

# Connectome Mapper 3: a software pipeline for multi-scale connectome mapping of multimodal MR data

## Poster No:

1174

## Submission Type:

Abstract Submission

## Authors:

Sebastien Tourbier<sup>1</sup>, Yasser Alemàn-Gòmez<sup>1</sup>, Emeline Mullier<sup>1</sup>, Alessandra Griffo<sup>2</sup>, Meritxell Bach Cuadra<sup>3</sup>, Patric Hagmann<sup>1</sup>

## Institutions:

<sup>1</sup>Connectomics Lab, Centre Hospitalier Universitaire Vaudois (CHUV) and University of Lausanne (UNIL), Lausanne, Vaud, <sup>2</sup>Medical Image Processing Lab (MIPLAB), Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Vaud, <sup>3</sup>Centre D'Imagerie BioMédicale (CIBM), University of Lausanne (UNIL), Lausanne, Vaud

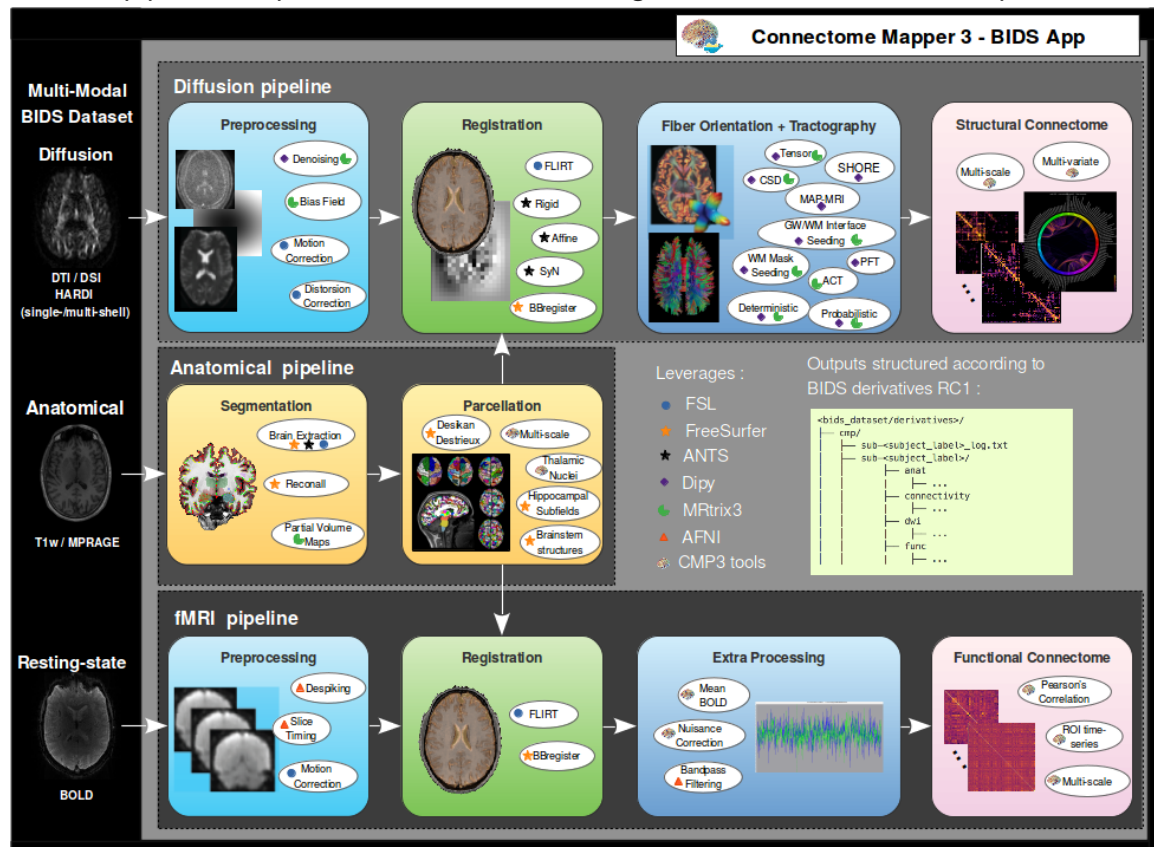
## Introduction:

Connectome Mapper (CMP) is an open-source software pipeline with a Graphical User Interface (GUI) written in Python and historically designed to help researchers in all the organization and processing steps needed to compute, from raw structural MRI (sMRI) and diffusion MRI (dMRI) data, a hierarchical multi-scale brain parcellation (Cammoun 2012) and the corresponding structural connectomes (Daducci 2012). While the two previous versions were designed with ease-of-use, modularity, configurability, re-executability and transparency in mind, they have shown to be limited in terms of interoperability, reusability, portability, and reproducibility. Following recent advances in the standardization of neuroimaging data organization (Gorgolewski 2016) and processing (Gorgolewski 2017), we present the third version of CMP (CMP3), which has evolved massively in terms of the underlying code, the tools used and the scope of functionality provided, been extended to the processing of resting-state fMRI (rfMRI) data.

## Methods:

CMP3 is developed following modern software practices and implements a full subject-level analysis workflow necessary to estimate a structural brain parcellation at five different macroscopic scales from sMRI with corresponding multivariate and multi-scale structural and functional connectomes from dMRI and rfMRI respectively. The workflow is encapsulated in a

Docker container image (Merkel 2014) and released as a BIDS App (Gorgolewski 2017), a framework which promotes interoperability, reusability, portability, and reproducibility. The processing workflow of CMP3 takes as input BIDS datasets (Gorgolewski 2016) and has a modular architecture composed of processing pipelines, each dedicated to one modality and composed of different stages that interface with one or more state-of-the-art tools (Figure 1). Each pipeline is described by a configuration file and represented in Nipype (Gorgolewski 2011), which facilitates its execution and the recordings of data and workflow provenance. This allows CMP3 workflow to be dynamically built and configured depending on the availability of sMRI, dMRI, rfMRI data and the parameters set in the different pipeline configuration files. The different pipeline outputs are structured following the BIDS derivatives RC1 specifications.

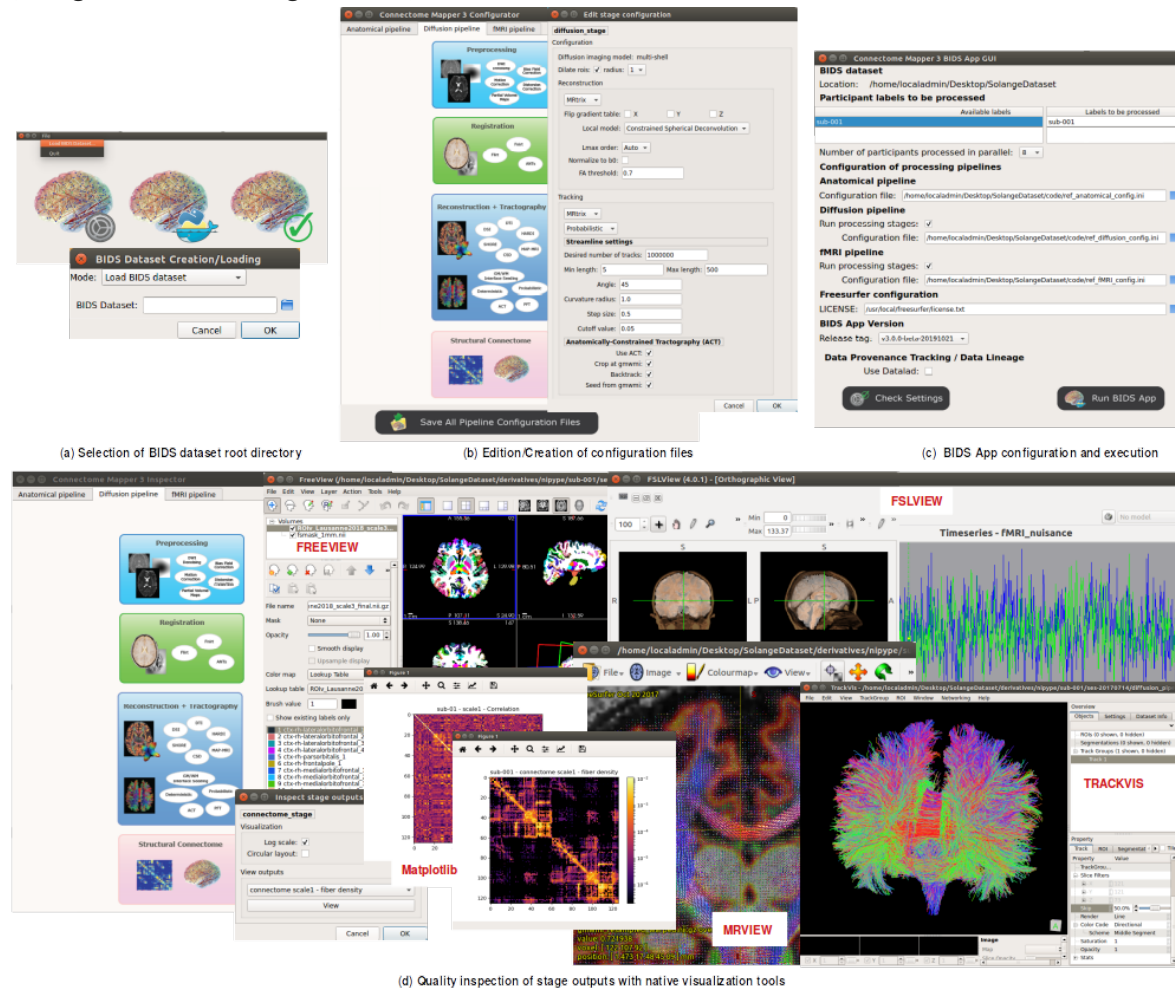


**Figure 1: Connectome Mapper 3 BIDS App Workflow** - The subject-level analysis workflow of the CMP3 BIDS App implements all the processing steps needed to compute a multi-scale brain parcellation and the corresponding multi-variate structural and/or functional connectomes from raw MRI data. It handles datasets structured following the BIDS standard (Gorgolewski 2016) that include at least a sMRI scan (T1w or MPAGE) and a dMRI scan (DTI, DSI, single/multi-shell HARDI) and/or a rfMRI scan. The workflow is staged in Nipype (Gorgolewski 2011) and has a modular architecture composed of three different pipelines (anatomical, diffusion and fMRI) dedicated to each modality (sMRI, dMRI and rfMRI). In particular, each pipeline consists of a number of processing stages implementing one or multiple specific tasks, where each task can interface with either a specific state-of-the-art tool included in FSL (Jenkinson 2012), FreeSurfer (Fischl 2012), ANTs (Avants 2008), Dipy (Garyfalidis 2014), MRtrix3 (Tournier 2019), AFNI (Cox 1997), or with an in-house tool. Main CMP3 derivatives of the analysis of one specific subject are placed in the `<bids_dataset/derivatives>/cmp/sub-<subject_label>` folder, structured according to the BIDS derivatives RC1 specifications, where sMRI-, dMRI-, and rfMRI-derived data are stored in their respective `anat`-, `dwi`-, and `func`-folder. Estimated connectomes are placed in the `connectivity` folder.

## Results:

CMP3 is distributed under the 3-Clause BSD license, hosted on GitHub at <https://github.com/connectomicslab/connectomemapper3> where issues and new feature requests are transparently discussed, and versions are released through continuous integration testing. For best user experience, CMP3 has a GUI that eases and supports all the steps involved in the configuration of the pipeline, the configuration of the BIDS App run and its execution, and the inspection of the stage outputs (Figure 2). While the configuration files can be easily created from the GUI, the execution of the BIDS App can also be scripted to guarantee a consistent and homogeneous processing on a collection of datasets at the same time. Adopting this procedure, CMP3 has

been successfully run on the range of supported diffusion schemes using the HCP test-retest (reorganized according to BIDS) and four in-house datasets.



**Figure 2: The Graphical User Interface of the Connectome Mapper 3.** It is designed in order to bring the best experience to the final user by facilitating all the steps required to perform an analysis. A typical procedure would consist of the selection of the root directory of the BIDS dataset to be analyzed (a), the creation/edition of the different pipeline configuration files (b), the configuration of the BIDS App run and its execution (c), and the inspection of the stage outputs using either fslview, or freeview, or mrview or trackvis depending on the software involved in the stage (d). Connectivity matrices are visualized using the matplotlib library.

## Conclusions:

The Connectome Mapper 3 provides a unique software pipeline solution for researchers to easily, reliably and transparently create a hierarchical multi-scale connectome representation of the structural and functional brain systems, on any dataset structured according to the BIDS standard. Thanks to its modular architecture, new pipelines and stages can be added with relatively little effort to account for additional imaging modalities and algorithms. At the time of writing, a new pipeline dedicated to the processing of EEG data is being implemented for instance. We believe that CMP3 will provide a solid multi-modal framework for the investigation of brain network function and organization at specific scales, as well as a map that links different spatial and temporal scales.

## Neuroinformatics and Data Sharing:

Workflows <sup>1</sup>

Informatics Other <sup>2</sup>

**Keywords:**

Data analysis  
Data Registration  
FUNCTIONAL MRI  
Informatics  
STRUCTURAL MRI  
Sub-Cortical  
Thalamus  
Tractography  
Workflows  
Other - BIDS App, Connectome

<sup>1|2</sup>Indicates the priority used for review

**My abstract is being submitted as a Software Demonstration.**

Yes

**Please indicate below if your study was a "resting state" or "task-activation" study.**

Other

**Healthy subjects only or patients (note that patient studies may also involve healthy subjects):**

Healthy subjects

**Was any human subjects research approved by the relevant Institutional Review Board or ethics panel? NOTE: Any human subjects studies without IRB approval will be automatically rejected.**

Not applicable

**Was any animal research approved by the relevant IACUC or other animal research panel? NOTE: Any animal studies without IACUC approval will be automatically rejected.**

Not applicable

**Please indicate which methods were used in your research:**

Functional MRI  
Structural MRI  
Diffusion MRI

**Provide references using author date format**

Avants B.B. (2008), 'Symmetric diffeomorphic image registration with cross-correlation: evaluating automated labeling of elderly and neurodegenerative brain', Med Image Anal., vol. 1, pp. 26-41

- Cammoun L. (2012), 'Mapping the human connectome at multiple scales with diffusion spectrum MRI', *J Neurosci Methods*, vol. 203, no. 2, pp. 386-97
- Cox R.W. (1996), 'AFNI: Software for analysis and visualization of functional magnetic resonance neuroimages', *Computers and Biomedical Research*, vol. 29, pp. 162-173.
- Daducci A. (2012), 'The Connectome Mapper: an open-source processing pipeline to map connectomes with MRI', *PLoS ONE*, vol. 7, no. 12, e48121
- Fischl B. (2012), 'FreeSurfer', *Neuroimage*, vol. 62, no. 2, pp. 774-781
- Garifallidis E. (2014), 'Dipy, a library for the analysis of diffusion MRI data', *Front. Neuroinform.*, vol. 8, no. 8
- Gorgolewski K.J. (2011), 'Nipype: a flexible, lightweight and extensible neuroimaging data processing framework in python', *Front Neuroinform*, vol. 5, pp. 13-13.
- Gorgolewski K.J. (2016), 'The brain imaging data structure, a format for organizing and describing outputs of neuroimaging', *Scientific Data*, vol. 3, no. 160044
- Gorgolewski K.J. (2017), 'BIDS apps: Improving ease of use, accessibility, and reproducibility of neuroimaging data analysis methods', *PLoS computational biology* vol. 13, no. 3, e1005209
- Jenkinson B. (2012), 'FSL', *Neuroimage*. vol. 62, no. 2, pp. 782-90
- Tournier J.-D. (2019), 'MRtrix3: A fast, flexible and open software framework for medical image processing and visualisation', *NeuroImage*, vol. 202, pp. 116-37