operators in Neuroimaging. It is a general tool which allows users to transform a collection of streamlines (a tractogram) obtained from diffusion magnetic resonance imaging (MRI) into a linear forward model of neuroimaging data. A particularity of Talon is that it allows the user to specify the forward model, therefore being very flexible on the definition of the linear operator. The structure of the operator is exploited, allowing Talon to solve problems with millions of variables and hundreds of millions of data points. By solving a linear system this operator, Talon assigns a weight to each streamline which represents its contribution to imaging data. The current version is directed at diffusion MRI data and supports solving linear systems with non-negative least squares, group sparsity, and hierarchical sparsity. In the future, it will be updated to support more varied structural and functional data.

Functional Description: Talon is a Python package that implements Tractograms As Linear Operators in Neuroimaging. It is a general tool that assigns a weight to each streamline of a collection (referred to as a tractogram) by fitting the diffusion MRI data. This allows, among other things, to filter a tractogram and remove redundant streamlines. The current version is directed at diffusion MRI data and supports solving linear systems with non-negative least squares, group sparsity, and hierarchical sparsity. In the future, it will be updated to support more varied structural and functional data.

Release Contributions: Initial version that implements the minimum requirements. This includes transforming a tractogram into a linear operator, solving the inverse problem associated to the filtering of a tractogram, and use GPUs to speed up these operations.

News of the Year: This first version contains the base functionality of the software.

Publication: hal-03116143

Authors: Matteo Frigo, Samuel Deslauriers-Gauthier, Mauro Zucchelli, Rachid Deriche

Contact: Samuel Deslauriers-Gauthier

5.1.4 BCI-VIZAPP

Name: BCI visual applications

Keywords: Health, Brain-Computer Interface, GUI (Graphical User Interface)

Scientific Description: Bci-Vizapp is a library that allows (in interaction with OpenViBE) to build BCI (Brain Computer Interfaces) applications based on the P300 speller principle. Bci-Vizapp provides a library that allows you to create the BCI's stimulation part as part of the Qt toolkit. Being able to use a standard toolkit to make BCI applications is a strong Bci-Vizapp originality. Indeed, in general the use of such toolkits is prohibited by the need for a very precise control of the display timings, which generally eliminates high-level graphic toolkits such as Qt.

Functional Description: BCI-VIZAPP includes a virtual keyboard for typing text, a photodiode monitoring application for checking timing issues. It communicates with the OpenViBE acquisition server for signal acquisition and with the OpenViBE designer for signal processing. The configuration is performed through a wizard.

This software is a new version following the CoAdapt P300 stimulator software.

News of the Year: Bci-Vizapp is undergoing a deep transmutation following, among other things, the impulse of the SED of CRISAM in the ADT BciBrowser. Signal processing which was once based only on OpenViBE can now be done internally by the software. This has led to the development of different substitutable "backends" which can do this processing. In 2022, this software has finalized the change to a new database format that logs all parameters to ease the reproducibility of results. Tools to deal with dry electrodes EEG caps were also added and will be used in a forthcoming P300 speller acquisition campaign.

Contact: Théodore Papadopoulo

Participants: Nathanaël Foy, Romain Lacroix, Maureen Clerc Gallagher, Théodore Papadopoulo, Yang Ji, Come Le Breton

6 New results

6.1 Computational Diffusion MRI

Computational Brain Connectivity Mapping : From Multi-Compartment Modeling To Network Topology Via Tractography Filtering

Participants: Matteo Frigo, Samuel Deslauriers-Gauthier, Rachid Deriche.

Mapping the human brain is one of the complex challenges of contemporary science. It is a task that concatenates several problems from acquisition design to preprocessing, modelling, analysis, visualisation and assessment of the coherence with the state-of-the-art knowledge on the architecture and functioning of the human brain. For each of these steps a plethora of solutions has been and is being developed. It is of fundamental importance that the assumptions made in each step align with each other, demanding extra care in the verification of the theoretical requirements of the employed tools. In this Ph.D thesis, we focus on three specific parts of the chain of problems that leads to a comprehensive view of the brain architecture, highlighting the theoretical aspects that characterise the posed challenges and providing experimental evidence of the soundness of the proposed solutions. We present four contributions on three topical research areas of diffusion MRI methods for human brain mapping: brain tissue microstructure, tractography filtering and topological analysis of brain networks. First, we propose a new method for the estimation of tissue-specific volume fractions by means of multi-compartment models of the single-TE diffusion MRI signal. Then, we review the state of the art of tractography filtering and unveil its effects on the graph-theoretical analysis of the structural connectomes of both healthy subjects and patients affected by traumatic brain injury. In addition, we propose a novel filtering technique that integrates structural and functional information in the process. Finally, we propose a new similarity measure between brain networks and a new graph alignment techniques, allowing to obtain original insights into the problem of selecting the suitable parcellation for brain connectivity studies.

This work has been published in [27].

Brain Tissue Microstructure Characterization Using dMRI Based Autoencoder Neural-Networks

Participants: Mauro Zucchelli, Samuel Deslauriers-Gauthier, Rachid Deriche.

In recent years, multi-compartmental models have been widely used to try to characterize brain tissue microstructure from Diffusion Magnetic Resonance Imaging (dMRI) data. One of the main drawbacks of this approach is that the number of microstructural features needs to be decided a priori and it is embedded in the model definition. However, the number of microstructural features which is possible to obtain from dMRI data given the acquisition scheme is still not clear. In this work, we aim at characterizing brain tissue using autoencoder neural networks in combination with rotation-invariant features. By changing the number of neurons in the autoencoder latent-space, we can effectively control the number of microstructural features that we obtained from the data. By plotting the autoencoder reconstruction error to the number of features we were able to find the optimal trade-off between data fidelity and the number of microstructural features. Our results show how this number is impacted by the number of shells and the bvalues used to sample the dMRI signal. We also show how our technique paves the way to a richer characterization of the brain tissue microstructure in-vivo.

This work has been published in [24].

Investigating the effect of DMRI signal representation on fully-connected neural networks brain tissue microstructure estimation

Participants: Mauro Zucchelli, Samuel Deslauriers-Gauthier, Rachid Deriche.

In this work, we evaluate the performance of three different diffusion MRI (dMRI) signal representations in the estimation of brain microstructural indices in combination with fully connected neural networks (FC-NN). The considered signal representations are the raw samples on the sphere, the spherical harmonics coefficients, and a novel set of recently presented rotation invariant features (RIF). To train FC-NN and validate our results, we create a synthetic dMRI dataset that mimics the signal properties of brain tissues and provides us a real ground truth for our experiments. We test 8 different network configurations changing both the depth of the networks and the number of perceptrons. Results show that our new RIF are able to estimate the brain microstructural indices more precisely than the diffusion signal samples or its spherical harmonics coefficients in all the tested network configurations. Finally, we apply the best-performing FC-NN in-vivo on a healthy human brain.

This work has been published in [25].

A spherical convolutional neural network for white matter structure imaging via dMRI

Participants: Sara Sedlar, Abib Alimi, Théodore Papadopoulo, Rachid Deriche, Samuel Deslauriers-Gauthier.

Diffusion Magnetic Resonance Imaging (dMRI) is a powerful non-invasive and in-vivo imaging modality for probing brain white matter structure. Convolutional neural networks (CNNs) have been shown to be a powerful tool for many computer vision problems where the signals are acquired on a regular grid and where translational invariance is important. However, as we are considering dMRI signals that are acquired on a sphere, rotational invariance, rather than translational, is desired. In this work, we propose a spherical CNN model with fully spectral domain convolutional and non-linear layers. It provides rotational invariance and is adapted to the real nature of dMRI signals and uniform random distribution of sampling points. The proposed model is positively evaluated on the problem of estimation of neurite orientation dispersion and density imaging (NODDI) parameters on the data from Human Connectome Project (HCP).

This work has been published in [23].

Multi Tissue Multi-Compartment Models of Diffusion MRI

Participants: Matteo Frigo, Rutger Fick *(TheraPanacea)*, Mauro Zucchelli, Samuel Deslauriers-Gauthier, Rachid Deriche.

State-of-the-art multi-compartment microstructural models of diffusion MRI (dMRI) in the human brain have limited capability to model multiple tissues at the same time. In particular, the available techniques that allow this multi-tissue modelling are based on multi-TE acquisitions. In this work, we propose a novel multi-tissue formulation of classical multi-compartment models that relies on more common single-TE acquisitions and can be employed in the analysis of previously acquired datasets. We show how modelling multiple tissues provides a new interpretation of the concepts of signal fraction and volume fraction in the context of multi-compartment modelling. The software that allows to inspect single-TE diffusion MRI data with multi-tissue multi-compartment models is included in the publicly available Dmipy Python package.

This work has been published in [28].

On the generalizability of diffusion MRI signal representations across acquisition parameters, sequences and tissue types: chronicles of the MEMENTO challenge.

Participants: Alberto De Luca *(PROVIDI Lab, Image Sciences Institute, University Medical Center Utrecht)*, Matteo Frigo, Rutger Fick *(TheraPanacea)*, Sara Sedlar, Abib Alimi, Enes Alpay, Mauro Zucchelli, Samuel Deslauriers-Gauthier, Rachid Deriche, Kurt Schilling *(Department of Neurology, Brain Center Rudolf Magnus, University Medical Center Utrecht)*.

Diffusion MRI (dMRI) has become an invaluable tool to assess the microstructural organization of brain tissue. Depending on the specific acquisition settings, the dMRI signal encodes specific properties of the underlying diffusion process. In the last two decades, several signal representations have been proposed to fit the dMRI signal and decode such properties. Most methods, however, are tested and developed on a limited amount of data, and their applicability to other acquisition schemes remains unknown. With this work, we aimed to shed light on the generalizability of existing dMRI signal representations to different brain tissue types for diffusion encoding parameters. To this end, we organized a community challenge - named MEMENTO, making available the same datasets for fair comparisons across algorithms and techniques. We considered two state-of-the-art diffusion datasets, including single-diffusion-encoding (SDE) spin-echo data from a human brain with over 3820 unique diffusion weightings (the MASSIVE dataset), and double (oscillating) diffusion encoding data (DDE/DODE) of a mouse brain including over 2520 unique data points. A subset of the data sampled in 5 different voxels was openly distributed, and the challenge participants were asked to predict the remaining part of the data. After one year, eight participant teams submitted a total of 80 signal fits. For each submission, we evaluated the mean squared error, the variance of the prediction error and the Bayesian information criteria. Most predictions predicted either multi-shell SDE data (39%) or DODE data (22,5%), followed by cartesian SDE data (20%) and DDE (22,5%). Most submissions predicted the signals measured with SDE remarkably well, with the exception of low and very strong diffusion weightings. The prediction of DDE and DODE data seemed more challenging, likely because none of the submissions explicitly accounted for diffusion time and frequency. Next to the choice of the model, decisions on fit procedure and hyperparameters play a major role in the prediction performance, highlighting the importance of optimizing and reporting such choices. This work is a community effort to highlight strength and limitations of the field at representing dMRI acquired with trending encoding schemes, gaining insights into how different models generalize to different tissue types and fiber configurations over a large range of diffusion encodings.

This work has been published in [16].

Network alignment and similarity reveal atlas-based topological differences in structural connectomes

Participants: Matteo Frigo, Emilio Cruciani *(Inria Coati)*, David Coudert *(Inria Coati)*, Rachid Deriche, Emanuele Natale *(Inria Coati)*, Samuel Deslauriers-Gauthier.

The interactions between different brain regions can be modeled as a graph, called connectome, whose nodes correspond to parcels from a predefined brain atlas. The edges of the graph encode the strength of the axonal connectivity between regions of the atlas that can be estimated via diffusion magnetic resonance imaging (MRI) tractography. In this work, we aim to provide a novel perspective on the problem of choosing a suitable atlas for structural connectivity studies by assessing how robustly an atlas captures the network topology across different subjects in a homogeneous cohort. We measure this robustness by assessing the alignability of the connectomes, namely the possibility to retrieve graph matchings that provide highly similar graphs. We introduce two novel concepts. First, the graph Jaccard index (GJI), a graph similarity measure based on the well-established Jaccard index between sets; the GJI exhibits natural mathematical properties that are not satisfied by previous approaches. Second, we devise WL-align, a new technique for aligning connectomes obtained by adapting the Weisfeiler-Leman (WL) graph-isomorphism test. We validated the GJI and WL-align on data from the Human Connectome Project database, inferring a strategy for choosing a suitable parcellation for structural connectivity studies. Code and data are publicly available.

This work has been published in [18].

6.2 Unveiling brain activity using M/EEG and its Applications to Brain Computer Interfaces

Autoregressive models for M/EEG signal analysis

Participants: Agathe Senellart, Igor Carrara, Côme Le Breton, Théodore Papadopoulo.

Electroencephalotherapy (EEG) is a widely used and inexpensive modality that serves as a support not only for experiments aimed at understanding the functioning of the brain when it performs certain tasks, but also for the characterization of certain pathologies (such as epilepsy [4]) or the development of brain-computer interfaces. But EEG signals are complex and difficult to characterize, in particular because of their variability, whether in the same subject through the repetition of the same experiment or a fortiori when one wants to carry out multi-subject analyses. They therefore require the use of specific and adapted signal processing methods. In a recent approach [41], sources were modeled as an auto-regressive model which explains a portion of a signal. This approach works at the level of the source space (i.e. the cortex), which requires modeling of the head and makes it quite expensive. However, EEG measurements can be considered as a linear mixture of sources and therefore it is possible to estimate an auto-regressive model directly at the measurement level. The objectives of this work is to explore the possibility of exploiting EEG/MEG auto-regressive models to extract as much information as possible without requiring the complex head modelling required for source reconstruction.

A shallow convolutional neural network with rank-1 Fourier domain weights for brain signal classification

Participants: Sara Sedlar, Samuel Deslauriers-Gauthier, Rachid Deriche, Théodore Papadopoulo.

Electro- and magneto-encephalography (MEG) signals are measured by sensors placed on the scalp (EEG) or slightly above it (MEG). Such measurements can be represented as linear combinations of source signals occurring in different cortical regions and are characterized by a high temporal, but low spatial resolution. Depending on the performed task, the signals exhibit different temporal and spatial patterns. These signals are affected by a significant amount of noise coming from measuring devices or from the subject itself and suffer from high intra- and inter-subject variability which make their analysis quite challenging. Deep learning approaches have been successfully used in different domains of medical signal analysis. However, they often require large amounts of data, otherwise they either suffer from over-fitting or exhibit poor generalization power. In this work, we propose a rank-1 convolutional neural

network (CNN) with Fourier domain kernels for MEEG signal classification. Since the spread of the source signals across sensors is instantaneous and linear, we have used rank-1 trainable kernels in our model, where both spatial and temporal components are represented in Fourier domain, which acts as a regularization space. Assuming that the head can be modeled by a sphere, spatial kernels are represented in the basis of spherical harmonics. This representation is less sensitive to the spatial distribution of sensors which varies between subjects and sessions. In order to constrain temporal kernels to focus on feature extraction from certain frequency range, they are represented as linear combinations of discrete cosine coefficients. The model is compared with the state-of-the-art CNN models on the passive brain computer interface problem of mental workload classification from EEG signals and motor-task MEG signal classification. We have shown that our model can achieve state-of-the art performance with significantly lower number of parameters and achieve improvement when the number of available training subjects is smaller. Given this and its speed both during train and test phase, it is well suited for portable devices in brain computer interfaces.

This work is currently under submission.

Automatic detection of interictal spikes and convulsive seizures

Participants: Daniel Diaz-Arce *(Côte d'Azur University)*, Anis Ghouma *(Côte d'Azur University)*, Pierre Guetschel, Théodore Papadopoulo, Massimo Mantegazza *(UCA, IPMC, INSERM)*, Fabrice Duprat *(UCA, IPMC, INSERM)*.

Epilepsy is a very invalidating and common brain disorder. The use of rodent models of epilepsy to test new anti-epileptic treatments is of great interest. To asses the characteristics of the treatment, mice are observed 24h/24h with video cameras with simultaneous recording of intracranial EEG (electrocorticograms). The ability to detect epileptic seizures in these mice models with automated or semi-automated methods is still a major challenge. Such tools would tremendous improve the work of experimenters, who otherwise have to examin manually hours and hours of recordings to label the few epileptic events that occur during a day. This works reports on the development of two new computer tools that enable 1) the non invasive semi-automated detection of convulsive seizures from videos and the automatic detection of interictal spikes from electrocorticogram recordings.

This work was published in [29].

Modeling of the human sensory thalamus somatotopy from responses evoked by directional deep brain stimulation in patients treated for refractory neuropathic pain

Participants: Sarah Mouffok, Denys Fontaine *(CHU Pasteur, Nice)*, Aurélie Leplus-Wuertzer *(CHU Pasteur, Nice)*, Théodore Papadopoulo.

Somatotopy is defined as the spatial representation of the body within neural structures. Somatotopic organization of the human sensory thalamus has been described using intraoperative data from micro-electrodes recordings and location of stimulation-induced paresthesias in patients treated by deep brain stimulation (DBS) for intractable pain. These data suggested a mediolateral somatotopic organization in the contralateral ventroposterior thalamus, the head and the inferior limb being represented respectively medially and laterally. The aim of the project is to explore the somatotopy of the sensory thalamus using location of paresthesias induced by directional DBS and to try to modelize its somatotopic organization based on this data.

EEG-Based Auditory Attention Detection and Its Possible Future Applications for Passive BCI

Participants: Joan Belo, Maureen Clerc, Daniele Schon *(CNRS, INS, Aix-Marseille Université)*.

The ability to discriminate and attend one specific sound source in a complex auditory environment is a fundamental skill for efficient communication. Indeed, it allows us to follow a family conversation or discuss with a friend in a bar. This ability is challenged in hearing-impaired individuals and more precisely in those with a cochlear implant (CI). Indeed, due to the limited spectral resolution of the implant, auditory perception remains quite poor in a noisy environment or in presence of simultaneous auditory sources. Recent methodological advances allow now to detect, on the basis of neural signals, which auditory stream within a set of multiple concurrent streams an individual is attending to. This approach, called EEG-based auditory attention detection (AAD), is based on fundamental research findings demonstrating that, in a multi speech scenario, cortical tracking of the envelope of the attended speech is enhanced compared to the unattended speech. Following these findings, other studies showed that it is possible to use EEG/MEG (Electroencephalography/Magnetoencephalography) to explore auditory attention during speech listening in a Cocktail-party-like scenario. Overall, these findings make it possible to conceive next-generation hearing aids combining customary technology and AAD. Importantly, AAD has also a great potential in the context of passive BCI, in the educational context as well as in the context of interactive music performances. In this mini review, we firstly present the different approaches of AAD and the main limitations of the global concept. We then expose its potential applications in the world of non-clinical passive BCI. The main rationale behind this mini-review is to bridge the EEG-based AAD and Passive BCI communities and to provide insights about how the emerging synergy will develop. While previous reviews have been published on technical aspects of AAD, this mini-review attempts to briefly present EEG-based AAD in a broader perspective and to guide the reader to the most relevant sources.

This work has been published in [14].

Long multi-stage training for a motor-impaired user in a BCI competition.

Participants: Federica Turi, Maureen Clerc, Théodore Papadopoulo.

In a Mental Imagery Brain-Computer Interface (BCI), the user has to perform a specific mental task that generates electroencephalography (EEG) components, which can be translated in commands to control a BCI system. The development of a high-performance MI-BCI requires a long training, lasting several weeks or months, in order to improve the ability of the user to manage his/her mental tasks. This works aims to present the design of a MI-BCI combining mental imaginary and cognitive tasks for a severely motor impaired user, involved in the BCI race of the Cybathlon event, a competition of people with severe motor disability. In the BCI-race, the user becomes a pilot in a virtual race game against up to three other pilots, in which each pilot has to control his/her virtual car by his/her mental tasks. We present all the procedures followed to realize an effective MI-BCI, from the user's first contact with a BCI technology to actually controlling a video-game through her EEG. We defined a multi-stage user-centered training protocol in order to successfully control a BCI, even in a stressful situation, such as that of a competition. We put a specific focus on the human aspects that influenced the long training phase of the system and the participation to the competition and we highlight that the emotional state of the user, in terms of stress and concentration, directly impacts the performance of the system, in particular in a live competition.

This work has been published in [20]

Usability and efficiency of a dry electrodes based P300 speller system

Participants: Guilherme Sola Dos Santos, Côme Le Breton, Marianne Bruno *(CHU Pasteur, Nice)*, Marie-Hélène Soriani *(CHU Pasteur, Nice)*, Théodore Papadopoulo.

The P300 signal is a modification of the brain response when it encounters a rare but expected situation. It can be measured with an EEG acquisition system and is used in Brain Computer Interfaces to do various

task. In particular, the P300 speller allows to communicate – i.e. to speller letters – using directly brain signals by using an on-screen keyboard with flashing letters (flashes are the expected but rare event).

The Athena team has invested quite some effort in creating such a P300 Speller in the past years, and this speller has been formerly tested on both healthy subjects but also on a cohort of ALS patient. A new iteration of this P300 Speller is currently developed in which the used EEG system relies on a limited number of dry electrodes (compared to more gel-electrodes in the previous work) and eventually subject-specific caps. The main goal of this evolution is to ease the usage of the device and reduce its cost. This iteration is set to be tested on SLA subjects to evaluate some of those criteria.

This work in progress seeks to prepare the campaign with SLA subjects by testing it on healthy subjects, improving its first implementation based on these tests and to compare it to gel-based electrodes both in terms of ease-of-use or in terms of performance.

Rank-1 CNN for mental workload classification from EEG

Participants: Sara Sedlar, Johann Benerradi, Côme Le Breton, Rachid Deriche, Théodore Papadopoulo, Max L. Wilson.

Brain-computer interfaces (BCIs) can be separated into two main types: active and passive BCIs. A BCI can be qualified of passive when the system uses signals involuntarily generated by the user. More specifically, this type of BCI is often used with the aim to assess the mental workload of users performing various task with different levels of mental demand, especially with electroencephalography (EEG). In most cases, those systems are built with a classifier that classifies brain signals into different categories. This relies on having collected labelled data beforehand. However, those systems are often developed in laboratory settings, where both the train and test set have known labels. The "Grand Challenge: Passive BCI Hackathon" organised for the Neuroergonomics 2021 conference enables to challenge researchers with a real-life scenario of a passive BCI: classifying data from unseen sessions, with labels concealed for them, preventing any kind of fine tuning on the test set. The dataset provided for this challenge was composed of EEG recordings of 15 participants performing in 3 distinct sessions the Multi-Attribute Task Battery-II (MATB-II) developed by the NASA. Each session is decomposed in blocks of different difficulties: easy, medium and difficult. The data provided consists in epochs of 2 seconds (with a sampling frequency of 250 Hz) from those blocks for a total 447 epochs for each session and each participant. Difficulty labels were provided only for the 2 first sessions.

This work has been published in [31].

Phase synchrony in neurofeedback protocols

Participants: Côme Le Breton, Théodore Papadopoulo, Maureen Clerc.

Online estimation of phase synchrony measures in EEG is subject to a number of pitfalls, which makes such neurofeedback protocols rare or inadequate, despite their potential in health care applications (epilepsy syndromes, attention deficit hyperactivity disorders...). This work explores three crucial points for using phase synchrony measures in EEG neurofeedback protocols : phase estimation mixes close frequency components, timely close phase estimations are statistically correlated and synchrony measures are redundant and / or complementary.

A framework for better understanding and interpreting phase extraction with the Morlet Wavelet Transform is provided, which shows that errors are often made when extracting and exploiting phase information in neurofeedback protocols.

This work has been published in [30].

6.3 Combined fMRI, M/EEG and dMRI and Applications

Incorporating transmission delays supported by diffusion MRI in MEG source reconstruction

Participants: Ivana Kojčić, Théodore Papadopoulo, Rachid Deriche, Samuel Deslauriers-Gauthier.

White matter fibers transfer the information between brain regions with delays that are measurable with magnetoencephalography and electroencephalography (M/EEG). In the context of regularizing the dynamics of M/EEG and recovering electrical activity of the brain from M/EEG measurements, this article proposes a graph representation-based framework to solve the M/EEG inverse problem, where prior information about transmission delays supported by diffusion MRI (dMRI) are included to enforce temporal smoothness. Results of the reconstruction of brain activity from simulated MEG measurements are compared to MNE, LORETA and CGS methods and we show that our approach improves MEG source localization when compared to these three state-of-theart approaches. In addition, we show preliminary qualitative results of the proposed reconstruction method on real MEG data for a sensory-motor task.

This work has been published in [22].

Structure-Function Mapping via Graph Neural Networks

Participants: Yang Ji, Samuel Deslauriers-Gauthier, Rachid Deriche.

Understanding the mapping between structural and functional brain connectivity is essential for understanding how cognitive processes emerge from their morphological substrates. Many studies have investigated the problem from an eigendecomposition viewpoint, however, few have taken a deep learning viewpoint, even less studies have been engaged within the framework of graph neural networks (GNNs). As deep learning has produced significant results in several fields, there has been an increasing interest in applying neural networks to graph problems. In this work, we investigate the structural connectivity and functional connectivity mapping within a deep learning GNNs based framework, including graph convolutional networks (GCN) and graph transformer networks (GTN). To our knowledge, this original GTN based framework has never been studied in the context of structure-function and brain connectivity mapping. To achieve this goal, we use a GNNs based encoder-decoder system, where the encoder takes structural connectivity (SC) matrix as input and generates a latent representation of each node in a lower dimension, then the decoder uses the latent representation to reconstruct or predict the associated functional connectivity (FC) matrix. Besides comparing different encoders for node embedding, we also demonstrate that a decoder, which projects lower dimension vectors onto higher dimensional space, can improve the model performance. Our experiments demonstrate that both GCN encoder and GTN encoder combined with the proposed decoder can provide better results on our data than the previously proposed GCN autoencoder model. GTN encoder is also shown to be much more effective when it comes to noisy data and outliers.

This work has been published in [26].

A Riemannian revisiting of structure–function mapping based on eigenmodes

Participants: Samuel Deslauriers-Gauthier, Mauro Zucchelli, Hiba Laghrissi, Rachid Deriche.

Understanding the link between brain structure and function may not only improve our knowledge of brain organization, but also lead to better quantification of pathology. To quantify this link, recent studies have attempted to predict the brain's functional connectivity from its structural connectivity. However, functional connectivity matrices live in the Riemannian manifold of the symmetric positive definite space and a specific attention must be paid to operate on this appropriate space. In this work we investigated the implications of using a distance based on an affine invariant Riemannian metric in the context of

structure–function mapping. Specifically, we revisit previously proposed structure–function mappings based on eigendecomposition and test them on 100 healthy subjects from the Human Connectome Project using this adapted notion of distance. First, we show that using this Riemannian distance significantly alters the notion of similarity between subjects from a functional point of view. We also show that using this distance improves the correlation between the structural and functional similarity of different subjects. Finally, by using a distance appropriate to this manifold, we demonstrate the importance of mapping function from structure under the Riemannian manifold and show in particular that it is possible to outperform the group average and the so–called glass ceiling on the performance of mappings based on eigenmodes.

This work has been submitted to the special issue on Advances in Brain Functional and Structural Networks Modeling via Graph Theory of Frontiers in NeuroImaging. It is currently under review.

Towards linking diffusion MRI based macro- and microstructure measures with cortico-cortical transmission in brain tumor patients

Participants: Patryk Filipiak, Fabien Almairac *(CHU Nice, UCA)*, Marie Onno *(CHU Nice, UCA)*, Théodore Papadopoulo, Denys Fontaine *(CHU Nice, UCA)*, Lydiane Mondot *(CHU Nice, UCA)*, Stéphane Chanalet *(CHU Nice, UCA)*, Rachid Deriche, Maureen Clerc, Demian Wassermann *(INRIA Parietal)*, Petru Isan *(CHU Nice, UCA)*.

We aimed to link macro- and microstructure measures of brain white matter obtained from diffusion MRI with effective connectivity measures based on a propagation of cortico-cortical evoked potentials induced with intrasurgical direct electrical stimulation. For this, we compared streamline lengths and log-transformed ratios of streamlines computed from presurgical diffusion-weighted images, and the delays and amplitudes of N1 peaks recorded intrasurgically with electrocorticography electrodes in a pilot study of 9 brain tumor patients. Our results showed positive correlation between these two modalities in the vicinity of the stimulation sites (Pearson coefficient 0.54±0.13 for N1 delays, and 0.47±0.23 for N1 amplitudes), which could correspond to the neural propagation via U-fibers. In addition, we reached high sensitivities (0.78±0.07) and very high specificities (0.93±0.03) in a binary variant of our comparison. Finally, we used the structural connectivity measures to predict the effective connectivity using a multiple linear regression model, and showed a significant role of brain microstructure-related indices in this relation.

This work has been published in [17].

Interpretable Deep Learning as a mean for decrypting disease signature in Multiple Sclerosis

Participants: Federica Cruciani *(University of Verona)*, Lorenza Brusini *(University of Verona)*, Mauro Zucchelli, Gustavo Retuci Pinheiro *(UNICAMP - Universidade Estadual de Campinas)*, Francesco Setti *(University of Verona)*, Ilaria Boscolo Galazzo *(University of Verona)*, Leticia Rittner *(University of Verona)*, Massimiliano Calabrese *(University of Verona)*, Rachid Deriche, Gloria Menegaz *(University of Verona)*.

The mechanisms driving multiple sclerosis (MS) are still largely unknown, calling for new methods allowing to detect and characterize tissue degeneration since the early stages of the disease. In this work, our aim is to decrypt the microstructural signatures of the Primary Progressive versus the Relapsing-Remitting state of disease based on diffusion and structural magnetic resonance imaging data. A selection of microstructural descriptors, based on the 3D-Simple Harmonics Oscillator Based Reconstruction and Estimation and the set of new algebraically independent Rotation Invariant spherical harmonics Features, was considered and used to feed convolutional neural networks (CNNs) models. Classical measures derived from diffusion tensor imaging, that are fractional anisotropy and mean diffusivity, were used as benchmark for diffusion MRI (dMRI). Finally, T1-weighted images were also considered for the sake of

comparison with the state-of-the-art. A CNN model was fit to each feature map and layerwise relevance propagation (LRP) heatmaps were generated for each model, target class and subject in the test set. Average heatmaps were calculated across correctly classified patients and size-corrected metrics were derived on a set of regions of interest to assess the LRP contrast between the two classes. Our results demonstrated that dMRI features extracted in grey matter tissues can help in disambiguating primary progressive multiple sclerosis from relapsing-remitting multiple sclerosis patients and, moreover, that LRP heatmaps highlight areas of high relevance which relate well with what is known from literature for MS disease. Within a patient stratification task, LRP allows detecting the input voxels that mostly contribute to the classification of the patients in either of the two classes for each feature, potentially bringing to light hidden data properties which might reveal peculiar disease-state factors.

This work has been published in [15].

Explainable 3D-CNN for Multiple Sclerosis patients stratification

Participants: Federica Cruciani *(University of Verona)*, Lorenza Brusini *(University of Verona)*, Mauro Zucchelli, Gustavo Retuci Pinheiro *(UNICAMP - Universidade Estadual de Campinas)*, Francesco Setti *(University of Verona)*, Ilaria Boscolo Galazzo *(University of Verona)*, Leticia Rittner *(University of Verona)*, Massimiliano Calabrese *(University of Verona)*, Rachid Deriche, Gloria Menegaz *(University of Verona)*.

The growing availability of novel interpretation techniques opened the way to the application of deep learning models in the clinical field, including neuroimaging, where their use is still largely underexploited. In this work, we focus the stratification of Multiple Sclerosis (MS) patients in the Primary Progressive versus the Relapsing-Remitting state of the disease using a 3D Convolutional Neural Network trained on structural MRI data. Within this task, the application of Layer-wise Relevance Propagation visualization allowed detecting the voxels of the input data mostly involved in the classification decision, potentially bringing to light brain regions which might reveal disease state.

This work has been published in [21].

Centering inclusivity in the design of online conferences—An OHBM–Open Science perspective

Participants: Elisabeth Levitis *(University College London)*, Matteo Frigo.

As the global health crisis unfolded, many academic conferences moved online in 2020. This move has been hailed as a positive step towards inclusivity in its attenuation of economic, physical, and legal barriers and effectively enabled many individuals from groups that have traditionally been underrepresented to join and participate. A number of studies have outlined how moving online made it possible to gather a more global community and has increased opportunities for individuals with various constraints, e.g., caregiving responsibilities.

Yet, the mere existence of online conferences is no guarantee that everyone can attend and participate meaningfully. In fact, many elements of an online conference are still significant barriers to truly diverse participation: the tools used can be inaccessible for some individuals; the scheduling choices can favour some geographical locations; the set-up of the conference can provide more visibility to well-established researchers and reduce opportunities for early-career researchers. While acknowledging the benefits of an online setting, especially for individuals who have traditionally been underrepresented or excluded, we recognize that fostering social justice requires inclusivity to actively be centered in every aspect of online conference design.

Here, we draw from the literature and from our own experiences to identify practices that purposefully encourage a diverse community to attend, participate in, and lead online conferences. Reflecting on how to design more inclusive online events is especially important as multiple scientific organizations have announced that they will continue offering an online version of their event when in-person conferences can resume.

This work has been published in [19].

7 Bilateral contracts and grants with industry

7.1 Bilateral Grants with Industry

Participants: Théodore Papadopoulo.

A BPI grant proposal has been submitted in 2021 with the startup Mag4Health (other partners are CNRS and INSERM). This company develops a new MEG machine working with optically pumped magnetometers (magnetic sensors), which potentially means lower costs and better measurements. ATHENA is in charge of developping a real time interface for signal visualisation, source reconstruction and epileptic spikes detection. The proposal is in final evaluation stage.

8 Partnerships and cooperations

8.1 International research visitors

8.1.1 Visits of international scientists

Other international visits to the team

Due to the epidemic outbreak virus in France, and to the severe restrictions imposed on travels, the planned visits of some of our collaborators outside of Europe have not been made possible for this year. Prof. Gloria Menegaz (University of Verona, Department of Computer Science, IT) visited Athena in July (5th - 31st) during which we contributed to our joint work and to the serie of videos-lectures produced within the framework of the ERC CoBCoM.

8.2 European initiatives

8.2.1 FP7 & H2020 projects

ERC AdG CoBCoM

- Program: H2020-EU.1.1. (ERC-ADG-2015 - ERC Advanced Grant)
- Project acronym: CoBCoM - **ID:** 694665
- Project title: *Computational Brain Connectivity Mapping*
- Start date: 2016-09-01, End date: 2021-08-31
- P.I. : R. Deriche
- Partners: ATHENA project-team
- Abstract:

  One third of the burden of all the diseases in Europe is due to problems caused by diseases affecting brain. Although exceptional progress has been obtained for exploring it during the past decades, **the brain is still terra-incognita** and calls for specific research efforts to better understand its architecture and functioning.

  CoBCoM is our response to this great challenge of modern science with the overall goal to **develop a joint Dynamical Structural-Functional Brain Connectivity Network (DSF-BCN)** solidly grounded on advanced and integrated methods for diffusion Magnetic Resonance Imaging (dMRI) and Electro & Magneto-Encephalography (EEG & MEG).

To take up this grand challenge and achieve new frontiers for brain connectivity mapping, CoBCoM develops a new generation of computational models and methods for identifying and characterizing the structural and functional connectivities. Our strategy is to break with the tradition to incrementally and separately contributing to structure or function and develop **a global approach involving strong interactions between structural and functional connectivities.** To solve the limited view of the brain provided just by one imaging modality, our models are developed under a rigorous computational framework integrating complementary non invasive imaging modalities: dMRI, EEG and MEG.

Capitalizing on the strengths of dMRI, MEG & EEG methodologies and building on the **bio-physical and mathematical foundations** of our new generation of computational models, CoBCoMwill be applied to high-impact diseases, and its **ground-breaking computational nature and added clinical value** will open new perspectives in neuroimaging.

We refer the interested reader to the CoBCoM URL to know more about the contributions including publications, workshops and videos lectures produced within the framework of this project.

8.3 National initiatives

3IA UCA Chair : AI-Based Computational Brain Connectomics

Participants: Rachid Deriche (P.I), Samuel Deslauriers-Gauthier, Théodore Papadopoulo, Sara Sedlar, Mauro Zucchelli.

Start date: 2019-10-01 **Duration:** *48 months.*

This project aims to reconstruct and analyse the network of neural connections of the brain, called the connectome via a computational brain connectomics framework based on ground-breaking AI algorithms and machine learning tools to gain insight into brain architecture, functioning and neurodegenerative diseases.

The avalanche of big data required to reconstruct the connectome and the study of the high complexity of structural and functional interactions within the connectome clearly position brain connectomics as a big data problem where AI & machine learning in particular, represent a very promising trend, as recently demonstrated in computer vision and in some biomedical image data-driven analysis. Partly related to the ERC AdG CoBCoM, the computational brain connectomics framework we develop in this project will construct networks specifically built on new generation of AI algorithms and machine learning tools to reconstruct a structural and functional connectome using advanced and integrated dMRI, EEG & MEG methods. This project completes CoBCoM by specifically investigating the AI added value in brain mapping, opens also exciting prospects and paves the way to translate the large amounts of high dimensional heterogeneous and complex brain data into knowledge for better contribute to neurodegenerative diseases detection and diagnosis.

ADT OpenMEEG

Participants: Théodore Papadopoulo, Maureen Clerc, Kostiantyn Maksymenko, Alexandre Gramfort *(PARIETAL)*, Joan Massich *(PARIETAL)*.

Duration: *24 months.*

The OpenMEEG ADT aims at improving OpenMEEG along 3 main directions:

- Offer a user interface for the creation and verification of head models most importantly for a simpler management of non-nested head models.
- Improve the Python interface (extension and reliability). This will also be useful to develop new research axes (in connection with point 3).

- Enrich the available operators and refactor the code to offer new possibilities in OpenMEEG and reduce the cost of maintenance.

In addition to the expected gains in code maintenance, these improvements will allow a number of new – more sophisticated – applications as well as open OpenMEEG to a larger audience with a simplified interface for classical use-cases.

This contract is part of the AMDT initiative.

8.4 Regional initiatives

The Ph.D, of Joan Belo is funded by a joint grant from Oticon Medical and Region Provence Alpes Côtes d'Azur entitled 'Analysis of auditory Attention During Naturalistic Music Listening'. The goal of the project is to better understand the link between the decoding of auditory attention during naturalistic music listening using recent EEG methods known as Auditory Attention Detection and several cognitive functions and behavioral indicators that are important for listening in complex auditory situation, such as working memory or mind wandering. This is done with the aim of improving the efficiency of next generation cochlear implants by taking into account the individual cognitive aspects.

9 Dissemination

9.1 Promoting scientific activities

Participants: Rachid Deriche, Théodore Papadopoulo, Samuel Deslauriers-Gauthier, Mauro Zucchelli.

9.1.1 Scientific events: selection

Reviewer

- R. Deriche served several international conferences (ISBI, MICCAI, ISMRM, ...) and international workshops (CD-MRI MICCAI, MFCA).
- S. Deslauriers-Gauthier served several international conferences (ISBI, MICCAI) and international workshops (CD-MRI MICCAI).
- S. Deslauriers-Gauthier served as co-chair of the Neuroimaging session of ISBI 2021.
- T. Papadopoulo served as a reviewer for the international conference ISBI 2021. He also was co-chair of the "Diffusion weighted imaging" session for this conference.

9.1.2 Journal

Member of the editorial boards

- R. Deriche is member of the Editorial Board of the Journal of Neural Engineering, editorial board member at Springer for the book series entitled Computational Imaging and Vision and member of the Editorial Board of the Medical Image Analysis Journal.
- S. Deslauriers-Gauthier serves as Guest Editor for the special issue on Advances in Brain Functional and Structural Networks Modeling via Graph Theory of the journal Frontiers in Neuroscience.
- T. Papadopoulo serves as Associate Editor in Frontiers: Brain Imaging Methods and as Review Editor for Frontiers: Artificial Intelligence in Radiology.

Reviewer - reviewing activities

- R. Deriche serves several international journals (NeuroImage, IEEE Transactions on Medical Imaging, Magnetic Resonance in Medicine, Medical Image Analysis Journal,Journal of Neural Engineering ...).

- T. Papadopoulo serves several international journals (Frontiers in Neuroscience, Brain Computer Interfaces, Journal of Neural Engneering, Computational and Applied Mathematics, Medical & Biological Engineering & Computing).

- S. Deslauriers-Gauthier serves several international journals (NeuroImage, IEEE Transactions on Biomedical Engineering, Journal of Neural Engineering, Medical Image Analysis, Science Advances).

- M. Zucchelli serves several international journals NeuroImage, BioMedical Engineering OnLine).

9.1.3 Invited talks

- S. Deslauriers-Gauthier presented his work titled "A Unified Framework for Multimodal Structure–function Mapping Based on Eigenmodes" to the Sherbrooke Connectivity Imaging Lab of the Université de Sherbrooke, Canada.

9.1.4 Scientific expertise

- R. Deriche served several national and international institutions in reviewing applications : 3IA UCA Chairs, ERC AdG and StG Grants, Swiss National Science Foundation, EPFL, the Netherlands Organisation for Scientific Research (NWO).

- T. Papadopoulo served in reviewing applications for the Neuromod institute of Université Côte d'Azur.

- T. Papadopoulo was member of the INSERM committee responsible for the selection of INSERM International Research Projects (IRP).

- T. Papadopoulo reviewed ANR project proposals and for a prize in University of Paris-Saclay.

9.1.5 Research administration

- T. Papadopoulo was member of the committee for INSERM research director competition in the neuroscience section (CSS4).

- T. Papadopoulo is elected member in the academic council of Côte d'Azur University.

- T. Papadopoulo is the head of the Technological Development Committee of Inria Sophia Antipolis Méditerranée.

9.2 Teaching - Supervision - Juries

9.2.1 Teaching

- Master: T. Papadopoulo, *Inverse problems for brain functional imaging*, 24 ETD, M2, Mathématiques, Vision et Apprentissage, ENS Cachan, France.

- Master: T. Papadopoulo, *Functional Brain Imaging*, 10 ETD, M1,M2 in the MSc Mod4NeuCog of Université Côte d'Azur.

9.2.2 Supervision

- PhD defended on Feb. 22th, 2021 Matteo Frigo, “Computational brain connectivity mapping: from multi-compartment modeling to network topology via tractography filtering” started Nov, 1st, 2017, Université Côte d’Azur. Supervisors: Rachid Deriche and Samuel Deslauriers-Gauthier.
- PhD in progress: Sara Sedlar, "Reconstruction and analysis of dynamical functional networks from EEG, MEG and dMRI Measurements", Université Côte d’Azur, started October 2018. Supervisors: Théodore Papadopoulo and Samuel Deslauriers-Gauthier
- PhD in progress: Ivana Kojcic, "Estimation of cortical activity and of the structure–function link using EEG and dMRI", Université Côte d’Azur, started October 2018. Supervisors: Théodore Papadopoulo and Samuel Deslauriers-Gauthier.
- PhD in progress: Côme Le Breton, "Non invasive analysis of epileptogenetic networks and their response to neurofeedback", started June 2019. Supervisors: Maureen Clerc and Théodore Papadopoulo.
- PhD in progress: Joan Belo, "Electroencephalography analysis of auditory attention when listening to music", started June 2019. Supervisors: Maureen Clerc and Daniele Schön.
- PhD in progress: I. Carrara, "Auto-regressive models for MEG/EEG processing", started in Oct. 2021. Supervisor: Théodore Papadopoulo.

9.2.3 Juries

- R. Deriche, S. Deslaurier-Gauthier and T. Papadopoulo participated in the PhD Jury of M. Frigo at Université Côte d’Azur on Feb. 22th, 2021.
- S. Deslauriers-Gauthier participated in the PhD Jury of Jonathan Rafael Patino Lopez at École polytechnique fédérale de Lausanne on June 7th 2021.
- S. Deslauriers-Gauthier participated in the Master thesis defense of Gabrielle Grenier at Université de Sherbrooke on December 17th 2021.

9.3 Popularization

9.3.1 Interventions

- T. Papadopoulo, C. Le Breton and G. Sola Dos Santos made a demonstration of the P300 speller to a public of young students twice in 2021.

10 Scientific production

10.1 Major publications

[1] B. Belaoucha and T. Papadopoulo. ‘Structural connectivity to reconstruct brain activation and effective connectivity between brain regions’. In: *Journal of Neural Engineering* 17.3 (1st June 2020), p. 035006. DOI: 10.1088/1741-2552/ab8b2b. URL: https://hal.inria.fr/hal-02945585.

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[3] E. Caruyer, C. Lenglet, G. Sapiro and R. Deriche. ‘Design of multishell sampling schemes with uniform coverage in diffusion MRI’. In: *Magnetic Resonance in Medicine* 69.6 (June 2013), pp. 1534–1540. DOI: 10.1002/mrm.24736. URL: http://hal.inria.fr/hal-00821688/.

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[9] M. Frigo, E. Cruciani, D. Coudert, R. Deriche, S. Deslauriers-Gauthier and E. Natale. 'Network alignment and similarity reveal atlas-based topological differences in structural connectomes'. In: *Network Neuroscience* (20th May 2021). DOI: 10.1162/netn_a_00199. URL: https://hal.archives-ouvertes.fr/hal-03033777.

[10] G. Girard, A. Daducci, L. Petit, J.-P. Thiran, K. Whittingstall, R. Deriche, D. Wassermann and M. Descoteaux. 'AxTract: Toward microstructure informed tractography'. In: *Human Brain Mapping* 38.11 (Nov. 2017), pp. 5485–5500. DOI: 10.1002/hbm.23741. URL: http://onlinelibrary.wiley.com/doi/10.1002/hbm.23741/abstract.

[11] S. Hitziger, M. Clerc, S. Saillet, C. Bénar and T. Papadopoulo. 'Adaptive Waveform Learning: A Framework for Modeling Variability in Neurophysiological Signals'. In: *IEEE Transactions on Signal Processing* 65 (15th Aug. 2017), pp. 4324–4338. DOI: 10.1109/TSP.2017.2698415. URL: https://hal.inria.fr/hal-01548428.

[12] S. Vallaghé and T. Papadopoulo. 'A Trilinear Immersed Finite Element Method for Solving the Electroencephalography Forward Problem'. In: *SIAM Journal on Scientific Computing* 32.4 (2010), pp. 2379–2394. DOI: 10.1137/09075038X. URL: https://epubs.siam.org/doi/pdf/10.1137/09075038X.

[13] M. Zucchelli, S. Deslauriers-Gauthier and R. Deriche. 'A Computational Framework For Generating Rotation Invariant Features And Its Application In Diffusion MRI'. In: *Medical Image Analysis* (Feb. 2020). DOI: 10.1016/j.media.2019.101597. URL: https://hal.inria.fr/hal-02370077.

10.2 Publications of the year

International journals

[14] J. Belo, M. Clerc and D. Schön. 'EEG-Based Auditory Attention Detection and Its Possible Future Applications for Passive BCI'. In: *Frontiers in Computer Science* 3 (30th Apr. 2021). DOI: 10.3389/fcomp.2021.661178. URL: https://hal.archives-ouvertes.fr/hal-03215168.

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[17] P. Filipiak, F. Almairac, T. Papadopoulo, D. Fontaine, L. Mondot, S. Chanalet, R. Deriche, M. Clerc and D. Wassermann. 'Towards Linking Diffusion MRI based Macro-and Microstructure Measures with Cortico-Cortical Transmission in Brain Tumor Patients'. In: *NeuroImage* (2021). DOI: 10.1016/j.neuroimage.2020.117567. URL: https://hal.inria.fr/hal-03015641.

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[20] F. Turi, M. Clerc and T. Papadopoulo. 'Long multi-stage training for a motor-impaired user in a BCI competition'. In: *Frontiers in Human Neuroscience* 15 (25th Mar. 2021). DOI: 10.3389/fnhum.2021.647908. URL: https://hal.inria.fr/hal-03192449.

International peer-reviewed conferences

[21] F. Cruciani, L. Brusini, M. Zucchelli, G. Retuci Pinheiro, F. Setti, I. Boscolo Galazzo, R. Deriche, L. Rittner, M. Calabrese and G. Menegaz. 'Explainable 3D-CNN for Multiple Sclerosis patients stratification'. In: Pattern Recognition. ICPR International Workshops and Challenges. Milan, Italy, 10th Jan. 2021. URL: https://hal.archives-ouvertes.fr/hal-02971361.

[22] I. Kojčić, T. Papadopoulo, R. Deriche and S. Deslauriers-Gauthier. 'Incorporating transmission delays supported by diffusion MRI in MEG source reconstruction'. In: ISBI 2021 - IEEE International Symposium on Biomedical Imaging. Nice, France, 13th Apr. 2021. URL: https://hal.inria.fr/hal-03143148.

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[24] M. Zucchelli, S. Deslauriers-Gauthier and R. Deriche. 'Brain Tissue Microstructure Characterization Using dMRI Based Autoencoder Neural-Networks'. In: MICCAI 2021 International Workshop on Computational Diffusion MRI. Strasbourg, France, 1st Oct. 2021. URL: https://hal.inria.fr/hal-03312453.

[25] M. Zucchelli, S. Deslauriers-Gauthier and R. Deriche. 'Investigating the effect of DMRI signal representation on fully-connected neural networks brain tissue microstructure estimation'. In: ISBI 2021 - IEEE International Symposium on Biomedical Imaging. Nice / Virtual, France, 13th Apr. 2021. URL: https://hal.inria.fr/hal-03174220.

Scientific book chapters

[26] Y. Ji, S. Deslauriers-Gauthier and R. Deriche. 'Structure-Function Mapping via Graph Neural Networks'. In: *Machine Learning in Clinical Neuroimaging. 4th International Workshop, MLCN 2021, Held in Conjunction with MICCAI 2021, Strasbourg, France, September 27, 2021, Proceedings*. Vol. 13001. Lecture Notes in Computer Science. Springer, 2021, pp. 135–144. DOI: 10.1007/978-3-030-87586-2_14. URL: https://hal.archives-ouvertes.fr/hal-03352550.

Doctoral dissertations and habilitation theses

[27] M. Frigo. 'Computational Brain Connectivity Mapping : From Multi-Compartment Modeling To Network Topology Via Tractography Filtering'. Université Côte d'Azur, 22nd Feb. 2021. URL: https://tel.archives-ouvertes.fr/tel-03273337.

Reports & preprints

[28] M. Frigo, R. H. Fick, M. Zucchelli, S. Deslauriers-Gauthier and R. Deriche. *Multi-Tissue Multi-Compartment Models of Diffusion MRI*. 29th Jan. 2021. URL: https://hal.archives-ouvertes.fr/hal-03125887.

Other scientific publications

[29] D. Diaz-Arce, A. Ghouma, P. Guetschel, T. Papadopoulo, M. Mantegazza and F. Duprat. 'Tools for convulsive seizures and interictal spikes detection'. In: Congrès Labex ICST. Nantes, France, 18th Nov. 2021. URL: https://hal.inria.fr/hal-03540822.

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10.3 Other

Softwares

[32] [SW] M. Frigo, M. Zucchelli, R. Deriche and S. Deslauriers-Gauthier, *TALON: Tractograms As Linear Operators in Neuroimaging* version 0.3.0, 19th Jan. 2021. LIC: MIT License. HAL: ⟨hal-03116143⟩, URL: https://hal.archives-ouvertes.fr/hal-03116143, VCS: https://gitlab.inria.fr/cobcom/talon, SWHID: ⟨swh:1:dir:f25157ad1b13cb20ac3457d4f6756b49ac63d079;origin=https://hal.archives-ouvertes.fr/hal-03116143;visit=swh:1:snp:465d89956196578717f4cb5155e456c279aa6a22;anchor=swh:1:rev:10247a14640a280b9140a27ce003d382d70cccac;path=/⟩.

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