

---

# **CMP3 Documentation**

***Release v3.0.3***

**Brain Communication Pathways Sinergia Consortium**

**Feb 21, 2022**



# GETTING STARTED

<b>1</b>	<b>About</b>	<b>3</b>
<b>2</b>	<b>License information</b>	<b>5</b>
<b>3</b>	<b>Aknowledgment</b>	<b>7</b>
3.1	Help/Questions . . . . .	7
<b>4</b>	<b>Eager to contribute?</b>	<b>9</b>
<b>5</b>	<b>Contents</b>	<b>11</b>
5.1	Installation Instructions for Users . . . . .	11
5.2	Connectome Mapper 3 and the BIDS standard . . . . .	13
5.3	Commandline Usage . . . . .	15
5.4	Graphical User Interface . . . . .	20
5.5	Outputs of Connectome Mapper 3 . . . . .	73
5.6	Packages and modules . . . . .	80
5.7	Adopting Datalad for collaboration . . . . .	238
5.8	Running on a cluster (HPC) . . . . .	244
5.9	Tutorial notebooks . . . . .	246
5.10	BSD 3-Clause License . . . . .	317
5.11	Changes . . . . .	318
5.12	Citing . . . . .	330
5.13	Contributors . . . . .	331
5.14	Contributing to Connectome Mapper 3 . . . . .	332
5.15	Support, Bugs and New Feature Requests . . . . .	337
<b>6</b>	<b>Funding</b>	<b>339</b>
	<b>Bibliography</b>	<b>341</b>
	<b>Python Module Index</b>	<b>343</b>
	<b>Index</b>	<b>345</b>



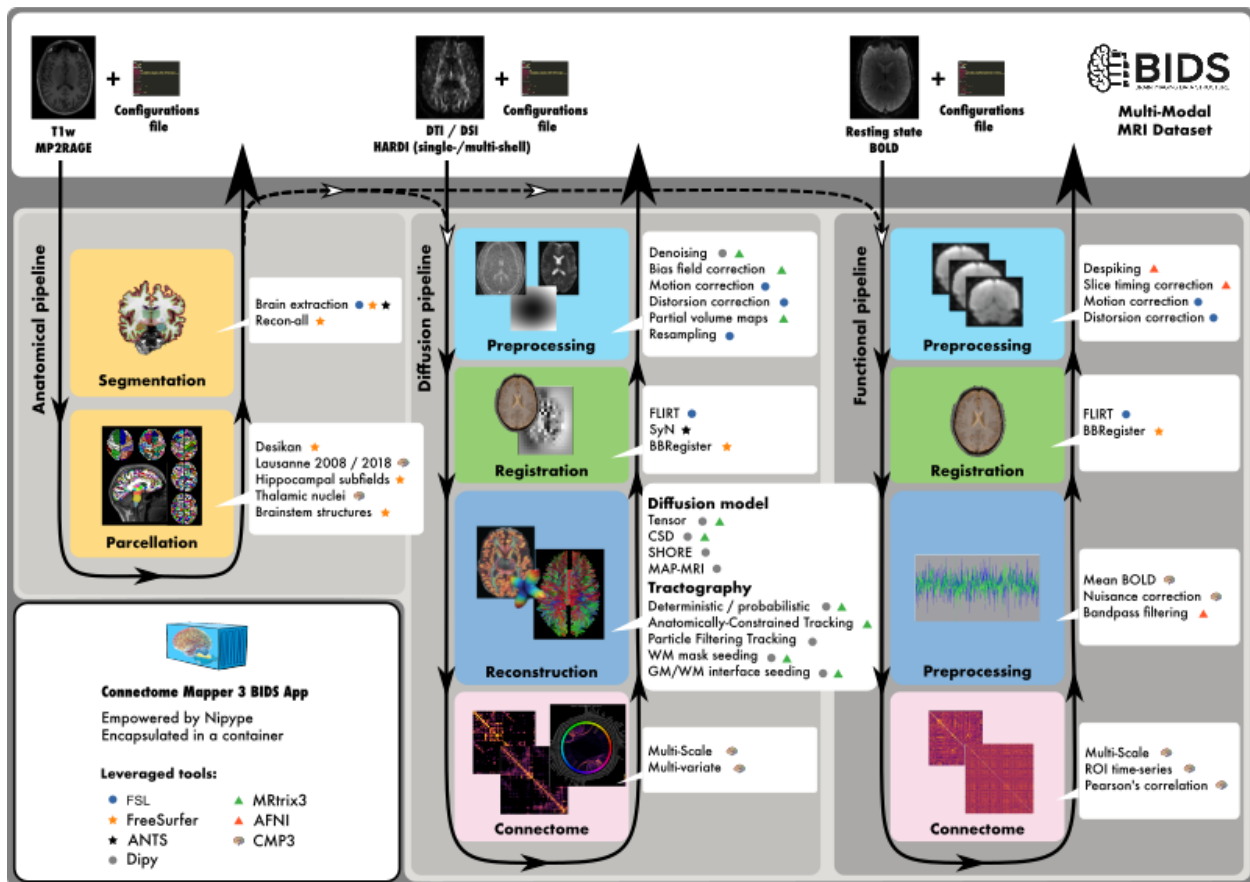


**Latest released version:** v3.0.3

This neuroimaging processing pipeline software is developed by the Connectomics Lab at the University Hospital of Lausanne (CHUV) for use within the [SNF Sinergia Project 170873](#), as well as for open-source software distribution. Source code is hosted on [GitHub](#).

<p><b>Warning:</b> THIS SOFTWARE IS FOR RESEARCH PURPOSES ONLY AND SHALL NOT BE USED FOR ANY CLINICAL USE. THIS SOFTWARE HAS NOT BEEN REVIEWED OR APPROVED BY THE FOOD AND DRUG ADMINISTRATION OR EQUIVALENT AUTHORITY, AND IS FOR NON-CLINICAL, IRB-APPROVED RESEARCH USE ONLY. IN NO EVENT SHALL DATA OR IMAGES GENERATED THROUGH THE USE OF THE SOFTWARE BE USED IN THE PROVISION OF PATIENT CARE.</p>
---





Connectome Mapper 3 is an open-source Python3 image processing pipeline software, with a Graphical User Interface (GUI), that implements full anatomical, diffusion and resting-state MRI processing pipelines, from raw T1 / Diffusion / BOLD data to multi-resolution connection matrices based on a new version of the Lausanne parcellation atlas, aka Lausanne2018.

Connectome Mapper 3 pipelines use a combination of tools from well-known software packages, including [FSL](#), [FreeSurfer](#), [ANTs](#), [MRtrix3](#), [Dipy](#) and [AFNI](#), empowered by the [Nipype](#) dataflow library. These pipelines are designed to provide the best software implementation for each state of processing at the time of conception, and can be easily updated as newer and better neuroimaging software become available.

To enhance reproducibility and replicability, the processing pipelines with all dependencies are encapsulated in a Docker image container, which handles datasets organized following the BIDS standard and is distributed as a [BIDS](#)

App @ [Docker Hub](#). For execution on high-performance computing cluster, a Singularity image is also made freely available @ [Sylabs Cloud](#).

To enhanced accessibility and reduce the risk of misconfiguration, Connectome Mapper 3 comes with an interactive GUI, aka `cmpbidsappmanager`, which supports the user in all the steps involved in the configuration of the pipelines, the configuration and execution of the BIDS App, and the control of the output quality. In addition, to facilitate the use by users not familiar with Docker and Singularity containers, Connectome Mapper 3 provides two Python commandline wrappers (`connectomemapper3_docker` and `connectomemapper3_singularity`) that will generate and run the appropriate command.

Since v3.0.3, CMP3 provides a new pipeline `py:class:EEGPipeline` dedicated to EEG modality with a collection of interfaces based on [MNE](#), [MNE-Connectivity](#), and [PyCartool](#). Please check [this notebook](#) for a demonstration using the public [VEPCON dataset](#).

---

### Carbon footprint estimation of BIDS App run

In support to the Organisation for Human Brain Mapping (OHBM) Sustainability and Environmental Action (OHBM-SEA) group, CMP3 enables you since v3.0.3 to be more aware about the adverse impact of your processing on the environment!

With the new `--track_carbon_footprint` option of the `connectomemapper3_docker` and `connectomemapper3_singularity` BIDS App python wrappers, and the new "Track carbon footprint" option of the BIDS Interface Window of `cmpbidsappmanager`, you can estimate the carbon footprint incurred by the execution of the BIDS App. Estimations are conducted using [codecarbon](#) to estimate the amount of carbon dioxide (CO2) produced to execute the code by the computing resources and save the results in `<bids_dir>/code/emissions.csv`.

Then, to visualize, interpret and track the evolution of the emitted CO2 emissions, you can use the visualization tool of [codecarbon](#) aka `carbonboard` that takes as input the `csv` created:

```
$ carbonboard --filepath="<bids_dir>/code/emissions.csv" --port=xxxx
```

Please check <https://ohbm-environment.org> to learn more about OHBM-SEA!

---

## LICENSE INFORMATION

This software is distributed under the open-source license Modified BSD. See [license](#) for more details.

All trademarks referenced herein are property of their respective holders.



## ACKNOWLEDGMENT

If you are using the Connectome Mapper 3 in your work, please acknowledge this software. See [Citing](#) for more details.

### 3.1 Help/Questions

If you run into any problems or have any questions, you can post to the [CMTK-users group](#). Code bugs can be reported by creating a “New Issue” on the [source code repository](#).





## EAGER TO CONTRIBUTE?

Connectome Mapper 3 is open-source and all kind of contributions (bug reporting, documentation, code,...) are welcome! See *[Contributing to Connectome Mapper](#)* for more details.



## CONTENTS

## 5.1 Installation Instructions for Users

**Warning:** This software is for research purposes only and shall not be used for any clinical use. This software has not been reviewed or approved by the Food and Drug Administration or equivalent authority, and is for non-clinical, IRB-approved Research Use Only. In no event shall data or images generated through the use of the Software be used in the provision of patient care.

The Connectome Mapper 3 is composed of a Docker image, namely the Connectome Mapper 3 BIDS App, and a Python Graphical User Interface, namely the Connectome Mapper BIDS App Manager.

- Installation instructions for the Connectome mapper 3 BIDS App are found in [Installation](#).
- Installation instructions for the Connectome mapper 3 BIDS App Manager are found in [Installation](#).

Make sure that you have installed the following prerequisites.

---

**Important:** On Mac and Windows, if you want to track the carbon emission incurred by the processing with the `--track_carbon_footprint` option flag, you will need to install in addition the Intel Power Gadget tool available [here](#).

---

### 5.1.1 The Connectome Mapper 3 BIDSApp

#### Prerequisites

- Install Docker Engine depending of your system:
  - For Ubuntu 14.04/16.04/18.04, follow the instructions at <https://docs.docker.com/install/linux/docker-ce/ubuntu/>
  - For Mac OSX ( $\geq 10.10.3$ ), get the .dmg installer at <https://store.docker.com/editions/community/docker-ce-desktop-mac>
  - For Windows ( $\geq 10$ ), get the installer at <https://store.docker.com/editions/community/docker-ce-desktop-windows>

---

**Note:** Connectome Mapper 3 BIDSApp has been tested only on Ubuntu and MacOSX. In principles, it should also run on Windows but it might require a few patches to make it work.

---

- Manage Docker as a non-root user

- Open a terminal
- Create the docker group:

```
$ sudo groupadd docker
```

- Add the current user to the docker group:

```
$ sudo usermod -G docker -a $USER
```

- Reboot
- After reboot, test if docker is managed as non-root:

```
$ docker run hello-world
```

## Installation

Installation of the Connectome Mapper 3 has been facilitated through the distribution of a BIDSApp relying on the Docker software container technology.

- Open a terminal
- Get the latest release (v3.0.3) of the BIDS App:

```
$ docker pull SebastienTournier/connectomemapper-bidsapp:v3.0.3
```

- To display all docker images available:

```
$ docker images
```

You should see the docker image “connectomemapper-bidsapp” with tag “v3.0.3” is now available.

- You are ready to use the Connectome Mapper 3 BIDS App from the terminal. See its [commandline usage](#).

### 5.1.2 The Connectome Mapper 3 BIDSApp Manager (GUI)

#### Prerequisites

- Download the Python 3 installer of miniconda3 corresponding to your 32/64bits MacOSX/Linux/Win system and install it following the instructions at <https://conda.io/miniconda.html>.

#### Installation

The installation of the Connectome Mapper 3, including `cmpbidsappmanager`, consists of the creation of conda environment with all python dependencies installed, and the installation of `connectomemapper` via the Python Package Index (PyPI) as follows:

- Download the appropriate [environment.yml](#) / [environment\\_macosx.yml](#).

---

**Important:** It seems there is no conda package for `git-annex` available on Mac. For your convenience, we created an additional `conda/environment_macosx.yml` miniconda3 environment where the line `- git-annex=XXXXXXX` has been removed. Git-annex should be installed on MacOSX using `brew` i.e. `brew install git-annex`. See <https://git-annex.branchable.com/install/> for more details.

Note that `git-annex` is only necessary if you wish to use BIDS datasets managed by Datalad (<https://www.datalad.org/>).

---

- Open a terminal.
- Create a miniconda3 environment where all python dependencies will be installed:

```
$ conda env create -f /path/to/downloaded/conda/environment[_macosx].yaml
```

- Activate the conda environment:

```
$ source activate py37cmp-gui
```

or:

```
$ conda activate py37cmp-gui
```

- Install finally the latest released version of Connectome Mapper 3 with the Python Package Index (PyPI) using `pip`:

```
(py37cmp-gui)$ pip install connectomemapper
```

- You are ready to use the Connectome Mapper 3 (1) via its Graphical User Interface (GUI) aka CMP BIDS App Manager (See [Graphical User Interface](#) for the user guide), (2) via its python `connectomemapper3_docker` and `connectomemapper3_singularity` wrappers (See [With the wrappers](#) for commandline usage), or (3) by interacting directly with the Docker / Singularity Engine (See [With the Docker / Singularity Engine](#) for commandline usage).

---

### In the future

If you wish to update Connectome Mapper 3 and the Connectome Mapper 3 BIDS App Manager, this could be easily done by running `pip install connectomemapper==v3.X.Y`.

---

## Help/Questions

If you run into any problems or have any questions, you can post to the [CMTK-users group](#). Code bugs can be reported by creating a “New Issue” on the [source code repository](#).

## 5.2 Connectome Mapper 3 and the BIDS standard

Connectome Mapper 3 (CMP3) adopts the BIDS (Brain Imaging Data Structure) standard for data organization and is developed following the BIDS App standard with a Graphical User Interface (GUI).

**This means CMP3 can be executed in two different ways:**

1. By running the BIDS App container image directly from the terminal or a script (See [Commandline Usage](#) section for more details).
2. By using its Graphical User Interface, designed to facilitate the configuration of all pipeline stages, the configuration of the BIDS App run and its execution, and the inspection of the different stage outputs with appropriate viewers (See [Graphical User Interface](#) section for more details) .

For more information about BIDS and BIDS-Apps, please consult the [BIDS Website](#), the [Online BIDS Specifications](#), and the [BIDSApps Website](#). [HeuDiConv](#) can assist you in converting DICOM brain imaging data to BIDS. A nice tutorial can be found @ [BIDS Tutorial Series: HeuDiConv Walkthrough](#).

### 5.2.1 Example BIDS dataset

For instance, a BIDS dataset with T1w, DWI and rs-fMRI images should adopt the following organization, naming, and file formats::

```
ds-example/

  README
  CHANGES
  participants.tsv
  dataset_description.json

  sub-01/
    anat/
      sub-01_T1w.nii.gz
      sub-01_T1w.json
    dwi/
      sub-01_dwi.nii.gz
      sub-01_dwi.json
      sub-01_dwi.bvec
      sub-01_dwi.bval
    func/
      sub-01_task-rest_bold.nii.gz
      sub-01_task-rest_bold.json

  ...

  sub-<subject_label>/
    anat/
      sub-<subject_label>_T1w.nii.gz
      sub-<subject_label>_T1w.json
    ...

  ...
```

---

**Important:** Before using any BIDS App, we highly recommend you to validate your BIDS structured dataset with the free, online [BIDS Validator](#).

---

## 5.3 Commandline Usage

Connectome Mapper 3 (CMP3) is distributed as a BIDS App which adopts the BIDS standard for data organization and takes as principal input the path of the dataset that is to be processed. The input dataset is required to be in valid BIDS format, and it must include at least a T1w or MPRAGE structural image and a DWI and/or resting-state fMRI image. See [Connectome Mapper 3 and the BIDS standard](#) page that provides links for more information about BIDS and BIDS-Apps as well as an example for dataset organization and naming.

**Warning:** As of CMP3 v3.0.0-RC2, the BIDS App includes a **tracking** system that anonymously reports the run of the BIDS App. This feature has been introduced to support us in the task of fund finding for the development of CMP3 in the future. However, users are still free to opt-out using the `--notrack` commandline argument.

**Important:** Since v3.0.0-RC4, configuration files adopt the JSON format. If you have your configuration files still in the *old* INI format, do not worry, the CMP3 BIDS App will convert them to the new JSON format automatically for you.

### 5.3.1 Commandline Arguments

The command to run CMP3 follows the [BIDS-Apps](#) definition standard with additional options for loading pipeline configuration files.

Entrypoint script of the BIDS-App Connectome Mapper version v3.0.3

```
usage: connectomemapper3 [-h]
                        [--participant_label PARTICIPANT_LABEL [PARTICIPANT_LABEL ...]]
                        [--session_label SESSION_LABEL [SESSION_LABEL ...]]
                        [--anat_pipeline_config ANAT_PIPELINE_CONFIG]
                        [--dwi_pipeline_config DWI_PIPELINE_CONFIG]
                        [--func_pipeline_config FUNC_PIPELINE_CONFIG]
                        [--number_of_threads NUMBER_OF_THREADS]
                        [--number_of_participants_processed_in_parallel NUMBER_OF_
↪PARTICIPANTS_PROCESSED_IN_PARALLEL]
                        [--mrtrix_random_seed MRTRIX_RANDOM_SEED]
                        [--ants_random_seed ANTS_RANDOM_SEED]
                        [--ants_number_of_threads ANTS_NUMBER_OF_THREADS]
                        [--fs_license FS_LICENSE] [--coverage] [--notrack]
                        [-v]
                        bids_dir output_dir {participant,group}
```

## Positional Arguments

<b>bids_dir</b>	The directory with the input dataset formatted according to the BIDS standard.
<b>output_dir</b>	The directory where the output files should be stored. If you are running group level analysis this folder should be prepopulated with the results of the participant level analysis.
<b>analysis_level</b>	Possible choices: participant, group  Level of the analysis that will be performed. Multiple participant level analyses can be run independently (in parallel) using the same output_dir.

## Named Arguments

<b>--participant_label</b>	The label(s) of the participant(s) that should be analyzed. The label corresponds to sub-<participant_label> from the BIDS spec (so it does not include “sub-“). If this parameter is not provided all subjects should be analyzed. Multiple participants can be specified with a space separated list.
<b>--session_label</b>	<b>The label(s) of the session that should be analyzed.</b> The label corresponds to ses-<session_label> from the BIDS spec (so it does not include “ses-“). If this parameter is not provided all sessions should be analyzed. Multiple sessions can be specified with a space separated list.
<b>--anat_pipeline_config</b>	Configuration .txt file for processing stages of the anatomical MRI processing pipeline
<b>--dwi_pipeline_config</b>	Configuration .txt file for processing stages of the diffusion MRI processing pipeline
<b>--func_pipeline_config</b>	Configuration .txt file for processing stages of the fMRI processing pipeline
<b>--number_of_threads</b>	The number of OpenMP threads used for multi-threading by Freesurfer (Set to [Number of available CPUs -1] by default).
<b>--number_of_participants_processed_in_parallel</b>	The number of subjects to be processed in parallel (One by default).  Default: 1
<b>--mrtrix_random_seed</b>	Fix MRtrix3 random number generator seed to the specified value
<b>--ants_random_seed</b>	Fix ANTS random number generator seed to the specified value
<b>--ants_number_of_threads</b>	Fix number of threads in ANTs. If not specified ANTs will use the same number as the number of OpenMP threads (see <code>—number_of_threads</code> option flag)
<b>--fs_license</b>	Freesurfer license.txt
<b>--coverage</b>	Run connectomemapper3 with coverage  Default: False
<b>--notrack</b>	Do not send event to Google analytics to report BIDS App execution, which is enabled by default.  Default: False
<b>-v, --version</b>	show program’s version number and exit



---

**Important:** Before using any BIDS App, we highly recommend you to validate your BIDS structured dataset with the free, online [BIDS Validator](#).

---

### 5.3.2 Participant Level Analysis

You can run CMP3 using the lightweight Docker or Singularity wrappers we created for convenience or you can interact directly with the Docker / Singularity Engine via the docker or singularity run command.

---

#### New in v3.0.2

You can now be aware about the adverse impact of your processing on the environment !

With the new `--track_carbon_footprint` option of the `connectomemapper3_docker` and `connectomemapper3_singularity` BIDS App python wrappers, you can use `codecarbon` to estimate the amount of carbon dioxide (CO2) produced to execute the code by the computing resources and save the results in `<bids_dir>/code/emissions.csv`.

Then, to visualize, interpret and track the evolution of the CO2 emissions incurred, you can use the visualization tool of `codecarbon` aka `carbonboard` that takes as input the `.csv` created:

```
$ carbonboard --filepath="<bids_dir>/code/emissions.csv" --port=xxxx
```

---

#### With the wrappers

When you run `connectomemapper3_docker`, it will generate a Docker command line for you, print it out for reporting purposes, and then execute it without further action needed, e.g.:

```
$ connectomemapper_docker \
  "/home/user/data/ds001" "/home/user/data/ds001/derivatives" \
  participant --participant_label 01 --session_label 01 \
  --fs_license "/usr/local/freesurfer/license.txt" \
  --config_dir "/home/user/data/ds001/code" \
  --track_carbon_footprint \
  --anat_pipeline_config "ref_anatomical_config.json" \
  (--dwi_pipeline_config "ref_diffusion_config.json" \)
  (--func_pipeline_config "ref_fMRI_config.json" \)
  (--number_of_participants_processed_in_parallel 1)
```

When you run `connectomemapper3_singularity`, it will generate a Singularity command line for you, print it out for reporting purposes, and then execute it without further action needed, e.g.:

```
$ connectomemapper3_singularity \
  "/home/user/data/ds001" "/home/user/data/ds001/derivatives" \
  participant --participant_label 01 --session_label 01 \
  --fs_license "/usr/local/freesurfer/license.txt" \
  --config_dir "/home/user/data/ds001/code" \
  --track_carbon_footprint \
  --anat_pipeline_config "ref_anatomical_config.json" \
  (--dwi_pipeline_config "ref_diffusion_config.json" \)
  (--func_pipeline_config "ref_fMRI_config.json" \)
  (--number_of_participants_processed_in_parallel 1)
```

## With the Docker / Singularity Engine

If you need a finer control over the container execution, or you feel comfortable with the Docker or Singularity Engine, avoiding the extra software layer of the wrapper might be a good decision.

### Docker

For instance, the previous call to the `connectomemapper3_docker` wrapper corresponds to:

```
$ docker run -t --rm -u $(id -u):$(id -g) \
-v /home/user/data/ds001:/bids_dir \
-v /home/user/data/ds001/derivatives:/output_dir \
(-v /usr/local/freesurfer/license.txt:/bids_dir/code/license.txt) \
sebastientourbier/connectomemapper-bidsapp:v3.0.3 \
/bids_dir /output_dir participant --participant_label 01 (--session_label_
↪01) \
--anat_pipeline_config /bids_dir/code/ref_anatomical_config.json \
(--dwi_pipeline_config /bids_dir/code/ref_diffusion_config.json \)
(--func_pipeline_config /bids_dir/code/ref_fMRI_config.json \)
(--number_of_participants_processed_in_parallel 1)
```

### Singularity

For instance, the previous call to the `connectomemapper3_singularity` wrapper corresponds to:

```
$ singularity run --containall \
--bind /home/user/data/ds001:/bids_dir \
--bind /home/user/data/ds001/derivatives:/output_dir \
--bind /usr/local/freesurfer/license.txt:/bids_dir/code/license.txt \
library://connectomicslab/default/connectomemapper-bidsapp:v3.0.3 \
/bids_dir /output_dir participant --participant_label 01 (--session_label_
↪01) \
--anat_pipeline_config /bids_dir/code/ref_anatomical_config.json \
(--dwi_pipeline_config /bids_dir/code/ref_diffusion_config.json \)
(--func_pipeline_config /bids_dir/code/ref_fMRI_config.json \)
(--number_of_participants_processed_in_parallel 1)
```

---

**Note:** The local directory of the input BIDS dataset (here: `/home/user/data/ds001`) and the output directory (here: `/home/user/data/ds001/derivatives`) used to process have to be mapped to the folders `/bids_dir` and `/output_dir` respectively using the `docker -v / singularity --bind` run option.

---

---

**Important:** The user is requested to use its own FreeSurfer license ([available here](#)). CMP expects by default to find a copy of the FreeSurfer `license.txt` in the `code/` folder of the BIDS directory. However, one can also mount a `freesurfer license.txt` with the `docker -v / singularity --bind` run option. This file can be located anywhere on the computer (as in the example above, i.e. `/usr/local/freesurfer/license.txt`) to the `code/` folder of the BIDS directory inside the docker container (i.e. `/bids_dir/code/license.txt`).

---

---

**Note:** At least a configuration file describing the processing stages of the anatomical pipeline should be provided. Diffusion and/or Functional MRI pipeline are performed only if a configuration file is set. The generation of such

---

configuration files, the execution of the BIDS App docker image and output inspection are facilitated through the use of the Connectome Mapper GUI, i.e. `cmpbidsappmanager` (see [dedicated documentation page](#))

### 5.3.3 Debugging

Logs are outputted into `<output_dir>/cmp/sub-<participant_label>/sub-<participant_label>_log-cmpbidsapp.txt`.

### 5.3.4 Already have Freesurfer outputs?

If you have already Freesurfer v5 / v6 output data available, CMP3 can use them if there are properly placed in your output / derivatives directory. Since v3.0.0, CMP3 expects to find a `freesurfer-7.2.0`, so make sure that your derivatives are organized as follows:

```
your_bids_dataset
|----- derivatives/
|         |----- freesurfer-7.2.0/
|         |         |----- sub-01[_ses-01]/
|         |         |         |----- label/
|         |         |         |----- mri/
|         |         |         |----- surf/
|         |         |         |----- ...
|         |         |----- ...
|         |----- sub-01/
|         |----- ...
```

### 5.3.5 Support, bugs and new feature requests

If you need any support or have any questions, you can post to the [CMTK-users group](#).

All bugs, concerns and enhancement requests for this software are managed on GitHub and can be submitted at <https://github.com/connectomicslab/connectomemapper3/issues>.

### 5.3.6 Not running on a local machine?

If you intend to run CMP3 on a remote system such as a high-performance computing cluster where Docker is not available due to root privileges, a Singularity image is also built for your convenience and available on [Sylabs.io](#). Please see instructions at [Running on a cluster \(HPC\)](#).

Also, you will need to make your data available within that system first. Comprehensive solutions such as [Datalad](#) will handle data transfers with the appropriate settings and commands. Datalad also performs version control over your data. A tutorial is provided in [Adopting Datalad for collaboration](#).

## 5.4 Graphical User Interface

### 5.4.1 Introduction

Connectome Mapper 3 comes with a Graphical User Interface, the Connectome Mapper BIDS App manager, designed to facilitate the configuration of all pipeline stages, the configuration of the BIDS App run and its execution, and the inspection of the different stage outputs with appropriate viewers.

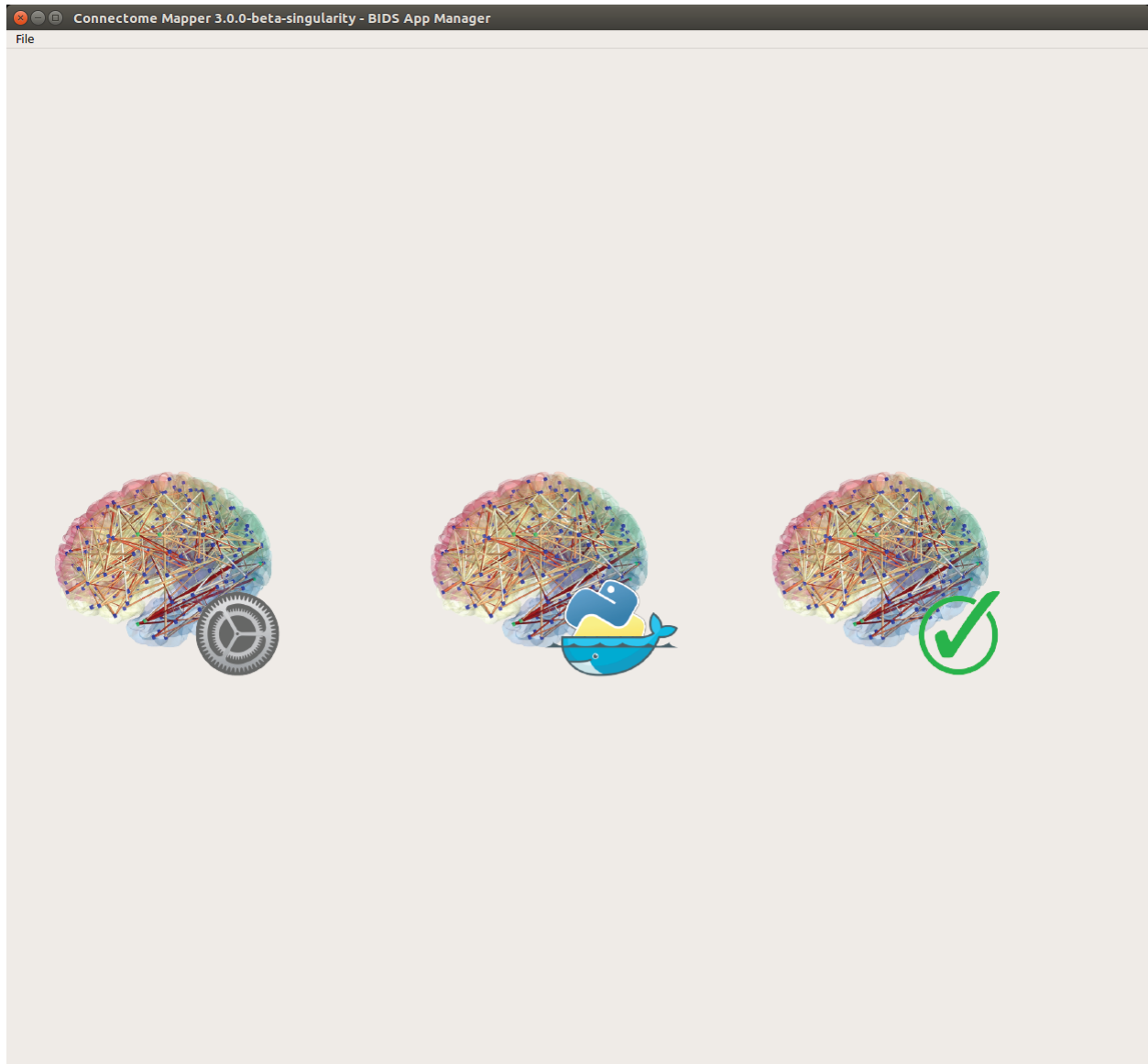


Fig. 1: Main window of the Connectome Mapper BIDS App Manager

## 5.4.2 Start the Graphical User Interface

In a terminal, enter to following:

```
$ source activate py37cmp-gui
```

or:

```
$ conda activate py37cmp-gui
```

Please see Section [Installation](#) for more details about installation.

After activation of the conda environment, start the graphical user interface called **Connectome Mapper 3 BIDS App Manager**

```
$ cmpbidsappmanager
```

## 5.4.3 Load a BIDS dataset

The **Connectome Mapper 3 BIDS App Manager** allows you to:

- load a BIDS dataset stored locally.

You only have to select the root directory of your valid BIDS dataset (see note below)

- create a new datalad/BIDS dataset locally from an existing local or remote datalad/BIDS dataset (This is a feature under development)

Select the mode “Install a Datalad/BIDS dataset”.

If ssh connection is used, make sure to enable the “install via ssh” and to provide all connection details (IP address / Remote host name, remote user, remote password)

---

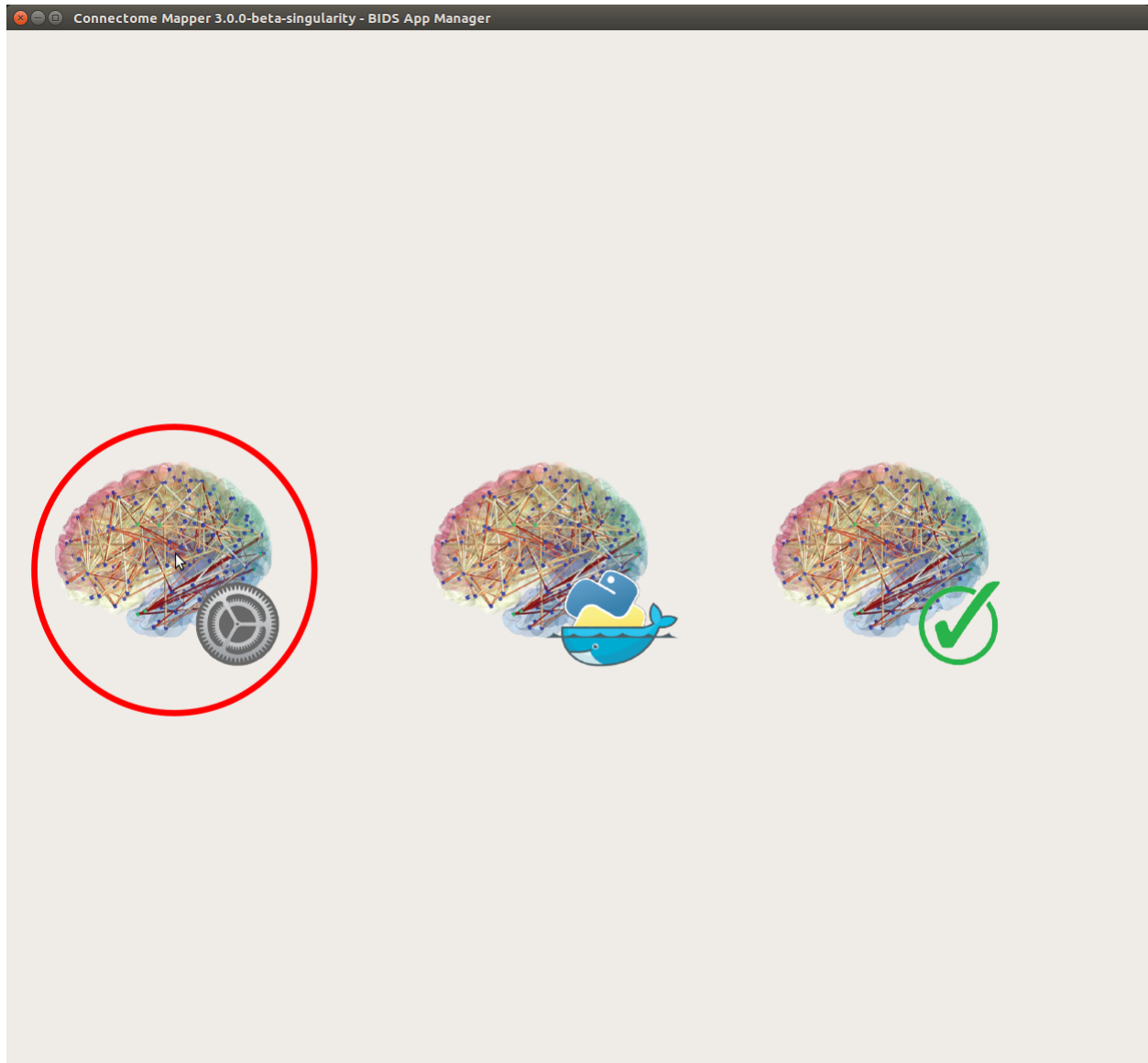
**Note:** The input dataset **MUST** be a valid BIDS structured dataset and must include at least one T1w or MPAGE structural image. We highly recommend that you validate your dataset with the free, online [BIDS Validator](#).

---

## 5.4.4 Pipeline stage configuration

### Start the Configurator Window

- From the main window, click on the left button to start the Configurator Window.



- The window of the Connectome Mapper BIDS App Configurator will appear, which will assist you note only in configuring the pipeline stages (each pipeline has a tab panel), but also in creating appropriate configuration files which could be used outside the Graphical User Interface.

The outputs depend on the chosen parameters.

## Anatomical pipeline stages

### Segmentation

Prior to Lausanne parcellation, CMP3 relies on **Freesurfer** for the segmentation of the different brain tissues and the reconstruction of the cortical surfaces. If you plan to use a custom parcellation, you will be required here to specify the pattern of the different existing segmentation files that follows BIDS derivatives (See *Custom segmentation*).

*Freesurfer*

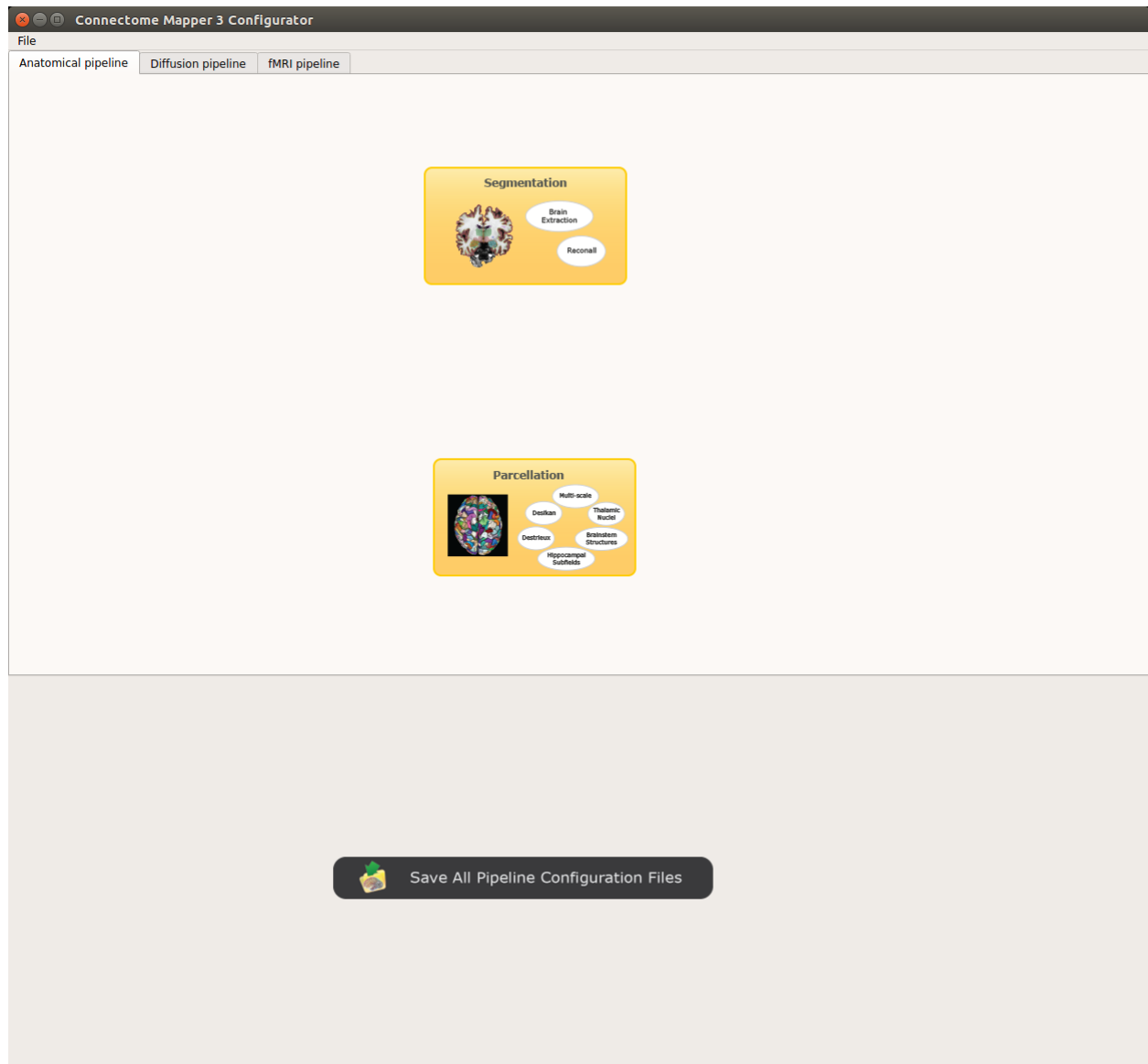


Fig. 2: Configurator Window of the Connectome Mapper

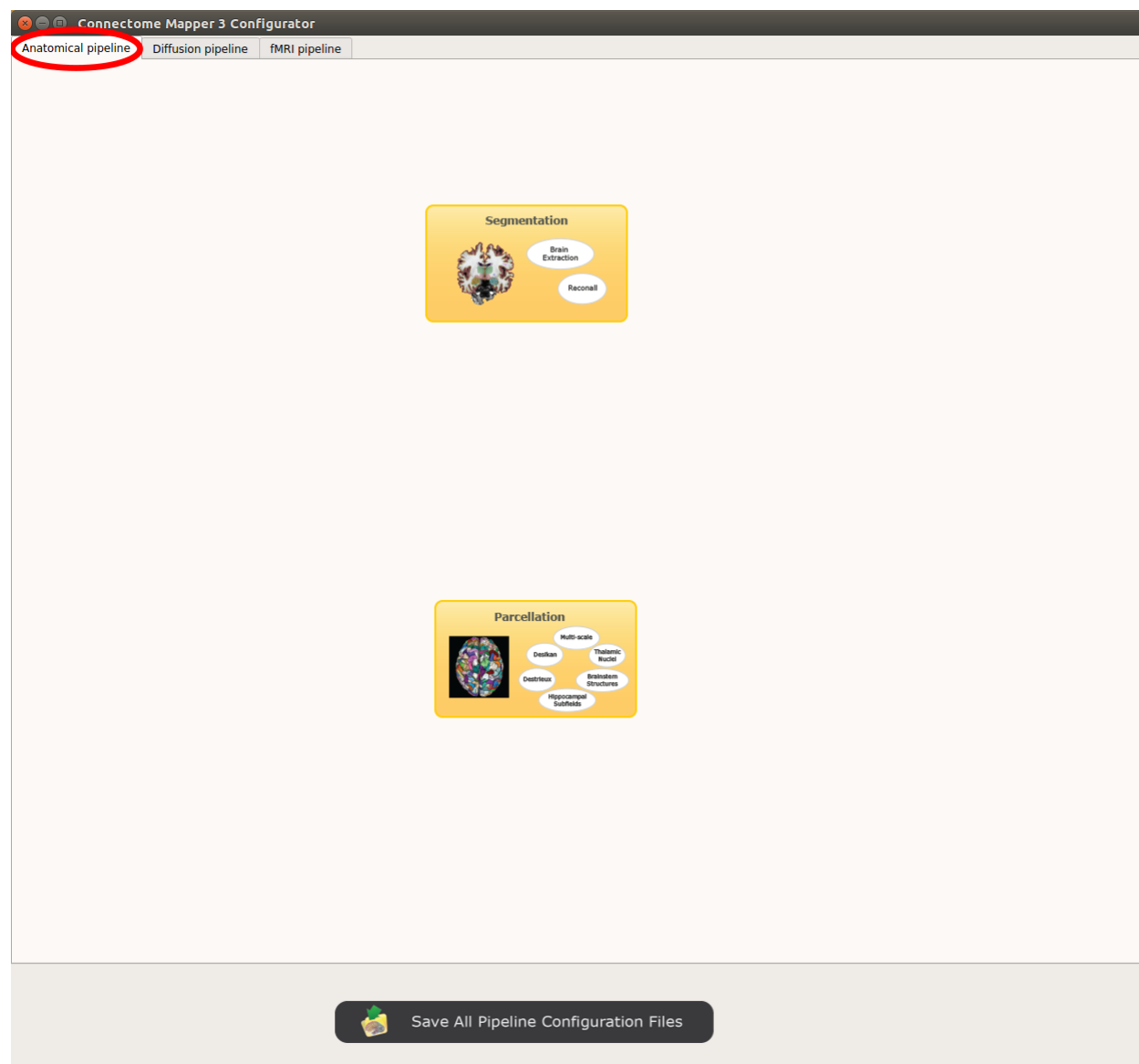
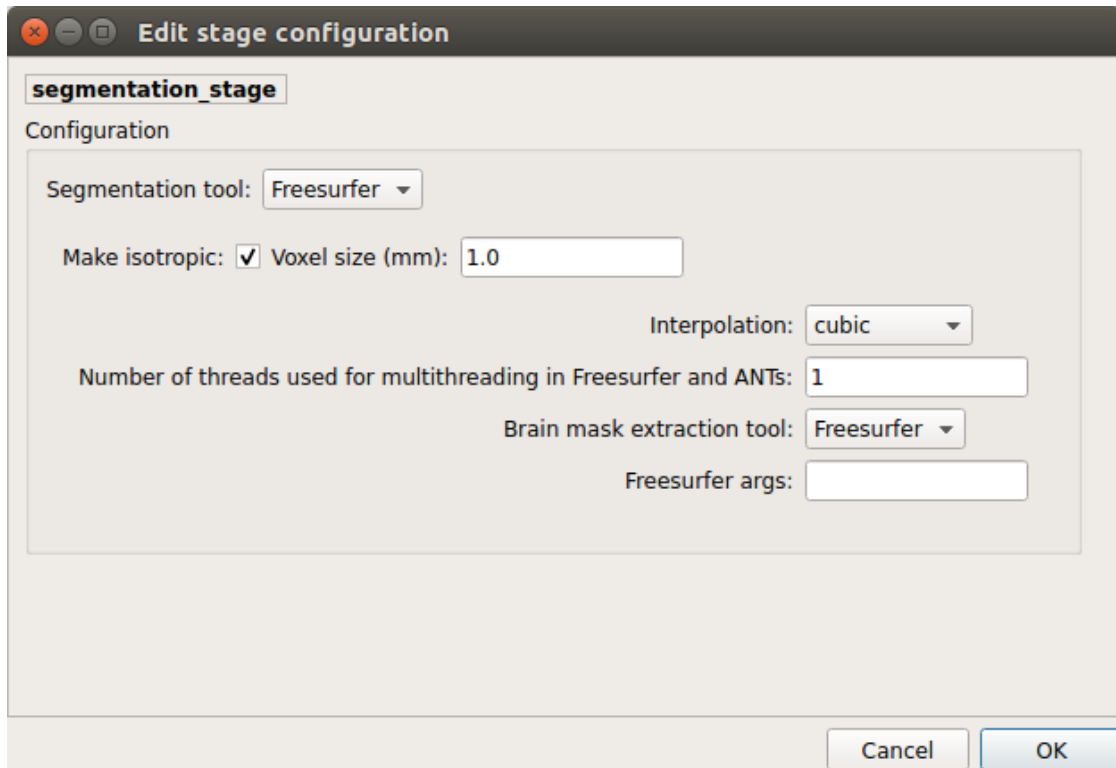


Fig. 3: Panel for configuration of anatomical pipeline stages





- *Number of threads*: used to specify how many threads are used for parallelization
- *Brain extraction tools*: alternative brain extraction methods injected in Freesurfer
- *Freesurfer args*: used to specify extra Freesurfer processing options

**Note:** If you have already Freesurfer v5 / v6 / v7 output data available, CMP3 can use them if there are placed in your output / derivatives directory. Note however that since v3.0.0, CMP3 expects to find a `freesurfer-7.2.0`, so make sure that your derivatives are organized as follows:

```
your_bids_dataset
derivatives/
  freesurfer-7.2.0/
    sub-01[_ses-01]/
      label/
      mri/
      surf/
      ...
    ...
  sub-01/
  ...
```

*Custom segmentation*

The screenshot shows a window titled "Edit stage configuration" with a sub-header "segmentation\_stage". Below this is a "Configuration" section containing several input fields for segmentation settings. The "Segmentation tool" is set to "Custom segmentation". There are five sections for custom masks: "Custom brain mask", "Custom gray matter mask", "Custom white matter mask", "Custom CSF mask", and "Custom Freesurfer aparc+aseg (used by MRtrix3 to build the 5TT image)". Each section has a "Derivatives directory" field (all set to "cmp-v3.0.2") and a "desc" field (all empty). The "label" and "suffix" are pre-filled for each mask type: brain (label: brain, suffix: mask), gray matter (label: GM, suffix: dseg), white matter (label: WM, suffix: dseg), CSF (label: CSF, suffix: dseg), and Freesurfer (label: aparcaseg, suffix: dseg). At the bottom right are "Cancel" and "OK" buttons.

**segmentation\_stage**

Configuration

Segmentation tool: Custom segmentation ▼

Custom brain mask

Derivatives directory: cmp-v3.0.2

desc: brain

suffix: mask

Custom gray matter mask

Derivatives directory: cmp-v3.0.2

desc:

label: GM

suffix: dseg

Custom white matter mask

Derivatives directory: cmp-v3.0.2

desc:

label: WM

suffix: dseg

Custom CSF mask

Derivatives directory: cmp-v3.0.2

desc:

label: CSF

suffix: dseg

Custom Freesurfer aparc+aseg (used by MRtrix3 to build the 5TT image)

Derivatives directory: cmp-v3.0.2

desc: aparcaseg

suffix: dseg

Cancel OK

You can use any parcellation scheme of your choice as long as you provide a list of segmentation files organized following the [BIDS derivatives specifications](#) for segmentation files, provide appropriate .tsv side-car files that describes the index/label/color mapping of the parcellation, and adopt the atlas-<label> entity to encode the name of the atlas, i.e:

```

<derivatives_directory>/
  sub-<participant_label>/
    anat/
      <source_entities>_desc-brain_mask.nii.gz
      <source_entities>_label-GM[_desc-<label>]_dseg.nii.gz
      <source_entities>_label-WM[_desc-<label>]_dseg.nii.gz
      <source_entities>_label-CSF[_desc-<label>]_dseg.nii.gz
      <source_entities>_desc-aparcaseg_dseg.nii.gz

```

The desc BIDS entity can be used to target specific mask and segmentation files.

For instance, the configuration above would allow us to re-use the outputs of the anatomical pipeline obtained with the previous v3.0.2 version of CMP3:

```

your_bids_dataset
derivatives/
  cmp-v3.0.2/
    sub-01/
      anat/
        sub-01_desc-brain_mask.nii.gz
        sub-01_label-GM_dseg.nii.gz
        sub-01_label-WM_dseg.nii.gz
        sub-01_label-CSF_dseg.nii.gz
        sub-01_desc-aparcaseg_dseg.nii.gz
        ...
      ...
    sub-01/
      ...

```

---

**Important:** If you plan to use either Anatomically Constrained or Particle Filtering tractography, you will still require to have Freesurfer 7 output data available in your output / derivatives directory, as described in the above note in [\\*Freesurfer\\*](#).

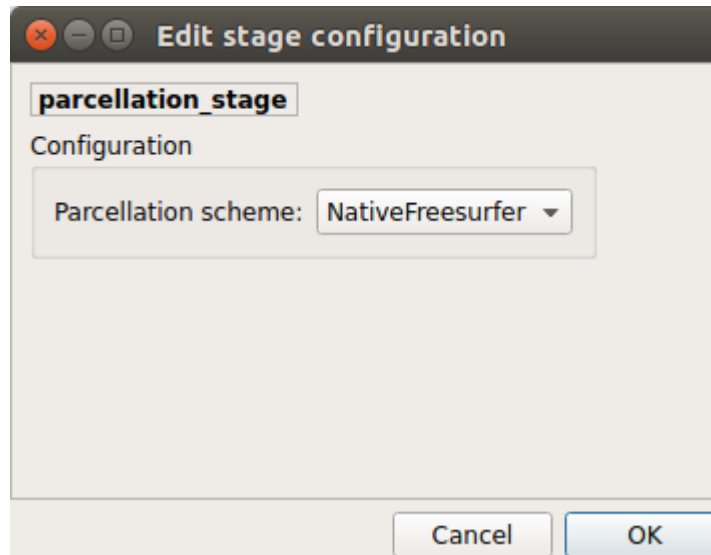
---

## Parcellation

Generates the Native Freesurfer or Lausanne2018 parcellation from Freesurfer data. Alternatively, since v3.0.3 you can use your own custom parcellation files.

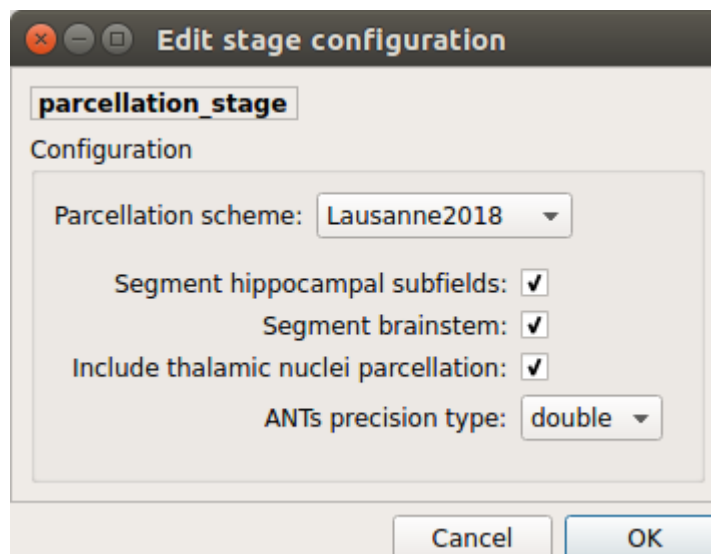
### Parcellation scheme

- *NativeFreesurfer:*



Atlas composed of 83 regions from the Freesurfer aparc+aseg file

- *Lausanne2018:*



New version of Lausanne parcellation atlas, corrected, and extended with 7 thalamic nuclei, 12 hippocampal subfields, and 4 brainstem sub-structure per hemisphere

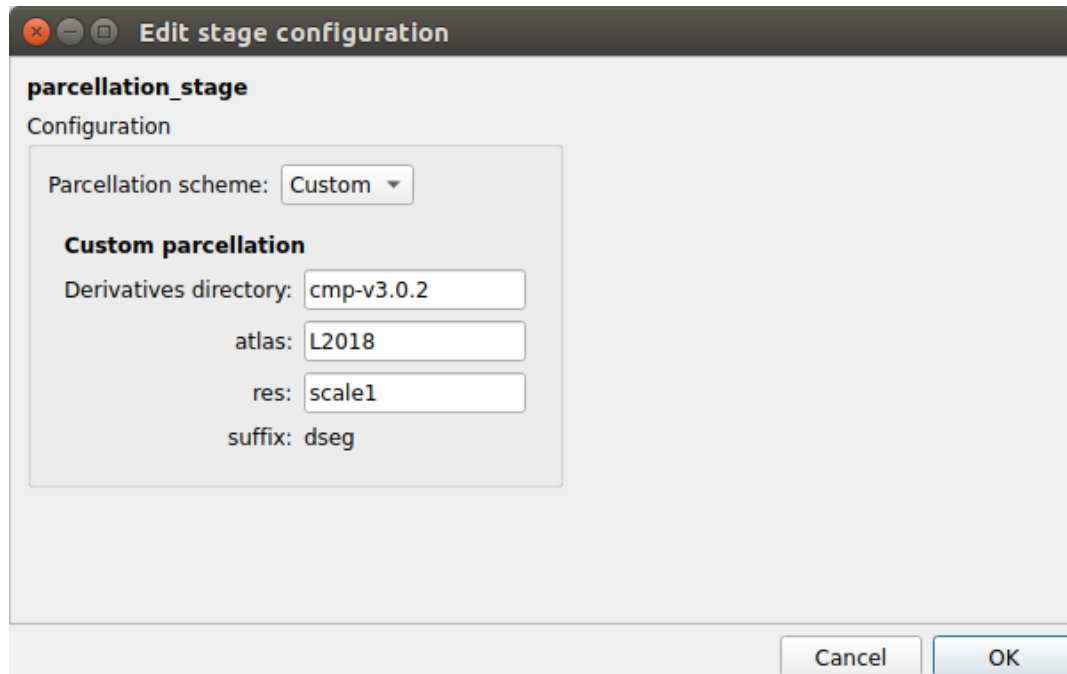
---

**Since v3.0.0, Lausanne2018 parcellation has completely replaced the old Lausanne2008 parcellation.**

As it provides improvements in the way Lausanne parcellation labels are generated, any code and data related to Lausanne2008 has been removed. If you still wish to use this old parcellation scheme, please use v3.0.0-RC4 which is the last version that supports it.

---

- *Custom:*



You can use any parcellation scheme of your choice as long as they follow the [BIDS derivatives specifications](#) for segmentation files, provide appropriate .tsv sidecar files that describes the index/label/color mapping of the parcellation, and adopt the atlas-<label> entity to encode the name of the atlas, i.e:

```
<derivatives_directory>/
  sub-<participant_label>/
    anat/
      <source_entities>[_space-<space>]_atlas-<label>[_res-<label>]_dseg.
      nii.gz
      <source_entities>[_space-<space>]_atlas-<label>[_res-<label>]_dseg.tsv
```

The res BIDS entity allows the differentiation between multiple scales of the same atlas.

For instance, the above configuration would allow us to re-use the scale 1 of the Lausanne parcellation generated by the anatomical pipeline obtained of the previous v3.0.2 version of CMP3:

```
your_bids_dataset
derivatives/
  cmp-v3.0.2/
    sub-01/
      anat/
        sub-01_atlas-L2018_res-scale1_dseg.nii.gz
        sub-01_atlas-L2018_res-scale1_dseg.tsv
        ...
      ...
    sub-01/
      ...
```

## Diffusion pipeline stages

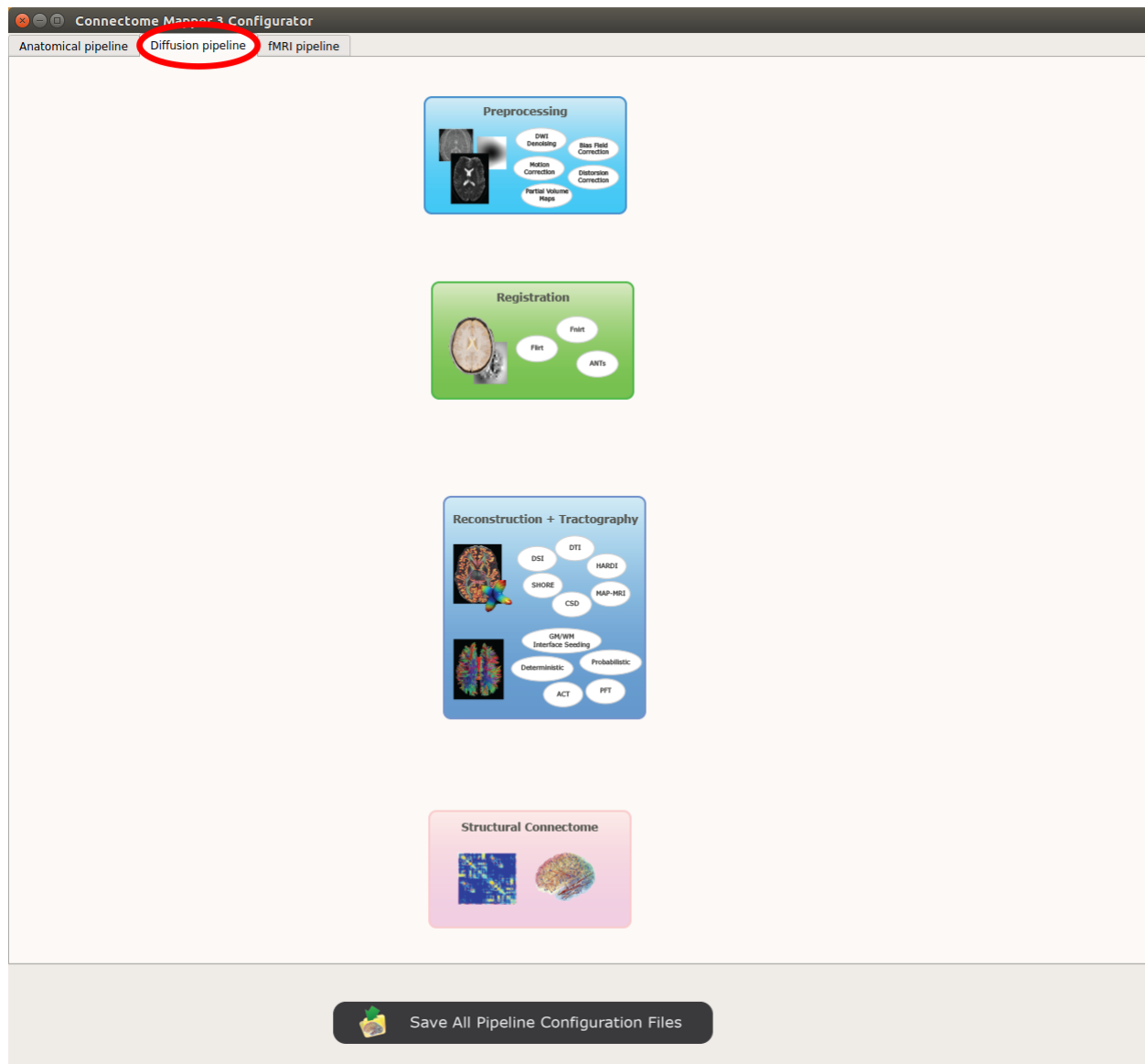


Fig. 4: Panel for configuration of diffusion pipeline stages

## Preprocessing

Preprocessing includes denoising, bias field correction, motion and eddy current correction for diffusion data.

The screenshot shows a window titled "Edit stage configuration" with a tab labeled "preprocessing\_stage". The window contains a "Configuration" section with two main groups of settings:

- Preprocessing steps:**
  - Denoising: ☒ Tool: **Dipy (NLM)** Noise model (Dipy): **Rician**
  - Bias field correction: ☒ Tool: **ANTS N4**
  - Eddy current and motion correction: ☒ Eddy correction algo: **FSL eddy\_correct**
  - Motion correction: ☒
- Final resampling:**
  - Voxel size (x,y,z): F0: **1** F1: **1** F2: **1**
  - Interpolation: **interpolate**

At the bottom right of the window are "Cancel" and "OK" buttons.

### *Denoising*

Remove noise from diffusion images using (1) MRtrix3 MP-PCA method or (2) Dipy Non-Local Mean (NLM) denoising with Gaussian or Rician noise models

### *Bias field correction*

Remove intensity inhomogeneities due to the magnetic resonance bias field using (1) MRtrix3 N4 bias field correction or (2) the bias field correction provided by FSL FAST

### *Motion correction*

Aligns diffusion volumes to the b0 volume using FSL's MCFLIRT

### *Eddy current correction*

Corrects for eddy current distortions using FSL's Eddy correct tool

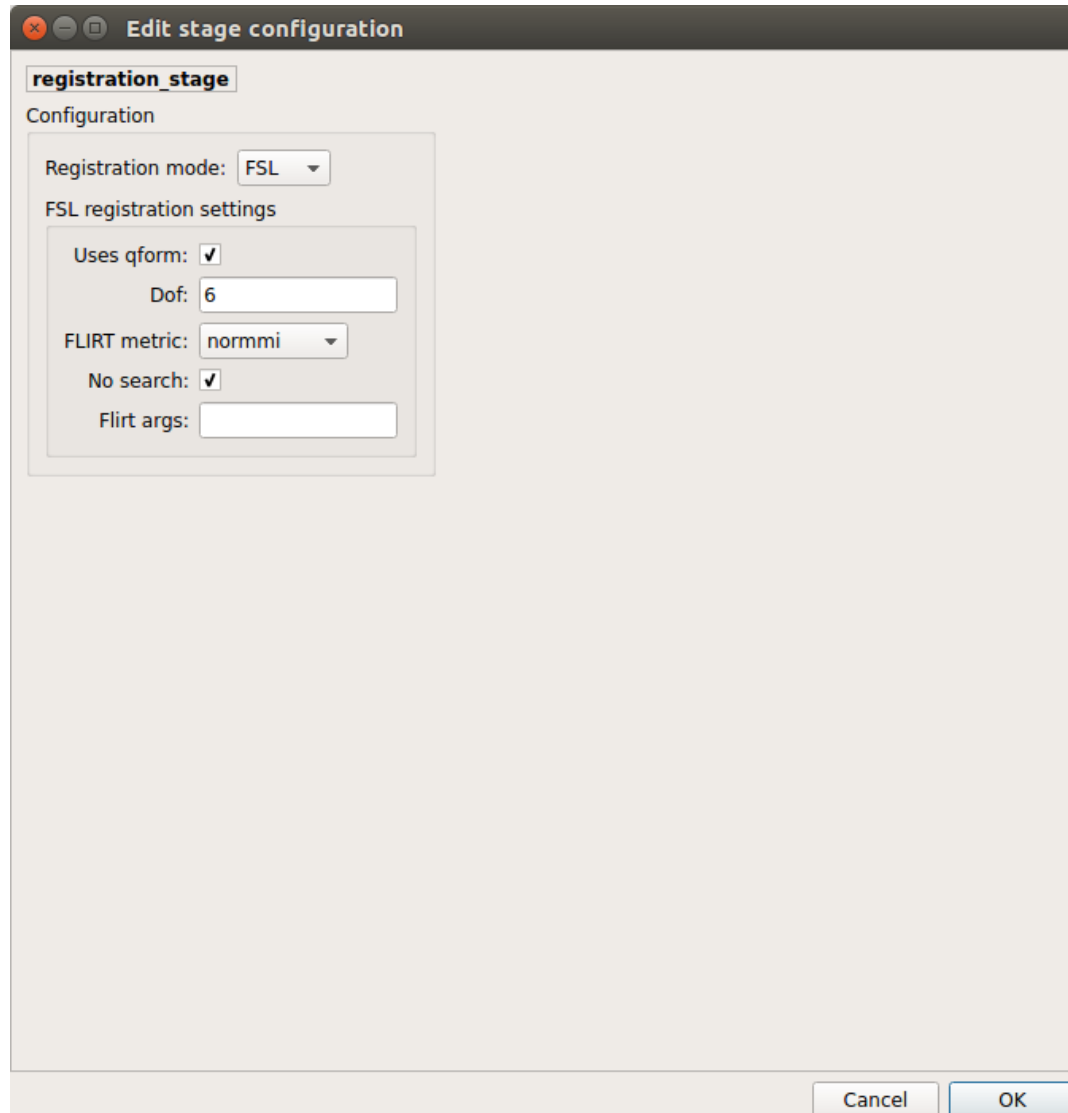
### *Resampling*

Resample morphological and diffusion data to F0 x F1 x F2 mm<sup>3</sup>

## Registration

### Registration mode

- FSL (Linear):



The screenshot shows a dialog box titled "Edit stage configuration" with a tab labeled "registration\_stage". The dialog is divided into a "Configuration" section and a larger empty area. The "Configuration" section contains the following settings:

- Registration mode: FSL (dropdown menu)
- FSL registration settings (grouped box):
  - Uses qform: ☒
  - Dof: 6 (text input)
  - FLIRT metric: normmi (dropdown menu)
  - No search: ☒
  - Flirt args: (empty text input)

At the bottom right of the dialog are "Cancel" and "OK" buttons.

Perform linear registration from T1 to diffusion b0 using FSL's flirt

- Non-linear (ANTS):



**Edit stage configuration**

**registration\_stage**

Configuration

Registration mode: **ANTs**

ANTs registration settings

**General**

Interpolation: **BSpline** Parameters: **5**

winsorize lower quantile: **0.005** winsorize upper quantile: **0.995**

Convergence threshold: **1e-06** Convergence window size: **10**

Use float precision to save memory: ☐

**Rigid + Affine**

Metric: **MI**

Gradient step size: **0.1**

Sampling strategy: **Regular** Sampling percentage: **0.25**

Gradient step size: **0.1**

Symmetric diffeomorphic SyN registration: ☒

**SyN (symmetric diffeomorphic registration)**

Metric: **CC**

Gradient step size: **0.1**

Update field variance in voxel space: **3.0**

Total field variance in voxel space: **0.0**

**Cancel** **OK**

Perform symmetric diffeomorphic SyN registration from T1 to diffusion b=0

## Diffusion reconstruction and tractography

Perform diffusion reconstruction and local deterministic or probabilistic tractography based on several tools. ROI dilation is required to map brain connections when the tracking only operates in the white matter.

### Reconstruction tool

**Dipy:** perform SHORE, tensor, CSD and MAP-MRI reconstruction

- SHORE:

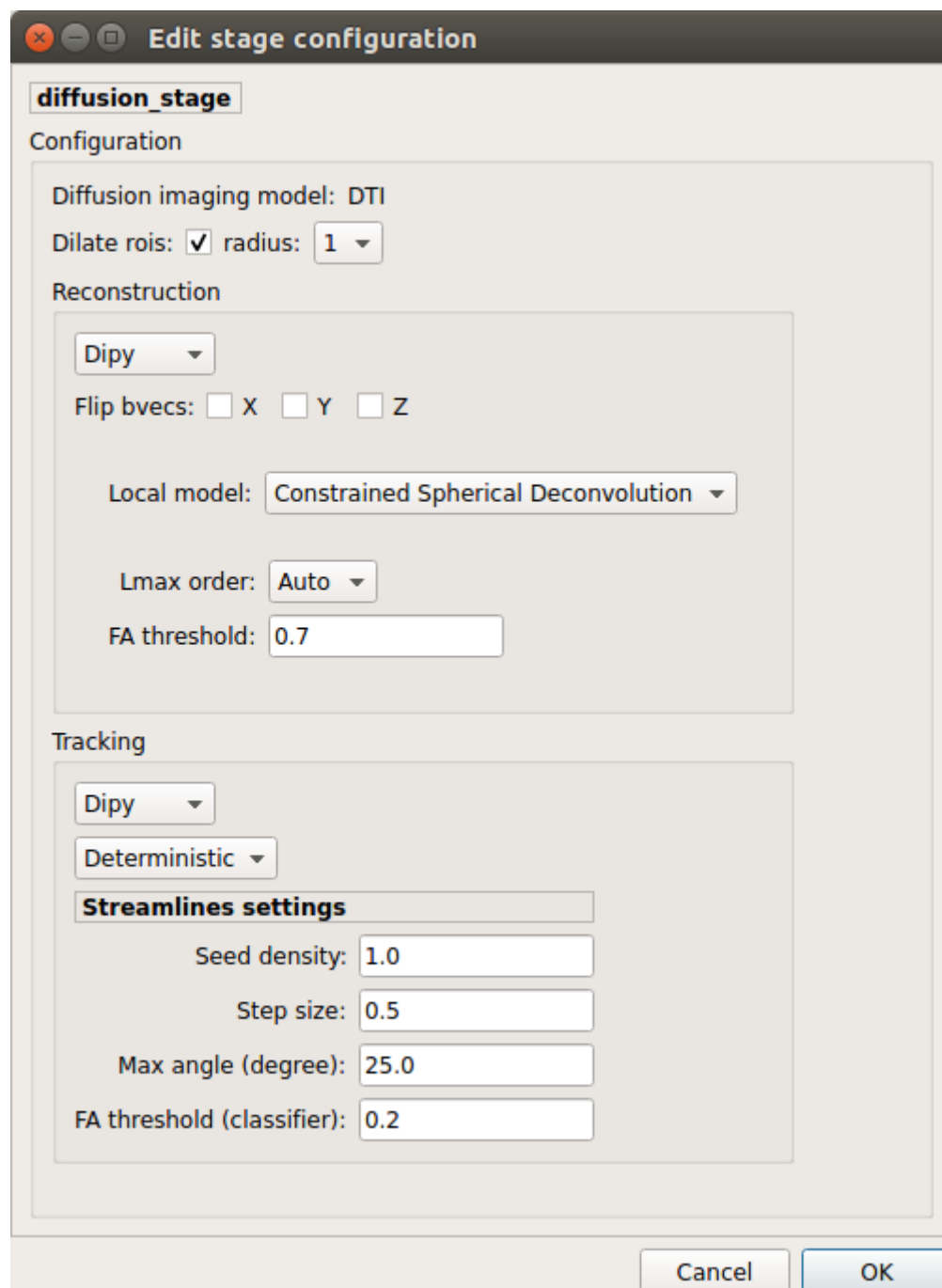


Fig. 5: Diffusion stage configuration window

Reconstruction

Dipy

Flip bvecs: ☐ X ☐ Y ☐ Z

**Parameters of SHORE reconstruction model**

Radial order: 6

Scale factor (zeta): 700

Radial regularization constant: 1e-08

Angular regularization constant: 1e-08

Diffusion time (s): 0.0253302959106

Constrain the optimization such that  $E(0) = 1$ . ☐

Constrain the propagator to be positive. ☐

Mapmri: ☐

SHORE performed only on DSI data

- Tensor:

Reconstruction

Dipy

Flip bvecs: ☐ X ☐ Y ☐ Z

Local model: Tensor

Tensor performed only on DTI data

- CSD:

Reconstruction

Dipy

Flip bvecs: ☐ X ☐ Y ☐ Z

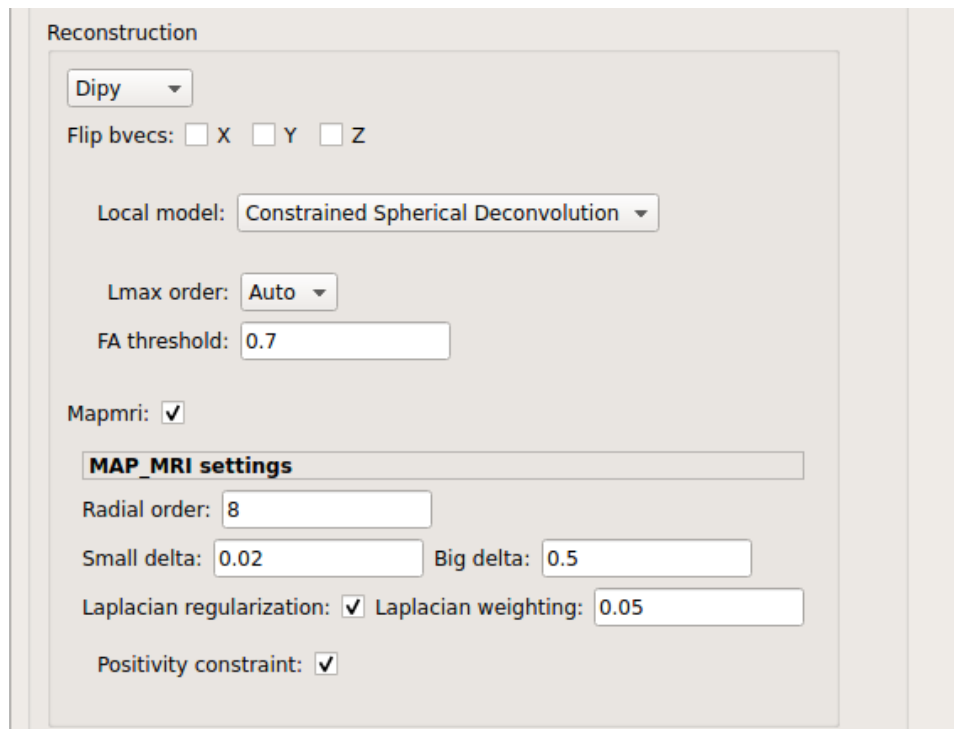
Local model: Constrained Spherical Deconvolution

Lmax order: Auto

FA threshold: 0.7

CSD performed on DTI and multi-shell data

- MAP\_MRI:

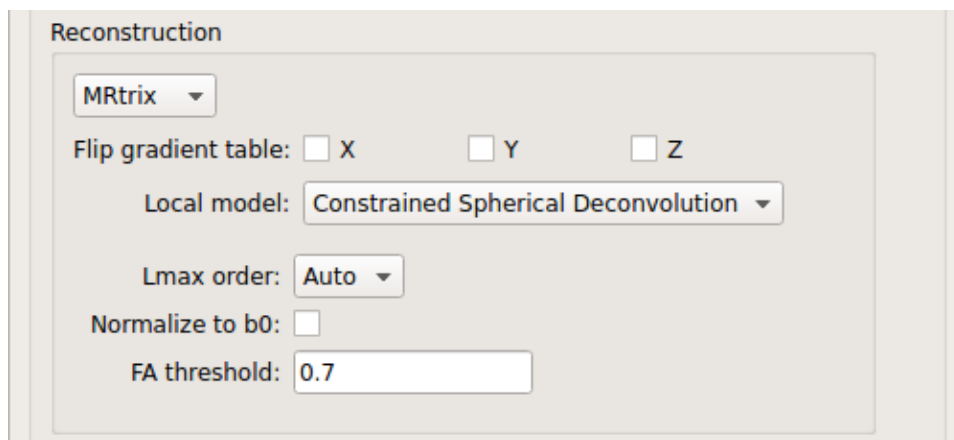


The screenshot shows the 'Reconstruction' panel in a software interface. At the top, a dropdown menu is set to 'Dipy'. Below it are three checkboxes for 'Flip bvecs' labeled X, Y, and Z, all of which are unchecked. The 'Local model' is set to 'Constrained Spherical Deconvolution' via a dropdown. 'Lmax order' is set to 'Auto' and 'FA threshold' is set to '0.7'. The 'Mapmri' checkbox is checked. A section titled 'MAP\_MRI settings' contains a 'Radial order' set to '8', 'Small delta' set to '0.02', 'Big delta' set to '0.5', 'Laplacian regularization' checked, 'Laplacian weighting' set to '0.05', and 'Positivity constraint' checked.

MAP-MRI performed only on multi-shell data

**MRtrix:** perform CSD reconstruction.

- CSD:



The screenshot shows the 'Reconstruction' panel with the dropdown menu set to 'MRtrix'. The 'Flip gradient table' checkboxes for X, Y, and Z are all unchecked. The 'Local model' remains 'Constrained Spherical Deconvolution'. 'Lmax order' is 'Auto'. The 'Normalize to b0' checkbox is unchecked. The 'FA threshold' is set to '0.7'.

CSD performed on DTI and multi-shell data

### Tractography tool

**Dipy:** perform deterministic and probabilistic fiber tracking as well as particle filtering tractography.

- Deterministic tractography:

Tracking

Dipy ▾

Deterministic ▾

**Streamlines settings**

Seed density: 1.0

Step size: 1.0

Max angle (degree): 25.0

FA threshold (classifier): 0.2

**Particle Filtering Tractography (PFT)**

Use PFT: ☐

Deterministic tractography (SD\_STREAM) performed on single tensor or CSD reconstruction

- Probabilistic tractography:

Tracking

Dipy ▾

Probabilistic ▾

**Streamlines settings**

Seed density: 1.0

Step size: 1.0

Max angle (degree): 25.0

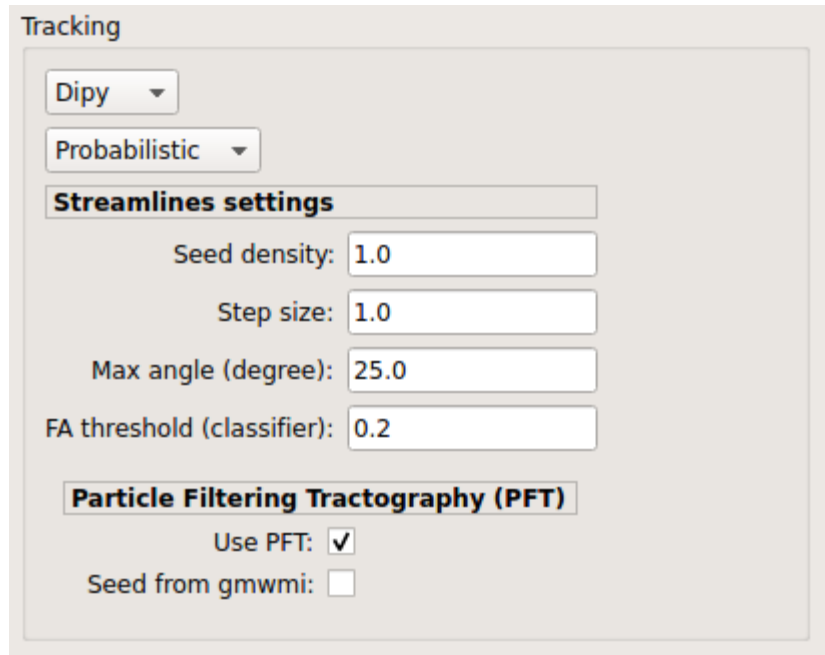
FA threshold (classifier): 0.2

**Particle Filtering Tractography (PFT)**

Use PFT: ☐

Probabilistic tractography (iFOD2) performed on SHORE or CSD reconstruction

- Probabilistic particle filtering tractography (PFT):



Tracking

Dipy ▾

Probabilistic ▾

**Streamlines settings**

Seed density: 1.0

Step size: 1.0

Max angle (degree): 25.0

FA threshold (classifier): 0.2

**Particle Filtering Tractography (PFT)**

Use PFT: ☒

Seed from gmwmi: ☐

Probabilistic PFT tracking performed on SHORE or CSD reconstruction. Seeding from the gray matter / white matter interface is possible.

---

**Note:** We noticed a shift of the center of tractograms obtained by dipy. As a result, tractograms visualized in TrackVis are not commonly centered despite the fact that the tractogram and the ROIs are properly aligned.

---

**MRtrix:** perform deterministic and probabilistic fiber tracking as well as anatomically-constrained tractography. ROI dilation is required to map brain connections when the tracking only operates in the white matter.

- Deterministic tractography:

Tracking

MRtrix ▾

Deterministic ▾

**Streamline settings**

Desired number of tracks: 5000000

Min length: 4.0 Max length: 200.0

Angle: 45.0

Curvature radius: 0.0

Step size: 0.5

Cutoff value: 0.05

**Anatomically-Constrained Tractography (ACT)**

Use ACT: ☐

**Streamline filtering**

Filter tractogram with SIFT: ☐

Deterministic tractography (SD\_STREAM) performed on single tensor or CSD reconstruction

- Deterministic anatomically-constrained tractography (ACT):

Tracking

MRtrix ▾

Deterministic ▾

**Streamline settings**

Desired number of tracks: 5000000

Min length: 4.0 Max length: 200.0

Angle: 45.0

Curvature radius: 0.0

Step size: 0.5

Cutoff value: 0.05

**Anatomically-Constrained Tractography (ACT)**

Use ACT: ☒

Crop at gmwmi: ☐

Backtrack: ☐

Seed from gmwmi: ☐

**Streamline filtering**

Filter tractogram with SIFT: ☐

Deterministic ACT tracking performed on single tensor or CSD reconstruction. Seeding from the gray matter / white matter interface is possible. Backtrack option is not available in deterministic tracking.

- Probabilistic tractography:



Tracking

MRtrix ▾

Probabilistic ▾

**Streamline settings**

Desired number of tracks: 5000000

Min length: 4.0 Max length: 200.0

Angle: 45.0

Curvature radius: 1.0

Step size: 0.5

Cutoff value: 0.05

**Anatomically-Constrained Tractography (ACT)**

Use ACT: ☐

**Streamline filtering**

Filter tractogram with SIFT: ☐

Probabilistic tractography (iFOD2) performed on SHORE or CSD reconstruction

- Probabilistic anatomically-constrained tractography (ACT):

Tracking

MRtrix ▾

Probabilistic ▾

**Streamline settings**

Desired number of tracks: 5000000

Min length: 4.0 Max length: 200.0

Angle: 45.0

Curvature radius: 1.0

Step size: 0.5

Cutoff value: 0.05

**Anatomically-Constrained Tractography (ACT)**

Use ACT: ☒

Crop at gmwmi: ☐

Backtrack: ☐

Seed from gmwmi: ☐

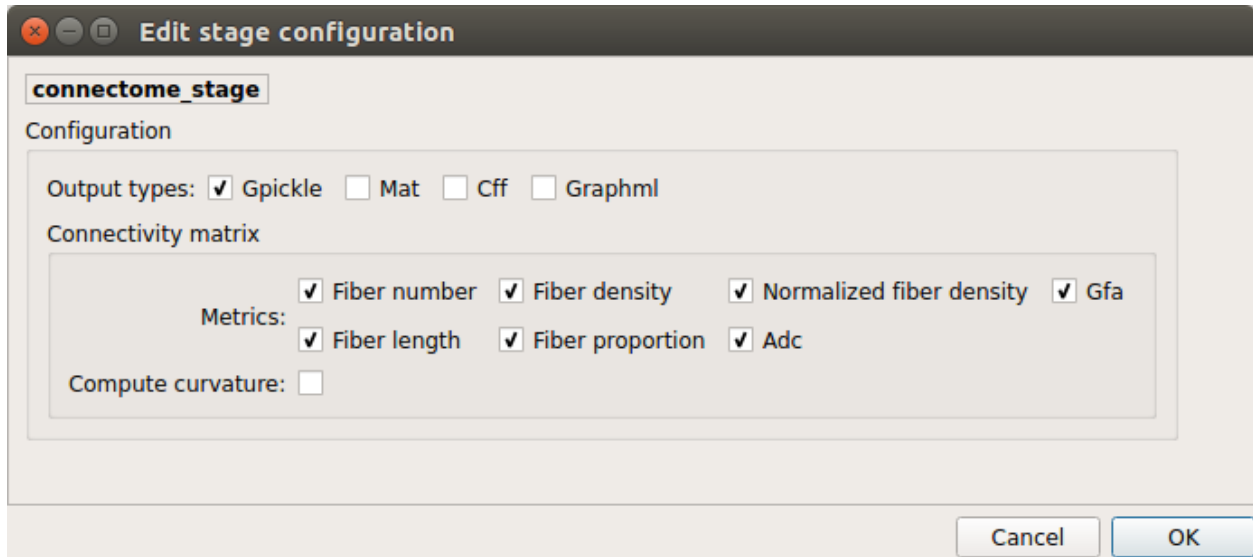
**Streamline filtering**

Filter tractogram with SIFT: ☐

Probabilistic ACT tracking performed on SHORE or CSD reconstruction. Seeding from the gray matter / white matter interface is possible.

## Connectome

Compute fiber length connectivity matrices. If DTI data is processed, FA additional map is computed. In case of DSI, additional maps include GFA and RTOP. In case of MAP-MRI, additional maps are RTPP, RTOP, ...



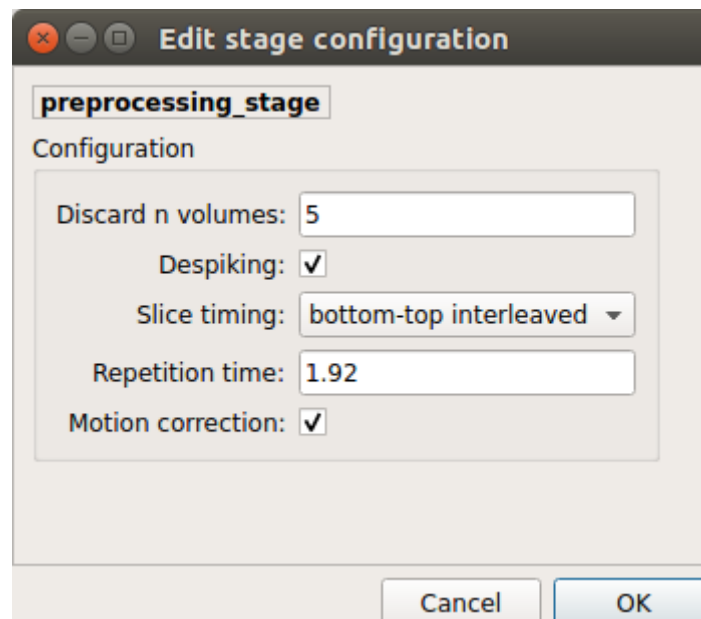
#### *Output types*

Select in which formats the connectivity matrices should be saved.

## FMRI pipeline stages

### Preprocessing

Preprocessing refers to processing steps prior to registration. It includes discarding volumes, despiking, slice timing correction and motion correction for fMRI (BOLD) data.



#### *Discard n volumes*

Discard n volumes from further analysis

#### *Despiking*

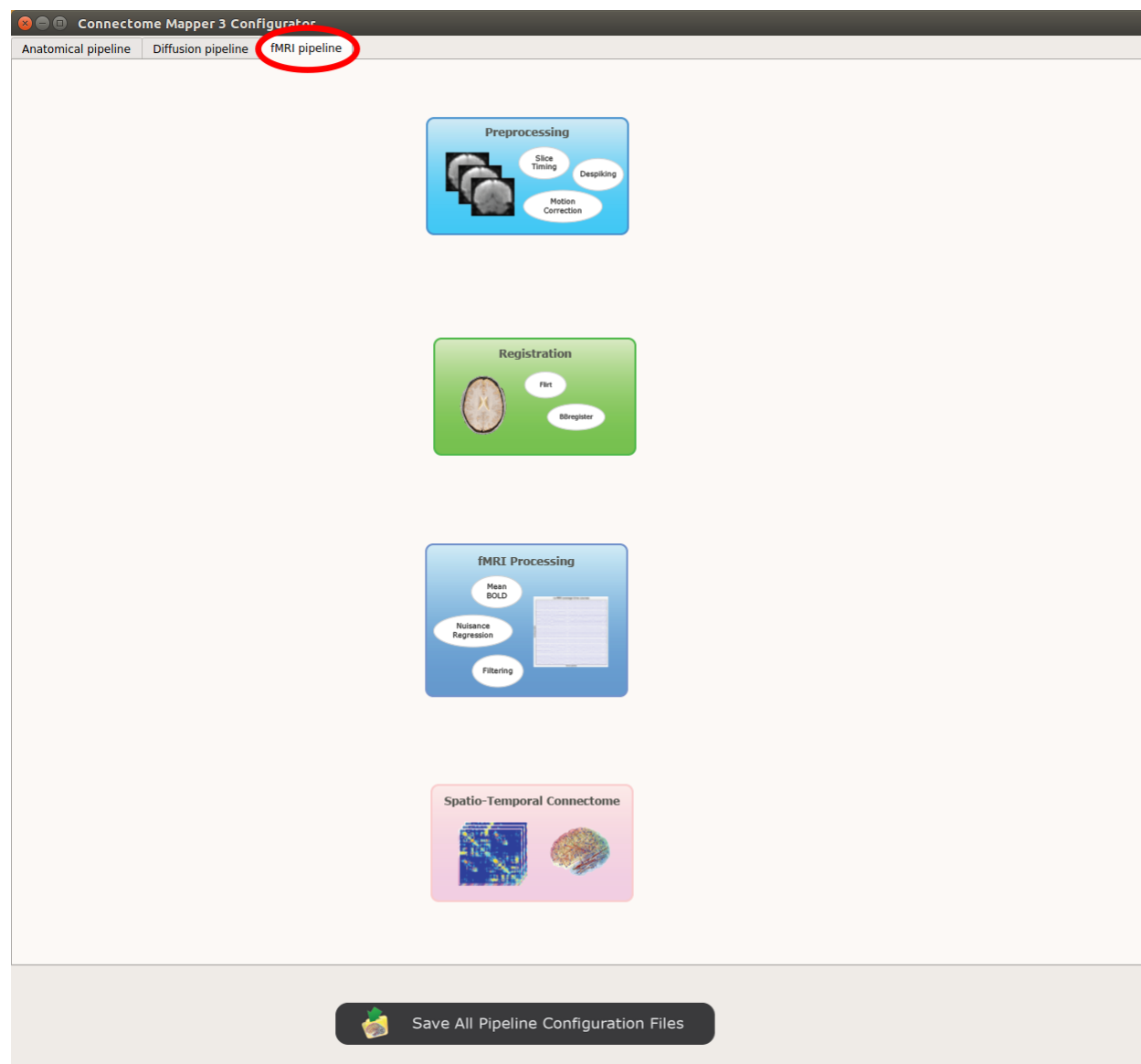


Fig. 6: Panel for configuration of fMRI pipeline stages

Perform despiking of the BOLD signal using AFNI.

#### *Slice timing and Repetition time*

Perform slice timing correction using FSL's slicetimer.

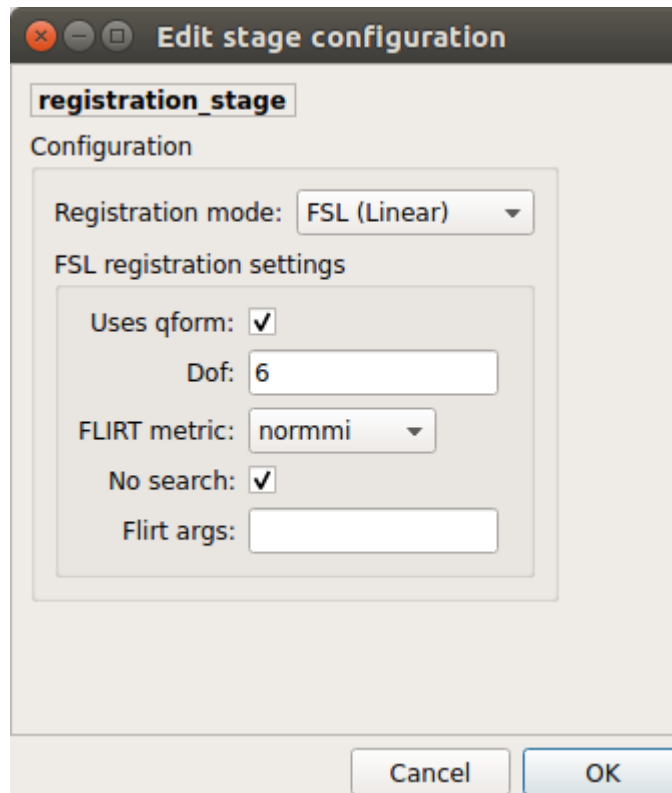
#### *Motion correction*

Align BOLD volumes to the mean BOLD volume using FSL's MCFLIRT.

## Registration

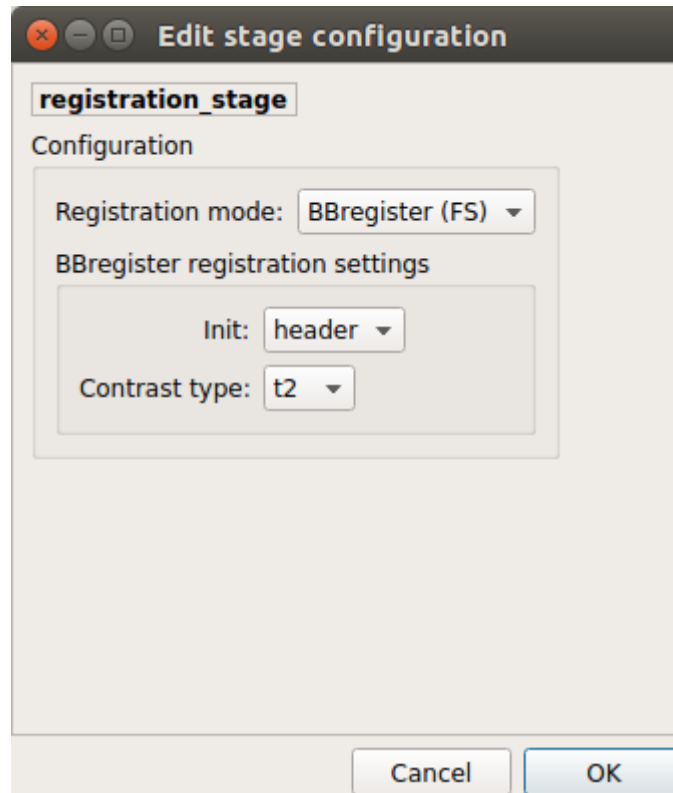
### Registration mode

- FSL (Linear):



Perform linear registration from T1 to mean BOLD using FSL's flirt.

- BBregister (FS)



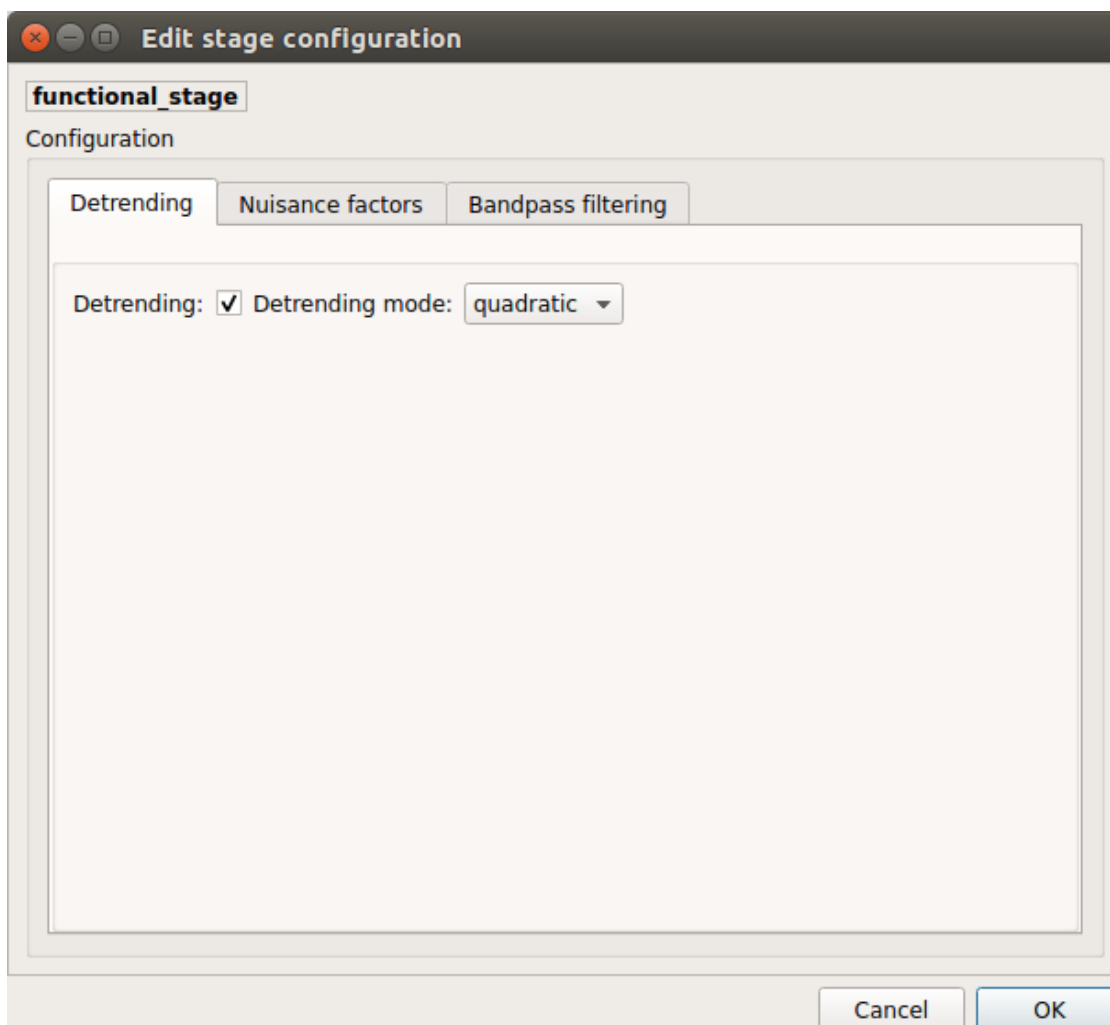
Perform linear registration using Freesurfer BBregister tool from T1 to mean BOLD via T2.

**Warning:** development in progress

## fMRI processing

Performs detrending, nuisance regression, bandpass filtering, diffusion reconstruction and local deterministic or probabilistic tractography based on several tools. ROI dilation is required to map brain connections when the tracking only operates in the white matter.

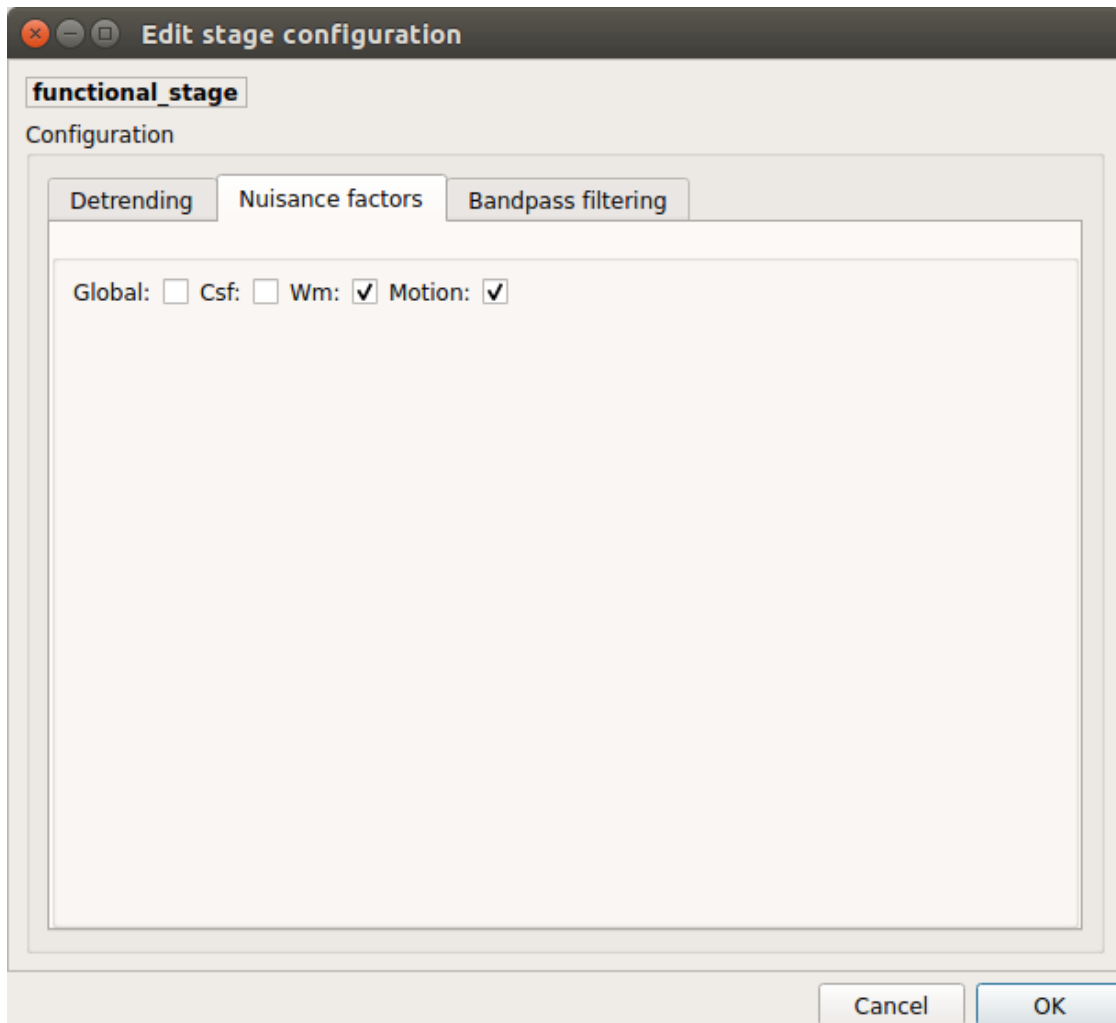
*Detrending*



Detrending of BOLD signal using:

1. *linear* trend removal algorithm provided by the *scipy* library
2. *quadratic* trend removal algorithm provided by the *obspy* library

*Nuisance regression*

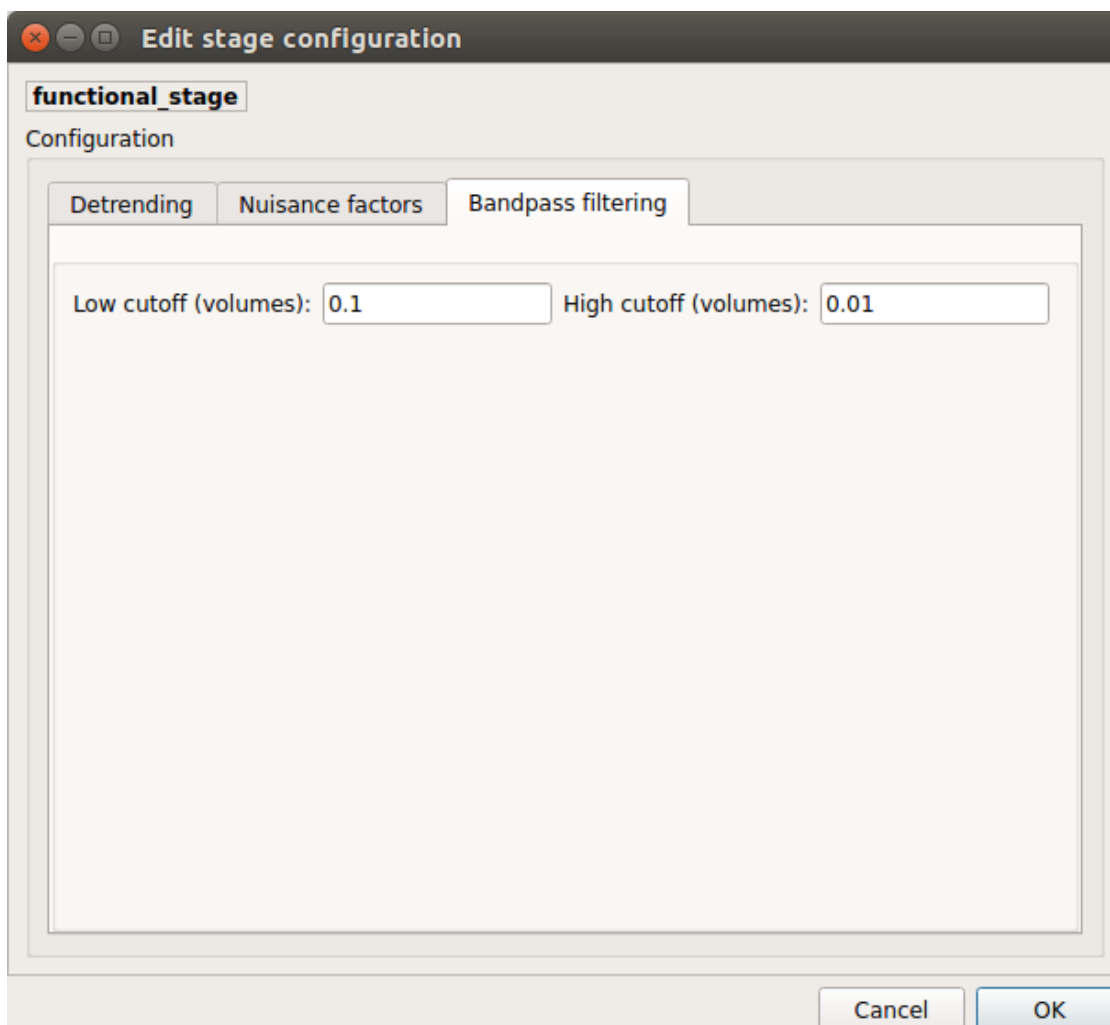


A number of options for removing nuisance signals is provided. They consist of:

1. *Global signal* regression
2. *CSF* regression
3. *WM* regression
4. *Motion parameters* regression

*Bandpass filtering*

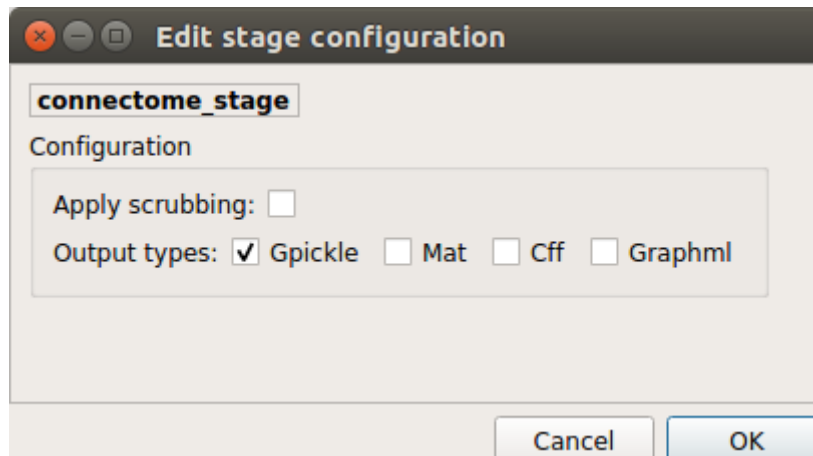




Perform bandpass filtering of the time-series using FSL's slicetimer

### Connectome

Computes ROI-averaged time-series and the correlation connectivity matrices.



### *Output types*

Select in which formats the connectivity matrices should be saved.

## Save the configuration files

You can save the pipeline stage configuration files in two different way:

1. You can save all configuration files at once by clicking on the **Save All Pipeline Configuration Files**. This will save automatically the configuration file of the anatomical / diffusion / fMRI pipeline to `<bids_dataset>/code/ref_anatomical_config.ini` / `<bids_dataset>/code/ref_diffusion_config.ini` / `<bids_dataset>/code/ref_fMRI_config.ini` respectively.
2. You can save individually each of the pipeline configuration files and edit its filename in the File menu (File -> Save anatomical/diffusion/fMRI configuration file as...)

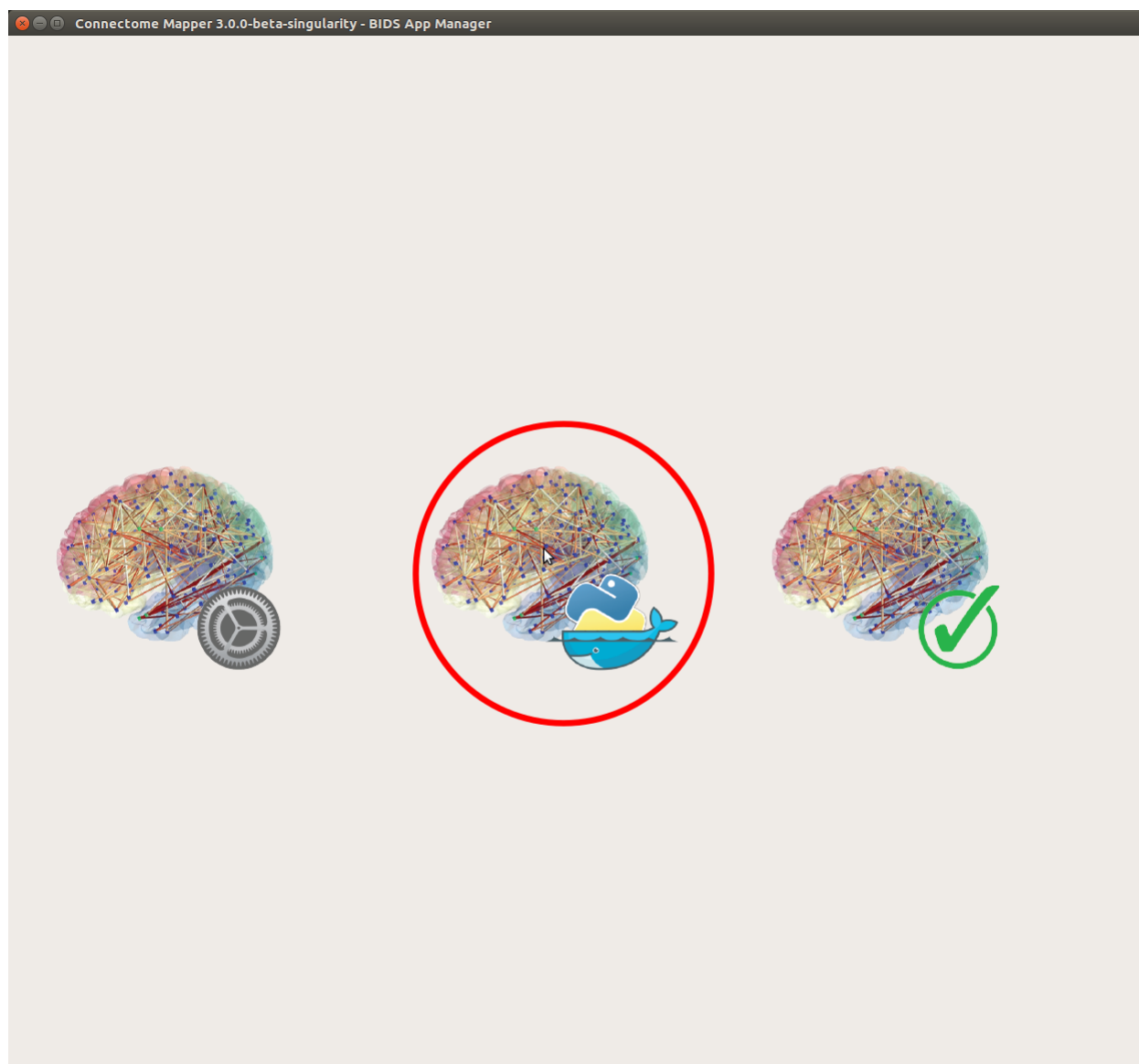
## Nipype

Connectome Mapper relies on Nipype. All intermediate steps for the processing are saved in the corresponding `<bids_dataset/derivatives>/nipype/sub-<participant_label>/<pipeline_name>/<stage_name>` stage folder (See *Nipype workflow outputs* for more details).

## 5.4.5 Run the BIDS App

### Start the Connectome Mapper BIDS App GUI

- From the main window, click on the middle button to start the Connectome Mapper BIDS App GUI.



- The window of the Connectome Mapper BIDS App GUI will appear, which will help you in setting up and launching the BIDS App run.

## Run configuration

- Select the output directory for data derivatives

**BIDS dataset**  
Input directory: /home/focaladmin/Data/ids-demo  
Output directory:

- Select the subject labels to be processed

Participant labels to be processed	
Available labels	Labels to be processed
sub-01	sub-01

Connectome Mapper 3 BIDS App GUI

**BIDS App Version**  
Tag: v3.0.3

**Environmental impact** Track carbon footprint: ☒

**BIDS dataset**  
Input directory: /home/localadmin/Data/ds-demo  
Output directory: /home/localadmin/Data/ds-demo/derivatives

**Participant labels to be processed**

Available labels	Labels to be processed
sub-01	

**Parallel processing** Number of participants processed in parallel: 1  1

**Advanced execution settings for each participant process**

**Multithreading**

Number of OpenMP threads:  Set seed of ANTS random number generator: ☐ Seed:

Set number of threads used by ANTs: ☐ Set seed of MRtrix random number generator: ☐ Seed:

Number of ITK threads used by ANTs registration:

**Configuration of processing pipelines**

**Anatomical pipeline**  
Configuration file: /home/localadmin/Data/ds-demo/code/ref\_anatomical\_config.json

**Diffusion pipeline**  
Run processing stages: ☒  
Configuration file: /home/localadmin/Data/ds-demo/code/ref\_diffusion\_config.json

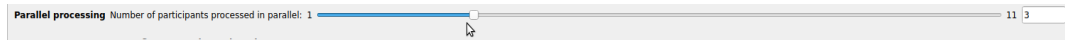
**fMRI pipeline**  
Run processing stages: ☒  
Configuration file: /home/localadmin/Data/ds-demo/code/ref\_fMRI\_config.json

**Freesurfer configuration**  
LICENSE: /usr/local/freesurfer/license.txt

**Data Provenance Tracking / Data Lineage**  
Use Datalad: ☐

Fig. 7: Window of the Connectome Mapper BIDS App GUI

- Tune the number of subjects to be processed in parallel



- Tune the advanced execution settings for each subject process. This include finer control on the number of threads used by each process as well as on the seed value of ANTs and MRtrix random number generators.



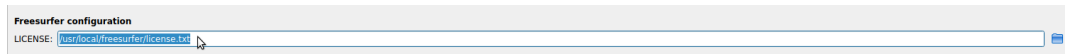
**Important:** Make sure the number of threads multiplied by the number of subjects being processed in parallel do not exceed the number of CPUs available on your system.

- Check/Uncheck the pipelines to be performed



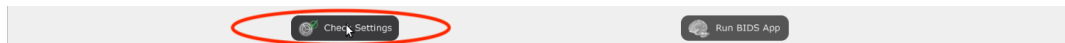
**Note:** The list of pipelines might vary as it is automatically updated based on the availability of diffusion MRI and resting-state fMRI data.

- Specify your Freesurfer license

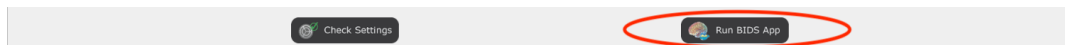


**Note:** Your Freesurfer license will be copied to your dataset directory as `<bids_dataset>/code/license.txt` which will be mounted inside the BIDS App container image.

- When the run is set up, you can click on the Check settings button.



- If the setup is complete and valid, this will enable the Run BIDS App button.



You are ready to launch the BIDS App run!

## Execute the BIDS App

- Click on the Run BIDS App button to execute the BIDS App



- You can see the complete docker run command generated by the Connectome Mapper BIDS App GUI from the terminal output such as in this example

```
Start BIDS App
> FreeSurfer license copy skipped as it already exists (BIDS App Manager)
> Datalad available: True
... BIDS App execution command: ['docker', 'run', '-it', '--rm', '-v', '/home/localadmin/Data/ds-demo:/bids_dir', '-v', '/home/localadmin/Data/ds-demo/derivatives:/output_dir', '-v', '/usr/local/freesurfer/license.txt:/bids_dir/code/license.txt', '-v', '/home/localadmin/Data/ds-demo/code/ref_anatomical_config.ini:/code/ref_anatomical_config.ini', '-v', '/home/localadmin/Data/ds-demo/code/ref_diffusion_config.ini:/code/ref_diffusion_config.ini', '-v', '/home/localadmin/Data/ds-demo/code/ref_fMRI_config.ini:/code/ref_fMRI_config.ini', '-u', '1000:1000', 'sebastientourbier/connectomemapper-bidsapp:v3.0.3', '/bids_dir', '/output_dir', 'participant', '--participant_label', '01', '--anat_pipeline_config', '/code/ref_anatomical_config.ini', '--dwi_pipeline_config', '/code/ref_diffusion_config.ini', '--func_pipeline_config', '/code/ref_fMRI_config.ini', '--fs_license', '/bids_dir/code/license.txt', '--number_of_participants_processed_in_parallel', '1', '--number_of_threads', '3', '--ants_number_of_threads', '3']
> BIDS dataset: /bids_dir
> Subjects to analyze : ['01']
> Set $FS_LICENSE which points to FreeSurfer license location (BIDS App)
... $FS_LICENSE : /bids_dir/code/license.txt
* Number of subjects to be processed in parallel set to 1 (Total of cores available: 11)
* Number of parallel threads set to 10 (total of cores: 11)
* OMP_NUM_THREADS set to 3 (total of cores: 11)
* ITK_GLOBAL_DEFAULT_NUMBER_OF_THREADS set to 3
Report execution to Google Analytics.
Thanks to support us in the task of finding new funds for CMP3 development!
> Sessions to analyze : ['ses-01']
> Process subject sub-103818 session ses-01
WARNING: rewriting config file /output_dir/cmp-v3.0.3/sub-01/ses-01/sub-01_ses-01_anatomical_config.ini
... Anatomical config created : /output_dir/cmp-v3.0.3/sub-01/ses-01/sub-01_ses-01_anatomical_config.ini
WARNING: rewriting config file /output_dir/cmp-v3.0.3/sub-01/ses-01/sub-01_ses-01_diffusion_config.ini
... Diffusion config created : /output_dir/cmp-v3.0.3/sub-01/ses-01/sub-01_ses-01_diffusion_config.ini
WARNING: rewriting config file /output_dir/cmp-v3.0.3/sub-01/ses-01/sub-01_ses-01_fMRI_config.ini
... fMRI config created : /output_dir/cmp-v3.0.3/sub-01/ses-01/sub-01_ses-01_fMRI_config.ini
... Running pipelines :
    - Anatomical MRI (segmentation and parcellation)
```

(continues on next page)

(continued from previous page)

```
- Diffusion MRI (structural connectivity matrices)
- fMRI (functional connectivity matrices)
... cmd : connectomemapper3 --bids_dir /bids_dir --output_dir /output_dir --
↪ participant_label sub-01 --session_label ses-01 --anat_pipeline_config /
↪ output_dir/cmp-v3.0.3/sub-01/ses-01/sub-01_ses-01_anatomical_config.ini --
↪ dwi_pipeline_config /output_dir/cmp-v3.0.3/sub-01/ses-01/sub-01_ses-01_
↪ diffusion_config.ini --func_pipeline_config /output_dir/cmp-v3.0.3/sub-01/
↪ ses-01/sub-01_ses-01_fMRI_config.ini --number_of_threads 3
```

---

**Note:** Also, this can be helpful in you wish to design your own batch scripts to call the BIDS App with the correct syntax.

---

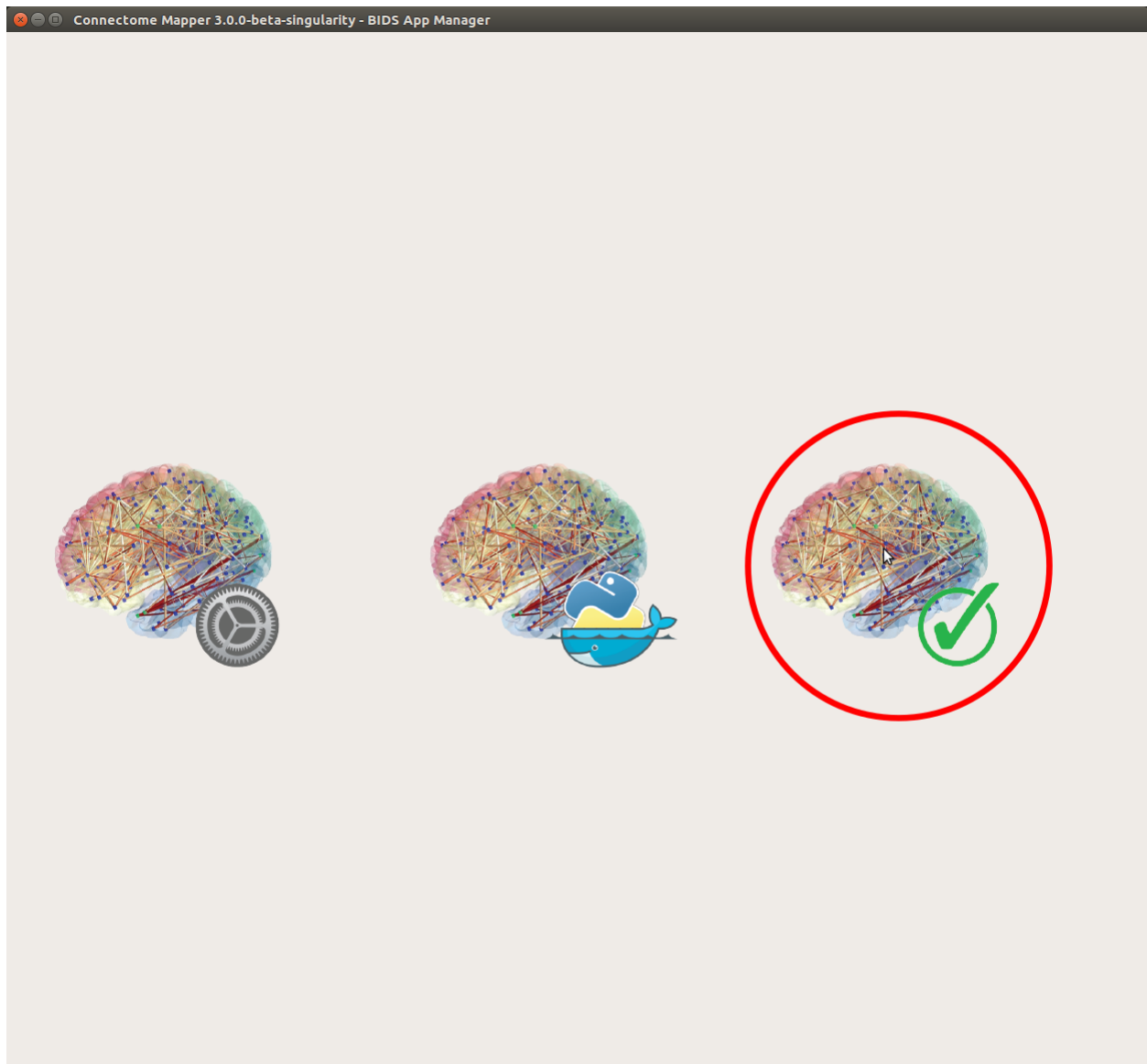
## Check progress

For each subject, the execution output of the pipelines are redirected to a log file, written as <bids\_dataset/derivatives>/cmp-v3.X.Y/sub-<subject\_label>\_log.txt. Execution progress can be checked by the means of these log files.

### 5.4.6 Check stages outputs

#### Start the Inspector Window

- From the main window, click on the right button to start the Inspector Window.



- The Connectome Mapper 3 Inspector Window will appear, which will assist you in inspecting outputs of the different pipeline stages (each pipeline has a tab panel).

### Anatomical pipeline stages

- Click on the stage you wish to check the output(s):



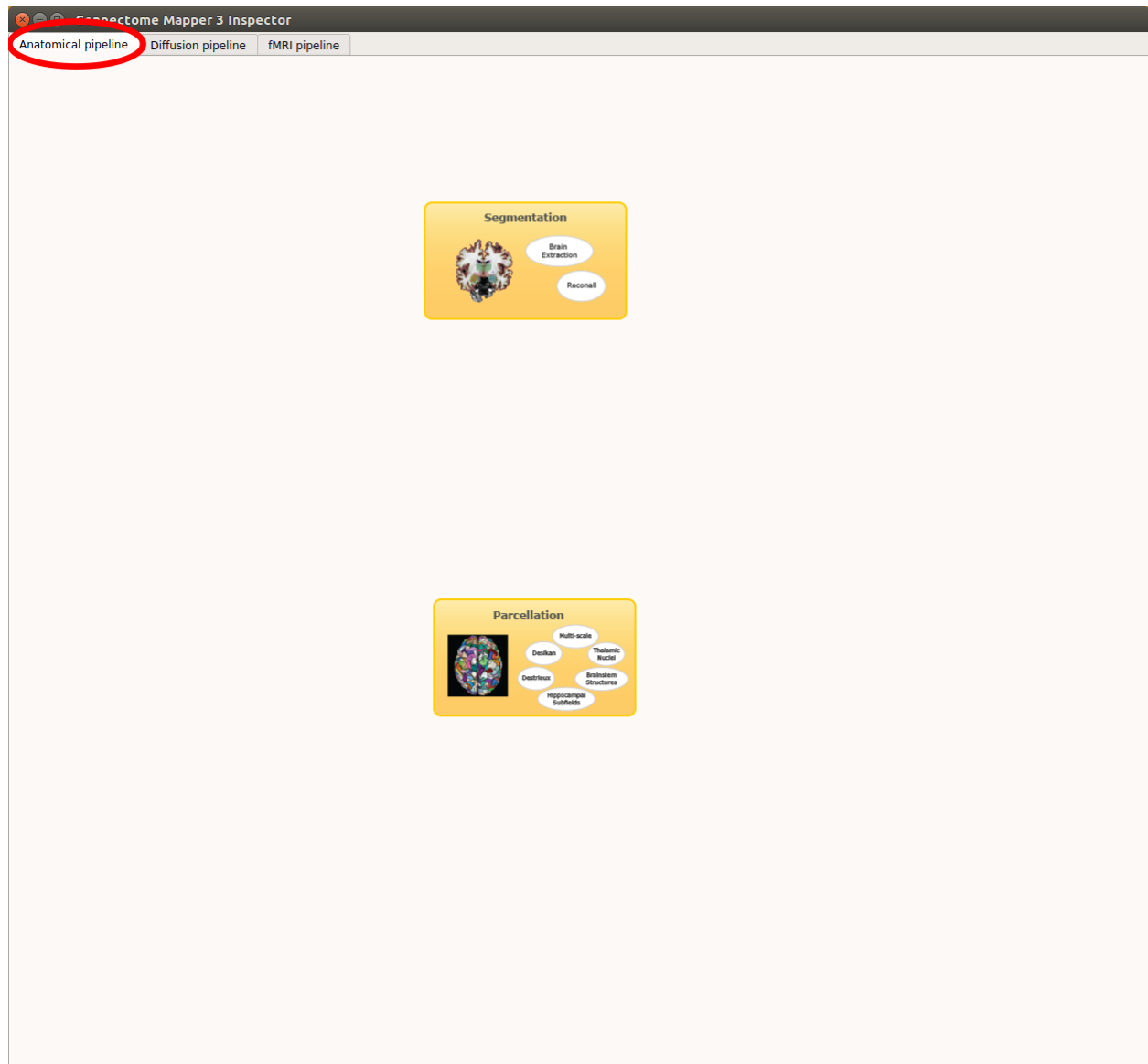
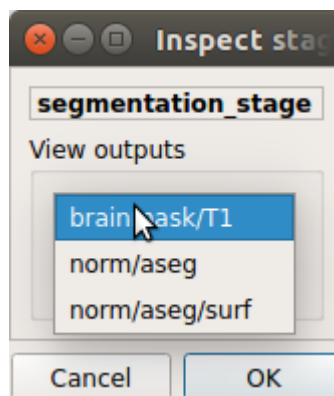


Fig. 8: Panel for configuration of anatomical pipeline stages

## Segmentation

- Select the desired output from the list and click on view:



## Segmentation results

Surfaces extracted using Freesurfer.

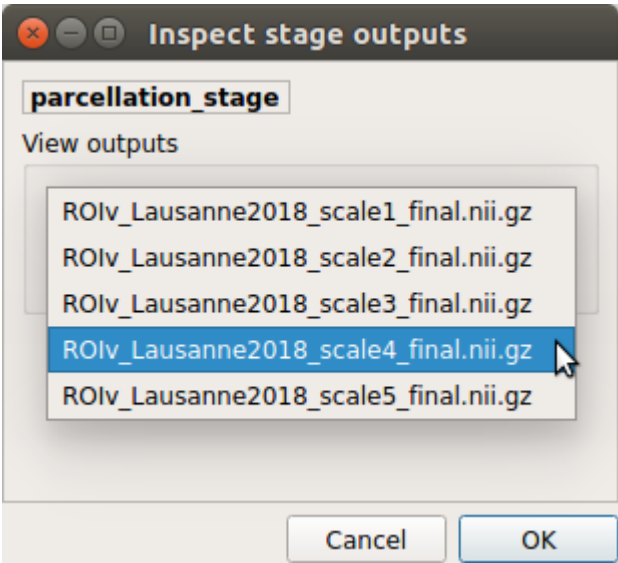


T1 segmented using Freesurfer.



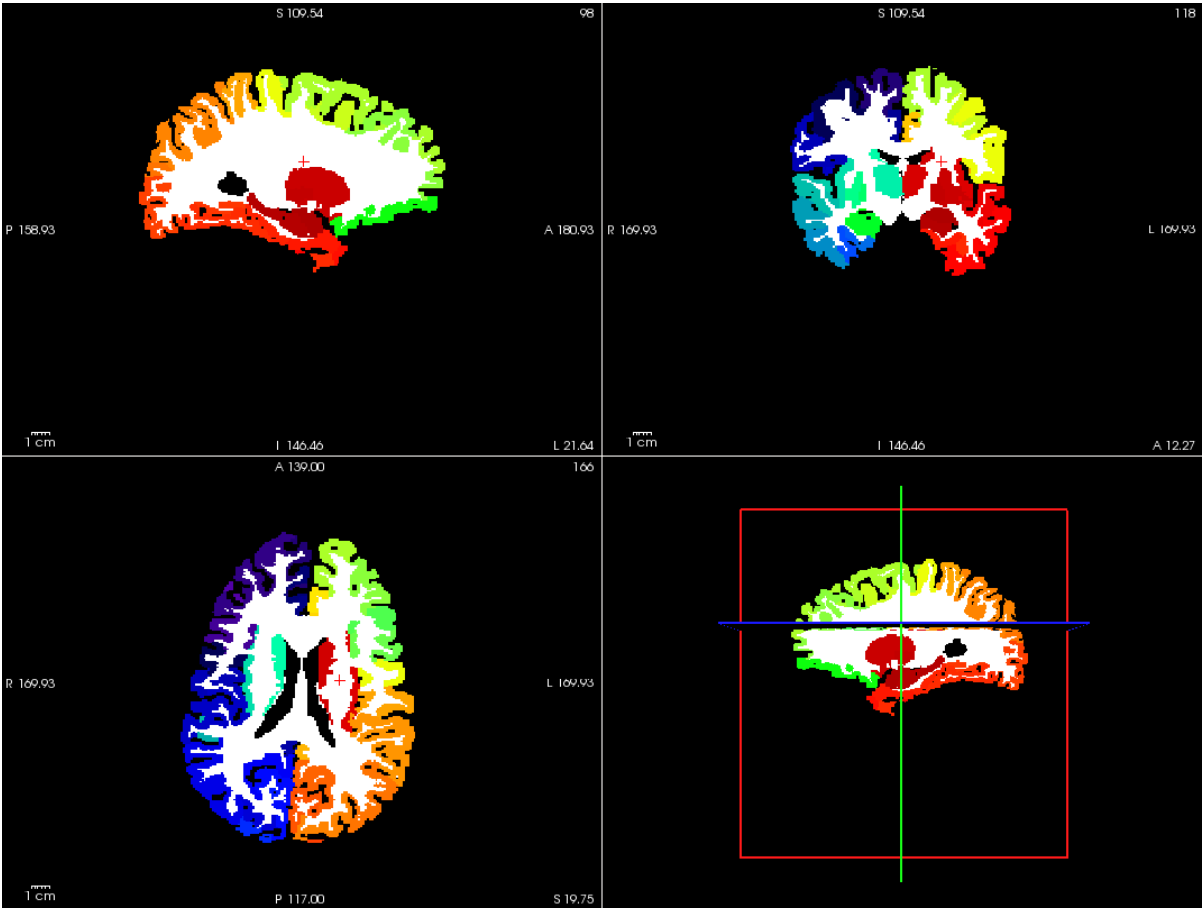
### Parcellation

- Select the desired output from the list and click on view:



Parcellation results

Cortical and subcortical parcellation are shown with Freeview.



## Diffusion pipeline stages

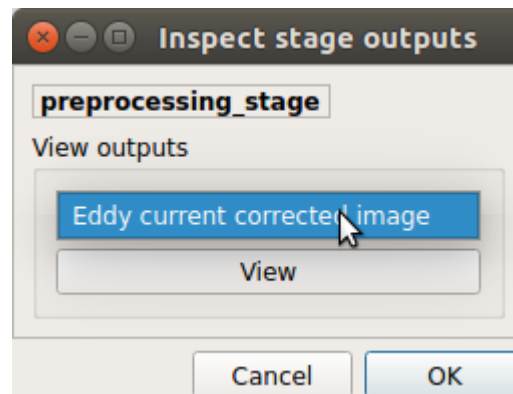
- Click on the stage you wish to check the output(s):



Fig. 9: Panel for configuration of diffusion pipeline stages

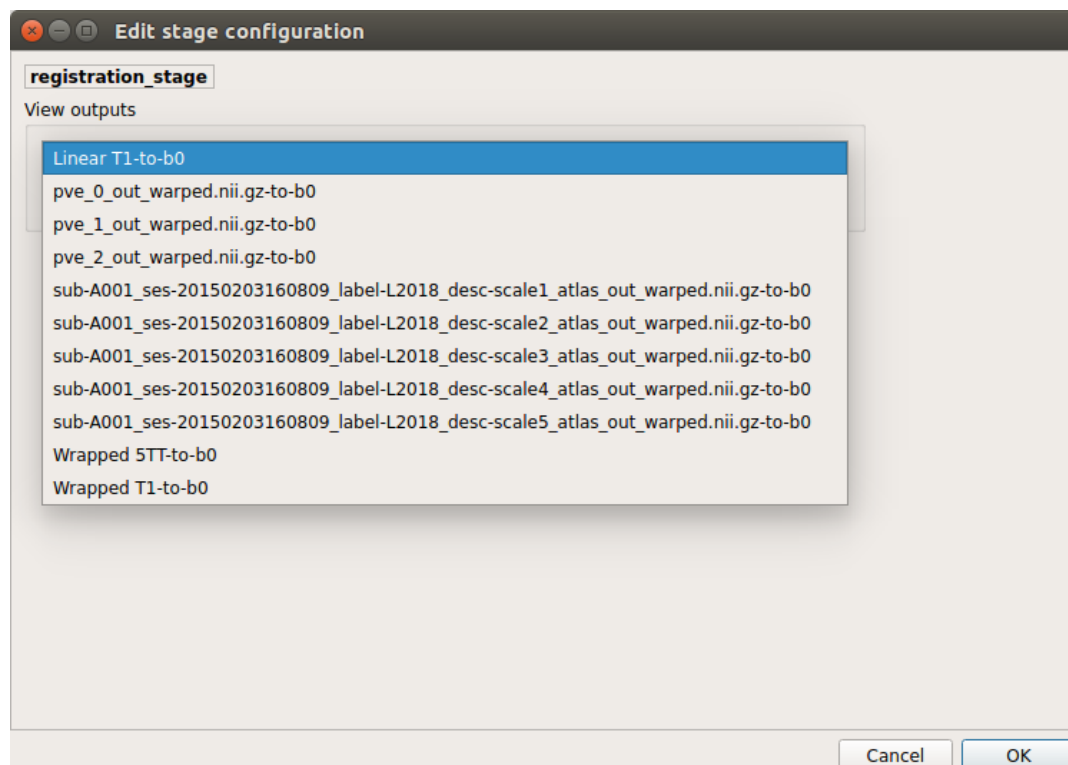
## Preprocessing

- Select the desired output from the list and click on view:



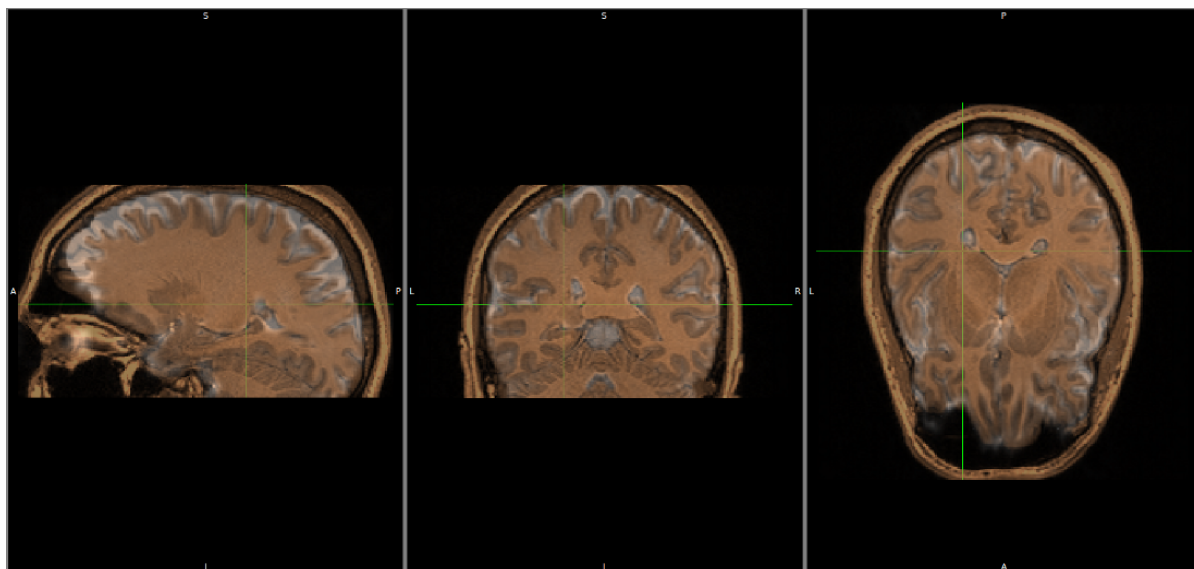
## Registration

- Select the desired output from the list and click on view:



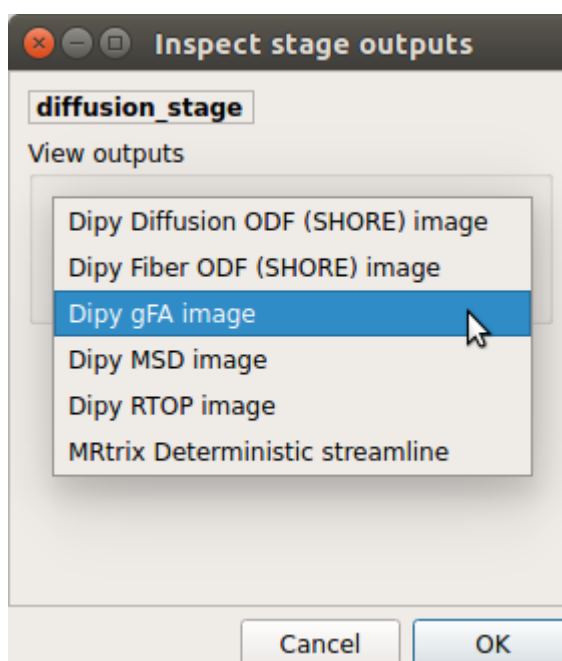
## Registration results

Registration of T1 to Diffusion space (b0). T1 in copper overlayed to the b0 image.



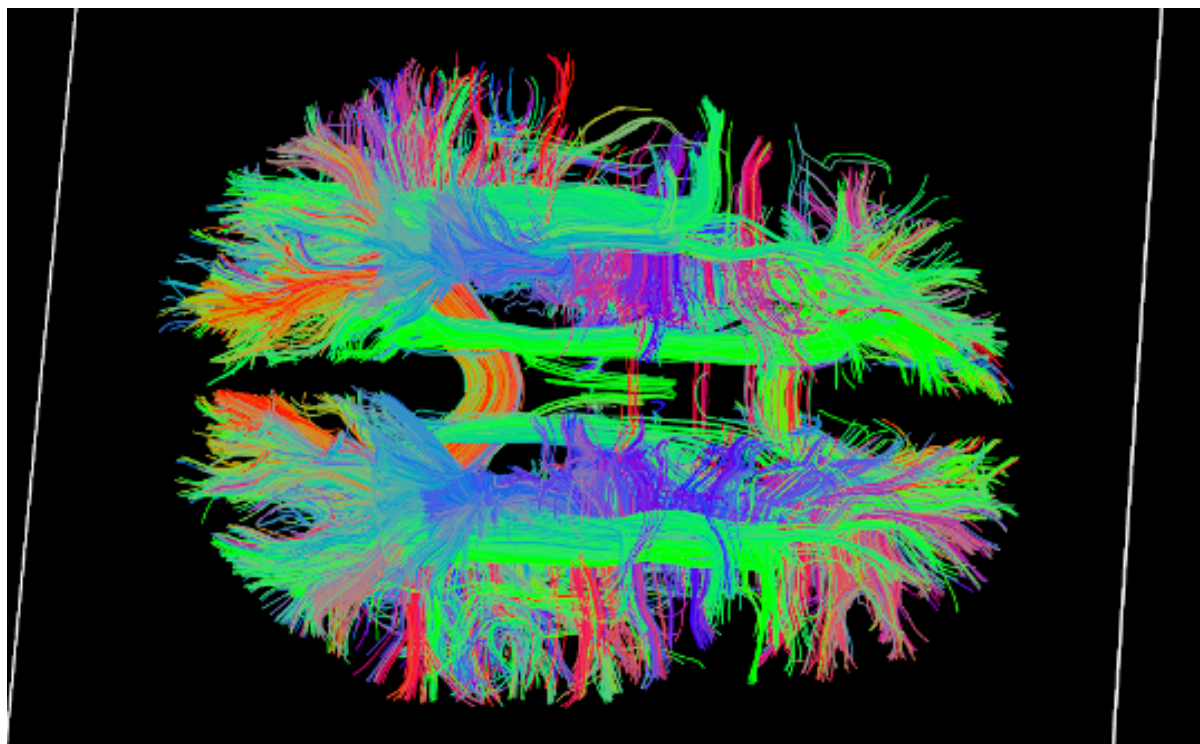
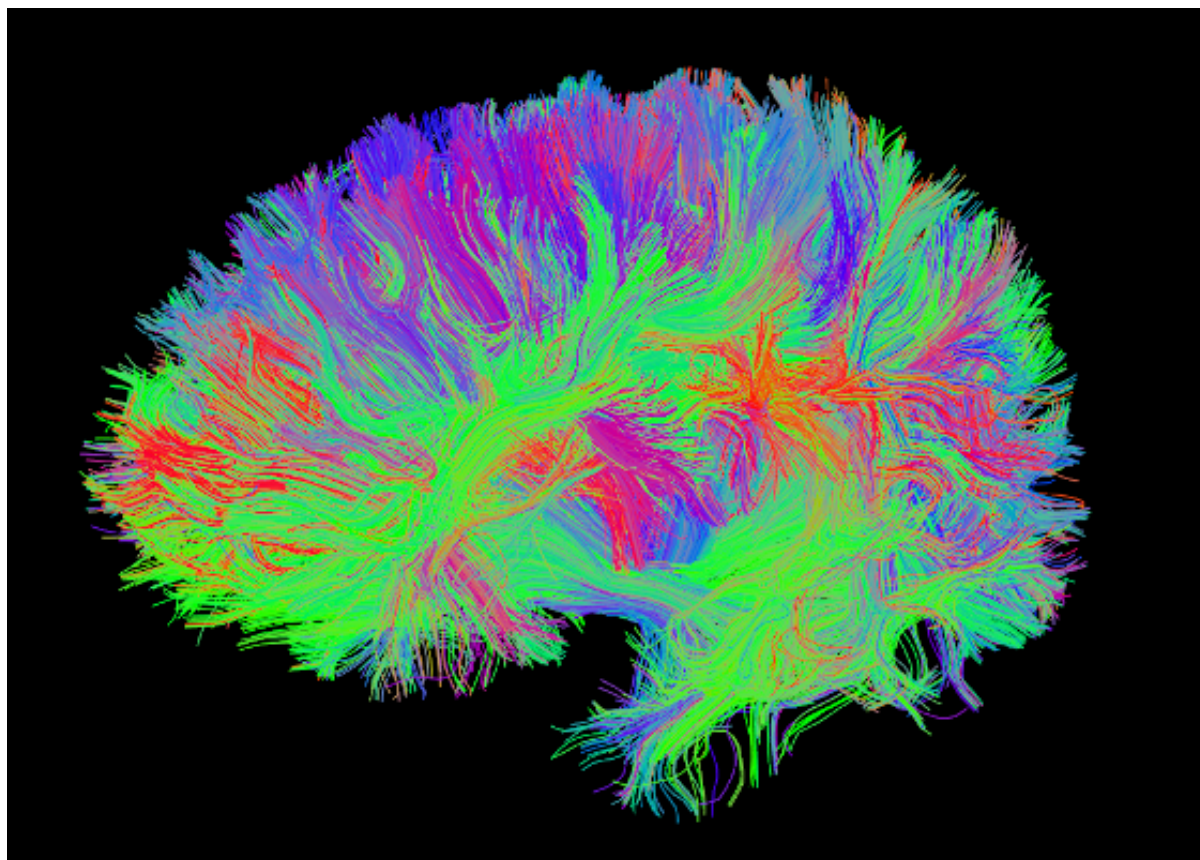
### Diffusion reconstruction and tractography

- Select the desired output from the list and click on view:



### Tractography results

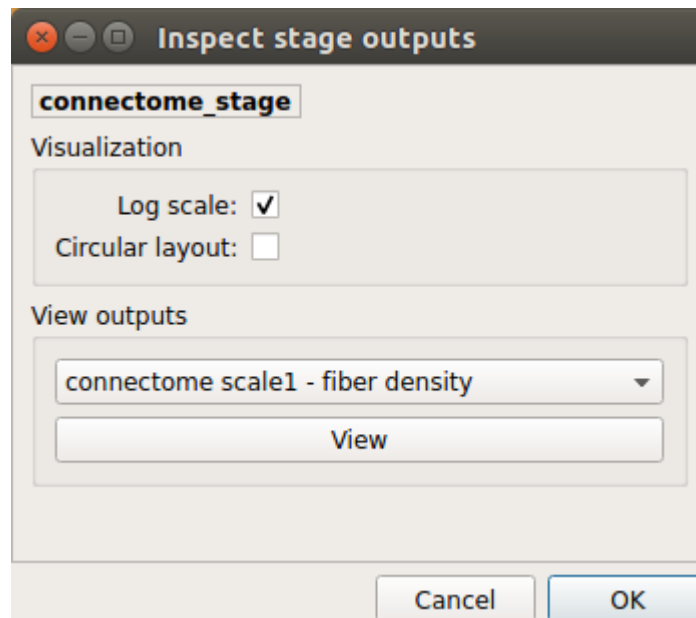
DSI Tractography results are displayed with TrackVis.





## Connectome

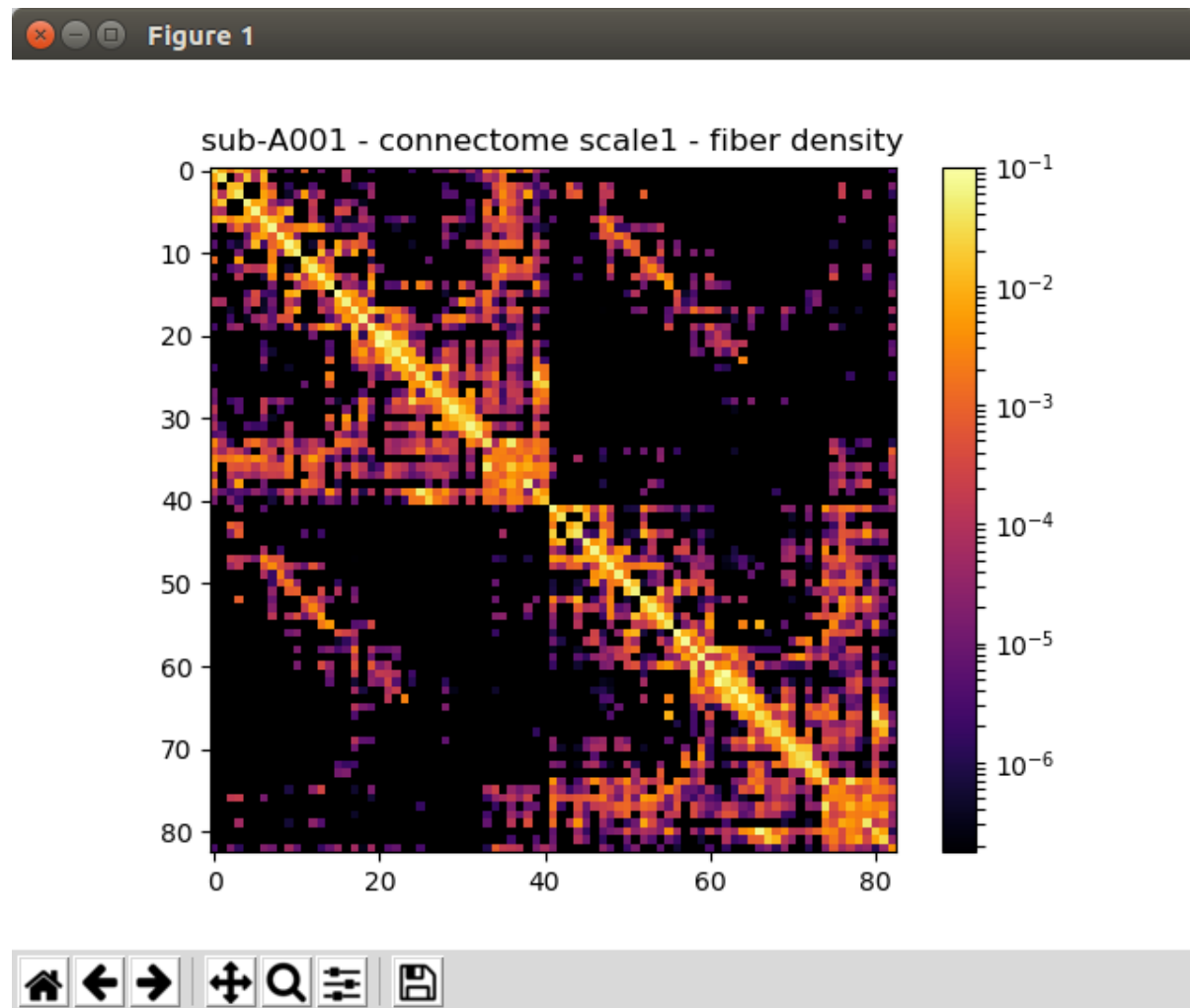
- Select the desired output from the list and click on view:



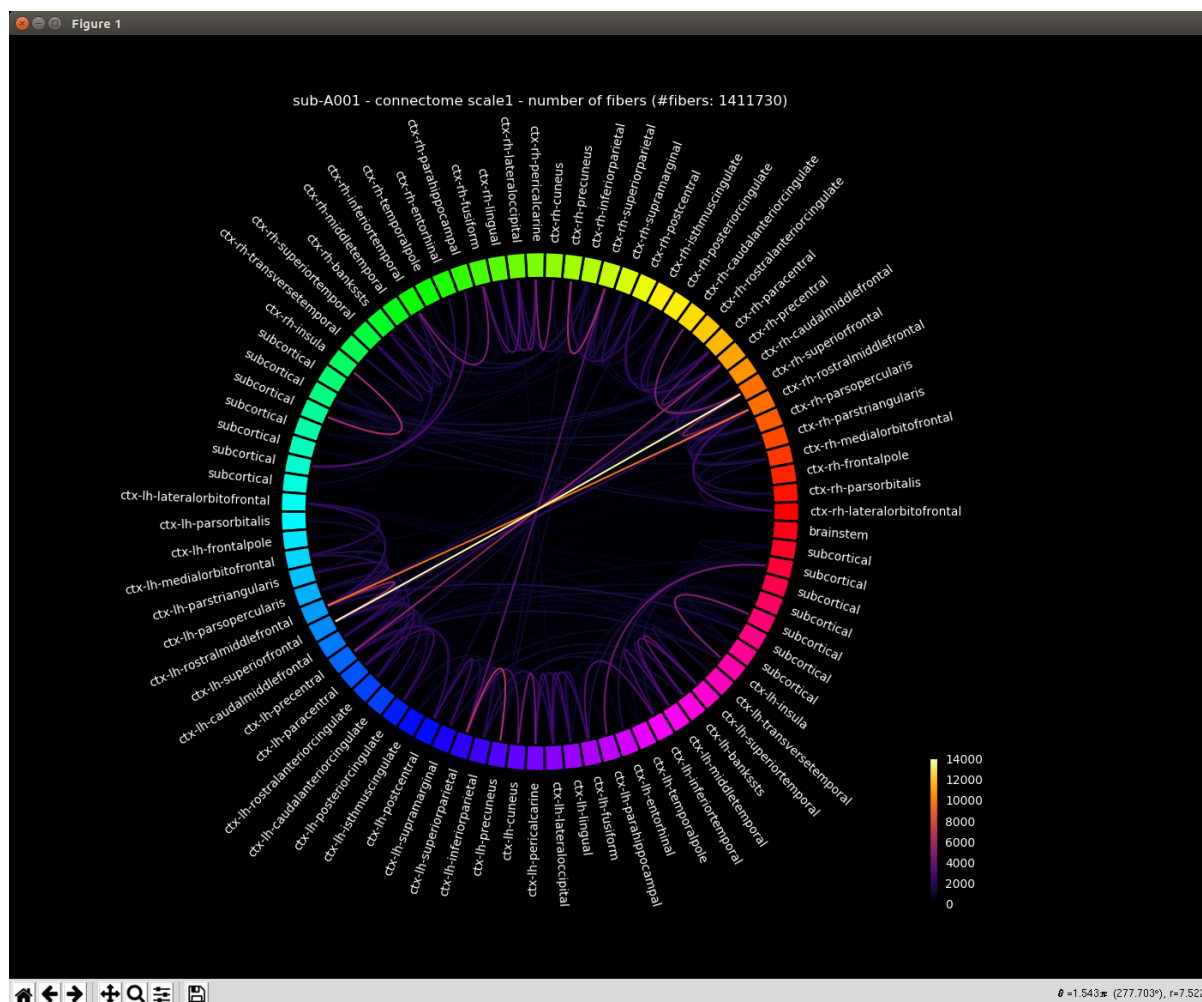
### Generated connection matrix

Displayed using a:

1. matrix layout with pyplot



2. circular layout with pyplot and MNE



## FMRI pipeline stages

- Click on the stage you wish to check the output(s):

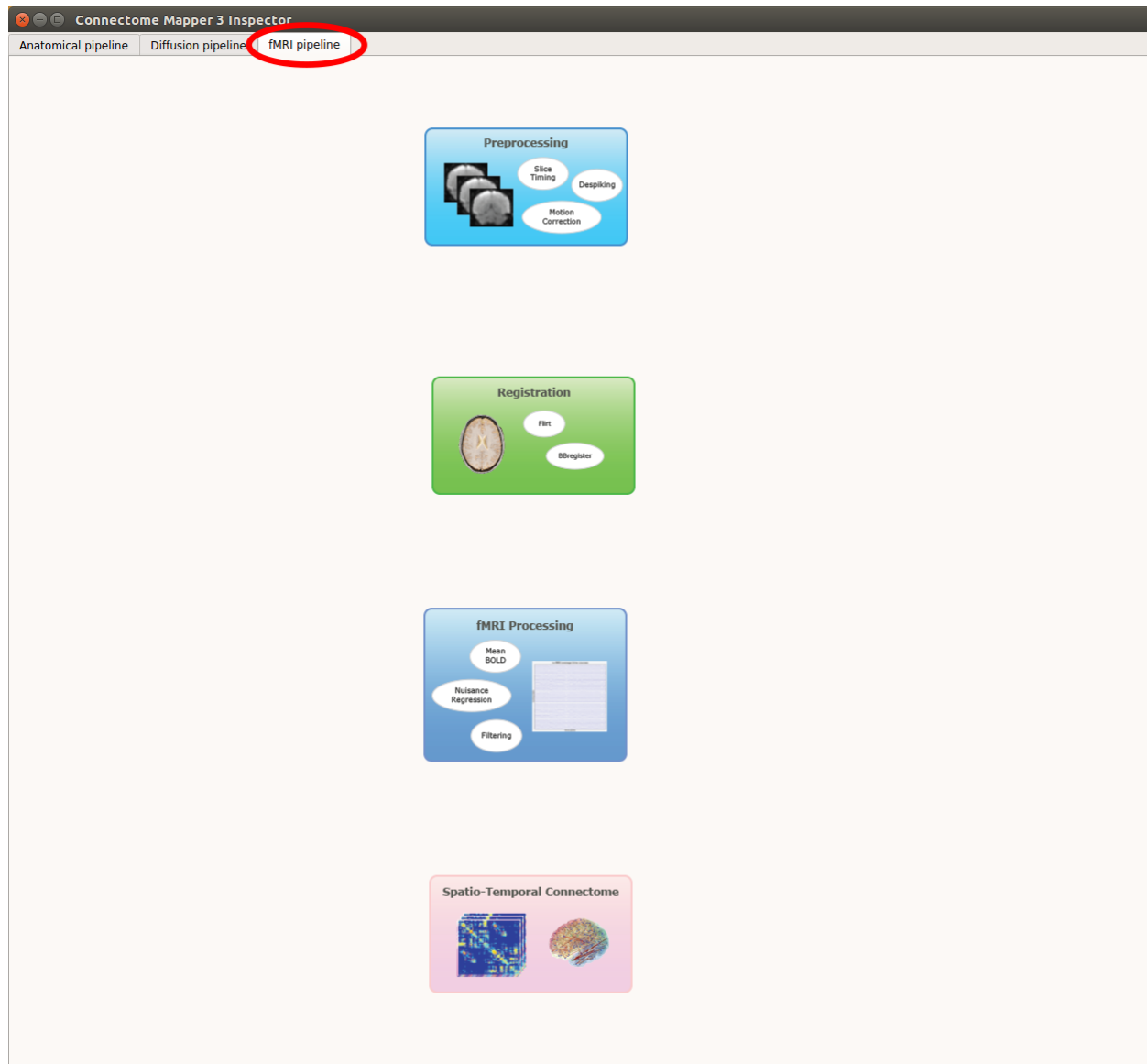
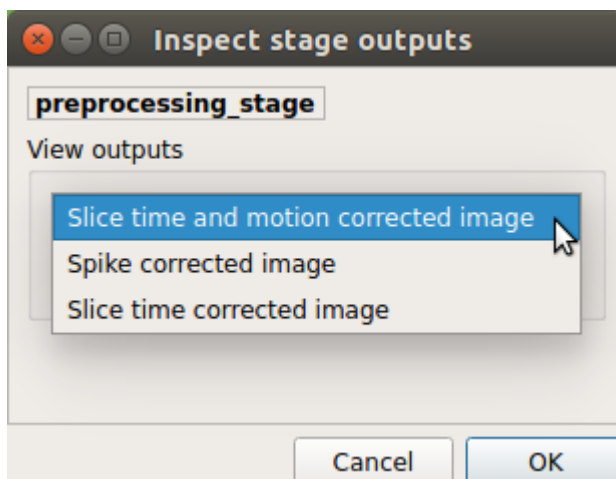


Fig. 10: Panel for configuration of fMRI pipeline stages

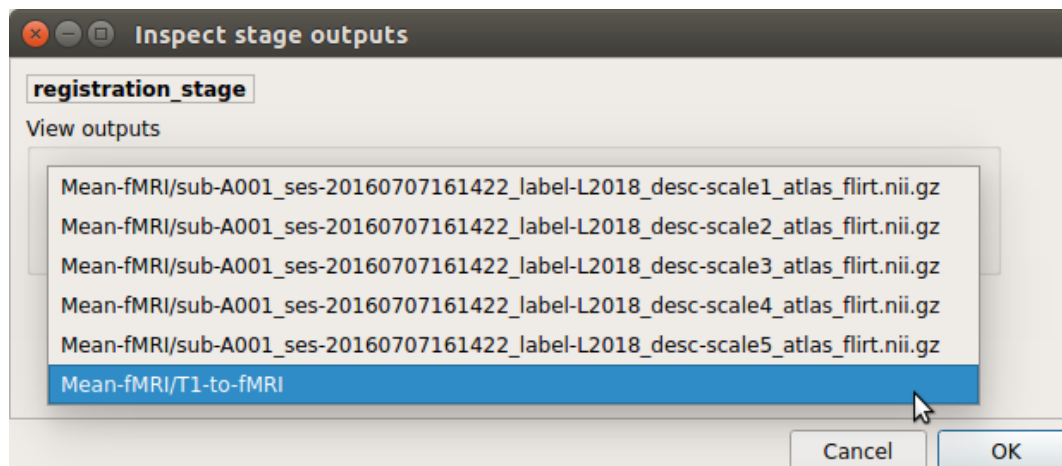
## Preprocessing

- Select the desired output from the list and click on view:



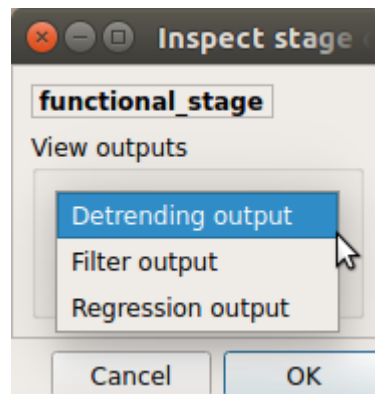
## Registration

- Select the desired output from the list and click on view:

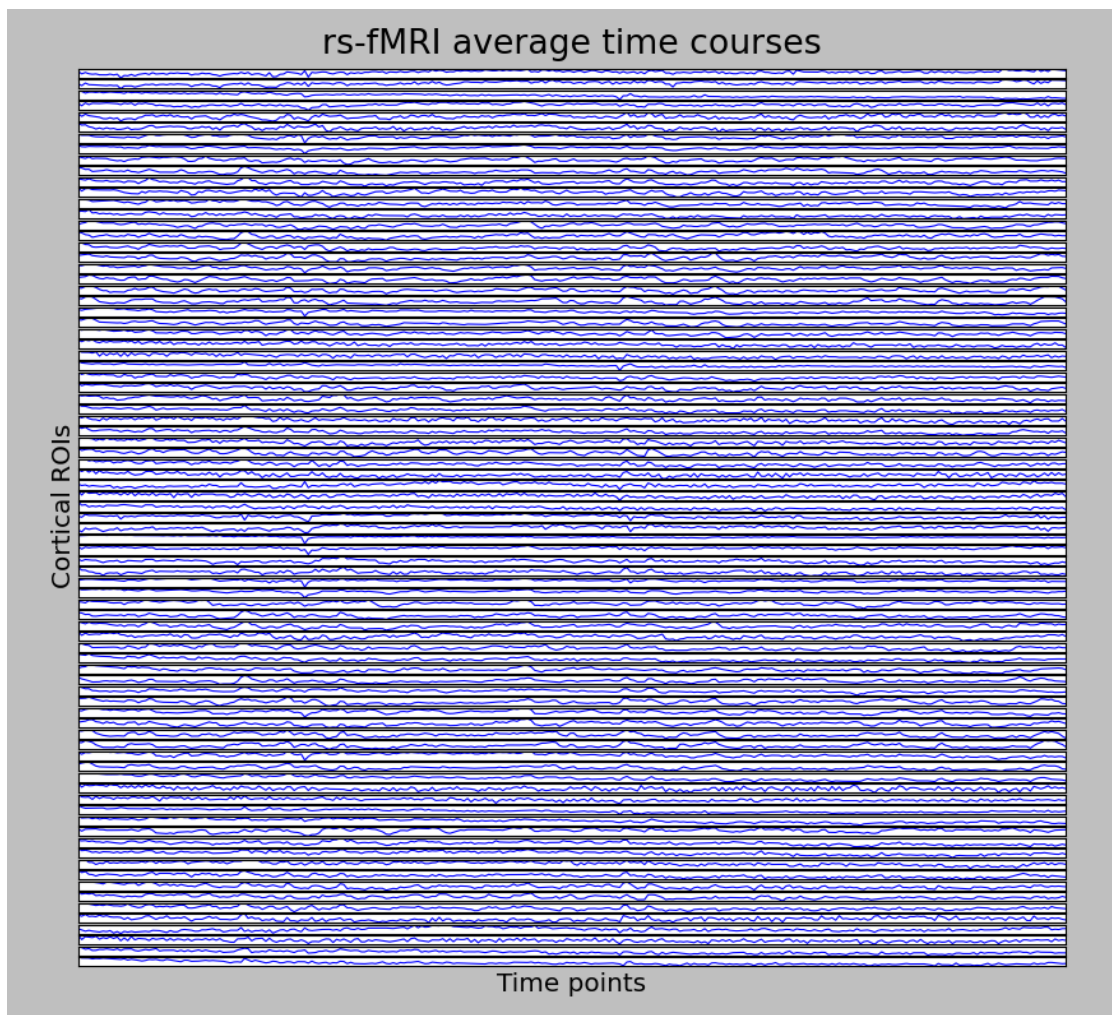


## fMRI processing

- Select the desired output from the list and click on view:

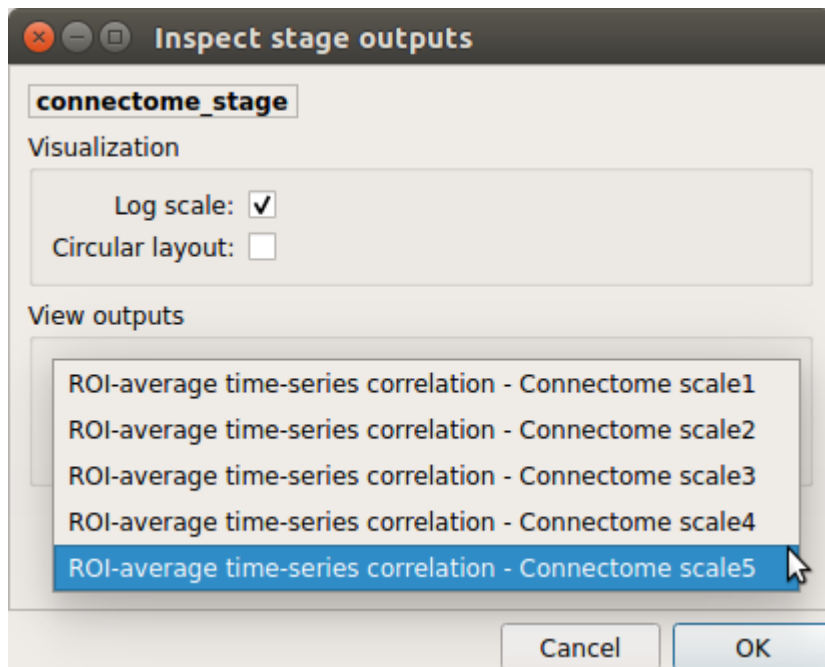


## ROI averaged time-series



## Connectome

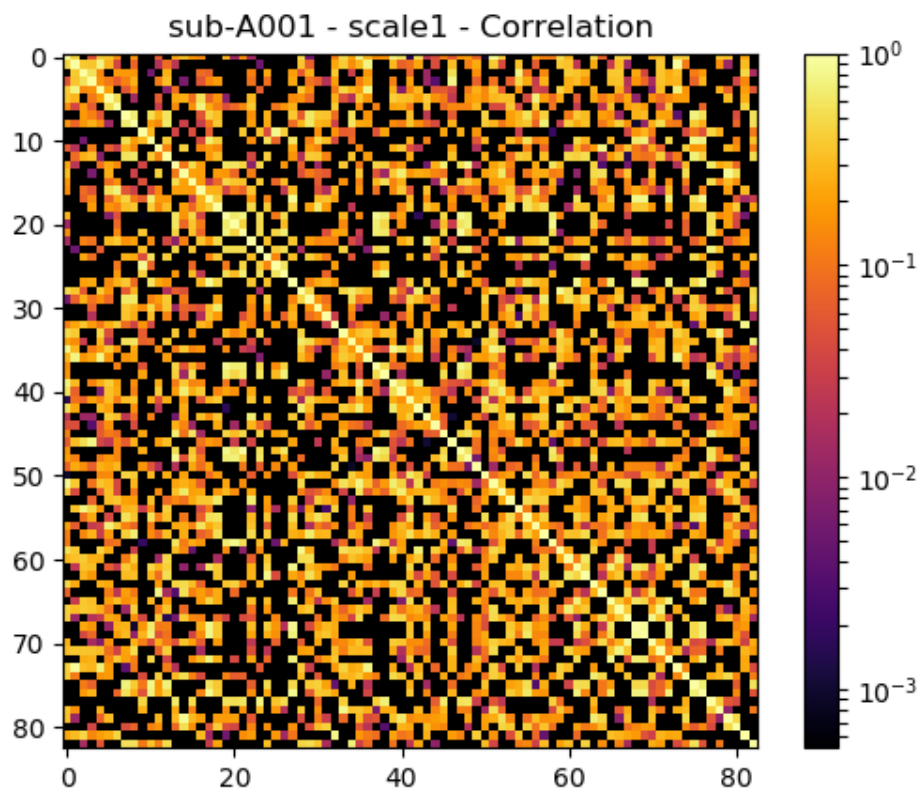
- Select the desired output from the list and click on view:



### Generated connection matrix

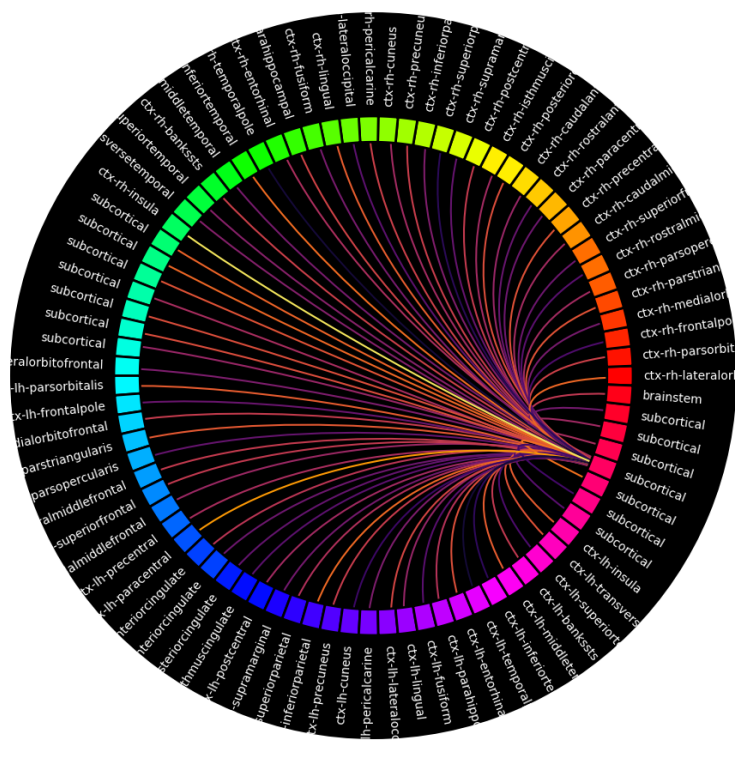
Displayed using a:

1. matrix layout with pyplot



2. circular layout with pyplot and MNE





## 5.5 Outputs of Connectome Mapper 3

Processed, or derivative, data are outputted to `< bids_dataset/derivatives >/`.

### 5.5.1 BIDS derivatives entities

Entity	Description
sub-<label>	Distinguish different subjects
ses-<label>	Distinguish different acquisition sessions
label-<label>	Describe the type of brain tissue segmented (for _probseg/dseg)
atlas-<label>	Distinguish data derived from different types of parcellation atlases
res-<label>	Distinguish data derived from the different scales of Lausanne2008 and Lausanne2018 parcellation atlases
space-DWI	Distinguish anatomical MRI derivatives in the target diffusion MRI space
model-<label>	Distinguish different diffusion signal models (DTI, CSD, SHORE, MAPMRI)

See [Original BIDS Entities Appendix](#) for more description.

---

**Note:** Connectome Mapper 3 introduced a new BIDS entity `atlas-<atlas_label>` (where `<atlas_label>`: Desikan/ L2008/ L2018), that is used in combination with the `res-<atlas_scale>` (where `<atlas_scale>`: scale1 / scale2 / scale3 / scale4 / scale5) entity to distinguish data derived from different parcellation atlases and different scales.

---

### 5.5.2 Main Connectome Mapper Derivatives

Main outputs produced by Connectome Mapper 3 are written to `cmp/sub-<subject_label>/`. In this folder, a configuration file generated for each modality pipeline (i.e. anatomical/diffusion/fMRI) and used for processing each participant is saved as `sub-<subject_label>_anatomical/diffusion/fMRI_config.ini`. It summarizes pipeline workflow options and parameters used for processing. An execution log of the full workflow is saved as `sub-<subject_label>_log.txt`.`

#### Anatomical derivatives

- Anatomical derivatives in the individual T1w space are placed in each subject's `anat/` subfolder, including:
  - The original T1w image:
    - \* `anat/sub-<subject_label>_desc-head_T1w.nii.gz`
  - The masked T1w image with its corresponding brain mask:
    - \* `anat/sub-<subject_label>_desc-brain_T1w.nii.gz`
    - \* `anat/sub-<subject_label>_desc-brain_mask.nii.gz`
  - The segmentations of the white matter (WM), gray matter (GM), and Cortical Spinal Fluid (CSF) tissues:
    - \* `anat/sub-<subject_label>_label-WM_dseg.nii.gz`

- \* anat/sub-<subject\_label>\_label-GM\_dseg.nii.gz
- \* anat/sub-<subject\_label>\_label-CSF\_dseg.nii.gz
- The five different brain parcellations:
  - \* anat/sub-<subject\_label>\_atlas-<atlas\_label>[\_res-<scale\_label>]\_dseg.nii.gz
  - where:
    - <atlas\_label>: Desikan / L2008 / L2018 is the parcellation scheme used
    - <scale\_label>: scale1, scale2, scale3, scale4, scale5 corresponds to the parcellation scale if applicable
  - with two tsv side-car files that follow the [BIDS derivatives](#), one describing the parcel label/index mapping (\_dseg.tsv), one reporting volumetry of the different parcels (\_stats.tsv), and two files used internally by CMP3, one describing the parcel labels in graphml format (dseg.graphml), one providing the color lookup table of the parcel labels in Freesurfer format which can be used directly in freeview (\_FreeSurferColorLUT.txt):
    - \* anat/sub-<subject\_label>\_atlas-<atlas\_label>[\_res-<scale\_label>]\_dseg.tsv
    - \* anat/sub-<subject\_label>\_atlas-<atlas\_label>[\_res-<scale\_label>]\_stats.tsv
    - \* anat/sub-<subject\_label>\_atlas-<atlas\_label>[\_res-<scale\_label>]\_dseg.graphml
    - \* anat/sub-<subject\_label>\_atlas-<atlas\_label>[\_res-<scale\_label>]\_FreeSurferColorLUT.txt
- Anatomical derivatives in the DWI space produced by the diffusion pipeline are placed in each subject's anat/ subfolder, including:
  - The unmasked T1w image:
    - \* anat/sub-<subject\_label>\_space-DWI\_desc-head\_T1w.nii.gz
  - The masked T1w image with its corresponding brain mask:
    - \* anat/sub-<subject\_label>\_space-DWI\_desc-brain\_T1w.nii.gz
    - \* anat/sub-<subject\_label>\_space-DWI\_desc-brain\_mask.nii.gz
  - The segmentation of WM tissue used for tractography seeding:
    - \* anat/sub-<subject\_label>\_space-DWI\_label-WM\_dseg.nii.gz
  - The five different brain parcellation are saved as:
    - \* anat/sub-<subject\_label>\_space-DWI\_atlas-<atlas\_label>[\_res-<scale\_label>]\_dseg.nii.gz
    - where:
      - <atlas\_label>: Desikan / L2008 / L2018 is the parcellation scheme used
      - <scale\_label>: scale1, scale2, scale3, scale4, scale5 corresponds to the parcellation scale if applicable
  - The 5TT image used for Anatomically Constrained Tractography (ACT):
    - \* anat/sub-<subject\_label>\_space-DWI\_label-5TT\_probseg.nii.gz

- The partial volume maps for white matter (WM), gray matter (GM), and Cortical Spinal Fluid (CSF) used for Particle Filtering Tractography (PFT), generated from 5TT image:
  - \* anat/sub-<subject\_label>\_space-DWI\_label-WM\_probseg.nii.gz
  - \* anat/sub-<subject\_label>\_space-DWI\_label-GM\_probseg.nii.gz
  - \* anat/sub-<subject\_label>\_space-DWI\_label-CSF\_probseg.nii.gz
- The GM/WM interface used for ACT and PFT seeding:
  - \* anat/sub-<subject\_label>\_space-DWI\_label-GWMI\_probseg.nii.gz

## Diffusion derivatives

Diffusion derivatives in the individual DWI space are placed in each subject's dwi/ subfolder, including:

- The final preprocessed DWI image used to fit the diffusion model for tensor or fiber orientation distribution estimation:
  - dwi/sub-<subject\_label>\_desc-preproc\_dwi.nii.gz
- The brain mask used to mask the DWI image:
  - dwi/sub-<subject\_label>\_desc-brain\_mask\_resampled.nii.gz
- The diffusion tensor (DTI) fit (if used for tractography):
  - dwi/sub-<subject\_label>]\_desc-WLS\_model-DTI\_diffmodel.nii.gzwith derived Fractional Anisotropic (FA) and Mean Diffusivity (MD) maps:
  - dwi/sub-<subject\_label>]\_model-DTI\_FA.nii.gz
  - dwi/sub-<subject\_label>]\_model-DTI\_MD.nii.gz
- The Fiber Orientation Distribution (FOD) image from Constrained Spherical Deconvolution (CSD) fit (if performed):
  - dwi/sub-<subject\_label>]\_model-CSD\_diffmodel.nii.gz
- The MAP-MRI fit for DSI and multi-shell DWI data (if performed):
  - dwi/sub-<subject\_label>]\_model-MAPMRI\_diffmodel.nii.gzwith derived Generalized Fractional Anisotropic (GFA), Mean Squared Displacement (MSD), Return-to-Origin Probability (RTOP) and Return-to-Plane Probability (RTPP) maps:
  - dwi/sub-<subject\_label>]\_model-MAPMRI\_GFA.nii.gz
  - dwi/sub-<subject\_label>]\_model-MAPMRI\_MSD.nii.gz
  - dwi/sub-<subject\_label>]\_model-MAPMRI\_RTOP.nii.gz
  - dwi/sub-<subject\_label>]\_model-MAPMRI\_RTPP.nii.gz
- The SHORE fit for DSI data:
  - dwi/sub-<subject\_label>]\_model-SHORE\_diffmodel.nii.gzwith derived Generalized Fractional Anisotropic (GFA), Mean Squared Displacement (MSD), Return-to-Origin Probability (RTOP) maps:
  - dwi/sub-<subject\_label>]\_model-SHORE\_GFA.nii.gz
  - dwi/sub-<subject\_label>]\_model-SHORE\_MSD.nii.gz
  - dwi/sub-<subject\_label>]\_model-SHORE\_RTOP.nii.gz

- The tractogram:
  - `dwi/sub-<subject_label>_model-<model_label>_desc-<label>_tractogram.trk`
 where:
  - \* `<model_label>` is the diffusion model used to drive tractography (DTI, CSD, SHORE)
  - \* `<label>` is the type of tractography algorithm employed (DET for deterministic, PROB for probabilistic)
- The structural connectivity (SC) graphs:
  - `dwi/sub-<subject_label>_atlas-<atlas_label>[_res-<scale_label>]_conndata-network_connectivity.<fmt>`
 where:
  - \* `<atlas_label>`: Desikan / L2008 / L2018 is the parcellation scheme used
  - \* `<scale_label>`: scale1, scale2, scale3, scale4, scale5 corresponds to the parcellation scale if applicable
  - \* `<fmt>`: mat / gpickle / tsv / graphml is the format used to store the graph

## Functional derivatives

Functional derivatives in the ‘meanBOLD’ (individual) space are placed in each subject’s `func/` subfolder including:

- The original BOLD image:
  - `func/sub-<subject_label>_task-rest_desc-cmp_bold.nii.gz`
- The mean BOLD image:
  - `func/sub-<subject_label>_meanBOLD.nii.gz`
- The fully preprocessed band-pass filtered used to compute ROI time-series:
  - `func/sub-<subject_label>_desc-bandpass_task-rest_bold.nii.gz`
- For scrubbing (if enabled):
  - The change of variance (DVARs):
    - \* `func/sub-<subject_label>_desc-scrubbing_DVARs.npy`
  - The frame displacement (FD):
    - \* `func/sub-<subject_label>_desc-scrubbing_FD.npy`
- Motion-related time-series:
  - `func/sub-<subject_label>_motion.tsv`
- The ROI time-series for each parcellation scale:
  - `func/sub-<subject_label>_atlas-<atlas_label>[_res-<scale_label>]_timeseries.npy`
  - `func/sub-<subject_label>_atlas-<atlas_label>[_res-<scale_label>]_timeseries.mat`
 where:
  - \* `<atlas_label>`: Desikan / L2008 / L2018 is the parcellation scheme used
  - \* `<scale_label>`: scale1, scale2, scale3, scale4, scale5 corresponds to the parcellation scale if applicable

- The functional connectivity (FC) graphs:
  - `func/sub-<subject_label>_atlas-<atlas_label>[_res-<scale_label>]_conndata-network_connectivity<fmt>`  
where:
    - \* `<atlas_label>`: Desikan / L2008 / L2018 is the parcellation scheme used
    - \* `<scale_label>`: scale1, scale2, scale3, scale4, scale5 corresponds to the parcellation scale if applicable
    - \* `<fmt>`: mat / gpickle / tsv / graphml is the format used to store the graph

## 5.5.3 FreeSurfer Derivatives

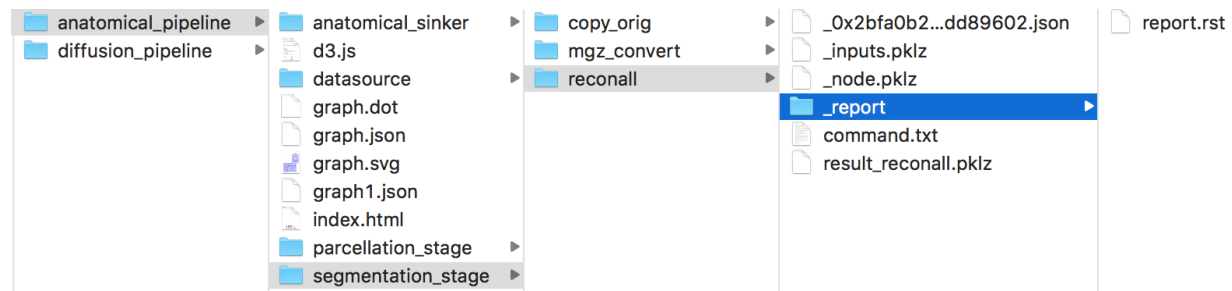
A FreeSurfer subjects directory is created in `<bids_dataset/derivatives>/freesurfer-7.2.0`.

```
freesurfer-7.2.0/  
  fsaverage/  
    mri/  
    surf/  
    ...  
  sub-<subject_label>/  
    mri/  
    surf/  
    ...  
  ...
```

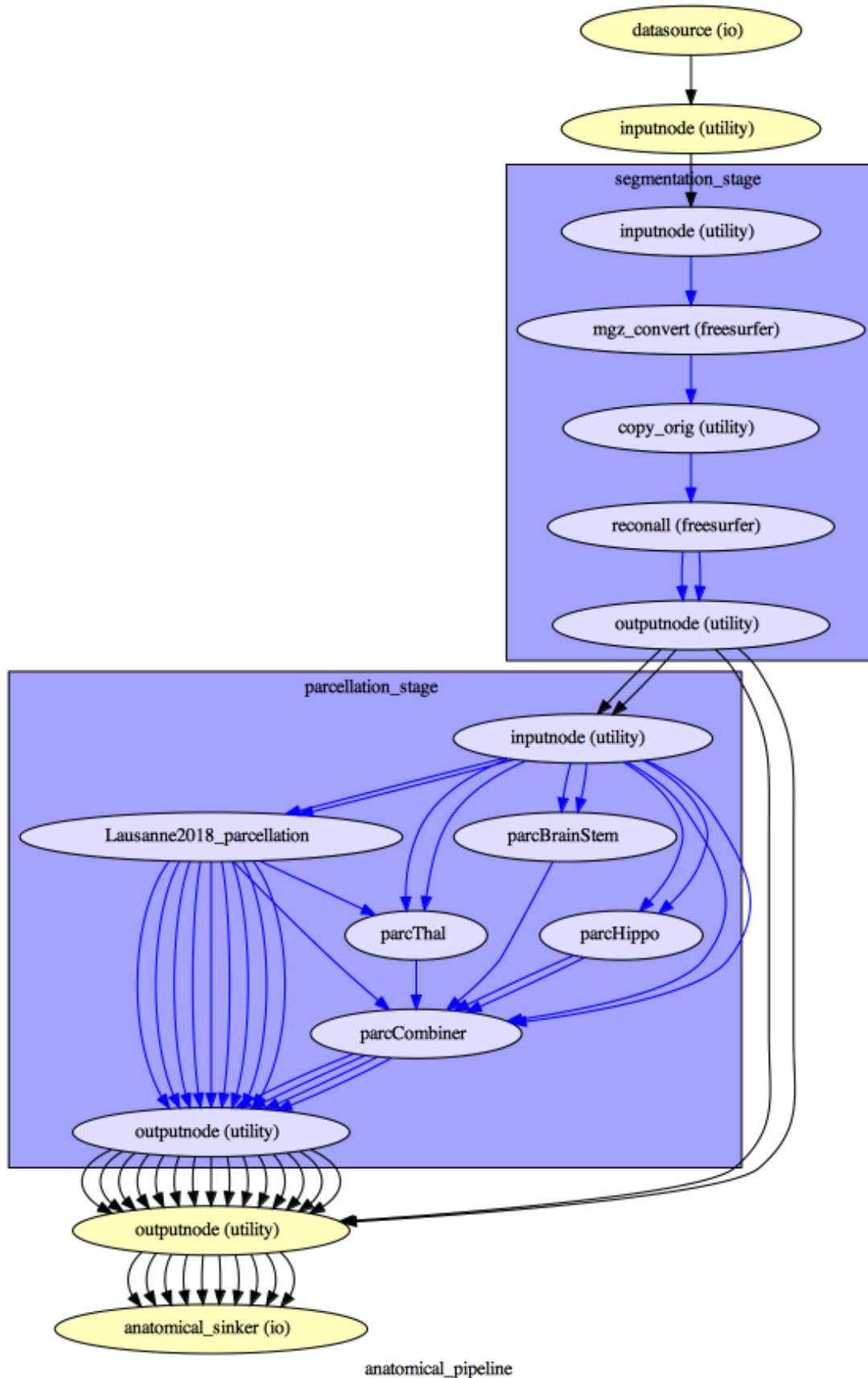
The fsaverage subject distributed with the running version of FreeSurfer is copied into this directory.

## 5.5.4 Nipype Workflow Derivatives

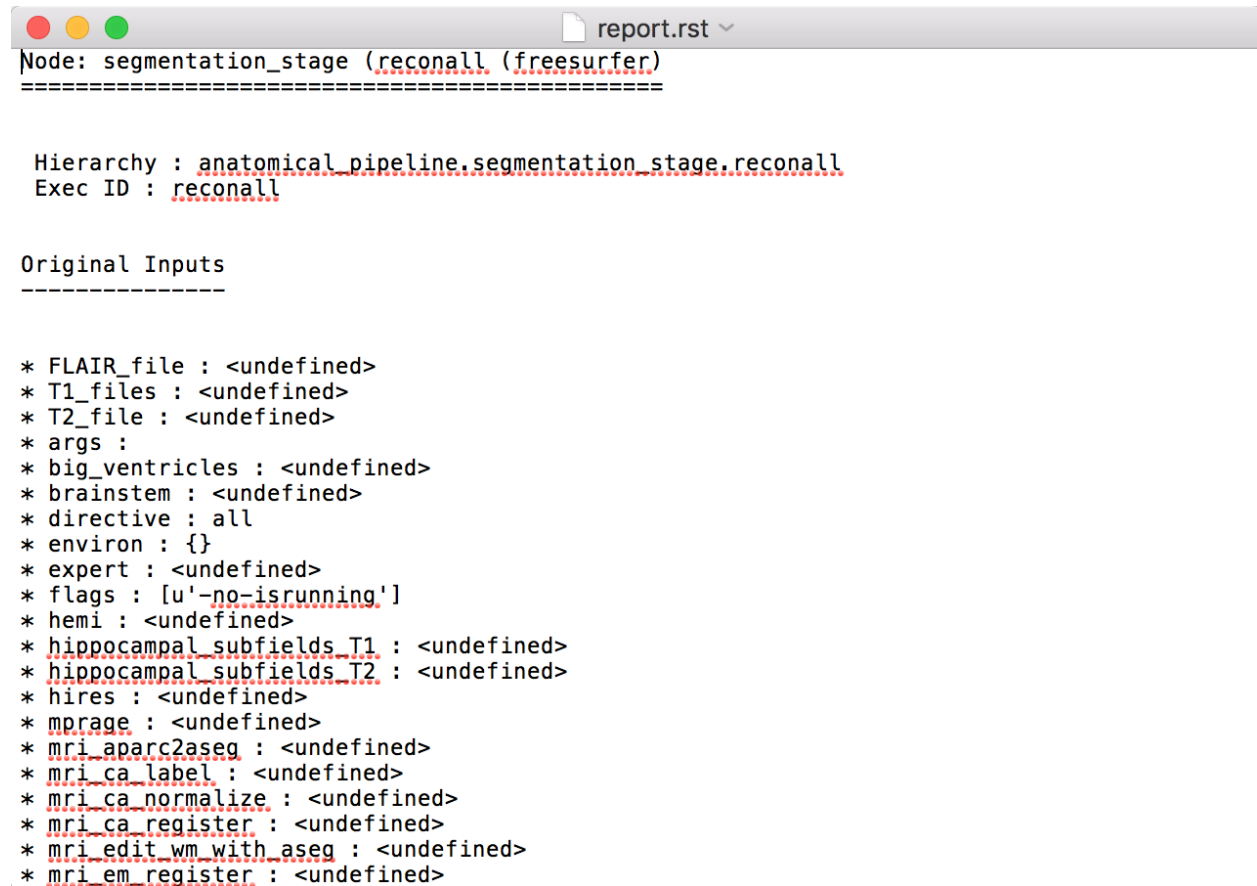
The execution of each Nipype workflow (pipeline) dedicated to the processing of one modality (i.e. anatomical/diffusion/fMRI) involves the creation of a number of intermediate outputs which are written to `<bids_dataset/derivatives>/nipype/sub-<subject_label>/<anatomical/diffusion/fMRI>_pipeline` respectively:



To enhance transparency on how data is processed, outputs include a pipeline execution graph saved as `<anatomical/diffusion/fMRI>_pipeline/graph.svg` which summarizes all processing nodes involved in the given processing pipeline:



Execution details (data provenance) of each interface (node) of a given pipeline are reported in `<anatomical/diffusion/fMRI>_pipeline/<stage_name>/<interface_name>/_report/report.rst`



```
report.rst
Node: segmentation_stage (reconall (freesurfer))
=====

Hierarchy : anatomical_pipeline.segmentation_stage.reconall
Exec ID : reconall

Original Inputs
-----

* FLAIR_file : <undefined>
* T1_files : <undefined>
* T2_file : <undefined>
* args :
* big_ventricles : <undefined>
* brainstem : <undefined>
* directive : all
* environ : {}
* expert : <undefined>
* flags : [u'-no-isrunning']
* hemi : <undefined>
* hippocampal_subfields_T1 : <undefined>
* hippocampal_subfields_T2 : <undefined>
* hires : <undefined>
* mprage : <undefined>
* mri_aparc2aseg : <undefined>
* mri_ca_label : <undefined>
* mri_ca_normalize : <undefined>
* mri_ca_register : <undefined>
* mri_edit_wm_with_aseg : <undefined>
* mri_em_register : <undefined>
```

---

**Note:** Connectome Mapper 3 outputs are currently being updated to conform to BIDS v1.4.0.

---

## 5.6 Packages and modules

### 5.6.1 cmp package

#### Submodules

##### cmp.parser module

Connectome Mapper 3 Commandline Parser.

`cmp.parser.get()` → `argparse.ArgumentParser`

Return the argparse parser of the BIDS App.

**Returns** `p` – Instance of `argparse.ArgumentParser`

**Return type** `argparse.ArgumentParser`

`cmp.parser.get_docker_wrapper_parser()` → `argparse.ArgumentParser`

Return the argparse parser of the Docker BIDS App.



**Returns** `p` – Instance of `argparse.ArgumentParser`

**Return type** `argparse.ArgumentParser`

`cmp.parser.get_singularity_wrapper_parser()` → `argparse.ArgumentParser`

Return the argparse parser of the Singularity BIDS App.

**Returns** `p` – Instance of `argparse.ArgumentParser`

**Return type** `argparse.ArgumentParser`

`cmp.parser.get_wrapper_parser()` → `argparse.ArgumentParser`

Create and return the parser object of the python wrappers of the BIDS App.

## cmp.project module

Definition of classes and functions for handling non-GUI general events.

**class** `cmp.project.ProjectInfo`

Bases: `traits.has_traits.HasTraits`

Class used to store all properties of a processing project.

**base\_directory**

BIDS dataset root directory

**Type** `traits.Directory`

**output\_directory**

Output directory

**Type** `traits.Directory`

**bids\_layout**

Instance of `pybids.BIDSLayout`

**Type** `bids.BIDSLayout`

**subjects**

List of subjects in the dataset

**Type** `traits.List`

**subject**

Subject being processed in the form `sub-XX`

**subject\_sessions**

List of sessions for the subject being processed

**Type** `traits.List`

**subject\_session**

Session of the subject being processed in the form `ses-YY`

**Type** `trait.Str`

**diffusion\_imaging\_model**

Diffusion imaging model that can be 'DSI', 'DTI', 'HARDI' or 'multishell'

**Type** `traits.Str`

**dmri\_bids\_acqs**

List diffusion imaging models extracted from `acq-<label>` filename part.

**Type** `traits.List`

**dmri\_bids\_acq**

Diffusion imaging model being processed

**anat\_runs**

List of run labels for T1w scans with multiple runs

**Type** traits.List

**anat\_run**

Run being processed for T1w scans with multiple runs

**Type** traits.Str

**dmri\_runs**

List of run labels for DWI scans with multiple runs

**Type** traits.List

**dmri\_run**

Run being processed for DWI scans with multiple runs

**Type** traits.Str

**fmri\_runs**

List of run labels for fMRI scans with multiple runs

**Type** traits.List

**fmri\_run**

Run being processed for fMRI scans with multiple runs

**Type** traits.Str

**parcellation\_scheme**

Parcellation scheme used (Default: 'Lausanne2018')

**Type** traits.Str

**atlas\_info**

Dictionary storing parcellation atlas information See ParcellationStage for more details

**Type** traits.Dict

**freesurfer\_subjects\_dir**

Freesurfer subjects directory

**Type** traits.Str

**freesurfer\_subject\_id**

Freesurfer subject ID

**Type** traits.Str

**t1\_available**

True if T1w scans were found (Default: False)

**Type** Bool

**dmri\_available**

True if DWI scans were found (Default: False)

**Type** Bool

**fmri\_available**

True if fMRI scans were found (Default: False)

**Type** Bool

**eeg\_available**

True if EEG recordings were found (Default: False)

**Type** Bool

**anat\_config\_error\_msg**

Error message for the anatomical pipeline configuration file

**Type** traits.Str

**anat\_config\_to\_load**

Path to a configuration file for the anatomical pipeline

**Type** traits.Str

**anat\_available\_config**

List of configuration files for the anatomical pipeline

**Type** traits.List

**anat\_stage\_names**

List of anatomical pipeline stage names

**Type** traits.List

**anat\_custom\_last\_stage**

Custom last anatomical pipeline stage to be processed

**Type** traits.Str

**dmri\_config\_error\_msg**

Error message for the diffusion pipeline configuration file

**Type** traits.Str

**dmri\_config\_to\_load**

Path to a configuration file for the diffusion pipeline

**Type** traits.Str

**dmri\_available\_config**

List of configuration files for the anatomical pipeline

**Type** traits.List

**dmri\_stage\_names**

List of diffusion pipeline stage names

**Type** traits.List

**dmri\_custom\_last\_stage**

Custom last diffusion pipeline stage to be processed

**Type** traits.Str

**fmri\_config\_error\_msg**

Error message for the fMRI pipeline configuration file

**Type** traits.Str

**fmri\_config\_to\_load**

Path to a configuration file for the fMRI pipeline

**Type** traits.Str

**fmri\_available\_config**

List of configuration files for the fMRI pipeline

**Type** traits.List

**fmri\_stage\_names**

List of fMRI pipeline stage names

**Type** traits.List

**fmri\_custom\_last\_stage**

Custom last fMRI pipeline stage to be processed

**Type** traits.Str

**eeg\_config\_error\_msg**

Error message for the EEG pipeline configuration file

**Type** traits.Str

**eeg\_config\_to\_load**

Path to a configuration file for the EEG pipeline

**Type** traits.Str

**eeg\_available\_config**

List of configuration files for the EEG pipeline

**Type** traits.List

**eeg\_stage\_names**

List of EEG pipeline stage names

**Type** traits.List

**eeg\_custom\_last\_stage**

Custom last EEG pipeline stage to be processed

**Type** traits.Str

**number\_of\_cores** [int] Number of cores used by Nipype workflow execution engine to distribute independent processing nodes (Must be in the range of your local resources)

`cmp.project.init_anat_project(project_info, is_new_project, debug=False)`

Initialize the anatomical processing pipeline.

**Parameters**

- **project\_info** (`cmp.project.ProjectInfo`) – Instance of `cmp.project.CMP_Project_Info` object
- **is\_new\_project** (*bool*) – Specify if it corresponds or not to a new project. If `True`, it will create initial pipeline configuration files.
- **debug** (*bool*) – If `True`, display extra prints to support debugging

**Returns** `anat_pipeline` – `AnatomicalPipeline` object instance

**Return type** `Instance(cmp.pipelines.anatomical.anatomical.AnatomicalPipeline)`

`cmp.project.init_dmri_project(project_info, bids_layout, is_new_project, gui=True, debug=False)`

Initialize the diffusion processing pipeline.

**Parameters**

- **project\_info** (`cmp.project.ProjectInfo`) – Instance of `cmp.project.CMP_Project_Info` object
- **bids\_layout** (`bids.BIDSLayout`) – Instance of `BIDSLayout` object

- **is\_new\_project** (*bool*) – Specify if it corresponds or not to a new project. If **True**, it will create initial pipeline configuration files.
- **gui** (*bool*) – Might be obsolete and removed in future versions
- **debug** (*bool*) – If **True**, display extra prints to support debugging

**Returns** **dmri\_pipeline** – DiffusionPipeline object instance

**Return type** Instance(*cmp.pipelines.diffusion.diffusion.DiffusionPipeline*)

`cmp.project.init_eeg_project(project_info, bids_layout, is_new_project, gui=False, debug=False)`  
Initialize the eeg processing pipeline.

#### Parameters

- **project\_info** (*cmp.project.CMP\_Project\_Info*) – Instance of `cmp.project.CMP_Project_Info` object
- **bids\_layout** (*bids.BIDSLayout*) – Instance of `BIDSLayout` object
- **is\_new\_project** (*bool*) – Specify if it corresponds or not to a new project. If **True**, it will create initial pipeline configuration files.
- **gui** (*bool*) – Might be obsolete and removed in future versions
- **debug** (*bool*) – If **True**, display extra prints to support debugging

**Returns** **eeg\_pipeline** – EEGPipeline object instance

**Return type** Instance(*cmp.pipelines.functional.eeg.EEGPipeline*)

`cmp.project.init_fmri_project(project_info, bids_layout, is_new_project, gui=True, debug=False)`  
Initialize the fMRI processing pipeline.

#### Parameters

- **project\_info** (*cmp.project.ProjectInfo*) – Instance of `cmp.project.CMP_Project_Info` object
- **bids\_layout** (*bids.BIDSLayout*) – Instance of `BIDSLayout` object
- **is\_new\_project** (*bool*) – Specify if it corresponds or not to a new project. If **True**, it will create initial pipeline configuration files.
- **gui** (*bool*) – Might be obsolete and removed in future versions
- **debug** (*bool*) – If **True**, display extra prints to support debugging

**Returns** **fmri\_pipeline** – fMRIPipeline object instance

**Return type** Instance(*cmp.pipelines.functional.fMRI.fMRIPipeline*)

`cmp.project.refresh_folder(bids_directory, derivatives_directory, subject, input_folders, session=None)`  
Creates (if needed) the folder hierarchy.

#### Parameters

- **bids\_directory** (*os.path*) – BIDS dataset root directory
- **derivatives\_directory** (*os.path*) – Output (derivatives) directory
- **subject** (*string*) – BIDS subject label (sub-XX)
- **input\_folders** (*List of string*) – List of folder to be created in `derivatives_directory/cmp-<version>/subject`
- **session** (*string*) – BIDS session label (ses-YY)

`cmp.project.run_individual(bids_dir, output_dir, participant_label, session_label, anat_pipeline_config, dwi_pipeline_config, func_pipeline_config, number_of_threads=1)`

Function that creates the processing pipeline for complete coverage.

#### Parameters

- **bids\_dir** (*string*) – BIDS dataset root directory
- **output\_dir** (*string*) – Output (derivatives) directory
- **participant\_label** (*string*) – BIDS participant / subject label (sub-XX)
- **session\_label** (*string*) – BIDS session label (ses-XX)
- **anat\_pipeline\_config** (*string*) – Path to anatomical pipeline configuration file
- **dwi\_pipeline\_config** (*string*) – Path to diffusion pipeline configuration file
- **func\_pipeline\_config** (*string*) – Path to fMRI pipeline configuration file
- **number\_of\_threads** (*int*) – Number of threads used by programs relying on the OpenMP library

`cmp.project.update_anat_last_processed(project_info, pipeline)`

Update last processing information of a [\*AnatomicalPipeline\*](#).

#### Parameters

- **project\_info** (`cmp.project.ProjectInfo`) – Instance of `CMP_Project_Info` object
- **pipeline** (`cmp.pipelines.anatomical.anatomical.AnatomicalPipeline`) – Instance of `AnatomicalPipeline` object

`cmp.project.update_dmri_last_processed(project_info, pipeline)`

Update last processing information of an [\*DiffusionPipeline\*](#).

#### Parameters

- **project\_info** (`cmp.project.ProjectInfo`) – Instance of `CMP_Project_Info` object
- **pipeline** (`cmp.pipelines.diffusion.diffusion.DiffusionPipeline`) – Instance of `DiffusionPipeline` object

`cmp.project.update_eeg_last_processed(project_info, pipeline)`

Update last processing information of a [\*EEGPipeline\*](#).

#### Parameters

- **project\_info** (`cmp.project.CMP_Project_Info`) – Instance of `CMP_Project_Info` object
- **pipeline** (`cmp.pipelines.functional.eeg.EEGPipeline`) – Instance of `EEGPipeline` object

`cmp.project.update_fmri_last_processed(project_info, pipeline)`

Update last processing information of an [\*fMRIPipeline\*](#).

#### Parameters

- **project\_info** (`cmp.project.ProjectInfo`) – Instance of `CMP_Project_Info` object
- **pipeline** (`cmp.pipelines.functional.fMRI.fMRIPipeline`) – Instance of `fMRIPipeline` object

## Pipelines and stages modules

### cmp.pipelines.common module

Definition of common parent classes for pipelines.

**class** cmp.pipelines.common.**Pipeline**(*project\_info*)

Bases: traits.has\_traits.HasTraits

Parent class that extends HasTraits and represents a processing pipeline.

It is extended by the various pipeline classes.

See also:

*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline*, *cmp.pipelines.diffusion.diffusion.DiffusionPipeline*, *cmp.pipelines.functional.fMRI.fMRIPipeline*

**anat\_flow** = None

**check\_config()**

Old method that was checking custom settings (obsolete).

**check\_stages\_execution()**

Check stage execution.

**clear\_stages\_outputs()**

Clear processing stage outputs.

**create\_stage\_flow**(*stage\_name*)

Create the sub-workflow of a processing stage.

**Parameters** *stage\_name* –

**fill\_stages\_outputs()**

Update processing stage output list for visual inspection.

**launch\_process()**

Launch the processing.

**number\_of\_cores** = 1

**subject** = 'sub-01'

**class** cmp.pipelines.common.**ProcessThread**(*group=None, target=None, name=None, args=()*,  
*kwargs=None, \*, daemon=None*)

Bases: `threading.Thread`

Class use to represent the pipeline process as a `threading.Thread`.

**pipeline** <Instance>

Any Pipeline instance

**pipeline** = <traits.trait\_types.Instance object>

**run()**

Execute the pipeline.

**class** cmp.pipelines.common.**ProgressThread**(*group=None, target=None, name=None, args=()*,  
*kwargs=None, \*, daemon=None*)

Bases: `threading.Thread`

Class use to monitor stage execution in a `threading.Thread`.

Information is display in the ProgressWindow (Not used anymore by CMP3)

```
pw = <traits.trait_types.Instance object>
run()
    Monitors stage execution a workflow.
stage_names = []
stages = {}
class cmp.pipelines.common.ProgressWindow
    Bases: traits.has_traits.HasTraits
    Progress window of stage execution
    (Not used anymore by CMP3)
```

## cmp.pipelines.anatomical package

### Submodules

#### cmp.pipelines.anatomical.anatomical module

Anatomical pipeline Class definition.

```
class cmp.pipelines.anatomical.anatomical.AnatomicalPipeline(project_info)
    Bases: cmp.pipelines.common.Pipeline
```

Class that extends a Pipeline and represents the processing pipeline for structural MRI.

It is composed of the segmentation stage that performs FreeSurfer recon-all and the parcellation stage that creates the Lausanne brain parcellations.

See also:

*cmp.stages.segmentation.segmentation.SegmentationStage*, *cmp.stages.parcellation.parcellation.ParcellationStage*

**check\_config()**

Check if custom white matter mask and custom atlas files specified in the configuration exist.

**Returns** *message* – String empty if all the checks pass, otherwise it contains the error message

**Return type** string

**check\_input(*layout*, *gui=True*)**

Check if inputs of the anatomical pipeline are available.

**Parameters**

- **layout** (*bids.BIDSLayout*) – Instance of BIDSLayout
- **gui** (*traits.Bool*) – Boolean used to display different messages but not really meaningful anymore since the GUI components have been migrated to *cmp.bidsappmanager*

**Returns** *valid\_inputs* – True if inputs are available

**Return type** traits.Bool

**check\_output()**

Check if outputs of an *AnatomicalPipeline* are available.

**Returns**

- *valid\_output* <Bool> – True if all outputs are found



- *error\_message* <string> – Error message if an output is not found.

**create\_datagrabber\_node**(*base\_directory*)

Create the appropriate Nipype DataGrabber node.

**Parameters** *base\_directory* (*Directory*) – Main CMP output directory of a subject e.g. /output\_dir/cmp/sub-XX/(ses-YY)

**Returns** *datasource* – Output Nipype Node with DataGrabber interface

**Return type** Output Nipype DataGrabber Node

**create\_datasinker\_node**(*base\_directory*)

Create the appropriate Nipype DataSink node depending on the *parcellation\_scheme*

**Parameters** *base\_directory* (*Directory*) – Main CMP output directory of a subject e.g. /output\_dir/cmp/sub-XX/(ses-YY)

**Returns** *sinker* – Output Nipype Node with DataSink interface

**Return type** Output Nipype DataSink Node

**create\_pipeline\_flow**(*cmp\_deriv\_subject\_directory*, *nipype\_deriv\_subject\_directory*)

Create the pipeline workflow.

**Parameters**

- *cmp\_deriv\_subject\_directory* (*Directory*) – Main CMP output directory of a subject e.g. /output\_dir/cmp/sub-XX/(ses-YY)
- *nipype\_deriv\_subject\_directory* (*Directory*) – Intermediate Nipype output directory of a subject e.g. /output\_dir/nipype/sub-XX/(ses-YY)

**Returns** *anat\_flow* – An instance of `nipype.pipeline.engine.Workflow`

**Return type** `nipype.pipeline.engine.Workflow`

**define\_custom\_mapping**(*custom\_last\_stage*)

Define the pipeline to be executed until a specific stages.

Not used yet by CMP3.

**Parameters** *custom\_last\_stage* (*string*) – Last stage to execute. Valid values are “Segmentation” and “Parcellation”

**global\_conf** = <`cmp.pipelines.anatomical.anatomical.GlobalConfig` object>

**init\_subject\_derivatives\_dirs**()

Return the paths to Nipype and CMP derivatives folders of a given subject / session.

## Notes

`self.subject` is updated to “sub-<participant\_label>\_ses-<session\_label>” when subject has multiple sessions.

**input\_folders** = ['anat']

**now** = '20220221\_2044'

**ordered\_stage\_list** = ['Segmentation', 'Parcellation']

**process**()

Executes the anatomical pipeline workflow and returns True if successful.

```
class cmp.pipelines.anatomical.anatomical.GlobalConfig
```

```
    Bases: traits.has_traits.HasTraits
```

```
    Global pipeline configurations.
```

```
    process_type
```

```
        Processing pipeline type
```

```
        Type 'anatomical'
```

```
    subjects
```

```
        List of subjects ID (in the form sub-XX)
```

```
        Type traits.List
```

```
    subject
```

```
        Subject to be processed (in the form sub-XX)
```

```
        Type traits.Str
```

```
    subject_session
```

```
        Subject session to be processed (in the form ses-YY)
```

```
        Type traits.Str
```

## cmp.pipelines.diffusion package

### Submodules

#### cmp.pipelines.diffusion.diffusion module

Diffusion pipeline Class definition.

```
class cmp.pipelines.diffusion.diffusion.DiffusionPipeline(project_info)
```

```
    Bases: cmp.pipelines.common.Pipeline
```

Class that extends a Pipeline and represents the processing pipeline for diffusion MRI.

It is composed of the preprocessing stage that preprocesses dMRI, the registration stage that co-registers T1w to the diffusion B0 and projects the parcellations to the native diffusion space, the diffusion stage that estimates tensors or fiber orientation distributions functions from the diffusion signal and reconstructs fiber using tractography, and finally the connectome stage that combines the output tractogram with the parcellations to create the structural connectivity matrices.

**See also:**

*cmp.stages.preprocessing.preprocessing.PreprocessingStage*, *cmp.stages.registration.registration.RegistrationStage*, *cmp.stages.diffusion.diffusion.DiffusionStage*, *cmp.stages.connectome.connectome.ConnectomeStage*

```
check_config()
```

Check if the list output formats in the configuration of the connectome stage is not empty.

**Returns message** – String that is empty if success, otherwise it contains the error message

**Return type** string

```
check_input(layout, gui=True)
```

Check if input of the diffusion pipeline are available.

**Parameters**

- **layout** (*bids.BIDSLayout*) – Instance of BIDSLayout
- **gui** (*traits.Bool*) – Boolean used to display different messages but not really meaningful anymore since the GUI components have been migrated to `cmp.bidsappmanager`

**Returns** **valid\_inputs** – True if inputs are available

**Return type** `traits.Bool`

**create\_datagrabber\_node**(*base\_directory, bids\_atlas\_label*)

Create the appropriate Nipype DataGrabber node depending on the `parcellation_scheme`

**Parameters**

- **base\_directory** (*Directory*) – Main CMP output directory of a subject e.g. `/output_dir/cmp/sub-XX/(ses-YY)`
- **bids\_atlas\_label** (*string*) – Parcellation atlas label

**Returns** **datasource** – Output Nipype Node with DataGrabber interface

**Return type** Output Nipype DataGrabber Node

**create\_datasinker\_node**(*base\_directory, bids\_atlas\_label, recon\_model, tracking\_model*)

Create the appropriate Nipype DataSink node depending on the `parcellation_scheme`

**Parameters**

- **base\_directory** (*Directory*) – Main CMP output directory of a subject e.g. `/output_dir/cmp/sub-XX/(ses-YY)`
- **bids\_atlas\_label** (*string*) – Parcellation atlas label
- **recon\_model** (*string*) – Diffusion signal model (DTI or CSD)
- **tracking\_model** (*string*) – Tractography algorithm (DET or PROB)

**Returns** **sinker** – Output Nipype Node with DataSink interface

**Return type** Output Nipype DataSink Node

**create\_field\_template\_dict**(*bids\_atlas\_label*)

Create the dictionary of input field template given to Nipype DataGrabber`

**Parameters** **bids\_atlas\_label** (*string*) – Parcellation atlas label

**Returns** **field\_template** – Output dictionary of template input formats given to Nipype DataGrabber

**Return type** `dict`

**create\_pipeline\_flow**(*cmp\_deriv\_subject\_directory, nipype\_deriv\_subject\_directory*)

Create the pipeline workflow.

**Parameters**

- **cmp\_deriv\_subject\_directory** (*Directory*) – Main CMP output directory of a subject e.g. `/output_dir/cmp/sub-XX/(ses-YY)`
- **nipype\_deriv\_subject\_directory** (*Directory*) – Intermediate Nipype output directory of a subject e.g. `/output_dir/nipype/sub-XX/(ses-YY)`

**Returns** **diffusion\_flow** – An instance of `nipype.pipeline.engine.Workflow`

**Return type** `nipype.pipeline.engine.Workflow`

**define\_custom\_mapping**(*custom\_last\_stage*)

Define the pipeline to be executed until a specific stages.

Not used yet by CMP3.

**Parameters** **custom\_last\_stage** (*string*) – Last stage to execute. Valid values are: “Preprocessing”, “Registration”, “Diffusion” and “Connectome”.

**get\_file**(*layout, subject, suffix, extension, session=None*)

Query files with PyBIDS and take the first file in the returned list or get a specific dmri file if BIDS acq-keyword is used in filename.

**Parameters**

- **layout** (*Instance(BIDSLayout)*) – Instance of pybids BIDSLayout
- **subject** (*str*) – BIDS subject/participant label i.e. XX in sub-XX
- **suffix** (*str*) – BIDS file suffix i.e. “T1w”, “dwi”, ...
- **extension** (*str*) – File extension i.e. “.nii.gz”, “.json”, “.bval”, ...
- **session** (*str*) – BIDS session label i.e. YY in ses-YY if the dataset has multiple sessions

**Returns** **out\_file** – The output filepath or None if no file was found

**Return type** *str*

**global\_conf** = <cmp.pipelines.diffusion.diffusion.GlobalConfig object>

**init\_subject\_derivatives\_dirs**()

Return the paths to Nipype and CMP derivatives folders of a given subject / session.

## Notes

self.subject is updated to “sub-<participant\_label>\_ses-<session\_label>” when subject has multiple sessions.

**input\_folders** = ['anat', 'dwi']

**now** = '20220221\_2044'

**ordered\_stage\_list** = ['Preprocessing', 'Registration', 'Diffusion', 'Connectome']

**process**()

Executes the diffusion pipeline workflow and returns True if successful.

**update\_outputs\_recon**(*new*)

Update list of of outputs of the diffusion stage when recon\_processing\_tool is updated.

**Parameters** **new** (*string*) – New value.

**update\_outputs\_tracking**(*new*)

Update list of of outputs of the diffusion stage when tracking\_processing\_tool is updated.

**Parameters** **new** (*string*) – New value.

**update\_preprocessing\_act**(*new*)

Update self.stages["Preprocessing"].config.act\_tracking when use\_act is updated.

**Parameters** **new** (*string*) – New value.

**update\_preprocessing\_gmwm**(*new*)

Update self.stages["Preprocessing"].config.gmwm\_seeding when seed\_from\_gmwm is updated.

**Parameters** **new** (*string*) – New value.

**update\_tracking\_tool** (*new*)

Update `self.stages["Preprocessing"].config.tracking_tool` when `tracking_processing_tool` is updated.

**Parameters** **new** (*string*) – New value.

**update\_vizualization\_layout** (*new*)

Update list of of outputs of the connectome stage when `circular_layout` is updated.

**Parameters** **new** (*string*) – New value.

**update\_vizualization\_logscale** (*new*)

Update list of of outputs of the connectome stage when `log_visualization` is updated.

**Parameters** **new** (*bool*) – New value.

**class** `cmp.pipelines.diffusion.diffusion.GlobalConfig`

Bases: `traits.has_traits.HasTraits`

Global pipeline configurations.

**process\_type**

Processing pipeline type

**Type** 'fMRI'

**subjects**

List of subjects ID (in the form sub-XX)

**Type** `traits.List`

**subject**

Subject to be processed (in the form sub-XX)

**Type** `traits.Str`

**subject\_session**

Subject session to be processed (in the form ses-YY)

**Type** `traits.Str`

**modalities**

List of available diffusion modalities red from the `acq-<modality>` filename keyword

**Type** `traits.List`

**dmri\_bids\_acq**

Diffusion modality to be processed

**Type** `traits.Str`

## `cmp.pipelines.functional` package

### Submodules

### `cmp.pipelines.functional.eeg` module

EEG pipeline Class definition.

**class** `cmp.pipelines.functional.eeg.EEGPipeline`(*project\_info*)

Bases: `cmp.pipelines.common.Pipeline`

Class that extends a Pipeline and represents the processing pipeline for EEG.

**It is composed of:**

- the EEG preparer stage that ...
- the EEG loader stage that ...
- the EEG inverse solution stage that ...

**See also:**

`cmp.stages.eeg.preparer.EEGPreparerStage`, `cmp.stages.eeg.loader.EEGLoaderStage`, `cmp.stages.eeg.inverse_solution.EEGInverseSolutionStage`

**check\_config()**

Old method that was checking custom settings (obsolete).

**check\_input**(*layout*, *gui=True*)

Check if input of the eeg pipeline are available (Not available yet).

**Parameters**

- **layout** (*bids.BIDSLayout*) – Instance of BIDSLayout
- **gui** (*traits.Bool*) – Boolean used to display different messages but not really meaningful anymore since the GUI components have been migrated to `cmp.bidsappmanager`

**Returns** **valid\_inputs** – True if inputs are available

**Return type** `traits.Bool`

**create\_datagrabber\_node**(*\*\*kwargs*)

Create the appropriate Nipype DataGrabber node depending on the `parcellation_scheme`

**Parameters**

- **base\_directory** (*Directory*) – Main CMP output directory of a subject e.g. `/output_dir/cmp/sub-XX/(ses-YY)`
- **bids\_atlas\_label** (*string*) – Parcellation atlas label

**Returns** **datasource** – Output Nipype Node with DataGrabber interface

**Return type** Output Nipype DataGrabber Node

**create\_pipeline\_flow**(*cmp\_deriv\_subject\_directory*, *nipype\_deriv\_subject\_directory*)

Create the workflow of the EEG pipeline.

**Parameters**

- **cmp\_deriv\_subject\_directory** (*Directory*) – Main CMP output directory of a subject e.g. `/output_dir/cmp/sub-XX/(ses-YY)`
- **nipype\_deriv\_subject\_directory** (*Directory*) – Intermediate Nipype output directory of a subject e.g. `/output_dir/nipype/sub-XX/(ses-YY)`

**Returns** **eeg\_flow** – An instance of `nipype.pipeline.engine.Workflow`

**Return type** `nipype.pipeline.engine.Workflow`

**global\_conf** = `<cmp.pipelines.functional.eeg.GlobalConfig object>`

**init\_subject\_derivatives\_dirs()**

Return the paths to Nipype and CMP derivatives folders of a given subject / session.

## Notes

`self.subject` is updated to “sub-<participant\_label>\_ses-<session\_label>” when subject has multiple sessions.

```
input_folders = ['anat', 'eeg']
```

```
now = '20220221_2044'
```

```
ordered_stage_list = ['EEGPreparer', 'EEGLoader', 'InverseSolution']
```

```
process()
```

Executes the anatomical pipeline workflow and returns True if successful.

```
class cmp.pipelines.functional.eeg.GlobalConfig
```

Bases: `traits.has_traits.HasTraits`

Global EEG pipeline configurations.

```
process_type
```

Processing pipeline type

**Type** ‘EEG’

```
subjects
```

List of subjects ID (in the form sub-XX)

**Type** `traits.List`

```
subject
```

Subject to be processed (in the form sub-XX)

**Type** `traits.Str`

```
subject_session
```

Subject session to be processed (in the form ses-YY)

**Type** `traits.Str`

## cmp.pipelines.functional.fMRI module

Functional pipeline Class definition.

```
class cmp.pipelines.functional.fMRI.GlobalConfig
```

Bases: `traits.has_traits.HasTraits`

Global pipeline configurations.

```
process_type
```

Processing pipeline type

**Type** ‘fMRI’

```
imaging_model
```

Imaging model used by RegistrationStage

**Type** ‘fMRI’

```
class cmp.pipelines.functional.fMRI.fMRIPipeline(project_info)
```

Bases: [cmp.pipelines.common.Pipeline](#)

Class that extends a Pipeline and represents the processing pipeline for structural MRI.

**It is composed of:**

- the preprocessing stage that can perform slice timing correction, deskipping and motion correction
- the registration stage that co-registered the anatomical T1w scan to the mean BOLD image and projects the parcellations to the native fMRI space
- the extra-preprocessing stage (`FunctionalMRISTage`) that can perform nuisance regression and band-pass filtering
- the connectome stage that extracts the time-series of each parcellation ROI and computes the Pearson's correlation coefficient between ROI time-series to create the functional connectome.

See also:

`cmp.stages.preprocessing.fmri_preprocessing.PreprocessingStage`, `cmp.stages.registration.registration.RegistrationStage`, `cmp.stages.functional.functionalMRI.FunctionalMRISTage`, `cmp.stages.connectome.fmri_connectome.ConnectomeStage`

#### **check\_config()**

Check if the fMRI pipeline parameters is properly configured.

**Returns** `message` – String that is empty if success, otherwise it contains the error message

**Return type** `string`

#### **check\_input(layout, gui=True)**

Check if input of the diffusion pipeline are available.

##### **Parameters**

- **layout** (`bids.BIDSLayout`) – Instance of `BIDSLayout`
- **gui** (`traits.Bool`) – Boolean used to display different messages but not really meaningful anymore since the GUI components have been migrated to `cmp.bidsappmanager`

**Returns** `valid_inputs` – True if inputs are available

**Return type** `traits.Bool`

#### **create\_datagrabber\_node(base\_directory, bids\_atlas\_label)**

Create the appropriate Nipype DataGrabber node depending on the `parcellation_scheme`

##### **Parameters**

- **base\_directory** (`Directory`) – Main CMP output directory of a subject e.g. `/output_dir/cmp/sub-XX/(ses-YY)`
- **bids\_atlas\_label** (`string`) – Parcellation atlas label

**Returns** `datasource` – Output Nipype Node with DataGrabber interface

**Return type** Output Nipype DataGrabber Node

#### **create\_datasinker\_node(base\_directory, bids\_atlas\_label)**

Create the appropriate Nipype DataSink node depending on the `parcellation_scheme`

##### **Parameters**

- **base\_directory** (`Directory`) – Main CMP output directory of a subject e.g. `/output_dir/cmp/sub-XX/(ses-YY)`
- **bids\_atlas\_label** (`string`) – Parcellation atlas label
- **recon\_model** (`string`) – Diffusion signal model (DTI or CSD)
- **tracking\_model** (`string`) – Tractography algorithm (DET or PROB)

**Returns** `sinker` – Output Nipype Node with DataSink interface



**Return type** Output Nipype DataSink Node

**create\_pipeline\_flow**(*cmp\_deriv\_subject\_directory*, *nipype\_deriv\_subject\_directory*)

Create the pipeline workflow.

**Parameters**

- **cmp\_deriv\_subject\_directory** (*Directory*) – Main CMP output directory of a subject e.g. /output\_dir/cmp/sub-XX/(ses-YY)
- **nipype\_deriv\_subject\_directory** (*Directory*) – Intermediate Nipype output directory of a subject e.g. /output\_dir/nipype/sub-XX/(ses-YY)

**Returns** **fMRI\_flow** – An instance of `nipype.pipeline.engine.Workflow`

**Return type** `nipype.pipeline.engine.Workflow`

**define\_custom\_mapping**(*custom\_last\_stage*)

Define the pipeline to be executed until a specific stages.

Not used yet by CMP3.

**Parameters** **custom\_last\_stage** (*string*) – Last stage to execute. Valid values are: “Preprocessing”, “Registration”, “FunctionalMRI” and “Connectome”.

**global\_conf** = <`cmp.pipelines.functional.fMRI.GlobalConfig` object>

**init\_subject\_derivatives\_dirs**()

Return the paths to Nipype and CMP derivatives folders of a given subject / session.

## Notes

`self.subject` is updated to “sub-<participant\_label>\_ses-<session\_label>” when subject has multiple sessions.

```
input_folders = ['anat', 'func']
```

```
now = '20220221_2044'
```

```
ordered_stage_list = ['Preprocessing', 'Registration', 'FunctionalMRI',
                      'Connectome']
```

**process**()

Executes the fMRI pipeline workflow and returns True if successful.

**update\_nuisance\_requirements**()

Update nuisance requirements.

Configure the registration to apply the estimated transformation to multiple segmentation masks depending on the Nuisance correction steps performed.

**update\_registration**()

Configure the list of registration tools.

**update\_scrubbing**()

Update to precompute or inputs for scrubbing during the FunctionalMRI stage.

## cmp.stages package

### Subpackages

## cmp.stages.connectome package

### Submodules

## cmp.stages.connectome.connectome module

Definition of config and stage classes for building structural connectivity matrices.

**class** cmp.stages.connectome.connectome.**ConnectomeConfig**

Bases: traits.has\_traits.HasTraits

Class used to store configuration parameters of a *ConnectomeStage* instance.

**compute\_curvature**

Compute fiber curvature (Default: False)

**Type** traits.Bool

**output\_types**

Output connectome format

**Type** ['gPickle', 'mat', 'graphml']

**connectivity\_metrics**

Set of connectome maps to compute

**Type** ['Fiber number', 'Fiber length', 'Fiber density', 'Fiber proportion', 'Normalized fiber density', 'ADC', 'gFA']

**log\_visualization**

Log visualization that might be obsolete as this has been detached after creation of the bidsappmanager (Default: True)

**Type** traits.Bool

**circular\_layout**

Visualization of the connectivity matrix using a circular layout that might be obsolete as this has been detached after creation of the bidsappmanager (Default: False)

**Type** traits.Bool

**subject**

BIDS subject ID (in the form sub-XX)

**Type** traits.Str

See also:

*cmp.stages.connectome.connectome.ConnectomeStage*

**class** cmp.stages.connectome.connectome.**ConnectomeStage**(*bids\_dir*, *output\_dir*)

Bases: *cmp.stages.common.Stage*

Class that represents the connectome building stage of a *DiffusionPipeline*.

**create\_workflow()**

Create the workflow of the diffusion *ConnectomeStage*

See also:

`cmp.pipelines.diffusion.diffusion.DiffusionPipeline`,  
`connectome.ConnectomeConfig`

`cmp.stages.connectome.`

**create\_workflow**(*flow*, *inputnode*, *outputnode*)

Create the stage workflow.

#### Parameters

- **flow** (`nipype.pipeline.engine.Workflow`) – The `nipype.pipeline.engine.Workflow` instance of the Diffusion pipeline
- **inputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the inputs of the stage
- **outputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs**()

Update the `inspect_outputs` class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**has\_run**()

Function that returns `True` if the stage has been run successfully.

#### Returns

**Return type** `True` if the stage has been run successfully

### `cmp.stages.connectome.fmri_connectome` module

Definition of config and stage classes for building functional connectivity matrices.

**class** `cmp.stages.connectome.fmri_connectome.ConnectomeConfig`

Bases: `traits.has_traits.HasTraits`

Class used to store configuration parameters of a `ConnectomeStage` instance.

**apply\_scrubbing**

Apply scrubbing before mapping the functional connectome if `True` (Default: `False`)

**Type** `traits.Bool`

**FD\_thr**

Framewise displacement threshold (Default: `0.2`)

**Type** `traits.Float`

**DVARS\_thr**

DVARS (RMS of variance over voxels) threshold (Default: `4.0`)

**Type** `traits.Float`

**output\_types**

Output connectome format

**Type** [`'gPickle'`, `'mat'`, `'cff'`, `'graphml'`]

**log\_visualization**

Log visualization that might be obsolete as this has been detached after creation of the `bidsappmanager` (Default: `True`)

**Type** `traits.Bool`

**circular\_layout**

Visualization of the connectivity matrix using a circular layout that might be obsolete as this has been detached after creation of the bidsappmanager (Default: False)

**Type** `traits.Bool`

**subject**

BIDS subject ID (in the form sub-XX)

**Type** `traits.Str`

**See also:**

[`cmp.stages.connectome.fmri\_connectome.ConnectomeStage`](#)

**class** `cmp.stages.connectome.fmri_connectome.ConnectomeStage(bids_dir, output_dir)`

Bases: [`cmp.stages.common.Stage`](#)

Class that represents the connectome building stage of a [`fMRIPipeline`](#).

**create\_workflow()**

Create the workflow of the fMRI [`ConnectomeStage`](#)

**See also:**

[`cmp.pipelines.functional.fMRI.fMRIPipeline`](#), [`cmp.stages.connectome.fmri\_connectome.ConnectomeConfig`](#)

**create\_workflow(flow, inputnode, outputnode)**

Create the stage workflow.

**Parameters**

- **flow** ([`nipype.pipeline.engine.Workflow`](#)) – The `nipype.pipeline.engine.Workflow` instance of the fMRI pipeline
- **inputnode** ([`nipype.interfaces.utility.IdentityInterface`](#)) – Identity interface describing the inputs of the stage
- **outputnode** ([`nipype.interfaces.utility.IdentityInterface`](#)) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs()**

Update the `inspect_outputs` class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**has\_run()**

Function that returns [`True`](#) if the stage has been run successfully.

**Returns**

**Return type** [`True`](#) if the stage has been run successfully

## cmp.stages.diffusion package

### Submodules

#### cmp.stages.diffusion.diffusion module

Definition of config and stage classes for diffusion reconstruction and tractography.

**class** cmp.stages.diffusion.diffusion.DiffusionConfig

Bases: traits.has\_traits.HasTraits

Class used to store configuration parameters of a *DiffusionStage* instance.

**diffusion\_imaging\_model\_editor**

Available diffusion imaging models

**Type** ['DSI', 'DTI', 'HARDI', 'multishell']

**diffusion\_imaging\_model**

Selected diffusion imaging model (Default: 'DTI')

**Type** traits.Str

**dilate\_rois**

Dilate parcellation regions-of-interest (Default: True)

**Type** traits.Bool

**dilation\_kernel**

Type of dilation kernel to used

**Type** traits.Enum(['Box', 'Gauss', 'Sphere'])

**dilation\_radius**

Radius of the dilation kernel

**Type** traits.Enum([1, 2, 3, 4])

**recon\_processing\_tool\_editor**

List of processing tools available for diffusion signal reconstruction

**Type** ['Dipy', 'MRtrix']

**tracking\_processing\_tool\_editor**

List of processing tools available for tractography

**Type** ['Dipy', 'MRtrix']

**processing\_tool\_editor**

List of processing tools available for diffusion signal reconstruction and tractography

**Type** ['Dipy', 'MRtrix']

**recon\_processing\_tool**

Processing tool to use for diffusion signal modeling (Default: 'MRtrix')

**Type** traits.Str

**tracking\_processing\_tool**

Processing tool to use for tractography (Default: 'MRtrix')

**Type** traits.Str

**custom\_track\_file**

Custom tractogram file to used as input to the connectome stage (obsolete)

**Type** traits.File

**dipy\_recon\_config**

Configuration instance of the Dipy reconstruction stage

**Type** Instance(HasTraits)

**mrtrix\_recon\_config**

Configuration instance of the MRtrix3 reconstruction stage

**Type** Instance(HasTraits)

**dipy\_tracking\_config**

Configuration instance of the Dipy tracking (tractography) stage

**Type** Instance(HasTraits)

**mrtrix\_tracking\_config**

Configuration instance of the MRtrix3 tracking (tractography) stage

**Type** Instance(HasTraits)

**diffusion\_model\_editor**

List of types of available local tractography algorithms.

**Type** ['Deterministic', 'Probabilistic']

**diffusion\_model**

Type of local tractography algorithm to use. (Default: 'Probabilistic')

**Type** traits.Str

**See also:**

*cmp.stages.diffusion.reconstruction.DipyReconConfig*, *cmp.stages.diffusion.reconstruction.MRtrixReconConfig*, *cmp.stages.diffusion.tracking.DipyTrackingConfig*, *cmp.stages.diffusion.tracking.MRtrixTrackingConfig*, *cmp.stages.diffusion.DiffusionStage*

**update\_dipy\_tracking\_SD(new)**

Update SD of dipy\_tracking\_config when local\_model is updated.

**Parameters** *new* (*string*) – New value of local\_model

**update\_dipy\_tracking\_sh\_order(new)**

Update sh\_order of dipy\_tracking\_config when lmax\_order is updated.

**Parameters** *new* (*int*) – New value of lmax\_order

**update\_mrtrix\_tracking\_SD(new)**

Update SD of mrtrix\_tracking\_config when local\_model is updated.

**Parameters** *new* (*string*) – New value of local\_model

**class** cmp.stages.diffusion.diffusion.DiffusionStage(*bids\_dir*, *output\_dir*)

Bases: *cmp.stages.common.Stage*

Class that represents the diffusion stage of a *DiffusionPipeline*.

The diffusion stage workflow is composed of two sub-workflows: 1. *recon\_flow* that estimates tensors or fiber orientation distribution functions from dMRI, 2. *track\_flow* that runs tractography from the output of *recon\_flow*.

**create\_workflow()**

Create the workflow of the *DiffusionStage*

See also:

*cmp.pipelines.diffusion.diffusion.DiffusionPipeline*, *cmp.stages.diffusion.diffusion.DiffusionConfig*, *cmp.stages.diffusion.reconstruction.DipyReconConfig*, *cmp.stages.diffusion.reconstruction.MRtrixReconConfig*, *cmp.stages.diffusion.tracking.DipyTrackingConfig*, *cmp.stages.diffusion.tracking.MRtrixTrackingConfig*, *cmp.stages.diffusion.reconstruction.create\_dipy\_recon\_flow*, *cmp.stages.diffusion.reconstruction.create\_mrtrix\_recon\_flow*, *cmp.stages.diffusion.tracking.create\_dipy\_tracking\_flow*, *cmp.stages.diffusion.tracking.create\_mrtrix\_tracking\_flow*

**create\_workflow(flow, inputnode, outputnode)**

Create the stage workflow.

**Parameters**

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of the Diffusion pipeline
- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the stage

See also:

*cmp.stages.diffusion.reconstruction.create\_dipy\_recon\_flow()*, *cmp.stages.diffusion.reconstruction.create\_mrtrix\_recon\_flow()*, *cmp.stages.diffusion.tracking.create\_dipy\_tracking\_flow()*, *cmp.stages.diffusion.tracking.create\_mrtrix\_tracking\_flow()*

**define\_inspect\_outputs()**

Update the *inspect\_outputs* class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**has\_run()**

Function that returns **True** if the stage has been run successfully.

**Returns**

**Return type** **True** if the stage has been run successfully

*cmp.stages.diffusion.diffusion.strip\_suffix(file\_input, prefix)*

Extract path of *file\_input* and add *prefix* to generate a prefix path for outputs.

**Parameters**

- **file\_input** (*os.path.abspath*) – Absolute path to an input file
- **prefix** (*os.path*) – Prefix to used in the generation of the output prefix path.

**Returns** *out\_prefix\_path* – The generated prefix path

**Return type** *os.path*

**cmp.stages.diffusion.reconstruction module**

Reconstruction methods and workflows.

**class** cmp.stages.diffusion.reconstruction.DipyReconConfig

Bases: traits.has\_traits.HasTraits

Class used to store Dipy diffusion reconstruction sub-workflow configuration parameters.

**imaging\_model**

Diffusion imaging model (For instance 'DTI')

**Type** Str

**flip\_table\_axis**

Axis to be flipped in the gradient table.

**Type** traits.List(['x', 'y', 'z'])

**local\_model\_editor**

List of reconstruction models

**Type** {False: '1:Tensor', True: '2:Constrained Spherical Deconvolution' }

**local\_model**

Reconstruction model selected (See [local\\_model\\_editor](#)) (Default: True, meaning Tensor is performed)

**Type** traits.Bool

**lmax\_order**

Choices of maximal order to use for Constrained Spherical Deconvolution

**Type** traits.Enum([2, 4, 6, 8, 10, 12, 14, 16])

**single\_fib\_thr**

FA threshold

**Type** traits.Float(0.7, min=0, max=1)

**recon\_mode**

Can be "Probabilistic" or "Deterministic"

**Type** traits.Str

**mapmri**

**Type** traits.Bool(False)

**tracking\_processing\_tool**

**Type** traits.Enum('MRtrix', 'Dipy')

**laplacian\_regularization**

Apply laplacian regularization in MAP-MRI if [True](#) (Default: True)

**Type** traits.Bool

**laplacian\_weighting**

Laplacian regularization weight in MAP-MRI (Default: 0.05)

**Type** traits.Float

**positivity\_constraint**

Apply positivity constraint in MAP-MRI if [True](#) (Default: True)

**Type** traits.Bool



**radial\_order**

MAP-MRI radial order (Default: 8)

**Type** traits.Int

**small\_delta**

Small data for gradient table (pulse duration) used by MAP-MRI (Default: 0.02)

**Type** traits.Float

**big\_delta**

Big data for gradient table (time interval) used by MAP-MRI (Default: 0.5)

**Type** traits.Float

**radial\_order\_values**

Choices of radial order values used by SHORE

**Type** traits.List([2, 4, 6, 8, 10, 12])

**shore\_radial\_order**

Even number that represents the order of the basis (Default: 6)

**Type** traits.Str

**shore\_zeta**

Scale factor in SHORE (Default: 700)

**Type** traits.Int

**shore\_lambda\_n**

Radial regularisation constant in SHORE (Default: 1e-8)

**Type** traits.Float

**shore\_lambda\_l**

Angular regularisation constant in SHORE (Default: 1e-8)

**Type** traits.Float

**shore\_tau**

Diffusion time used by SHORE. By default the value that makes  $q$  equal to the square root of the b-value (Default: 0.025330295910584444)

**Type** traits.Float

**shore\_constrain\_e0**

Constrain SHORE optimization such that  $E(0) = 1$  (Default: False)

**Type** traits.Bool

**shore\_positive\_constraint**

Constrain the SHORE propagator to be positive (Default: False)

**Type** traits.Bool

**class cmp.stages.diffusion.reconstruction.MRtrixReconConfig**

Bases: traits.has\_traits.HasTraits

Class used to store Dipy diffusion reconstruction sub-workflow configuration parameters.

**flip\_table\_axis**

Axis to be flipped in the gradient table.

**Type** traits.List(['x', 'y', 'z'])

**local\_model\_editor**

List of reconstruction models

**Type** {False: '1:Tensor', True: '2:Constrained Spherical Deconvolution' }

**local\_model**

Reconstruction model selected (See [local\\_model\\_editor](#)) (Default: True, meaning Tensor is performed)

**Type** traits.Bool

**lmax\_order**

Choices of maximal order to use for Constrained Spherical Deconvolution

**Type** traits.Enum([2, 4, 6, 8, 10, 12, 14, 16])

**single\_fib\_thr**

FA threshold

**Type** traits.Float(0.7, min=0, max=1)

**recon\_mode**

Can be “Probabilistic” or “Deterministic”

**Type** traits.Str

`cmp.stages.diffusion.reconstruction.create_dipy_recon_flow(config)`

Create the reconstruction sub-workflow of the DiffusionStage using Dipy.

**Parameters** *config* ([DipyReconConfig](#)) – Workflow configuration

**Returns** *flow* – Built reconstruction sub-workflow

**Return type** `nipype.pipeline.engine.Workflow`

`cmp.stages.diffusion.reconstruction.create_mrtrix_recon_flow(config)`

Create the reconstruction sub-workflow of the DiffusionStage using MRtrix3.

**Parameters** *config* ([DipyReconConfig](#)) – Workflow configuration

**Returns** *flow* – Built reconstruction sub-workflow

**Return type** `nipype.pipeline.engine.Workflow`

**cmp.stages.diffusion.tracking module**

Tracking methods and workflows of the diffusion stage.

**class** `cmp.stages.diffusion.tracking.DipyTrackingConfig`

Bases: `traits.has_traits.HasTraits`

Class used to store Dipy diffusion reconstruction sub-workflow configuration parameters.

**imaging\_model**

Diffusion imaging model (For example ‘DTI’)

**Type** traits.Str

**tracking\_mode**

Type of local tractography algorithm (Can be “Deterministic” or “Probabilistic”)

**Type** traits.Str

**SD**

If [True](#), inputs are coming from Constrained Spherical Deconvolution reconstruction

**Type** traits.Bool

**number\_of\_seeds**

Number of seeds (Default: 1000)

**Type** traits.Int

**seed\_density**

Number of seeds to place along each direction where a density of 2 is the same as [2, 2, 2] and will result in a total of 8 seeds per voxel (Default: 1.0)

**Type** traits.Float

**fa\_thresh**

Fractional Anisotropy (FA) threshold (Default: 0.2)

**Type** traits.Float

**step\_size**

Tractography algorithm step size (Default: 0.5)

**Type** traits.trait.Float

**max\_angle**

Maximum streamline angle allowed (Default: 25.0)

**Type** traits.Float

**sh\_order**

Order used for Constrained Spherical Deconvolution reconstruction (Default: 8)

**Type** traits.Int

**use\_act**

Use FAST for partial volume estimation and Anatomically-Constrained Tractography (ACT) tissue classifier (Default: False)

**Type** traits.Bool

**seed\_from\_gmwmi**

Seed from Grey Matter / White Matter interface (requires Anatomically-Constrained Tractography (ACT)) (Default: False)

**Type** traits.Bool

**class** cmp.stages.diffusion.tracking.MRtrixTrackingConfig

Bases: traits.has\_traits.HasTraits

Class used to store Dipy diffusion reconstruction sub-workflow configuration parameters.

**tracking\_mode**

Type of local tractography algorithm (Can be “Deterministic” or “Probabilistic”)

**Type** traits.Str

**SD**

If **True**, inputs are coming from Constrained Spherical Deconvolution reconstruction

**Type** traits.Bool

**desired\_number\_of\_tracks**

Desired number of output streamlines in the tractogram (Default: 1M)

**Type** traits.Int

**curvature = Float**

Maximum streamline curvature (Default: 2.0)

**min\_length = Float**

Minimal streamline length (Default: 5)

**max\_length = Float**

Maximal streamline length (Default: 500)

**angle**

Maximum streamline angle allowed (Default: 45.0)

**Type** traits.Float

**cutoff\_value**

Cut-off value to terminate streamline (Default: 0.05)

**Type** traits.Float

**use\_act**

Use 5ttgen for brain tissue types estimation and Anatomically-Constrained Tractography (ACT) tissue classifier (Default: False)

**Type** traits.Bool

**seed\_from\_gmwmi**

Seed from Grey Matter / White Matter interface (requires Anatomically-Constrained Tractography (ACT)) (Default: False)

**Type** traits.Bool

**crop\_at\_gmwmi**

Crop streamline endpoints more precisely as they cross the GM-WM interface (requires Anatomically-Constrained Tractography (ACT)) (Default: True)

**Type** traits.Bool

**backtrack**

Allow tracks to be truncated (requires Anatomically-Constrained Tractography (ACT)) (Default: True)

**Type** traits.Bool

**sift**

Filter tractogram using mrtrix3 SIFT (Default: True)

**Type** traits.Bool

`cmp.stages.diffusion.tracking.create_dipy_tracking_flow(config)`

Create the tractography sub-workflow of the DiffusionStage using Dipy.

**Parameters** *config* ([DipyTrackingConfig](#)) – Sub-workflow configuration object

**Returns** *flow* – Built tractography sub-workflow

**Return type** `nipype.pipeline.engine.Workflow`

`cmp.stages.diffusion.tracking.create_mrtrix_tracking_flow(config)`

Create the tractography sub-workflow of the DiffusionStage using MRtrix3.

**Parameters** *config* ([MRtrixTrackingConfig](#)) – Sub-workflow configuration object

**Returns** *flow* – Built tractography sub-workflow

**Return type** `nipype.pipeline.engine.Workflow`

`cmp.stages.diffusion.tracking.get_freesurfer_parcellation(roi_files)`

Return the first file in the list of parcellation files

**Parameters** `roi_files` (*list of traits.File*) – List of parcellation files

## cmp.stages.eeg package

### Submodules

#### cmp.stages.eeg.inverse\_solution module

Definition of config and stage classes for computing brain parcellation.

**class** `cmp.stages.eeg.inverse_solution.EEGInverseSolutionConfig`

Bases: `traits.has_traits.HasTraits`

Class used to store configuration parameters of a [EEGInverseSolutionStage](#) instance.

**invsol\_format**

Specify the inverse solution algorithm (Default: Cartool-LAURA)

**Type** ['Cartool-LAURA', 'Cartool-LORETA', 'mne-sLORETA']

**See also:**

[cmp.stages.eeg.inverse\\_solution.EEGInverseSolutionStage](#)

**class** `cmp.stages.eeg.inverse_solution.EEGInverseSolutionStage(bids_dir, output_dir)`

Bases: [cmp.stages.common.Stage](#)

Class that represents the reconstruction of the inverse solutions stage of a [EEGPipeline](#).

This stage consists of three processing interfaces:

- **CreateFwd**: Create the forward solution (leadfield) from the BEM and the source space.
- **CreateCov**: Create the noise covariance matrix from the data.
- **MNEInverseSolution**: Create and apply the actual inverse operator to generate the ROI time courses.

**create\_workflow()**

Create the workflow of the [EEGInverseSolutionStage](#)

**See also:**

[cmp.pipelines.functional.eeg.EEGPipeline](#),  
[EEGInverseSolutionConfig](#)

[cmp.stages.eeg.inverse\\_solution.](#)

**create\_workflow(flow, inputnode, outputnode)**

Create the stage workflow.

**Parameters**

- **flow** (`nipype.pipeline.engine.Workflow`) – The `nipype.pipeline.engine.Workflow` instance of the Diffusion pipeline
- **inputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the inputs of the stage
- **outputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs()**

**has\_run()**

Function that returns **True** if the stage has been run successfully.

**Returns**

**Return type** **True** if the stage has been run successfully

## cmp.stages.eeg.loader module

Definition of config and stage classes for computing brain parcellation.

**class** `cmp.stages.eeg.loader.EEGLoaderConfig`

Bases: `traits.has_traits.HasTraits`

Class used to store configuration parameters of a *EEGLoaderStage* instance.

**invsol\_format**

Specify the inverse solution algorithm (Default: Cartool-LAURA)

**Type** ['Cartool-LAURA', 'Cartool-LORETA', 'mne-sLORETA']

**See also:**

*cmp.stages.eeg.loader.EEGLoaderStage*

**class** `cmp.stages.eeg.loader.EEGLoaderStage(bids_dir, output_dir)`

Bases: *cmp.stages.common.Stage*

Class that represents inverse solution input loader stage of a *EEGPipeline*.

This stage consists of one processing interface:

- **EEGloader:** Use `nipype.interfaces.io.BIDSDataGrabber` to query all the necessary files to be passed as inputs to the inverse solution stage of the EEG pipeline.

**create\_workflow()**

Create the workflow of the *EEGLoaderStage*

**See also:**

*cmp.pipelines.functional.eeg.EEGPipeline*, *cmp.stages.eeg.loader.EEGLoaderConfig*

**create\_workflow(flow, inputnode, outputnode)**

Create the stage workflow.

**Parameters**

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of the Diffusion pipeline
- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs()**

**has\_run()**

Function that returns **True** if the stage has been run successfully.

**Returns**

**Return type** **True** if the stage has been run successfully

**cmp.stages.eeg.preparer module**

Definition of config and stage classes for computing brain parcellation.

**class** cmp.stages.eeg.preparer.**EEGPreparerConfig**

Bases: traits.has\_traits.HasTraits

Class used to store configuration parameters of a *EEGPreparerStage* instance.

**eeg\_format**

Specify the format in which EGG data is stored (Default: *set*)

**Type** Enum(['.set', '.fif'])

**epochs**

Name of file containing EEG epochs

**Type** File

**invsol\_format**

Specify the inverse solution algorithm (Default: Cartool-LAURA)

**Type** Enum(['Cartool-LAURA', 'Cartool-LORETA', 'mne-sLORETA'])

**parcellation = Dict({'label'**

Dictionary used to differentiate parcellation files

**Type** 'aparc', 'desc':', 'suffix:'.})

**cartool\_dir = Str**

Name of cartool derivatives directory (Default: 'cartool-v3.80')

**cmp3\_dir = Str**

Name of cartool derivatives directory (Default: 'cmp')

**EEG\_params = Dict()**

Dictionary storing extra EEG parameters

**See also:**

*cmp.stages.eeg.preparer.EEGPreparerStage*

**class** cmp.stages.eeg.preparer.**EEGPreparerStage**(*bids\_dir*, *output\_dir*)

Bases: *cmp.stages.common.Stage*

Class that represents the preparing stage of a *EEGPipeline*.

This stage consists of three processing interfaces:

- **EEGLAB2fif**: Reads eeglab data and converts them to MNE format (*fif* file extension).
- **CreateSrc**: Creates the dipole locations along the surface of the brain.
- **CreateBEM**: Creates the boundary element method.

**create\_workflow()**

Create the workflow of the *EEGPreparerStage*

**See also:**

*cmp.pipelines.functional.eeg.EEGPipeline*, *cmp.stages.eeg.preparer.EEGPreparerConfig*

**create\_workflow**(*flow*, *inputnode*, *outputnode*)

Create the stage workflow.

**Parameters**

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of the Diffusion pipeline
- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs()**

**has\_run()**

Function that returns **True** if the stage has been run successfully.

**Returns**

**Return type** **True** if the stage has been run successfully

## cmp.stages.functional package

### Submodules

#### cmp.stages.functional.functionalMRI module

Definition of config and stage classes for the extra functional preprocessing stage.

**class** `cmp.stages.functional.functionalMRI.FunctionalMRIConfig`

Bases: `traits.has_traits.HasTraits`

Class used to store configuration parameters of a `FunctionalMRIStage` object.

**global\_nuisance**

Perform global nuisance regression (Default: False)

**Type** `traits.Bool`

**csf**

Perform CSF nuisance regression (Default: True)

**Type** `traits.Bool`

**wm**

Perform White-Matter nuisance regression (Default: True)

**Type** `traits.Bool`

**motion**

Perform motion nuisance regression (Default: True)

**Type** `traits.Bool`

**detrending = Bool**

Perform detrending (Default: True)

**detrending\_mode = Enum("linear", "quadratic")**

Detrending mode (Default: "Linear")

**lowpass\_filter = Float**

Lowpass filter frequency (Default: 0.01)

**highpass\_filter = Float**

Highpass filter frequency (Default: 0.1)



**scrubbing = Bool**

Perform scrubbing (Default: True)

See also:

*cmp.stages.functional.functionalMRI.FunctionalMRIStage*

**class** *cmp.stages.functional.functionalMRI.FunctionalMRIStage*(*bids\_dir*, *output\_dir*)

Bases: *cmp.stages.common.Stage*

Class that represents the post-registration preprocessing stage of the fMRIPipeline.

**create\_workflow()**

Create the workflow of the *FunctionalMRIStage*

See also:

*cmp.pipelines.functional.fMRI.fMRIPipeline*, *cmp.stages.functional.functionalMRI.FunctionalMRIConfig*

**create\_workflow**(*flow*, *inputnode*, *outputnode*)

Create the stage workflow.

#### Parameters

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of the fMRI pipeline
- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs()**

Update the *inspect\_outputs* class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**has\_run()**

Function that returns **True** if the stage has been run successfully.

#### Returns

**Return type** **True** if the stage has been run successfully

## cmp.stages.parcellation package

### Submodules

#### cmp.stages.parcellation.parcellation module

Definition of config and stage classes for computing brain parcellation.

**class** *cmp.stages.parcellation.parcellation.ParcellationConfig*

Bases: *traits.has\_traits.HasTraits*

Class used to store configuration parameters of a *ParcellationStage* object.

**pipeline\_mode**

Distinguish if a parcellation is run in a “Diffusion” or in a fMRI pipeline

**Type** *traits.Enum*([“Diffusion”, “fMRI”])

**parcellation\_scheme**

Parcellation scheme used (Default: 'Lausanne2018')

**Type** traits.Str

**parcellation\_scheme\_editor**

Choice of parcellation schemes

**Type** traits.List(['NativeFreesurfer', 'Lausanne2018', 'Custom'])

**include\_thalamic\_nuclei\_parcellation**

Perform and include thalamic nuclei segmentation in 'Lausanne2018' parcellation (Default: True)

**Type** traits.Bool

**ants\_precision\_type**

Specify ANTs used by thalamic nuclei segmentation to adopt single / double precision float representation to reduce memory usage. (Default: 'double')

**Type** traits.Enum(['double', 'float'])

**segment\_hippocampal\_subfields**

Perform and include FreeSurfer hippocampal subfields segmentation in 'Lausanne2018' parcellation (Default: True)

**Type** traits.Bool

**segment\_brainstem**

Perform and include FreeSurfer brainstem segmentation in 'Lausanne2018' parcellation (Default: True)

**Type** traits.Bool

**atlas\_info**

Dictionary storing information of atlases in the form >>> atlas\_info = { >>> "atlas\_name": { >>> 'number\_of\_regions': 83, >>> 'node\_information\_graphml': "/path/to/file.graphml" >>> } >>> } # doctest: +SKIP

**Type** traits.Dict

**custom\_parcellation**

Instance of *CustomParcellationBIDSFile* that describes the custom BIDS-formatted brain parcellation file

**Type** traits.Instance(*CustomParcellationBIDSFile*)

See also:

*cmp.stages.parcellation.parcellation.ParcellationStage*

**class** *cmp.stages.parcellation.parcellation.ParcellationStage*(*pipeline\_mode*, *subject*, *session*,  
*bids\_dir*, *output\_dir*)

Bases: *cmp.stages.common.Stage*

Class that represents the parcellation stage of a *AnatomicalPipeline*.

**create\_workflow()**

Create the workflow of the *ParcellationStage*

See also:

*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline*, *cmp.stages.parcellation.parcellation.ParcellationConfig*

**create\_workflow**(*flow*, *inputnode*, *outputnode*)

Create the stage workflow.

**Parameters**

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of the anatomical pipeline
- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the parcellation stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the parcellation stage

**create\_workflow\_custom**(*flow, outputnode*)

Create the stage workflow when custom inputs are specified.

**Parameters**

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of the anatomical pipeline
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the parcellation stage

**define\_inspect\_outputs**()

Update the `inspect_outputs` class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**has\_run**()

Function that returns `True` if the stage has been run successfully.

**Returns**

**Return type** `True` if the stage has been run successfully

**cmp.stages.preprocessing package****Submodules****cmp.stages.preprocessing.fmri\_preprocessing module**

Definition of config and stage classes for pre-registration fMRI preprocessing.

**class** `cmp.stages.preprocessing.fmri_preprocessing.PreprocessingConfig`

Bases: `traits.has_traits.HasTraits`

Class used to store configuration parameters of a *PreprocessingStage* object.

**discard\_n\_volumes**

(Default: '5')

**Type** `traits.Int`

**despiking**

(Default: True)

**Type** `traits.Bool`

**slice\_timing**

Slice acquisition order for slice timing correction that can be: “bottom-top interleaved”, “bottom-top interleaved”, “top-bottom interleaved”, “bottom-top”, and “top-bottom” (Default: “none”)

**Type** `traits.Enum`

**repetition\_time**

Repetition time (Default: 1.92)

**Type** traits.Float**motion\_correction**

Perform motion correction (Default: True)

**Type** traits.Bool**See also:**[\*cmp.stages.preprocessing.fmri\\_preprocessing.PreprocessingStage\*](#)**class** [`cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingStage`](#)(*bids\_dir, output\_dir*)Bases: [\*cmp.stages.common.Stage\*](#)Class that represents the pre-registration preprocessing stage of a [\*fMRIPipeline\*](#) instance.**create\_workflow()**Create the workflow of the [\*PreprocessingStage\*](#)**See also:**[\*cmp.pipelines.functional.fMRI.fMRIPipeline\*](#),  
[\*fmri\\_preprocessing.PreprocessingConfig\*](#)[\*cmp.stages.preprocessing.\*](#)**create\_workflow**(*flow, inputnode, outputnode*)

Create the stage workflow.

**Parameters**

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of the fMRI pipeline
- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs()**Update the `inspect_outputs` class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**has\_run()**Function that returns `True` if the stage has been run successfully.**Returns****Return type** `True` if the stage has been run successfully**cmp.stages.preprocessing.preprocessing module**

Definition of config and stage classes for diffusion MRI preprocessing.

**class** [`cmp.stages.preprocessing.preprocessing.PreprocessingConfig`](#)Bases: `traits.has_traits.HasTraits`Class used to store configuration parameters of a [\*PreprocessingStage\*](#) instance.**total\_readout**

Acquisition total readout time used by FSL Eddy (Default: 0.0)

**Type** traits.Float

**description**

Description (Default: 'description')

**Type** traits.Str

**denoising**

Perform diffusion MRI denoising (Default: False)

**Type** traits.Bool

**denoising\_algo**

Type of denoising algorithm (Default: 'MRtrix (MP-PCA)')

**Type** traits.Enum(['MRtrix (MP-PCA)', 'Dipy (NLM)'])

**dipy\_noise\_model**

Type of noise model when Dipy denoising is performed that can be: 'Rician' or 'Gaussian' (Default: 'Rician')

**Type** traits.Enum

**bias\_field\_correction**

Perform diffusion MRI bias field correction (Default: False)

**Type** traits.Bool

**bias\_field\_algo**

Type of bias field correction algorithm that can be: 'ANTs N4' or 'FSL FAST' (Default: 'ANTs N4')

**Type** traits.Enum, ['ANTs N4', 'FSL FAST'])

**eddy\_current\_and\_motion\_correction**

Perform eddy current and motion correction (Default: True)

**Type** traits.Bool

**eddy\_correction\_algo**

Algorithm used for eddy current correction that can be: 'FSL eddy\_correct' or 'FSL eddy' (Default: 'FSL eddy\_correct')

**Type** traits.Enum

**eddy\_correct\_motion\_correction**

Perform eddy current and motion correction MIGHT BE OBSOLETE (Default: True)

**Type** traits.Bool

**partial\_volume\_estimation**

Estimate partial volume maps from brain tissues segmentation (Default: True)

**Type** traits.Bool

**fast\_use\_priors**

Use priors when FAST is used for partial volume estimation (Default: True)

**Type** traits.Bool

**resampling**

Tuple describing the target resolution (Default: (1, 1, 1))

**Type** traits.Tuple

**interpolation**

Type of interpolation used when resampling that can be: 'interpolate', 'weighted', 'nearest', 'sinc', or 'cubic' (Default: 'interpolate')

**Type** traits.Enum

**tracking\_tool**

Tool used for tractography

**Type** Enum(['Dipy', 'MRtrix'])

**act\_tracking**

True if Anatomically-Constrained or Particle Filtering Tractography is enabled (Default: False)

**Type** Bool

**gmwmi\_seeding**

True if tractography seeding is performed from the gray-matter / white-matter interface (Default: False)

**Type** Bool

**See also:**

[\*cmp.stages.preprocessing.preprocessing.PreprocessingStage\*](#)

**class** `cmp.stages.preprocessing.preprocessing.PreprocessingStage`(*bids\_dir*, *output\_dir*)

Bases: [\*cmp.stages.common.Stage\*](#)

Class that represents the pre-registration preprocessing stage of a [\*DiffusionPipeline\*](#) instance.

**create\_workflow()**

Create the workflow of the [\*PreprocessingStage\*](#)

**See also:**

[\*cmp.pipelines.diffusion.diffusion.DiffusionPipeline\*](#), [\*cmp.stages.preprocessing.preprocessing.PreprocessingConfig\*](#)

**create\_workflow**(*flow*, *inputnode*, *outputnode*)

Create the stage workflow.

**Parameters**

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of the Diffusion pipeline
- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs()**

Update the `inspect_outputs` class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**has\_run()**

Function that returns **True** if the stage has been run successfully.

**Returns**

**Return type** **True** if the stage has been run successfully

## cmp.stages.registration package

### Submodules

#### cmp.stages.registration.registration module

Definition of config and stage classes for MRI co-registration.

**class** cmp.stages.registration.registration.RegistrationConfig

Bases: traits.has\_traits.HasTraits

Class used to store configuration parameters of a *RegistrationStage* instance.

**pipeline**

Pipeline type (Default: “Diffusion”)

**Type** traits.Enum([“Diffusion”, “fMRI”])

**registration\_mode\_trait**

Choices of registration tools updated depending on the pipeline type. (Default: [‘FSL’, ‘ANTs’] if “Diffusion”, [‘FSL’, ‘BRegister (FS)’] if “fMRI”)

**Type** traits.List([‘FSL’, ‘ANTs’, ‘BRegister (FS)’])

**registration\_mode**

Registration tool used from the *registration\_mode\_trait* list (Default: ‘ANTs’)

**Type** traits.Str

**diffusion\_imaging\_model**

Diffusion imaging model (‘DTI’ for instance)

**Type** traits.Str

**use\_float\_precision**

Use ‘single’ instead of ‘double’ float representation to reduce memory usage of ANTs (Default: False)

**Type** traits.Bool

**ants\_interpolation**

Interpolation type used by ANTs that can be: ‘Linear’, ‘NearestNeighbor’, ‘CosineWindowedSinc’, ‘WelchWindowedSinc’, ‘HammingWindowedSinc’, ‘LanczosWindowedSinc’, ‘BSpline’, ‘MultiLabel’, or ‘Gaussian’ (Default: ‘Linear’)

**Type** traits.Enum

**ants\_bspline\_interpolation\_parameters**

ANTs BSpline interpolation parameters (Default: traits.Tuple(Int(3)))

**Type** traits.Tuple

**ants\_gauss\_interpolation\_parameters**

ANTs Gaussian interpolation parameters (Default: traits.Tuple(Float(5), Float(5)))

**Type** traits.Tuple

**ants\_multilab\_interpolation\_parameters**

ANTs Multi-label interpolation parameters (Default: traits.Tuple(Float(5), Float(5)))

**Type** traits.Tuple

**ants\_lower\_quantile**

ANTs lower quantile (Default: 0.005)

**Type** traits.Float

**ants\_upper\_quantile**

ANTs upper quantile (Default: 0.995)

**Type** traits.Float

**ants\_convergence\_thresh**

ANTs convergence threshold (Default: 1e-06)

**Type** traits.Float

**ants\_convergence\_winsize**

ANTs convergence window size (Default: 10)

**Type** traits.Int

**ants\_linear\_gradient\_step**

ANTS linear gradient step size (Default: 0.1)

**Type** traits.Float

**ants\_linear\_cost**

Metric used by ANTs linear registration phase that can be 'CC', 'MeanSquares', 'Demons', 'GC', 'MI', or 'Mattes' (Default: 'MI')

**Type** traits.Enum

**ants\_linear\_sampling\_strategy**

ANTS sampling strategy for the linear registration phase that can be 'None', 'Regular', or 'Random' (Default: 'Regular')

**Type** traits.Enum

**ants\_linear\_sampling\_perc**

Percentage used if random sampling strategy is employed in the linear registration phase (Default: 0.25)

**Type** traits.Float

**ants\_perform\_syn**

(Default: True)

**Type** traits.Bool

**ants\_nonlinear\_gradient\_step**

(Default: 0.1)

**Type** traits.Float

**ants\_nonlinear\_cost**

Metric used by ANTs nonlinear (SyN) registration phase that can be 'CC', 'MeanSquares', 'Demons', 'GC', 'MI', or 'Mattes' (Default: 'CC')

**Type** traits.Enum

**ants\_nonlinear\_update\_field\_variance**

Weight to update field variance in ANTs nonlinear (SyN) registration phase (Default: 3.0)

**Type** traits.Float

**ants\_nonlinear\_total\_field\_variance**

Weight to give to total field variance in ANTs nonlinear (SyN) registration phase (Default: 0.0)

**Type** traits.Float



**flirt\_args**

FLIRT extra arguments that will be append to the FSL FLIRT command (Default: None)

**Type** traits.Str

**uses\_qform**

FSL FLIRT uses qform (Default: True)

**Type** traits.Bool

**dof**

Specify number of degree-of-freedom to FSL FLIRT (Default: 6)

**Type** traits.Int

**fsl\_cost**

Metric used by FSL registration that can be ‘mutualinfo’, ‘corratio’, ‘normcorr’, ‘normmi’, ‘leastsq’, or ‘labeldiff’ (Default: ‘normmi’)

**Type** traits.Enum

**no\_search**

Enable FSL FLIRT “no search” option (Default: True)

**Type** traits.Bool

**init**

Initialization type of FSL registration: ‘spm’, ‘fsl’, or ‘header’ (Default: ‘spm’)

**Type** traits.Enum(‘header’, [‘spm’, ‘fsl’, ‘header’])

**contrast\_type**

Contrast type specified to BBRegister: ‘t1’, ‘t2’, or ‘dti’ (Default: ‘dti’)

**Type** traits.Enum(‘dti’, [‘t1’, ‘t2’, ‘dti’])

**apply\_to\_eroded\_wm**

Apply estimated transform to eroded white-matter mask (Default: True)

**Type** traits.Bool

**apply\_to\_eroded\_csf**

Apply estimated transform to eroded cortico spinal fluid mask (Default: True)

**Type** traits.Bool

**apply\_to\_eroded\_brain**

Apply estimated transform to eroded brain mask (Default: False)

**Type** traits.Bool

**tracking\_tool**

Tool used for tractography

**Type** Enum([‘Dipy’, ‘MRtrix’])

**act\_tracking**

True if Anatomically-Constrained or Particle Filtering Tractography is enabled (Default: False)

**Type** traits.Bool

**gmwmi\_seeding**

True if tractography seeding is performed from the gray-matter / white-matter interface (Default: False)

**Type** traits.Bool

See also:

[`cmp.stages.registration.registration.RegistrationStage`](#)

```
class cmp.stages.registration.registration.RegistrationStage(pipeline_mode,
                                                            fs_subjects_dir=None,
                                                            fs_subject_id=None, bids_dir="",
                                                            output_dir="")
```

Bases: [`cmp.stages.common.Stage`](#)

Class that represents the registration stage of both DiffusionPipeline and fMRIPipeline.

**fs\_subjects\_dir**

Freesurfer subjects directory (needed by BBRegister)

**Type** `traits.Directory`

**fs\_subject\_id**

Freesurfer subject (being processed) directory (needed by BBRegister)

**Type** `traits.Str`

**create\_workflow()**

Create the workflow of the [`RegistrationStage`](#)

See also:

[`cmp.pipelines.diffusion.diffusion.DiffusionPipeline`](#), [`cmp.pipelines.functional.fMRI.fMRIPipeline`](#), [`cmp.stages.registration.registration.RegistrationConfig`](#)

**create\_ants\_workflow(flow, inputnode, outputnode)**

Create the registration workflow using [`ANTs`](#).

**Parameters**

- **flow** (`nipype.pipeline.engine.Workflow`) – The `nipype.pipeline.engine.Workflow` instance of the Diffusion pipeline
- **inputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the inputs of the stage
- **outputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the outputs of the stage

**create\_bbregister\_workflow(flow, inputnode, outputnode)**

Create the workflow of the registration stage using [`FreeSurfer BBRegister`](#).

**Parameters**

- **flow** (`nipype.pipeline.engine.Workflow`) – The `nipype.pipeline.engine.Workflow` instance of the fMRI pipeline
- **inputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the inputs of the stage
- **outputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the outputs of the stage

**create\_flirt\_workflow(flow, inputnode, outputnode)**

Create the workflow of the registration stage using [`FSL FLIRT`](#).

**Parameters**

- **flow** (`nipype.pipeline.engine.Workflow`) – The `nipype.pipeline.engine.Workflow` instance of either the Diffusion pipeline or the fMRI pipeline

- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the stage

**create\_workflow**(*flow, inputnode, outputnode*)

Create the stage workflow.

#### Parameters

- **flow** (*nipype.pipeline.engine.Workflow*) – The *nipype.pipeline.engine.Workflow* instance of either the Diffusion pipeline or the fMRI pipeline
- **inputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the inputs of the stage
- **outputnode** (*nipype.interfaces.utility.IdentityInterface*) – Identity interface describing the outputs of the stage

**define\_inspect\_outputs**()

Update the `inspect_outputs` class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**has\_run**()

Function that returns `True` if the stage has been run successfully.

#### Returns

**Return type** `True` if the stage has been run successfully

## cmp.stages.segmentation package

### Submodules

#### cmp.stages.segmentation.segmentation module

Definition of config and stage classes for segmentation.

**class** `cmp.stages.segmentation.segmentation.SegmentationConfig`

Bases: `traits.has_traits.HasTraits`

Class used to store configuration parameters of a *SegmentationStage* object.

**seg\_tool**

Choice of segmentation tool that can be “Freesurfer”

**Type** `traits.Enum(["Freesurfer", "Custom segmentation"])`

**make\_isotropic**

Resample to isotropic resolution (Default: False)

**Type** `traits.Bool`

**isotropic\_vox\_size**

Isotropic resolution to be resampled (Default: 1.2, desc=)

**Type** `traits.Float`

**isotropic\_interpolation**

Interpolation type used for resampling that can be: ‘cubic’, ‘weighted’, ‘nearest’, ‘sinc’, or ‘interpolate’, (Default: ‘cubic’)

**Type** traits.Enum

**brain\_mask\_extraction\_tool**

Choice of brain extraction tool: “Freesurfer”, “BET”, or “ANTs” (Default: Freesurfer)

**Type** traits.Enum

**ants\_templatefile**

Anatomical template used by ANTS brain extraction

**Type** traits.File

**ants\_probmaskfile**

Brain probability mask used by ANTS brain extraction

**Type** traits.File

**ants\_regmaskfile**

Mask (defined in the template space) used during registration in ANTs brain extraction. To limit the metric computation to a specific region.

**Type** traits.File

**use\_fsl\_brain\_mask**

Use FSL BET for brain extraction (Default: False)

**Type** traits.Bool

**use\_existing\_freesurfer\_data**

(Default: False)

**Type** traits.Bool

**freesurfer\_subjects\_dir**

Freesurfer subjects directory path usually /output\_dir/freesurfer

**Type** traits.Str

**freesurfer\_subject\_id**

Freesurfer subject (being processed) ID in the form sub-XX(\_ses-YY)

**Type** traits.Str

**freesurfer\_args**

Extra Freesurfer recon-all arguments

**Type** traits.Str

**custom\_brainmask**

Instance of *CustomBrainMaskBIDSFile* that describes the custom BIDS formatted brain mask

**Type** traits.Instance(*CustomBrainMaskBIDSFile*)

**custom\_wm\_mask**

Instance of *CustomWMMaskBIDSFile* that describes the custom BIDS formatted white-matter mask

**Type** traits.Instance(*CustomWMMaskBIDSFile*)

**custom\_gm\_mask**

Instance of *CustomGMMaskBIDSFile* that describes the custom BIDS formatted gray-matter mask

**Type** traits.Instance(*CustomGMMaskBIDSFile*)

**custom\_csf\_mask**

Instance of *CustomCSFMaskBIDSFile* that describes the custom BIDS formatted CSF mask

**Type** `traits.Instance(CustomCSFMaskBIDSFile)`

**custom\_aparcaseg**

Instance of *CustomAparcAsegBIDSFile* that describes the custom BIDS formatted Freesurfer aparc-aseg file

**Type** `traits.Instance(CustomAparcAsegBIDSFile)`

**number\_of\_threads**

Number of threads leveraged by OpenMP and used in the stage by Freesurfer and ANTs (Default: 1)

**Type** `traits.Int`

**See also:**

`cmp.stages.segmentation.segmentation.SegmentationStage`, `cmtklib.bids.io.CustomBrainMaskBIDSFile`, `cmtklib.bids.io.CustomWMMaskBIDSFile`, `cmtklib.bids.io.CustomGMMaskBIDSFile`, `cmtklib.bids.io.CustomCSFMaskBIDSFile`

**class** `cmp.stages.segmentation.segmentation.SegmentationStage`(*subject, session, bids\_dir, output\_dir*)

Bases: `cmp.stages.common.Stage`

Class that represents the segmentation stage of a *AnatomicalPipeline*.

**create\_workflow()**

Create the workflow of the *SegmentationStage*

**See also:**

`cmp.pipelines.anatomical.anatomical.AnatomicalPipeline`, `cmp.stages.segmentation.segmentation.SegmentationConfig`

**create\_workflow**(*flow, inputnode, outputnode*)

Create the stage workflow.

**Parameters**

- **flow** (`nipype.pipeline.engine.Workflow`) – The `nipype.pipeline.engine.Workflow` instance of the anatomical pipeline
- **inputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the inputs of the segmentation stage
- **outputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the outputs of the segmentation stage

**create\_workflow\_custom**(*flow, inputnode, outputnode*)

Create the stage workflow when custom inputs are specified.

**Parameters**

- **flow** (`nipype.pipeline.engine.Workflow`) – The `nipype.pipeline.engine.Workflow` instance of the anatomical pipeline
- **inputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the inputs of the segmentation stage
- **outputnode** (`nipype.interfaces.utility.IdentityInterface`) – Identity interface describing the outputs of the segmentation stage

**define\_inspect\_outputs**(*debug=False*)

Update the `inspect_outputs` class attribute.

It contains a dictionary of stage outputs with corresponding commands for visual inspection.

**Parameters** `debug` (*bool*) – If `True`, show printed output

**has\_run**()

Function that returns `True` if the stage has been run successfully.

**Returns**

**Return type** `True` if the stage has been run successfully

## Submodules

### `cmp.stages.common` module

Definition of common parent classes for stages.

**class** `cmp.stages.common.Stage`

Bases: `traits.has_traits.HasTraits`

Parent class that extends `HasTraits` and represents a processing pipeline stage.

It is extended by the various pipeline stage subclasses.

**bids\_subject\_label**

BIDS subject (participant) label

**Type** `traits.Str`

**bids\_session\_label**

BIDS session label

**Type** `traits.Str`

**bids\_dir**

BIDS dataset root directory

**Type** `traits.Str`

**output\_dir**

Output directory

**Type** `traits.Str`

**inspect\_outputs**

Dictionary of stage outputs with corresponding commands for visual inspection (Initialization: 'Outputs not available')

**Type** `traits.Dict`

**inspect\_outputs\_enum**

Choice of output to be visually inspected (values='inspect\_outputs')

**Type** `traits.Enum`

**enabled**

Stage enabled in the pipeline (Default: `True`)

**Type** `traits.Bool`

**config**

Instance of stage configuration

**Type** Instance(HasTraits)**See also:**

*cmp.stages.preprocessing.preprocessing.PreprocessingStage*, *cmp.stages.diffusion.diffusion.DiffusionStage*, *cmp.stages.registration.registration.RegistrationStage*, *cmp.stages.connectome.connectome.ConnectomeStage*, *cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingStage*, *cmp.stages.functional.functionalMRI.FunctionalMRIStage*, *cmp.stages.connectome.fmri\_connectome.ConnectomeStage*

**enabled** = True**inspect\_outputs** = ['Outputs not available']**is\_running()**

Return the number of unfinished files in the stage.

**Returns** **nb\_of\_unfinished\_files** – Number of unfinished files in the stage**Return type** int**GUI modules****cmp.bidsappmanager.gui package**

Module that provides the definition of all classes, functions, and variables dedicated to the GUI of Connectome Mapper 3.

**Submodules****cmp.bidsappmanager.gui.bidsapp module**

Connectome Mapper BIDS App Interface Window.

```
class cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow(project_info=None, bids_root="",
                                                             subjects=None, anat_config="",
                                                             dmri_config="", fmri_config="")
```

**Bases:** traits.has\_traits.HasTraits

Class that defines the Window of the BIDS App Interface.

**project\_info**

Instance of CMP\_Project\_Info that represents the processing project

**Type** *ProjectInfo***bids\_root**

BIDS root dataset directory

**Type** traits.Directory**output\_dir**

Output directory

**Type** traits.Directory

**subjects**

List of subjects (in the form sub-XX) present in the dataset

**Type** traits.List

**number\_of\_participants\_processed\_in\_parallel**

Number of participants / subjects to be processed in parallel that takes values in the [1, # of CPUs - 1] range

**Type** traits.Range

**number\_threads\_max**

Maximal number of threads to be used by OpenMP programs (4 by default)

**Type** traits.Int

**number\_of\_threads**

Number of threads to be used by OpenMP programs that takes values in the [1, number\_threads\_max] range

**Type** traits.Range

**fs\_file**

Path to Freesurfer license file

**Type** traits.File

**list\_of\_subjects\_to\_be\_processed**

Selection of subjects to be processed from the subjects list

**Type** List(Str)

**dmri\_inputs\_checked**

True if dMRI data is available in the dataset

**Type** traits.Bool

**fmri\_inputs\_checked**

rue if fMRI data is available in the dataset

**Type** traits.Bool

**anat\_config**

Configuration file for the anatomical MRI pipeline

**Type** traits.File

**dmri\_config**

Configuration file for the diffusion MRI pipeline

**Type** traits.File

**fmri\_config**

Configuration file for the functional MRI pipeline

**Type** traits.File

**run\_anat\_pipeline**

If True, run the anatomical pipeline

**Type** traits.Bool

**run\_dmri\_pipeline**

If True, run the diffusion pipeline

**Type** traits.Bool



**run\_fmri\_pipeline**

If True, run the functional pipeline

**Type** traits.Bool

**bidsapp\_tag**

Selection of BIDS App version to use

**Type** traits.Enum

**data\_provenance\_tracking**

If set and if datalad\_is\_available is True run the BIDS App using datalad (False by default)

**Type** traits.Bool

**datalad\_update\_environment**

If True and data\_provenance\_tracking is True, tell to datalad to update the BIDS App container image if there was a previous execution (True by default)

**Type** traits.Bool

**datalad\_is\_available**

Boolean used to store if datalad is available in the computing environment (False by default)

**Type** traits.Bool

**track\_carbon\_footprint**

Track carbon footprint if **True** (True by default)

**Type** traits.Bool

**carbon\_emission\_msg**

Carbon footprint reporting message

**Type** traits.Str

**check**

Button to check if all parameters are properly set for execution of the BIDS App

**Type** traits.ui.Button

**start\_bidsapp**

Button to run the BIDS App

**Type** traits.ui.Button

**traits\_view**

TraitsUI QtView that describes the content of the window

**Type** QtView

**check\_settings()**

Checks if all the parameters of the BIDS App run are properly set before execution.

**classmethod manage\_bidsapp\_procs(proclist)**

Manage parallelized process at the participant level

**Parameters proclist** (*List of subprocess.Popen*) – List of Popen processes

**number\_of\_parallel\_procs\_updated(new)**

Callback function when number\_of\_parallel\_procs is updated.

**classmethod run(command, env=None, cwd='/home/docs/checkouts/readthedocs.org/user\_builds/connectome-mapper-3/checkouts/v3.0.3/docs')**

Function to run datalad commands.

It runs the command specified as input via `subprocess.run()`.

#### Parameters

- **command** (*string*) – String containing the command to be executed (required)
- **env** (*os.environ*) – Specify a custom `os.environ`
- **cwd** (*os.path*) – Specify a custom current working directory

#### Examples

```
>>> cmd = 'datalad save -m my dataset change message'
>>> run(cmd)
```

#### **start\_bids\_app()**

Function executed when the Run BIDS App button is clicked.

It implements all steps in the creation and execution of the BIDS App with or without datalad.

#### **start\_bidsapp\_participant\_level\_process**(*bidsapp\_tag, participant\_labels*)

Create and run the BIDS App command.

#### Parameters

- **bidsapp\_tag** (*traits.Str*) – Version tag of the CMP 3 BIDS App
- **participant\_labels** (*traits.List*) – List of participants labels in the form ["01", "03", "04", ...]

#### **start\_bidsapp\_participant\_level\_process\_with\_datalad**(*bidsapp\_tag, participant\_labels*)

Create and run the BIDS App command with Datalad.

#### Parameters

- **bidsapp\_tag** (*traits.Str*) – Version tag of the CMP 3 BIDS App
- **participant\_labels** (*traits.List*) – List of participants labels in the form ["01", "03", "04", ...]

#### **update\_checksettings**(*new*)

Function that reset `settings_checked` attribute to False.

#### **update\_run\_anat\_pipeline**(*new*)

Callback function when `run_anat_pipeline` is updated.

#### **update\_run\_dmri\_pipeline**(*new*)

Callback function when `run_dmri_pipeline` is updated.

#### **update\_run\_fmri\_pipeline**(*new*)

Callback function when `run_fmri_pipeline` is updated.

**cmp.bidsappmanager.gui.config module**

Connectome Mapper Pipeline Configurator Window.

```
class cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow(project_info=None,
                                                                anat_pipeline=None,
                                                                dmri_pipeline=None,
                                                                fmri_pipeline=None,
                                                                anat_inputs_checked=False,
                                                                dmri_inputs_checked=False,
                                                                fmri_inputs_checked=False)
```

Bases: `traits.has_traits.HasTraits`

Class that defines the Pipeline Configurator Window.

**project\_info**

Instance of `CMP_Project_Info` that represents the processing project

**Type** `cmp.project.ProjectInfo`

**anat\_pipeline**

Instance of anatomical MRI pipeline UI

**Type** `Instance(HasTraits)`

**dmri\_pipeline**

Instance of diffusion MRI pipeline UI

**Type** `Instance(HasTraits)`

**fmri\_pipeline**

Instance of functional MRI pipeline UI

**Type** `Instance(HasTraits)`

**anat\_inputs\_checked**

Boolean that indicates if anatomical pipeline inputs are available (Default: `False`)

**dmri\_inputs\_checked** = `[traits.Bool]` Boolean that indicates if diffusion pipeline inputs are available (Default: `False`)

**fmri\_inputs\_checked** `[traits.Bool]` Boolean that indicates if functional pipeline inputs are available (Default: `False`)

**Type** `traits.Bool`

**anat\_save\_config**

TraitsUI Action to save the anatomical pipeline configuration

**Type** `traits.ui.Action`

**dmri\_save\_config**

TraitsUI Action to save the diffusion pipeline configuration

**Type** `traits.ui.Action`

**fmri\_save\_config**

TraitsUI Action to save the functional pipeline configuration

**Type** `traits.ui.Action`

**save\_all\_config**

Button to save all configuration files at once

**Type** traits.ui.Button

**traits\_view**

TraitsUI QtView that describes the content of the window

**Type** QtView

**anat\_save\_config**

An action on a menu bar in a Traits UI window or panel.

**dmri\_save\_config**

An action on a menu bar in a Traits UI window or panel.

**fmri\_save\_config**

An action on a menu bar in a Traits UI window or panel.

**update\_diffusion\_imaging\_model**(*new*)**cmp.bidsappmanager.gui.globals module**

Modules that defines multiple variables and functions used by the different windows of the GUI.

**cmp.bidsappmanager.gui.globals.get\_icon**(*icon\_fname*)

Return an instance of ImageResource or None is there is not graphical backend.

**Parameters** *icon\_fname* (*string*) – Filename to an icon image

**Returns** *icon* – Return the full path to the icon file or None is there is not graphical backend.

**Return type** string

**cmp.bidsappmanager.gui.handlers module****class cmp.bidsappmanager.gui.handlers.BIDSAppInterfaceWindowHandler**

Bases: traitsui.handler.Handler

Event handler of the BIDS App Interface window.

**docker\_process**

Instance of subprocess.Popen where BIDS App docker image is run

**Type** subprocess.Popen

**check\_settings**(*ui\_info*)

Function that checks if all parameters are properly set before execution of the BIDS App.

**Parameters** *ui\_info* (*QtView*) – TraitsUI QtView associated with self

**classmethod manage\_bidsapp\_procs**(*proclist*)

Function that managed the parallelized BIDS App Popen process.

**Parameters** *proclist* – List of Popen processes running the BIDS App on a single subject

**start\_bids\_app**(*ui\_info*)

Main function that runs the BIDS App on a set or sub-set of participants.

**Parameters** *ui\_info* (*QtView*) – TraitsUI QtView associated with this handler

**classmethod** `start_bidsapp_process(participant_label)`

Function that runs the BIDS App on a single subject.

**Parameters**

- **ui\_info** (*QtView*) – TraitsUI QtView associated with this handler
- **participant\_label** (*string*) – Label of the participant / subject (e.g. "01", no "sub-" prefix)

**classmethod** `stop_bids_app()`

Function that stops the BIDS execution.

**Parameters** **ui\_info** (*QtView*) – TraitsUI QtView associated with this handler

**class** `cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler`

Bases: `traitsui.handler.Handler`

Event handler of the Configurator and Inspector (Quality Control) windows.

**project\_loaded**

Indicate if project has been successfully loaded (Default: False)

**Type** `traits.Bool`

**anat\_pipeline**

Instance of `AnatomicalPipelineUI` class

**Type** `Instance(HasTraits)`

**anat\_inputs\_checked**

Indicate if anatomical pipeline inputs are available (Default: False)

**Type** `traits.Bool`

**anat\_outputs\_checked**

Indicate if anatomical pipeline outputs are available (Default: False)

**Type** `traits.Bool`

**anatomical\_processed**

Indicate if anatomical pipeline was run (Default: False)

**Type** `traits.Bool`

**dmri\_pipeline**

Instance of `DiffusionPipelineUI` class

**Type** `Instance(HasTraits)`

**dmri\_inputs\_checked**

Indicate if diffusion pipeline inputs are available (Default: False)

**Type** `traits.Bool`

**dmri\_processed**

Indicate if diffusion pipeline was run (Default: False)

**Type** `traits.Bool`

**fmri\_pipeline**

Instance of `fMRIPipelineUI` class

**Type** `Instance(HasTraits)`

**fmri\_inputs\_checked**

Indicate if fMRI pipeline inputs are available (Default: False)

**Type** traits.Bool

**fmri\_processed**

Indicate if fMRI pipeline was run (Default: False)

**Type** traits.Bool

**load\_anat\_config\_file(ui\_info)**

Function that loads the anatomical pipeline configuration file.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**load\_dmri\_config\_file(ui\_info)**

Function that loads the diffusion pipeline configuration file.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**load\_fmri\_config\_file(ui\_info)**

Function that loads the fMRI pipeline configuration file.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**load\_project(ui\_info)**

Function that creates a new *ProjectInfoUI* instance from an existing project.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**new\_project(ui\_info)**

Function that creates a new *ProjectInfoUI* instance.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**classmethod save\_anat\_config\_file(ui\_info)**

Function that saves the anatomical pipeline configuration file.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**classmethod save\_dmri\_config\_file(ui\_info)**

Function that saves the diffusion pipeline configuration file.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**classmethod save\_fmri\_config\_file(ui\_info)**

Function that saves the fMRI pipeline configuration file.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**classmethod show\_bidsapp\_window()**

Function that shows the BIDS App Interface Window.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with this handler

**update\_subject\_anat\_pipeline(ui\_info)**

Function that updates attributes of the *AnatomicalPipelineUI* instance.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**update\_subject\_dmri\_pipeline(ui\_info)**

Function that updates attributes of the *DiffusionPipelineUI* instance.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

**update\_subject\_fmri\_pipeline(ui\_info)**

Function that updates attributes of the *fMRIPipelineUI* instance.

**Parameters** **ui\_info** (*QtView*) – TraitsUI *QtView* associated with *self*

---

```

class cmp.bidsappmanager.gui.handlers.MainWindowHandler
    Bases: traitsui.handler.Handler

    Event handler of the Configurator and Inspector (Quality Control) windows.

    project_loaded
        Indicate if project has been successfully loaded (Default: False)

        Type traits.Bool

    anat_pipeline
        Instance of AnatomicalPipelineUI class

        Type Instance(HasTraits)

    anat_inputs_checked
        Indicate if anatomical pipeline inputs are available (Default: False)

        Type traits.Bool

    anat_outputs_checked
        Indicate if anatomical pipeline outputs are available (Default: False)

        Type traits.Bool

    anatomical_processed
        Indicate if anatomical pipeline was run (Default: False)

        Type traits.Bool

    dmri_pipeline
        Instance of DiffusionPipelineUI class

        Type Instance(HasTraits)

    dmri_inputs_checked
        Indicate if diffusion pipeline inputs are available (Default: False)

        Type traits.Bool

    dmri_processed
        Indicate if diffusion pipeline was run (Default: False)

        Type traits.Bool

    fmri_pipeline
        Instance of fMRIPipelineUI class

        Type Instance(HasTraits)

    fmri_inputs_checked
        Indicate if fMRI pipeline inputs are available (Default: False)

        Type traits.Bool

    fmri_processed
        Indicate if fMRI pipeline was run (Default: False)

        Type traits.Bool

    load_dataset(ui_info, debug=False)
        Function that creates a new ProjectInfoUI instance from an existing project.

        Parameters
            • ui_info (QtView) – TraitsUI QtView associated with self

```

- **debug** (*bool*) – If True, print more information for debugging

### **cmp.bidsappmanager.gui.principal module**

Connectome Mapper Main Window.

**class** `cmp.bidsappmanager.gui.principal.MainWindow`

Bases: `traits.has_traits.HasTraits`

Class that defines the Main window of the Connectome Mapper 3 GUI.

**project\_info**

Instance of `CMP_Project_InfoUI` that represents the processing project

**Type** `cmp.bidsappmanager.project.ProjectInfoUI`

**anat\_pipeline**

Instance of anatomical MRI pipeline UI

**Type** `Instance(HasTraits)`

**dmri\_pipeline**

Instance of diffusion MRI pipeline UI

**Type** `Instance(HasTraits)`

**fmri\_pipeline**

Instance of functional MRI pipeline UI

**Type** `Instance(HasTraits)`

**configurator\_ui**

Instance of `PipelineConfiguratorWindow`

**Type** `PipelineConfiguratorWindow`

**bidsapp\_ui**

Instance of `BIDSAppInterfaceWindow`

**Type** `BIDSAppInterfaceWindow`

**quality\_control\_ui**

Instance of `QualityInspectorWindow`

**Type** `QualityInspectorWindow`

**load\_dataset**

`TraitsUI` Action to load a BIDS dataset

**Type** `traits.ui.Action`

**bidsapp**

Button that displays the BIDS App Interface window

**Type** `traits.ui.Button`

**configurator**

Button that displays the pipeline Configurator window

**Type** `traits.ui.Button`

**quality\_control**

Button that displays the pipeline Quality Control / Inspector window

**Type** `traits.ui.Button`



**manager\_group**

TraitsUI View that describes the content of the main window

**Type** traits.ui.View

**traits\_view**

TraitsUI QtView that includes `manager_group` and parameterize the window with menu

**Type** QtView

**load\_dataset**

An action on a menu bar in a Traits UI window or panel.

**view\_mode** = 1

**cmp.bidsappmanager.gui.qc module**

Connectome Mapper Output Quality Inspector Window.

```
class cmp.bidsappmanager.gui.qc.QualityInspectorWindow(project_info=None,
                                                         anat_inputs_checked=False,
                                                         dmri_inputs_checked=False,
                                                         fmri_inputs_checked=False)
```

Bases: traits.has\_traits.HasTraits

Class that defines the Quality Inspector Window.

**project\_info**

Instance of `CMP_Project_Info` that represents the processing project

**Type** *cmp.project.ProjectInfo*

**anat\_pipeline**

Instance of anatomical MRI pipeline

**Type** Instance(HasTraits)

**dmri\_pipeline**

Instance of diffusion MRI pipeline

**Type** Instance(HasTraits)

**fmri\_pipeline**

Instance of functional MRI pipeline

**Type** Instance(HasTraits)

**anat\_inputs\_checked**

Indicates if inputs of anatomical pipeline are available (Default: False)

**Type** traits.Bool

**dmri\_inputs\_checked**

Indicates if inputs of diffusion pipeline are available (Default: False)

**Type** traits.Bool

**fmri\_inputs\_checked**

Indicates if inputs of functional pipeline are available (Default: False)

**Type** traits.Bool

**output\_anat\_available**

Indicates if outputs of anatomical pipeline are available (Default: False)

**Type** traits.Bool

**output\_dmri\_available**

Indicates if outputs of diffusion pipeline are available (Default: False)

**Type** traits.Bool

**output\_fmri\_available**

Indicates if outputs of functional pipeline are available (Default: False)

**Type** traits.Bool

**traits\_view**

TraitsUI QtView that describes the content of the window

**Type** QtView

**select\_subject()**

Function to select the subject and session for which to inspect outputs.

**update\_diffusion\_imaging\_model(*new*)**

Function called when diffusion\_imaging\_model is updated.

### **cmp.bidsappmanager.gui.traits module**

Module that defines traits-based classes for Connectome Mapper 3 BIDS App Interface TraitsUI View.

**class** cmp.bidsappmanager.gui.traits.**MultiSelectAdapter**

Bases: traitsui.tabular\_adapter.TabularAdapter

This adapter is used by left and right tables for selection of subject to be processed.

### **cmp.bidsappmanager.project module**

Connectome Mapper Controller for handling GUI and non GUI general events.

**class** cmp.bidsappmanager.project.**ProjectInfoUI**

Bases: [cmp.project.ProjectInfo](#)

Class that extends the ProjectInfo with graphical components.

It supports graphically the setting of all processing properties / attributes of an ProjectInfo instance.

**creation\_mode**

Mode for loading the dataset. Valid values are 'Load BIDS dataset', 'Install Datalad BIDS dataset'

**Type** traits.Enum

**install\_datalad\_dataset\_via\_ssh**

If set to True install the datalad dataset from a remote server via ssh.(True by default)

**Type** traits.Bool

**ssh\_user**

Remote server username. (Required if install\_datalad\_dataset\_via\_ssh is True)

**Type** traits.Str

**ssh\_pwd <traits.Password>**

Remote server password. (Required if install\_datalad\_dataset\_via\_ssh is True)

**ssh\_remote**

Remote server IP or URL. (Required if `install_datalad_dataset_via_ssh` is True)

**Type** `traits.Str`

**datalad\_dataset\_path**

Path to the datalad dataset on the remote server. (Required if `install_datalad_dataset_via_ssh` is True)

**Type** `traits.Directory`

**summary\_view\_button**

Button that shows the pipeline processing summary table

**Type** `traits.ui.Button`

**pipeline\_processing\_summary\_view**

TraitsUI VGroup that contains `Item('pipeline_processing_summary')`

**Type** `traits.ui.VGroup`

**dataset\_view**

TraitsUI View that shows a summary of project settings and modality available for a given subject

**Type** `traits.ui.View`

**traits\_view**

TraitsUI QtView that includes the View 'dataset\_view'

**Type** `QtView`

**create\_view**

Dialog view to create a BIDS Dataset

**Type** `traits.ui.View`

**subject\_view**

Dialog view to select of subject

**Type** `traits.ui.View`

**subject\_session\_view**

Dialog view to select the subject session

**Type** `traits.ui.View`

**dmri\_bids\_acq\_view**

Dialog view to select the diffusion acquisition model

**Type** `traits.ui.View`

**anat\_warning\_view**

View that displays a warning message regarding the anatomical T1w data

**Type** `traits.ui.View`

**anat\_config\_error\_view**

Error view that displays an error message regarding the configuration of the anatomical pipeline

**Type** `traits.ui.View`

**dmri\_warning\_view**

View that displays a warning message regarding the diffusion MRI data

**Type** `traits.ui.View`

**dmri\_config\_error\_view**

View that displays an error message regarding the configuration of the diffusion pipeline

**Type** traits.ui.View

**fmri\_warning\_view**

View that displays a warning message regarding the functional MRI data

**Type** traits.ui.View

**fmri\_config\_error\_view**

View that displays an error message regarding the configuration of the fMRI pipeline

**Type** traits.ui.View

**open\_view**

Dialog view to load a BIDS Dataset

**Type** traits.ui.View

**anat\_select\_config\_to\_load**

Dialog view to load the configuration file of the anatomical pipeline

**Type** traits.ui.View

**diffusion\_imaging\_model\_select\_view**

Dialog view to select the diffusion acquisition model

**Type** traits.ui.View

**dmri\_select\_config\_to\_load**

Dialog view to load the configuration file of the diffusion MRI pipeline

**Type** traits.ui.View

**fmri\_select\_config\_to\_load**

Dialog view to load the configuration file of the fMRI pipeline

**Type** traits.ui.View

`cmp.bidsappmanager.project.clean_cache(bids_root)`

Clean cache stored in /tmp.

Target issue related to that a dataset directory is mounted into /tmp and used for caching by java/matlab/matplotlib/xvfb-run in the container image.

**Parameters** `bids_root` (*string*) – BIDS root dataset directory

`cmp.bidsappmanager.project.init_anat_project(project_info, is_new_project)`

Create and initialize a AnatomicalPipelineUI instance

**Parameters**

- **project\_info** (*ProjectInfoUI*) – Instance of *ProjectInfoUI* class
- **is\_new\_project** (*bool*) – If True, this is a new project which has been never processed

`cmp.bidsappmanager.project.init_dmri_project(project_info, bids_layout, is_new_project, gui=True)`

Create and initialize a DiffusionPipelineUI instance

**Parameters**

- **project\_info** (*ProjectInfoUI*) – Instance of *ProjectInfoUI* class
- **bids\_layout** (*bids.BIDSLayout*) – PyBIDS BIDS Layout object describing the BIDS dataset

- **is\_new\_project** (*bool*) – If True, this is a new project which has been never processed
- **gui** (*bool*) – If True, display messages in GUI

`cmp.bidsappmanager.project.init_fmri_project(project_info, bids_layout, is_new_project, gui=True)`  
Create and initialize a fMRIPipelineUI instance

#### Parameters

- **project\_info** (*ProjectInfoUI*) – Instance of *ProjectInfoUI* class
- **bids\_layout** (*bids.BIDSLayout*) – PyBIDS BIDS Layout object describing the BIDS dataset
- **is\_new\_project** (*bool*) – If True, this is a new project which has been never processed
- **gui** (*bool*) – If True, display messgae in GUI

`cmp.bidsappmanager.project.is_tool(name)`  
Check whether name is on PATH.

`cmp.bidsappmanager.project.refresh_folder(derivatives_directory, subject, input_folders, session=None)`  
Creates (if needed) the folder hierarchy.

#### Parameters

- **derivatives\_directory** (*string*) –
- **subject** (*string*) – Subject label (sub-XX) for which we create the output folder hierarchy
- **session** (*string*) – Subject session label (ses-YY)
- **input\_folders** (*list of string*) – List of folders to create in `derivative_directory/sub-XX/(ses-YY)/` folder for the given subject

`cmp.bidsappmanager.project.update_anat_last_processed(project_info, pipeline)`  
Update anatomical pipeline processing information

#### Parameters

- **project\_info** (*ProjectInfoUI*) – Instance of *ProjectInfoUI* class
- **pipeline** (*AnatomicalPipelineUI*) – Instance of *AnatomicalPipelineUI*

`cmp.bidsappmanager.project.update_dmri_last_processed(project_info, pipeline)`  
Update diffusion pipeline processing information

#### Parameters

- **project\_info** (*ProjectInfoUI*) – Instance of *ProjectInfoUI* class
- **pipeline** (*DiffusionPipelineUI*) – Instance of *DiffusionPipelineUI*

`cmp.bidsappmanager.project.update_fmri_last_processed(project_info, pipeline)`  
Update functional MRI pipeline processing information

#### Parameters

- **project\_info** (*ProjectInfoUI*) – Instance of *ProjectInfoUI* class
- **pipeline** (*fMRIPipelineUI*) – Instance of *fMRIPipelineUI*

## cmp.bidsappmanager.pipelines.anatomical package

### Submodules

#### cmp.bidsappmanager.pipelines.anatomical.anatomical module

Anatomical pipeline UI Class definition.

**class** `cmp.bidsappmanager.pipelines.anatomical.anatomical.AnatomicalPipelineUI(project_info)`  
Bases: `cmp.pipelines.anatomical.anatomical.AnatomicalPipeline`

Class that extends the `AnatomicalPipeline` with graphical components.

##### **segmentation**

Button to open the window for configuration or quality inspection of the segmentation stage depending on the `view_mode`

**Type** `traits.ui.Button`

##### **parcellation**

Button to open the window for configuration or quality inspection of the segmentation stage depending on the `view_mode`

**Type** `traits.ui.Button`

##### **view\_mode**

Variable used to control the display of either (1) the configuration or (2) the quality inspection of stage of the pipeline

**Type** `['config_view', 'inspect_outputs_view']`

##### **pipeline\_group**

Panel defining the layout of the buttons of the stages with corresponding images

**Type** `traitsUI panel`

##### **traits\_view**

QtView that includes the `pipeline_group` panel

**Type** `QtView`

##### **See also:**

`cmp.pipelines.anatomical.anatomical.AnatomicalPipeline`

##### **check\_input(*layout*)**

Method that checks if inputs of the anatomical pipeline are available in the datasets.

**Parameters** `layout` (`bids.BIDSLayout`) – `BIDSLayout` object used to query

**Returns** `valid_inputs` – True in all inputs of the anatomical pipeline are available

**Return type** `bool`

##### **check\_output()**

Method that checks if outputs of the anatomical pipeline are available.

##### **Returns**

- **valid\_output** (`bool`) – True is all outputs are found
- **error\_message** (`string`) – Message in case there is an error

## cmp.bidsappmanager.pipelines.diffusion package

### Submodules

## cmp.bidsappmanager.pipelines.diffusion.diffusion module

Diffusion pipeline UI Class definition.

**class** `cmp.bidsappmanager.pipelines.diffusion.diffusion.DiffusionPipelineUI(project_info)`

Bases: `cmp.pipelines.diffusion.diffusion.DiffusionPipeline`

Class that extends the `DiffusionPipeline` with graphical components.

#### **preprocessing**

Button to open the window for configuration or quality inspection of the preprocessing stage depending on the `view_mode`

**Type** `traits.ui.Button`

#### **registration**

Button to open the window for configuration or quality inspection of the registration stage depending on the `view_mode`

**Type** `traits.ui.Button`

#### **diffusion**

Button to open the window for configuration or quality inspection of the diffusion reconstruction and tractography stage depending on the `view_mode`

**Type** `traits.ui.Button`

#### **connectome**

Button to open the window for configuration or quality inspection of the connectome stage depending on the `view_mode`

**Type** `traits.ui.Button`

#### **view\_mode**

Variable used to control the display of either (1) the configuration or (2) the quality inspection of stage of the pipeline

**Type** `['config_view', 'inspect_outputs_view']`

#### **pipeline\_group**

Panel defining the layout of the buttons of the stages with corresponding images

**Type** `traitsUI panel`

#### **traits\_view**

QtView that includes the `pipeline_group` panel

**Type** `QtView`

See also:

`cmp.pipelines.diffusion.diffusion.DiffusionPipeline`

**check\_input(*layout*, *gui=True*)**

Method that checks if inputs of the diffusion pipeline are available in the datasets.

#### **Parameters**

- **layout** (`bids.BIDSLayout`) – `BIDSLayout` object used to query

- **gui** (*bool*) – If True, display message in GUI

**Returns** **valid\_inputs** – True in all inputs of the anatomical pipeline are available

**Return type** *bool*

## **cmp.bidsappmanager.pipelines.functional package**

### **Submodules**

#### **cmp.bidsappmanager.pipelines.functional.eeg module**

EEG pipeline Class definition

#### **cmp.bidsappmanager.pipelines.functional.fMRI module**

Functional pipeline UI Class definition.

**class** `cmp.bidsappmanager.pipelines.functional.fMRI.fMRIPipelineUI(project_info)`

Bases: `cmp.pipelines.functional.fMRI.fMRIPipeline`

Class that extends the `fMRIPipeline` with graphical components.

##### **preprocessing**

Button to open the window for configuration or quality inspection of the preprocessing stage depending on the `view_mode`

**Type** `traits.ui.Button`

##### **registration**

Button to open the window for configuration or quality inspection of the registration stage depending on the `view_mode`

**Type** `traits.ui.Button`

##### **functionalMRI**

Button to open the window for configuration or quality inspection of the extra preprocessing stage stage depending on the `view_mode`

**Type** `traits.ui.Button`

##### **connectome**

Button to open the window for configuration or quality inspection of the connectome stage depending on the `view_mode`

**Type** `traits.ui.Button`

##### **view\_mode**

Variable used to control the display of either (1) the configuration or (2) the quality inspection of stage of the pipeline

**Type** `['config_view', 'inspect_outputs_view']`

##### **pipeline\_group**

Panel defining the layout of the buttons of the stages with corresponding images

**Type** `traitsUI panel`

##### **traits\_view**

QtView that includes the `pipeline_group` panel



**Type** QtView

**See also:**

[\*cmp.pipelines.functional.fMRI.fMRIPipeline\*](#)

**check\_input**(*layout*, *gui=True*)

Method that checks if inputs of the fMRI pipeline are available in the datasets.

**Parameters**

- **layout** (*bids.BIDSLayout*) – BIDSLayout object used to query
- **gui** (*bool*) – If True, display message in GUI

**Returns** **valid\_inputs** – True in all inputs of the fMRI pipeline are available

**Return type** *bool*

## cmp.bidsappmanager.stages package

### Subpackages

#### cmp.bidsappmanager.stages.connectome package

### Submodules

#### cmp.bidsappmanager.stages.connectome.connectome module

Definition of structural connectome config and stage UI classes.

**class** `cmp.bidsappmanager.stages.connectome.connectome.ConnectomeConfigUI`

Bases: [\*cmp.stages.connectome.connectome.ConnectomeConfig\*](#)

Class that extends the ConnectomeConfig with graphical components.

**output\_types**

A list of output\_types. Valid output\_types are 'gPickle', 'mat', 'cff', 'graphml'

**Type** list of string

**connectivity\_metrics**

A list of connectivity metrics to stored. Valid connectivity\_metrics are 'Fiber number', 'Fiber length', 'Fiber density', 'Fiber proportion', 'Normalized fiber density', 'ADC', 'gFA'

**Type** list of string

**traits\_view**

TraitsUI view that displays the Attributes of this class

**Type** traits.ui.View

**See also:**

[\*cmp.stages.connectome.connectome.ConnectomeConfig\*](#)

**class** `cmp.bidsappmanager.stages.connectome.connectome.ConnectomeStageUI`(*bids\_dir*, *output\_dir*)

Bases: [\*cmp.stages.connectome.connectome.ConnectomeStage\*](#)

Class that extends the ConnectomeStage with graphical components.

**log\_visualization**

If True, display with a log transformation

**Type** traits.Bool

**circular\_layout**

If True, display the connectivity matrix using a circular layout

**Type** traits.Bool

**inspect\_output\_button**

Button that displays the selected connectivity matrix in the graphical component for quality inspection

**Type** traits.ui.Button

**inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** traits.ui.View

**config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** traits.ui.View

**See also:**

[\*cmp.stages.connectome.connectome.ConnectomeStage\*](#)

**cmp.bidsappmanager.stages.connectome.fmri\_connectome module**

Definition of functional connectome config and stage UI classes.

**class** `cmp.bidsappmanager.stages.connectome.fmri_connectome.ConnectomeConfigUI`

Bases: [\*cmp.stages.connectome.fmri\\_connectome.ConnectomeConfig\*](#)

Class that extends the `ConnectomeConfig` with graphical components.

**output\_types**

A list of output\_types. Valid output\_types are 'gPickle', 'mat', 'cff', 'graphml'

**Type** list of string

**traits\_view**

TraitsUI view that displays the Attributes of this class

**Type** traits.ui.View

**See also:**

[\*cmp.stages.connectome.fmri\\_connectome.ConnectomeConfig\*](#)

**class** `cmp.bidsappmanager.stages.connectome.fmri_connectome.ConnectomeStageUI` (*bids\_dir*,  
*output\_dir*)

Bases: [\*cmp.stages.connectome.fmri\\_connectome.ConnectomeStage\*](#)

Class that extends the `ConnectomeStage` with graphical components.

**log\_visualization**

If True, display with a log transformation

**Type** traits.Bool

**circular\_layout**

If True, display the connectivity matrix using a circular layout

**Type** traits.Bool

**inspect\_output\_button**

Button that displays the selected connectivity matrix in the graphical component for quality inspection

**Type** traits.ui.Button

**inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** traits.ui.View

**config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** traits.ui.View

**See also:**

[\*cmp.stages.connectome.fmri\\_connectome.ConnectomeStage\*](#)

## cmp.bidsappmanager.stages.diffusion package

### Submodules

### cmp.bidsappmanager.stages.diffusion.diffusion module

Definition of diffusion reconstruction and tracking config and stage UI classes.

**class** `cmp.bidsappmanager.stages.diffusion.diffusion.DiffusionConfigUI`

Bases: [\*cmp.stages.diffusion.diffusion.DiffusionConfig\*](#)

Class that extends the DiffusionConfig with graphical components.

It includes the graphical components defining the configuration of the diffusion reconstruction and tractography sub-stages.

**traits\_view**

TraitsUI view that displays the Diffusion Stage Parameter Attributes of this class

**Type** traits.ui.View

**See also:**

[\*cmp.stages.diffusion.diffusion.DiffusionConfig\*](#)

**class** `cmp.bidsappmanager.stages.diffusion.diffusion.DiffusionStageUI(bids_dir, output_dir)`

Bases: [\*cmp.stages.diffusion.diffusion.DiffusionStage\*](#)

Class that extends the DiffusionStage with graphical components.

**inspect\_output\_button**

Button that displays the selected output in an appropriate viewer (present only in the window for quality inspection)

**Type** traits.ui.Button

**inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** traits.ui.View

**config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** traits.ui.View

**See also:**

[\*cmp.stages.diffusion.diffusion.DiffusionStage\*](#)

**cmp.bidsappmanager.stages.diffusion.reconstruction module**

Definition of diffusion reconstruction config UI classes.

**class** `cmp.bidsappmanager.stages.diffusion.reconstruction.Dipy_recon_configUI`

Bases: [\*cmp.stages.diffusion.reconstruction.DipyReconConfig\*](#)

Class that extends the DipyReconConfig with graphical components.

**flip\_table\_axis**

List of axis to flip in the gradient table. Valid values are 'x', 'y', 'z'

**Type** list of string

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for diffusion reconstruction using Dipy

**Type** traits.ui.View

**See also:**

[\*cmp.stages.diffusion.reconstruction.DipyReconConfig\*](#)

**class** `cmp.bidsappmanager.stages.diffusion.reconstruction.MRtrix_recon_configUI`

Bases: [\*cmp.stages.diffusion.reconstruction.MRtrixReconConfig\*](#)

Class that extends the MRtrixReconConfig with graphical components.

**flip\_table\_axis**

List of axis to flip in the gradient table. Valid values are 'x', 'y', 'z'

**Type** list of string

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for diffusion reconstruction using MRtrix

**Type** traits.ui.View

**See also:**

[\*cmp.stages.diffusion.reconstruction.MRtrixReconConfig\*](#)

## cmp.bidsappmanager.stages.diffusion.tracking module

Definition of diffusion tracking config UI classes.

**class** `cmp.bidsappmanager.stages.diffusion.tracking.Dipy_tracking_configUI`

Bases: `cmp.stages.diffusion.tracking.DipyTrackingConfig`

Class that extends the DipyTrackingConfig with graphical components.

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for diffusion tractography using Dipy

**Type** `traits.ui.View`

**See also:**

`cmp.stages.diffusion.tracking.DipyTrackingConfig`

**class** `cmp.bidsappmanager.stages.diffusion.tracking.MRtrix_tracking_configUI`

Bases: `cmp.stages.diffusion.tracking.MRtrixTrackingConfig`

Class that extends the MRtrixTrackingConfig with graphical components.

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for tractography using MRtrix

**Type** `traits.ui.View`

**See also:**

`cmp.stages.diffusion.reconstruction.MRtrixTrackingConfig`

## cmp.bidsappmanager.stages.functional package

### Submodules

## cmp.bidsappmanager.stages.functional.functionalMRI module

Definition of extra preprocessing of functional MRI (post-registration) config and stage UI classes.

**class** `cmp.bidsappmanager.stages.functional.functionalMRI.FunctionalMRIConfigUI`

Bases: `cmp.stages.functional.functionalMRI.FunctionalMRIConfig`

Class that extends the FunctionalMRIConfig with graphical components.

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for the stage

**Type** `traits.ui.View`

**See also:**

`cmp.stages.functional.functionalMRI.FunctionalMRIConfig`

**class** `cmp.bidsappmanager.stages.functional.functionalMRI.FunctionalMRIStageUI` (*bids\_dir*,  
*output\_dir*)

Bases: `cmp.stages.functional.functionalMRI.FunctionalMRIStage`

Class that extends the FunctionalMRIStage with graphical components.

**inspect\_output\_button**

Button that displays the selected output in an appropriate viewer (present only in the window for quality inspection)

**Type** traits.ui.Button

**inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** traits.ui.View

**config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** traits.ui.View

**See also:**

*cmp.stages.functional.functionalMRI.FunctionalMRIStage*

**cmp.bidsappmanager.stages.parcellation package****Submodules****cmp.bidsappmanager.stages.parcellation.parcellation module**

Definition of parcellation config and stage UI classes.

**class** cmp.bidsappmanager.stages.parcellation.parcellation.ParcellationConfigUI

Bases: *cmp.stages.parcellation.parcellation.ParcellationConfig*

Class that extends the ParcellationConfig with graphical components.

**custom\_parcellation\_view**

VGroup that displays the different parts of a custom BIDS parcellation file

**Type** traits.ui.View

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for the stage

**Type** traits.ui.View

**See also:**

*cmp.stages.parcellation.parcellation.ParcellationConfig*

**class** cmp.bidsappmanager.stages.parcellation.parcellation.ParcellationStageUI(*pipeline\_mode,*  
*subject,*  
*session,*  
*bids\_dir,*  
*output\_dir*)

Bases: *cmp.stages.parcellation.parcellation.ParcellationStage*

Class that extends the ParcellationStage with graphical components.

**inspect\_output\_button**

Button that displays the selected output in an appropriate viewer (present only in the window for quality inspection)

**Type** traits.ui.Button

**inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** traits.ui.View

**config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** traits.ui.View

**See also:**

*cmp.stages.parcellation.parcellation.ParcellationStage*

**cmp.bidsappmanager.stages.preprocessing package****Submodules****cmp.bidsappmanager.stages.preprocessing.fmri\_preprocessing module**

Definition of fMRI preprocessing config and stage UI classes.

**class** cmp.bidsappmanager.stages.preprocessing.fmri\_preprocessing.PreprocessingConfigUI

Bases: *cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingConfig*

Class that extends the (functional) PreprocessingConfig with graphical components.

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for the stage

**Type** traits.ui.View

**See also:**

*cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingConfig*

**class** cmp.bidsappmanager.stages.preprocessing.fmri\_preprocessing.PreprocessingStageUI(*bids\_dir*,  
*out-put\_dir*)

Bases: *cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingStage*

Class that extends the (functional) PreprocessingStage with graphical components.

**inspect\_output\_button**

Button that displays the selected output in an appropriate viewer (present only in the window for quality inspection)

**Type** traits.ui.Button

**inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** traits.ui.View

**config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** traits.ui.View

**See also:**

*cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingStage*

## cmp.bidsappmanager.stages.preprocessing.preprocessing module

Definition of diffusion preprocessing config and stage UI classes.

**class** `cmp.bidsappmanager.stages.preprocessing.preprocessing.PreprocessingConfigUI`

Bases: `cmp.stages.preprocessing.preprocessing.PreprocessingConfig`

Class that extends the (diffusion) `PreprocessingConfig` with graphical components.

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for the stage

**Type** `traits.ui.View`

**See also:**

`cmp.stages.preprocessing.preprocessing.PreprocessingConfig`

**class** `cmp.bidsappmanager.stages.preprocessing.preprocessing.PreprocessingStageUI` (*bids\_dir*,  
*out-put\_dir*)

Bases: `cmp.stages.preprocessing.preprocessing.PreprocessingStage`

Class that extends the (diffusion) `PreprocessingStage` with graphical components.

**inspect\_output\_button**

Button that displays the selected output in an appropriate viewer (present only in the window for quality inspection)

**Type** `traits.ui.Button`

**inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** `traits.ui.View`

**config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** `traits.ui.View`

**See also:**

`cmp.stages.preprocessing.preprocessing.PreprocessingStage`

## cmp.bidsappmanager.stages.registration package

### Submodules

## cmp.bidsappmanager.stages.registration.registration module

Definition of registration config and stage UI classes.

**class** `cmp.bidsappmanager.stages.registration.registration.RegistrationConfigUI`

Bases: `cmp.stages.registration.registration.RegistrationConfig`

Class that extends the `RegistrationConfig` with graphical components.

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for the stage

**Type** `traits.ui.View`



See also:

[\*cmp.stages.registration.registration.RegistrationConfig\*](#)

```
class cmp.bidsappmanager.stages.registration.registration.RegistrationStageUI(pipeline_mode,
                                                                              fs_subjects_dir=None,
                                                                              fs_subject_id=None,
                                                                              bids_dir="",
                                                                              output_dir="")
```

Bases: [\*cmp.stages.registration.registration.RegistrationStage\*](#)

Class that extends the RegistrationStage with graphical components.

#### **inspect\_output\_button**

Button that displays the selected output in an appropriate viewer (present only in the window for quality inspection)

**Type** traits.ui.Button

#### **inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** traits.ui.View

#### **config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** traits.ui.View

See also:

[\*cmp.stages.registration.registration.RegistrationStage\*](#)

## **cmp.bidsappmanager.stages.segmentation package**

### **Submodules**

#### **cmp.bidsappmanager.stages.segmentation.segmentation module**

Definition of segmentation config and stage UI classes.

```
class cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationConfigUI
```

Bases: [\*cmp.stages.segmentation.segmentation.SegmentationConfig\*](#)

Class that extends the SegmentationConfig with graphical components.

#### **custom\_brainmask\_group**

VGroup that displays the different parts of a custom BIDS brain mask file

**Type** traits.ui.VGroup

#### **custom\_gm\_mask\_group**

VGroup that displays the different parts of a custom BIDS gray matter mask file

**Type** traits.ui.VGroup

#### **custom\_wm\_mask\_group**

VGroup that displays the different parts of a custom BIDS white matter mask file

**Type** traits.ui.VGroup

**custom\_csf\_mask\_group**

VGroup that displays the different parts of a custom BIDS CSF mask file

**Type** traits.ui.VGroup

**custom\_aparcaseg\_group**

VGroup that displays the different parts of a custom BIDS-formatted Freesurfer's aparc+aseg file

**Type** traits.ui.VGroup

**traits\_view**

TraitsUI view that displays the attributes of this class, e.g. the parameters for the stage

**Type** traits.ui.View

**See also:**

[\*cmp.stages.segmentation.segmentation.SegmentationConfig\*](#)

```
class cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationStageUI(subject,  
                                                                           session,  
                                                                           bids_dir,  
                                                                           output_dir)
```

Bases: [\*cmp.stages.segmentation.segmentation.SegmentationStage\*](#)

Class that extends the SegmentationStage with graphical components.

**inspect\_output\_button**

Button that displays the selected output in an appropriate viewer (present only in the window for quality inspection)

**Type** traits.ui.Button

**inspect\_outputs\_view**

TraitsUI view that displays the quality inspection window of this stage

**Type** traits.ui.View

**config\_view**

TraitsUI view that displays the configuration window of this stage

**Type** traits.ui.View

**See also:**

[\*cmp.stages.segmentation.segmentation.SegmentationStage\*](#)

## 5.6.2 cmtklib package

### Subpackages

#### cmtklib.bids package

### Submodules

#### cmtklib.bids.io module

This module provides classes to handle custom BIDS derivatives file input.

**class** `cmtklib.bids.io.CustomAparcAsegBIDSFile`

Bases: `cmtklib.bids.io.CustomBIDSFile`

Represent a custom BIDS-formatted Freesurfer aparc+aseg file in the form sub-<label>\_desc-aparcaseg\_dseg.nii.gz.

**class** `cmtklib.bids.io.CustomBIDSFile`(*p\_toolbox\_derivatives\_dir*="", *p\_suffix*="", *p\_extension*="", *p\_acquisition*="", *p\_atlas*="", *p\_res*="", *p\_label*="", *p\_desc*="")

Bases: `traits.has_traits.HasTraits`

Base class used to represent a BIDS-formatted file inside a custom BIDS derivatives directory.

**toolbox\_derivatives\_dir**

Toolbox folder name in the derivatives/ of the BIDS dataset

**Type** Str

**suffix**

Filename suffix e.g. sub-01\_T1w.nii.gz has suffix T1w

**Type** Str

**acquisition**

Label used in \_acq-<label>\_

**Type** Str

**res**

Label used in \_res-<label>\_

**Type** Str

**extension**

File extension

**Type** Str

**atlas**

Label used in \_atlas-<label>\_

**Type** Str

**label**

Label used in \_label-<label>\_

**Type** Str

**desc**

Label used in \_desc-<label>\_

**Type** Str

**get\_filename\_path**(*base\_dir*, *subject*, *session*=None, *debug*=True)

Return the number of regions by reading its associated TSV side car file describing the nodes.

**Parameters**

- **base\_dir** (*str*) – BIDS root directory or derivatives/ directory in BIDS root directory
- **subject** (*str*) – Subject filename entity e.g. “sub-01”
- **session** (*str*) – Session filename entity e.g. “ses-01” if applicable (Default: None)
- **debug** (*bool*) – Debug mode (Extra outputted messages) if **True**

**get\_query\_dict**()

Return the dictionary to be passed to BIDSDataGrabber to query a list of files.

**get\_toolbox\_derivatives\_dir()**

Return the value of `custom_derivatives_dir` attribute.

**class** `cmtklib.bids.io.CustomBrainMaskBIDSFile`

Bases: `cmtklib.bids.io.CustomBIDSFile`

Represent a custom brain mask in the form `sub-<label>_desc-brain_mask.nii.gz`.

**class** `cmtklib.bids.io.CustomCSFMaskBIDSFile`

Bases: `cmtklib.bids.io.CustomBIDSFile`

Represent a custom CSF mask in the form `sub-<label>_label-CSF_dseg.nii.gz`.

**class** `cmtklib.bids.io.CustomGMMaskBIDSFile`

Bases: `cmtklib.bids.io.CustomBIDSFile`

Represent a custom gray-matter mask in the form `sub-<label>_label-GM_dseg.nii.gz`.

**class** `cmtklib.bids.io.CustomParcellationBIDSFile`

Bases: `cmtklib.bids.io.CustomBIDSFile`

Represent a custom parcellation files in the form `sub-<label>_atlas-<label>[_res-<label>]_dseg.nii.gz`.

**get\_nb\_of\_regions**(*bids\_dir*, *subject*, *session=None*, *debug=True*)

Return the number of regions by reading its associated TSV side car file describing the nodes.

#### Parameters

- **bids\_dir** (*str*) – BIDS root directory
- **subject** (*str*) – Subject filename entity e.g. “sub-01”
- **session** (*str*) – Session filename entity e.g. “ses-01” if applicable (Default: None)
- **debug** (*bool*) – Debug mode (Extra outputted messages) if **True**

**class** `cmtklib.bids.io.CustomWMMaskBIDSFile`

Bases: `cmtklib.bids.io.CustomBIDSFile`

Represent a custom white-matter mask in the form `sub-<label>_label-WM_dseg.nii.gz`.

## cmtklib.bids.network module

This module provides functions to handle connectome networks / graphs generated by CMP3.

**cmtklib.bids.network.load\_graphs**(*output\_dir*, *subjects*, *parcellation\_scheme*, *weight*)

Return a dictionary of connectivity matrices (graph adjacency matrices).

Still in development

#### Parameters

- **output\_dir** (*string*) – Output/derivatives directory
- **subjects** (*list*) – List of subject
- **parcellation\_scheme** (`['NativeFreesurfer', 'Lausanne2018', 'Custom']`) – Parcellation scheme
- **weight** (`['number_of_fibers', 'fiber_density', ...]`) – Edge metric to extract from the graph

**Returns** **connmats** – Dictionary of connectivity matrices

**Return type** dict

## cmtklib.bids.utils module

This module provides CMTK Utility functions to handle BIDS datasets.

### CreateBIDSStandardParcellationLabelIndexMappingFile

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Creates the BIDS standard generic label-index mapping file that describes parcellation nodes.

**roi\_colorlut** [a pathlike object or string representing an existing file] Path to FreesurferColorLUT.txt file that describes the RGB color of the graph nodes for a given parcellation.

**roi\_graphml** [a pathlike object or string representing an existing file] Path to graphml file that describes graph nodes for a given parcellation.

**verbose** [a boolean] Verbose mode.

**roi\_bids\_tsv** [a pathlike object or string representing a file] Output BIDS standard generic label-index mapping file that describes parcellation nodes.

### CreateCMPParcellationNodeDescriptionFilesFromBIDSFile

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Creates CMP graphml and FreeSurfer colorLUT files that describe parcellation nodes from the BIDS TSV file

**roi\_bids\_tsv** [a pathlike object or string representing an existing file] Output BIDS standard generic label-index mapping file that describes parcellation nodes.

**roi\_colorlut** [a pathlike object or string representing a file] Path to FreesurferColorLUT.txt file that describes the RGB color of the graph nodes for a given parcellation.

**roi\_graphml** [a pathlike object or string representing a file] Path to graphml file that describes graph nodes for a given parcellation.

### CreateMultipleCMPParcellationNodeDescriptionFilesFromBIDSFile

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Creates CMP graphml and FreeSurfer colorLUT files describing parcellation nodes from a list of BIDS TSV files

**roi\_bids\_tsvs** : a list of items which are a pathlike object or string representing an existing file

**roi\_colorluts** : a list of items which are a pathlike object or string representing a file **roi\_graphmls** : a list of items which are a pathlike object or string representing a file

`cmtklib.bids.utils.get_native_space_files(filepathlist)`

Return a list of files without `_space-<label>_` in the filename.

`cmtklib.bids.utils.get_native_space_no_desc_files(filepathlist)`

Return a list of files without `_space-<label>_` and `_desc-<label>_` in the filename.

`cmtklib.bids.utils.get_native_space_tsv_sidecar_files(filepathlist)`

Return path to tsv sidecar file of a list of niftis (`nii.gz`) without `_space-<label>_` in their filename.

`cmtklib.bids.utils.write_derivative_description(bids_dir, deriv_dir, pipeline_name)`

Write a `dataset_description.json` in each type of CMP derivatives.

#### Parameters

- **bids\_dir** (*string*) – BIDS root directory
- **deriv\_dir** (*string*) – Output/derivatives directory
- **pipeline\_name** (*string*) – Type of derivatives (`['cmp-<version>', 'freesurfer-<version>', 'nipype-<version>']`)

## cmtklib.interfaces package

### Submodules

#### cmtklib.interfaces.afni module

The AFNI module provides Nipype interfaces for the AFNI toolbox missing in nipype or modified.

### Bandpass

[Link to code](#)

Bases: `nipype.interfaces.afni.base.AFNICCommand`

Wrapped executable: `3dBandpass`.

Program to lowpass and/or highpass each voxel time series in a dataset.

Calls the `3dBandpass` tool from AFNI, offering more/different options than Fourier.

For complete details, see the [3dBandpass Documentation](#).

### Examples

```
>>> from nipype.interfaces import afni as afni
>>> from nipype.testing import example_data
>>> bandpass = afni.Bandpass()
>>> bandpass.inputs.in_file = example_data('functional.nii')
>>> bandpass.inputs.highpass = 0.005
>>> bandpass.inputs.lowpass = 0.1
>>> res = bandpass.run()
```

**highpass** [a float] Highpass. Maps to a command-line argument: `%f` (position: -3).

**in\_file** [a pathlike object or string representing an existing file] Input file to `3dBandpass`. Maps to a command-line argument: `%s` (position: -1).

- lowpass** [a float] Lowpass. Maps to a command-line argument: %f (position: -2).
- args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.
- automask** [a boolean] Create a mask from the input dataset. Maps to a command-line argument: -automask.
- blur** [a float] Blur (inside the mask only) with a filter width (FWHM) of 'fff' millimeters. Maps to a command-line argument: -blur %f.
- despike** [a boolean] Despike each time series before other processing. Hopefully, you don't actually need to do this, which is why it is optional. Maps to a command-line argument: -despike.
- environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})
- localPV** [a float] Replace each vector by the local Principal Vector (AKA first singular vector) from a neighborhood of radius 'rrr' millimeters. Note that the PV time series is L2 normalized. This option is mostly for Bob Cox to have fun with. Maps to a command-line argument: -localPV %f.
- mask** [a pathlike object or string representing an existing file] Mask file. Maps to a command-line argument: -mask %s (position: 2).
- nfft** [an integer] Set the FFT length [must be a legal value]. Maps to a command-line argument: -nfft %d.
- no\_detrend** [a boolean] Skip the quadratic detrending of the input that occurs before the FFT-based band-passing. ++ You would only want to do this if the dataset had been detrended already in some other program. Maps to a command-line argument: -nodetrend.
- normalize** [a boolean] Make all output time series have L2 norm = 1 ++ i.e., sum of squares = 1. Maps to a command-line argument: -norm.
- notrans** [a boolean] Don't check for initial positive transients in the data: The test is a little slow, so skipping it is OK, if you KNOW the data time series are transient-free. Maps to a command-line argument: -notrans.
- num\_threads** [an integer] Set number of threads. (Nipype **default** value: 1)
- orthogonalize\_dset** [a pathlike object or string representing an existing file] Orthogonalize each voxel to the corresponding voxel time series in dataset 'fset', which must have the same spatial and temporal grid structure as the main input dataset. At present, only one '-dsort' option is allowed. Maps to a command-line argument: -dsort %s.
- orthogonalize\_file** [a list of items which are a pathlike object or string representing an existing file] Also orthogonalize input to columns in f.1D Multiple '-ort' options are allowed. Maps to a command-line argument: -ort %s.
- out\_file** [a pathlike object or string representing a file] Output file from 3dBandpass. Maps to a command-line argument: -prefix %s (position: 1).
- outputtype** ['NIFTI' or 'AFNI' or 'NIFTI\_GZ'] AFNI output filetype.
- tr** [a float] Set time step (TR) in sec [default=from dataset header]. Maps to a command-line argument: -dt %f.
- out\_file** [a pathlike object or string representing an existing file] Output file.

## Despike

[Link to code](#)

Bases: `nipype.interfaces.afni.base.AFNICCommand`

Wrapped executable: `3dDespike`.

Removes ‘spikes’ from the 3D+time input dataset.

It calls the `3dDespike` tool from AFNI.

For complete details, see the [3dDespike Documentation](#).

### Examples

```
>>> from nipype.interfaces import afni
>>> despike = afni.Despike()
>>> despike.inputs.in_file = 'functional.nii'
>>> res = despike.run()
```

**in\_file** [a pathlike object or string representing an existing file] Input file to `3dDespike`. Maps to a command-line argument: `%s` (position: -1).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class ‘str’ and with values which are a bytes or None or a value of class ‘str’] Environment variables. (Nipype **default** value: `{}`)

**num\_threads** [an integer] Set number of threads. (Nipype **default** value: 1)

**out\_file** [a pathlike object or string representing a file] Output image file name. Maps to a command-line argument: `-prefix %s`.

**outputtype** [‘NIFTI’ or ‘AFNI’ or ‘NIFTI\_GZ’] AFNI output filetype.

**out\_file** [a pathlike object or string representing an existing file] Output file.

## cmtklib.interfaces.ants module

The ANTs module provides Nipype interfaces for the ANTs registration toolbox missing in nipype or modified.

### MultipleANTsApplyTransforms

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Apply linear and deformable transforms estimated by ANTS to a list of images.

It calls the `antsApplyTransform` on a series of images.



## Examples

```
>>> apply_tf = MultipleANTsApplyTransforms()
>>> apply_tf.inputs.input_images = ['/path/to/sub-01_atlas-L2018_desc-scale1_
↳dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale2_
↳dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale3_
↳dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale4_
↳dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale5_
↳dseg.nii.gz']
>>> apply_tf.inputs.transforms = ['/path/to/final1Warp.nii.gz',
>>>                                '/path/to/final0GenericAffine.mat']
>>> apply_tf.inputs.reference_image = File(mandatory=True, exists=True)
>>> apply_tf.inputs.interpolation = 'NearestNeighbor'
>>> apply_tf.inputs.default_value = 0.0
>>> apply_tf.inputs.out_postfix = "_transformed"
>>> apply_tf.run()
```

`reference_image` : a string or `os.PathLike` object referring to an existing file  
`transforms` : a list of items which are a string or `os.PathLike` object referring to an existing file

Transform files: will be applied in reverse order. For example, the last specified transform will be applied first.

`default_value` : a float  
`input_images` : a list of items which are a string or `os.PathLike` object referring to an existing file  
`interpolation` : 'Linear' or 'NearestNeighbor' or 'CosineWindowedSinc' or 'WelchWindowedSinc' or 'HammingWindowedSinc' or 'LanczosWindowedSinc' or 'MultiLabel' or 'Gaussian' or 'BSpline'

(Nipype **default** value: Linear)

**out\_postfix** [a string] (Nipype **default** value: `_transformed`)

`output_images` : a list of items which are a string or `os.PathLike` object

## cmtklib.interfaces.dipy module

The Dipy module provides Nipype interfaces to the algorithms in dipy.

## CSD

[Link to code](#)

Bases: `nipype.interfaces.dipy.base.DipyDiffusionInterface`

Uses CSD [Tournier2007] to generate the fODF of DWIs.

The interface uses `dipy`, as explained in [dipy's CSD example](#).

## References

### Example

```
>>> from cmtklib.interfaces.dipy import CSD
>>> csd = CSD()
>>> csd.inputs.in_file = '4d_dwi.nii'
>>> csd.inputs.in_bval = 'bvals'
>>> csd.inputs.in_bvec = 'bvecs'
>>> res = csd.run()
```

**in\_bval** [a pathlike object or string representing an existing file] Input b-values table.

**in\_bvec** [a pathlike object or string representing an existing file] Input b-vectors table.

**in\_file** [a pathlike object or string representing an existing file] Input diffusion data.

**b0\_thres** [an integer] B0 threshold. (Nipype **default** value: 700)

**fa\_thresh** [a float] FA threshold used for response estimation. (Nipype **default** value: 0.7)

**in\_mask** [a pathlike object or string representing an existing file] Input mask in which compute tensors.

**out\_fods** [a pathlike object or string representing a file] FODFs output file name.

**out\_prefix** [a string] Output prefix for file names.

**out\_shm\_coeff** [a pathlike object or string representing a file] Spherical Harmonics Coefficients output file name.

**response** [a pathlike object or string representing an existing file] Single fiber estimated response.

**save\_fods** [a boolean] Save fODFs in file. (Nipype **default** value: True)

**save\_shm\_coeff** [a boolean] Save Spherical Harmonics Coefficients in file. (Nipype **default** value: True)

**sh\_order** [an integer] Maximal shperical harmonics order. (Nipype **default** value: 8)

**tracking\_processing\_tool** : ‘mrtrix’ or ‘dipy’

**model** [a pathlike object or string representing a file] Python pickled object of the CSD model fitted.

**out\_fods** [a pathlike object or string representing a file] FODFs output file name.

**out\_shm\_coeff** [a pathlike object or string representing a file] Spherical Harmonics Coefficients output file name.

## DTIEstimateResponseSH

[Link to code](#)

Bases: nipype.interfaces.dipy.base.DipyDiffusionInterface

Uses dipy to compute the single fiber response to be used by spherical deconvolution methods.

**The single fiber response is computed in a similar way to MRTrix’s command estimate\_response.**

## Example

```
>>> from cmtklib.interfaces.dipy import DTIEstimateResponseSH
>>> dti = DTIEstimateResponseSH()
>>> dti.inputs.in_file = '4d_dwi.nii'
>>> dti.inputs.in_bval = 'bvals'
>>> dti.inputs.in_bvec = 'bvecs'
>>> res = dti.run()
```

**in\_bval** [a pathlike object or string representing an existing file] Input b-values table.

**in\_bvec** [a pathlike object or string representing an existing file] Input b-vectors table.

**in\_file** [a pathlike object or string representing an existing file] Input diffusion data.

**auto** [a boolean] Use the auto\_response estimator from dipy. Mutually **exclusive** with inputs: **recursive**.

**b0\_thres** [an integer] B0 threshold. (Nipype **default** value: 700)

**fa\_thresh** [a float] FA threshold. (Nipype **default** value: 0.7)

**in\_mask** [a pathlike object or string representing an existing file] Input mask in which we find single fibers.

**out\_mask** [a pathlike object or string representing a file] Computed wm mask. (Nipype **default** value: `wm_mask.nii.gz`)

**out\_prefix** [a string] Output prefix for file names.

**recursive** [a boolean] Use the recursive response estimator from dipy. Mutually **exclusive** with inputs: **auto**.

**response** [a pathlike object or string representing a file] The output response file. (Nipype **default** value: `response.txt`)

**roi\_radius** [an integer] ROI radius to be used in auto\_response. (Nipype **default** value: 10)

**ad\_file** : a pathlike object or string representing an existing file **dti\_model** : a pathlike object or string representing an existing file

DTI model object.

**fa\_file** : a pathlike object or string representing an existing file **md\_file** : a pathlike object or string representing an existing file **out\_mask** : a pathlike object or string representing an existing file

Output wm mask.

**rd\_file** : a pathlike object or string representing an existing file **response** : a pathlike object or string representing an existing file

The response file.

## DirectionGetterTractography

[Link to code](#)

Bases: `nipy.interfaces.dipy.base.DipyBaseInterface`

Streamline tractography using Dipy Deterministic Maximum Direction Getter.

### Example

```
>>> from cmtklib.interfaces import dipy as ndp
>>> track = ndp.DirectionGetterTractography()
>>> track.inputs.in_file = '4d_dwi.nii'
>>> track.inputs.in_model = 'model.pklz'
>>> track.inputs.tracking_mask = 'dilated_wm_mask.nii'
>>> res = track.run()
```

**fa\_thresh** [a float] FA threshold to build the tissue classifier. (Nipype **default** value: 0.2)

**in\_fa** [a pathlike object or string representing an existing file] Input FA.

**in\_file** [a pathlike object or string representing an existing file] Input diffusion data.

**in\_model** [a pathlike object or string representing an existing file] Input f/d-ODF model extracted from.

**max\_angle** [a float] Maximum angle. (Nipype **default** value: 25.0)

**multiprocess** [a boolean] Use multiprocessing. (Nipype **default** value: True)

**num\_seeds** [an integer] Desired number of tracks in tractography. (Nipype **default** value: 10000)

**save\_seeds** [a boolean] Save seeding voxels coordinates. (Nipype **default** value: False)

**seed\_mask** [a list of items which are a pathlike object or string representing an existing file] ROI files registered to diffusion space.

**step\_size** [a float] Step size. (Nipype **default** value: 0.5)

**tracking\_mask** [a pathlike object or string representing an existing file] Input mask within which perform tracking.

**algo** ['deterministic' or 'probabilistic'] Use either deterministic maximum (default) or probabilistic direction getter tractography. (Nipype **default** value: deterministic)

**fod\_file** [a pathlike object or string representing an existing file] Input fod file (if SHORE).

**gmwmi\_file** [a pathlike object or string representing an existing file] Input Gray Matter / White Matter interface image.

**in\_partial\_volume\_files** [a list of items which are a pathlike object or string representing an existing file] Partial volume estimation result files (required if performing ACT).

**out\_prefix** [a string] Output prefix for file names.

**recon\_model** ['CSD' or 'SHORE'] Use either fODFs from CSD (default) or SHORE models. (Nipype **default** value: CSD)

**recon\_order** [an integer] Spherical harmonics order.

**seed\_density** [a float] Density of seeds. (Nipype **default** value: 1)

**seed\_from\_gmwmi** [a boolean] Seed from the Gray Matter / White Matter interface.

**use\_act** [a boolean] Use FAST for partial volume estimation and Anatomically-Constrained Tractography (ACT) tissue classifier.

**out\_seeds** [a pathlike object or string representing a file] File containing the (N,3) *voxel* coordinates used in seeding.

**streamlines** [a pathlike object or string representing a file] Numpy array of streamlines.

**tracks** [a pathlike object or string representing a file] TrackVis file containing extracted streamlines.

**tracks2** [a pathlike object or string representing a file] TrackVis file containing extracted streamlines.

**tracks3** [a pathlike object or string representing a file] TrackVis file containing extracted streamlines.

## MAPMRI

[Link to code](#)

Bases: `nipy.interfaces.dipy.base.DipyDiffusionInterface`

Computes the MAP MRI model.

### Example

```
>>> from cmtklib.interfaces.dipy import MAPMRI
>>> mapmri = MAPMRI()
>>> mapmri.inputs.in_file = '4d_dwi.nii'
>>> mapmri.inputs.in_bval = 'bvals'
>>> mapmri.inputs.in_bvec = 'bvecs'
>>> res = mapmri.run()
```

**big\_delta** [a float] Small data for gradient table.

**in\_bval** [a pathlike object or string representing an existing file] Input b-values table.

**in\_bvec** [a pathlike object or string representing an existing file] Input b-vectors table.

**in\_file** [a pathlike object or string representing an existing file] Input diffusion data.

**small\_delta** [a float] Small data for gradient table.

**b0\_thres** [an integer] B0 threshold. (Nipype **default** value: 700)

**laplacian\_regularization** [a boolean] Apply laplacian regularization. (Nipype **default** value: True)

**laplacian\_weighting** [a float] Regularization weight. (Nipype **default** value: 0.05)

**out\_prefix** [a string] Output prefix for file names.

**positivity\_constraint** [a boolean] Apply positivity constraint. (Nipype **default** value: True)

**radial\_order** [an integer] Maximal shperical harmonics order. (Nipype **default** value: 8)

**model** [a pathlike object or string representing a file] Python pickled object of the MAP-MRI model fitted.

**msd\_file** [a pathlike object or string representing a file] Msd output file name.

**ng\_file** [a pathlike object or string representing a file] Ng output file name.

**ng\_para\_file** [a pathlike object or string representing a file] Ng parallel output file name.

**ng\_perp\_file** [a pathlike object or string representing a file] Ng perpendicular output file name.

**qiv\_file** [a pathlike object or string representing a file] Qiv output file name.  
**rtap\_file** [a pathlike object or string representing a file] Rtap output file name.  
**rtop\_file** [a pathlike object or string representing a file] Rtop output file name.  
**rtpv\_file** [a pathlike object or string representing a file] Rtpv output file name.

## SHORE

[Link to code](#)

Bases: `nipy.interfaces.dipy.base.DipyDiffusionInterface`

Uses SHORE [Merlet2013] to generate the fODF of DWIs.

The interface uses **dipy**, as explained in [dipy's SHORE example](#).

### References

### Example

```
>>> from cmtklib.interfaces.dipy import SHORE
>>> asm = SHORE(radial_order=6, zeta=700, lambda_n=1e-8, lambda_l=1e-8)
>>> asm.inputs.in_file = '4d_dwi.nii'
>>> asm.inputs.in_bval = 'bvals'
>>> asm.inputs.in_bvec = 'bvecs'
>>> res = asm.run()
```

**in\_bval** [a pathlike object or string representing an existing file] Input b-values table.  
**in\_bvec** [a pathlike object or string representing an existing file] Input b-vectors table.  
**in\_file** [a pathlike object or string representing an existing file] Input diffusion data.  
**b0\_thres** [an integer] B0 threshold. (Nipype **default** value: 700)  
**constrain\_e0** [a boolean] Constrain the optimization such that  $E(0) = 1$ . (Nipype **default** value: False)  
**in\_mask** [a pathlike object or string representing an existing file] Input mask in which compute SHORE solution.  
**lambda\_l** [a float] Angular regularisation constant. (Nipype **default** value:  $1e-08$ )  
**lambda\_n** [a float] Radial regularisation constant. (Nipype **default** value:  $1e-08$ )  
**out\_prefix** [a string] Output prefix for file names.  
**positive\_constraint** [a boolean] Constrain the optimization such that  $E(0) = 1$ . (Nipype **default** value: False)  
**radial\_order** [an integer] Even number that represents the order of the basis. (Nipype **default** value: 6)  
**response** [a pathlike object or string representing an existing file] Single fiber estimated response.  
**tau** [a float] Diffusion time. By default the value that makes  $q$  equal to the square root of the b-value.  
**tracking\_processing\_tool** : 'mrtix' or 'dipy' **zeta** : an integer  
Scale factor. (Nipype **default** value: 700)  
**GFA** [a pathlike object or string representing a file] Generalized Fractional Anisotropy output file name.

**MSD** [a pathlike object or string representing a file] Mean Square Displacement output file name.

**RTOP** [a pathlike object or string representing a file] Return To Origin Probability output file name.

**dodf** [a pathlike object or string representing a file] Fiber Orientation Distribution Function output file name.

**fodf** [a pathlike object or string representing a file] Fiber Orientation Distribution Function output file name.

**model** [a pathlike object or string representing a file] Python pickled object of the SHORE model fitted.

## TensorInformedEudXTractography

[Link to code](#)

Bases: `nipy.interfaces.dipy.base.DipyBaseInterface`

Streamline tractography using Dipy Deterministic Maximum Direction Getter.

### Example

```
>>> from cmtklib.interfaces import dipy as ndp
>>> track = ndp.TensorInformedEudXTractography()
>>> track.inputs.in_file = '4d_dwi.nii'
>>> track.inputs.in_model = 'model.pklz'
>>> track.inputs.tracking_mask = 'dilated_wm_mask.nii'
>>> res = track.run()
```

**fa\_thresh** [a float] FA threshold to build the tissue classifier. (Nipype **default** value: 0.2)

**in\_fa** [a pathlike object or string representing an existing file] Input FA.

**in\_file** [a pathlike object or string representing an existing file] Input diffusion data.

**in\_model** [a pathlike object or string representing an existing file] Input Tensor model extracted from.

**max\_angle** [a float] Maximum angle. (Nipype **default** value: 25.0)

**multiprocess** [a boolean] Use multiprocessing. (Nipype **default** value: True)

**num\_seeds** [an integer] Desired number of tracks in tractography. (Nipype **default** value: 10000)

**save\_seeds** [a boolean] Save seeding voxels coordinates. (Nipype **default** value: False)

**seed\_mask** [a list of items which are a pathlike object or string representing an existing file] ROI files registered to diffusion space.

**step\_size** [a float] Step size. (Nipype **default** value: 0.5)

**tracking\_mask** [a pathlike object or string representing an existing file] Input mask within which perform tracking.

**out\_prefix** [a string] Output prefix for file names.

**out\_seeds** [a pathlike object or string representing a file] File containing the (N,3) *voxel* coordinates used in seeding.

**tracks** [a pathlike object or string representing a file] TrackVis file containing extracted streamlines.

## cmtklib.interfaces.eeg module

Module that defines CMTK Nipype interfaces for EEG.

### CreateRois

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Create Cartool-reconstructed sources / parcellation ROI mapping files.

### Examples

```
>>> from cmtklib.interfaces.eeg import CreateRois
>>> createrois = CreateRois()
>>> createrois.inputs.subject = 'sub-01'
>>> createrois.inputs.bids_dir = '/path/to/bids_dataset'
>>> createrois.inputs.parcellation = {'label': 'L2008', 'desc': 'scale1'}
>>> createrois.inputs.cartool_dir = 'Cartool-v3.80'
>>> createrois.inputs.cmp3_dir = 'cmp-v3.0.3'
>>> createrois.inputs.output_query = {}
>>> createrois.inputs.derivative_list = []
>>> createrois.run()
```

**bids\_dir** [a string] Base directory.

**cartool\_dir** [a string] Cartool directory.

**cmp3\_dir** [a string] CMP3 directory.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**output\_query** [a dictionary with keys which are any value and with values which are any value] BIDS-DataGrabber output\_query.

**parcellation** [a string] Parcellation scheme.

**subject** [a string] Subject.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**output\_query** [a dictionary with keys which are any value and with values which are any value] BIDS-DataGrabber output\_query.

### EEGLoader

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Create Cartool-reconstructed sources / parcellation ROI mapping files.



## Examples

```
>>> from cmtklib.interfaces.eeg import EEGLoader
>>> eeg_loader = EEGLoader()
>>> eeg_loader.inputs.base_directory = '/path/to/bids_dataset'
>>> eeg_loader.inputs.subject = 'sub-01'
>>> eeg_loader.inputs.invsol_format = 'Cartool-LAURA'
>>> eeg_loader.inputs.output_query = {
...     "rois" : {"extension": ["pickle.rois"]},
...     "src" : {"extension": ["spi"]},
...     "invsol" = {"extension": ["LAURA.is"]}
... }
>>> eeg_loader.inputs.derivative_list = ['/path/to/cartool/derivatives']
>>> eeg_loader.run()
```

**base\_directory** [a string or os.PathLike object referring to an existing directory] BIDS data directory.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**output\_query** [a dictionary with keys which are any value and with values which are any value] Output query for BIDSDataGrabber.

**subject** [a string] Subject.

**invsol\_format** ['Cartool-LAURA' or 'Cartool-LORETA' or 'mne-sLORETA'] Cartool vs mne.

**verbose\_mode** [a boolean] Print extra information.

**EEG** [a list of items which are any value] Eeg \* epochs in .fif format.

**bem** [a list of items which are any value] Boundary surfaces for MNE head model.

**invsol** [a list of items which are any value] Inverse solution (.is file loaded with pycartool).

**rois** [a list of items which are any value] Parcellation scheme.

**src** [a list of items which are any value] Src (spi loaded with pycartool or source space created with MNE).

## cmtklib.interfaces.freesurfer module

The FreeSurfer module provides Nipype interfaces for Freesurfer tools missing in nipype or modified.

## BBRegister

[Link to code](#)

Bases: nipype.interfaces.freesurfer.base.FSCommand

Wrapped executable: bregister.

Use FreeSurfer bregister to register a volume to the Freesurfer anatomical.

**This program performs within-subject, cross-modal registration using a** boundary-based cost function. The registration is constrained to be 6 DOF (rigid).

**It is required that you have an anatomical scan of the subject that has** already been recon-all-ed using freesurfer.

## Examples

```
>>> from cmtklib.interfaces.freesurfer import BBRegister
>>> bgreg = BBRegister(subject_id='me',
>>>                    source_file='structural.nii',
>>>                    init='header',
>>>                    contrast_type='t2')
>>> bgreg.run()
```

**contrast\_type** ['t1' or 't2' or 'dti'] Contrast type of image. Maps to a command-line argument: `--%s`.

**init** ['spm' or 'fsl' or 'header'] Initialize registration spm, fsl, header. Maps to a command-line argument: `--init-%s`. Mutually **exclusive** with inputs: `init_reg_file`.

**init\_reg\_file** [a pathlike object or string representing an existing file] Existing registration file. Mutually **exclusive** with inputs: `init`.

**source\_file** [a pathlike object or string representing a file] Source file to be registered. Maps to a command-line argument: `--mov %s`.

**subject\_id** [a string] Freesurfer subject id. Maps to a command-line argument: `--s %s`.

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**epi\_mask** [a boolean] Mask out B0 regions in stages 1 and 2. Maps to a command-line argument: `--epi-mask`.

**intermediate\_file** [a pathlike object or string representing an existing file] Intermediate image, e.g. in case of partial FOV. Maps to a command-line argument: `--int %s`.

**out\_fsl\_file** [a boolean or a pathlike object or string representing a file] Write the transformation matrix in FSL FLIRT format. Maps to a command-line argument: `--fslmat %s`.

**out\_reg\_file** [a pathlike object or string representing a file] Output registration file. Maps to a command-line argument: `--reg %s`.

**reg\_frame** [an integer] 0-based frame index for 4D source file. Maps to a command-line argument: `--frame %d`. Mutually **exclusive** with inputs: `reg_middle_frame`.

**reg\_middle\_frame** [a boolean] Register middle frame of 4D source file. Maps to a command-line argument: `--mid-frame`. Mutually **exclusive** with inputs: `reg_frame`.

**registered\_file** [a boolean or a pathlike object or string representing a file] Output warped sourcefile either True or filename. Maps to a command-line argument: `--o %s`.

**spm\_nifti** [a boolean] Force use of nifti rather than analyze with SPM. Maps to a command-line argument: `--spm-nii`.

**subjects\_dir** [a pathlike object or string representing an existing directory] Subjects directory.

**min\_cost\_file** [a pathlike object or string representing an existing file] Output registration minimum cost file.

**out\_fsl\_file** [a pathlike object or string representing a file] Output FLIRT-style registration file.

**out\_reg\_file** [a pathlike object or string representing an existing file] Output registration file.

**registered\_file** [a pathlike object or string representing a file] Registered and resampled source file.

## Tkregister2

[Link to code](#)

Bases: `nipype.interfaces.base.core.CommandLine`

Wrapped executable: `tkregister2`.

Performs image co-registration using Freesurfer `tkregister2`.

### Examples

```
>>> from cmtklib.interfaces.freesurfer import Tkregister2
>>> tkreg = Tkregister2()
>>> tkreg.inputs.in_file = 'sub-01_desc-brain_mask.nii.gz'
>>> tkreg.inputs.subject_dir = '/path/to/output_dir/freesurfer/sub-01'
>>> tkreg.inputs.subjects_dir = '/path/to/output_dir/freesurfer'
>>> tkreg.inputs.subject_id = 'sub-01'
>>> tkreg.inputs.regheader = True
>>> tkreg.inputs.in_file = '/path/to/moving_image.nii.gz'
>>> tkreg.inputs.target_file = '/path/to/fixed_image.nii.gz'
>>> tkreg.inputs.fslreg_out = 'motions.par'
>>> tkreg.inputs.noedit = True
>>> tkreg.run()
```

**fslreg\_out** [a string] FSL-Style registration output matrix. Maps to a command-line argument: `--fslregout %s`.

**in\_file** [a pathlike object or string representing a file] Movable volume. Maps to a command-line argument: `--mov %s`.

**reg\_out** [a string] Input/output registration file. Maps to a command-line argument: `--reg %s`.

**target\_file** [a pathlike object or string representing a file] Target volume. Maps to a command-line argument: `--targ %s`.

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**noedit** [a boolean] Do not open edit window (exit) - for conversions. Maps to a command-line argument: `--noedit`.

**regheader** [a boolean] Compute registration from headers. Maps to a command-line argument: `--regheader`.

**subject\_id** [a string] Set subject id. Maps to a command-line argument: `--s %s`.

**subjects\_dir** [a pathlike object or string representing an existing directory] Use dir as SUBJECTS\_DIR. Maps to a command-line argument: `--sd %s`.

**fslregout\_file** [a pathlike object or string representing a file] Resulting FSL-Style registration matrix.

**regout\_file** [a pathlike object or string representing a file] Resulting registration file.

## copyBrainMaskToFreesurfer

[Link to code](#)

Bases: `nipype.interfaces.io.IOBase`

Copy a custom brain mask in the freesurfer subject `mri/` directory.

**It replaces the brainmask files generated by Freesurfer recon-all** in order to re-run recon-all with a custom brain mask.

### Examples

```
>>> from cmtklib.interfaces.freesurfer import copyBrainMaskToFreesurfer
>>> copy_mask_fs = copyBrainMaskToFreesurfer()
>>> copy_mask_fs.inputs.in_file = 'sub-01_desc-brain_mask.nii.gz'
>>> copy_mask_fs.inputs.subject_dir = '/path/to/output_dir/freesurfer/sub-01'
>>> copy_mask_fs.run()
```

`in_file` : a pathlike object or string representing an existing file `subject_dir` : a pathlike object or string representing an existing directory

`out_brainmask_file` : a pathlike object or string representing an existing file `out_brainmaskauto_file` : a pathlike object or string representing an existing file

## copyFileToFreesurfer

[Link to code](#)

Bases: `nipype.interfaces.io.IOBase`

Copy a file to an output specified.

---

**Note:** Not used.

---

`in_file` : a pathlike object or string representing an existing file `out_file` : a pathlike object or string representing a file

`out_file` : a pathlike object or string representing an existing file

## cmtklib.interfaces.fsl module

The FSL module provides Nipype interfaces for FSL functions missing in Nipype or modified.

## ApplymultipleWarp

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Apply a deformation field estimated by FSL `fnirt` to a list of images.

### Example

```
>>> from cmtklib.interfaces import fsl
>>> apply_warp = fsl.ApplymultipleWarp()
>>> apply_warp.inputs.in_files = ['/path/to/sub-01_atlas-L2018_desc-scale1_
↳dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale2_
↳dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale3_
↳dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale4_
↳dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale5_
↳dseg.nii.gz']
>>> apply_warp.inputs.field_file = '/path/to/fnirt_deformation.nii.gz'
>>> apply_warp.inputs.ref_file = '/path/to/sub-01_meanBOLD.nii.gz'
>>> apply_warp.run()
```

**field\_file** [a pathlike object or string representing an existing file] Deformation field.

**ref\_file** [a pathlike object or string representing an existing file] Reference image used for target space.

**in\_files** [a list of items which are a pathlike object or string representing an existing file] Files to be registered.

**interp** ['nn' or 'trilinear' or 'sinc' or 'spline'] Interpolation method. Maps to a command-line argument: `--interp=%s` (position: -2).

**out\_files** [a list of items which are a pathlike object or string representing a file] Warped files.

## ApplymultipleXfm

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Apply an XFM transform estimated by FSL `flirt` to a list of images.

### Example

```
>>> from cmtklib.interfaces import fsl
>>> apply_xfm = fsl.ApplymultipleXfm
>>> apply_xfm.inputs.in_files = ['/path/to/sub-01_atlas-L2018_desc-scale1_dseg.
↳nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale2_dseg.
↳nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale3_dseg.
↳nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale4_dseg.
↳nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale5_dseg.
↳nii.gz']
>>> apply_xfm.inputs.xfm_file = '/path/to/flirt_transform.xfm'
>>> apply_xfm.inputs.reference = '/path/to/sub-01_meanBOLD.nii.gz'
>>> apply_xfm.run()
```

**reference** [a pathlike object or string representing an existing file] Reference image used for target space.

**xfm\_file** [a pathlike object or string representing an existing file] Transform file.

**in\_files** [a list of items which are a pathlike object or string representing an existing file] Files to be registered.

**interp** ['nearestneighbour' or 'spline'] Interpolation used.

**out\_files** [a list of items which are a pathlike object or string representing a file] Transformed files.

### BinaryThreshold

[Link to code](#)

Bases: `nipy.interfaces.fsl.base.FSLCommand`

Wrapped executable: `fslmaths`.

Use `fslmaths` to apply a threshold to an image in a variety of ways.

### Examples

```
>>> from cmtklib.interfaces.fsl import BinaryThreshold
>>> thresh = BinaryThreshold()
>>> thresh.inputs.in_file = '/path/to/probseg.nii.gz'
>>> thresh.inputs.thresh = 0.5
>>> thresh.inputs.out_file = '/path/to/output_binseg.nii.gz'
>>> thresh.run()
```

**in\_file** [a pathlike object or string representing an existing file] Image to operate on. Maps to a command-line argument: `%s` (position: 2).

**out\_file** [a pathlike object or string representing a file] Image to write. Maps to a command-line argument: `%s` (position: 5).

**thresh** [a float] Threshold value. Maps to a command-line argument: `-thr %s` (position: 3).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**binarize** [a boolean] Maps to a command-line argument: `-bin` (position: 4).

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**output\_type** ['NIFTI' or 'NIFTI\_PAIR' or 'NIFTI\_GZ' or 'NIFTI\_PAIR\_GZ'] FSL output type.

**out\_file** [a pathlike object or string representing an existing file] Image written after calculations.

## CreateAcqpFile

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Create an acquisition Acqp file for FSL eddy.

---

**Note:** This value can be extracted from dMRI data acquired on Siemens scanner

---

### Examples

```
>>> from cmtklib.interfaces.fsl import CreateAcqpFile
>>> create_acqp = CreateAcqpFile()
>>> create_acqp.inputs.total_readout = 0.28
>>> create_acqp.run()
```

`total_readout` : a float

`acqp` : a pathlike object or string representing an existing file

## CreateIndexFile

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Create an index file for FSL eddy from a `mrtrix` diffusion gradient table.

### Examples

```
>>> from cmtklib.interfaces.fsl import CreateIndexFile
>>> create_index = CreateIndexFile()
>>> create_index.inputs.in_grad_mrtrix = 'grad.txt'
>>> create_index.run()
```

**in\_grad\_mrtrix** [a pathlike object or string representing an existing file] Input DWI gradient table in MRTrx format.

`index` : a pathlike object or string representing an existing file

## Eddy

[Link to code](#)

Bases: `nipype.interfaces.fsl.base.FSLCommand`

Wrapped executable: `eddy`.

Performs eddy current distortion correction using FSL `eddy`.

### Example

```
>>> from cmtklib.interfaces import fsl
>>> eddyc = fsl.Eddy(in_file='diffusion.nii',
>>>                  bvecs='diffusion.bvecs',
>>>                  bvals='diffusion.bvals',
>>>                  out_file="diffusion_eddyc.nii")
>>> eddyc.run()
```

**acqp** [a pathlike object or string representing an existing file] File containing acquisition parameters. Maps to a command-line argument: `--acqp=%s` (position: 3).

**bvals** [a pathlike object or string representing an existing file] File containing the b-values for all volumes in `-imain`. Maps to a command-line argument: `--bvals=%s` (position: 5).

**bvecs** [a pathlike object or string representing an existing file] File containing the b-vectors for all volumes in `-imain`. Maps to a command-line argument: `--bvecs=%s` (position: 4).

**in\_file** [a pathlike object or string representing an existing file] File containing all the images to estimate distortions for. Maps to a command-line argument: `--imain=%s` (position: 0).

**index** [a pathlike object or string representing an existing file] File containing indices for all volumes in `-imain` into `-acqp` and `-topup`. Maps to a command-line argument: `--index=%s` (position: 2).

**mask** [a pathlike object or string representing an existing file] Mask to indicate brain. Maps to a command-line argument: `--mask=%s` (position: 1).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**out\_file** [a pathlike object or string representing a file] Basename for output. Maps to a command-line argument: `--out=%s` (position: 6).

**output\_type** ['NIFTI' or 'NIFTI\_PAIR' or 'NIFTI\_GZ' or 'NIFTI\_PAIR\_GZ'] FSL output type.

**verbose** [a boolean] Display debugging messages. Maps to a command-line argument: `--verbose` (position: 7).

**bvecs\_rotated** [a pathlike object or string representing an existing file] Path/name of rotated DWI gradient bvecs file.

**eddy\_corrected** [a pathlike object or string representing an existing file] Path/name of 4D eddy corrected DWI file.



## EddyOpenMP

[Link to code](#)

Bases: `nipy.interfaces.fsl.base.FSLCommand`

Wrapped executable: `eddy_openmp`.

Performs eddy current distortion correction using FSL `eddy_openmp`.

### Example

```
>>> from cmtklib.interfaces import fsl
>>> eddyc = fsl.EddyOpenMP(in_file='diffusion.nii',
>>>                        bvecs='diffusion.bvecs',
>>>                        bvals='diffusion.bvals',
>>>                        out_file="diffusion_eddyc.nii")
>>> eddyc.run()
```

**acqp** [a pathlike object or string representing an existing file] File containing acquisition parameters. Maps to a command-line argument: `--acqp=%s` (position: 3).

**bvals** [a pathlike object or string representing an existing file] File containing the b-values for all volumes in `-imain`. Maps to a command-line argument: `--bvals=%s` (position: 5).

**bvecs** [a pathlike object or string representing an existing file] File containing the b-vectors for all volumes in `-imain`. Maps to a command-line argument: `--bvecs=%s` (position: 4).

**in\_file** [a pathlike object or string representing an existing file] File containing all the images to estimate distortions for. Maps to a command-line argument: `--imain=%s` (position: 0).

**index** [a pathlike object or string representing an existing file] File containing indices for all volumes in `-imain` into `-acqp` and `-topup`. Maps to a command-line argument: `--index=%s` (position: 2).

**mask** [a pathlike object or string representing an existing file] Mask to indicate brain. Maps to a command-line argument: `--mask=%s` (position: 1).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**out\_file** [a pathlike object or string representing a file] Basename for output. Maps to a command-line argument: `--out=%s` (position: 6).

**output\_type** ['NIFTI' or 'NIFTI\_PAIR' or 'NIFTI\_GZ' or 'NIFTI\_PAIR\_GZ'] FSL output type.

**verbose** [a boolean] Display debugging messages. Maps to a command-line argument: `--verbose` (position: 7).

**bvecs\_rotated** [a pathlike object or string representing an existing file] Path/name of rotated DWI gradient bvecs file.

**eddy\_corrected** [a pathlike object or string representing an existing file] Path/name of 4D eddy corrected DWI file.

## FSLCreateHD

[Link to code](#)

Bases: `nipy.interfaces.base.core.CommandLine`

Wrapped executable: `fslcreatehd`.

Calls the `fslcreatehd` command to create an image for space / dimension reference.

### Examples

```
>>> from cmtklib.interfaces.fsl import FSLCreateHD
>>> fsl_create = FSLCreateHD()
>>> fsl_create.inputs.im_size = [256, 256, 256, 1]
>>> fsl_create.inputs.vox_size = [1, 1, 1]
>>> fsl_create.inputs.tr = 0
>>> fsl_create.inputs.origin = [0, 0, 0]
>>> fsl_create.inputs.datatype = '16' # 16: float
>>> fsl_create.inputs.out_filename = '/path/to/generated_image.nii.gz'
>>> fsl_create.run()
```

**datatype** ['2' or '4' or '8' or '16' or '32' or '64'] Datatype values: 2=char, 4=short, 8=int, 16=float, 64=double. Maps to a command-line argument: %s (position: 5).

**im\_size** [a list of from 4 to 4 items which are an integer] Image size : xsize , ysize, zsize, tsize . Maps to a command-line argument: %s (position: 1).

**origin** [a list of from 3 to 3 items which are an integer] Origin coordinates : xorig, yorig, zorig. Maps to a command-line argument: %s (position: 4).

**out\_filename** [a pathlike object or string representing a file]  
the output temp reference image created.

Maps to a command-line argument: %s (position: 6).

**tr** [an integer] <tr>. Maps to a command-line argument: %s (position: 3).

**vox\_size** [a list of from 3 to 3 items which are an integer] Voxel size : xvoxsize, yvoxsize, zvoxsize. Maps to a command-line argument: %s (position: 2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**out\_file** [a pathlike object or string representing an existing file] Path/name of the output reference image created.

## MathsCommand

[Link to code](#)

Bases: `nipy.interfaces.fsl.base.FSLCommand`

Wrapped executable: `fslmaths`.

Calls the `fslmaths` command in a variety of ways.

### Examples

```
>>> from cmtklib.interfaces.fsl import MathsCommand
>>> fsl_maths = MathsCommand()
>>> fsl_maths.inputs.in_file = '/path/to/image_with_nans.nii.gz'
>>> fsl_maths.inputs.nan2zeros = True
>>> fsl_maths.inputs.out_file = '/path/to/image_with_no_nans.nii.gz'
>>> fsl_maths.run()
```

**in\_file** [a pathlike object or string representing an existing file] Image to operate on. Maps to a command-line argument: `%s` (position: 2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**internal\_datatype** ['float' or 'char' or 'int' or 'short' or 'double' or 'input'] Datatype to use for calculations (default is float). Maps to a command-line argument: `-dt %s` (position: 1).

**nan2zeros** [a boolean] Change NaNs to zeros before doing anything. Maps to a command-line argument: `-nan` (position: 3).

**out\_file** [a pathlike object or string representing a file] Image to write. Maps to a command-line argument: `%s` (position: -2).

**output\_datatype** ['float' or 'char' or 'int' or 'short' or 'double' or 'input'] Datatype to use for output (default uses input type). Maps to a command-line argument: `-odt %s` (position: -1).

**output\_type** ['NIFTI' or 'NIFTI\_PAIR' or 'NIFTI\_GZ' or 'NIFTI\_PAIR\_GZ'] FSL output type.

**out\_file** [a pathlike object or string representing an existing file] Image written after calculations.

## Orient

[Link to code](#)

Bases: `nipy.interfaces.fsl.base.FSLCommand`

Wrapped executable: `fslorient`.

Use `fslorient` to get/set orientation information from an image's header.

Advanced tool that reports or sets the orientation information in a file. Note that only in NIFTI files can the orientation be changed - Analyze files are always treated as “radiological” (meaning that they could be simply rotated into the same alignment as the MNI152 standard images - equivalent to the appropriate `sform` or `qform` in a NIFTI file having a negative determinant).

## Examples

```
>>> from cmtklib.interfaces.fsl import Orient
>>> fsl_orient = Orient()
>>> fsl_orient.inputs.in_file = 'input_image.nii.gz'
>>> fsl_orient.inputs.force_radiological = True
>>> fsl_orient.inputs.out_file = 'output_image.nii.gz'
>>> fsl_orient.run()
```

**in\_file** [a pathlike object or string representing an existing file] Input image. Maps to a command-line argument: %s (position: 2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**copy\_qform2sform** [a boolean] Sets the sform equal to the qform - code and matrix. Maps to a command-line argument: -copyqform2sform (position: 1). Mutually **exclusive** with inputs: get\_orient, get\_sform, get\_qform, set\_sform, set\_qform, get\_sformcode, get\_qformcode, set\_sformcode, set\_qformcode, copy\_sform2qform, copy\_qform2sform, delete\_orient, force\_radiological, force\_neurological, swap\_orient.

**copy\_sform2qform** [a boolean] Sets the qform equal to the sform - code and matrix. Maps to a command-line argument: -copysform2qform (position: 1). Mutually **exclusive** with inputs: get\_orient, get\_sform, get\_qform, set\_sform, set\_qform, get\_sformcode, get\_qformcode, set\_sformcode, set\_qformcode, copy\_sform2qform, copy\_qform2sform, delete\_orient, force\_radiological, force\_neurological, swap\_orient.

**delete\_orient** [a boolean] Removes orient info from header. Maps to a command-line argument: -deleteorient (position: 1). Mutually **exclusive** with inputs: get\_orient, get\_sform, get\_qform, set\_sform, set\_qform, get\_sformcode, get\_qformcode, set\_sformcode, set\_qformcode, copy\_sform2qform, copy\_qform2sform, delete\_orient, force\_radiological, force\_neurological, swap\_orient.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**force\_neurological** [a boolean] Makes FSL neurological header - not Analyze. Maps to a command-line argument: -forceneurological (position: 1). Mutually **exclusive** with inputs: get\_orient, get\_sform, get\_qform, set\_sform, set\_qform, get\_sformcode, get\_qformcode, set\_sformcode, set\_qformcode, copy\_sform2qform, copy\_qform2sform, delete\_orient, force\_radiological, force\_neurological, swap\_orient.

**force\_radiological** [a boolean] Makes FSL radiological header. Maps to a command-line argument: -forceradiological (position: 1). Mutually **exclusive** with inputs: get\_orient, get\_sform, get\_qform, set\_sform, set\_qform, get\_sformcode, get\_qformcode, set\_sformcode, set\_qformcode, copy\_sform2qform, copy\_qform2sform, delete\_orient, force\_radiological, force\_neurological, swap\_orient.

**get\_orient** [a boolean] Gets FSL left-right orientation. Maps to a command-line argument: -getorient (position: 1). Mutually **exclusive** with inputs: get\_orient, get\_sform, get\_qform, set\_sform, set\_qform, get\_sformcode, get\_qformcode, set\_sformcode, set\_qformcode, copy\_sform2qform, copy\_qform2sform, delete\_orient, force\_radiological, force\_neurological, swap\_orient.

**get\_qform** [a boolean] Gets the 16 elements of the qform matrix. Maps to a command-line argument: -getqform (position: 1). Mutually **exclusive** with inputs: get\_orient, get\_sform, get\_qform, set\_sform, set\_qform, get\_sformcode, get\_qformcode, set\_sformcode, set\_qformcode, copy\_sform2qform, copy\_qform2sform, delete\_orient, force\_radiological, force\_neurological, swap\_orient.

**get\_qformcode** [a boolean] Gets the qform integer code. Maps to a command-line argument: `-getqformcode` (position: 1). Mutually **exclusive** with inputs: `get_orient`, `get_sform`, `get_qform`, `set_sform`, `set_qform`, `get_sformcode`, `get_qformcode`, `set_sformcode`, `set_qformcode`, `copy_sform2qform`, `copy_qform2sform`, `delete_orient`, `force_radiological`, `force_neurological`, `swap_orient`.

**get\_sform** [a boolean] Gets the 16 elements of the sform matrix. Maps to a command-line argument: `-getsform` (position: 1). Mutually **exclusive** with inputs: `get_orient`, `get_sform`, `get_qform`, `set_sform`, `set_qform`, `get_sformcode`, `get_qformcode`, `set_sformcode`, `set_qformcode`, `copy_sform2qform`, `copy_qform2sform`, `delete_orient`, `force_radiological`, `force_neurological`, `swap_orient`.

**get\_sformcode** [a boolean] Gets the sform integer code. Maps to a command-line argument: `-getsformcode` (position: 1). Mutually **exclusive** with inputs: `get_orient`, `get_sform`, `get_qform`, `set_sform`, `set_qform`, `get_sformcode`, `get_qformcode`, `set_sformcode`, `set_qformcode`, `copy_sform2qform`, `copy_qform2sform`, `delete_orient`, `force_radiological`, `force_neurological`, `swap_orient`.

**output\_type** ['NIFTI' or 'NIFTI\_PAIR' or 'NIFTI\_GZ' or 'NIFTI\_PAIR\_GZ'] FSL output type.

**set\_qform** [a list of from 16 to 16 items which are a float] <m11 m12 ... m44> sets the 16 elements of the qform matrix. Maps to a command-line argument: `-setqform %f` (position: 1). Mutually **exclusive** with inputs: `get_orient`, `get_sform`, `get_qform`, `set_sform`, `set_qform`, `get_sformcode`, `get_qformcode`, `set_sformcode`, `set_qformcode`, `copy_sform2qform`, `copy_qform2sform`, `delete_orient`, `force_radiological`, `force_neurological`, `swap_orient`.

**set\_qformcode** [an integer] <code> sets qform integer code. Maps to a command-line argument: `-setqormcode %d` (position: 1). Mutually **exclusive** with inputs: `get_orient`, `get_sform`, `get_qform`, `set_sform`, `set_qform`, `get_sformcode`, `get_qformcode`, `set_sformcode`, `set_qformcode`, `copy_sform2qform`, `copy_qform2sform`, `delete_orient`, `force_radiological`, `force_neurological`, `swap_orient`.

**set\_sform** [a list of from 16 to 16 items which are a float] <m11 m12 ... m44> sets the 16 elements of the sform matrix. Maps to a command-line argument: `-setsform %f` (position: 1). Mutually **exclusive** with inputs: `get_orient`, `get_sform`, `get_qform`, `set_sform`, `set_qform`, `get_sformcode`, `get_qformcode`, `set_sformcode`, `set_qformcode`, `copy_sform2qform`, `copy_qform2sform`, `delete_orient`, `force_radiological`, `force_neurological`, `swap_orient`.

**set\_sformcode** [an integer] <code> sets sform integer code. Maps to a command-line argument: `-setformcode %d` (position: 1). Mutually **exclusive** with inputs: `get_orient`, `get_sform`, `get_qform`, `set_sform`, `set_qform`, `get_sformcode`, `get_qformcode`, `set_sformcode`, `set_qformcode`, `copy_sform2qform`, `copy_qform2sform`, `delete_orient`, `force_radiological`, `force_neurological`, `swap_orient`.

**swap\_orient** [a boolean] Swaps FSL radiological and FSL neurological. Maps to a command-line argument: `-swaporient` (position: 1). Mutually **exclusive** with inputs: `get_orient`, `get_sform`, `get_qform`, `set_sform`, `set_qform`, `get_sformcode`, `get_qformcode`, `set_sformcode`, `set_qformcode`, `copy_sform2qform`, `copy_qform2sform`, `delete_orient`, `force_radiological`, `force_neurological`, `swap_orient`.

**orient** [a string] FSL left-right orientation.

**out\_file** [a pathlike object or string representing an existing file] Image with modified orientation.

**qform** [a list of from 16 to 16 items which are a float] The 16 elements of the qform matrix.

**qformcode** [an integer] Qform integer code.

**sform** [a list of from 16 to 16 items which are a float] The 16 elements of the sform matrix.

**sformcode** [an integer] Sform integer code.

`Orient.aggregate_outputs(runtime=None, needed_outputs=None)`  
Collate expected outputs and apply output traits validation.

## `cmtklib.interfaces.misc` module

### `ConcatOutputsAsTuple`

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Concatenate 2 different output file as a Tuple of 2 files.

#### Examples

```
>>> from cmtklib.interfaces.misc import ConcatOutputsAsTuple
>>> concat_outputs = ConcatOutputsAsTuple()
>>> concat_outputs.inputs.input1 = 'output_interface1.nii.gz'
>>> concat_outputs.inputs.input2 = 'output_interface2.nii.gz'
>>> concat_outputs.run()
```

`input1` : a pathlike object or string representing an existing file  
`input2` : a pathlike object or string representing an existing file

`out_tuple` : a tuple of the form: (a pathlike object or string representing an existing file, a pathlike object or string representing an existing file)

### `ExtractHeaderVoxel2WorldMatrix`

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Write in a text file the voxel-to-world transform matrix from the header of a Nifti image.

#### Examples

```
>>> from cmtklib.interfaces.misc import ExtractHeaderVoxel2WorldMatrix
>>> extract_mat = ExtractHeaderVoxel2WorldMatrix()
>>> extract_mat.inputs.in_file = 'sub-01_T1w.nii.gz'
>>> extract_mat.run()
```

`in_file` [a pathlike object or string representing an existing file] Input image file.

`out_matrix` [a pathlike object or string representing an existing file] Output voxel to world affine transform file.

## ExtractImageVoxelSizes

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Returns a list of voxel sizes from an image.

### Examples

```
>>> from cmtklib.interfaces.misc import ExtractImageVoxelSizes
>>> extract_voxel_sizes = ExtractImageVoxelSizes()
>>> extract_voxel_sizes.inputs.in_file = 'sub-01_T1w.nii.gz'
>>> extract_voxel_sizes.run()
```

`in_file` : a pathlike object or string representing an existing file

`voxel_sizes` : a list of items which are any value

## Rename001

[Link to code](#)

Bases: `nipype.interfaces.utility.base.Rename`

Change the name of a file based on a mapped format string.

To use additional inputs that will be defined at run-time, the class constructor must be called with the format template, and the fields identified will become inputs to the interface. Additionally, you may set the `parse_string` input, which will be run over the input filename with a regular expressions search, and will fill in additional input fields from matched groups. Fields set with inputs have precedence over fields filled in with the regexp match.

It corresponds to the `nipype.interfaces.utility.base.Rename` interface that has been modified to force hard link during copy

### Examples

```
>>> from nipype.interfaces.utility import Rename
>>> rename1 = Rename()
>>> rename1.inputs.in_file = os.path.join(datadir, "zstat1.nii.gz") # datadir_
↳ is a directory with exemplary files, defined in conftest.py
>>> rename1.inputs.format_string = "Faces-Scenes.nii.gz"
>>> res = rename1.run()
>>> res.outputs.out_file
'Faces-Scenes.nii.gz'
```

```
>>> rename2 = Rename(format_string="%(subject_id)s_func_run%(run)02d")
>>> rename2.inputs.in_file = os.path.join(datadir, "functional.nii")
>>> rename2.inputs.keep_ext = True
>>> rename2.inputs.subject_id = "subj_201"
>>> rename2.inputs.run = 2
>>> res = rename2.run()
```

(continues on next page)

(continued from previous page)

```
>>> res.outputs.out_file
'subj_201_func_run02.nii'

>>> rename3 = Rename(format_string="%(%subject_id)s_%(seq)s_run%(run)02d.nii")
>>> rename3.inputs.in_file = os.path.join(datadir, "func_epi_1_1.nii")
>>> rename3.inputs.parse_string = r"func_(?P<seq>\w*)_*"
>>> rename3.inputs.subject_id = "subj_201"
>>> rename3.inputs.run = 2
>>> res = rename3.run()
>>> res.outputs.out_file
'subj_201_epi_run02.nii'
```

## References

Adapted from <https://github.com/nipy/nipype/blob/cd4c34d935a43812d1756482fdc4034844e485b8/nipype/interfaces/utility/base.py#L232-L272>

**format\_string** [a string] Python formatting string for output template.

**in\_file** [a pathlike object or string representing an existing file] File to rename.

**keep\_ext** [a boolean] Keep in\_file extension, replace non-extension component of name.

**parse\_string** [a string] Python regexp parse string to define replacement inputs.

**use\_fullpath** [a boolean] Use full path as input to regex parser. (Nipype **default** value: False)

**out\_file** [a pathlike object or string representing an existing file] Softlink to original file with new name.

## cmtklib.interfaces.mne module

The MNE module provides Nipype interfaces for MNE tools missing in Nipype or modified.

## CreateBEM

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Use MNE to create the BEM surfaces.

## Examples

```
>>> from cmtklib.interfaces.mne import CreateBEM
>>> create_bem = CreateBEM()
>>> create_bem.inputs.subject = 'sub-01'
>>> create_bem.inputs.bids_dir = '/path/to/bids_dataset'
>>> create_bem.inputs.output_query = {"src": {"suffix": "src", "extension": [
↪ "fif"]}}
>>> create_bem.inputs.derivative_list = ['cmp-v3.0.3']
>>> create_bem.run()
```



## References

- [https://mne.tools/stable/generated/mne.bem.make\\_watershed\\_bem.html](https://mne.tools/stable/generated/mne.bem.make_watershed_bem.html)
- [https://mne.tools/stable/generated/mne.make\\_bem\\_model.html](https://mne.tools/stable/generated/mne.make_bem_model.html)
- [https://mne.tools/stable/generated/mne.write\\_bem\\_solution.html](https://mne.tools/stable/generated/mne.write_bem_solution.html)

**bids\_dir** [a string] Base directory.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**output\_query** [a dictionary with keys which are any value and with values which are any value] BIDS-DataGrabber output\_query.

**subject** [a string] Subject.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**output\_query** [a dictionary with keys which are any value and with values which are any value] BIDS-DataGrabber output\_query.

## CreateCov

Link to code

Bases: `nipy.interfaces.base.core.BaseInterface`

Use MNE to create the noise covariance matrix.

## Examples

```
>>> from cmtdlib.interfaces.mne import CreateCov
>>> create_cov = CreateCov()
>>> create_cov.inputs.epochs_fif_fname = 'sub-01_epo.fif'
>>> create_cov.inputs.noise_cov_fname = 'sub-01_noisecov.fif'
>>> create_cov.run()
```

## References

- <https://mne.tools/stable/generated/mne.Covariance.html>

**epochs\_fif\_fname** [a string or `os.PathLike` object referring to an existing file] Eeg \* epochs in .set format.

**noise\_cov\_fname** [a string or `os.PathLike` object] Location and name to store noise covariance matrix in fif format.

**has\_run** [a boolean] If true, covariance matrix has been produced.

**noise\_cov\_fname** [a string or `os.PathLike` object referring to an existing file] Location and name to store noise covariance matrix in fif format.

## CreateFwd

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Use MNE to calculate the forward solution.

## Examples

```
>>> from cmtklib.interfaces.mne import CreateFwd
>>> create_fwd = CreateFwd()
>>> create_fwd.inputs.epochs_fif_fname = 'sub-01_epo.fif'
>>> create_fwd.inputs.fwd_fname = 'sub-01_fwd.fif'
>>> create_fwd.inputs.src = 'sub-01_src.fif'
>>> create_fwd.inputs.bem = 'sub-01_bem.fif'
>>> create_fwd.inputs.trans_fname = 'sub-01_trans.fif'
>>> create_fwd.run()
```

## References

- [https://mne.tools/stable/generated/mne.make\\_forward\\_solution.html](https://mne.tools/stable/generated/mne.make_forward_solution.html)

**bem** [a list of items which are any value] Boundary surfaces for MNE head model.

**epochs\_fif\_fname** [a string or `os.PathLike` object] Eeg \* epochs in .fif format, containing information about electrode montage.

**src** [a list of items which are any value] Source space created with MNE.

**fwd\_fname** [a string or `os.PathLike` object] Forward solution created with MNE.

**trans\_fname** [a string or `os.PathLike` object referring to an existing file] Trans.fif file containing co-registration information (electrodes x MRI).

**has\_run** [a boolean] If true, forward solution has been produced.

## CreateSrc

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Use MNE to set up bilateral hemisphere surface-based source space with subsampling and write source spaces to a file.

## Examples

```
>>> from cmtklib.interfaces.mne import CreateSrc
>>> create_src = CreateSrc()
>>> create_src.inputs.subject = 'sub-01'
>>> create_src.inputs.bids_dir = '/path/to/bids_dataset'
>>> create_src.inputs.output_query = {"src": {"suffix": "src", "extension": [
↪ "fif"]}}
>>> create_src.inputs.derivative_list = ['cmp-v3.0.3']
>>> create_src.run()
```

## References

- [https://mne.tools/stable/generated/mne.setup\\_source\\_space.html](https://mne.tools/stable/generated/mne.setup_source_space.html)
- [https://mne.tools/stable/generated/mne.write\\_source\\_spaces.html](https://mne.tools/stable/generated/mne.write_source_spaces.html)

**bids\_dir** [a string] Base directory.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**output\_query** [a dictionary with keys which are any value and with values which are any value] BIDS-DataGrabber output\_query.

**subject** [a string] Subject.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**output\_query** [a dictionary with keys which are any value and with values which are any value] BIDS-DataGrabber output\_query.

## EEGLAB2fif

Link to code

Bases: `nipy.interfaces.base.core.BaseInterface`

Use MNE to convert EEG data from EEGLab to MNE format.

## Examples

```
>>> from cmtklib.interfaces.mne import EEGLAB2fif
>>> eeglab2fif = EEGLAB2fif()
>>> eeglab2fif.inputs.eeg_ts_file = ['sub-01_task-faces_desc-preproc_eeg.set']
>>> eeglab2fif.inputs.behav_file = ['sub-01_task-faces_events.tsv']
>>> eeglab2fif.inputs.epochs_fif_fname = 'sub-01_epo.fif'
>>> eeglab2fif.inputs.electrode_positions_file = 'sub-01_eeg.xyz'
>>> eeglab2fif.inputs.EEG_params = {"expe_name": "faces",
                                   EEG_event_IDs": {"SCRAMBLED": 0, "FACES": 1},
                                   "start_t": -0.2, "end_t": 0.6}
>>> eeglab2fif.inputs.output_query = {"src": {"suffix": "src", "extension": [
↪ "fif"]}}
>>> eeglab2fif.inputs.derivative_list = ['cmp-v3.0.3']
>>> eeglab2fif.run()
```

## References

- [https://mne.tools/stable/generated/mne.read\\_epochs\\_eeglab.html](https://mne.tools/stable/generated/mne.read_epochs_eeglab.html)
- [https://mne.tools/stable/generated/mne.channels.make\\_dig\\_montage.html](https://mne.tools/stable/generated/mne.channels.make_dig_montage.html)
- [https://mne.tools/stable/generated/mne.Epochs.html?highlight=set\\_montage#mne.Epochs.set\\_montage](https://mne.tools/stable/generated/mne.Epochs.html?highlight=set_montage#mne.Epochs.set_montage)
- [https://mne.tools/stable/generated/mne.Epochs.html?highlight=set\\_montage#mne.Epochs.save](https://mne.tools/stable/generated/mne.Epochs.html?highlight=set_montage#mne.Epochs.save)

**behav\_file** [a list of items which are any value] Epochs metadata in \_behav.txt.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**eeg\_ts\_file** [a list of items which are any value] Eeg \* epochs in .set format.

**epochs\_fif\_fname** [a string or os.PathLike object] Eeg \* epochs in .fif format.

**output\_query** [a dictionary with keys which are any value and with values which are any value] BIDS-DataGrabber output\_query.

**EEG\_params** [a dictionary with keys which are any value and with values which are any value] Dictionary defining EEG parameters.

**electrode\_positions\_file** [a string or os.PathLike object referring to an existing file] Positions of EEG electrodes in a txt file.

**derivative\_list** [a list of items which are any value] List of derivatives to add to the datagrabber.

**epochs\_fif\_fname** [a string or os.PathLike object referring to an existing file] Eeg \* epochs in .fif format.

**output\_query** [a dictionary with keys which are any value and with values which are any value] BIDS-DataGrabber output\_query.

## MNEInverseSolution

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Use MNE to convert EEG data from EEGLab to MNE format.

## Examples

```
>>> from cmcklib.interfaces.mne import MNEInverseSolution
>>> inv_sol = MNEInverseSolution()
>>> inv_sol.inputs.subject = 'sub-01'
>>> inv_sol.inputs.bids_dir = '/path/to/bids_dataset'
>>> inv_sol.inputs.epochs_fif_fname = 'sub-01_epo.fif'
>>> inv_sol.inputs.src_file = ['sub-01_src.fif']
>>> inv_sol.inputs.bem_file = ['sub-01_bem.fif']
>>> inv_sol.inputs.cov_has_run = 'True'
>>> inv_sol.inputs.noise_cov_fname = 'sub-01_noisecov.fif'
>>> inv_sol.inputs.fwd_has_run = 'True'
>>> inv_sol.inputs.fwd_fname = 'sub-01_fwd.fif'
>>> inv_sol.inputs.inv_fname = 'sub-01_inv.fif'
>>> inv_sol.inputs.parcellation = 'lausanne2018.scale1'
```

(continues on next page)

(continued from previous page)

```
>>> inv_sol.inputs.roi_ts_file = 'sub-01_atlas-L2018_res-scale1_desc-epo_
↳timeseries.npy'
>>> inv_sol.run()
```

## References

- [https://mne.tools/stable/generated/mne.read\\_forward\\_solution.html](https://mne.tools/stable/generated/mne.read_forward_solution.html)
- [https://mne.tools/stable/generated/mne.minimum\\_norm.make\\_inverse\\_operator.html](https://mne.tools/stable/generated/mne.minimum_norm.make_inverse_operator.html)
- [https://mne.tools/stable/generated/mne.minimum\\_norm.apply\\_inverse\\_epochs.html](https://mne.tools/stable/generated/mne.minimum_norm.apply_inverse_epochs.html)
- [https://mne.tools/stable/generated/mne.read\\_labels\\_from\\_annot.html](https://mne.tools/stable/generated/mne.read_labels_from_annot.html)
- [https://mne.tools/stable/generated/mne.extract\\_label\\_time\\_course.html](https://mne.tools/stable/generated/mne.extract_label_time_course.html)

**bem\_file** [a list of items which are any value] Surfaces for head model.

**bids\_dir** [a string] Base directory.

**cov\_has\_run** [a boolean] Indicate if covariance matrix has been produced.

**epochs\_fif\_fname** [a string or os.PathLike object referring to an existing file] Eeg \* epochs in .fif format.

**fwd\_fname** [a string or os.PathLike object] Forward solution in fif format.

**inv\_fname** [a string or os.PathLike object] Inverse operator in fif format.

**noise\_cov\_fname** [a string or os.PathLike object referring to an existing file] Noise covariance matrix in fif format.

**src\_file** [a list of items which are any value] Source space created with MNE.

**subject** [a string] Subject.

**fwd\_has\_run** [a boolean] Indicate if forward solution has been produced.

**parcellation** [a string] Parcellation scheme.

**roi\_ts\_file** [a string or os.PathLike object] Rois \* time series in .npy format.

**fwd\_fname** [a string or os.PathLike object referring to an existing file] Forward solution in fif format.

**roi\_ts\_file** [a string or os.PathLike object referring to an existing file] Rois \* time series in .npy format.

## cmtklib.interfaces.mrtrix3 module

The MRTrix3 module provides Nipype interfaces for MRTrix3 tools missing in Nipype or modified.

## ApplymultipleMRConvert

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Apply `mrconvert` tool to multiple images.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> mrconvert = mrt.ApplymultipleMRConvert()
>>> mrconvert.inputs.in_files = ['dwi_FA.mif', 'dwi_MD.mif']
>>> mrconvert.inputs.extension = 'nii'
>>> mrconvert.run()
```

**extension** [`'mif'` or `'nii'` or `'float'` or `'char'` or `'short'` or `'int'` or `'long'` or `'double'`] “i.e. Bfloat”. Can be `“char”`, `“short”`, `“int”`, `“long”`, `“float”` or `“double”`. (Nipype **default** value: `mif`)

**in\_files** [a list of items which are a pathlike object or string representing an existing file] Files to be registered.

**output\_datatype** [`'float32'` or `'float32le'` or `'float32be'` or `'float64'` or `'float64le'` or `'float64be'` or `'int64'` or `'uint64'` or `'int64le'` or `'uint64le'` or `'int64be'` or `'uint64be'` or `'int32'` or `'uint32'` or `'int32le'` or `'uint32le'` or `'int32be'` or `'uint32be'` or `'int16'` or `'uint16'` or `'int16le'` or `'uint16le'` or `'int16be'` or `'uint16be'` or `'cfloat32'` or `'cfloat32le'` or `'cfloat32be'` or `'cfloat64'` or `'cfloat64le'` or `'cfloat64be'` or `'int8'` or `'uint8'` or `'bit'`] Specify output image data type. Valid choices are: `float32`, `float32le`, `float32be`, `float64`, `float64le`, `float64be`, `int64`, `uint64`, `int64le`, `int64be`, `uint64le`, `uint64be`, `int32`, `uint32`, `int32le`, `int32be`, `uint32le`, `uint32be`, `int16`, `uint16`, `int16le`, `uint16le`, `int16be`, `uint16be`, `cfloat32`, `cfloat32le`, `cfloat32be`, `cfloat64`, `cfloat64le`, `cfloat64be`, `int8`, `uint8`, `bit`. Maps to a command-line argument: `-datatype %s` (position: 2).

**stride** [a list of from 3 to 4 items which are an integer] Three to four comma-separated numbers specifying the strides of the output data in memory. The actual strides produced will depend on whether the output image format can support it.. Maps to a command-line argument: `-stride %s` (position: 3).

**converted\_files** [a list of items which are a pathlike object or string representing a file] Output files.

## ApplymultipleMRCrop

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Apply `MRCrop` to a list of images.

### Example

```
>>> from cmtklib.interfaces.mrtrix3 import ApplymultipleMRCrop
>>> multi_crop = ApplymultipleMRCrop()
>>> multi_crop.inputs.in_files = ['/sub-01_atlas-L2018_desc-scale1_dseg.nii.gz
↳ ',
>>>                                     'sub-01_atlas-L2018_desc-scale2_dseg.nii.gz',
>>>                                     'sub-01_atlas-L2018_desc-scale3_dseg.nii.gz',
>>>                                     'sub-01_atlas-L2018_desc-scale4_dseg.nii.gz',
>>>                                     'sub-01_atlas-L2018_desc-scale5_dseg.nii.gz']
>>> multi_crop.inputs.template_image = 'sub-01_T1w.nii.gz'
>>> multi_crop.run()
```

See also:

`cmtklib.interfaces.mrtrix3.MRCrop`

**template\_image** [a pathlike object or string representing an existing file] Template image.

**in\_files** [a list of items which are a pathlike object or string representing an existing file] Files to be cropped.

**out\_files** [a list of items which are a pathlike object or string representing a file] Cropped files.

### ApplymultipleMRTransforms

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Apply MRTransform to a list of images.

### Example

```
>>> from cmtklib.interfaces.mrtrix3 import ApplymultipleMRTransforms
>>> multi_transform = ApplymultipleMRTransforms()
>>> multi_transform.inputs.in_files = ['/sub-01_atlas-L2018_desc-scale1_dseg.
↳ nii.gz',
>>>                                     'sub-01_atlas-L2018_desc-scale2_dseg.
↳ nii.gz',
>>>                                     'sub-01_atlas-L2018_desc-scale3_dseg.
↳ nii.gz',
>>>                                     'sub-01_atlas-L2018_desc-scale4_dseg.
↳ nii.gz',
>>>                                     'sub-01_atlas-L2018_desc-scale5_dseg.
↳ nii.gz']
>>> multi_transform.inputs.template_image = 'sub-01_T1w.nii.gz'
>>> multi_transform.run()
```

See also:

`cmtklib.interfaces.mrtrix3.MRTransform`

**template\_image** [a pathlike object or string representing an existing file] Template image.

**in\_files** [a list of items which are a pathlike object or string representing an existing file] Files to be transformed.

**out\_files** [a list of items which are a pathlike object or string representing a file] Transformed files.

## ConstrainedSphericalDeconvolution

[Link to code](#)

Bases: `nipy.interfaces.base.core.CommandLine`

Wrapped executable: `dwi2fod`.

Perform non-negativity constrained spherical deconvolution using `dwi2fod`.

Note that this program makes use of implied symmetries in the diffusion profile. First, the fact the signal attenuation profile is real implies that it has conjugate symmetry, i.e.  $Y(l, -m) = Y(l, m)^*$  (where  $*$  denotes the complex conjugate). Second, the diffusion profile should be antipodally symmetric (i.e.  $S(\mathbf{x}) = S(-\mathbf{x})$ ), implying that all odd  $l$  components should be zero. Therefore, this program only computes the even elements. Note that the spherical harmonics equations used here differ slightly from those conventionally used, in that the  $(-1)^m$  factor has been omitted. This should be taken into account in all subsequent calculations. Each volume in the output image corresponds to a different spherical harmonic component, according to the following convention:

- [0]  $Y(0,0)$
- [1]  $\text{Im} \{Y(2,2)\}$
- [2]  $\text{Im} \{Y(2,1)\}$
- [3]  $Y(2,0)$
- [4]  $\text{Re} \{Y(2,1)\}$
- [5]  $\text{Re} \{Y(2,2)\}$
- [6]  $\text{Im} \{Y(4,4)\}$
- [7]  $\text{Im} \{Y(4,3)\}$

## Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> csdeconv = mrt.ConstrainedSphericalDeconvolution()
>>> csdeconv.inputs.in_file = 'dwi.mif'
>>> csdeconv.inputs.encoding_file = 'encoding.txt'
>>> csdeconv.run()
```

**algorithm** [`'csd'`] Use CSD algorithm for FOD estimation. Maps to a command-line argument: `%s` (position: -4).

**in\_file** [a pathlike object or string representing an existing file] Diffusion-weighted image. Maps to a command-line argument: `%s` (position: -3).

**response\_file** [a pathlike object or string representing an existing file] The diffusion-weighted signal response function for a single fibre population (see `EstimateResponse`). Maps to a command-line argument: `%s` (position: -2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.



- directions\_file** [a pathlike object or string representing an existing file] A text file containing the [ el az ] pairs for the directions: Specify the directions over which to apply the non-negativity constraint (by default, the built-in 300 direction set is used). Maps to a command-line argument: `-directions %s` (position: -2).
- encoding\_file** [a pathlike object or string representing an existing file] Gradient encoding, supplied as a 4xN text file with each line is in the format [ X Y Z b ], where [ X Y Z ] describe the direction of the applied gradient, and b gives the b-value in units (1000 s/mm<sup>2</sup>). See FSL2MRTrix. Maps to a command-line argument: `-grad %s` (position: 1).
- environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})
- filter\_file** [a pathlike object or string representing an existing file] A text file containing the filtering coefficients for each even harmonic order.the linear frequency filtering parameters used for the initial linear spherical deconvolution step (default = [ 1 1 1 0 0 ]). Maps to a command-line argument: `-filter %s` (position: -2).
- iterations** [an integer] The maximum number of iterations to perform for each voxel (default = 50). Maps to a command-line argument: `-niter %s`.
- lambda\_value** [a float] The regularisation parameter lambda that controls the strength of the constraint (default = 1.0). Maps to a command-line argument: `-norm_lambda %s`.
- mask\_image** [a pathlike object or string representing an existing file] Only perform computation within the specified binary brain mask image. Maps to a command-line argument: `-mask %s` (position: 2).
- maximum\_harmonic\_order** [an integer] Set the maximum harmonic order for the output series. By default, the program will use the highest possible lmax given the number of diffusion-weighted images. Maps to a command-line argument: `-lmax %s`.
- out\_filename** [a pathlike object or string representing a file] Output filename. Maps to a command-line argument: `%s` (position: -1).
- threshold\_value** [a float] The threshold below which the amplitude of the FOD is assumed to be zero, expressed as a fraction of the mean value of the initial FOD (default = 0.1). Maps to a command-line argument: `-threshold %s`.
- spherical\_harmonics\_image** [a pathlike object or string representing an existing file] Spherical harmonics image.

## DWI2Tensor

[Link to code](#)

Bases: `nipype.interfaces.base.core.CommandLine`

Wrapped executable: `dwi2tensor`.

Converts diffusion-weighted images to tensor images using `dwi2tensor`.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> dwi2tensor = mrt.DWI2Tensor()
>>> dwi2tensor.inputs.in_file = 'dwi.mif'
>>> dwi2tensor.inputs.encoding_file = 'encoding.txt'
>>> dwi2tensor.run()
```

**in\_file** [a list of items which are any value] Diffusion-weighted images. Maps to a command-line argument: %s (position: -2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**debug** [a boolean] Display debugging messages. Maps to a command-line argument: -debug (position: 1).

**encoding\_file** [a pathlike object or string representing a file] Encoding file, , supplied as a 4xN text file with each line is in the format [ X Y Z b ], where [ X Y Z ] describe the direction of the applied gradient, and b gives the b-value in units (1000 s/mm<sup>2</sup>). See FSL2MRTrix(). Maps to a command-line argument: -grad %s (position: 2).

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**ignore\_slice\_by\_volume** [a list of from 2 to 2 items which are an integer] Requires two values (i.e. [34 1] for [Slice Volume] Ignores the image slices specified when computing the tensor. Slice here means the z coordinate of the slice to be ignored. Maps to a command-line argument: -ignoreslices %s (position: 2).

**ignore\_volumes** [a list of at least 1 items which are an integer] Requires two values (i.e. [2 5 6] for [Volumes] Ignores the image volumes specified when computing the tensor. Maps to a command-line argument: -ignorevolumes %s (position: 2).

**in\_mask\_file** [a pathlike object or string representing an existing file] Input DWI mask. Maps to a command-line argument: -mask %s (position: -3).

**out\_filename** [a pathlike object or string representing a file] Output tensor filename. Maps to a command-line argument: %s (position: -1).

**quiet** [a boolean] Do not display information messages or progress status. Maps to a command-line argument: -quiet (position: 1).

**tensor** [a pathlike object or string representing an existing file] Path/name of output diffusion tensor image.

### DWIBiasCorrect

[Link to code](#)

Bases: nipype.interfaces.base.core.CommandLine

Wrapped executable: dwibiascorrect.

Correct for bias field in diffusion MRI data using the dwibiascorrect tool.

## Example

```
>>> from cmtklib.interfaces.mrtrix3 import DWIBiasCorrect
>>> dwi_biascorr = DWIBiasCorrect()
>>> dwi_biascorr.inputs.in_file = 'sub-01_dwi.nii.gz'
>>> dwi_biascorr.inputs.use_ants = True
>>> dwi_biascorr.run()
```

**in\_file** [a pathlike object or string representing an existing file] The input image series to be corrected. Maps to a command-line argument: %s (position: -2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**debug** [a boolean] Display debugging messages. Maps to a command-line argument: -debug (position: 5).

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**force\_writing** [a boolean] Force file overwriting. Maps to a command-line argument: -force (position: 4).

**mask** [a pathlike object or string representing a file] Manually provide a mask image for bias field estimation (optional). Maps to a command-line argument: -mask %s (position: 2).

**out\_bias** [a pathlike object or string representing a file] Output the estimated bias field. Maps to a command-line argument: -bias %s (position: 3).

**out\_file** [a pathlike object or string representing a file] The output corrected image series. Maps to a command-line argument: %s (position: -1).

**use\_ants** [a boolean] Use ANTS N4 to estimate the inhomogeneity field. Maps to a command-line argument: ants (position: 1). Mutually **exclusive** with inputs: use\_ants, use\_fsl.

**use\_fsl** [a boolean] Use FSL FAST to estimate the inhomogeneity field. Maps to a command-line argument: fsl (position: 1). Mutually **exclusive** with inputs: use\_ants, use\_fsl.

**out\_bias** [a pathlike object or string representing an existing file] Output estimated bias field.

**out\_file** [a pathlike object or string representing an existing file] Output corrected DWI image.

## DWIDenoise

[Link to code](#)

Bases: nipype.interfaces.base.core.CommandLine

Wrapped executable: dwidenoise.

Denoise diffusion MRI data using the dwidenoise tool.

### Example

```
>>> from cmtklib.interfaces.mrtrix3 import DWIDenoise
>>> dwi_denoise = DWIDenoise()
>>> dwi_denoise.inputs.in_file = 'sub-01_dwi.nii.gz'
>>> dwi_denoise.inputs.out_file = 'sub-01_desc-denoised_dwi.nii.gz'
>>> dwi_denoise.inputs.out_noisemap = 'sub-01_mod-dwi_noisemap.nii.gz'
>>> dwi_denoise.run()
```

**in\_file** [a pathlike object or string representing an existing file] Input diffusion-weighted image filename. Maps to a command-line argument: %s (position: -2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**debug** [a boolean] Display debugging messages. Maps to a command-line argument: -debug (position: 5).

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**extent\_window** [a list of from 3 to 3 items which are a float] Three comma-separated numbers giving the window size of the denoising filter. Maps to a command-line argument: -extent %s (position: 2).

**force\_writing** [a boolean] Force file overwriting. Maps to a command-line argument: -force (position: 4).

**mask** [a pathlike object or string representing a file] Only perform computation within the specified binary brain mask image. (optional). Maps to a command-line argument: -mask %s (position: 1).

**out\_file** [a pathlike object or string representing a file] Output denoised DWI image filename. Maps to a command-line argument: %s (position: -1).

**out\_noisemap** [a pathlike object or string representing a file] Output noise map filename. Maps to a command-line argument: -noise %s (position: 3).

**out\_file** [a pathlike object or string representing an existing file] Output denoised DWI image.

**out\_noisemap** [a pathlike object or string representing an existing file] Output noise map (if generated).

### Erode

[Link to code](#)

Bases: nipype.interfaces.base.core.CommandLine

Wrapped executable: `maskfilter`.

Erode (or dilates) a mask (i.e. binary) image using the `maskfilter` tool.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> erode = mrt.Erode()
>>> erode.inputs.in_file = 'mask.mif'
>>> erode.run()
```

**in\_file** [a pathlike object or string representing an existing file] Input mask image to be eroded. Maps to a command-line argument: %s (position: -3).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**debug** [a boolean] Display debugging messages. Maps to a command-line argument: -debug (position: 1).

**dilate** [a boolean] Perform dilation rather than erosion. Maps to a command-line argument: -dilate (position: 1).

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**filtertype** ['clean' or 'connect' or 'dilate' or 'erode' or 'median'] The type of filter to be applied (clean, connect, dilate, erode, median). Maps to a command-line argument: %s (position: -2).

**number\_of\_passes** [an integer] The number of passes (default: 1). Maps to a command-line argument: -npass %s.

**out\_filename** [a pathlike object or string representing a file] Output image filename. Maps to a command-line argument: %s (position: -1).

**quiet** [a boolean] Do not display information messages or progress status. Maps to a command-line argument: -quiet (position: 1).

**out\_file** [a pathlike object or string representing an existing file] The output image.

### EstimateResponseForSH

[Link to code](#)

Bases: nipype.interfaces.base.core.CommandLine

Wrapped executable: dwi2response.

Estimates the fibre response function for use in spherical deconvolution using dwi2response.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> estresp = mrt.EstimateResponseForSH()
>>> estresp.inputs.in_file = 'dwi.mif'
>>> estresp.inputs.mask_image = 'dwi_WMPProb.mif'
>>> estresp.inputs.encoding_file = 'encoding.txt'
>>> estresp.run()
```

**encoding\_file** [a pathlike object or string representing an existing file] Gradient encoding, supplied as a 4xN text file with each line is in the format [ X Y Z b ], where [ X Y Z ] describe the direction of the applied gradient, and b gives the b-value in units (1000 s/mm<sup>2</sup>). See FSL2MRTrix. Maps to a command-line argument: -grad %s (position: -2).

**in\_file** [a pathlike object or string representing an existing file] Diffusion-weighted images. Maps to a command-line argument: %s (position: 2).

**mask\_image** [a pathlike object or string representing an existing file] Only perform computation within the specified binary brain mask image. Maps to a command-line argument: -mask %s (position: -1).

**algorithm** ['dhollander' or 'fa' or 'manual' or 'msmt\_5tt' or 'tax' or 'tournier'] Select the algorithm to be used to derive the response function; additional details and options become available once an algorithm is nominated. Options are: dhollander, fa, manual, msmt\_5tt, tax, tournier. Maps to a command-line argument: %s (position: 1).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**debug** [a boolean] Display debugging messages. Maps to a command-line argument: -debug.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**maximum\_harmonic\_order** [an integer] Set the maximum harmonic order for the output series. By default, the program will use the highest possible lmax given the number of diffusion-weighted images. Maps to a command-line argument: -lmax %s (position: -3).

**out\_filename** [a pathlike object or string representing a file] Output filename. Maps to a command-line argument: %s (position: 3).

**quiet** [a boolean] Do not display information messages or progress status. Maps to a command-line argument: -quiet.

**response** [a pathlike object or string representing an existing file] Spherical harmonics image.

## ExtractFSLGrad

[Link to code](#)

Bases: nipype.interfaces.base.core.CommandLine

Wrapped executable: mrinfo.

Use mrinfo to extract FSL gradient.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> fsl_grad = mrt.ExtractFSLGrad()
>>> fsl_grad.inputs.in_file = 'sub-01_dwi.mif'
>>> fsl_grad.inputs.out_grad_fsl = ['sub-01_dwi.bvecs', 'sub-01_dwi.bvals']
>>> fsl_grad.run()
```

**in\_file** [a pathlike object or string representing an existing file] Input images to be read. Maps to a command-line argument: %s (position: -2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**out\_grad\_fsl** [a tuple of the form: (a pathlike object or string representing a file, a pathlike object or string representing a file)] Export the DWI gradient table to files in FSL (bvecs / bvals) format. Maps to a command-line argument: -export\_grad\_fsl %s %s.

**out\_grad\_fsl** [a tuple of the form: (a pathlike object or string representing an existing file, a pathlike object or string representing an existing file)] Outputs [bvecs, bvals] DW gradient scheme (FSL format) if set.

## ExtractMRTrixGrad

[Link to code](#)

Bases: `nipype.interfaces.base.core.CommandLine`

Wrapped executable: `mrinfo`.

Use `mrinfo` to extract mrtrix gradient text file.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> mrtrix_grad = mrt.ExtractMRTrixGrad()
>>> mrtrix_grad.inputs.in_file = 'sub-01_dwi.mif'
>>> mrtrix_grad.inputs.out_grad_mrtrix = 'sub-01_gradient.txt'
>>> mrtrix_grad.run()
```

**in\_file** [a pathlike object or string representing an existing file] Input images to be read. Maps to a command-line argument: `%s` (position: -2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**out\_grad\_mrtrix** [a pathlike object or string representing a file] Export the DWI gradient table to file in MRtrix format. Maps to a command-line argument: `-export_grad_mrtrix %s`.

**out\_grad\_mrtrix** [a pathlike object or string representing a file] Output MRtrix gradient text file if set.

## FilterTractogram

[Link to code](#)

Bases: *MRTrix3Base*

Wrapped executable: `tcksift`.

Spherical-deconvolution informed filtering of tractograms using `tcksift` [Smith2013SIFT].

### References

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as cmp_mrt
>>> mrtrix_sift = cmp_mrt.FilterTractogram()
>>> mrtrix_sift.inputs.in_tracks = 'tractogram.tck'
>>> mrtrix_sift.inputs.in_fod = 'spherical_harmonics_image.nii.gz'
>>> mrtrix_sift.inputs.out_file = 'sift_tractogram.tck'
>>> mrtrix_sift.run()
```

**in\_fod** [a pathlike object or string representing an existing file] Input image containing the spherical harmonics of the fibre orientation distributions. Maps to a command-line argument: %s (position: -2).

**in\_tracks** [a pathlike object or string representing an existing file] Input track file in TCK format. Maps to a command-line argument: %s (position: -3).

**act\_file** [a pathlike object or string representing an existing file] ACT 5TT image file. Maps to a command-line argument: -act %s (position: -4).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**out\_file** [a pathlike object or string representing a file] Output filtered tractogram. Maps to a command-line argument: %s (position: -1).

**out\_tracks** [a pathlike object or string representing an existing file] Output filtered tractogram.

## Generate5tt

[Link to code](#)

Bases: nipype.interfaces.base.core.CommandLine

Wrapped executable: 5ttgen.

Generate a 5TT image suitable for ACT using the selected algorithm using 5ttgen.

## Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> gen5tt = mrt.Generate5tt()
>>> gen5tt.inputs.in_file = 'T1.nii.gz'
>>> gen5tt.inputs.algorithm = 'fsl'
>>> gen5tt.inputs.out_file = '5tt.mif'
>>> gen5tt.cmdline
'5ttgen fsl T1.nii.gz 5tt.mif'
>>> gen5tt.run()
```

**algorithm** ['fsl' or 'gif' or 'freesurfer' or 'hsvs'] Tissue segmentation algorithm. Maps to a command-line argument: %s (position: -3).

**in\_file** [a pathlike object or string representing an existing file] Input image. Maps to a command-line argument: -nocrop -sgm\_amyg\_hipp %s (position: -2).

**out\_file** [a pathlike object or string representing a file] Output image. Maps to a command-line argument: %s (position: -1).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**out\_file** [a pathlike object or string representing an existing file] Output image.



## GenerateGMWMInterface

[Link to code](#)

Bases: `nipype.interfaces.base.core.CommandLine`

Wrapped executable: `5tt2gmwmi`.

Generate a grey matter-white matter interface mask from the 5TT image using `5tt2gmwmi`.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as cmp_mrt
>>> genWMGMI = cmp_mrt.Generate5tt()
>>> genWMGMI.inputs.in_file = '5tt.mif'
>>> genWMGMI.inputs.out_file = 'gmwmi.mif'
>>> genWMGMI.run()
```

**in\_file** [a pathlike object or string representing an existing file] Input 5TT image. Maps to a command-line argument: `%s` (position: -2).

**out\_file** [a pathlike object or string representing a file] Output GW/WM interface image. Maps to a command-line argument: `%s` (position: -1).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**out\_file** [a pathlike object or string representing an existing file] Output image.

## MRConvert

[Link to code](#)

Bases: `nipype.interfaces.base.core.CommandLine`

Wrapped executable: `mrconvert`.

Perform conversion with `mrconvert` between different file types and optionally extract a subset of the input image.

If used correctly, this program can be a very useful workhorse. In addition to converting images between different formats, it can be used to extract specific studies from a data set, extract a specific region of interest, flip the images, or to scale the intensity of the images.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> mrconvert = mrt.MRConvert()
>>> mrconvert.inputs.in_file = 'dwi_FA.mif'
>>> mrconvert.inputs.out_filename = 'dwi_FA.nii'
>>> mrconvert.run()
```

- in\_dir** [a pathlike object or string representing an existing directory] Directory containing DICOM files. Maps to a command-line argument: %s (position: -2). Mutually **exclusive** with inputs: **in\_file**, **in\_dir**.
- in\_file** [a pathlike object or string representing an existing file] Voxel-order data filename. Maps to a command-line argument: %s (position: -2). Mutually **exclusive** with inputs: **in\_file**, **in\_dir**.
- args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.
- environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})
- extension** ['mif' or 'nii' or 'float' or 'char' or 'short' or 'int' or 'long' or 'double'] "i.e. Bfloat". Can be "char", "short", "int", "long", "float" or "double". (Nipype **default** value: mif)
- extract\_at\_axis** [1 or 2 or 3] Extract data only at the coordinates specified. This option specifies the Axis. Must be used in conjunction with **extract\_at\_coordinate**. . Maps to a command-line argument: -coord %s (position: 1).
- extract\_at\_coordinate** [a list of from 1 to 3 items which are an integer] Extract data only at the coordinates specified. This option specifies the coordinates. Must be used in conjunction with **extract\_at\_axis**. Three comma-separated numbers giving the size of each voxel in mm. Maps to a command-line argument: %s (position: 2).
- force\_writing** [a boolean] Force file overwriting. Maps to a command-line argument: -force.
- grad** [a pathlike object or string representing an existing file] Gradient encoding, supplied as a 4xN text file with each line is in the format [ X Y Z b ], where [ X Y Z ] describe the direction of the applied gradient, and b gives the b-value in units (1000 s/mm^2). See FSL2MRTrix. Maps to a command-line argument: -grad %s (position: 9).
- grad\_fsl** [a tuple of the form: (a pathlike object or string representing an existing file, a pathlike object or string representing an existing file)] [bvecs, bvals] DW gradient scheme (FSL format). Maps to a command-line argument: -fslgrad %s %s.
- layout** ['nii' or 'float' or 'char' or 'short' or 'int' or 'long' or 'double'] Specify the layout of the data in memory. The actual layout produced will depend on whether the output image format can support it. Maps to a command-line argument: -output %s (position: 5).
- offset\_bias** [a float] Apply offset to the intensity values. Maps to a command-line argument: -scale %d (position: 7).
- out\_filename** [a pathlike object or string representing a file] Output filename. Maps to a command-line argument: %s (position: -1).
- output\_datatype** ['float32' or 'float32le' or 'float32be' or 'float64' or 'float64le' or 'float64be' or 'int64' or 'uint64' or 'int64le' or 'uint64le' or 'int64be' or 'uint64be' or 'int32' or 'uint32' or 'int32le' or 'uint32le' or 'int32be' or 'uint32be' or 'int16' or 'uint16' or 'int16le' or 'uint16le' or 'int16be' or 'uint16be' or 'cfloat32' or 'cfloat32le' or 'cfloat32be' or 'cfloat64' or 'cfloat64le' or 'cfloat64be' or 'int8' or 'uint8' or 'bit'] Specify output image data type. Valid choices are: float32, float32le, float32be, float64, float64le, float64be, int64, uint64, int64le, uint64le, int64be, uint64be, int32, uint32, int32le, uint32le, int32be, uint32be, int16, uint16, int16le, uint16le, int16be, uint16be, cfloat32, cfloat32le, cfloat32be, cfloat64, cfloat64le, cfloat64be, int8, uint8, bit.". Maps to a command-line argument: -datatype %s (position: 2).
- prs** [a boolean] Assume that the DW gradients are specified in the PRS frame (Siemens DICOM only). Maps to a command-line argument: -prs (position: 3).
- quiet** [a boolean] Do not display information messages or progress status. Maps to a command-line argument: -quiet.

- replace\_nan\_with\_zero** [a boolean] Replace all NaN values with zero. Maps to a command-line argument: `-zero` (position: 8).
- resample** [a float] Apply scaling to the intensity values. Maps to a command-line argument: `-scale %d` (position: 6).
- stride** [a list of from 3 to 4 items which are an integer] Three to four comma-separated numbers specifying the strides of the output data in memory. The actual strides produced will depend on whether the output image format can support it.. Maps to a command-line argument: `-stride %s` (position: 3).
- voxel\_dims** [a list of from 3 to 3 items which are a float] Three comma-separated numbers giving the size of each voxel in mm. Maps to a command-line argument: `-vox %s` (position: 3).
- converted** [a pathlike object or string representing an existing file] Path/name of 4D volume in voxel order.

## MRCrop

[Link to code](#)

Bases: `nipy.interfaces.base.core.CommandLine`

Wrapped executable: `mrcrop`.

Crops a NIFTI image using the `mrcrop` tool.

## Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> mrcrop = mrt.MRCrop()
>>> mrcrop.inputs.in_file = 'sub-01_dwi.nii.gz'
>>> mrcrop.inputs.in_mask_file = 'sub-01_mod-dwi_desc-brain_mask.nii.gz'
>>> mrcrop.inputs.out_filename = 'sub-01_desc-cropped_dwi.nii.gz'
>>> mrcrop.run()
```

- in\_file** [a pathlike object or string representing an existing file] Input image. Maps to a command-line argument: `%s` (position: -2).
- args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.
- debug** [a boolean] Display debugging messages. Maps to a command-line argument: `-debug` (position: 1).
- environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)
- in\_mask\_file** [a pathlike object or string representing an existing file] Input mask. Maps to a command-line argument: `-mask %s` (position: -3).
- out\_filename** [a pathlike object or string representing a file] Output cropped image. Maps to a command-line argument: `%s` (position: -1).
- quiet** [a boolean] Do not display information messages or progress status. Maps to a command-line argument: `-quiet` (position: 1).
- cropped** [a pathlike object or string representing an existing file] The output cropped image.

## MRThreshold

[Link to code](#)

Bases: `nipy.interfaces.base.core.CommandLine`

Wrapped executable: `mrthreshold`.

Threshold an image using the `mrthreshold` tool.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> mrthresh = mrt.MRCrop()
>>> mrthresh.inputs.in_file = 'sub-01_dwi.nii.gz'
>>> mrthresh.inputs.out_file = 'sub-01_desc-thresholded_dwi.nii.gz'
>>> mrthresh.run()
```

**in\_file** [a pathlike object or string representing an existing file] The input image to be thresholded. Maps to a command-line argument: `%s` (position: -3).

**out\_file** [a pathlike object or string representing a file]

the output binary image mask.

Maps to a command-line argument: `%s` (position: -2).

**abs\_value** [a float] Specify threshold value as absolute intensity. Maps to a command-line argument: `-abs %s` (position: -1).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**force\_writing** [a boolean] Force file overwriting. Maps to a command-line argument: `-force`.

**quiet** [a boolean] Do not display information messages or progress status. Maps to a command-line argument: `-quiet`.

**thresholded** [a pathlike object or string representing an existing file] Path/name of the output binary image mask.

## MRTransform

[Link to code](#)

Bases: `nipy.interfaces.base.core.CommandLine`

Wrapped executable: `mrtransform`.

Apply spatial transformations or reslice images using the `mrtransform` tool.

## Example

```
>>> from cmtklib.interfaces.mrtrix3 import MRTransform
>>> MRxform = MRTransform()
>>> MRxform.inputs.in_files = 'anat_coreg.mif'
>>> MRxform.inputs.interp = 'cubic'
>>> MRxform.run()
```

**in\_files** [a list of items which are any value] Input images to be transformed. Maps to a command-line argument: %s (position: -2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**debug** [a boolean] Display debugging messages. Maps to a command-line argument: -debug (position: 1).

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**flip\_x** [a boolean] Assume the transform is supplied assuming a coordinate system with the x-axis reversed relative to the MRtrix convention (i.e. x increases from right to left). This is required to handle transform matrices produced by FSL's FLIRT command. This is only used in conjunction with the -reference option. Maps to a command-line argument: -flipx (position: 1).

**interp** ['nearest' or 'linear' or 'cubic' or 'sinc'] Set the interpolation method to use when reslicing (choices: nearest,linear, cubic, sinc. Default: cubic). Maps to a command-line argument: -interp %s.

**invert** [a boolean] Invert the specified transform before using it. Maps to a command-line argument: -inverse (position: 1).

**out\_filename** [a pathlike object or string representing a file] Output image. Maps to a command-line argument: %s (position: -1).

**quiet** [a boolean] Do not display information messages or progress status. Maps to a command-line argument: -quiet (position: 1).

**reference\_image** [a pathlike object or string representing an existing file] In case the transform supplied maps from the input image onto a reference image, use this option to specify the reference. Note that this implicitly sets the -replace option. Maps to a command-line argument: -reference %s (position: 1).

**replace\_transform** [a boolean] Replace the current transform by that specified, rather than applying it to the current transform. Maps to a command-line argument: -replace (position: 1).

**template\_image** [a pathlike object or string representing an existing file] Reslice the input image to match the specified template image. Maps to a command-line argument: -template %s (position: 1).

**transformation\_file** [a pathlike object or string representing an existing file] The transform to apply, in the form of a 4x4 ascii file. Maps to a command-line argument: -transform %s (position: 1).

**out\_file** [a pathlike object or string representing an existing file] The output image of the transformation.

## MRtrix3Base

[Link to code](#)

Bases: `nipype.interfaces.base.core.CommandLine`

“MRtrix3Base base class inherited by `FilterTractogram` class.

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class ‘str’ and with values which are a bytes or None or a value of class ‘str’] Environment variables. (Nipype **default** value: `{}`)

## MRtrix\_mul

[Link to code](#)

Bases: `nipype.interfaces.base.core.CommandLine`

Wrapped executable: `mrcalc`.

Multiply two images together using `mrcalc` tool.

### Examples

```
>>> from cmtklib.interfaces.mrtrix3 import MRtrix_mul
>>> multiply = MRtrix_mul()
>>> multiply.inputs.input1 = 'image1.nii.gz'
>>> multiply.inputs.input2 = 'image2.nii.gz'
>>> multiply.inputs.out_filename = 'result.nii.gz'
>>> multiply.run()
```

**input1** [a pathlike object or string representing an existing file] Input1 file. Maps to a command-line argument: `%s` (position: 1).

**input2** [a pathlike object or string representing an existing file] Input2 file. Maps to a command-line argument: `%s` (position: 2).

**out\_filename** [a string] Out filename. Maps to a command-line argument: `-mult %s` (position: 3).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**environ** [a dictionary with keys which are a bytes or None or a value of class ‘str’ and with values which are a bytes or None or a value of class ‘str’] Environment variables. (Nipype **default** value: `{}`)

**out\_file** [a pathlike object or string representing a file] Multiplication result file.

## SIFT2

[Link to code](#)

Bases: *MRtrix3Base*

Wrapped executable: `tcksift2`.

Determine an appropriate cross-sectional area multiplier for each streamline using `tcksift2` [Smith2015SIFT2].

## References

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as cmp_mrt
>>> mrtrix_sift2 = cmp_mrt.SIFT2()
>>> mrtrix_sift2.inputs.in_tracks = 'tractogram.tck'
>>> mrtrix_sift2.inputs.in_fod = 'spherical_harmonics_image.nii.gz'
>>> mrtrix_sift2.inputs.out_file = 'sift2_fiber_weights.txt'
>>> mrtrix_sift2.run()
```

**in\_fod** [a pathlike object or string representing an existing file] Input image containing the spherical harmonics of the fibre orientation distributions. Maps to a command-line argument: %s (position: -2).

**in\_tracks** [a pathlike object or string representing an existing file] Input track file in TCK format. Maps to a command-line argument: %s (position: -3).

**act\_file** [a pathlike object or string representing an existing file] ACT 5TT image file. Maps to a command-line argument: -act %s (position: -4).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})

**out\_file** [a pathlike object or string representing a file] Output filtered tractogram. Maps to a command-line argument: %s (position: -1).

**out\_tracks** [a pathlike object or string representing an existing file] Output filtered tractogram.

## StreamlineTrack

[Link to code](#)

Bases: nipype.interfaces.base.core.CommandLine

Wrapped executable: tckgen.

Performs tractography using tckgen.

It can use one of the following models:

```
'dt_prob', 'dt_stream', 'sd_prob', 'sd_stream'
```

where 'dt' stands for diffusion tensor, 'sd' stands for spherical deconvolution, and 'prob' stands for probabilistic.

### Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> strack = mrt.StreamlineTrack()
>>> strack.inputs.inputmodel = 'SD_PROB'
>>> strack.inputs.in_file = 'data.Bfloat'
>>> strack.inputs.seed_file = 'seed_mask.nii'
>>> strack.run()
```

- in\_file** [a pathlike object or string representing an existing file] The image containing the source data. The type of data required depends on the type of tracking as set in the preceeding argument. For DT methods, the base DWI are needed. For SD methods, the SH harmonic coefficients of the FOD are needed. Maps to a command-line argument: %s (position: 2).
- act\_file** [a pathlike object or string representing an existing file] Use the Anatomically-Constrained Tractography framework during tracking; provided image must be in the 5TT (five - tissue - type) format. Maps to a command-line argument: -act %s.
- angle** [a float] Set the maximum angle between successive steps (default is 90deg x stepsize / voxelsize). Maps to a command-line argument: -angle %s.
- args** [a string] Additional parameters to the command. Maps to a command-line argument: %s.
- backtrack** [a boolean] Allow tracks to be truncated. Maps to a command-line argument: -backtrack.
- crop\_at\_gmwmi** [a boolean] Crop streamline endpoints more precisely as they cross the GM-WM interface. Maps to a command-line argument: -crop\_at\_gmwmi.
- cutoff\_value** [a float] Set the FA or FOD amplitude cutoff for terminating tracks (default is 0.5). Maps to a command-line argument: -cutoff %s.
- desired\_number\_of\_tracks** [an integer] Sets the desired number of tracks. The program will continue to generate tracks until this number of tracks have been selected and written to the output file (default is 100 for \*\_STREAM methods, 1000 for \*\_PROB methods). Maps to a command-line argument: -select %d.
- do\_not\_precompute** [a boolean] Turns off precomputation of the legendre polynomial values. Warning: this will slow down the algorithm by a factor of approximately 4. Maps to a command-line argument: -noprocomputed.
- environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: {})
- gradient\_encoding\_file** [a pathlike object or string representing an existing file] Gradient encoding, supplied as a 4xN text file with each line is in the format [ X Y Z b ] where [ X Y Z ] describe the direction of the applied gradient, and b gives the b-value in units (1000 s/mm<sup>2</sup>). See FSL2MRTrix. Maps to a command-line argument: -grad %s.
- initial\_cutoff\_value** [a float] Sets the minimum FA or FOD amplitude for initiating tracks (default is twice the normal cutoff). Maps to a command-line argument: -seed\_cutoff %s.
- initial\_direction** [a list of from 2 to 2 items which are an integer] Specify the initial tracking direction as a vector. Maps to a command-line argument: -seed\_direction %s.
- inputmodel** ['FACT' or 'iFOD1' or 'iFOD2' or 'Nulldist1' or 'Nulldist2' or 'SD\_Stream' or 'Seedtest' or 'Tensor\_Det' or 'Tensor\_Prob'] Specify the tractography algorithm to use. Valid choices are: FACT, iFOD1, iFOD2, Nulldist1, Nulldist2, SD\_Stream, Seedtest, Tensor\_Det, Tensor\_Prob (default: iFOD2). Maps to a command-line argument: -algorithm %s (position: -3). (Nipype **default** value: FACT)
- mask\_file** [a pathlike object or string representing an existing file] Mask file. Only tracks within mask. Maps to a command-line argument: -mask %s.
- maximum\_number\_of\_seeds** [an integer] Sets the maximum number of tracks to generate. The program will not generate more tracks than this number, even if the desired number of tracks hasn't yet been reached (default is 1000 x number of streamlines). Maps to a command-line argument: -seeds %d.
- maximum\_tract\_length** [a float] Sets the maximum length of any track in millimeters (default is 500 mm). Maps to a command-line argument: -maxlength %s.



**minimum\_tract\_length** [a float] Sets the minimum length of any track in millimeters (default is 5 mm). Maps to a command-line argument: `-minlength %s`.

**out\_file** [a pathlike object or string representing a file] Output data file. Maps to a command-line argument: `%s` (position: -1).

**rk4** [a boolean] Use 4th-order Runge-Kutta integration (slower, but eliminates curvature overshoot in 1st-order deterministic methods). Maps to a command-line argument: `-rk4`.

**seed\_file** [a pathlike object or string representing an existing file] Seed file. Maps to a command-line argument: `-seed_image %s`.

**seed\_gmwmi** [a pathlike object or string representing an existing file] Seed from the grey matter - white matter interface (only valid if using ACT framework). Maps to a command-line argument: `-seed_gmwmi %s`. **Requires** inputs: `act_file`.

**seed\_spec** [a list of from 4 to 4 items which are an integer] Seed specification in voxels and radius (x y z r). Maps to a command-line argument: `-seed_sphere %s`.

**step\_size** [a float] Set the step size of the algorithm in mm (default is 0.5). Maps to a command-line argument: `-step %s`.

**stop** [a boolean] Stop track as soon as it enters any of the include regions. Maps to a command-line argument: `-stop`.

**unidirectional** [a boolean] Track from the seed point in one direction only (default is to track in both directions). Maps to a command-line argument: `-seed_unidirectional`.

**tracked** [a pathlike object or string representing an existing file] Output file containing reconstructed tracts.

## Tensor2Vector

[Link to code](#)

Bases: `nipy.interfaces.base.core.CommandLine`

Wrapped executable: `tensor2metric`.

Generates a map of the major eigenvectors of the tensors in each voxel using `tensor2metric`.

## Example

```
>>> import cmtklib.interfaces.mrtrix3 as mrt
>>> tensor2vector = mrt.Tensor2Vector()
>>> tensor2vector.inputs.in_file = 'dwi_tensor.mif'
>>> tensor2vector.run()
```

**in\_file** [a pathlike object or string representing an existing file] Diffusion tensor image. Maps to a command-line argument: `%s` (position: -2).

**args** [a string] Additional parameters to the command. Maps to a command-line argument: `%s`.

**debug** [a boolean] Display debugging messages. Maps to a command-line argument: `-debug` (position: 1).

**environ** [a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str'] Environment variables. (Nipype **default** value: `{}`)

**out\_filename** [a pathlike object or string representing a file] Output vector filename. Maps to a command-line argument: `-vector %s` (position: -1).

**quiet** [a boolean] Do not display information messages or progress status. Maps to a command-line argument: `-quiet` (position: 1).

**vector** [a pathlike object or string representing an existing file] The output image of the major eigenvectors of the diffusion tensor image.

## cmtklib.interfaces.pycartool module

The PyCartool module provides Nipype interfaces with Cartool using pycartool.

### CartoolInverseSolutionROIExtraction

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Use Pycartool to load inverse solutions estimated by Cartool.

### Examples

```
>>> from cmtklib.interfaces.pycartool import _
↳ CartoolInverseSolutionROIExtraction
>>> cartool_inv_sol = CartoolInverseSolutionROIExtraction()
>>> cartool_inv_sol.inputs.eeg_ts_file = 'sub-01_task-faces_desc-preproc_eeg.
↳ set'
>>> cartool_inv_sol.inputs.invsol_file = 'sub-01_eeg.LORETA.is'
>>> cartool_inv_sol.inputs.rois_file = 'sub-01_label-L2008_desc-scale1.rois'
>>> cartool_inv_sol.inputs.invsol_params = {'lamda': 6, 'svd_params': {'toi_
↳ begin': 0, 'toi_end': 0.25}}
>>> cartool_inv_sol.inputs.roi_ts_file = 'sub-01_task-faces_label-L2008_desc-
↳ scale1_LORETA.npy'
>>> cartool_inv_sol.run()
```

### References

- [https://pycartool.readthedocs.io/en/latest/pycartool.io.html#module-pycartool.io.inverse\\_solution](https://pycartool.readthedocs.io/en/latest/pycartool.io.html#module-pycartool.io.inverse_solution)

**eeg\_ts\_file** [a list of items which are any value] Eeg \* epochs in .set format.

**invsol\_file** [a list of items which are any value] Inverse solution (.is file loaded with pycartool).

**invsol\_params** [a dictionary with keys which are any value and with values which are any value] Parameters for inverse solution and roi tc extraction.

**rois\_file** [a list of items which are any value] Rois file, loaded with pickle.

**roi\_ts\_file** [a string or `os.PathLike` object] Rois \* time series in .npy format.

**roi\_ts\_file** [a string or `os.PathLike` object referring to an existing file] Rois \* time series in .npy format.

```
static CartoolInverseSolutionROIExtraction.apply_inverse_epochs_cartool(epochs_file,
                                                                    in-
                                                                    vsol_file,
                                                                    lamda,
                                                                    rois_file,
                                                                    svd_params)
```

## Submodules

### cmtklib.carbonfootprint module

Module that defines CMTK functions for converting CO2 emissions estimated with codecarbon.

```
cmtklib.carbonfootprint.create_carbon_footprint_message(bids_dir, emissions_csv_file,
                                                         nb_of_subjects_processed)
```

Return a string containing the carbon footprint print message to be passed to `print()`.

#### Parameters

- **bids\_dir** (*string*) – Path to root directory of the BIDS dataset
- **emissions\_csv\_file** (*string*) – Path to the `emissions.csv` file generated by Codecarbon.
- **nb\_of\_subjects\_processed** (*int*) – Number of subject processed.

**Returns** **carbon\_footprint\_msg** – String formatted containing the carbon footprint message to be passed to `print()`

**Return type** `string`

```
cmtklib.carbonfootprint.create_emissions_tracker(bids_root)
```

Return a new instance of `codecarbon.EmissionsTracker`.

**Parameters** **bids\_root** (*string*) – Path to the root directory of the BIDS dataset

**Returns** **tracker** – Return a new instance of `codecarbon.EmissionsTracker`

**Return type** `codecarbon.EmissionsTracker`

## References

[https://github.com/mlco2/codecarbon/blob/v1.2.0/codecarbon/emissions\\_tracker.py](https://github.com/mlco2/codecarbon/blob/v1.2.0/codecarbon/emissions_tracker.py)

```
cmtklib.carbonfootprint.create_html_carbon_footprint_report(emissions_csv_file,
                                                            nb_of_subjects_processed)
```

Return a string containing the content of html report to be passed to `traits.Str` with `HTMLEditor`.

#### Parameters

- **emissions\_csv\_file** (*string*) – Path to the `emissions.csv` file generated by Codecarbon.
- **nb\_of\_subjects\_processed** (*int*) – Number of subject processed.

```
cmtklib.carbonfootprint.get_emission_car_miles_equivalent(emissions)
```

Return the equivalent of CO2 emissions [Kg] in terms of kms traveled by an average car.

## References

<https://github.com/mlco2/codecarbon/blob/c6aebb9681186a71573748e381b6a3c9731de2d3/codecarbon/viz/data.py#L53>

`cmtklib.carbonfootprint.get_emission_tv_time_equivalent(emissions)`

Return the equivalent of CO2 emissions [Kg] in terms of kms traveled by an average car.

## References

<https://github.com/mlco2/codecarbon/blob/c6aebb9681186a71573748e381b6a3c9731de2d3/codecarbon/viz/data.py#L66>

`cmtklib.carbonfootprint.load_and_compute_carbon_footprint_metrics(emissions_csv_file, nb_of_subjects_processed) → dict`

Return a dictionary storing the different metrics and variables displayed in the carbon footprint report.

The dictionary has the different fields: 'country\_name', 'region\_name', 'country\_emissions\_per\_kwh', 'duration', 'energy\_consumed', 'emissions', 'car\_kms', 'tv\_time', 'pred\_energy\_consumed', 'pred\_emissions', 'pred\_car\_kms', 'pred\_tv\_time'.

### Parameters

- **emissions\_csv\_file** (*string*) – Path to the emissions.csv file generated by Codecarbon.
- **nb\_of\_subjects\_processed** (*int*) – Number of subject processed.

## cmtklib.config module

Module that defines methods for handling CMP3 configuration files.

`cmtklib.config.anat_load_config_json(pipeline, config_path)`

Load the JSON configuration file of an anatomical pipeline.

### Parameters

- **pipeline** (*Instance(cmp.pipelines.anatomical.anatomical.AnatomicalPipeline)*) – Instance of AnatomicalPipeline
- **config\_path** (*string*) – Path of the JSON configuration file

`cmtklib.config.anat_save_config(pipeline, config_path)`

Save the configuration file of an anatomical pipeline.

### Parameters

- **pipeline** (*Instance(cmp.pipelines.anatomical.anatomical.AnatomicalPipeline)*) – Instance of AnatomicalPipeline
- **config\_path** (*string*) – Path of the JSON configuration file

`cmtklib.config.check_configuration_format(config_path)`

Check format of the configuration file.

**Parameters** **config\_path** (*string*) – Path to pipeline configuration file

**Returns** **ext** – Format extension of the pipeline configuration file

**Return type** 'ini' or 'json'

`cmtklib.config.check_configuration_version(config)`

Check the version of CMP3 used to generate a configuration.

**Parameters** `config` (*Dict*) – Dictionary of configuration parameters loaded from JSON file

**Returns** `is_same` – `True` if the version used to generate the configuration matches the version currently used (`cmp.info.__version__`).

**Return type** `bool`

`cmtklib.config.convert_config_ini_2_json(config_ini_path)`

Convert a configuration file in old INI format to new JSON format.

**Parameters** `config_ini_path` (*string*) – Path to configuration file in old INI format

**Returns** `config_json_path` – Path to converted configuration file in new JSON format

**Return type** `string`

`cmtklib.config.create_configparser_from_pipeline(pipeline, debug=False)`

Create a ConfigParser object from a Pipeline instance.

**Parameters**

- `pipeline` (*Instance(Pipeline)*) – Instance of pipeline
- `debug` (*bool*) – If `True`, show additional prints

**Returns** `config` – Instance of ConfigParser

**Return type** `Instance(configparser.ConfigParser)`

`cmtklib.config.create_subject_configuration_from_ref(project, ref_conf_file, pipeline_type, multiproc_number_of_cores=1)`

Create the pipeline configuration file for an individual subject from a reference given as input.

**Parameters**

- `project` (`cmp.project.ProjectInfo`) – Instance of `cmp.project.CMP_Project_Info`
- `ref_conf_file` (*string*) – Reference configuration file
- `pipeline_type` (*'anatomical', 'diffusion', 'fMRI', 'EEG'*) – Type of pipeline
- `multiproc_number_of_cores` (*int*) – Number of threads used by Nipype

**Returns** `subject_conf_file` – Configuration file of the individual subject

**Return type** `string`

`cmtklib.config.dmri_load_config_json(pipeline, config_path)`

Load the JSON configuration file of a diffusion pipeline.

**Parameters**

- `pipeline` (*Instance(cmp.pipelines.diffusion.diffusion.DiffusionPipeline)*) – Instance of DiffusionPipeline
- `config_path` (*string*) – Path of the JSON configuration file

`cmtklib.config.dmri_save_config(pipeline, config_path)`

Save the INI configuration file of a diffusion pipeline.

**Parameters**

- `pipeline` (*Instance(cmp.pipelines.diffusion.diffusion.DiffusionPipeline)*) – Instance of DiffusionPipeline

- **config\_path** (*string*) – Path of the JSON configuration file

`cmtklib.config.eeg_load_config_json(pipeline, config_path)`

Load the JSON configuration file of a eeg pipeline.

#### Parameters

- **pipeline** (*Instance*(`cmp.pipelines.functional.eeg.EEGPipeline`)) – Instance of EEGPipeline
- **config\_path** (*string*) – Path of the JSON configuration file

`cmtklib.config.eeg_save_config(pipeline, config_path)`

Save the INI configuration file of a eeg pipeline.

#### Parameters

- **pipeline** (*Instance*(`cmp.pipelines.functional.eeg.EEGPipeline`)) – Instance of EEGPipeline
- **config\_path** (*string*) – Path of the JSON configuration file

`cmtklib.config.fmri_load_config_json(pipeline, config_path)`

Load the JSON configuration file of a fMRI pipeline.

#### Parameters

- **pipeline** (*Instance*(`cmp.pipelines.functional.fmri.fMRIPipeline`)) – Instance of fMRIPipeline
- **config\_path** (*string*) – Path of the JSON configuration file

`cmtklib.config.fmri_save_config(pipeline, config_path)`

Save the INI configuration file of a fMRI pipeline.

#### Parameters

- **pipeline** (*Instance*(`cmp.pipelines.functional.fmri.fMRIPipeline`)) – Instance of fMRIPipeline
- **config\_path** (*string*) – Path of the JSON configuration file

`cmtklib.config.get_anat_process_detail_json(project_info, section, detail)`

Get the value for a parameter key (detail) in the stage section of the anatomical JSON config file.

#### Parameters

- **project\_info** (*Instance*(`cmp.project.ProjectInfo`)) – Instance of `cmp.project.ProjectInfo` class
- **section** (*string*) – Stage section name
- **detail** (*string*) – Parameter key

#### Returns

**Return type** The parameter value

`cmtklib.config.get_dmri_process_detail_json(project_info, section, detail)`

Get the value for a parameter key (detail) in the stage section of the diffusion JSON config file.

#### Parameters

- **project\_info** (*Instance*(`cmp.project.ProjectInfo`)) – Instance of `cmp.project.ProjectInfo` class
- **section** (*string*) – Stage section name

- **detail** (*string*) – Parameter key

**Returns**

**Return type** The parameter value

`cmtklib.config.get_eeg_process_detail_json(project_info, section, detail)`

Get the value for a parameter key (detail) in the stage section of the EEG JSON config file.

**Parameters**

- **project\_info** (*Instance(cmp.project.CMP\_Project\_Info)*) – Instance of `cmp.project.CMP_Project_Info` class
- **section** (*string*) – Stage section name
- **detail** (*string*) – Parameter key

**Returns**

**Return type** The parameter value

`cmtklib.config.get_fmri_process_detail_json(project_info, section, detail)`

Get the value for a parameter key (detail) in the stage section of the fMRI JSON config file.

**Parameters**

- **project\_info** (*Instance(cmp.project.ProjectInfo)*) – Instance of `cmp.project.ProjectInfo` class
- **section** (*string*) – Stage section name
- **detail** (*string*) – Parameter key

**Returns**

**Return type** The parameter value

`cmtklib.config.get_process_detail_json(project_info, section, detail)`

Get the value for a parameter key (detail) in the global section of the JSON config file.

**Parameters**

- **project\_info** (*Instance(cmp.project.ProjectInfo)*) – Instance of `cmp.project.ProjectInfo` class
- **section** (*string*) – Stage section name
- **detail** (*string*) – Parameter key

**Returns**

**Return type** The parameter value

`cmtklib.config.save_configparser_as_json(config, config_json_path, ini_mode=False, debug=False)`

Save a ConfigParser to JSON file.

**Parameters**

- **config** (*Instance(configparser.ConfigParser)*) – Instance of ConfigParser
- **config\_json\_path** (*string*) – Output path of JSON configuration file
- **ini\_mode** (*bool*) – If `True`, handles all content stored in strings
- **debug** (*bool*) – If `True`, show additional prints

`cmtklib.config.set_pipeline_attributes_from_config(pipeline, config, debug=False)`

Set the pipeline stage attributes given a configuration.

### Parameters

- **pipeline** (*Instance(Pipeline)*) – Instance of pipeline
- **config** (*Dict*) – Dictionary of configuration parameter loaded from the JSON configuration file
- **debug** (*bool*) – If `True`, show additional prints

## cmtklib.connectome module

Module that defines CMTK functions and Nipype interfaces for connectome mapping.

### DmriCmat

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Creates the structural connectivity matrices for a given parcellation scheme.

### Examples

```
>>> from cmtklib.connectome import DmriCmat
>>> cmat = DmriCmat()
>>> cmat.inputs.base_dir = '/my_directory'
>>> cmat.inputs.track_file = '/path/to/sub-01_tractogram.trk'
>>> cmat.inputs.roi_volumes = ['/path/to/sub-01_space-DWI_atlas-L2018_desc-
↳scale1_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-DWI_atlas-L2018_desc-
↳scale2_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-DWI_atlas-L2018_desc-
↳scale3_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-DWI_atlas-L2018_desc-
↳scale4_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-DWI_atlas-L2018_desc-
↳scale5_dseg.nii.gz']
>>> cmat.inputs.roi_graphmls = ['/path/to/sub-01_atlas-L2018_desc-scale1_dseg.
↳graphml',
>>>                               '/path/to/sub-01_atlas-L2018_desc-scale2_dseg.
↳graphml',
>>>                               '/path/to/sub-01_atlas-L2018_desc-scale3_dseg.
↳graphml',
>>>                               '/path/to/sub-01_atlas-L2018_desc-scale4_dseg.
↳graphml',
>>>                               '/path/to/sub-01_atlas-L2018_desc-scale5_dseg.
↳graphml']
>>> cmat.inputs.parcellation_scheme = 'Lausanne2018'
>>> cmat.inputs.output_types = ['gPickle', 'mat', 'graphml']
>>> cmat.run()
```

**track\_file** [a list of items which are a pathlike object or string representing an existing file] Tractography result.



**additional\_maps** [a list of items which are a pathlike object or string representing a file] Additional calculated maps (ADC, gFA, ...).

**atlas\_info** [a dictionary with keys which are any value and with values which are any value] Custom atlas information.

**compute\_curvature** [a boolean] Compute curvature. (Nipype **default** value: True)

**output\_types** [a list of items which are a string] Output types of the connectivity matrices.

**parcellation\_scheme** ['Lausanne2018' or 'NativeFreesurfer' or 'Custom'] Parcellation scheme. (Nipype **default** value: Lausanne2018)

**roi\_graphmls** [a list of items which are a pathlike object or string representing an existing file] GraphML description of ROI volumes (Lausanne2018).

**roi\_volumes** [a list of items which are a pathlike object or string representing an existing file] ROI volumes registered to diffusion space.

**voxel\_connectivity** [a list of items which are a pathlike object or string representing an existing file] ProbtrackX connectivity matrices (# seed voxels x # target ROIs).

**connectivity\_matrices** [a list of items which are a pathlike object or string representing a file] Connectivity matrices.

**endpoints\_file** [a pathlike object or string representing a file] Numpy files storing the list of fiber endpoint.

**endpoints\_mm\_file** [a pathlike object or string representing a file] Numpy files storing the list of fiber endpoint in mm.

**filtered\_fiberslabel\_files** [a list of items which are a pathlike object or string representing a file] List of fiber start end ROI parcellation label after filtering.

**final\_fiberlabels\_files** [a list of items which are a pathlike object or string representing a file] List of fiber start end ROI parcellation label.

**final\_fiberslength\_files** [a list of items which are a pathlike object or string representing a file] List of fiber length.

**streamline\_final\_file** [a pathlike object or string representing a file] Final tractogram of fibers considered in the creation of connectivity matrices.

## RsfmriCmat

[Link to code](#)

Bases: nipype.interfaces.base.core.BaseInterface

Creates the functional connectivity matrices for a given parcellation scheme.

**It applies scrubbing (if enabled), computes the average GM ROI time-series and computes the Pearson's correlation coefficient between each GM ROI time-series pair.**

## Examples

```
>>> from cmtklib.connectome import RsfmriCmat
>>> cmat = RsfmriCmat()
>>> cmat.inputs.base_dir = '/my_directory'
>>> cmat.inputs.func_file = '/path/to/sub-01_task-rest_desc-preproc_bold.nii.gz'
>>> cmat.inputs.roi_volumes = ['/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳ desc-scale1_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳ desc-scale2_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳ desc-scale3_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳ desc-scale4_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳ desc-scale5_dseg.nii.gz']
>>> cmat.inputs.roi_graphmls = ['/path/to/sub-01_atlas-L2018_desc-scale1_dseg.
↳ graphml',
>>>                               '/path/to/sub-01_atlas-L2018_desc-scale2_dseg.
↳ graphml',
>>>                               '/path/to/sub-01_atlas-L2018_desc-scale3_dseg.
↳ graphml',
>>>                               '/path/to/sub-01_atlas-L2018_desc-scale4_dseg.
↳ graphml',
>>>                               '/path/to/sub-01_atlas-L2018_desc-scale5_dseg.
↳ graphml']
>>> cmat.inputs.parcellation_scheme = 'Lausanne2018'
>>> cmat.inputs.apply_scrubbing = False
>>> cmat.inputs.output_types = ['gPickle', 'mat', 'graphml']
>>> cmat.run()
```

**func\_file** [a pathlike object or string representing an existing file] FMRI volume.

**DVARS** [a pathlike object or string representing an existing file] DVARS file if scrubbing is performed.

**DVARS\_th** [a float] DVARS threshold.

**FD** [a pathlike object or string representing an existing file] FD file if scrubbing is performed.

**FD\_th** [a float] FD threshold.

**apply\_scrubbing** [a boolean] Apply scrubbing.

**atlas\_info** [a dictionary with keys which are any value and with values which are any value] Custom atlas information.

**output\_types** [a list of items which are a string] Output types of the connectivity matrices.

**parcellation\_scheme** ['Lausanne2018' or 'NativeFreesurfer' or 'Custom'] Parcellation scheme. (Nipype default value: Lausanne2018)

**roi\_graphmls** [a list of items which are a pathlike object or string representing an existing file] GraphML description file for ROI volumes (used only if parcellation\_scheme == Lausanne2018).

**roi\_volumes** [a list of items which are a pathlike object or string representing an existing file] ROI volumes registered to functional space.

**avg\_timeseries** [a list of items which are a pathlike object or string representing an existing file] ROI average timeseries.

**connectivity\_matrices** [a list of items which are a pathlike object or string representing an existing file] Functional connectivity matrices.

**scrubbed\_idx** [a pathlike object or string representing an existing file] Scrubbed indices.

```
cmtklib.connectome.cmat(intrk, roi_volumes=None, roi_graphmls=None, parcellation_scheme=None,
                        compute_curvature=True, additional_maps=None, output_types=None,
                        atlas_info=None)
```

Create the connection matrix for each resolution using fibers and ROIs.

#### Parameters

- **intrk** (*TRK file*) – Reconstructed tractogram
- **roi\_volumes** (*list*) – List of parcellation files for a given parcellation scheme
- **roi\_graphmls** (*list*) – List of graphmls files that describes parcellation nodes
- **parcellation\_scheme** (*['NativeFreesurfer', 'Lausanne2018', 'Custom']*) –
- **compute\_curvature** (*Boolean*) –
- **additional\_maps** (*dict*) – A dictionary of key/value for each additional map where the value is the path to the map
- **output\_types** (*['gPickle', 'mat', 'graphml']*) –
- **atlas\_info** (*dict*) – Dictionary storing information such as path to files related to a parcellation atlas / scheme.

```
cmtklib.connectome.compute_curvature_array(fib)
```

Computes the curvature array.

```
cmtklib.connectome.create_endpoints_array(fib, voxelSize, print_info)
```

Create the endpoints arrays for each fiber.

#### Parameters

- **fib** (*the fibers data*) –
- **voxelSize** (*3-tuple*) – It contains the voxel size of the ROI image
- **print\_info** (*bool*) – If True, print extra information

#### Returns

- **endpoints** (*matrix of size [#fibers, 2, 3] containing for each fiber the*) – index of its first and last point in the voxelSize volume
- **endpointsmm** (*endpoints in milimeter coordinates*)

```
cmtklib.connectome.group_analysis_sconn(output_dir, subjects_to_be_analyzed)
```

Perform group level analysis of structural connectivity matrices.

```
cmtklib.connectome.save_fibers(oldhdr, oldfib, fname, indices)
```

Stores a new trackvis file *fname* using only given indices.

#### Parameters

- **oldhdr** (*the tractogram header*) – Tractogram header to use as reference
- **oldfib** (*the fibers data*) – Input fibers
- **fname** (*string*) – Output tractogram filename

- **indices** (*list*) – Indices of fibers included

### **cmtklib.data.parcellation.util module**

Module that defines CMTK utility functions for retrieving Lausanne parcellation files.

`cmtklib.data.parcellation.util.get_lausanne2018_parcellation_annot(scale='scale1', hemi='lh')`  
Return the path of the Freesurfer `.annot` file corresponding to a specific scale and hemisphere.

#### **Parameters**

- **scale** (`{'scale1', 'scale2', 'scale3', 'scale4', 'scale5'}`) – Lausanne 2018 parcellation scale
- **hemi** (`{'lh', 'rh'}`) – Brain hemisphere

**Returns** `annot_file_path` – Absolute path to the queried `.annot` file

**Return type** `string`

`cmtklib.data.parcellation.util.get_lausanne2018_parcellation_mni_coords(scale='scale1')`  
Return label regions cut coordinates in MNI space (mm).

**Parameters** **scale** (`{'scale1', 'scale2', 'scale3', 'scale4', 'scale5'}`) – Lausanne 2018 parcellation scale

**Returns** `coords` – Label regions cut coordinates in MNI space (mm)

**Return type** `numpy.array`

### **cmtklib.data.parcellation.viz module**

### **cmtklib.eeg module**

Module that defines CMTK utility functions for the EEG pipeline.

`cmtklib.eeg.save_eeg_connectome_file(output_dir, output_basename, con_res, roi_labels, output_types=None)`

Save a dictionary of connectivity matrices with corresponding keys to the metrics in the multiple formats of CMP3.

#### **Parameters**

- **output\_dir** (*str*) – Output directory for the connectome file(s)
- **output\_basename** (*str*) – Base name for the connectome file(s) i.e., `sub-01_atlas-L20018_res-scale1_conndata-network_connectivity`
- **con\_res** (*dict*) – Dictionary of connectivity metric / matrix pairs
- **roi\_labels** (*list*) – List of parcellation roi labels extracted from the `epo.pkl` file generated with MNE
- **output\_types** (`['tsv', 'gpickle', 'mat', 'graphml']`) – List of output format in which to save the connectome files. (Default: `None`)

## cmtklib.diffusion module

Module that defines CMTK utility functions for the diffusion pipeline.

### ExtractPVEsFrom5TT

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Create Partial Volume Estimation maps for CSF, GM, WM tissues from `mrtrix3` 5TT image.

#### Examples

```

>>> from cmtklib.diffusion import ExtractPVEsFrom5TT
>>> pves = ExtractPVEsFrom5TT()
>>> pves.inputs.in_5tt = 'sub-01_desc-5tt_dseg.nii.gz'
>>> pves.inputs.ref_image = 'sub-01_T1w.nii.gz'
>>> pves.inputs.pve_csf_file = '/path/to/output_csf_pve.nii.gz'
>>> pves.inputs.pve_gm_file = '/path/to/output_gm_pve.nii.gz'
>>> pves.inputs.pve_wm_file = '/path/to/output_wm_pve.nii.gz'
>>> pves.run()

```

**in\_5tt** [a pathlike object or string representing an existing file] Input 5TT (4D) image.

**pve\_csf\_file** [a pathlike object or string representing a file] CSF Partial Volume Estimation volume estimated from.

**pve\_gm\_file** [a pathlike object or string representing a file] GM Partial Volume Estimation volume estimated from.

**pve\_wm\_file** [a pathlike object or string representing a file] WM Partial Volume Estimation volume estimated from.

**ref\_image** [a pathlike object or string representing an existing file] Reference 3D image to be used to save 3D PVE volumes.

**partial\_volume\_files** [a list of items which are a pathlike object or string representing a file] CSF/GM/WM Partial Volume Estimation images estimated from.

### FlipBvec

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Return a diffusion bvec file with flipped axis as specified by `flipping_axis` input.

## Examples

```
>>> from cmtklib.diffusion import FlipBvec
>>> flip_bvec = FlipBvec()
>>> flip_bvec.inputs.bvecs = 'sub-01_dwi.bvecs'
>>> flip_bvec.inputs.flipping_axis = ['x']
>>> flip_bvec.inputs.delimiter = ' '
>>> flip_bvec.inputs.header_lines = 0
>>> flip_bvec.inputs.orientation = 'h'
>>> flip_bvec.run()
```

**bvecs** [a pathlike object or string representing an existing file] Input diffusion gradient bvec file.

**delimiter** [a string] Delimiter used in the table.

**flipping\_axis** [a list of items which are any value] List of axis to be flipped.

**header\_lines** [an integer] Line number of table header.

**orientation** ['v' or 'h'] Orientation of the table.

**bvecs\_flipped** [a pathlike object or string representing an existing file] Output bvec file with flipped axis.

## FlipTable

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Flip axis and rewrite a gradient table.

## Examples

```
>>> from cmtklib.diffusion import FlipTable
>>> flip_table = FlipTable()
>>> flip_table.inputs.table = 'sub-01_mod-dwi_gradient.txt'
>>> flip_table.inputs.flipping_axis = ['x']
>>> flip_table.inputs.orientation = 'v'
>>> flip_table.inputs.delimiter = ','
>>> flip_table.run()
```

**delimiter** [a string] Delimiter used in the table.

**flipping\_axis** [a list of items which are any value] List of axis to be flipped.

**header\_lines** [an integer] Line number of table header.

**orientation** ['v' or 'h'] Orientation of the table.

**table** [a pathlike object or string representing an existing file] Input diffusion gradient table.

**table** [a pathlike object or string representing an existing file] Output table with flipped axis.

## Tck2Trk

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Convert a tractogram in `mrtrix` TCK format to `trackvis` TRK format.

### Examples

```
>>> from cmtklib.diffusion import Tck2Trk
>>> tck_to_trk = Tck2Trk()
>>> tck_to_trk.inputs.in_tracks = 'sub-01_tractogram.tck'
>>> tck_to_trk.inputs.in_image = 'sub-01_desc-preproc_dwi.nii.gz'
>>> tck_to_trk.inputs.out_tracks = 'sub-01_tractogram.trk'
>>> tck_to_trk.run()
```

**in\_image** [a pathlike object or string representing an existing file] Input image used to extract the header.

**in\_tracks** [a pathlike object or string representing an existing file] Input track file in MRtrix .tck format.

**out\_tracks** [a pathlike object or string representing a file] Output track file in Trackvis .trk format.

**out\_tracks** [a pathlike object or string representing an existing file] Output track file in Trackvis .trk format.

## UpdateGMWMInterfaceSeeding

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Add extra Lausanne2018 structures to the Gray-matter/White-matter interface for tractography seeding.

### Examples

```
>>> from cmtklib.diffusion import UpdateGMWMInterfaceSeeding
>>> update_gmwmi = UpdateGMWMInterfaceSeeding()
>>> update_gmwmi.inputs.in_gmwmi_file = 'sub-01_label-gmwmi_desc-orig_dseg.nii.
↳ gz'
>>> update_gmwmi.inputs.out_gmwmi_file = 'sub-01_label-gmwmi_desc-modif_dseg.
↳ nii.gz'
>>> update_gmwmi.inputs.in_roi_volumes = ['sub-01_space-DWI_atlas-L2018_desc-
↳ scale1_dseg.nii.gz',
>>>                                     'sub-01_space-DWI_atlas-L2018_desc-
↳ scale2_dseg.nii.gz',
>>>                                     'sub-01_space-DWI_atlas-L2018_desc-
↳ scale3_dseg.nii.gz',
>>>                                     'sub-01_space-DWI_atlas-L2018_desc-
↳ scale4_dseg.nii.gz',
>>>                                     'sub-01_space-DWI_atlas-L2018_desc-
↳ scale5_dseg.nii.gz']
>>> update_gmwmi.run()
```

**in\_gmwmi\_file** [a pathlike object or string representing an existing file] Input GMWM interface image used for streamline seeding.

**in\_roi\_volumes** [a list of items which are a pathlike object or string representing an existing file] Input parcellation images.

**out\_gmwmi\_file** [a pathlike object or string representing a file] Output GM WM interface used for streamline seeding.

**out\_gmwmi\_file** [a pathlike object or string representing an existing file] Output GM WM interface used for streamline seeding.

`cmtklib.diffusion.compute_length_array(trkfile=None, streams=None, savefname='lengths.npy')`  
Computes the length of the fibers in a tractogram and returns an array of length.

#### Parameters

- **trkfile** (*TRK file*) – Path to the tractogram in TRK format
- **streams** (*the fibers data*) – The fibers from which we want to compute the length
- **savefname** (*string*) – Output filename to write the length array

**Returns** **fibers\_length** – Array of fiber lengths

**Return type** `numpy.array`

`cmtklib.diffusion.filter_fibers(intrk, outtrk="", fiber_cutoff_lower=20, fiber_cutoff_upper=500)`  
Filters a tractogram based on lower / upper cutoffs.

#### Parameters

- **intrk** (*TRK file*) – Path to a tractogram file in TRK format
- **outtrk** (*TRK file*) – Output path for the filtered tractogram
- **fiber\_cutoff\_lower** (*int*) – Lower number of fibers cutoff (Default: 20)
- **fiber\_cutoff\_upper** (*int*) – Upper number of fibers cutoff (Default: 500)

## cmtklib.functionalMRI module

Module that defines CMTK Nipype interfaces for the Functional MRI pipeline.

### Detrending

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Apply linear, quadratic or cubic detrending on the Functional MRI signal.



## Examples

```
>>> from cmtklib.functionalMRI import Detrending
>>> detrend = Detrending()
>>> detrend.inputs.base_dir = '/my_directory'
>>> detrend.inputs.in_file = '/path/to/sub-01_task-rest_desc-preproc_bold.nii.
↳gz'
>>> detrend.inputs.gm_file = ['/path/to/sub-01_space-meanBOLD_atlas-L2018_desc-
↳scale1_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale2_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale3_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale4_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale5_dseg.nii.gz']
>>> detrend.inputs.mode = 'quadratic'
>>> detrend.run()
```

**in\_file** [a string or os.PathLike object referring to an existing file] FMRI volume to detrend.

**gm\_file** [a list of items which are a string or os.PathLike object referring to an existing file] ROI files registered to fMRI space.

**mode** ['linear' or 'quadratic' or 'cubic'] Detrending order.

**out\_file** [a string or os.PathLike object referring to an existing file] Detrended fMRI volume.

## DiscardTP

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Discards the n first time frame in functional MRI data.

## Examples

```
>>> from cmtklib.functionalMRI import DiscardTP
>>> discard = DiscardTP()
>>> discard.inputs.base_dir = '/my_directory'
>>> discard.inputs.in_file = '/path/to/sub-01_task-rest_desc-preproc_bold.nii.
↳gz'
>>> discard.inputs.n_discard = 5
>>> discard.run()
```

**in\_file** [a string or os.PathLike object referring to an existing file] Input 4D fMRI image.

**n\_discard** [an integer] Number of n first frames to discard.

**out\_file** [a string or os.PathLike object referring to an existing file] Output 4D fMRI image with discarded frames.

## NuisanceRegression

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Regress out nuisance signals (WM, CSF, movements) through GLM.

### Examples

```
>>> from cmtklib.functionalMRI import NuisanceRegression
>>> nuisance = NuisanceRegression()
>>> nuisance.inputs.base_dir = '/my_directory'
>>> nuisance.inputs.in_file = '/path/to/sub-01_task-rest_desc-preproc_bold.nii.
↳gz'
>>> nuisance.inputs.wm_file = '/path/to/sub-01_task-rest_desc-preproc_bold.nii.
↳gz'
>>> nuisance.inputs.csf_file = '/path/to/sub-01_task-rest_desc-preproc_bold.
↳nii.gz'
>>> nuisance.inputs.motion_file = '/path/to/sub-01_motions.par'
>>> nuisance.inputs.gm_file = ['/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale1_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale2_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale3_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale4_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_
↳desc-scale5_dseg.nii.gz']
>>> nuisance.inputs.global_nuisance = False
>>> nuisance.inputs.csf_nuisance = True
>>> nuisance.inputs.wm_nuisance = True
>>> nuisance.inputs.motion_nuisance = True
>>> nuisance.inputs.nuisance_motion_nb_reg = 36
>>> nuisance.inputs.n_discard = 5
>>> nuisance.run()
```

**brainfile** [a string or `os.PathLike` object] Eroded brain mask registered to fMRI space.

**csf\_file** [a string or `os.PathLike` object] Eroded CSF mask registered to fMRI space.

**csf\_nuisance** [a boolean] If `True` perform CSF nuisance regression.

**global\_nuisance** [a boolean] If `True` perform global nuisance regression.

**gm\_file** [a list of items which are a string or `os.PathLike` object] GM atlas files registered to fMRI space.

**in\_file** [a string or `os.PathLike` object referring to an existing file] Input fMRI volume.

**motion\_file** [a string or `os.PathLike` object] Motion nuisance effect.

**motion\_nuisance** [a boolean] If `True` perform motion nuisance regression.

**n\_discard** [an integer] Number of volumes discarded from the fMRI sequence during preprocessing.

**nuisance\_motion\_nb\_reg** [an integer] Number of reg to use in motion nuisance regression.

**wm\_file** [a string or `os.PathLike` object] Eroded WM mask registered to fMRI space.

**wm\_nuisance** [a boolean] If `True` perform WM nuisance regression.

**averageCSF\_mat** [a string or `os.PathLike` object] Output matrix of CSF regression.

**averageCSF\_npy** [a string or `os.PathLike` object] Output of CSF regression in `np`y format.

**averageGlobal\_mat** [a string or `os.PathLike` object] Output matrix of global regression.

**averageGlobal\_npy** [a string or `os.PathLike` object] Output of global regression in `np`y format.

**averageWM\_mat** [a string or `os.PathLike` object] Output matrix of WM regression.

**averageWM\_npy** [a string or `os.PathLike` object] Output of WM regression in `np`y format.

**out\_file** [a string or `os.PathLike` object referring to an existing file] Output fMRI Volume.

## Scrubbing

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Computes scrubbing parameters: FD and DVARS.

## Examples

```
>>> from cmtklib.functionalMRI import Scrubbing
>>> scrub = Scrubbing()
>>> scrub.inputs.base_dir = '/my_directory'
>>> scrub.inputs.in_file = '/path/to/sub-01_task-rest_desc-preproc_bold.nii.gz'
>>> scrub.inputs.gm_file = ['/path/to/sub-01_space-meanBOLD_atlas-L2018_desc-
↳scale1_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_desc-
↳scale2_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_desc-
↳scale3_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_desc-
↳scale4_dseg.nii.gz',
>>>                               '/path/to/sub-01_space-meanBOLD_atlas-L2018_desc-
↳scale5_dseg.nii.gz']
>>> scrub.inputs.wm_mask = '/path/to/sub-01_space-meanBOLD_label-WM_dseg.nii.gz
↳'
>>> scrub.inputs.gm_file = '/path/to/sub-01_space-meanBOLD_label-GM_dseg.nii.gz
↳'
>>> scrub.inputs.mode = 'quadratic'
>>> scrub.run()
```

**in\_file** [a string or `os.PathLike` object referring to an existing file] FMRI volume to scrub.

**gm\_file** [a list of items which are a string or `os.PathLike` object referring to an existing file] ROI volumes registered to fMRI space.

**motion\_parameters** [a string or `os.PathLike` object referring to an existing file] Motion parameters from preprocessing stage.

**wm\_mask** [a string or `os.PathLike` object referring to an existing file] WM mask registered to fMRI space.

**dvars\_mat** [a string or `os.PathLike` object referring to an existing file] DVARS matrix for scrubbing.

**dvars\_npy** [a string or os.PathLike object referring to an existing file] DVARs in .npy format.

**fd\_mat** [a string or os.PathLike object referring to an existing file] FD matrix for scrubbing.

**fd\_npy** [a string or os.PathLike object referring to an existing file] FD in .npy format.

## cmtklib.parcellation module

Module that defines CMTK utility functions and Nipype interfaces for anatomical parcellation.

### CombineParcellations

[Link to code](#)

Bases: nipype.interfaces.base.core.BaseInterface

Creates the final parcellation.

It combines the original cortico sub-cortical parcellation with the following extra segmented structures:

- Segmentation of the 8 thalamic nuclei per hemisphere
- Segmentation of 14 hippocampal subfields per hemisphere
- Segmentation of 3 brainstem sub-structures

It also generates by defaults the corresponding (1) description of the nodes in **graphml** format and (2) color lookup tables in FreeSurfer format that can be displayed in **freeview**.

### Examples

```
>>> parc_combine = CombineParcellations()
>>> parc_combine.inputs.input_rois = ['/path/to/sub-01_atlas-L2018_desc-scale1_
↳ dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale2_
↳ dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale3_
↳ dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale4_
↳ dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale5_
↳ dseg.nii.gz']
>>> parc_combine.inputs.lh_hippocampal_subfields = '/path/to/lh_hippocampal_
↳ subfields.nii.gz'
>>> parc_combine.inputs.rh_hippocampal_subfields = '/path/to/rh_hippocampal_
↳ subfields.nii.gz'
>>> parc_combine.inputs.brainstem_structures = '/path/to/brainstem_structures.
↳ nii.gz'
>>> parc_combine.inputs.thalamus_nuclei = '/path/to/thalamus_nuclei.nii.gz'
>>> parc_combine.inputs.create_colorLUT = True
>>> parc_combine.inputs.create_graphml = True
>>> parc_combine.inputs.subjects_dir = '/path/to/output_dir/freesurfer')
>>> parc_combine.inputs.subject_id = 'sub-01'
>>> parc_combine.run()
```

**brainstem\_structures** [a pathlike object or string representing a file] Brainstem segmentation file.

**create\_colorLUT** [a boolean] If **True**, create the color lookup table in Freesurfer format.

**create\_graphml** [a boolean] If **True**, create the parcellation node description files in **graphml** format.

**input\_rois** [a list of items which are a pathlike object or string representing an existing file] Input parcellation files.

**lh\_hippocampal\_subfields** [a pathlike object or string representing a file] Input hippocampal subfields file for left hemisphere.

**rh\_hippocampal\_subfields** [a pathlike object or string representing a file] Input hippocampal subfields file for right hemisphere.

**subject\_id** [a string] Freesurfer subject id.

**subjects\_dir** [a pathlike object or string representing a directory] Freesurfer subjects dir.

**thalamus\_nuclei** [a pathlike object or string representing a file] Thalamic nuclei segmentation file.

**verbose\_level** [1 or 2] Verbose level (1: partial (default) / 2: full).

**aparc\_aseg** [a pathlike object or string representing a file] Modified Freesurfer aparc+aseg file.

**colorLUT\_files** [a list of items which are a pathlike object or string representing an existing file] Color lookup table files in Freesurfer format.

**graphML\_files** [a list of items which are a pathlike object or string representing an existing file] Parcellation node description files in **graphml** format.

**output\_rois** [a list of items which are a pathlike object or string representing an existing file] Output parcellation with all structures combined.

`CombineParcellations.ismember(b)`

## ComputeParcellationRoiVolumes

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Computes the volumes of each ROI for each parcellation scale.

### Examples

```
>>> compute_vol = ComputeParcellationRoiVolumes()
>>> compute_vol.inputs.roi_volumes = ['/path/to/sub-01_atlas-L2018_desc-scale1_
↳ dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale2_
↳ dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale3_
↳ dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale4_
↳ dseg.nii.gz',
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale5_
↳ dseg.nii.gz']
>>> compute_vol.inputs.roi_graphmls = ['/path/to/sub-01_atlas-L2018_desc-
↳ scale1_dseg.graphml',
```

(continues on next page)

(continued from previous page)

```
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale2_dseg.  
↳graphml',  
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale3_dseg.  
↳graphml',  
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale4_dseg.  
↳graphml',  
>>>                                     '/path/to/sub-01_atlas-L2018_desc-scale5_dseg.  
↳graphml']  
>>> compute_vol.inputs.parcellation_scheme = ['Lausanne2018']  
>>> compute_vol.run()
```

**parcellation\_scheme** ['NativeFreesurfer' or 'Lausanne2018' or 'Custom'] Parcellation scheme. (Nipype **default** value: Lausanne2018)

**roi\_graphMLs** [a list of items which are a pathlike object or string representing an existing file] GraphML description of ROI volumes (Lausanne2018).

**roi\_volumes** [a list of items which are a pathlike object or string representing an existing file] ROI volumes registered to diffusion space.

**roi\_volumes\_stats** [a list of items which are a pathlike object or string representing a file] TSV files with computed parcellation ROI volumes.

## Parcellate

[Link to code](#)

Bases: nipype.interfaces.base.core.BaseInterface

Subdivides segmented ROI file into smaller subregions.

**This interface interfaces with the CMTK parcellation functions** available in [cmtklib](#). [parcellation](#) module for all parcellation resolutions of a given scheme.

## Example

```
>>> from cmtklib.parcellation import Parcellate  
>>> parcellate = Parcellate()  
>>> parcellate.inputs.subjects_dir = '/path/to/output_dir/freesurfer'  
>>> parcellate.inputs.subject_id = 'sub-01'  
>>> parcellate.inputs.parcellation_scheme = 'Lausanne2018'  
>>> parcellate.run()
```

**subject\_id** [a string] Subject ID.

**erode\_masks** [a boolean] If **True** erode the masks.

**parcellation\_scheme** ['Lausanne2018' or 'NativeFreesurfer'] Parcellation scheme. (Nipype **default** value: Lausanne2018)

**subjects\_dir** [a pathlike object or string representing a directory] Freesurfer main directory.

**T1** [a pathlike object or string representing a file] T1 image file.

**aparc\_aseg** [a pathlike object or string representing a file] APArc+ASeg image file (in native space).

**aseg** [a pathlike object or string representing a file] ASeg image file (in native space).

**brain** [a pathlike object or string representing a file] Brain-masked T1 image file.

**brain\_eroded** [a pathlike object or string representing a file] Eroded brain file in original space.

**brain\_mask** [a pathlike object or string representing a file] Brain mask file.

**csf\_eroded** [a pathlike object or string representing a file] Eroded csf file in original space.

**csf\_mask\_file** [a pathlike object or string representing a file] Cerebrospinal fluid (CSF) mask file.

**gray\_matter\_mask\_file** [a pathlike object or string representing a file] Cortical gray matter (GM) mask file.

**ribbon\_file** [a pathlike object or string representing an existing file] Image file detailing the cortical ribbon.

**roi\_files\_in\_structural\_space** [a list of items which are a pathlike object or string representing an existing file] ROI image resliced to the dimensions of the original structural image.

**white\_matter\_mask\_file** [a pathlike object or string representing a file] White matter (WM) mask file.

**wm\_eroded** [a pathlike object or string representing a file] Eroded wm file in original space.

### ParcellateBrainstemStructures

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Parcellates the brainstem sub-structures using Freesurfer [Iglesias2015Brainstem].

#### References

#### Examples

```
>>> parc_bstem = ParcellateBrainstemStructures()
>>> parc_bstem.inputs.subjects_dir = '/path/to/derivatives/freesurfer'
>>> parc_bstem.inputs.subject_id = 'sub-01'
>>> parc_bstem.run()
```

**subject\_id** [a string] Subject ID.

**subjects\_dir** [a pathlike object or string representing a directory] Freesurfer main directory.

**brainstem\_structures** [a pathlike object or string representing a file] Parcellated brainstem structures file.

### ParcellateHippocampalSubfields

[Link to code](#)

Bases: `nipy.interfaces.base.core.BaseInterface`

Parcellates the hippocampal subfields using Freesurfer [Iglesias2015Hippo].

## References

### Examples

```
>>> parc_hippo = ParcellateHippocampalSubfields()
>>> parc_hippo.inputs.subjects_dir = '/path/to/derivatives/freesurfer'
>>> parc_hippo.inputs.subject_id = 'sub-01'
>>> parc_hippo.run()
```

**subject\_id** [a string] Subject ID.

**subjects\_dir** [a pathlike object or string representing a directory] Freesurfer main directory.

**lh\_hipposubfields** [a pathlike object or string representing a file] Left hemisphere hippocampal subfields file.

**rh\_hipposubfields** [a pathlike object or string representing a file] Right hemisphere hippocampal subfields file.

## ParcellateThalamus

[Link to code](#)

Bases: `nipype.interfaces.base.core.BaseInterface`

Parcellates the thalamus into 8 nuclei using an atlas-based method [Najdenovska18].

## References

### Examples

```
>>> parc_thal = ParcellateThalamus()
>>> parc_thal.inputs.T1w_image = File(mandatory=True, desc='T1w image to be
↳ parcellated')
>>> parc_thal.inputs.bids_dir = Directory(desc='BIDS root directory')
>>> parc_thal.inputs.subject = '01'
>>> parc_thal.inputs.template_image = '/path/to/atlas/T1w.nii.gz'
>>> parc_thal.inputs.thalamic_nuclei_maps = '/path/to/atlas/nuclei/probability/
↳ map.nii.gz'
>>> parc_thal.inputs.subjects_dir = '/path/to/output_dir/freesurfer'
>>> parc_thal.inputs.subject_id = 'sub-01'
>>> parc_thal.inputs.ants_precision_type = 'float'
>>> parc_thal.run()
```

**T1w\_image** [a pathlike object or string representing a file] T1w image to be parcellated.

**subject\_id** [a string] Subject ID.

**subjects\_dir** [a pathlike object or string representing a directory] Freesurfer main directory.

**template\_image** [a pathlike object or string representing a file] Template T1w.

**thalamic\_nuclei\_maps** [a pathlike object or string representing a file] Probability maps of thalamic nuclei (4D image) in template space.

**ants\_precision\_type** ['double' or 'float'] Precision type used during computation.



**bids\_dir** [a pathlike object or string representing a directory] BIDS root directory.

**session** [a string] Session id.

**subject** [a string] Subject id.

**inverse\_warped\_image** [a pathlike object or string representing a file] Inverse warped template.

**max\_prob\_registered** [a pathlike object or string representing a file] Max probability label image (native).

**prob\_maps\_registered** [a pathlike object or string representing a file] Probabilistic map of thalamus nuclei (native).

**thalamus\_mask** [a pathlike object or string representing a file] Thalamus mask.

**transform\_file** [a pathlike object or string representing a file] Transform file.

**warp\_file** [a pathlike object or string representing a file] Deformation file.

**warped\_image** [a pathlike object or string representing a file] Template registered to T1w image (native).

`cmtklib.parcellation.create_T1_and_Brain(subject_id, subjects_dir)`

Generates T1, T1 masked and aseg+aparc Freesurfer images in NIFTI format.

#### Parameters

- **subject\_id** (*string*) – Freesurfer subject id
- **subjects\_dir** (*string*) – Freesurfer subjects dir (Typically /path/to/output\_dir/freesurfer)

`cmtklib.parcellation.create_roi(subject_id, subjects_dir, v=True)`

Iteratively creates the ROI\_%s.nii.gz files using the given Lausanne2018 parcellation information from networks.

#### Parameters

- **subject\_id** (*string*) – Freesurfer subject id
- **subjects\_dir** (*string*) – Freesurfer subjects dir (Typically /path/to/output\_dir/freesurfer)
- **v** (*Boolean*) – Verbose mode

`cmtklib.parcellation.create_wm_mask(subject_id, subjects_dir, v=True)`

Creates the white-matter mask using the Freesurfer ribbon as basis in the Lausanne2018 framework.

#### Parameters

- **subject\_id** (*string*) – Freesurfer subject id
- **subjects\_dir** (*string*) – Freesurfer subjects dir (Typically /path/to/output\_dir/freesurfer)
- **v** (*Boolean*) – Verbose mode

`cmtklib.parcellation.crop_and_move_WM_and_GM(subject_id, subjects_dir)`

Convert Freesurfer images back to original native space when NativeFreesurfer parcellation scheme is used.

#### Parameters

- **subject\_id** (*string*) – Freesurfer subject id
- **subjects\_dir** (*string*) – Freesurfer subjects dir (Typically /path/to/output\_dir/freesurfer)

`cmtklib.parcellation.crop_and_move_datasets(subject_id, subjects_dir)`

Convert Freesurfer images back to original native space when Lausanne2018 parcellation schemes are used.

**Parameters**

- **subject\_id** (*string*) – Freesurfer subject id
- **subjects\_dir** (*string*) – Freesurfer subjects dir (Typically /path/to/output\_dir/freesurfer)

`cmtklib.parcellation.erode_mask(fsd, mask_file)`

Erodes the mask and saves it the Freesurfer subject directory.

**Parameters**

- **fsdir** (*string*) – Freesurfer subject directory
- **mask\_file** (*string*) – Path to mask file

`cmtklib.parcellation.extract(Z, shape, position, fill)`

Extract voxel neighbourhood.

**Parameters**

- **Z** (*numpy.array*) – The original data
- **shape** (*tuple*) – Tuple containing neighbourhood dimensions
- **position** (*tuple*) – Tuple containing central point indexes
- **fill** (*value*) – Value for the padding of Z

**Returns** **R** – The output neighbourhood of the specified point in Z

**Return type** `numpy.array`

`cmtklib.parcellation.generate_WM_and_GM_mask(subject_id, subjects_dir)`

Generates the white-matter and gray-matter masks when NativeFreesurfer parcellation is used.

**Parameters**

- **subject\_id** (*string*) – Freesurfer subject id
- **subjects\_dir** (*string*) – Freesurfer subjects dir (Typically /path/to/output\_dir/freesurfer)

`cmtklib.parcellation.get_parcellation(parcel='NativeFreesurfer')`

Returns a dictionary containing atlas information.

---

**Note:** `atlas_info` often used in the code refers to such a dictionary.

---

**Parameters** **parcel** (*parcellation scheme*) – It can be: 'NativeFreesurfer' or 'Lausanne2018'

**cmtklib.util module**

Module that defines CMTK Utility functions.

**class** `cmtklib.util.BColors`

Bases: `object`

Utility class for color unicode.

**BOLD** = `'\x1b[1m'`

**ENDC** = `'\x1b[0m'`

```
FAIL = '\x1b[91m'
```

```
HEADER = '\x1b[95m'
```

```
OKBLUE = '\x1b[94m'
```

```
OKGREEN = '\x1b[92m'
```

```
UNDERLINE = '\x1b[4m'
```

```
WARNING = '\x1b[93m'
```

```
cmtklib.util.check_directory_exists(mandatory_dir)
```

Makes sure the mandatory directory exists.

**Raises** `FileNotFoundError` – Raised when the directory is not found.

```
cmtklib.util.convert_list_to_tuple(lists)
```

Convert list of files to tuple of files.

(Duplicated with preprocessing, could be moved to utils in the future)

**Parameters** `lists` (`[bvecs, bvals]`) – List of files containing bvecs and bvals

**Returns** `out_tuple` – Tuple of files containing bvecs and bvals

**Return type** (`bvecs, bvals`)

```
cmtklib.util.extract_freesurfer_subject_dir(reconall_report, local_output_dir=None, debug=False)
```

Extract Freesurfer subject directory from the report created by Nipype Freesurfer Recon-all node.

**Parameters**

- **reconall\_report** (`string`) – Path to the recon-all report
- **local\_output\_dir** (`string`) – Local output / derivatives directory
- **debug** (`bool`) – If `True`, show printed outputs

**Returns** `fs_subject_dir` – Freesurfer subject directory

**Return type** `string`

```
cmtklib.util.extract_reconall_base_dir(file)
```

Extract Recon-all base directory from a file.

**Parameters** `file` (`File`) – File generated by Recon-all

**Returns** `out_path` – Recon-all base directory

**Return type** `string`

```
cmtklib.util.get_basename(path)
```

Return `os.path.basename()` of a path.

**Parameters** `path` (`os.path`) – Path to extract the containing directory

**Returns** `path` – Path to the containing directory

**Return type** `os.path`

```
cmtklib.util.get_freesurfer_subject_id(file)
```

Extract Freesurfer subject ID from file generated by recon-all.

**Parameters** `file` (`str`) – File generated by recon-all

**Returns** `out` – Freesurfer subject ID

**Return type** `str`

`cmtklib.util.get_pipeline_dictionary_outputs(datasink_report, local_output_dir=None, debug=False)`  
Read the Nipype datasink report and return a dictionary of pipeline outputs.

**Parameters**

- **datasink\_report** (*string*) – Path to the datasink report
- **local\_output\_dir** (*string*) – Local output / derivatives directory
- **debug** (*bool*) – If **True**, print output dictionary

**Returns** **dict\_outputs** – Dictionary of pipeline outputs

**Return type** `dict`

`cmtklib.util.isavailable(file)`

Check if file is available and return the file if it is.

Used for debugging.

**Parameters** **file** (*File*) – Input file

**Returns** **file** – Output file

**Return type** `File`

`cmtklib.util.length(xyz, along=False)`

Euclidean length of track line.

**Parameters**

- **xyz** (*array-like shape (N, 3)*) – array representing x,y,z of N points in a track
- **along** (*bool, optional*) – If **True**, return array giving cumulative length along track, otherwise (default) return scalar giving total length.

**Returns** **L** – scalar in case of **along == False**, giving total length, array if **along == True**, giving cumulative lengths.

**Return type** scalar or array shape (N-1,)

## Examples

```
>>> xyz = np.array([[1,1,1],[2,3,4],[0,0,0]])
>>> expected_lens = np.sqrt([1+2**2+3**2, 2**2+3**2+4**2])
>>> length(xyz) == expected_lens.sum()
True
>>> len_along = length(xyz, along=True)
>>> np.allclose(len_along, expected_lens.cumsum())
True
>>> length([])
0
>>> length([[1, 2, 3]])
0
>>> length([], along=True)
array([0])
```

`cmtklib.util.magn(xyz, n=1)`

Returns the vector magnitude

**Parameters**

- **xyz** (*vector*) – Input vector
- **n** (*int*) – Tile by n if n>1 before return

`cmtklib.util.mean_curvature(xyz)`

Calculates the mean curvature of a curve.

**Parameters** **xyz** (*array-like shape (N,3)*) – array representing x,y,z of N points in a curve

**Returns** **m** – float representing the mean curvature

**Return type** `float`

## Examples

Create a straight line and a semi-circle and print their mean curvatures

```
>>> from dipy.tracking import metrics as tm
>>> import numpy as np
>>> x=np.linspace(0,1,100)
>>> y=0*x
>>> z=0*x
>>> xyz=np.vstack((x,y,z)).T
>>> m=tm.mean_curvature(xyz) # mean curvature straight line
>>> theta=np.pi*np.linspace(0,1,100)
>>> x=np.cos(theta)
>>> y=np.sin(theta)
>>> z=0*x
>>> xyz=np.vstack((x,y,z)).T
>>> m=tm.mean_curvature(xyz) # mean curvature for semi-circle
```

`cmtklib.util.print_blue(message)`

Print blue-colored message

**Parameters** **message** (*string*) – The string of the message to be printed

`cmtklib.util.print_error(message)`

Print red-colored error message

**Parameters** **message** (*string*) – The string of the message to be printed

`cmtklib.util.print_warning(message)`

Print yellow-colored warning message

**Parameters** **message** (*string*) – The string of the message to be printed

`cmtklib.util.return_button_style_sheet(image, image_disabled=None, verbose=False)`

Return Qt style sheet for QPushButton with image

**Parameters**

- **image** (*string*) – Path to image to use as icon when button is enabled
- **image\_disabled** (*string*) – Path to image to use as icon when button is disabled
- **verbose** (*Bool*) – Print the style sheet if True Default: False

**Returns** **button\_style\_sheet** – Qt style sheet for QPushButton with image

**Return type** `string`

`cmtklib.util.unicode2str(text)`

Convert a unicode to a string using system's encoding.

**Parameters** `text` (*bytes*) – Unicode bytes representation of a string

**Returns** `out_str` – Output string

**Return type** `str`

## 5.7 Adopting Datalad for collaboration

Datalad is a powerful tool for the versioning and sharing of raw and processed data as well as for the tracking of data provenance (i.e. the recording on how data was processed). This page was created with the intention to share with the user how we adopted datalad to manage and process datasets with Connectome Mapper 3 in our lab, following the YODA principles to our best.

You may ask “What are the YODA principles?”. They are basic principles behind creating, sharing, and publishing reproducible, understandable, and open data analysis projects with DataLad.

For more details and tutorials on Datalad and YODA, please check the recent [Datalad Handbook](#) and the [YODA principles](#).

### Happy Collaborative and Reproducible Connectome Mapping!

---

**Note:** This was tested on Ubuntu 16.04 with Datalad 0.14.0, its extensions `datalad-container 1.1.2`, `datalad-neuroimaging 0.3.1`, and `git-annex 8.20210127`.

---

### 5.7.1 Prerequisites

- Python3 must be installed with Datalad and all dependencies. You can use the conda environment `py37cmp-gui` for instance. See [Installation of py37cmp-gui](#) for more installation details.
- A recent version of `git-annex` and `liblzma` (included in `py37cmp-gui` for Ubuntu/Debian).
- Docker must be installed on systems running Connectome Mapper 3. See [Prerequisites of Connectome Mapper 3](#) for more installation instructions.

### 5.7.2 Copy BIDS dataset to server

Copy the raw BIDS dataset using `rsync`:

```
rsync -P -avz -e 'ssh' \  
--exclude 'derivatives' \  
--exclude 'code' \  
--exclude '.datalad' \  
--exclude '.git' \  
--exclude '.gitattributes' \  
/path/to/ds-example/* \  
<SERVER_USERNAME>@<SERVER_IP_ADDRESS>:/archive/data/ds-example
```

where:

- `-P` is used to show progress during transfer

- `-v` increases verbosity
- `-e` specifies the remote shell to use (ssh)
- `-a` indicates archive mode
- `-z` enables file data compression during the transfer
- `--exclude DIR_NAME` exclude the specified DIR\_NAME from the copy

### 5.7.3 Remote datalad dataset creation on Server

#### Connect to Server

To connect with SSH:

```
ssh <SERVER_USERNAME>@<SERVER_IP_ADDRESS>
```

#### Creation of Datalad dataset

Go to the source dataset directory:

```
cd /archive/data/ds-example
```

Initialize the Datalad dataset:

```
datalad create -f -c text2git -D "Original example dataset on lab server" -d .
```

where:

- `-f` forces to create the datalad dataset if not empty
- `-c text2git` configures Datalad to use git to manage text file
- `-D` gives a brief description of the dataset
- `-d` specify the location where the Datalad dataset is created

Track all files contained in the dataset with Datalad:

```
datalad save -m "Source (Origin) BIDS dataset" --version-tag origin
```

where:

- `-m MESSAGE` is the description of the state or the changes made to the dataset
- `--version-tag` tags the state of the Dataset

Report on the state of dataset content:

```
datalad status -r
git log
```

## 5.7.4 Processing using the Connectome Mapper BIDS App on Alice's workstation

### Processed dataset creation

Initialize a datalad dataset with the YODA procedure:

```
datalad create -c text2git -c yoda \  
-D "Processed example dataset by Alice with CMP3" \  
/home/alice/data/ds-example-processed
```

This will create a datalad dataset with:

- a code directory in your dataset
- three files for human consumption (README.md, CHANGELOG.md)
- everything in the code/ directory configured to be tracked by Git, not git-annex
- README.md and CHANGELOG.md configured in the root of the dataset to be tracked by Git
- Text files configured to be tracked by Git

Go to the created dataset directory:

```
cd /home/alice/data/ds-example-processed
```

Create the derivatives output directory:

```
mkdir derivatives
```

### Raw BIDS dataset installation

Install the remote datalad dataset ds-example in /home/alice/data/ds-example-processed/input/:

```
datalad install -d . -s ssh://<SERVER_USERNAME>@<SERVER_IP_ADDRESS>:/archive/data/ds-  
example \  
/home/alice/data/ds-example-processed/input/
```

where:

- -s SOURCE specifies the URL or local path of the installation source

### Get T1w and Diffusion images to be processed

For reproducibility, create and write datalad get commands to get\_required\_files\_for\_analysis.sh:

```
echo "datalad get input/sub-*/ses-*/anat/sub-*_T1w.nii.gz" > code/get_required_files_for_  
analysis.sh  
echo "datalad get input/sub-*/ses-*/dwi/sub-*_dwi.nii.gz" >> code/get_required_files_for_  
analysis.sh  
echo "datalad get input/sub-*/ses-*/dwi/sub-*_dwi.bvec" >> code/get_required_files_for_  
analysis.sh  
echo "datalad get input/sub-*/ses-*/dwi/sub-*_dwi.bval" >> code/get_required_files_for_  
analysis.sh
```

Save the script to the dataset's history:



```
datalad save -m "Add script to get the files required for analysis by Alice"
```

Execute the script:

```
sh code/get_required_files_for_analysis.sh
```

### Link the container image with the dataset

Add Connectome Mapper's container image to the datalad dataset:

```
datalad containers-add connectomemapper-bidsapp-<VERSION_TAG> \
--url dhub://sebastientourbier/connectomemapper-bidsapp:<VERSION_TAG> \
-d . \
--call-fmt \
"docker run --rm -t \
  -v "$(pwd)/input":/bids_dir \
  -v "$(pwd)/code":/bids_dir/code \
  -v "$(pwd)/derivatives:/output_dir \
  -u "$(id -u)": "$(id -g)" \
  sebastientourbier/connectomemapper-bidsapp:<VERSION_TAG> {cmd}"
```

**Note:** `--call-fmt` specifies a custom docker run command. The current directory is assumed to be the BIDS root directory and retrieve with `"$(pwd)/input` and the output directory is inside the `derivatives/` folder.

**Important:** The name of the container-name registered to Datalad cannot have dot as character so that a `<VERSION_TAG>` of `v3.X.Y` would need to be rewritten as `v3-X-Y`

Copy existing reference pipeline configuration files to `code` folder:

```
cp /path/to/existing/ref_anatomical_config.json \
code/ref_anatomical_config.json
cp /path/to/existing/ref_diffusion_config.json \
code/ref_diffusion_config.json
```

Copy FreeSurfer license file to `code` folder:

```
cp /path/to/freesurfer/license.txt \
code/license.txt
```

Save the state of the dataset prior to analysis:

```
datalad save -m "Alice's test dataset on local \
workstation ready for analysis with connectomemapper-bidsapp:<VERSION_TAG>" \
--version-tag ready4analysis-<date>-<time>
```

## Run Connectome Mapper with Datalad

Run Connectome Mapper on all subjects:

```
datalad containers-run --container-name connectomemapper-bidsapp-<VERSION_TAG> \
--input code/ref_anatomical_config.json \
--input code/ref_diffusion_config.json \
--output derivatives \
/bids_dir /output_dir participant \
--anat_pipeline_config '/bids_dir/{inputs[0]}' \
--dwi_pipeline_config '/bids_dir/{inputs[1]}'
```

---

**Note:** `datalad containers-run` will take of replacing the `{inputs[i]}` by the value specified by the *i* `--input` flag (Indexing start at 0).

---

Save the state:

```
datalad save -m "Alice's test dataset on local \
workstation processed by connectomemapper-bidsapp:<VERSION_TAG>, {Date/Time}" \
--version-tag processed-<date>-<time>
```

Report on the state of dataset content:

```
datalad status -r
git log
```

## Configure a datalad dataset target on the Server

Create a remote dataset repository and configures it as a dataset sibling to be used as a publication target:

```
datalad create-sibling --name remote -d . \
<SERVER_USERNAME>@<SERVER_IP_ADDRESS>:/archive/data/ds-example-processed
```

See the documentation of `datalad create-sibling` command for more details.

## Update the remote datalad dataset

Push the datalad dataset with data derivatives to the server:

```
datalad push -d . --to remote
```

---

**Note:** `--to remote` specifies the remote dataset sibling i.e. `ssh://<SERVER_USERNAME>@<SERVER_IP_ADDRESS>:/archive/data/ds-example-processed` previously configured.

---

### Uninstall all files accessible from the remote

With DataLad we don't have to keep those inputs around so you can safely uninstall them without losing the ability to reproduce an analysis:

```
datalad uninstall input/sub-*/*
```

## 5.7.5 Local collaboration with Bob for Electrical Source Imaging

### Processed dataset installation on Bob's workstation

Install the processed datalad dataset ds-example-processed in /home/bob/data/ds-example-processed:

```
datalad install -s ssh://<SERVER_USERNAME>@<SERVER_IP_ADDRESS>:/archive/data/ds-example-processed \
/home/bob/data/ds-example-processed
```

Go to datalad dataset clone directory:

```
cd /home/bob/data/ds-example-processed
```

### Get connectome mapper output files (Brain Segmentation and Multi-scale Parcellation) used by Bob in his analysis

For reproducibility, write datalad get commands to get\_required\_files\_for\_analysis\_by\_bob.sh:

```
echo "datalad get derivatives/cmp/sub-*/ses-*/anat/sub-*_mask.nii.gz" \
> code/get_required_files_for_analysis_by_bob.sh
echo "datalad get derivatives/cmp/sub-*/ses-*/anat/sub-*_class-*_dseg.nii.gz" \
>> code/get_required_files_for_analysis_by_bob.sh
echo "datalad get derivatives/cmp/sub-*/ses-*/anat/sub-*_scale*_atlas.nii.gz" \
>> code/get_required_files_for_analysis_by_bob.sh
```

Save the script to the dataset's history:

```
datalad save -m "Add script to get the files required for analysis by Bob"
```

Execute the script:

```
sh code/get_required_files_for_analysis_by_bob.sh
```

### Update derivatives

Update derivatives with data produced by Cartool:

```
cd /home/bob/data/ds-example
mkdir derivatives/cartool
cp [...]
```

Save the state:

```
datalad save -m "Bob's test dataset on local \
workstation processed by cartool:<CARTOOL_VERSION>, {Date/Time}" \
--version-tag processed-<date>-<time>
```

Report on the state of dataset content:

```
datalad status -r
git log
```

### Update the remote datalad dataset

Update the remote datalad dataset with data derivatives:

```
datalad push -d . --to origin
```

---

**Note:** `--to origin` specifies the origin dataset sibling i.e. `ssh://<SERVER_USERNAME>@<SERVER_IP_ADDRESS>:/archive/data/ds-example-processed` from which it was cloned.

---

### Uninstall all files accessible from the remote

Again, with DataLad we don't have to keep those inputs around so you can safely uninstall them without losing the ability to reproduce an analysis:

```
datalad uninstall derivatives/cmp-*/**
datalad uninstall derivatives/freesurfer-*/**
datalad uninstall derivatives/nipype-*/**
```

---

**Authors** Sebastien Tourbier

**Version** Revision: 2.1 (Last modification: 2022 Feb 09)

## 5.8 Running on a cluster (HPC)

Connectome Mapper 3 BIDS App can be run on a cluster using Singularity.

For your convenience, the Singularity image is automatically built along the docker image using Singularity 3.8.4 and deployed to [Sylabs.io](https://sylabs.io) (equivalent of DockerHub for Singularity) during continuous integration on CircleCI. It can be freely downloaded with the following command:

```
$ singularity pull library://connectomicslab/default/connectomemapper-bidsapp:latest
```

If you prefer, you can still build the Singularity image on your side using one of the 2 methods described in [Conversion to a Singularity image](#).

A list of useful singularity command can be found in [Useful singularity commands](#). For more documentation about Singularity, please check the [official documentation website](#).

**Happy Large-Scale Connectome Mapping!**

### 5.8.1 Prerequisites

- Singularity must be installed. Check the [official documentation webpage](#) for installation instructions.

### 5.8.2 Running the singularity image

The following example shows how to call from the terminal the Singularity image of the CMP3 BIDS App to perform both anatomical and diffusion pipelines for sub-01, sub-02 and sub-03 of a BIDS dataset whose root directory is located at `${localDir}`:

```
$ singularity run --containall \
  --bind ${localDir}:/bids_dir --bind ${localDir}/derivatives:/output_dir \
  library://connectomicslab/default/connectomemapper-bidsapp:|release| \
  /bids_dir /output_dir participant --participant_label 01 02 03 \
  --anat_pipeline_config /bids_dir/code/ref_anatomical_config.json \
  --dwi_pipeline_config /bids_dir/code/ref_diffusion_config.json \
  --fs_license /bids_dir/code/license.txt \
  --number_of_participants_processed_in_parallel 3
```

**Note:** As you can see, the `singularity run` command is slightly different from the `docker run`. The `docker` option flag `-v` is replaced by the `singularity --bind` to map local folders inside the container. Last but not least, while `docker` containers are executed in total isolation, `singularity` images **MUST** run with the option flag `--containall`. Otherwise your `$HOME` and `$TMP` directories or your local environment variables might be shared inside the container.

### 5.8.3 Conversion to a Singularity image

It actually exists two options for Docker to Singularity container image conversion. Let's say we want to store Singularity-compatible image file in `~/Softwares/singularity/`.

#### Option 1 (recommended): Using the Docker image `docker2singularity`

1. Build locally in a `/tmp/test` folder:

```
$ mkdir -p /tmp/test
$ docker run -v /var/run/docker.sock:/var/run/docker.sock \
  -v /tmp/test:/output --privileged -t --rm \
  singularityware/docker2singularity \
  --name cmp-v3.0.3.simg \
  sebastientourbier/connectomemapper-bidsapp:v3.0.3
```

2. Move the converted image `cmp-|release|` to the `~/Softwares/singularity` folder on the cluster (via `ssh` using `scp` for instance)

```
$ scp -v /tmp/test/cmp-v3.0.3.simg <user>@<cluster_url>:~/Softwares/singularity/
↪ cmp-v3.0.3.simg
```

**Advantage(s):** Has never failed

**Disadvantage(s):** Have to make a-priori the conversion locally on a workstation where `docker` is installed and then upload the converted image to the cluster

### Option 2 : Using singularity directly

```
$ singularity build ~/Softwares/singularity/cmp-v3.0.3.simg \
    docker://sebastientourbier/connectomemapper-bidsapp:v3.0.3
```

This command will directly download the latest version release of the Docker image from the DockerHub and convert it to a Singularity image.

**Advantage(s):** Can be executed on the cluster directly

**Disadvantage(s):** Has shown to fail because of some docker / singularity version incompatibilities

## 5.8.4 Useful singularity commands

- Display a container's metadata:

```
$ singularity inspect ~/Softwares/singularity/cmp-v3.0.3.simg
```

- Clean cache:

```
$ singularity cache clean
```

---

**Authors** Sebastien Tourbier

**Version** Revision: 2 (Last modification: 2021 Jan 04)

## 5.9 Tutorial notebooks

### 5.9.1 Analysis Tutorial

This tutorial demonstrates how to analyze and interpret the outputs from Connectomemapper 3. In particular it will tell you how to:

- Get the list of connectome files with [Pybids](#)
- Read the .tsv connectome files with [Networkx](#) and [Pandas](#)
- Read the .gpickle files with [Networkx](#)
- Read the .mat files with [Scipy](#)
- Compute the connectome harmonics with [PyGSP](#)
- Visualize the harmonics with the plot functions of [Nilearn](#)

### Setup instructions

If you want to reproduce all the results of this notebook on your side, a conda `environment.yml` file can be downloaded at the following link: [tutorial\\_environment.yml](#). The original `.ipynb` notebook file can be downloaded at the following link: [analysis\\_tutorial.ipynb](#).

Once you have downloaded the conda environment file, install the environment as follows:

```
$ conda create env -f /path/to/downloaded/analysis_tutorial.yml
```

This will install all the packages needed to run this notebook including jupyter lab.

You can then activate it, go to the directory where you downloaded the `analysis_tutorial.ipynb`, and launch jupyter lab as follows:

```
$ cd /directory/of/downloaded/analysis_tutorial.ipynb/
$ conda activate cmp3-tutorial
$ jupyter lab
```

You are ready to open and interact with the notebook!

### Loading the external python packages

```
[1]: # General
import os
import sys
import subprocess
import copy

# Dataset management
import datalad.api as dl

# Data handling
import pandas as pd
import numpy as np
import nibabel as nib
import scipy.io as sio

# BIDS dataset handling
from bids import BIDSLayout

# Network / Graph
import pygsp
import networkx as nx

# Visualization
import seaborn as sns
import matplotlib.pyplot as plt
from matplotlib.colors import LogNorm
import nilearn
from nilearn import plotting, image, datasets

/Applications/miniconda3/envs/cmp3-tutorial/lib/python3.7/site-packages/nilearn/datasets/
↳__init__.py:96: FutureWarning: Fetchers from the nilearn.datasets module will be
↳updated in version 0.9 to return python strings instead of bytes and Pandas dataframes.
↳instead of Numpy arrays.
  "Numpy arrays.", FutureWarning)
```

## Loading the connectome files

For demonstration, we are going to use the latest version of VEPCON dataset, available on [Open Neuro](#) that already contains output from Connectome Mapper v3.0.3. A full description of the dataset can be found in [Pascucci, Tourbier, et al. 2022](#).

In case you want to rerun the notebook, make sure to remove any `ds003505_demo` folder in the directory of the notebook. Otherwise, datalad install will complain.

```
[ ]: %%time
# Download example dataset with datalad
dataset_dir = os.path.join(".", "ds003505_demo")
vepcon_data = dl.install(
    path=dataset_dir,
    source="git@github.com:OpenNeuroDatasets/ds003505.git"
)

[INFO] Cloning dataset to Dataset(/Users/sebastientourbier/Documents/GitHub/
↳connectomemapper3/docs/notebooks/ds003505_demo)
[INFO] Attempting to clone from git@github.com:OpenNeuroDatasets/ds003505.git to /Users/
↳sebastientourbier/Documents/GitHub/connectomemapper3/docs/notebooks/ds003505_demo
[INFO] Start enumerating objects
[INFO] Start counting objects
[INFO] Start compressing objects
[INFO] Start receiving objects
[INFO] Start resolving deltas
[INFO] Completed clone attempts for Dataset(/Users/sebastientourbier/Documents/GitHub/
↳connectomemapper3/docs/notebooks/ds003505_demo)
[INFO] scanning for annexed files (this may take some time)
[INFO] Unable to parse git config from origin
[INFO] [ERROR] BrokenPipeError([Errno 32] Broken pipe) (BrokenPipeError)
[INFO] Remote origin does not have git-annex installed; setting annex-ignore
[INFO] This could be a problem with the git-annex installation on the remote. Please
↳make sure that git-annex-shell is available in PATH when you ssh into the remote. Once
↳you have fixed the git-annex installation, run: git annex enableremote origin
[INFO] access to 1 dataset sibling s3-PRIVATE not auto-enabled, enable with:
|           datalad siblings -d "/Users/sebastientourbier/Documents/GitHub/
↳connectomemapper3/docs/notebooks/ds003505_demo" enable -s s3-PRIVATE

CPU times: user 115 ms, sys: 73 ms, total: 188 ms
Wall time: 45.5 s
```

As the dataset is in [BIDS](#), we can use [Pybids](#) to help us with the task of interacting with the files of the dataset.

```
[ ]: # Represent the BIDS dataset as a PyBIDS BIDSLayout
layout = BIDSLayout(vepcon_data.path)
# Add derivative folder containing the connectivity matrices
layout.add_derivatives(os.path.join(vepcon_data.path, "derivatives", "cmp-v3.0.3"))
```

Now we can easily query for the filenames of the files we are interested in using `layout.get`. We will ask for the connectivity matrix of subject 01, scale 3, in tsv format.

It will be returned as a list of file paths (in this case containing just one element). Note that at this stage the Datalad dataset contains mostly file annexes.



As the connectome in TSV format, are just text files, they are directly managed by Git, such that we do have to retrieve its actual content before querying them.

```
[4]: # Query the connectome file path
conn_tsv_scale3 = layout.get(
    subject='01',
    datatype='dwi',
    atlas='L2018',
    res='scale3',
    suffix='connectivity',
    extension='tsv',
    return_type='filename'
)
conn_tsv_scale3
```

```
[4]: ['/Users/sebastientourbier/Documents/GitHub/connectomemapper3/docs/notebooks/ds003505_
↳demo/derivatives/cmp-v3.0.3/sub-01/dwi/sub-01_atlas-L2018_res-scale3_conndata-network_
↳connectivity.tsv']
```

We can then use [Pandas](#) to read the file and display it as a table.

```
[5]: edges = pd.read_csv(conn_tsv_scale3[0], delimiter="\t")
edges.head()
```

```
[5]:
```

	source	target	number_of_fibers	fiber_length_mean	fiber_length_median	\
0	1	1	193	6.800518	6.000000	
1	1	8	23	16.173914	17.000004	
2	1	3	98	9.382652	8.000008	
3	1	4	5	23.299999	23.000008	
4	1	111	63	9.484127	8.499999	

	fiber_length_std	fiber_proportion	fiber_density	\
0	2.242513	0.118146	0.007391	
1	5.212046	0.014080	0.000411	
2	3.732647	0.059991	0.002899	
3	0.678231	0.003061	0.000070	
4	3.311797	0.038566	0.001030	

	normalized_fiber_density	FA_mean	FA_std	FA_median	ADC_mean	\
0	0.052092	0.196300	0.084466	0.177124	0.000785	
1	0.002896	0.227573	0.094389	0.218950	0.000815	
2	0.020433	0.195890	0.081233	0.185918	0.000786	
3	0.000490	0.229370	0.093624	0.229142	0.000787	
4	0.007262	0.242134	0.064675	0.254462	0.000816	

	ADC_std	ADC_median
0	0.000082	0.000777
1	0.000067	0.000813
2	0.000069	0.000790
3	0.000086	0.000782
4	0.000096	0.000803

Using [Networkx](#), we can convert this table to a network graph. From that, we can convert individual measures to a [Numpy](#) array. The array format is especially useful, as it allows us to plot the edge weights easily.

```
[6]: G = nx.from_pandas_edgelist(edges, edge_attr=True)
A_fiber_density = nx.to_numpy_array(G, weight="fiber_density")
A_fiber_density

[6]: array([[0.00739067, 0.00041088, 0.00289892, ..., 0.          , 0.          ,
0.          ],
[0.00041088, 0.00541092, 0.00340868, ..., 0.          , 0.          ,
0.          ],
[0.00289892, 0.00340868, 0.0055656 , ..., 0.          , 0.          ,
0.          ],
...,
[0.          , 0.          , 0.          , ..., 0.00909844, 0.          ,
0.          ],
[0.          , 0.          , 0.          , ..., 0.          , 0.00863366,
0.          ],
[0.          , 0.          , 0.          , ..., 0.          , 0.          ,
0.00504128]])
```

Alternatively, we can also load the matrices in network format, by reading the gpickle files using Networkx:

```
[7]: # Retrieve content of the connectome file with datalad
vepcon_data.get('derivatives/cmp-v3.0.3/sub-01/dwi/sub-01_atlas-L2018_res-scale3_
↳conndata-network_connectivity.gpickle')
# Query the connectome file path
conn_gpickle_scale3 = layout.get(
    subject='01',
    datatype='dwi',
    atlas='L2018',
    res='scale3',
    suffix='connectivity',
    extension='gpickle',
    return_type='filename'
)
G = nx.read_gpickle(conn_gpickle_scale3[0]) # same format as with tsv
A_fiber_density = nx.to_numpy_array(G, weight="fiber_density")
A_fiber_density

[7]: array([[7.39067471e-03, 4.01920257e-04, 2.89891974e-03, ...,
0.00000000e+00, 0.00000000e+00, 0.00000000e+00],
[4.01920257e-04, 7.98799252e-03, 6.66710786e-03, ...,
0.00000000e+00, 0.00000000e+00, 0.00000000e+00],
[2.89891974e-03, 6.66710786e-03, 5.56559629e-03, ...,
0.00000000e+00, 0.00000000e+00, 0.00000000e+00],
...,
[0.00000000e+00, 0.00000000e+00, 0.00000000e+00, ...,
5.84868693e-03, 6.47767105e-04, 1.57817881e-04],
[0.00000000e+00, 0.00000000e+00, 0.00000000e+00, ...,
6.47767105e-04, 1.18190323e-03, 1.05523480e-05],
[0.00000000e+00, 0.00000000e+00, 0.00000000e+00, ...,
1.57817881e-04, 1.05523480e-05, 8.37270426e-05]])
```

...or load the .mat files with [Scipy](#):

```
[8]: # Retrieve content of the connectome file with datalad
```

(continues on next page)

(continued from previous page)

```

vepcon_data.get('derivatives/cmp-v3.0.3/sub-01/dwi/sub-01_atlas-L2018_res-scale3_
↳ conndata-network_connectivity.mat')
# Query the connectome file path
conn_mat_scale3 = layout.get(
    subject='01',
    datatype='dwi',
    atlas='L2018',
    res='scale3',
    suffix='connectivity',
    extension='mat',
    return_type='filename'
)
A_mat = sio.loadmat(conn_mat_scale3[0])

```

The adjacency matrices here can be accessed as followss:

```

[9]: A_mat["sc"]["fiber_density"][0][0]
[9]: array([[7.39067471e-03, 4.01920257e-04, 2.89891974e-03, ...,
            0.00000000e+00, 0.00000000e+00, 0.00000000e+00],
            [4.01920257e-04, 7.98799252e-03, 6.66710786e-03, ...,
            0.00000000e+00, 0.00000000e+00, 0.00000000e+00],
            [2.89891974e-03, 6.66710786e-03, 5.56559629e-03, ...,
            0.00000000e+00, 0.00000000e+00, 0.00000000e+00],
            ...,
            [0.00000000e+00, 0.00000000e+00, 0.00000000e+00, ...,
            5.84868693e-03, 6.47767105e-04, 1.57817881e-04],
            [0.00000000e+00, 0.00000000e+00, 0.00000000e+00, ...,
            6.47767105e-04, 1.18190323e-03, 1.05523480e-05],
            [0.00000000e+00, 0.00000000e+00, 0.00000000e+00, ...,
            1.57817881e-04, 1.05523480e-05, 8.37270426e-05]])

```

Note that in these two situations, the connectome files are not directly managed by Git and their actual content need to be first retrieved with the datalad get command.

## Plotting the adjacency matrices

Let's plot some of those adjacency matrices using [Matplotlib](#) and [Seaborn](#):

```

[10]: # Create color map to handle zeros with log visualization
custom_cmap = copy.copy(plt.cm.get_cmap("inferno"))
# Copy the default cmap (0,0,0.5156)
custom_cmap.set_bad((0, 0, 0))

# Define the metrics to plot
cols_to_plot = ["number_of_fibers", "fiber_length_mean",
                "fiber_proportion", "fiber_density",
                "FA_mean", "normalized_fiber_density"]

# Plot with log-scale for all metrics except FA_mean
fig, axs = plt.subplots(3,2, figsize=(12,15))
axs = axs.flatten()

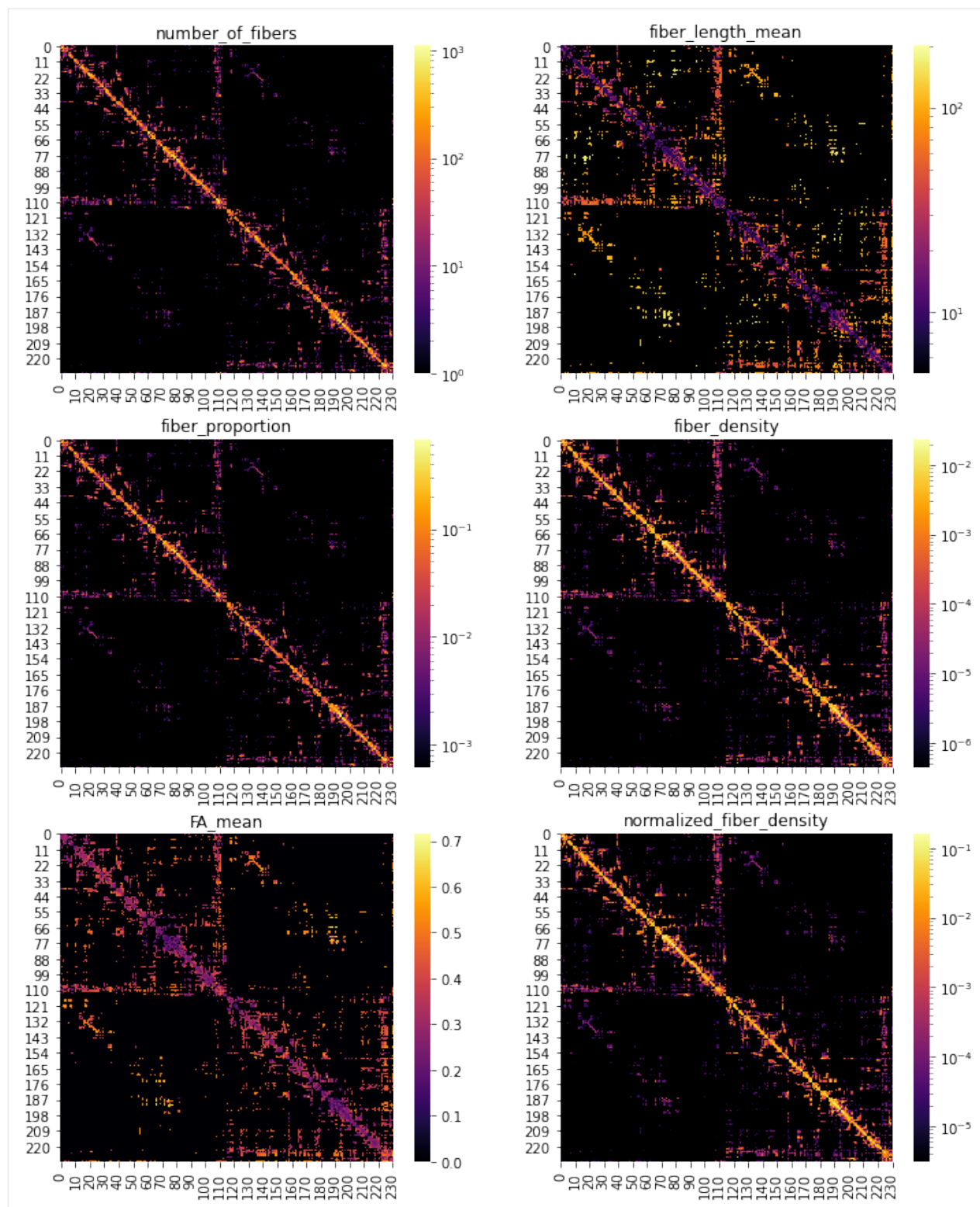
```

(continues on next page)

(continued from previous page)

```
for c, ax in zip(cols_to_plot, axs):
    A = nx.to_numpy_array(G, weight=c)
    sns.heatmap(A, ax=ax, cmap=custom_cmap, norm=(LogNorm()
                                                    if c != "FA_mean"
                                                    else None))

    ax.set_title(c)
```



## Graph signal processing with structural connectivity and visualization

The package `PyGSP` offers a range of graph signal processing tools we can use on our structural connectivity data. In particular, we can do an eigendecomposition of the `graph Laplacian` to get the Fourier basis - the connectome harmonics.

Even though it is possible to also do this for subcortical regions, for the sake of plotting it is easier just to work with the cortical regions. To identify those, we need the parcellation labels.

```
[11]: # Query the BIDS index/label mapping TSV file for the corresponding scale
label_path = layout.get(subject='01',
                        datatype='anat',
                        atlas='L2018',
                        res='scale3',
                        suffix='dseg',
                        extension='tsv',
                        return_type='filename')
print(f' BIDS index/label mapping TSV filepath: {label_path[0]}')

BIDS index/label mapping TSV filepath: /Users/sebastientourbier/Documents/GitHub/
↪connectomemapper3/docs/notebooks/ds003505_demo/derivatives/cmp-v3.0.3/sub-01/anat/sub-
↪01_atlas-L2018-res-scale3_dseg.tsv
```

```
[12]: # Load the TSV content
labels = pd.read_csv(label_path[0], sep="\t", index_col=0)
# Reset index to start at 0
labels.reset_index(inplace=True)
# Select cortex labels
labels_ctx = labels["name"][[n.startswith("ctx") for n in labels["name"]]].copy()
idx = list(labels_ctx.index)
# Select rows with cortical areas
# A_fd_ctx = A_fiber_density[idx]
A = nx.to_numpy_array(G, weight="FA_mean")
A_fd_ctx = A[idx]
# Select columns with cortical areas
A_fd_ctx = A_fd_ctx[:,idx]
```

```
[ ]: # Display the shape of the matrix
A_fd_ctx.shape
```

Now we can compute the harmonics:

```
[ ]: np.fill_diagonal(A_fd_ctx, 0) # PyGSP does not support self-loops
G_fd = pygsp.graphs.Graph(A_fd_ctx) # PyGSP graph
G_fd.compute_laplacian(lap_type="normalized")
G_fd.compute_fourier_basis() # compute connectome harmonics
```

The harmonics have the same dimensions as our original adjacency matrix.

```
[ ]: # Display the shape of the matrix
G_fd.U.shape
```

Each column contains one basis vector.

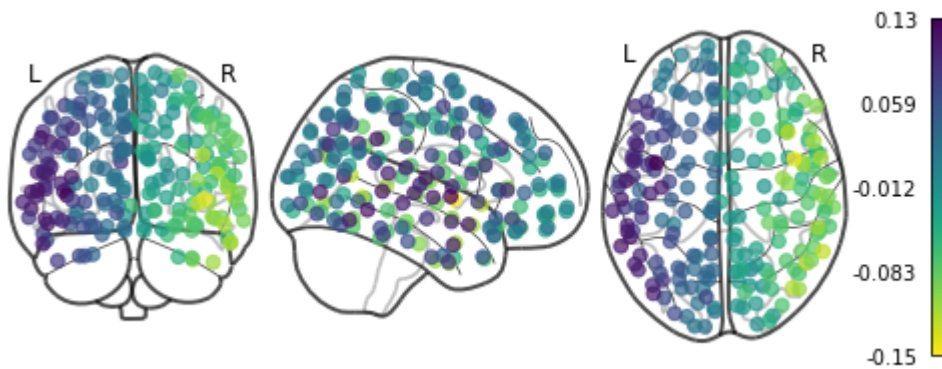
## Basic visualization with Nilearn

Nilearn offers a quick and easy way to plot them using `plot_markers`. For this, we need the center coordinates of each region in the parcellation in MNI space. For your convenience, they have been already computed and can be easily retrieved with the `get_lausanne2018_parcellation_mni_coords(scale)` utility function of CMP3.

```
[ ]: # Import the util function
    from cmcklib.data.parcellation.util import get_lausanne2018_parcellation_mni_coords

[17]: # Load coordinates with the utility function provided by CMP3
    coords_ctx = get_lausanne2018_parcellation_mni_coords('scale3')
    # Plot
    plotting.plot_markers(G_fd.U[:,1], coords_ctx)

[17]: <nilearn.plotting.displays.OrthoProjector at 0x7f95ec10d610>
```



## Advanced visualization with Nilearn

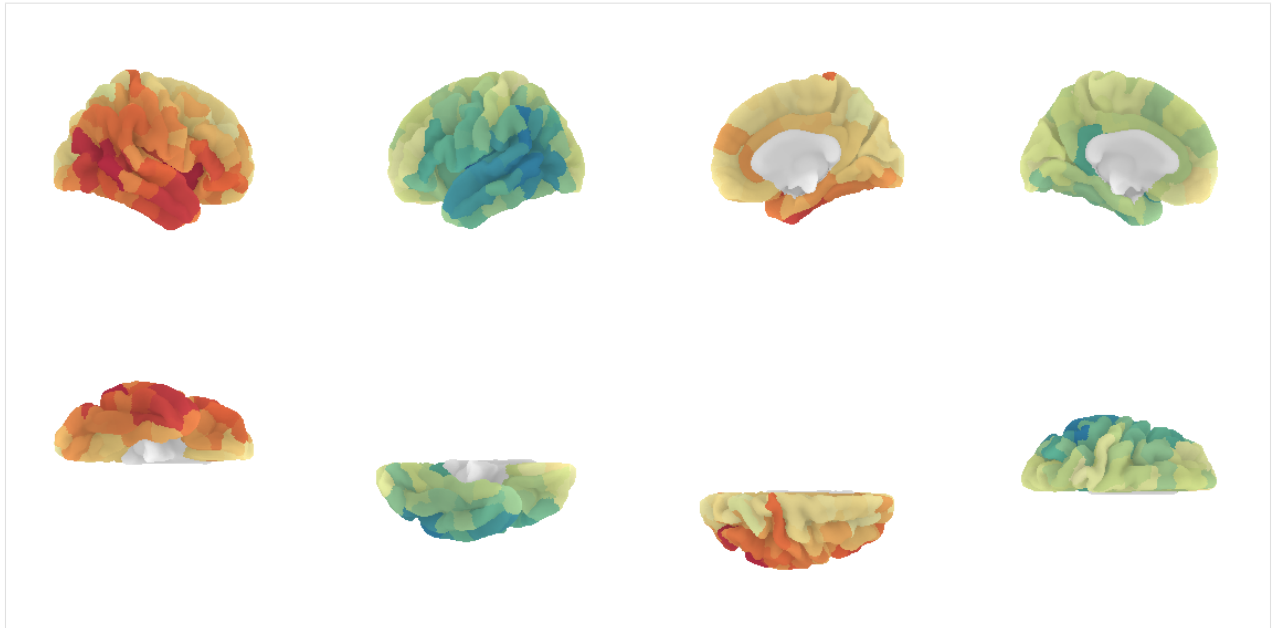
A prettier version is to plot the connectome harmonics on a brain surface using Nilearn `plot_surf_roi()`. For your convenience, a multiple view plot can be easily generated and saved with the `plot_lausanne2018_surface_ctx()` of the `cmcklib.data.parcellation.viz` module of CMP3, by specifying the scale to use.

These figures take a few minutes to generate, so you might need to be a bit patient.

```
[18]: # Import the viz function
    from cmcklib.data.parcellation.viz import plot_lausanne2018_surface_ctx

[19]: %%time
    # Plot
    plot_lausanne2018_surface_ctx(G_fd.U[:,1], scale='scale3', save_fig=True)

CPU times: user 1min 35s, sys: 3.72 s, total: 1min 38s
Wall time: 1min 18s
```



Pretty, right? This concludes the tutorial. We hope you enjoy it and any feedback or suggestions to improve it are very welcome! Just please open a [new issue](#) on GitHub and share your thoughts with us.

### Want to learn more about connectome harmonics?

Here are some references:

- Human brain networks function in connectome-specific harmonic waves (Atasoy et al., 2016, [link](#)): Landmark paper that first applied graph signal processing to brain connectivity.
- Functional harmonics reveal multi-dimensional basis functions underlying cortical organization (Glomb et al., 2021, [link](#)): Connectome harmonics of functional connectivity.
- The connectome spectrum as a canonical basis for a sparse representation of fast brain activity (Ru  -Queralt et al., 2021, [link](#)): EEG and connectome harmonics.

[ ]:

## 5.9.2 EEG Pipeline Tutorial

In this notebook, we will demonstrate how to use the newly implemented EEG pipeline of CMP3, using the “VEPCON” dataset, available at <https://openneuro.org/datasets/ds003505/versions/1.1.1>.

It is important to note that CMP3 *does not* include preprocessing of EEG data, so it is expected that you have your data ready to be analyzed.

---

**Important:** Note that the skull-surfaces provided with the dataset (“bem”, see below) which are needed to create the head model are obtained from non-defaced MRIs. You will not be able to proceed with surfaces created from VEPCon dataset alone.

---



## Setup instructions

If you want to reproduce all the results of this notebook on your side, a conda `environment.yml` file can be downloaded at the following link: [EEG\\_tutorial\\_environment.yml](#). The original `.ipynb` notebook file can be downloaded at the following link: [EEG\\_pipeline\\_tutorial.ipynb](#).

Once you have downloaded the conda environment file, install the environment `py37cmp-eeg` as follows:

```
$ conda create env -f /path/to/downloaded/EEG_tutorial_environment.yml
```

This will install all the packages needed to run this notebook including jupyter lab.

You can then activate it, go to the directory where you downloaded the `EEG_pipeline_tutorial.ipynb`, and launch jupyter lab as follows:

```
$ cd /directory/of/downloaded/EEG_pipeline_tutorial.ipynb
$ conda activate py37cmp-eeg
$ jupyter lab
```

You are ready to open and interact with the notebook!

## Loading the python packages used in the notebook

```
[1]: # General
import sys
import os
import argparse
import subprocess
import pdb
import pickle
import shutil
import json
from IPython.display import SVG, display
import warnings

# Dataset management
import datalad.api as dl

# Data/graph handling and visualization
import numpy as np
import matplotlib.pyplot as plt
import networkx as nx

# BIDS import
from bids import BIDSLayout

# MNE imports
import mne
import mne_connectivity as mnec

# CMP3 imports
import cmp.project
from cmp.info import __version__, __copyright__
from cmcklib.util import print_error, print_blue, print_warning
```

(continues on next page)

(continued from previous page)

```

from cmtklib.bids.io import __nipype_directory__, __cartool_directory__, __eeglab_
↳directory__, __cmp_directory__

# other
from EEG_tutorial_utils import create_trans_files

```

## Loading the BIDS dataset

For demonstration, we are going to use the latest version of VEPCON dataset, available on [Open Neuro](#) that already contains outputs from Connectome Mapper v3.0.3 and Freesurfer 7.1.1. A full description of the dataset can be found in [Pascucci, Tourbier, et al. 2022](#).

In case you want to rerun the notebook, make sure to remove any `ds003505_demo` folder in the directory of the notebook. Otherwise, datalad install will complain.

```

[2]: %%time
# Download example dataset with datalad
bids_dir = os.path.join(".", "ds003505_demo") # Adjust path to your BIDS dataset as
↳needed
vepcon_data = dl.install(
    path=bids_dir,
    source="git@github.com:OpenNeuroDatasets/ds003505.git"
)

[INFO] Cloning dataset to Dataset(/home/localadmin/Softwares/GitHub/connectomemapper3/
↳docs/notebooks/ds003505_demo)
[INFO] Attempting to clone from git@github.com:OpenNeuroDatasets/ds003505.git to /home/
↳localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo
[INFO] Start enumerating objects
[INFO] Start counting objects
[INFO] Start compressing objects
[INFO] Start receiving objects
[INFO] Start resolving deltas
[INFO] Completed clone attempts for Dataset(/home/localadmin/Softwares/GitHub/
↳connectomemapper3/docs/notebooks/ds003505_demo)
[INFO] scanning for annexed files (this may take some time)
[INFO] Unable to parse git config from origin
[INFO] Remote origin does not have git-annex installed; setting annex-ignore
[INFO] This could be a problem with the git-annex installation on the remote. Please
↳make sure that git-annex-shell is available in PATH when you ssh into the remote. Once
↳you have fixed the git-annex installation, run: git annex enableremote origin
[INFO] access to 1 dataset sibling s3-PRIVATE not auto-enabled, enable with:
|           datalad siblings -d "/home/localadmin/Softwares/GitHub/connectomemapper3/
↳docs/notebooks/ds003505_demo" enable -s s3-PRIVATE

CPU times: user 157 ms, sys: 148 ms, total: 304 ms
Wall time: 10.6 s

```

## Running the EEG pipeline

As of now, the EEG pipeline can only be run directly from the application programming interface (API) as demonstrated in this notebook. As soon as possible, we will integrate it into the graphical user interface (GUI) and the command line interface (CLI).

First, we need to configure the following user-defined arguments. Please modify them as needed.

```
[3]: # Adjust path to your BIDS dataset as needed
      bids_dir = vepcon_data.path

      # Adjust path of the output directory as needed
      output_dir = os.path.join(bids_dir, 'derivatives')

      # Adjust the subject to be processed as needed
      participant_label = 'sub-01'

      # Adjust path to the anatomical pipeline configuration file as needed
      anat_pipeline_config = os.path.join(bids_dir, 'code', 'ConnectomeMapper-Docker', 'ref_
      ↪ anatomical_config.json')

      # Adjust path to the MNE-based pipeline configuration file as needed
      eeg_pipeline_config = os.path.join('.', 'ref_mne_eeg_config.json')
```

The eeg pipeline config .json file contains information that CMP3 needs to correctly load EEG data and associated information like electrode positions, names of conditions, which parcellation to use, etc. as seen below:

```
[4]: %cat ref_mne_eeg_config.json

{
  "Global": {
    "process_type": "eeg",
    "subjects": [
      "sub-01"
    ],
    "subject": "sub-01",
    "version": "v3.0.3"
  },
  "eeg_preparer_stage": {
    "eeg_format": ".set",
    "epochs": "sub-01_task-faces_desc-preproc_eeg.set",
    "invsol_format": "mne-sLORETA",
    "parcellation": {
      "atlas": "lausanne2018",
      "res": "scale1"
    },
  },
  "number_of_threads": 1,
  "EEG_params": {
    "expe_name": "faces",
    "EEG_event_IDS": {
      "SCRAMBLED" : 0,
      "FACES" : 1
    },
    "start_t": -0.2,
    "end_t" : 0.6
  }
}
```

(continues on next page)

(continued from previous page)

```

    }
  },
  "eeg_inverse_solution_stage": {
    "eeg_format": ".set",
    "number_of_threads": 1
  },
  "Multi-processing": {
    "number_of_cores": 1
  }
}

```

**Note:** If you would like to run another subject (all available subjects except subjects 5 and 15 can be run), you will need to modify the config files (replacing sub-<label> accordingly).

Then, we need to tell datalad to download the actual content of the structural MRI and EEG files that will be input to the pipelines.

```

[5]: %%time
# Raw MRI
vepcon_data.get(f'{participant_label}/anat/')
# CMP3 and Freesurfer derivatives
vepcon_data.get(f'derivatives/cmp-v3.0.3/{participant_label}/anat/')
vepcon_data.get(f'derivatives/freesurfer-7.1.1/{participant_label}/')
# Electrode position
vepcon_data.get(f'derivatives/{__cartool_directory__}/{participant_label}/' +
                f'eeg/{participant_label}_eeg.xyz')
# Preprocessed EEG in EEGLab .fdt/.set format
vepcon_data.get(f'derivatives/{__eeglab_directory__}/{participant_label}/eeg/' +
                f'{participant_label}_task-faces_desc-preproc_eeg.fdt')
vepcon_data.get(f'derivatives/{__eeglab_directory__}/{participant_label}/eeg/' +
                f'{participant_label}_task-faces_desc-preproc_eeg.set')

```

CPU times: user 1.38 s, sys: 273 ms, total: 1.65 s

Wall time: 3min 58s

```

[5]: [{'type': 'file',
      'refds': '/home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_
      demo',
      'status': 'ok',
      'path': '/home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_
      demo/derivatives/eeglab-v14.1.1/sub-01/eeg/sub-01_task-faces_desc-preproc_eeg.set',
      'action': 'get',
      'annexkey': 'MD5E-s3318272--2421186ff914211599affe7be30985ba.set',
      'message': 'from s3-PUBLIC...'}]

```

Once the files are available, we need to configure a new CMP3 project.

```

[6]: # initialize project
project = cmp.project.ProjectInfo()
project.base_directory = os.path.abspath(bids_dir)
project.output_directory = os.path.abspath(output_dir)
project.subjects = ["{}".format(participant_label)]

```

(continues on next page)

(continued from previous page)

```

project.subject = "{}".format(participant_label)

# VEPCON dataset does not have a subject/sessions structure
project.subject_sessions = [""]
project.subject_session = ""

# Set the path to the anatomical pipeline configuration file
project.anat_config_file = os.path.abspath(anat_pipeline_config)

```

As the dataset is in [BIDS](#), we can use [Pybids](#) to help us with the task of interacting with the files of the dataset.

```

[7]: # Represent the BIDS dataset as a PyBIDS BIDSLayout
      bids_layout = BIDSLayout(project.base_directory)
      # Add derivative folder containing the connectivity matrices
      bids_layout.add_derivatives(os.path.join(project.base_directory, "derivatives", "cmp-v3.
      ↳0.3"))

```

Once set, we can run the anatomical pipeline, in order to obtain, among other things, Freesurfer derivatives necessary for the MNE pipeline.

Freesurfer and CMP3 derivatives are indeed provided with the VEPCON dataset, so we do not need to run it, but if run on a fresh dataset, it can take several hours (per subject).

```

[8]: %%time
      # Do not run again the anatomical pipeline
      # You will have to set it to True on a fresh dataset
      run = False

      # Initialize the anatomical pipeline reading the configuration file
      anat_pipeline = cmp.project.init_anat_project(project, False)

      if anat_pipeline is not None:
          # Check if inputs to anatomical pipeline are valid
          anat_valid_inputs = anat_pipeline.check_input(bids_layout, gui=False)
          if anat_valid_inputs:
              if run:
                  print(">> Process anatomical pipeline")
                  anat_pipeline.process()
              else:
                  print_error(" .. ERROR: Invalid inputs")
                  exit_code = 1

      # Check if outputs to anatomical pipeline are valid
      anat_valid_outputs, msg = anat_pipeline.check_output()

      # Set the freesurfer subjects directory and the subject id
      project.freesurfer_subjects_dir = anat_pipeline.stages['Segmentation'].config.freesurfer_
      ↳subjects_dir
      project.freesurfer_subject_id = anat_pipeline.stages['Segmentation'].config.freesurfer_
      ↳subject_id

```

```

Created directory /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↳ds003505_demo/derivatives/nipype-1.7.0/sub-01

```

(continues on next page)

(continued from previous page)

```

.. LOAD: Load anatomical config file : /home/localadmin/Softwares/GitHub/
↪connectomemapper3/docs/notebooks/ds003505_demo/code/ConnectomeMapper-Docker/ref_
↪anatomical_config.json
.. WARNING: CMP3 version used to generate the configuration files (v3.0.2) and
↪version of CMP3 used (v3.0.3) differ
**** Check Inputs ****
> Looking in /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_
↪demo for...
/home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↪derivatives/cmp-v3.0.3/sub-01/anat/sub-01_desc-brain_T1w.nii.gz
... t1_file : /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↪ds003505_demo/derivatives/cmp-v3.0.3/sub-01/anat/sub-01_desc-brain_T1w.nii.gz
/home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↪derivatives/cmp-v3.0.3/sub-01/anat/sub-01_desc-cmp_T1w.json
... t1_json_file : /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↪ds003505_demo/derivatives/cmp-v3.0.3/sub-01/anat/sub-01_desc-cmp_T1w.json
Inputs check finished successfully.
Only anatomical data (T1) available.
.. INFO: Valid derivatives for anatomical pipeline
CPU times: user 57.5 ms, sys: 4.16 ms, total: 61.7 ms
Wall time: 57 ms

```

```
[9]: project.freesurfer_subjects_dir
```

```
[9]: '/home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↪derivatives/freesurfer-7.1.1'
```

In VEPCON, the electrode positions are provided in a file in the Cartool-derivatives folder, but CMP3 expects them in the EEGLAB-derivatives folder.

```
[10]: # Copy the file to the appropriate location
cartool_file_location = os.path.join(
    bids_dir, 'derivatives', __cartool_directory__,
    participant_label, 'eeg', participant_label + '_eeg.xyz'
)
eeglab_file_location = os.path.join(
    bids_dir, 'derivatives', 'eeglab-v14.1.1',
    participant_label, 'eeg', participant_label + '_eeg.xyz')

if not os.path.exists(eeglab_file_location):
    _ = shutil.copyfile(cartool_file_location, eeglab_file_location)

```

Since we are using non-defaced MRIs, which are not exactly the same as the ones provided on OpenNeuro, we need an additional transform that will be applied to the electrode positions.

```
[11]: # The following line creates the appropriate file with this transform in derivatives/cmp-
↪v3.0.3:
create_trans_files(bids_dir, participant_label)

```

Finally, you can run the EEG pipeline.

```
[12]: %%time
# Set the path to the EEG pipeline configuration file

```

(continues on next page)

(continued from previous page)

```

project.eeg_config_file = os.path.abspath(eeg_pipeline_config)

if anat_valid_outputs:
    # Initialize the EEG pipeline reading the configuration file and check input validity
    eeg_valid_inputs, eeg_pipeline = cmp.project.init_eeg_project(project, bids_layout,
↪False)
    if eeg_pipeline is not None:
        eeg_pipeline.parcellation_scheme = anat_pipeline.parcellation_scheme
        eeg_pipeline.atlas_info = anat_pipeline.atlas_info

        if eeg_valid_inputs:
            print(">> Process EEG pipeline")
            eeg_pipeline.process()
        else:
            print(" .. ERROR: Invalid inputs")
            exit_code = 1
    else:
        print_error(f' .. ERROR: Invalid anatomical outputs for eeg pipeline')
        print_error(f'{msg}')
        exit_code = 1

**** Check Inputs is still not implemented ****
.. LOAD: Load eeg config file : /home/localadmin/Softwares/GitHub/connectomemapper3/
↪docs/notebooks/ref_mne_eeg_config.json
.. INFO: Generated with the same CMP3 version
>> Process EEG pipeline
220221-10:54:42,107 nipype.interface INFO:
    **** Processing ****
Parcellation atlas: lausanne2018
Parcellation resolution: scale1
220221-10:54:42,447 nipype.workflow INFO:
    Generated workflow graph: /home/localadmin/Softwares/GitHub/connectomemapper3/
↪docs/notebooks/ds003505_demo/derivatives/nipype-1.7.0/sub-01/eeg_pipeline/graph.svg
↪(graph2use=colored, simple_form=True).
220221-10:54:42,469 nipype.workflow INFO:
    Workflow eeg_pipeline settings: ['check', 'execution', 'logging', 'monitoring']
220221-10:54:42,480 nipype.workflow INFO:
    Running in parallel.
220221-10:54:42,483 nipype.workflow INFO:
    [MultiProc] Running 0 tasks, and 1 jobs ready. Free memory (GB): 28.20/28.20,
↪Free processors: 1/1.
220221-10:54:42,609 nipype.workflow INFO:
    [Node] Setting-up "eeg_pipeline.eeg_preparer_stage.eeglab2fif" in "/home/
↪localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/derivatives/
↪nipype-1.7.0/sub-01/eeg_pipeline/eeg_preparer_stage/eeglab2fif".
220221-10:54:42,614 nipype.workflow INFO:
    [Node] Executing "eeglab2fif" <cmtklib.interfaces.mne.EEGLAB2fif>
Extracting parameters from /home/localadmin/Softwares/GitHub/connectomemapper3/docs/
↪notebooks/ds003505_demo/derivatives/eeglab-v14.1.1/sub-01/eeg/sub-01_task-faces_desc-
↪preproc_eeg.set...
Not setting metadata
Not setting metadata

```

(continues on next page)

(continued from previous page)

```

588 matching events found
No baseline correction applied
0 projection items activated
Ready.
Applying baseline correction (mode: mean)
Adding average EEG reference projection.
1 projection items deactivated
Average reference projection was added, but has not been applied yet. Use the apply_proj_
↳method to apply it.
220221-10:54:43,765 nipy.workflow INFO:
    [Node] Finished "eeglab2fif", elapsed time 1.148652s.
220221-10:54:44,486 nipy.workflow INFO:
    [Job 0] Completed (eeg_pipeline.eeg_preparer_stage.eeglab2fif).
220221-10:54:44,492 nipy.workflow INFO:
    [MultiProc] Running 0 tasks, and 2 jobs ready. Free memory (GB): 28.20/28.20,↳
↳Free processors: 1/1.
220221-10:54:44,677 nipy.workflow INFO:
    [Node] Setting-up "eeg_pipeline.eeg_preparer_stage.create_src" in "/home/
↳localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/derivatives/
↳nipy-1.7.0/sub-01/eeg_pipeline/eeg_preparer_stage/create_src".
220221-10:54:44,681 nipy.workflow INFO:
    [Node] Executing "create_src" <cmtklib.interfaces.mne.CreateSrc>
Setting up the source space with the following parameters:

SUBJECTS_DIR = /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↳ds003505_demo/derivatives/freesurfer-7.1.1
Subject      = sub-01
Surface      = white
Octahedron subdivision grade 6

>>> 1. Creating the source space...

Doing the octahedral vertex picking...
Loading /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↳derivatives/freesurfer-7.1.1/sub-01/surf/lh.white...
Mapping lh sub-01 -> oct (6) ...
    Triangle neighbors and vertex normals...
Loading geometry from /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↳ds003505_demo/derivatives/freesurfer-7.1.1/sub-01/surf/lh.sphere...
Setting up the triangulation for the decimated surface...
loaded lh.white 4098/149863 selected to source space (oct = 6)

Loading /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↳derivatives/freesurfer-7.1.1/sub-01/surf/rh.white...
Mapping rh sub-01 -> oct (6) ...
    Triangle neighbors and vertex normals...
Loading geometry from /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↳ds003505_demo/derivatives/freesurfer-7.1.1/sub-01/surf/rh.sphere...
Setting up the triangulation for the decimated surface...
loaded rh.white 4098/147183 selected to source space (oct = 6)

Calculating source space distances (limit=inf mm)...
```

(continues on next page)



(continued from previous page)

```

220221-10:54:46,488 nipype.workflow INFO:
    [MultiProc] Running 1 tasks, and 1 jobs ready. Free memory (GB): 28.00/28.20,
↪Free processors: 0/1.
        Currently running:
            * eeg_pipeline.eeg_preparer_stage.createsrc
Computing patch statistics...
Patch information added...
Computing patch statistics...
Patch information added...
You are now one step closer to computing the gain matrix
Write a source space...
[done]
Write a source space...
[done]
2 source spaces written
220221-11:03:00,105 nipype.workflow INFO:
    [Node] Finished "createsrc", elapsed time 495.422403s.
220221-11:03:00,974 nipype.workflow INFO:
    [Job 1] Completed (eeg_pipeline.eeg_preparer_stage.createsrc).
220221-11:03:00,979 nipype.workflow INFO:
    [MultiProc] Running 0 tasks, and 2 jobs ready. Free memory (GB): 28.20/28.20,
↪Free processors: 1/1.
220221-11:03:01,116 nipype.workflow INFO:
    [Node] Setting-up "eeg_pipeline.eeg_inverse_solution_stage.createcov" in "/home/
↪localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/derivatives/
↪nipype-1.7.0/sub-01/eeg_pipeline/eeg_inverse_solution_stage/createcov".
220221-11:03:01,121 nipype.workflow INFO:
    [Node] Executing "createcov" <cmtklib.interfaces.mne.CreateCov>
Reading /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↪derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_epo.fif ...
    Read a total of 1 projection items:
        Average EEG reference (1 x 128) idle
    Found the data of interest:
        t = -200.00 ... 600.00 ms
        0 CTF compensation matrices available
Not setting metadata
Not setting metadata
588 matching events found
No baseline correction applied
Created an SSP operator (subspace dimension = 1)
1 projection items activated
Computing rank from data with rank=None
    Using tolerance 3.2e-11 (2.2e-16 eps * 128 dim * 1.1e+03 max singular value)
    Estimated rank (eeg): 127
    EEG: rank 127 computed from 128 data channels with 1 projector
    Created an SSP operator (subspace dimension = 1)
    Setting small EEG eigenvalues to zero (without PCA)
Reducing data rank from 128 -> 127
Estimating covariance using SHRUNK
220221-11:03:02,977 nipype.workflow INFO:
    [MultiProc] Running 1 tasks, and 1 jobs ready. Free memory (GB): 28.00/28.20,
↪Free processors: 0/1.

```

(continues on next page)

(continued from previous page)

```

                Currently running:
                * eeg_pipeline.eeg_inverse_solution_stage.createcov
Done.
Estimating covariance using EMPIRICAL
Done.
Using cross-validation to select the best estimator.
Number of samples used : 29988
log-likelihood on unseen data (descending order):
    shrunk: 71.788
    empirical: -373.964
selecting best estimator: shrunk
[done]
220221-11:03:06,998 nipy.workflow INFO:
    [Node] Finished "createcov", elapsed time 5.873837s.
220221-11:03:08,982 nipy.workflow INFO:
    [Job 2] Completed (eeg_pipeline.eeg_inverse_solution_stage.createcov).
220221-11:03:08,984 nipy.workflow INFO:
    [MultiProc] Running 0 tasks, and 1 jobs ready. Free memory (GB): 28.20/28.20,
    ↪Free processors: 1/1.
220221-11:03:09,119 nipy.workflow INFO:
    [Node] Setting-up "eeg_pipeline.eeg_preparer_stage.createbem" in "/home/
    ↪localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/derivatives/
    ↪nipy-1.7.0/sub-01/eeg_pipeline/eeg_preparer_stage/createbem".
220221-11:03:09,126 nipy.workflow INFO:
    [Node] Executing "createbem" <cmtklib.interfaces.mne.CreateBEM>
Creating the BEM geometry...
Going from 5th to 4th subdivision of an icosahedron (n_tri: 20480 -> 5120)
Going from 5th to 4th subdivision of an icosahedron (n_tri: 20480 -> 5120)
Going from 5th to 4th subdivision of an icosahedron (n_tri: 20480 -> 5120)
outer skin CM is -1.05 -8.88 11.57 mm
outer skull CM is -1.05 -8.80 11.09 mm
inner skull CM is -1.05 -10.32 19.78 mm
Checking that surface outer skull is inside surface outer skin ...
220221-11:03:10,985 nipy.workflow INFO:
    [MultiProc] Running 1 tasks, and 0 jobs ready. Free memory (GB): 28.00/28.20,
    ↪Free processors: 0/1.
                Currently running:
                * eeg_pipeline.eeg_preparer_stage.createbem
Checking that surface inner skull is inside surface outer skull ...
Checking distance between outer skin and outer skull surfaces...
Minimum distance between the outer skin and outer skull surfaces is approximately 1.
    ↪6 mm
Checking distance between outer skull and inner skull surfaces...
Minimum distance between the outer skull and inner skull surfaces is approximately 1.
    ↪8 mm
Surfaces passed the basic topology checks.
Complete.

Approximation method : Linear collocation

Three-layer model surfaces loaded.
Computing the linear collocation solution...

```

(continues on next page)

(continued from previous page)

```

Matrix coefficients...
    outer skin (2562) -> outer skin (2562) ...
    outer skin (2562) -> outer skull (2562) ...
    outer skin (2562) -> inner skull (2562) ...
    outer skull (2562) -> outer skin (2562) ...
    outer skull (2562) -> outer skull (2562) ...
    outer skull (2562) -> inner skull (2562) ...
    inner skull (2562) -> outer skin (2562) ...
    inner skull (2562) -> outer skull (2562) ...
    inner skull (2562) -> inner skull (2562) ...
Inverting the coefficient matrix...
IP approach required...
Matrix coefficients (homog)...
    inner skull (2562) -> inner skull (2562) ...
Inverting the coefficient matrix (homog)...
Modify the original solution to incorporate IP approach...
    Combining...
    Scaling...
Solution ready.
BEM geometry computations complete.
220221-11:04:28,211 nipype.workflow INFO:
    [Node] Finished "createbem", elapsed time 79.081617s.
220221-11:04:29,61 nipype.workflow INFO:
    [Job 3] Completed (eeg_pipeline.eeg_preparer_stage.createbem).
220221-11:04:29,65 nipype.workflow INFO:
    [MultiProc] Running 0 tasks, and 1 jobs ready. Free memory (GB): 28.20/28.20,
    ↪Free processors: 1/1.
220221-11:04:29,195 nipype.workflow INFO:
    [Node] Setting-up "eeg_pipeline.eeg_loader_stage.eegloader" in "/home/
    ↪localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/derivatives/
    ↪nipype-1.7.0/sub-01/eeg_pipeline/eeg_loader_stage/eegloader".
220221-11:04:29,198 nipype.workflow INFO:
    [Node] Executing "eegloader" <cmrklb.interfaces.eeg.EEGLoader>
220221-11:04:31,63 nipype.workflow INFO:
    [MultiProc] Running 1 tasks, and 0 jobs ready. Free memory (GB): 28.00/28.20,
    ↪Free processors: 0/1.
    Currently running:
        * eeg_pipeline.eeg_loader_stage.eegloader
220221-11:04:37,177 nipype.workflow INFO:
    [Node] Finished "eegloader", elapsed time 7.977005s.
220221-11:04:39,71 nipype.workflow INFO:
    [Job 4] Completed (eeg_pipeline.eeg_loader_stage.eegloader).
220221-11:04:39,76 nipype.workflow INFO:
    [MultiProc] Running 0 tasks, and 1 jobs ready. Free memory (GB): 28.20/28.20,
    ↪Free processors: 1/1.
220221-11:04:39,217 nipype.workflow INFO:
    [Node] Setting-up "eeg_pipeline.eeg_inverse_solution_stage.createfwd" in "/home/
    ↪localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/derivatives/
    ↪nipype-1.7.0/sub-01/eeg_pipeline/eeg_inverse_solution_stage/createfwd".
220221-11:04:39,222 nipype.workflow INFO:
    [Node] Executing "createfwd" <cmrklb.interfaces.mne.CreateFwd>
Reading /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
    ↪derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_epo.fif ...

```

(continues on next page)

(continued from previous page)

```

Read a total of 1 projection items:
  Average EEG reference (1 x 128)  idle
Found the data of interest:
  t =      -200.00 ...      600.00 ms
  0 CTF compensation matrices available
Not setting metadata
Not setting metadata
588 matching events found
No baseline correction applied
Created an SSP operator (subspace dimension = 1)
1 projection items activated
Source space      : /home/localadmin/Softwares/GitHub/connectomemapper3/docs/
↳notebooks/ds003505_demo/derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_src.fif
MRI -> head transform : /home/localadmin/Softwares/GitHub/connectomemapper3/docs/
↳notebooks/ds003505_demo/derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_trans.fif
Measurement data   : instance of Info
Conductor model    : /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↳ds003505_demo/derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_bem.fif
Accurate field computations
Do computations in head coordinates
Free source orientations

Reading /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↳derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_src.fif...
Read 2 source spaces a total of 8196 active source locations

Coordinate transformation: MRI (surface RAS) -> head
  1.000000  0.000000  0.000000      0.00 mm
  0.000000  1.000000  0.000000      9.00 mm
  0.000000  0.000000  1.000000     -11.00 mm
  0.000000  0.000000  0.000000      1.00

Read 128 EEG channels from info
Head coordinate coil definitions created.
Source spaces are now in head coordinates.

Setting up the BEM model using /home/localadmin/Softwares/GitHub/connectomemapper3/docs/
↳notebooks/ds003505_demo/derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_bem.fif...

Loading surfaces...

Loading the solution matrix...

Three-layer model surfaces loaded.
Loaded linear_collocation BEM solution from /home/localadmin/Softwares/GitHub/
↳connectomemapper3/docs/notebooks/ds003505_demo/derivatives/cmp-v3.0.3/sub-01/eeg/sub-
↳01_bem.fif
Employing the head->MRI coordinate transform with the BEM model.
BEM model sub-01_bem.fif is now set up

Source spaces are in head coordinates.
Checking that the sources are inside the surface (will take a few...)

```

(continues on next page)

(continued from previous page)

```

Skipping interior check for 1736 sources that fit inside a sphere of radius 53.7 mm
Skipping solid angle check for 0 points using Qhull

```

```
[Parallel(n_jobs=4)]: Using backend LokyBackend with 4 concurrent workers.
```

```
220221-11:04:41,74 nipype.workflow INFO:
```

```

    [MultiProc] Running 1 tasks, and 0 jobs ready. Free memory (GB): 28.00/28.20,
    ↪Free processors: 0/1.

```

```
    Currently running:
```

```
        * eeg_pipeline.eeg_inverse_solution_stage.createfwd
```

```
[Parallel(n_jobs=4)]: Done 2 out of 4 | elapsed: 6.6s remaining: 6.6s
```

```
[Parallel(n_jobs=4)]: Done 4 out of 4 | elapsed: 6.6s remaining: 0.0s
```

```
[Parallel(n_jobs=4)]: Done 4 out of 4 | elapsed: 6.6s finished
```

```

Skipping interior check for 1721 sources that fit inside a sphere of radius 53.7 mm
Skipping solid angle check for 0 points using Qhull

```

```
[Parallel(n_jobs=4)]: Using backend LokyBackend with 4 concurrent workers.
```

```
[Parallel(n_jobs=4)]: Done 2 out of 4 | elapsed: 0.3s remaining: 0.3s
```

```
[Parallel(n_jobs=4)]: Done 4 out of 4 | elapsed: 0.4s remaining: 0.0s
```

```
[Parallel(n_jobs=4)]: Done 4 out of 4 | elapsed: 0.4s finished
```

```
Setting up for EEG...
```

```
Computing EEG at 8196 source locations (free orientations)...
```

```
[Parallel(n_jobs=4)]: Using backend LokyBackend with 4 concurrent workers.
```

```
[Parallel(n_jobs=4)]: Done 2 out of 4 | elapsed: 1.6s remaining: 1.6s
```

```
[Parallel(n_jobs=4)]: Done 4 out of 4 | elapsed: 1.7s remaining: 0.0s
```

```
[Parallel(n_jobs=4)]: Done 4 out of 4 | elapsed: 1.7s finished
```

```
Finished.
```

```
    Write a source space...
```

```
    [done]
```

```
    Write a source space...
```

```
    [done]
```

```
    2 source spaces written
```

```
220221-11:04:50,779 nipype.workflow INFO:
```

```
    [Node] Finished "createfwd", elapsed time 11.554622s.
```

```
220221-11:04:51,82 nipype.workflow INFO:
```

```
    [Job 5] Completed (eeg_pipeline.eeg_inverse_solution_stage.createfwd).
```

```
220221-11:04:51,87 nipype.workflow INFO:
```

```

    [MultiProc] Running 0 tasks, and 1 jobs ready. Free memory (GB): 28.20/28.20,
    ↪Free processors: 1/1.

```

```
220221-11:04:51,217 nipype.workflow INFO:
```

```

    [Node] Setting-up "eeg_pipeline.eeg_inverse_solution_stage.invsol" in "/home/
    ↪localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/derivatives/
    ↪nipype-1.7.0/sub-01/eeg_pipeline/eeg_inverse_solution_stage/invsol".

```

```
220221-11:04:51,227 nipype.workflow INFO:
```

```
    [Node] Executing "invsol" <cmtklib.interfaces.mne.MNEInverseSolution>
```

```

Reading /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
    ↪derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_epo.fif ...

```

```
    Read a total of 1 projection items:
```

```
        Average EEG reference (1 x 128) idle
```

(continues on next page)

(continued from previous page)

```

Found the data of interest:
    t =    -200.00 ...    600.00 ms
    0 CTF compensation matrices available
Not setting metadata
Not setting metadata
588 matching events found
No baseline correction applied
Created an SSP operator (subspace dimension = 1)
1 projection items activated
Reading forward solution from /home/localadmin/Softwares/GitHub/connectomemapper3/docs/
↳ notebooks/ds003505_demo/derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_fwd.fif...
    Reading a source space...
    Computing patch statistics...
    Patch information added...
    Distance information added...
    [done]
    Reading a source space...
    Computing patch statistics...
    Patch information added...
    Distance information added...
    [done]
    2 source spaces read
    Desired named matrix (kind = 3523) not available
    Read EEG forward solution (8196 sources, 128 channels, free orientations)
    Source spaces transformed to the forward solution coordinate frame
    128 x 128 full covariance (kind = 1) found.
    Read a total of 1 projection items:
        Average EEG reference (1 x 128) active
    Reading a source space...
    Computing patch statistics...
    Patch information added...
    Distance information added...
    [done]
    Reading a source space...
    Computing patch statistics...
    Patch information added...
    Distance information added...
    [done]
    2 source spaces read
Computing inverse operator with 128 channels.
    128 out of 128 channels remain after picking
Selected 128 channels
Whitening the forward solution.
    Created an SSP operator (subspace dimension = 1)
Computing rank from covariance with rank=None
    Using tolerance 1.2e-14 (2.2e-16 eps * 128 dim * 0.43 max singular value)
220221-11:04:53,84 nipy.workflow INFO:
    [MultiProc] Running 1 tasks, and 0 jobs ready. Free memory (GB): 28.00/28.20,
↳ Free processors: 0/1.
        Currently running:
            * eeg_pipeline.eeg_inverse_solution_stage.invsol
    Estimated rank (eeg): 127

```

(continues on next page)

(continued from previous page)

```

    EEG: rank 127 computed from 128 data channels with 1 projector
    Setting small EEG eigenvalues to zero (without PCA)
Creating the source covariance matrix
Adjusting source covariance matrix.
Computing SVD of whitened and weighted lead field matrix.
    largest singular value = 11.2136
    scaling factor to adjust the trace = 4.17725e+26 (nchan = 128 nzero = 1)
Write inverse operator decomposition in /home/localadmin/Softwares/GitHub/
↪connectomemapper3/docs/notebooks/ds003505_demo/derivatives/cmp-v3.0.3/sub-01/eeg/sub-
↪01_inv.fif...
    Write a source space...
    [done]
    Write a source space...
    [done]
    2 source spaces written
    Writing inverse operator info...
    Writing noise covariance matrix.
    Writing source covariance matrix.
    Writing orientation priors.
    [done]
Preparing the inverse operator for use...
    Scaled noise and source covariance from nave = 1 to nave = 588
    Created the regularized inverter
    Created an SSP operator (subspace dimension = 1)
    Created the whitener using a noise covariance matrix with rank 127 (1 small
↪eigenvalues omitted)
    Computing noise-normalization factors (sLORETA)...
[done]
Picked 128 channels from the data
Computing inverse...
    Eigenleads need to be weighted ...
Processing epoch : 1 / 588
combining the current components...
Processing epoch : 2 / 588
combining the current components...
Processing epoch : 3 / 588
combining the current components...
Processing epoch : 4 / 588
combining the current components...
Processing epoch : 5 / 588
combining the current components...
Processing epoch : 6 / 588
combining the current components...
Processing epoch : 7 / 588
combining the current components...
Processing epoch : 8 / 588
combining the current components...
Processing epoch : 9 / 588
combining the current components...
Processing epoch : 10 / 588
combining the current components...
Processing epoch : 11 / 588

```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 12 / 588
combining the current components...
Processing epoch : 13 / 588
combining the current components...
Processing epoch : 14 / 588
combining the current components...
Processing epoch : 15 / 588
combining the current components...
Processing epoch : 16 / 588
combining the current components...
Processing epoch : 17 / 588
combining the current components...
Processing epoch : 18 / 588
combining the current components...
Processing epoch : 19 / 588
combining the current components...
Processing epoch : 20 / 588
combining the current components...
Processing epoch : 21 / 588
combining the current components...
Processing epoch : 22 / 588
combining the current components...
Processing epoch : 23 / 588
combining the current components...
Processing epoch : 24 / 588
combining the current components...
Processing epoch : 25 / 588
combining the current components...
Processing epoch : 26 / 588
combining the current components...
Processing epoch : 27 / 588
combining the current components...
Processing epoch : 28 / 588
combining the current components...
Processing epoch : 29 / 588
combining the current components...
Processing epoch : 30 / 588
combining the current components...
Processing epoch : 31 / 588
combining the current components...
Processing epoch : 32 / 588
combining the current components...
Processing epoch : 33 / 588
combining the current components...
Processing epoch : 34 / 588
combining the current components...
Processing epoch : 35 / 588
combining the current components...
Processing epoch : 36 / 588
combining the current components...
Processing epoch : 37 / 588
```

(continues on next page)



(continued from previous page)

```
combining the current components...
Processing epoch : 38 / 588
combining the current components...
Processing epoch : 39 / 588
combining the current components...
Processing epoch : 40 / 588
combining the current components...
Processing epoch : 41 / 588
combining the current components...
Processing epoch : 42 / 588
combining the current components...
Processing epoch : 43 / 588
combining the current components...
Processing epoch : 44 / 588
combining the current components...
Processing epoch : 45 / 588
combining the current components...
Processing epoch : 46 / 588
combining the current components...
Processing epoch : 47 / 588
combining the current components...
Processing epoch : 48 / 588
combining the current components...
Processing epoch : 49 / 588
combining the current components...
Processing epoch : 50 / 588
combining the current components...
Processing epoch : 51 / 588
combining the current components...
Processing epoch : 52 / 588
combining the current components...
Processing epoch : 53 / 588
combining the current components...
Processing epoch : 54 / 588
combining the current components...
Processing epoch : 55 / 588
combining the current components...
Processing epoch : 56 / 588
combining the current components...
Processing epoch : 57 / 588
combining the current components...
Processing epoch : 58 / 588
combining the current components...
Processing epoch : 59 / 588
combining the current components...
Processing epoch : 60 / 588
combining the current components...
Processing epoch : 61 / 588
combining the current components...
Processing epoch : 62 / 588
combining the current components...
Processing epoch : 63 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 64 / 588
combining the current components...
Processing epoch : 65 / 588
combining the current components...
Processing epoch : 66 / 588
combining the current components...
Processing epoch : 67 / 588
combining the current components...
Processing epoch : 68 / 588
combining the current components...
Processing epoch : 69 / 588
combining the current components...
Processing epoch : 70 / 588
combining the current components...
Processing epoch : 71 / 588
combining the current components...
Processing epoch : 72 / 588
combining the current components...
Processing epoch : 73 / 588
combining the current components...
Processing epoch : 74 / 588
combining the current components...
Processing epoch : 75 / 588
combining the current components...
Processing epoch : 76 / 588
combining the current components...
Processing epoch : 77 / 588
combining the current components...
Processing epoch : 78 / 588
combining the current components...
Processing epoch : 79 / 588
combining the current components...
Processing epoch : 80 / 588
combining the current components...
Processing epoch : 81 / 588
combining the current components...
Processing epoch : 82 / 588
combining the current components...
Processing epoch : 83 / 588
combining the current components...
Processing epoch : 84 / 588
combining the current components...
Processing epoch : 85 / 588
combining the current components...
Processing epoch : 86 / 588
combining the current components...
Processing epoch : 87 / 588
combining the current components...
Processing epoch : 88 / 588
combining the current components...
Processing epoch : 89 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 90 / 588
combining the current components...
Processing epoch : 91 / 588
combining the current components...
Processing epoch : 92 / 588
combining the current components...
Processing epoch : 93 / 588
combining the current components...
Processing epoch : 94 / 588
combining the current components...
Processing epoch : 95 / 588
combining the current components...
Processing epoch : 96 / 588
combining the current components...
Processing epoch : 97 / 588
combining the current components...
Processing epoch : 98 / 588
combining the current components...
Processing epoch : 99 / 588
combining the current components...
Processing epoch : 100 / 588
combining the current components...
Processing epoch : 101 / 588
combining the current components...
Processing epoch : 102 / 588
combining the current components...
Processing epoch : 103 / 588
combining the current components...
Processing epoch : 104 / 588
combining the current components...
Processing epoch : 105 / 588
combining the current components...
Processing epoch : 106 / 588
combining the current components...
Processing epoch : 107 / 588
combining the current components...
Processing epoch : 108 / 588
combining the current components...
Processing epoch : 109 / 588
combining the current components...
Processing epoch : 110 / 588
combining the current components...
Processing epoch : 111 / 588
combining the current components...
Processing epoch : 112 / 588
combining the current components...
Processing epoch : 113 / 588
combining the current components...
Processing epoch : 114 / 588
combining the current components...
Processing epoch : 115 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 116 / 588
combining the current components...
Processing epoch : 117 / 588
combining the current components...
Processing epoch : 118 / 588
combining the current components...
Processing epoch : 119 / 588
combining the current components...
Processing epoch : 120 / 588
combining the current components...
Processing epoch : 121 / 588
combining the current components...
Processing epoch : 122 / 588
combining the current components...
Processing epoch : 123 / 588
combining the current components...
Processing epoch : 124 / 588
combining the current components...
Processing epoch : 125 / 588
combining the current components...
Processing epoch : 126 / 588
combining the current components...
Processing epoch : 127 / 588
combining the current components...
Processing epoch : 128 / 588
combining the current components...
Processing epoch : 129 / 588
combining the current components...
Processing epoch : 130 / 588
combining the current components...
Processing epoch : 131 / 588
combining the current components...
Processing epoch : 132 / 588
combining the current components...
Processing epoch : 133 / 588
combining the current components...
Processing epoch : 134 / 588
combining the current components...
Processing epoch : 135 / 588
combining the current components...
Processing epoch : 136 / 588
combining the current components...
Processing epoch : 137 / 588
combining the current components...
Processing epoch : 138 / 588
combining the current components...
Processing epoch : 139 / 588
combining the current components...
Processing epoch : 140 / 588
combining the current components...
Processing epoch : 141 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 142 / 588
combining the current components...
Processing epoch : 143 / 588
combining the current components...
Processing epoch : 144 / 588
combining the current components...
Processing epoch : 145 / 588
combining the current components...
Processing epoch : 146 / 588
combining the current components...
Processing epoch : 147 / 588
combining the current components...
Processing epoch : 148 / 588
combining the current components...
Processing epoch : 149 / 588
combining the current components...
Processing epoch : 150 / 588
combining the current components...
Processing epoch : 151 / 588
combining the current components...
Processing epoch : 152 / 588
combining the current components...
Processing epoch : 153 / 588
combining the current components...
Processing epoch : 154 / 588
combining the current components...
Processing epoch : 155 / 588
combining the current components...
Processing epoch : 156 / 588
combining the current components...
Processing epoch : 157 / 588
combining the current components...
Processing epoch : 158 / 588
combining the current components...
Processing epoch : 159 / 588
combining the current components...
Processing epoch : 160 / 588
combining the current components...
Processing epoch : 161 / 588
combining the current components...
Processing epoch : 162 / 588
combining the current components...
Processing epoch : 163 / 588
combining the current components...
Processing epoch : 164 / 588
combining the current components...
Processing epoch : 165 / 588
combining the current components...
Processing epoch : 166 / 588
combining the current components...
Processing epoch : 167 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 168 / 588
combining the current components...
Processing epoch : 169 / 588
combining the current components...
Processing epoch : 170 / 588
combining the current components...
Processing epoch : 171 / 588
combining the current components...
Processing epoch : 172 / 588
combining the current components...
Processing epoch : 173 / 588
combining the current components...
Processing epoch : 174 / 588
combining the current components...
Processing epoch : 175 / 588
combining the current components...
Processing epoch : 176 / 588
combining the current components...
Processing epoch : 177 / 588
combining the current components...
Processing epoch : 178 / 588
combining the current components...
Processing epoch : 179 / 588
combining the current components...
Processing epoch : 180 / 588
combining the current components...
Processing epoch : 181 / 588
combining the current components...
Processing epoch : 182 / 588
combining the current components...
Processing epoch : 183 / 588
combining the current components...
Processing epoch : 184 / 588
combining the current components...
Processing epoch : 185 / 588
combining the current components...
Processing epoch : 186 / 588
combining the current components...
Processing epoch : 187 / 588
combining the current components...
Processing epoch : 188 / 588
combining the current components...
Processing epoch : 189 / 588
combining the current components...
Processing epoch : 190 / 588
combining the current components...
Processing epoch : 191 / 588
combining the current components...
Processing epoch : 192 / 588
combining the current components...
Processing epoch : 193 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 194 / 588
combining the current components...
Processing epoch : 195 / 588
combining the current components...
Processing epoch : 196 / 588
combining the current components...
Processing epoch : 197 / 588
combining the current components...
Processing epoch : 198 / 588
combining the current components...
Processing epoch : 199 / 588
combining the current components...
Processing epoch : 200 / 588
combining the current components...
Processing epoch : 201 / 588
combining the current components...
Processing epoch : 202 / 588
combining the current components...
Processing epoch : 203 / 588
combining the current components...
Processing epoch : 204 / 588
combining the current components...
Processing epoch : 205 / 588
combining the current components...
Processing epoch : 206 / 588
combining the current components...
Processing epoch : 207 / 588
combining the current components...
Processing epoch : 208 / 588
combining the current components...
Processing epoch : 209 / 588
combining the current components...
Processing epoch : 210 / 588
combining the current components...
Processing epoch : 211 / 588
combining the current components...
Processing epoch : 212 / 588
combining the current components...
Processing epoch : 213 / 588
combining the current components...
Processing epoch : 214 / 588
combining the current components...
Processing epoch : 215 / 588
combining the current components...
Processing epoch : 216 / 588
combining the current components...
Processing epoch : 217 / 588
combining the current components...
Processing epoch : 218 / 588
combining the current components...
Processing epoch : 219 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 220 / 588
combining the current components...
Processing epoch : 221 / 588
combining the current components...
Processing epoch : 222 / 588
combining the current components...
Processing epoch : 223 / 588
combining the current components...
Processing epoch : 224 / 588
combining the current components...
Processing epoch : 225 / 588
combining the current components...
Processing epoch : 226 / 588
combining the current components...
Processing epoch : 227 / 588
combining the current components...
Processing epoch : 228 / 588
combining the current components...
Processing epoch : 229 / 588
combining the current components...
Processing epoch : 230 / 588
combining the current components...
Processing epoch : 231 / 588
combining the current components...
Processing epoch : 232 / 588
combining the current components...
Processing epoch : 233 / 588
combining the current components...
Processing epoch : 234 / 588
combining the current components...
Processing epoch : 235 / 588
combining the current components...
Processing epoch : 236 / 588
combining the current components...
Processing epoch : 237 / 588
combining the current components...
Processing epoch : 238 / 588
combining the current components...
Processing epoch : 239 / 588
combining the current components...
Processing epoch : 240 / 588
combining the current components...
Processing epoch : 241 / 588
combining the current components...
Processing epoch : 242 / 588
combining the current components...
Processing epoch : 243 / 588
combining the current components...
Processing epoch : 244 / 588
combining the current components...
Processing epoch : 245 / 588
```

(continues on next page)



(continued from previous page)

```
combining the current components...
Processing epoch : 246 / 588
combining the current components...
Processing epoch : 247 / 588
combining the current components...
Processing epoch : 248 / 588
combining the current components...
Processing epoch : 249 / 588
combining the current components...
Processing epoch : 250 / 588
combining the current components...
Processing epoch : 251 / 588
combining the current components...
Processing epoch : 252 / 588
combining the current components...
Processing epoch : 253 / 588
combining the current components...
Processing epoch : 254 / 588
combining the current components...
Processing epoch : 255 / 588
combining the current components...
Processing epoch : 256 / 588
combining the current components...
Processing epoch : 257 / 588
combining the current components...
Processing epoch : 258 / 588
combining the current components...
Processing epoch : 259 / 588
combining the current components...
Processing epoch : 260 / 588
combining the current components...
Processing epoch : 261 / 588
combining the current components...
Processing epoch : 262 / 588
combining the current components...
Processing epoch : 263 / 588
combining the current components...
Processing epoch : 264 / 588
combining the current components...
Processing epoch : 265 / 588
combining the current components...
Processing epoch : 266 / 588
combining the current components...
Processing epoch : 267 / 588
combining the current components...
Processing epoch : 268 / 588
combining the current components...
Processing epoch : 269 / 588
combining the current components...
Processing epoch : 270 / 588
combining the current components...
Processing epoch : 271 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 272 / 588
combining the current components...
Processing epoch : 273 / 588
combining the current components...
Processing epoch : 274 / 588
combining the current components...
Processing epoch : 275 / 588
combining the current components...
Processing epoch : 276 / 588
combining the current components...
Processing epoch : 277 / 588
combining the current components...
Processing epoch : 278 / 588
combining the current components...
Processing epoch : 279 / 588
combining the current components...
Processing epoch : 280 / 588
combining the current components...
Processing epoch : 281 / 588
combining the current components...
Processing epoch : 282 / 588
combining the current components...
Processing epoch : 283 / 588
combining the current components...
Processing epoch : 284 / 588
combining the current components...
Processing epoch : 285 / 588
combining the current components...
Processing epoch : 286 / 588
combining the current components...
Processing epoch : 287 / 588
combining the current components...
Processing epoch : 288 / 588
combining the current components...
Processing epoch : 289 / 588
combining the current components...
Processing epoch : 290 / 588
combining the current components...
Processing epoch : 291 / 588
combining the current components...
Processing epoch : 292 / 588
combining the current components...
Processing epoch : 293 / 588
combining the current components...
Processing epoch : 294 / 588
combining the current components...
Processing epoch : 295 / 588
combining the current components...
Processing epoch : 296 / 588
combining the current components...
Processing epoch : 297 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 298 / 588
combining the current components...
Processing epoch : 299 / 588
combining the current components...
Processing epoch : 300 / 588
combining the current components...
Processing epoch : 301 / 588
combining the current components...
Processing epoch : 302 / 588
combining the current components...
Processing epoch : 303 / 588
combining the current components...
Processing epoch : 304 / 588
combining the current components...
Processing epoch : 305 / 588
combining the current components...
Processing epoch : 306 / 588
combining the current components...
Processing epoch : 307 / 588
combining the current components...
Processing epoch : 308 / 588
combining the current components...
Processing epoch : 309 / 588
combining the current components...
Processing epoch : 310 / 588
combining the current components...
Processing epoch : 311 / 588
combining the current components...
Processing epoch : 312 / 588
combining the current components...
Processing epoch : 313 / 588
combining the current components...
Processing epoch : 314 / 588
combining the current components...
Processing epoch : 315 / 588
combining the current components...
Processing epoch : 316 / 588
combining the current components...
Processing epoch : 317 / 588
combining the current components...
Processing epoch : 318 / 588
combining the current components...
Processing epoch : 319 / 588
combining the current components...
Processing epoch : 320 / 588
combining the current components...
Processing epoch : 321 / 588
combining the current components...
Processing epoch : 322 / 588
combining the current components...
Processing epoch : 323 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 324 / 588
combining the current components...
Processing epoch : 325 / 588
combining the current components...
Processing epoch : 326 / 588
combining the current components...
Processing epoch : 327 / 588
combining the current components...
Processing epoch : 328 / 588
combining the current components...
Processing epoch : 329 / 588
combining the current components...
Processing epoch : 330 / 588
combining the current components...
Processing epoch : 331 / 588
combining the current components...
Processing epoch : 332 / 588
combining the current components...
Processing epoch : 333 / 588
combining the current components...
Processing epoch : 334 / 588
combining the current components...
Processing epoch : 335 / 588
combining the current components...
Processing epoch : 336 / 588
combining the current components...
Processing epoch : 337 / 588
combining the current components...
Processing epoch : 338 / 588
combining the current components...
Processing epoch : 339 / 588
combining the current components...
Processing epoch : 340 / 588
combining the current components...
Processing epoch : 341 / 588
combining the current components...
Processing epoch : 342 / 588
combining the current components...
Processing epoch : 343 / 588
combining the current components...
Processing epoch : 344 / 588
combining the current components...
Processing epoch : 345 / 588
combining the current components...
Processing epoch : 346 / 588
combining the current components...
Processing epoch : 347 / 588
combining the current components...
Processing epoch : 348 / 588
combining the current components...
Processing epoch : 349 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 350 / 588
combining the current components...
Processing epoch : 351 / 588
combining the current components...
Processing epoch : 352 / 588
combining the current components...
Processing epoch : 353 / 588
combining the current components...
Processing epoch : 354 / 588
combining the current components...
Processing epoch : 355 / 588
combining the current components...
Processing epoch : 356 / 588
combining the current components...
Processing epoch : 357 / 588
combining the current components...
Processing epoch : 358 / 588
combining the current components...
Processing epoch : 359 / 588
combining the current components...
Processing epoch : 360 / 588
combining the current components...
Processing epoch : 361 / 588
combining the current components...
Processing epoch : 362 / 588
combining the current components...
Processing epoch : 363 / 588
combining the current components...
Processing epoch : 364 / 588
combining the current components...
Processing epoch : 365 / 588
combining the current components...
Processing epoch : 366 / 588
combining the current components...
Processing epoch : 367 / 588
combining the current components...
Processing epoch : 368 / 588
combining the current components...
Processing epoch : 369 / 588
combining the current components...
Processing epoch : 370 / 588
combining the current components...
Processing epoch : 371 / 588
combining the current components...
Processing epoch : 372 / 588
combining the current components...
Processing epoch : 373 / 588
combining the current components...
Processing epoch : 374 / 588
combining the current components...
Processing epoch : 375 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 376 / 588
combining the current components...
Processing epoch : 377 / 588
combining the current components...
Processing epoch : 378 / 588
combining the current components...
Processing epoch : 379 / 588
combining the current components...
Processing epoch : 380 / 588
combining the current components...
Processing epoch : 381 / 588
combining the current components...
Processing epoch : 382 / 588
combining the current components...
Processing epoch : 383 / 588
combining the current components...
Processing epoch : 384 / 588
combining the current components...
Processing epoch : 385 / 588
combining the current components...
Processing epoch : 386 / 588
combining the current components...
Processing epoch : 387 / 588
combining the current components...
Processing epoch : 388 / 588
combining the current components...
Processing epoch : 389 / 588
combining the current components...
Processing epoch : 390 / 588
combining the current components...
Processing epoch : 391 / 588
combining the current components...
Processing epoch : 392 / 588
combining the current components...
Processing epoch : 393 / 588
combining the current components...
Processing epoch : 394 / 588
combining the current components...
Processing epoch : 395 / 588
combining the current components...
Processing epoch : 396 / 588
combining the current components...
Processing epoch : 397 / 588
combining the current components...
Processing epoch : 398 / 588
combining the current components...
Processing epoch : 399 / 588
combining the current components...
Processing epoch : 400 / 588
combining the current components...
Processing epoch : 401 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 402 / 588
combining the current components...
Processing epoch : 403 / 588
combining the current components...
Processing epoch : 404 / 588
combining the current components...
Processing epoch : 405 / 588
combining the current components...
Processing epoch : 406 / 588
combining the current components...
Processing epoch : 407 / 588
combining the current components...
Processing epoch : 408 / 588
combining the current components...
Processing epoch : 409 / 588
combining the current components...
Processing epoch : 410 / 588
combining the current components...
Processing epoch : 411 / 588
combining the current components...
Processing epoch : 412 / 588
combining the current components...
Processing epoch : 413 / 588
combining the current components...
Processing epoch : 414 / 588
combining the current components...
Processing epoch : 415 / 588
combining the current components...
Processing epoch : 416 / 588
combining the current components...
Processing epoch : 417 / 588
combining the current components...
Processing epoch : 418 / 588
combining the current components...
Processing epoch : 419 / 588
combining the current components...
Processing epoch : 420 / 588
combining the current components...
Processing epoch : 421 / 588
combining the current components...
Processing epoch : 422 / 588
combining the current components...
Processing epoch : 423 / 588
combining the current components...
Processing epoch : 424 / 588
combining the current components...
Processing epoch : 425 / 588
combining the current components...
Processing epoch : 426 / 588
combining the current components...
Processing epoch : 427 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 428 / 588
combining the current components...
Processing epoch : 429 / 588
combining the current components...
Processing epoch : 430 / 588
combining the current components...
Processing epoch : 431 / 588
combining the current components...
Processing epoch : 432 / 588
combining the current components...
Processing epoch : 433 / 588
combining the current components...
Processing epoch : 434 / 588
combining the current components...
Processing epoch : 435 / 588
combining the current components...
Processing epoch : 436 / 588
combining the current components...
Processing epoch : 437 / 588
combining the current components...
Processing epoch : 438 / 588
combining the current components...
Processing epoch : 439 / 588
combining the current components...
Processing epoch : 440 / 588
combining the current components...
Processing epoch : 441 / 588
combining the current components...
Processing epoch : 442 / 588
combining the current components...
Processing epoch : 443 / 588
combining the current components...
Processing epoch : 444 / 588
combining the current components...
Processing epoch : 445 / 588
combining the current components...
Processing epoch : 446 / 588
combining the current components...
Processing epoch : 447 / 588
combining the current components...
Processing epoch : 448 / 588
combining the current components...
Processing epoch : 449 / 588
combining the current components...
Processing epoch : 450 / 588
combining the current components...
Processing epoch : 451 / 588
combining the current components...
Processing epoch : 452 / 588
combining the current components...
Processing epoch : 453 / 588
```

(continues on next page)



(continued from previous page)

```
combining the current components...
Processing epoch : 454 / 588
combining the current components...
Processing epoch : 455 / 588
combining the current components...
Processing epoch : 456 / 588
combining the current components...
Processing epoch : 457 / 588
combining the current components...
Processing epoch : 458 / 588
combining the current components...
Processing epoch : 459 / 588
combining the current components...
Processing epoch : 460 / 588
combining the current components...
Processing epoch : 461 / 588
combining the current components...
Processing epoch : 462 / 588
combining the current components...
Processing epoch : 463 / 588
combining the current components...
Processing epoch : 464 / 588
combining the current components...
Processing epoch : 465 / 588
combining the current components...
Processing epoch : 466 / 588
combining the current components...
Processing epoch : 467 / 588
combining the current components...
Processing epoch : 468 / 588
combining the current components...
Processing epoch : 469 / 588
combining the current components...
Processing epoch : 470 / 588
combining the current components...
Processing epoch : 471 / 588
combining the current components...
Processing epoch : 472 / 588
combining the current components...
Processing epoch : 473 / 588
combining the current components...
Processing epoch : 474 / 588
combining the current components...
Processing epoch : 475 / 588
combining the current components...
Processing epoch : 476 / 588
combining the current components...
Processing epoch : 477 / 588
combining the current components...
Processing epoch : 478 / 588
combining the current components...
Processing epoch : 479 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 480 / 588
combining the current components...
Processing epoch : 481 / 588
combining the current components...
Processing epoch : 482 / 588
combining the current components...
Processing epoch : 483 / 588
combining the current components...
Processing epoch : 484 / 588
combining the current components...
Processing epoch : 485 / 588
combining the current components...
Processing epoch : 486 / 588
combining the current components...
Processing epoch : 487 / 588
combining the current components...
Processing epoch : 488 / 588
combining the current components...
Processing epoch : 489 / 588
combining the current components...
Processing epoch : 490 / 588
combining the current components...
Processing epoch : 491 / 588
combining the current components...
Processing epoch : 492 / 588
combining the current components...
Processing epoch : 493 / 588
combining the current components...
Processing epoch : 494 / 588
combining the current components...
Processing epoch : 495 / 588
combining the current components...
Processing epoch : 496 / 588
combining the current components...
Processing epoch : 497 / 588
combining the current components...
Processing epoch : 498 / 588
combining the current components...
Processing epoch : 499 / 588
combining the current components...
Processing epoch : 500 / 588
combining the current components...
Processing epoch : 501 / 588
combining the current components...
Processing epoch : 502 / 588
combining the current components...
Processing epoch : 503 / 588
combining the current components...
Processing epoch : 504 / 588
combining the current components...
Processing epoch : 505 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 506 / 588
combining the current components...
Processing epoch : 507 / 588
combining the current components...
Processing epoch : 508 / 588
combining the current components...
Processing epoch : 509 / 588
combining the current components...
Processing epoch : 510 / 588
combining the current components...
Processing epoch : 511 / 588
combining the current components...
Processing epoch : 512 / 588
combining the current components...
Processing epoch : 513 / 588
combining the current components...
Processing epoch : 514 / 588
combining the current components...
Processing epoch : 515 / 588
combining the current components...
Processing epoch : 516 / 588
combining the current components...
Processing epoch : 517 / 588
combining the current components...
Processing epoch : 518 / 588
combining the current components...
Processing epoch : 519 / 588
combining the current components...
Processing epoch : 520 / 588
combining the current components...
Processing epoch : 521 / 588
combining the current components...
Processing epoch : 522 / 588
combining the current components...
Processing epoch : 523 / 588
combining the current components...
Processing epoch : 524 / 588
combining the current components...
Processing epoch : 525 / 588
combining the current components...
Processing epoch : 526 / 588
combining the current components...
Processing epoch : 527 / 588
combining the current components...
Processing epoch : 528 / 588
combining the current components...
Processing epoch : 529 / 588
combining the current components...
Processing epoch : 530 / 588
combining the current components...
Processing epoch : 531 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 532 / 588
combining the current components...
Processing epoch : 533 / 588
combining the current components...
Processing epoch : 534 / 588
combining the current components...
Processing epoch : 535 / 588
combining the current components...
Processing epoch : 536 / 588
combining the current components...
Processing epoch : 537 / 588
combining the current components...
Processing epoch : 538 / 588
combining the current components...
Processing epoch : 539 / 588
combining the current components...
Processing epoch : 540 / 588
combining the current components...
Processing epoch : 541 / 588
combining the current components...
Processing epoch : 542 / 588
combining the current components...
Processing epoch : 543 / 588
combining the current components...
Processing epoch : 544 / 588
combining the current components...
Processing epoch : 545 / 588
combining the current components...
Processing epoch : 546 / 588
combining the current components...
Processing epoch : 547 / 588
combining the current components...
Processing epoch : 548 / 588
combining the current components...
Processing epoch : 549 / 588
combining the current components...
Processing epoch : 550 / 588
combining the current components...
Processing epoch : 551 / 588
combining the current components...
Processing epoch : 552 / 588
combining the current components...
Processing epoch : 553 / 588
combining the current components...
Processing epoch : 554 / 588
combining the current components...
Processing epoch : 555 / 588
combining the current components...
Processing epoch : 556 / 588
combining the current components...
Processing epoch : 557 / 588
```

(continues on next page)

(continued from previous page)

```
combining the current components...
Processing epoch : 558 / 588
combining the current components...
Processing epoch : 559 / 588
combining the current components...
Processing epoch : 560 / 588
combining the current components...
Processing epoch : 561 / 588
combining the current components...
Processing epoch : 562 / 588
combining the current components...
Processing epoch : 563 / 588
combining the current components...
Processing epoch : 564 / 588
combining the current components...
Processing epoch : 565 / 588
combining the current components...
Processing epoch : 566 / 588
combining the current components...
Processing epoch : 567 / 588
combining the current components...
Processing epoch : 568 / 588
combining the current components...
Processing epoch : 569 / 588
combining the current components...
Processing epoch : 570 / 588
combining the current components...
Processing epoch : 571 / 588
combining the current components...
Processing epoch : 572 / 588
combining the current components...
Processing epoch : 573 / 588
combining the current components...
Processing epoch : 574 / 588
combining the current components...
Processing epoch : 575 / 588
combining the current components...
Processing epoch : 576 / 588
combining the current components...
Processing epoch : 577 / 588
combining the current components...
Processing epoch : 578 / 588
combining the current components...
Processing epoch : 579 / 588
combining the current components...
Processing epoch : 580 / 588
combining the current components...
Processing epoch : 581 / 588
combining the current components...
Processing epoch : 582 / 588
combining the current components...
Processing epoch : 583 / 588
```

(continues on next page)

(continued from previous page)

[illegible]

(continues on next page)

[illegible]

(continued from previous page)

[illegible]

(continues on next page)



[illegible]

(continued from previous page)

[illegible]

(continues on next page)

[illegible]

(continued from previous page)

[illegible]

(continues on next page)



(continued from previous page)

[illegible]

(continues on next page)



(continued from previous page)

[illegible]

(continues on next page)





(continued from previous page)

```

220221-11:12:23,523 nipype.workflow INFO:
    [MultiProc] Running 0 tasks, and 0 jobs ready. Free memory (GB): 28.20/28.20,
    ↳Free processors: 1/1.
220221-11:12:25,653 nipype.interface INFO:
    ***** Processing finished *****
CPU times: user 3.85 s, sys: 924 ms, total: 4.78 s
Wall time: 17min 43s

/home/localadmin/Softwares/miniconda3/envs/py37cmp-eeg/lib/python3.7/site-packages/
↳joblib/externals/loky/backend/resource_tracker.py:320: UserWarning: resource_tracker:
↳There appear to be 3 leaked folder objects to clean up at shutdown
    (len(rtype_registry), rtype))

```

## A closer look at the EEG pipeline outputs

Let's have a closer look at the outputs that the EEG pipeline produces.

First of all: Connectomemapper works in such a way that the pipeline is first assembled and only afterwards, it is executed. During the assembly stage, input and output variables are connected and CMP3 produces a graph that visualizes this.

```

[13]: %matplotlib inline
path_to_svg = os.path.join(output_dir,__nipype_directory__,participant_label,'eeg_
↳pipeline','graph.svg')
display(SVG(filename=path_to_svg))

```

Apart from the input (“datasource”) and output (“eeg sinker”) nodes that are apart, you can see three blue boxes that represent the stages of the pipeline flow:

```

* Preparer stage
* Loader stage
* Inverse solution stage

```

Each of the stages, again, has an input and an output node, as well as several nodes representing processing steps. Each processing step has its own “interface” which you can find in `cmtklib/interfaces` (“mne” in parentheses indicates that they are defined in the file `mne.py`).

In the following, we will go over the interfaces and show what output they produce.

## Preparer stage

Let's first have a look at the information given by the config file regarding this stage:

```

[...]
"eeg_preparer_stage": {
    "eeg_format": ".set",
    "epochs": "sub-01_task-faces_desc-preproc_eeg.set",
    "invsol_format": "mne-sLORETA",
    "parcellation": {
        "label": "lausanne2008",
        "desc": "",

```

(continues on next page)

(continued from previous page)

```

        "suffix": "scale1"
    },
    "number_of_threads": 1,
    "EEG_params": {
        "expe_name": "faces",
        "EEG_event_IDs": {
            "SCRAMBLED" : 0,
            "FACES" : 1
        },
        "start_t": -0.2,
        "end_t" : 0.6
    }
},
[...]
```

The preparer stage has three processing steps:

- `eeglab2fif`: reads eeglab data and converts them to MNE format (.fif file extension)
- `createsrc`: creates the dipole locations along the surface of the brain
- `createbem`: creates the boundary element method

### eeglab2fif

If your data are not already in MNE format (.fif file extension), they have to be read and re-saved. The `eeglab2fif` interface does this for EEGLAB-format data (.set file extension). The interface produces a file named `sub-01_epo.fif` in the `derivatives/cmp-v3.0.3` folder. Critically, the saved epochs contain a montage, i.e. the sensor locations which have to be supplied in a file names `sub-01.xyz` inside the subject's EEGLAB derivatives folder (`derivatives/eeglab/sub-01/eeg/sub-01.xyz`).

```
[14]: # Let's have a look at the EEG data
with warnings.catch_warnings(): # suppress some irrelevant warnings coming from mne.read_
    epochs_eeglab()
    warnings.simplefilter("ignore")
    epochs_eeglab = mne.read_epochs_eeglab(
        os.path.join(output_dir, __eeglab_directory__,
                      participant_label, 'eeg',
                      participant_label+'_task-faces_desc-preproc_eeg.set')
    ) # sub-01_FACES_250HZ_prepd.set

# eeglab2fif removes a baseline and crops the epochs according to parameters start_t and_
    end_t in config file
start_t = -0.2
end_t = 0.6
epochs_eeglab.apply_baseline((start_t,0))
epochs_eeglab.crop(tmin=start_t,tmax=end_t)
evoked_eeglab = epochs_eeglab.average().pick('eeg')

# compare to what eeglab2fif saved
epochs_mne = mne.read_epochs(
    os.path.join(output_dir, __cmp_directory__,
                  participant_label, 'eeg',
```

(continues on next page)

(continued from previous page)

```

        participant_label+'_epo.fif'))
evoked_mne = epochs_mne.average().pick('eeg')

Extracting parameters from /home/localadmin/Softwares/GitHub/connectomemapper3/docs/
↳ notebooks/ds003505_demo/derivatives/eeglab-v14.1.1/sub-01/eeg/sub-01_task-faces_desc-
↳ preproc_eeg.set...
Not setting metadata
Not setting metadata
588 matching events found
No baseline correction applied
0 projection items activated
Ready.
Applying baseline correction (mode: mean)
Reading /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↳ derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_epo.fif ...
    Read a total of 1 projection items:
        Average EEG reference (1 x 128)  idle
    Found the data of interest:
        t =      -200.00 ...      600.00 ms
        0 CTF compensation matrices available
Not setting metadata
Not setting metadata
588 matching events found
No baseline correction applied
Created an SSP operator (subspace dimension = 1)
1 projection items activated

```

```

[15]: # plot and convince yourself it's the same
      %matplotlib inline
      fig = plt.figure()
      plt.rcParams['figure.figsize'] = (15, 10)

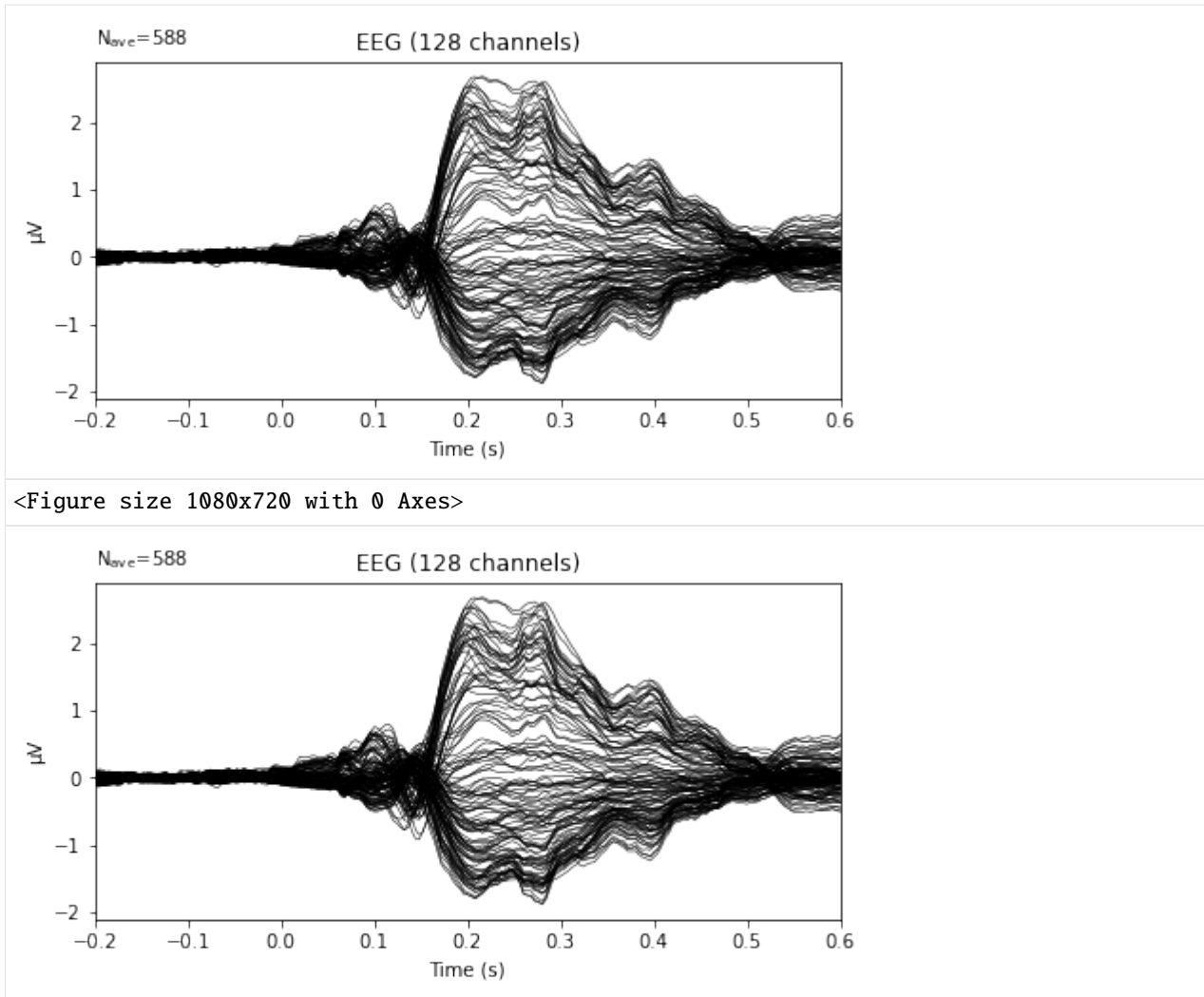
      _=evoked_mne.plot(time_unit='s')

      fig = plt.figure()
      plt.rcParams['figure.figsize'] = (15, 10)

      _=evoked_eeglab.plot(time_unit='s')

      <Figure size 432x288 with 0 Axes>

```



### createsrc

MNE is able to create volume- and surface-based source spaces, but in our pipeline, we use surface-based only. In order to do this, MNE takes advantage of the Freesurfer-created outputs in the `derivatives/freesurfer-7.1.1` derivatives directory.

### createbem

The BEM (boundary element model) is the head model we use, in our case, it is based on the individual's structural MRI and, again, related freesurfer derivatives. Its creation consists of two steps:

1. The necessary surfaces (brain, inner skull, outer skull, and outer skin) are extracted using `mne.bem.make_watershed_bem()`. The surfaces are saved in the subject's freesurfer-directory in a new folder `bem/watershed`.
2. The model itself is created using `mne.make_bem_model()` and `mne.make_bem_solution()`. In this step, the surfaces and the tissue conductivities between the surfaces are used.

```
[16]: # Let's visualize the BEM surfaces and source space
src = mne.read_source_spaces(os.path.join(output_dir,__cmp_directory__,\
                                         participant_label,'eeg',participant_label+'_src.fif'))
# plot will appear in separate window
%matplotlib qt
# lines are the surfaces, pink dots are the sources (dipoles)
_=mne.viz.plot_bem(subject=participant_label, subjects_dir=project.freesurfer_subjects_
↳dir,
                    brain_surfaces='white', src=src, orientation='sagittal')
```

```
Reading a source space...
Computing patch statistics...
Patch information added...
Distance information added...
[done]
Reading a source space...
Computing patch statistics...
Patch information added...
Distance information added...
[done]
2 source spaces read
Using surface: /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↳ds003505_demo/derivatives/freesurfer-7.1.1/sub-01/bem/inner_skull.surf
Using surface: /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↳ds003505_demo/derivatives/freesurfer-7.1.1/sub-01/bem/outer_skull.surf
Using surface: /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/
↳ds003505_demo/derivatives/freesurfer-7.1.1/sub-01/bem/outer_skin.surf
```

## Loader stage

During the preparer stage, we have told CMP3 which file extensions and keywords to look for that are going to be used in the actual inverse solution. Using nipype's "BIDS datagrabber", it gathers the necessary inputs in this step.

## Inverse solution stage

The only implemented inverse solution algorithm right now is sLORETA.

This stage has again three processing steps:

- `createfwd`: creates the forward solution (leadfield) from the BEM and the source space
- `createcov`: creates the noise covariance matrix from the data
- `invsol_MNE`: creates the actual inverse operator and applies it, resulting in ROI-time courses

**createfwd**

MNE first computes a forward solution that describes how electrical currents propagate from the sources created earlier (via `createsrc`) through the tissues of the head modelled by the BEM (created via `createbem`) to the electrodes. Thus, the electrode positions have to be known and be aligned to the head model.

```
[17]: # Let's check the alignment between MRI and electrode positions.
trans = mne.read_trans(os.path.join(output_dir,__cmp_directory__,\
                                participant_label,'eeg',participant_label+'_trans.fif'))
mne.viz.plot_alignment(epochs_mne.info, trans=trans, subject=participant_label,
                      subjects_dir=project.freesurfer_subjects_dir, dig=False,
                      surfaces=dict(head=0.95), coord_frame='mri')
```

Using mayavi 3d backend.

Using `outer_skin.surf` for head surface.

Channel types:: eeg: 128

```
2022-02-21 11:12:43.725 ( 3.624s) [ 23F39700]vtkInteractorStyleTrack:27
↳WARN| vtkInteractorStyleTrackball (0x55ed299ef300): vtkInteractorStyleTrackball will
↳be deprecated in
the next release after VTK 4.0. Please use
vtkInteractorStyleSwitch instead.
```

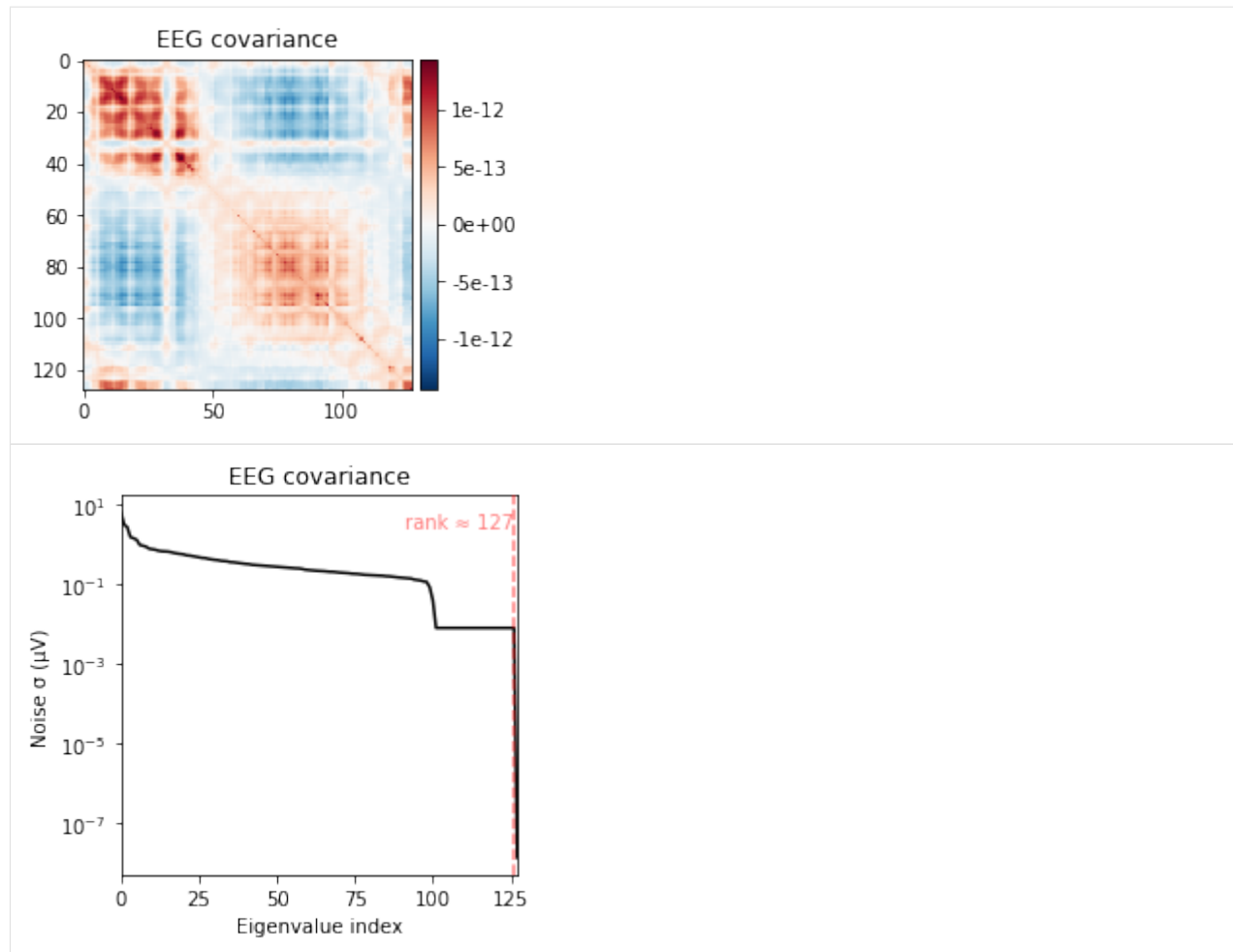
```
[17]: <mayavi.core.scene.Scene at 0x7f972ef24290>
```

**createcov**

MNE uses an estimate of signal to noise ratio in its creation of the inverse solution. For that, it considers the pre-stimulus period of the EEG recordings.

```
[18]: # Let's have a look at the noise covariance.
%matplotlib inline
noise_cov = mne.read_cov(os.path.join(output_dir,__cmp_directory__,\
                                participant_label,'eeg',participant_label+'_noisecov.fif'
                                ))
fig_cov, fig_spectra = mne.viz.plot_cov(noise_cov, epochs_mne.info)
```

```
128 x 128 full covariance (kind = 1) found.
Read a total of 1 projection items:
  Average EEG reference (1 x 128) active
Computing rank from covariance with rank=None
Using tolerance 1.2e-14 (2.2e-16 eps * 128 dim * 0.43 max singular value)
Estimated rank (eeg): 127
EEG: rank 127 computed from 128 data channels with 0 projectors
```



## invsol\_MNE

Now, everything comes together to create the inverse operator, which is then applied to the EEG data to create source time courses. In the last step, the source time courses are converted to ROI-time courses according to the selected parcellation.

The outputs that are necessary for this step to work were created in the previous processing steps, namely:

- the EEG epochs in .fif-format
- the electrode montage
- the head model
- the source point locations
- the forward operator
- the noise covariance

First, the inverse operator is created using `mne.minimum_norm.make_inverse_operator()`. We use the options

```
loose=1, depth=None, fixed=False
```



This means that we are obtaining full 3-dimensional dipoles whose orientation is not fixed or constrained to be (somewhat) orthogonal to surface; and we are not applying any depth weighting. The solution is written to a file `sub-01_inv.fif` in the same directory as the other outputs (`derivatives/cmp-v3.0.3/sub-01/eeg`).

In a subsequent step in the same interface, this inverse operator is then applied to the epochs (not the evoked time course averaged over trials) using `mne.minimum_norm.apply_inverse_epochs`.

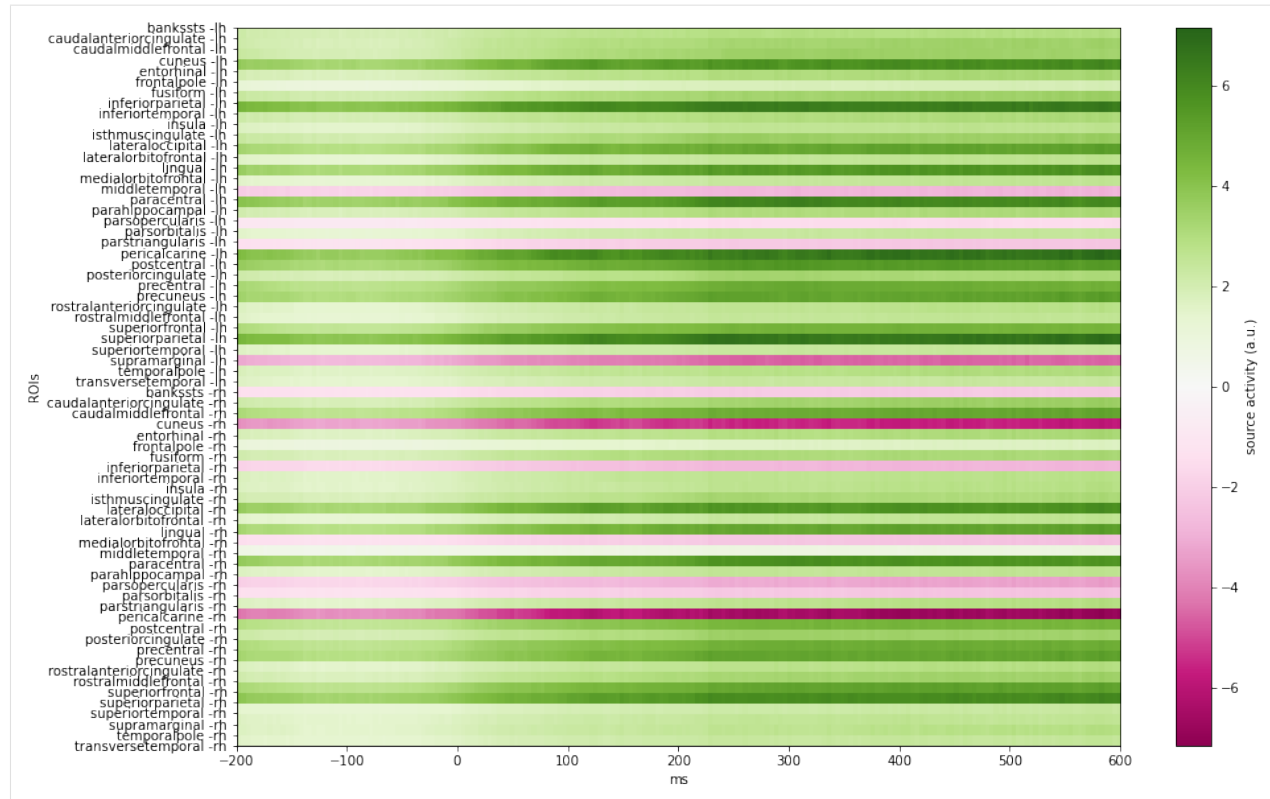
The final step performed by this interface and by the EEG pipeline is to use `mne.extract_label_time_course` to create ROI-time courses according to `mne.read_labels_from_annot()`. As given in the config file, we use “lausanne2008” scale 1, which is the Desikan-atlas. The time courses and the ROI-names are stored in `sub-01_atlas-L2018_res-scale1_desc-epo_timeseries.pkl`, i.e. a format that is not specific to MNE.

Let’s have a look at the time courses.

```
[19]: with open(os.path.join(output_dir,__cmp_directory__,participant_label,'eeg',participant_
      ↪label + '_atlas-L2018_res-scale1_desc-epo_timeseries.pkl'), 'rb') as f:
          rtc_epo = pickle.load(f)
          # for some reason, MNE writes label time courses as lists. convert to numpy array
          rtc_epo['data'] = np.array(rtc_epo['data'])
```

```
[20]: # sort labels to make the time courses look nicer
N = len(rtc_epo['labels'])-2 # two "unknown" regions - do not plot
sorting = list(np.arange(0,N,2))+list(np.arange(1,N,2)) # left and right always_
      ↪alternating
# list of ROI names
labels_list_left = [i.name for i in rtc_epo['labels'][0::2] if i.name!='unknown -lh']
labels_list_right = [i.name for i in rtc_epo['labels'][1::2] if i.name!='unknown -rh']
labels_list = labels_list_left+labels_list_right
```

```
[21]: # plot
%matplotlib inline
to_plot = np.mean(rtc_epo['data'][:, :-2, :], axis=0)
vminmax = np.max(abs(to_plot))
plt.rcParams['figure.figsize'] = (15, 10)
plt.imshow(to_plot[sorting, :], aspect='auto', extent=[-200, 600, 0, 67], interpolation='None',
      ↪vmin=-vminmax, vmax=vminmax, cmap='PiYG');
plt.xlabel('ms')
plt.ylabel('ROIs')
cbar = plt.colorbar()
cbar.set_label('source activity (a.u.)')
locs = np.arange(0,N)
_=plt.yticks(locs, labels_list[-1::-1] )
```



We can see that some of the time courses are “flipped” (have the opposite sign of the others). We will not address this problem here, but this is because of the step where dipole time courses are summarized for each brain region, using PCA. The direction of the resulting vector is not uniquely defined.

## Connectivity measures

Of course, the idea of CMP3 is to provide connectomes! This interface is not implemented yet in the pipeline, but with the ROI-time courses, it is easy to obtain functional connectivity matrices using [MNE-Connectivity](#).

Keep in mind that we only plot a single subject’s connectivity here, so it is not surprising if you do not see exactly what you would expect.

```
[22]: %%time
sfreq = epochs_mne.info['sfreq'] # the sampling frequency
con_methods = ['pli', 'wpli2_debiased', 'ciplv']

label_ts = rtc_epo['data']

con = mnec.spectral_connectivity(
    label_ts, method=con_methods, mode='multitaper', sfreq=sfreq,
    faverage=True, mt_adaptive=True, n_jobs=1,
    verbose='WARNING')

# Prepare the connectivity data for saving with CMP3 the connectome files
# con is a 3D array, get the connectivity for the first (and only) freq. band
# for each method
con_res = dict()
```

(continues on next page)

```
CPU times: user 54.6 s, sys: 0 ns, total: 54.6 s
Wall time: 54.7 s
```

```
conn_output = os.path.join(
    bids_dir, 'derivatives', 'cmp-v3.0.3', participant_label, 'eeg'
)

conn_basename = f'{participant_label}_atlas-L2018_res-scale1_conndata-network_
↪connectivity'

save_eeg_connectome_file(
    con_res=con_res,
    roi_labels=[label.name for label in rtc_epo['labels']], # Get parcellationlabels_
↪used by MNE
    output_dir=conn_output,
    output_basename=conn_basename,
    output_types=['tsv', 'gpickle', 'mat', 'graphml']
)
```

```
Save /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↳ derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_atlas-L2018_res-scale1_conndata-network_
↳ connectivity.gpickle...
```

```
Save /home/localadmin/Softwares/GitHub/connectomemapper3/docs/notebooks/ds003505_demo/
↳ derivatives/cmp-v3.0.3/sub-01/eeg/sub-01_atlas-L2018_res-scale1_conndata-network_
↳ connectivity.graphml...
```

```
G = nx.read_gpickle(os.path.join(conn_output, f"{conn_basename}.gpickle")) # same_
↪ format with tsv
A_wpli2_debiased = nx.to_numpy_array(G, weight="wpli2_debiased")
A_wpli2_debiased
```

```
array([[ 0.00000000e+00, -3.66497642e-04, -4.44626249e-04, ...,
         2.61330892e-04, -6.55801234e-04, -7.51796246e-04],
       [-3.66497642e-04,  0.00000000e+00,  1.73599618e-03, ...,
         1.88210359e-03,  2.06624042e-03,  1.58885857e-03],
       [-4.44626249e-04,  1.73599618e-03,  0.00000000e+00, ...,
         1.20817345e-03, -1.18799242e-03, -1.27701877e-03],
       ...,
```

(continued from previous page)

```
[ 2.61330892e-04, 1.88210359e-03, 1.20817345e-03, ...,
 0.00000000e+00, 2.14315916e-03, -8.06204062e-05],
[-6.55801234e-04, 2.06624042e-03, -1.18799242e-03, ...,
 2.14315916e-03, 0.00000000e+00, 1.98345454e-03],
[-7.51796246e-04, 1.58885857e-03, -1.27701877e-03, ...,
 -8.06204062e-05, 1.98345454e-03, 0.00000000e+00]])
```

You can then visualize the connectivity matrix in a pretty circular layout with [MNE-Connectivity viz](#). `plot_connectivity_circle()`:

```
[26]: %%time
label_names = [label.name for label in rtc_epo['labels']]

lh_labels = [name for name in label_names if name.endswith('lh')]

# Get the y-location of the label
label_ypos = list()
for name in lh_labels:
    idx = label_names.index(name)
    ypos = np.mean(rtc_epo['labels'][idx].pos[:, 1])
    label_ypos.append(ypos)

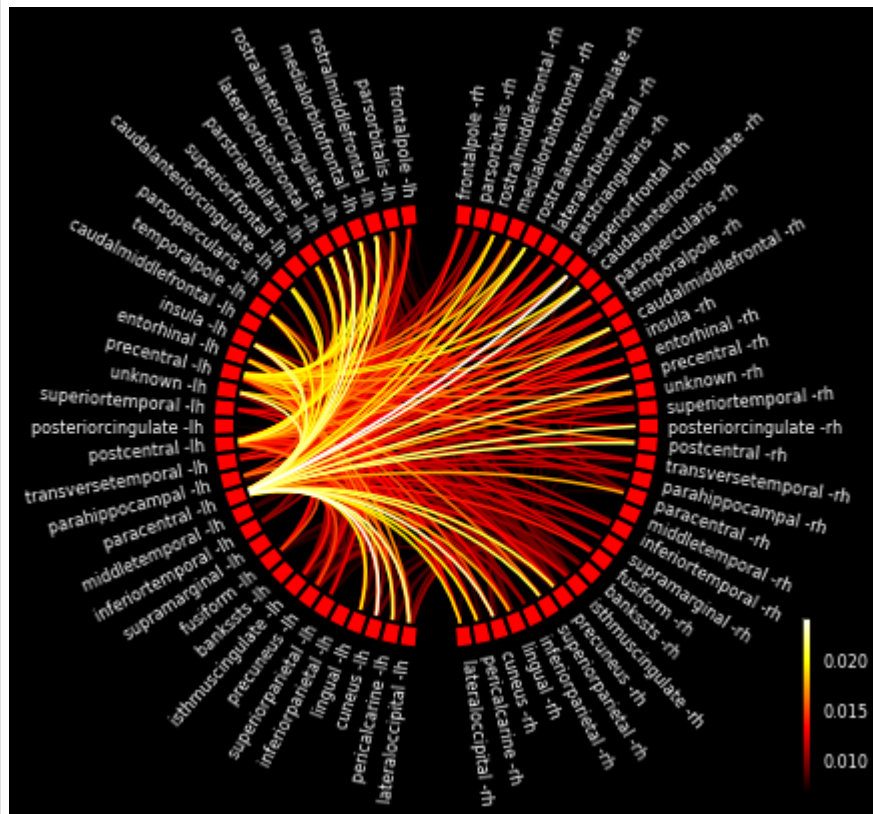
# Reorder the labels based on their location
lh_labels = [label for (yp, label) in sorted(zip(label_ypos, lh_labels))]

# For the right hemi
rh_labels = [label[:-2] + 'rh' for label in lh_labels]

# Save the plot order and create a circular layout
node_order = list()
node_order.extend(lh_labels[::-1]) # reverse the order
node_order.extend(rh_labels)

node_angles = mnec.viz.circular_layout(label_names, node_order, start_pos=90,
                                       group_boundaries=[0, len(label_names) / 2])

# Plot the graph using node colors from the FreeSurfer parcellation. We only
# show the 300 strongest connections.
# plot will appear in separate window
%matplotlib inline
mnec.viz.plot_connectivity_circle(A_wpli2_debiased, label_names, n_lines=300,
                                node_angles=node_angles, node_colors='r',
                                title='')
```



CPU times: user 14.1 s, sys: 182 ms, total: 14.2 s

Wall time: 14 s

[26]: (<Figure size 576x576 with 2 Axes>, <PolarAxesSubplot:>)

This concludes the tutorial !

We hope you enjoy it and any feedback or suggestions to improve it are very welcome! Just please open a [new issue](#) on GitHub and share your thoughts with us.

[ ]:

## 5.10 BSD 3-Clause License

Copyright (C) 2009-2022, Ecole Polytechnique Fédérale de Lausanne (EPFL) and Hospital Center and University of Lausanne (UNIL-CHUV), Switzerland, & Contributors, All rights reserved.

Redistribution and use in source and binary forms, with or without modification, are permitted provided that the following conditions are met:

- Redistributions of source code must retain the above copyright notice, this list of conditions and the following disclaimer.
- Redistributions in binary form must reproduce the above copyright notice, this list of conditions and the following disclaimer in the documentation and/or other materials provided with the distribution.
- Neither the name of the Ecole Polytechnique Fédérale de Lausanne (EPFL) and Hospital Center and University of Lausanne (UNIL-CHUV) nor the names of its contributors may be used to endorse or promote products derived from this software without specific prior written permission.

THIS SOFTWARE IS PROVIDED BY THE COPYRIGHT HOLDERS AND CONTRIBUTORS “AS IS” AND ANY EXPRESS OR IMPLIED WARRANTIES, INCLUDING, BUT NOT LIMITED TO, THE IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS FOR A PARTICULAR PURPOSE ARE DISCLAIMED. IN NO EVENT SHALL “Ecole Polytechnique Fédérale de Lausanne (EPFL) and Hospital Center and University of Lausanne (UNIL-CHUV)” BE LIABLE FOR ANY DIRECT, INDIRECT, INCIDENTAL, SPECIAL, EXEMPLARY, OR CONSEQUENTIAL DAMAGES (INCLUDING, BUT NOT LIMITED TO, PROCUREMENT OF SUBSTITUTE GOODS OR SERVICES; LOSS OF USE, DATA, OR PROFITS; OR BUSINESS INTERRUPTION) HOWEVER CAUSED AND ON ANY THEORY OF LIABILITY, WHETHER IN CONTRACT, STRICT LIABILITY, OR TORT (INCLUDING NEGLIGENCE OR OTHERWISE) ARISING IN ANY WAY OUT OF THE USE OF THIS SOFTWARE, EVEN IF ADVISED OF THE POSSIBILITY OF SUCH DAMAGE.

**Warning:** THIS SOFTWARE IS FOR RESEARCH PURPOSES ONLY AND SHALL NOT BE USED FOR ANY CLINICAL USE. THIS SOFTWARE HAS NOT BEEN REVIEWED OR APPROVED BY THE FOOD AND DRUG ADMINISTRATION OR EQUIVALENT AUTHORITY, AND IS FOR NON-CLINICAL, IRB-APPROVED RESEARCH USE ONLY. IN NO EVENT SHALL DATA OR IMAGES GENERATED THROUGH THE USE OF THE SOFTWARE BE USED IN THE PROVISION OF PATIENT CARE.

## 5.11 Changes

### 5.11.1 Version 3.0.3

Date: Feb 18, 2022

This version introduces the new pipeline dedicated to EEG modality with a tutorial, updates `Freesurfer` to 7.1.1, and adds a new tutorial that shows how to analyze the CMP3 connectomes.

#### What’s Changed

##### *New features*

- CMP3 provides a new pipeline `cmp.pipelines.functional.eeg.EEGPipeline` dedicated to EEG modality with a collection of interfaces implemented by the following modules: `cmtklib.eeg`, `cmtklib.interfaces.eeg`, `cmtklib.interfaces.mne`, and `cmtklib.interfaces.pycartool`. See [PR #82](#) for more details.

##### *Updates*

- `Freesurfer` has been updated from 6.1.0 to 7.1.1. See [PR #147](#) for more details.

##### *Bug fix*

- **FIX:** List of outputs are empty in inspector window of the parcellation and fmri\_connectome stages. See [PR #145](#) for more details.
- Correct way GM mask is generated and clean code in `cmtklib/parcellation.py`.
- Add interface to copy 001.mgz using `hardlink`.

##### *Documentation*

- Add documentation of new classes and functions introduced by the EEG pipeline.
- Add two ipython notebooks in `docs/notebooks` that are integrated directly in the docs with `nbsphinx`:
  - `analysis_tutorial.ipynb`: Show how to interact, analyze, and visualize CMP3 outputs.
  - `EEG_pipeline_tutorial.ipynb`: Show how to use the new API dedicated to the EEG pipeline.

##### *Contributors*

- Sebastien Tourbier
- Joan Rue Queralt
- Katharina Glomb
- Mikkel Schoettner

*More...*

Please check the main [PR #146](#) page for more details.

### 5.11.2 Version 3.0.2

Date: Jan 31, 2021

This version mostly introduces the capability to estimate carbon footprint of CMP3 execution and fix problem of conflicts during the creation of the conda environment. It incorporates in particular the following changes.

#### *New features*

- Allow the estimation of the carbon footprint while using the BIDS App python wrappers and the GUI. Estimations are conducted using [codecarbon](#). All functions supporting this features have been implemented in the new module [cmtklib.carbonfootprint](#). See [PR #136](#) for more details.

#### *Code changes*

- Creation of `init_subject_derivatives_dirs()` for `AnatomicalPipeline`, `DiffusionPipeline`, and `fMRIPipeline` that return the paths to Nipype and CMP derivatives folders of a given subject / session for a given pipeline. This removed all the implicated code from the `process()` method and improve modularity and readability. In the future, the different functions could be merged as there is a lot of code duplication between them.
- `AnatomicalPipeline`, `DiffusionPipeline`, and `fMRIPipeline` workflows are run with the `MultiProc` plugin.

#### *Bug fix*

- Major update of the `conda/environment.yml` and `conda/environment_macosx.yml` to correct the problems of conflicts in the previous version, as reported in [issue #137](#). This has resulted in the following package updates:
  - `pip`: 20.1.1 -> 21.3.1
  - `numpy`: 1.19.2 -> 1.21.5
  - `matplotlib`: 3.2.2 -> 3.5.1
  - `traits`: 6.2.0 -> 6.3.2
  - `traitsui`: 7.0.0 -> 7.2.0
  - `graphviz`: 2.40.1 -> 2.50.0
  - `configparser`: 5.0.0 -> 5.2.0
  - `git-annex`: 8.20210127 -> 8.20211123
  - `pyside2`: 5.9.0a1 -> 5.13.2
  - `indexed_gzip`: 1.2.0 -> 1.6.4
  - `cvxpy`: 1.1.7 -> 1.1.18
  - `fsleyes`: 0.33.0 -> 1.3.3

- mrtrix3: 3.0.2 -> 3.0.3
- duecredit: 0.8.0 -> 0.9.1
- mne: 0.20.7 -> 0.24.1
- datalad: 0.14.0 -> 0.15.4
- datalad-container: 1.1.2 -> 1.1.5
- statsmodels: 0.11.1 -> 0.13.1
- networkx: 2.4 -> 2.6.3
- pydicom: 2.0.0 -> 2.2.2

See commit [483931f](#) for more details.

#### *Documentation*

- Add description of carbon footprint estimation feature.
- Improve description on how to use already computed Freesurfer derivatives.

#### *Misc*

- Add bootstrap CSS and jquery JS as resources to `cmtklib/data/report/carbonfootprint`. They are used to display the carbon footprint report in the GUI.
- Clean the resources related to parcellation in `cmtklib/data/parcellation` and rename all files and mentions of `lausanne2008` to `lausanne2018`.
- Removed unused `cmtklib.interfaces.camino`, `cmtklib.interfaces.camino2trackvis`, and `cmtklib.interfaces.diffusion` modules
- Specify to `Coverage.py` with `# pragma: no cover` part of the code we know it won't be executed
- Create and use a `coveragerc` file to set the run of `Coverage.py` with `--concurrency=multiprocessing` to be allow to track code inside Nipype interfaces, now managed by multiprocessing.

#### *Code style*

- Correct a number of code style issues with class names.

#### *Contributors*

- [Sebastien Tourbier](#)
- [Joan Rue Queralt](#)

#### *More...*

Please check the main [PR #140](#) page for more details.

### **5.11.3 Version 3.0.1**

Date: Jan 05, 2021

This version is mostly a bug fix release that allows the python packages of Connectome Mapper 3 to be available on PyPI. It incorporates [Pull Request #132](#) which includes the following changes.

#### *Bug fix*

- Rename the project name in `setup.py` and `setup_pypi.py` from "cmp" to "connectomemapper". Such a "cmp" project name was already existing on PyPI, that caused continuous integration on CircleCI to fail during the last v3.0.0 release, while uploading the python packages of CMP3 to PyPI.



#### *Code refactoring*

- Make `cmp.bidsappmanager.gui.py` more lightweight by splitting the classes defined there in different files. (See [Issue #129](#) for more discussion details)
- Split the `create_workflow()` method of the `RegistrationStage` into the `create_ants_workflow()`, `create_flirt_workflow()`, and `create_bbrregister_workflow()`. (See [Issue #95](#) for more discussion details)

#### *Code style*

- Correct a number of code style issues with class names

#### *Contributors*

- [Sebastien Tourbier](#)

Please check the [main pull request 132 page](#) for more details.

### 5.11.4 Version 3.0.0

Date: Dec 24, 2021

This version corresponds to the first official release of Connectome Mapper 3 (CMP3). It incorporates [Pull Request #88](#) (>450 commits) which includes the following changes.

#### *Updates*

- traits has been updated from 6.0.0 to 6.2.0.
- traitsui has been updated from 6.1.3 to 7.0.0.
- pybids has been updated from 0.10.2 to 0.14.0.
- nipy has been updated to 1.5.1 to 1.7.0.
- dipy has been updated from 1.1.0 to 1.3.0.
- obspy has been updated from 1.2.1 to 1.2.2.

#### *New features*

- CMP3 can take custom segmentation (brain, white-matter, gray-matter and CSF masks, Freesurfer's aparcaseg - used for ACT for PFT) and parcellation files as long as they comply to [BIDS Derivatives specifications](#), by providing the label value for the different entity in the filename. This has led to the creation of the new module [cmrplib.bids.io](#), which provides different classes to represent the diversity of custom input BIDS-formatted files. (PR #88)
- CMP3 generates generic label-index mapping tsv files along with the parcellation files, in accordance to [BIDS derivatives](#). This has led to the creation of the `CreateBIDSStandardParcellationLabelIndexMappingFile` and `CreateCMPParcellationNodeDescriptionFilesFromBIDSFile` interfaces, which allows us to create the BIDS label-index mapping file from the parcellation node description files employed by CMP3 (that includes `_FreeSurferColorLUT.txt` and `_dseg.graphml`), and vice versa.
- CMP3 provide python wrappers to the Docker and Singularity container images (`connectomemapper3_docker` and `connectomemapper3_singularity`) that will generate and execute the appropriate command to run the BIDS App. (PR #109,

[PR #115](#), [PR #130](#))

#### *Major changes*

- Lausanne2018 parcellation has completely replaced the old Lausanne2008 parcellation. In brief, the new parcellation was introduced to provide (1) symmetry of labels between hemispheres, and (2) a more optimal generation of the volumetric parcellation images, that now are generated at once from `annot` files. This fixes the issue of overwritten labels encountered by in the process of creating the Lausanne2008 parcellation. Any code and data related to Lausanne2008 has been removed. If one still wish to use this old parcellation scheme, one should use CMP3 (v3.0.0-RC4).

#### *Output updates*

- Directories for the derivatives produced by `cmp` (`cmp`, `freesurfer`, `nipype`) were renamed to `cmp-`, `freesurfer-`, and `nipype-` to comply with BIDS 1.4.0+. (PR #3 (fork))

#### *Code refactoring*

- Creation in `AnatomicalPipeline`, `DiffusionPipeline`, `fMRIPipeline` of `create_datagrabber_node()` and `create_datasinker_node()` methods to reduce the code in `create_workflow()`.
- The `run(command)` function of `cmp.bidsappmanager.core` has been moved to `cmtklib.process`, which is used by the python wrappers in `cmp.cli`.

#### *Pipeline Improvements*

- Better handle of existing Freesurfer outputs. In this case, CMP3 does not re-create the `mri/orig/001.mgz` and connect the reconall interface anymore.
- Creation of 5TT, gray-matter / white-matter interface, and partial volume maps images are performed in the preprocessing stage of the diffusion pipeline only if necessary

#### *Code Style*

- Clean code and remove a number of commented lines that are now obsolete. Code related to the connection of nodes in the Nipype Workflow adopts a specific format and are protected from being reformatted by BLACK with the `# fmt: off` and `# fmt: on` tags.

#### *Documentation*

- Add instructions to use custom segmentation and parcellation files as inputs.
- Add description in contributing page of format for code related to the connection of the nodes in a Nipype Workflow.
- Add instructions to use the python wrappers for running the BIDS App. (PR #115)
- Add notification about the removal of the old Lausanne2008 parcellation, and remove any other mentions in the documentation.

#### *Software container*

- Define multiple build stages in Dockerfile, which can be run in parallel at build with BUILDKIT. (PR #88)

#### *Software development life cycle*

- Update the list of outputs of circleci tests with the new names of directories produced by `cmp` in `output_dir/`.
- Following major changes in the pricing plans of CircleCI but also to improve its readability, `circleci/config.yml` has been dramatically refactored, including: \* Use BUILDKIT in docker build to take advantage of the multi-stage build \* Reordering and modularization of the tests:
  - tests 01-02 (Docker): anatomical pipeline for each parcellation scheme
  - tests 03-06 (Docker): diffusion pipeline for dipy/mrtrix deterministic/probabilistic tractography
  - tests 07-08 (Docker): fMRI pipeline for FLIRT and BBRegistration registrations
  - test 09 (Singularity): anatomical pipeline for Lausanne2018 scheme

- Creation of commands for steps that are shared between jobs to reduce code duplication

(PR #88)

#### Contributors

- Sebastien Tourbier
- Anil Tuncel
- Jakub Jancovic
- Jonathan Wirsich

Please check the [main pull request 88](#) page for more details.

### 5.11.5 Version 3.0.0-RC4

Date: March 07, 2021

This version corresponds to the fourth and final release candidate of Connectome Mapper 3 (CMP3). It incorporates the relatively large [Pull Request #74](#) (~270 commits) which includes the following changes such that it marks the end of the release candidate phase.

#### New features

- CMP3 pipeline configuration files adopt JSON as new format. (PR #76)
- CMP3 is compatible with PyPI for installation. (PR #78)
- BIDS convention naming of data derived from parcellation atlas adopt now the new BIDS entity `atlas-<atlas_label>` to distinguish data derived from different parcellation atlases. The use of the entity `desc-<scale_label>` to distinguish between parcellation scale has been replaced by the use of the entity `res-<scale_label>`. (PR #79)

#### Updates

- Content of `dataset_description.json` for each derivatives folder has been updated to conform to BIDS version 1.4.0. (PR #79)

#### Code refactoring

- Major refactoring of the `cmtklib.config` module with the addition and replacement of a number of new methods to handle JSON configuration files. (See [full diff on GitHub](#)) Configuration files in the old INI format can be converted automatically with the help of the two new methods `check_configuration_format()` and `convert_config_ini_2_json()` to detect if configuration files are in the INI format and to make the conversion. (PR #76)
- Major changes to make `cmp` and `cmpbidsappmanager` compatible with the Python Package Index (pip) for package distribution and installation. This includes the merge of `setup.py` and `setup_gui.py`, which have been merged into one `setup.py` and a major refactoring to make pip happy, as well as the creation of a new `cmp.cli` module, migration to `cmp.cli` module and refactoring of the scripts `connectomemapper3`, `showmatrix_gpickle`, and `cmpbidsappmanager` with correction of code style issues and addition of missing docstrings. (PR #78)

#### Improvements

- Clean parameters to be saved in configuration files with the new API. (PR #74)
- Clean output printed by the `cmpbidsappmanager` Graphical User Interface. (PR #74)
- Add in `cmtklib.config` the three new functions `print_error`, `print_blue`, and `print_warning` to use different colors to differentiate general info (default color), error (red), command or action (blue), and highlight or warning (yellow). (PR #74)

- Clean code and remove a number of commented lines that are now obsolete. (PR #74, PR #79)

### Documentation

- Review usage and add a note regarding the adoption of the new JSON format for configuration files. (PR #76)
- Update tutorial on using CMP3 and Datalad for collaboration. (PR #77)
- Update installation instruction of `cmpbidsappmanager` using `pip install ..` (PR #78)
- Update list of outputs following the new BIDS derivatives naming convention introduced. (PR #79)

### Bug fixes

- Correct attributes related to the diffusion imaging model type `multishell`. (PR #74)
- Review code in `cmtklib/connectome.py` for saving functional connectome files in GRAPHML format. (PR #74)

### Software Updates

- Update version of datalad and dependencies (PR #77):
  - `datalad[full]==0.13.0` to `datalad[full]==0.14.0`.
  - `datalad-container==0.3.1` to `datalad-container==1.1.2`.
  - `datalad_neuroimaging==0.2.0` to `datalad-neuroimaging==0.3.1`.
  - `git-annex=8.20200617` to `git-annex=8.20210127`.
  - `datalad-revolution` was removed.

### Software development life cycle

- Improve code coverage by calling the methods `check_stages_execution()` and `fill_stages_outputs()` on each pipeline when executed with coverage. (PR #75)
- Improve code coverage by saving in test-01 structural connectome files in MAT and GRAPHML format. (PR #74)
- Improve code coverage by saving in test-07 functional connectome files in GRAPHML format. (PR #74)
- Update the list of outputs for all tests. (PR #74)
- Add `test-python-install` job that test the build and installation of `cmp` and `cmpbidsappmanager` packages compatible with `pip`. (PR #78)

Please check the [main pull request 74](#) page for more details.

## 5.11.6 Version 3.0.0-RC3

Date: February 05, 2021

This version corresponds to the third release candidate of Connectome Mapper 3. In particular, it integrates [Pull Request #62](#) which includes:

### Updates

- MRtrix3 has been updated from `3.0_RC3_latest` to `3.0.2`.
- Numpy has been updated from `1.18.5` to `1.19.2`.
- Nipype has been updated to `1.5.0` to `1.5.1`.
- Dipy has been updated from `1.0.0` to `1.3.0`.
- CVXPY has been updated from `1.1.5` to `1.1.7`.

*Documentation*

- Update outdated screenshots for GUI documentation page at [readthedocs](#) reported at [CMTK user-group](#).
- Correction of multiple typos.

*Bug fixes*

- Update code for Dipy tracking with DTI model following major changes in Dipy 1.0 (Fix reported issue [#54](#)).
- Update to Dipy 1.3.0 has removed the deprecated warnings related to CVXPY when using MAP\_MRI ([#63](#))
- Do not set anymore OMP\_NUM\_THREADS at execution due to allocation errors raised when using numpy function dot in Dipy.

*Software development life cycle*

- Add Test 08 that runs anatomical and fMRI pipelines with: Lausanne2018 parcellation, FSL FLIRT co-registration, all nuisance regression, linear detrending and scrubbing
- Add Test 09 that runs anatomical and dMRI pipelines with: Lausanne2018 parcellation, FSL FLIRT, Dipy SHORE, MRtrix SD\_Stream tracking, MRtrix SIFT tractogram filtering
- Remove `deploy_singularity_latest` from the workflow for the sake of space on Sylabs.io.

Please check the [main pull request 62 page](#) for more details.

### 5.11.7 Version 3.0.0-RC2-patch1

Date: February 4, 2021

This version fixes bugs in the second release candidate of Connectome Mapper 3 (v3.0.0-RC2). In particular, it includes:

*Bug fixes*

- Fix the error to save connectome in GraphML format reported in [#65](#) and ([Pull Request #66](#)).

*Software development life cycle*

- Remove publication of the Singularity image to sylabs.io when the master branch is updated for the sake of space (11GB limit)

*Commits*

- CI: remove publication of latest tag image on sylabs.io for space (2 days ago) - commit [c765f79](#)
- Merge pull request [#66](#) from connectomicslab/v3.0.0-RC2-hotfix1 (3 days ago) - commit [0a2603e](#)
- FIX: update `g2.node` to `g2.nodes` when saving connectomes as graphml (fix [#65](#)) (6 days ago) - commit [d629eef](#)
- FIX: enabled/disabled gray-out button “Run BIDS App” with Qt Style sheet [skip ci] (3 weeks ago) - commit [10e78d9](#)
- MAINT: removed commented lines in `cmpbidsappmanager/gui.py` [skip ci] (3 weeks ago) - commit [4cc11e7](#)
- FIX: check availability of modalities in the BIDS App manager window [skip ci] (3 weeks ago) - commit [80fbee2](#)
- MAINT: update copyright year [skip ci] (3 weeks ago) - commit [f7d0ffb](#)
- CI: delete previous container with latest TAG on sylabs.io [skip ci] (4 weeks ago) - commit [15c9b18](#)
- DOC: update tag to latest in `runonhpc.rst` [skip ci] (4 weeks ago) - commit [3165bcc](#)
- CI: comment lines related to version for singularity push (4 weeks ago) - commit [3952d46](#)

### 5.11.8 Version 3.0.0-RC2

Date: December 24, 2020

This version corresponds to the second release candidate of Connectome Mapper 3. In particular, it integrates [Pull Request #45](#) which includes:

#### *New feature*

- Add SIFT2 tractogram filtering (requested in [#48](#), [PR #52](#)).
- Add a tracker to support us seeking for new funding. User is still free to opt-out and disable it with the new option flag `--notrack`.
- Add options suggested by [Theaud G et al. \(2020\)](#) to better control factors having impacts on reproducibility. It includes:
  - Set the number of ITK threads used by ANTs for registration (option flag `--ants_number_of_threads`).
  - Set the seed of the random number generator used by ANTs for registration (option flag `--ants_random_seed`).
  - Set the seed of the random number generator used by MRtrix for tractography seeding and track propagation (option flag `--mrtrix_random_seed`).
- Full support of Singularity (see [Software development life cycle](#)).

#### *Code refactoring*

- A number of classes describing interfaces to `fsl` and `mrtrix3` have been moved from `cmtklib/interfaces/util.py` to `cmtklib/interfaces/fsl.py` and `cmtklib/interfaces/mrtrix3.py`.
- Capitalize the first letter of a number of class names.
- Lowercase a number of variable names in `cmtklib/parcellation.py`.

#### *Graphical User Interface*

- Improve display of `qpushbuttons` with images in the GUI ([PR #52](#)).
- Make the window to control BIDS App execution scrollable.
- Allow to specify a custom output directory.
- Tune new options in the window to control BIDS App multi-threading (OpenMP and ANTs) and random number generators (ANTs and MRtrix).

#### *Documentation*

- Full code documentation with *numpydoc*-style docstrings.
- API documentation page at [readthedocs](#).

#### *Bug fixes*

- Fix the error reported in [#17](#) if it is still occurring.
- Review statements for creating contents of BIDS App entrypoint scripts to fix issue with Singularity converted images reported in [#47](#).
- Install `dc` package inside the BIDS App to fix the issue with FSL BET reported in [#50](#).
- Install `libopenblas` package inside the BIDS App to fix the issue with FSL EDDY\_OPENMP reported in [#49](#).

#### *Software development life cycle*

- Add a new job `test_docker_fmri` that test the fMRI pipeline.

- Add `build_singularity`, `test_singularity_parcellation`, `deploy_singularity_latest`, and `deploy_singularity_release` jobs to build, test and deploy the Singularity image in CircleCI (PR #56).

Please check the [main pull request 45](#) page for more details.

### 5.11.9 Version 3.0.0-RC1

Date: August 03, 2020

This version corresponds to the first release candidate of Connectome Mapper 3. In particular, it integrates Pull Request #40 where the last major changes prior to its official release have been made, which includes in particular:

#### *Migration to Python 3*

- Fixes automatically with 2to3 and manually a number of Python 2 statements invalid in python 3 including the `print()` function
- Correct automatically PEP8 code style issues with `autopep8`
- Correct manually a number of code stly issues reported by Codacy (`bandits/pylints/flake8`)
- Major dependency upgrades including:
  - `dipy 0.15 -> 1.0` and related code changes in `cmtklib/interfaces/dipy` (Check [here](#) for more details about Dipy 1.0 changes)

**Warning:** Interface for tractography based on Dipy DTI model and EuDX tractography, which has been drastically changed in Dipy 1.0, has not been updated yet, It will be part of the next release candidate.

```

– nipy 1.1.8 -> 1.5.0
– pybids 0.9.5 -> 0.10.2
– pydicom 1.4.2 -> 2.0.0
– networkX 2.2 -> 2.4
– statsmodels 0.9.0 -> 0.11.1
– obspy 1.1.1 -> 1.2.1
– traits 5.1 -> 6.0.0
– traitsui 6.0.0 -> 6.1.3
– numpy 1.15.4 -> 1.18.5
– matplotlib 1.1.8 -> 1.5.0
– fsleyes 0.27.3 -> 0.33.0
– mne 0.17.1 -> 0.20.7
– sphinx 1.8.5 -> 3.1.1
– sphinx_rtd_theme 0.4.3 -> 0.5.0
– recommonmark 0.5.0 -> 0.6.0

```

#### *New feature*

- Option to run Freesurfer recon-all in parallel and to specify the number of threads used by not only Freesurfer but also all softwares relying on OpenMP for multi-threading. This can be achieved by running the BIDS App with the new option flag `--number_of_threads`.

### *Changes in BIDS derivatives*

- Renamed connectivity graph files to better conform to the [BIDS extension proposal on connectivity data schema](#). They are now saved by default in a TSV file as a list of edges.

### *Code refactoring*

- Functions to save and load pipeline configuration files have been moved to `cmtklib/config.py`

### *Bug fixes*

- Major changes in how inspection of stage/pipeline outputs with the graphical user interface (`cmpbidsappmanager`) which was not working anymore after migration to Python3
- Fixes to compute the structural connectivity matrices following migration to python 3
- Fixes to computes ROI volumetry for Lausanne2008 and NativeFreesurfer parcellation schemes
- Add missing renaming of the ROI volumetry file for the NativeFreesurfer parcellation scheme following BIDS
- Create the mask used for computing peaks from the Dipy CSD model when performing Particle Filtering Tractography (development still on-going)
- Add missing renaming of Dipy tensor-related maps (AD, RD, MD) following BIDS
- Remove all references to use Custom segmentation / parcellation / diffusion FOD image / tractogram, inherited from CMP2 but not anymore functional following the adoption of BIDS standard inside CMP3.

### *Software development life cycle*

- Use [Codacy](#) to support code reviews and monitor code quality over time.
- Use [coveragepy](#) in CircleCI during regression tests of the BIDS app and create code coverage reports published on our [Codacy project page](#).
- **Add new regression tests in CircleCI to improve code coverage:**
  - Test 01: Lausanne2018 (full) parcellation + Dipy SHORE + Mrtrix3 SD\_STREAM tractography
  - Test 02: Lausanne2018 (full) parcellation + Dipy SHORE + Mrtrix3 ACT iFOV2 tractography
  - Test 03: Lausanne2018 (full) parcellation + Dipy SHORE + Dipy deterministic tractography
  - Test 04: Lausanne2018 (full) parcellation + Dipy SHORE + Dipy Particle Filtering tractography
  - Test 05: Native Freesurfer (Desikan-Killiany) parcellation
  - Test 06: Lausanne2008 parcellation (as implemented in CMP2)
- Moved pipeline configurations for regression tests in CircleCI from `config/` to `.circle/tests/configuration_files`
- Moved lists of expected regression test outputs in CircleCI from `.circle/` to `.circle/tests/expected_outputs`

Please check the [pull request 40](#) page for more details.



### 5.11.10 Version 3.0.0-beta-RC2

Date: June 02, 2020

This version integrates Pull Request #33 which corresponds to the last beta release that still relies on Python 2.7. It includes in particular:

#### *Upgrade*

- Uses `fsleyes` instead of `fslview` (now deprecated), which now included in the conda environment of the GUI (`py27cmp-gui`).

#### *New feature*

- Computes of ROI volumetry stored in `<output_dir>/sub-<label>(/ses<label>)/anat` folder, recognized by their `_stats.tsv` file name suffix.

#### *Improved replicability*

- Sets the `MATRIX_RNG_SEED` environment variable (used by MRtrix) and seed for the numpy random number generator (`numpy.random.seed()`)

#### *Bug fixes*

- Fixes the output inspector window of the `cmpbidsappmanager` (GUI) that fails to find existing outputs, after adoption of `/bids_dir` and `/output_dir` in the bidsapp docker image.
- Fixes the way to get the list of networkx edge attributes in `inspect_outputs()` of `ConnectomeStage` for the output inspector window of the `cmpbidsappmanager` (GUI)
- Added missing package dependencies ( `fury` and  `vtk`) that fixes `dipy_CSD` execution error when trying to import module `actor` from `dipy.viz` to save the results in a png
- Fixes a number of unresolved references identified by pycharm code inspection tool

#### *Code refactoring*

- Interfaces for fMRI processing were moved to `cmtklib/functionalMRI.py`.
- Interface for fMRI connectome creation (`rsfmri_conmat`) moved to `cmtklib/connectome.py`

Please check the [pull request 33](#) page for change details.

### 5.11.11 Version 3.0.0-beta-RC1

Date: March 26, 2020

This version integrates Pull Request #28 which includes in summary:

- A major revision of continuous integration testing and deployment with CircleCI which closes [Issue 14](#) integrates an in-house dataset published and available on Zenodo @ <https://doi.org/10.5281/zenodo.3708962>.
- Multiple bug fixes and enhancements incl. close [Issue 30](#) , update mrtrix3 to RC3 version, bids-app run command generated by the GUI, location of the configuration and log files to be more BIDS compliant.
- Change in tagging beta version which otherwise might not be meaningful in accordance with the release date (especially when the expected date is delayed due to unexpected errors that might take longer to be fixed than expected).

Please check the [pull request 28](#) page for a full list of changes.

### 5.11.12 Version 3.0.0-beta-20200227

Date: February 27, 2020

This version addresses multiple issues to make successful conversion and run of the CMP3 BIDS App on HPC (Clusters) using Singularity.

- Revised the build of the master and BIDS App images:
  - Install locales and set `$LC_ALL` and `$LANG` to make freesurfer hippocampal subfields and brainstem segmentation (matlab-based) modules working when run in the converted Singularity image
  - BIDS input and output directories inside the BIDS App container are no longer the `/tmp` and `/tmp/derivatives` folders but `/bids_dir` and `/output_dir`. .. warning:: this might affect the use of Datalad container (To be confirmed.)
  - Fix the branch of `mrtrix3` to check out
  - Updated metadata
- Fix the configuration of CircleCI to not use Docker layer cache feature anymore as this feature is not included anymore in the free plan for open source projects.
- Improved documentation where the latest version should be dynamically generated everywhere it should appear.

### 5.11.13 Version 3.0.0-beta-20200206

Date: February 06, 2020

- Implementation of an in-house Nipype interface to AFNI 3DBandPass which can handle to check output as `..++orig.BRIK` or as `..tlrc.BRIK` (The later can occur with HCP preprocessed fmri data)

### 5.11.14 Version 3.0.0-beta-20200124

Date: January 24, 2020

- Updated multi-scale parcellation with a new symmetric version:
  1. The right hemisphere labels were projected in the left hemisphere to create a symmetric version of the multiscale cortical parcellation proposed by [Cammoun2012](#).
  2. For scale 1, the boundaries of the projected regions over the left hemisphere were matched to the boundaries of the original parcellation for the left hemisphere.
  3. This transformation was applied for the rest of the scales.
- Updated documentation with list of changes

## 5.12 Citing

---

### Important:


- If you are using the Connectome Mapper 3 in your work, a manuscript is in preparation, but for now, please acknowledge this software with the following two entries:
1. Tourbier S, Aleman-Gomez Y, Mullier E, Griffa A, Wirsich J, Tuncel A, Bach Cuadra M, Hagmann P. (2022). connectomicslab/connectomemapper3: Connectome Mapper v3.0.3 (Version v3.0.3). Zenodo. <http://doi.org/10.5281/zenodo.3475969>.

2. Tourbier S, Aleman-Gomez Y, Mullier E, Griffa A, Bach Cuadra M, Hagmann P (2020, June). Connectome Mapper 3: a software pipeline for multi-scale connectome mapping of multimodal MR data. 26th Annual Meeting of the Organization for Human Brain Mapping (OHBM), abstract #1174, poster #1892.

## 5.12.1 Poster

- Organization for Human Brain Mapping 2020 (Abstract; Poster)

**1892**




Connectome Mapper 3

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

S. Tourbier<sup>1</sup>, Y. Alemán-Gómez<sup>1,4</sup>, E. Mullier<sup>1</sup>, A. Griffa<sup>2</sup>, M. Bach Cuadra<sup>3</sup>, P. Hagmann<sup>1</sup>

<sup>1</sup> Department of Radiology, University Hospital of Lausanne (CHUV) and University of Lausanne (UNIL), Lausanne, Switzerland  
<sup>2</sup> Medical Image Processing Lab (MIP/LAB), École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland  
<sup>3</sup> Medical Image Analysis Laboratory (MIAL), Centre d'Imagerie BioMédicale (CIBM), Lausanne, Switzerland



OHBM 2020

#### MOTIVATION

Connectome Mapper (CMP) is an open-source software pipeline, written in Python with a Graphical User Interface (GUI) 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 and the corresponding structural connectomes.

Designed with *ease-of-use, modularity, configurability, re-executability and transparency* in mind.

But two previous versions limited in terms of *interoperability and reusability, portability, and reproducibility*, with dependencies not easy to install.

#### OBJECTIFS

- Provide a unique software pipeline solution with a GUI for researchers to easily, reliably and transparently create a hierarchical multi-scale connectome representation of the structural and functional brain systems.
- Adopt recent advances in the standardization of neuroimaging data organization [2] and processing [4-5] that:
- promote processing interoperability, reusability, portability and reproducibility, and
- have proven to be capable of effective large scale collaboration

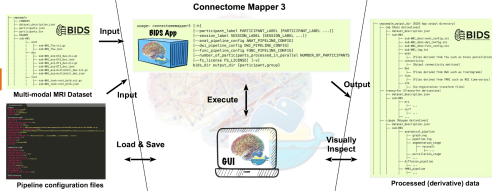
#### HIGHLIGHTS

- Extend the 5-scale brain gray matter parcellation [2] derived from the Desikan-Killiany atlas [6] with:
  - a subdivision of the thalamus into 7 nuclei [7],
  - the hippocampus into 12 subfields [8] and
  - the brainstem into 4 sub-structures [9].
- *unique multi-scale hierarchical brain parcellation*
- Read datasets following the *Brain Imaging Data Structure (BIDS)* standard [3]
- *Outputs (derivatives)* structured according to *BIDS derivatives* draft (see [complete list](#))
  - interoperable, reusable
- Use *ConfigParser*, *Traits* and *Nipype* [4] to implement a modular processing workflow composed of configurable pipelines, each dedicated to one modality (anatomical, diffusion, fMRI), that interface with tools from *FSL* [10], *Freesurfer* [11], *ANTs* [12], *Dipy* [13], *MRtrix3* [14], *AFNI* [15], and the in-house *Connectome Mapper* library (cm3lib)
- modular, configurable, scalable, re-executable with data provenance tracking
- Workflow encapsulated in a software container image following the *BIDS Apps* standard [5]
  - *easy-to-be-installed, easy-to-interface, portable, scalable and reproducible*
- Provide a GUI to ease and support all the steps involved in (1) the configuration of the pipeline, (2) the configuration of the BIDS App run and its execution, and (3) the inspection of the stage outputs.
  - *accessible, easy-to-be-installed, easy-to-use*
- Distributed under the *3-Clause BSD license*
- Hosted on [GitHub](#) @ <https://github.com/connectome-mapper/connectome-mapper> where issues and new feature requests are transparently discussed, and versions are released through continuous integration testing
  - modern community-driven software practices

#### ARCHITECTURE

Software bundle which contains:

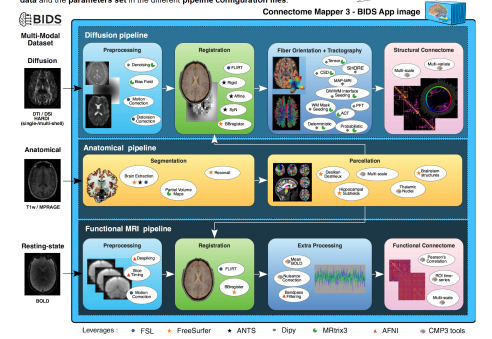
- **The Connectome Mapper BIDS App**: the processing core encapsulating the processing workflow in a software container image (Docker [16] and Singularity [17] on HPC) that takes as main input a BIDS dataset and specific pipeline configuration files.
- **The Connectome Mapper BIDS App Manager**: the user-friendly graphical user interface (GUI) which relies on the *traktatsUI* windowing framework, and allows you to easily configure and run the pipelines and inspect the outputs.



#### PROCESSING WORKFLOW

Thanks to its modular architecture and the use of *Nipype* and *traktatsUI* libraries, new pipelines and stages with GUI components can be added with relatively little effort to account for additional imaging modalities and algorithms.

Dynamically built and configured depending on the availability of sMRI, dMRI, fMRI data and the parameters set in the different pipeline configuration files.



Leverages: FSL • FreeSurfer • ANTs • Dipy • MRtrix3 • AFNI • CMP3 tools

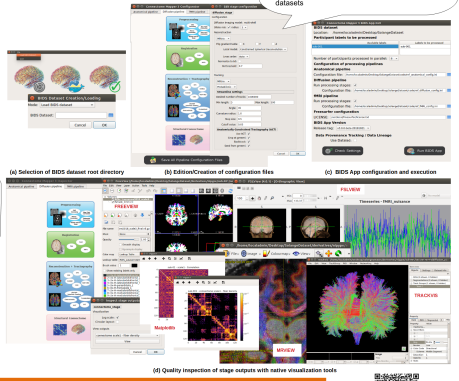
#### GRAPHICAL USER INTERFACE

A typical use case consists only of a few steps which are:

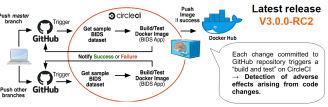
- (a) the selection of the root directory of the **BIDS dataset** to be analyzed,
- (b) the **creation/editing of each pipeline configuration file**,
- (c) the **configuration of the BIDS App run and its execution**,
- (d) the **inspection of the stage outputs** using either *reviewer*, or *reviewer* or *trackvis* depending on the software involved in the stage. Connectivity matrices are visualized using *nine* and the *matplotlib* library.

• 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



#### CONTINUOUS INTEGRATION TESTING



Latest release **V3.0.0-RC2**

Each change committed to GitHub repository triggers a "build and test" on GitHub Actions. Selection of adverse effects arising from code changes.

#### UPCOMING

- Implementation of EEG pipeline initiated during Global Brainhack Geneva 2019 (see [Project](#)) and discussed in the following [GitHub issue](#).
- BIDS and CMP3 Training at the upcoming [ReproNim/Sinergica Summer School 2020](#) that will be held in Lausanne, Switzerland (expected to June 2021, date to be confirmed). See [website](#) for more details.

#### OTHER LINKS

License BIDS App

Code Docs

For rapid news and support, please also consult our [CMP3 User Group forum](#).

## 5.13 Contributors

Thanks goes to these wonderful people (emoji key):

Thanks also goes to all these wonderful people that contributed to the two first versions of Connectome Mapper:

- Collaborators from Signal Processing Laboratory (LTS5), EPFL, Lausanne:
  - Jean-Philippe Thiran
  - Leila Cammoun
  - Adrien Birbaumer (abirba)
  - Alessandro Daducci (daducci)
  - Stephan Gerhard (unidesigner)

- Christophe Chênes (Cwis)
- Oscar Esteban (oesteban)
- David Romascano (davidrs06)
- Alia Lemkaddem (allem)
- Xavier Gigandet
- Collaborators from Children’s Hospital, Boston:
  - Ellen Grant
  - Daniel Ginsburg (danginsburg)
  - Rudolph Pienaar (rudolphpienaar)
  - Nicolas Rannou (NicolasRannou)

This project follows the [all-contributors](#) specification. Contributions of any kind are welcome!

See [contributing page](#) for more details about how to join us!

## 5.14 Contributing to Connectome Mapper 3

### Contents

- *Contributing to Connectome Mapper 3*
  - *Philosophy*
  - *Contribution Types*
    - \* *Report Bugs*
    - \* *Fix Bugs*
    - \* *Implement Features*
    - \* *Write Documentation*
    - \* *Submit Feedback*
  - *Get Started!*
    - \* *Pull Request Guidelines*
    - \* *How to build the BIDS App locally*
    - \* *How to build the documentation locally*

### 5.14.1 Philosophy

The development philosophy for this new version of the Connectome Mapper is to:

- I. Enhance interoperability by working with datasets structured following the Brain Imaging Data Structure structured dataset.
- II. Keep the code of the processing as much as possible outside of the actual main Connectome Mapper code, through the use and extension of existing Nipype interfaces and an external library (dubbed cmtklib).
- III. Separate the code of the graphical interface and the actual main Connectome Mapper code through inheritance of the classes of the actual main stages and pipelines.
- IV. Enhance portability by freezing the computing environment with all software dependencies installed, through the adoption of the BIDS App framework relying on light software container technologies.
- V. Adopt best modern open-source software practices that includes to continuously test the build and execution of the BIDS App with code coverage and to follow the PEP8 and PEP257 conventions for python code and docstring style conventions. The use of an integrated development environment such as PyCharm or SublimeText with a python linter (code style checker) is strongly recommended.
- VI. Follow the [all contributors](#) specification to acknowledge any kind of contribution.

This means that contributions in many different ways (discussed in the following subsections) are welcome and will be properly acknowledged! If you have contributed to CMP3 and are not listed as contributor, please add yourself and make a pull request.

This also means that further development, typically additions of other tools and configuration options should go in this direction.

### 5.14.2 Contribution Types

#### Report Bugs

Report bugs at <https://github.com/connectomicslab/connectomemapper3/issues>.

If you are reporting a bug, please include:

- Your operating system name and version.
- Any details about your local setup that might be helpful in troubleshooting.
- Detailed steps to reproduce the bug.

#### Fix Bugs

Look through the GitHub issues for bugs. Anything tagged with “bug” and “help wanted” is open to whoever wants to implement it.

## Implement Features

Look through the GitHub issues for features. Anything tagged with “enhancement” and “help wanted” is open to whoever wants to implement it.

Possible enhancements are probably to be included in the following list:

- I. Adding of a configuration option to an existing stage
- II. Adding a new interface to *cmtklib*
- III. Adding of a new stage
- IV. Adding of a new pipeline

The adding of newer configuration options to existing stages should be self-understandable. If the addition is large enough to be considered a “sub-module” of an existing stage, see the Diffusion stage example.

Adding a new stage implies the addition of the stage folder to the `cmp/stages` and `cmp/bidsappmanager/stages` directory and according modification of the parent pipeline along with insertion of a new image in `cmp/bidsappmanager/stages`. Copy-paste of existing stage (such as segmentation stage) is recommended. Note that CMP3 adopts a specific style for code dedicated to the connection of stages and interfaces, which is as follows:

```
[...]
# fmt: off
anat_flow.connect(
    [
        (seg_flow, parc_flow, [("outputnode.subjects_dir", "inputnode.subjects_
↪ dir"),
                                ("outputnode.subject_id", "inputnode.subject_id
↪ ")]),
        (seg_flow, anat_outputnode, [("outputnode.subjects_dir", "subjects_dir
↪ "),
                                    ("outputnode.subject_id", "subject_id")]),
        [...]
    ]
)
# fmt: on
[...]
```

The `# fmt: off` and `# fmt: on` flags protect the lines to be reformatted by BLACK.

Adding a new pipeline implies the creation of a new pipeline script and folder in the `cmp/pipelines` and `cmp/bidsappmanager/pipelines` directories. Again copy-pasting an existing pipeline is the better idea here. Modification of `cmp/project.py` and `cmp/bidsappmanager/project.py` file is also needed.

Each new module, class or function should be properly documented with a docstring in accordance to the [Numpy docstring style](#).

## Write Documentation

CMP3 could always use more documentation, whether as part of the official CMP3 docs, in docstrings, or even on the web in blog posts, articles, and such.

When you commit changes related to the documentation, please always insert at the end of your message `[skip ci]` to not perform continuous integration of the whole project with CircleCI.

## Submit Feedback

The best way to send feedback is to create an issue at <https://github.com/connectomicslab/connectomemapper3/issues>.

If you are proposing a feature:

- Explain in detail how it would work.
- Keep the scope as narrow as possible, to make it easier to implement.
- Remember that this is a volunteer-driven project, and that contributions are welcome :)

### 5.14.3 Get Started!

Ready to contribute? Here's how to set up Connectome Mapper 3 for local development.

1. Fork the `connectomemapper3` repo on GitHub.
2. Clone your fork locally:

```
git clone git@github.com:your_name_here/connectomemapper3.git
cd connectomemapper3
```

3. Create a branch for local development:

```
git checkout -b name-of-your-bugfix-or-feature
```

4. Now you can make your changes locally. If you add a new node in a pipeline or a completely new pipeline, we encourage you to rebuild the BIDS App Docker image (See *BIDS App build instructions*).

---

**Note:** Please keep your commit the most specific to a change it describes. It is highly advice to track un-staged files with `git status`, add a file involved in the change to the stage one by one with `git add <file>`. The use of `git add .` is highly discouraged. When all the files for a given change are staged, commit the files with a brief message using `git commit -m "[COMMIT_TYPE]: Your detailed description of the change."` that describes your change and where `[COMMIT_TYPE]` can be `[FIX]` for a bug fix, `[ENH]` for a new feature, `[MAINT]` for code maintenance and typo fix, `[DOC]` for documentation, `[CI]` for continuous integration testing, `[UPD]` for dependency update, `[MISC]` for miscellaneous.

---

5. When you're done making changes, push your branch to GitHub:

```
git push origin name-of-your-bugfix-or-feature
```

6. Submit a pull request through the GitHub website.

## Pull Request Guidelines

Before you submit a pull request, check that it meets these guidelines:

1. If the pull request adds functionality, the docs and tests should be updated (See [documentation build instructions](#)).
2. Python code and docstring should comply with [PEP8](#) and [PEP257](#) standards.
3. The pull request should pass all tests on GitHub.

## How to build the BIDS App locally

1. Go to the clone directory of your fork and run the script `build_bidsapp.sh`

```
cd connectomemapper3
sh scripts/build_bidsapp.sh
```

---

**Note:** Tag of the version of the image is extracted from `cmp/info.py`. You might want to change the version in this file to not overwrite an other existing image with the same version.

---

## How to build the documentation locally

To generate the documentation:

1. Install the CMP3 conda environment `py37cmp-gui`:

```
$ cd connectomemapper3
$ conda env create -f environment.yml
```

2. Activate CMP3 conda environment `py37cmp-gui`:

```
$ conda activate py37cmp-gui
```

3. Install all dependencies such as sphinx and its extensions, required for the build:

```
(py37cmp-gui)$ pip install -r docs/requirements.txt
```

4. Install `connectomemapper3`:

```
(py37cmp-gui)$ pip install .
```

5. Run the script `scripts/build_docs.sh` to generate the HTML documentation in `docs/_build/html`:

```
(py37cmp-gui)$ sh scripts/build_docs.sh
```

---

**Note:** Make sure to have (1) activated the conda environment `py37cmp-gui` and (2) reinstalled `connectomemapper3` with `pip` before running `build_docs.sh`.

---

---

**Authors** Sebastien Tourbier, Adrien Birbaumer



**Version** Revision: 2

### Acknowledgments

We thanks the authors of [these great contributing guidelines](#), from which part of this document has been inspired and adapted.

## 5.15 Support, Bugs and New Feature Requests

If you need any support or have any questions, you can post to the [CMTK-users](#) group.

All bugs, concerns and enhancement requests for this software are managed on GitHub and can be submitted at <https://github.com/connectomicslab/connectomemapper3/issues>. (See *Contribute to Connectome Mapper* for more details)



## FUNDING

Work supported by the SNF Sinergia Grant 170873 (<http://p3.snf.ch/Project-170873>).



## BIBLIOGRAPHY

- [Tournier2007] Tournier, J.D., et al. NeuroImage 2007. Robust determination of the fibre orientation distribution in diffusion MRI: Non-negativity constrained super-resolved spherical deconvolution
- [Merlet2013] Merlet S. et. al, Medical Image Analysis, 2013. “Continuous diffusion signal, EAP and ODF estimation via Compressive Sensing in diffusion MRI”
- [Smith2013SIFT] R.E. Smith et al., NeuroImage 67 (2013), pp. 298–312, <<https://www.ncbi.nlm.nih.gov/pubmed/23238430>>.
- [Smith2015SIFT2] Smith RE et al., Neuroimage, 2015, 119:338-51. <<https://doi.org/10.1016/j.neuroimage.2015.06.092>>.
- [Iglesias2015Brainstem] Iglesias et al., NeuroImage, 113, June 2015, 184-195. <[http://www.nmr.mgh.harvard.edu/~iglesias/pdf/Neuroimage\\_2015\\_brainstem.pdf](http://www.nmr.mgh.harvard.edu/~iglesias/pdf/Neuroimage_2015_brainstem.pdf)>
- [Iglesias2015Hippo] Iglesias et al., Neuroimage, 115, July 2015, 117-137. <<http://www.nmr.mgh.harvard.edu/~iglesias/pdf/subfieldsNeuroimage2015preprint.pdf>>
- [Najdenovska18] Najdenovska et al., Sci Data 5, 180270 (2018). <<https://doi.org/10.1038/sdata.2018.270>>



## PYTHON MODULE INDEX

### C

cmp, 80  
 cmp.bidsappmanager.gui, 127  
 cmp.bidsappmanager.gui.bidsapp, 127  
 cmp.bidsappmanager.gui.config, 131  
 cmp.bidsappmanager.gui.globals, 132  
 cmp.bidsappmanager.gui.handlers, 132  
 cmp.bidsappmanager.gui.principal, 136  
 cmp.bidsappmanager.gui.qc, 137  
 cmp.bidsappmanager.gui.traits, 138  
 cmp.bidsappmanager.pipelines.anatomical, 142  
 cmp.bidsappmanager.pipelines.anatomical.anatomical, 142  
 cmp.bidsappmanager.pipelines.diffusion, 143  
 cmp.bidsappmanager.pipelines.diffusion.diffusion, 143  
 cmp.bidsappmanager.pipelines.functional, 144  
 cmp.bidsappmanager.pipelines.functional.eeg, 144  
 cmp.bidsappmanager.pipelines.functional.fMRI, 144  
 cmp.bidsappmanager.project, 138  
 cmp.bidsappmanager.stages, 145  
 cmp.bidsappmanager.stages.connectome, 145  
 cmp.bidsappmanager.stages.connectome.connectome, 145  
 cmp.bidsappmanager.stages.connectome.fMRI\_connectome, 146  
 cmp.bidsappmanager.stages.diffusion, 147  
 cmp.bidsappmanager.stages.diffusion.diffusion, 147  
 cmp.bidsappmanager.stages.diffusion.reconstruction, 148  
 cmp.bidsappmanager.stages.diffusion.tracking, 149  
 cmp.bidsappmanager.stages.functional, 149  
 cmp.bidsappmanager.stages.functional.functionalMRI, 149  
 cmp.bidsappmanager.stages.parcellation, 150  
 cmp.bidsappmanager.stages.parcellation.parcellation, 150  
 cmp.bidsappmanager.stages.preprocessing, 151  
 cmp.bidsappmanager.stages.preprocessing.fMRI\_preprocessing, 151  
 cmp.bidsappmanager.stages.preprocessing.preprocessing, 152  
 cmp.bidsappmanager.stages.registration, 152  
 cmp.bidsappmanager.stages.registration.registration, 152  
 cmp.bidsappmanager.stages.segmentation, 153  
 cmp.bidsappmanager.stages.segmentation.segmentation, 153  
 cmp.parser, 80  
 cmp.pipelines.anatomical, 88  
 cmp.pipelines.anatomical.anatomical, 88  
 cmp.pipelines.common, 87  
 cmp.pipelines.diffusion, 90  
 cmp.pipelines.diffusion.diffusion, 90  
 cmp.pipelines.functional, 93  
 cmp.pipelines.functional.eeg, 93  
 cmp.pipelines.functional.fMRI, 95  
 cmp.project, 81  
 cmp.stages, 98  
 cmp.stages.common, 126  
 cmp.stages.connectome, 98  
 cmp.stages.connectome.connectome, 98  
 cmp.stages.connectome.fMRI\_connectome, 99  
 cmp.stages.diffusion, 101  
 cmp.stages.diffusion.diffusion, 101  
 cmp.stages.diffusion.reconstruction, 104  
 cmp.stages.diffusion.tracking, 106  
 cmp.stages.eeg, 109  
 cmp.stages.eeg.inverse\_solution, 109  
 cmp.stages.eeg.loader, 110  
 cmp.stages.eeg.preparer, 111  
 cmp.stages.functional, 112  
 cmp.stages.functional.functionalMRI, 112  
 cmp.stages.parcellation, 113  
 cmp.stages.parcellation.parcellation, 113  
 cmp.stages.preprocessing, 115  
 cmp.stages.preprocessing.fMRI\_preprocessing, 115  
 cmp.stages.preprocessing.preprocessing, 116  
 cmp.stages.registration, 119

- `cmp.stages.registration.registration`, 119
- `cmp.stages.segmentation`, 123
- `cmp.stages.segmentation.segmentation`, 123
- `cmtklib`, 154
  - `cmtklib.bids`, 154
    - `cmtklib.bids.io`, 154
    - `cmtklib.bids.network`, 156
    - `cmtklib.bids.utils`, 157
  - `cmtklib.carbonfootprint`, 211
  - `cmtklib.config`, 212
  - `cmtklib.connectome`, 216
  - `cmtklib.data.parcellation.util`, 220
  - `cmtklib.diffusion`, 221
  - `cmtklib.eeg`, 220
  - `cmtklib.functionalMRI`, 224
  - `cmtklib.interfaces`, 158
    - `cmtklib.interfaces.afni`, 158
    - `cmtklib.interfaces.ants`, 160
    - `cmtklib.interfaces.dipy`, 161
    - `cmtklib.interfaces.eeg`, 168
    - `cmtklib.interfaces.freesurfer`, 169
    - `cmtklib.interfaces.fsl`, 172
    - `cmtklib.interfaces.misc`, 182
    - `cmtklib.interfaces.mne`, 184
    - `cmtklib.interfaces.mrtrix3`, 189
    - `cmtklib.interfaces.pycartool`, 210
  - `cmtklib.parcellation`, 228
  - `cmtklib.util`, 234



## INDEX

### A

acquisition (*cmtklib.bids.io.CustomBIDSFile* attribute), 155  
 act\_tracking (*cmp.stages.preprocessing.preprocessing.PreprocessingConfig* attribute), 118  
 act\_tracking (*cmp.stages.registration.registration.RegistrationConfig* attribute), 121  
 aggregate\_outputs() (*cmtklib.interfaces.fsl.Orient* method), 181  
 anat\_available\_config (*cmp.project.ProjectInfo* attribute), 83  
 anat\_config (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 128  
 anat\_config\_error\_msg (*cmp.project.ProjectInfo* attribute), 83  
 anat\_config\_error\_view (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 139  
 anat\_config\_to\_load (*cmp.project.ProjectInfo* attribute), 83  
 anat\_custom\_last\_stage (*cmp.project.ProjectInfo* attribute), 83  
 anat\_flow (*cmp.pipelines.common.Pipeline* attribute), 87  
 anat\_inputs\_checked (*cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow* attribute), 131  
 anat\_inputs\_checked (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler* attribute), 133  
 anat\_inputs\_checked (*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135  
 anat\_inputs\_checked (*cmp.bidsappmanager.gui.qc.QualityInspectorWindow* attribute), 137  
 anat\_load\_config\_json() (in module *cmtklib.config*), 212  
 anat\_outputs\_checked (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler* attribute), 133  
 anat\_outputs\_checked (*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135  
 anat\_pipeline (*cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow* attribute), 131  
 anat\_pipeline (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler* attribute), 133  
 anat\_pipeline (*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135  
 anat\_pipeline (*cmp.bidsappmanager.gui.principal.MainWindow* attribute), 136  
 anat\_pipeline (*cmp.bidsappmanager.gui.qc.QualityInspectorWindow* attribute), 137  
 anat\_run (*cmp.project.ProjectInfo* attribute), 82  
 anat\_runs (*cmp.project.ProjectInfo* attribute), 82  
 anat\_save\_config (*cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow* attribute), 131, 132  
 anat\_save\_config() (in module *cmtklib.config*), 212  
 anat\_select\_config\_to\_load (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 140  
 anat\_stage\_names (*cmp.project.ProjectInfo* attribute), 83  
 anat\_warning\_view (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 139  
 anatomical\_processed (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler* attribute), 133  
 anatomical\_processed (*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135  
 AnatomicalPipeline (class in *cmp.pipelines.anatomical.anatomical*), 88  
 AnatomicalPipelineUI (class in *cmp.bidsappmanager.pipelines.anatomical.anatomical*), 142  
 angle (*cmp.stages.diffusion.tracking.MRtrixTrackingConfig* attribute), 108  
 ants\_bspline\_interpolation\_parameters (*cmp.stages.registration.registration.RegistrationConfig* attribute), 119  
 ants\_convergence\_thresh (*cmp.stages.registration.registration.RegistrationConfig* attribute), 119

attribute), 120  
 ants\_convergence\_winsize (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_gauss\_interpolation\_parameters (cmp.stages.registration.registration.RegistrationConfig attribute), 119  
 ants\_interpolation (cmp.stages.registration.registration.RegistrationConfig attribute), 119  
 ants\_linear\_cost (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_linear\_gradient\_step (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_linear\_sampling\_perc (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_linear\_sampling\_strategy (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_lower\_quantile (cmp.stages.registration.registration.RegistrationConfig attribute), 119  
 ants\_multilab\_interpolation\_parameters (cmp.stages.registration.registration.RegistrationConfig attribute), 119  
 ants\_nonlinear\_cost (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_nonlinear\_gradient\_step (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_nonlinear\_total\_field\_variance (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_nonlinear\_update\_field\_variance (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_perform\_syn (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 ants\_precision\_type (cmp.stages.parcellation.parcellation.ParcellationConfig attribute), 114  
 ants\_probmaskfile (cmp.stages.segmentation.segmentation.SegmentationConfig attribute), 124  
 ants\_regmaskfile (cmp.stages.segmentation.segmentation.SegmentationConfig attribute), 124  
 ants\_templatefile (cmp.stages.segmentation.segmentation.SegmentationConfig attribute), 124  
 ants\_upper\_quantile (cmp.stages.registration.registration.RegistrationConfig attribute), 120  
 apply\_inverse\_epochs\_cartool() (cmtk-lib.interfaces.pycartool.CartoolInverseSolutionROIExtractor static method), 210  
 apply\_scrubbing (cmp.stages.connectome.fmri\_connectome.Connectome attribute), 99  
 apply\_to\_eroded\_brain (cmp.stages.registration.registration.RegistrationConfig attribute), 121  
 apply\_to\_eroded\_csf (cmp.stages.registration.registration.RegistrationConfig attribute), 121  
 apply\_to\_eroded\_wm (cmp.stages.registration.registration.RegistrationConfig attribute), 121  
 ApplymultipleMRConvert, 189  
 ApplymultipleMRCrop, 190  
 ApplymultipleMRTransforms, 191  
 ApplymultipleWarp, 172  
 ApplymultipleXfm, 173  
 atlas (cmtklib.bids.io.CustomBIDSFile attribute), 155  
 atlas\_info (cmp.project.ProjectInfo attribute), 82  
 atlas\_info (cmp.stages.parcellation.parcellation.ParcellationConfig attribute), 114  
 B  
 backtrack (cmp.stages.diffusion.tracking.MRtrixTrackingConfig attribute), 108  
 Bandpass, 158  
 base\_directory (cmp.project.ProjectInfo attribute), 81  
 BBRegister, 169  
 Builders (class in cmtklib.util), 234  
 bias\_field\_algo (cmp.stages.preprocessing.preprocessing.PreprocessingConfig attribute), 117  
 bias\_field\_correction (cmp.stages.preprocessing.preprocessing.PreprocessingConfig attribute), 117  
 bids\_dir (cmp.stages.common.Stage attribute), 126  
 bids\_layout (cmp.project.ProjectInfo attribute), 81  
 bids\_root (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow attribute), 127  
 bids\_session\_label (cmp.stages.common.Stage attribute), 126  
 bids\_subject\_label (cmp.stages.common.Stage attribute), 126  
 bidsapp (cmp.bidsappmanager.gui.principal.MainWindow attribute), 136  
 bidsapp\_tag (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow attribute), 129  
 bidsapp\_ui (cmp.bidsappmanager.gui.principal.MainWindow attribute), 136  
 BIDSAppInterfaceWindow (class in cmp.bidsappmanager.gui.bidsapp), 127  
 BIDSAppInterfaceWindowHandler (class in cmp.bidsappmanager.gui.handlers), 132  
 big\_delta (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105  
 BinaryThreshold, 174

BOLD (*cmklib.util.BColors* attribute), 234

brain\_mask\_extraction\_tool

(*cmp.stages.segmentation.segmentation.Segmentation* attribute), 124

## C

carbon\_emission\_msg

(*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 129

CartoolInverseSolutionROIExtraction, 210

check (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 129

check\_config() (*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* method), 88

check\_config() (*cmp.pipelines.common.Pipeline* method), 87

check\_config() (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline* method), 90

check\_config() (*cmp.pipelines.functional.eeg.EEGPipeline* method), 94

check\_config() (*cmp.pipelines.functional.fMRI.fMRIPipeline* method), 96

check\_configuration\_format() (in module *cmklib.config*), 212

check\_configuration\_version() (in module *cmklib.config*), 212

check\_directory\_exists() (in module *cmklib.util*), 235

check\_input() (*cmp.bidsappmanager.pipelines.anatomical.anatomical.anatomical.Pipeline* method), 142

check\_input() (*cmp.bidsappmanager.pipelines.diffusion.diffusion.diffusion.Pipeline* method), 143

check\_input() (*cmp.bidsappmanager.pipelines.functional.fMRI.fMRIPipeline* method), 145

check\_input() (*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* method), 88

check\_input() (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline* method), 90

check\_input() (*cmp.pipelines.functional.eeg.EEGPipeline* method), 94

check\_input() (*cmp.pipelines.functional.fMRI.fMRIPipeline* method), 96

check\_output() (*cmp.bidsappmanager.pipelines.anatomical.anatomical.anatomical.Pipeline* method), 142

check\_output() (*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* method), 88

check\_settings() (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* method), 129

check\_settings() (*cmp.bidsappmanager.gui.handlers.BIDSAppInterfaceWindowHandler* method), 132

check\_stages\_execution()  
(*cmp.pipelines.common.Pipeline* method), 87

circular\_layout (*cmp.bidsappmanager.stages.connectome.connectome.Connectome* attribute), 146

circular\_layout (*cmp.bidsappmanager.stages.connectome.fmri\_connectome.Connectome* attribute), 146

circular\_layout (*cmp.stages.connectome.connectome.ConnectomeConfig* attribute), 98

circular\_layout (*cmp.stages.connectome.fmri\_connectome.ConnectomeConfig* attribute), 100

clean\_cache() (in module *cmp.bidsappmanager.project*), 140

clear\_stages\_outputs() (*cmp.pipelines.common.Pipeline* method), 87

cmat() (in module *cmklib.connectome*), 219

cmp module, 80

*cmp.bidsappmanager.gui* module, 127

*cmp.bidsappmanager.gui.bidsapp* module, 127

*cmp.bidsappmanager.gui.config* module, 131

*cmp.bidsappmanager.gui.globals* module, 132

*cmp.bidsappmanager.gui.handlers* module, 132

*cmp.bidsappmanager.gui.principal* module, 136

*cmp.bidsappmanager.gui.qc* module, 137

*cmp.bidsappmanager.gui.traits* module, 138

*cmp.bidsappmanager.pipelines.anatomical* module, 142

*cmp.bidsappmanager.pipelines.anatomical.anatomical* module, 142

*cmp.bidsappmanager.pipelines.diffusion* module, 143

*cmp.bidsappmanager.pipelines.diffusion.diffusion* module, 143

*cmp.bidsappmanager.pipelines.functional* module, 144

*cmp.bidsappmanager.pipelines.functional.eeg* module, 144

*cmp.bidsappmanager.pipelines.functional.fMRI* module, 144

*cmp.bidsappmanager.project* module, 138

*cmp.bidsappmanager.stages* module, 145

*cmp.bidsappmanager.stages.connectome* module, 145

*cmp.bidsappmanager.stages.connectome.connectome* module, 145

<code>cmp.bidsappmanager.stages.connectome.fmri_connectome</code>	<code>cmp.stages.common</code>
module, 146	module, 126
<code>cmp.bidsappmanager.stages.diffusion</code>	<code>cmp.stages.connectome</code>
module, 147	module, 98
<code>cmp.bidsappmanager.stages.diffusion.diffusion</code>	<code>cmp.stages.connectome.connectome</code>
module, 147	module, 98
<code>cmp.bidsappmanager.stages.diffusion.reconstruction</code>	<code>cmp.stages.connectome.fmri_connectome</code>
module, 148	module, 99
<code>cmp.bidsappmanager.stages.diffusion.tracking</code>	<code>cmp.stages.diffusion</code>
module, 149	module, 101
<code>cmp.bidsappmanager.stages.functional</code>	<code>cmp.stages.diffusion.diffusion</code>
module, 149	module, 101
<code>cmp.bidsappmanager.stages.functional.functionalMRI</code>	<code>cmp.stages.diffusion.reconstruction</code>
module, 149	module, 104
<code>cmp.bidsappmanager.stages.parcellation</code>	<code>cmp.stages.diffusion.tracking</code>
module, 150	module, 106
<code>cmp.bidsappmanager.stages.parcellation.parcellation</code>	<code>cmp.stages.eeg</code>
module, 150	module, 109
<code>cmp.bidsappmanager.stages.preprocessing</code>	<code>cmp.stages.eeg.inverse_solution</code>
module, 151	module, 109
<code>cmp.bidsappmanager.stages.preprocessing.fmri_preprocessing</code>	<code>cmp.stages.eeg.loader</code>
module, 151	module, 110
<code>cmp.bidsappmanager.stages.preprocessing.preprocessing</code>	<code>cmp.stages.eeg.preparer</code>
module, 152	module, 111
<code>cmp.bidsappmanager.stages.registration</code>	<code>cmp.stages.functional</code>
module, 152	module, 112
<code>cmp.bidsappmanager.stages.registration.registration</code>	<code>cmp.stages.functional.functionalMRI</code>
module, 152	module, 112
<code>cmp.bidsappmanager.stages.segmentation</code>	<code>cmp.stages.parcellation</code>
module, 153	module, 113
<code>cmp.bidsappmanager.stages.segmentation.segmentation</code>	<code>cmp.stages.parcellation.parcellation</code>
module, 153	module, 113
<code>cmp.parser</code>	<code>cmp.stages.preprocessing</code>
module, 80	module, 115
<code>cmp.pipelines.anatomical</code>	<code>cmp.stages.preprocessing.fmri_preprocessing</code>
module, 88	module, 115
<code>cmp.pipelines.anatomical.anatomical</code>	<code>cmp.stages.preprocessing.preprocessing</code>
module, 88	module, 116
<code>cmp.pipelines.common</code>	<code>cmp.stages.registration</code>
module, 87	module, 119
<code>cmp.pipelines.diffusion</code>	<code>cmp.stages.registration.registration</code>
module, 90	module, 119
<code>cmp.pipelines.diffusion.diffusion</code>	<code>cmp.stages.segmentation</code>
module, 90	module, 123
<code>cmp.pipelines.functional</code>	<code>cmp.stages.segmentation.segmentation</code>
module, 93	module, 123
<code>cmp.pipelines.functional.eeg</code>	<code>cmtklib</code>
module, 93	module, 154
<code>cmp.pipelines.functional.fMRI</code>	<code>cmtklib.bids</code>
module, 95	module, 154
<code>cmp.project</code>	<code>cmtklib.bids.io</code>
module, 81	module, 154
<code>cmp.stages</code>	<code>cmtklib.bids.network</code>
module, 98	module, 156

cmtklib.bids.utils  
     module, 157  
 cmtklib.carbonfootprint  
     module, 211  
 cmtklib.config  
     module, 212  
 cmtklib.connectome  
     module, 216  
 cmtklib.data.parcellation.util  
     module, 220  
 cmtklib.diffusion  
     module, 221  
 cmtklib.eeg  
     module, 220  
 cmtklib.functionalMRI  
     module, 224  
 cmtklib.interfaces  
     module, 158  
 cmtklib.interfaces.afni  
     module, 158  
 cmtklib.interfaces.ants  
     module, 160  
 cmtklib.interfaces.dipy  
     module, 161  
 cmtklib.interfaces.eeg  
     module, 168  
 cmtklib.interfaces.freesurfer  
     module, 169  
 cmtklib.interfaces.fsl  
     module, 172  
 cmtklib.interfaces.misc  
     module, 182  
 cmtklib.interfaces.mne  
     module, 184  
 cmtklib.interfaces.mrtrix3  
     module, 189  
 cmtklib.interfaces.pycartool  
     module, 210  
 cmtklib.parcellation  
     module, 228  
 cmtklib.util  
     module, 234  
 CombineParcellations, 228  
 compute\_curvature(*cmp.stages.connectome.connectome.ConnectomeStage*  
     attribute), 98  
 compute\_curvature\_array() (in module *cmtklib.connectome*), 219  
 compute\_length\_array() (in module *cmtklib.diffusion*), 224  
 ComputeParcellationRoiVolumes, 229  
 ConcatOutputsAsTuple, 182  
 config(*cmp.stages.common.Stage* attribute), 126  
 config\_view(*cmp.bidsappmanager.stages.connectome.connectome.ConnectomeStage*  
     attribute), 146  
 config\_view(*cmp.bidsappmanager.stages.connectome.fmri\_connectome.ConnectomeStage*  
     attribute), 147  
 config\_view(*cmp.bidsappmanager.stages.diffusion.diffusion.DiffusionStage*  
     attribute), 147  
 config\_view(*cmp.bidsappmanager.stages.functional.functionalMRI.FunctionalMRIStage*  
     attribute), 150  
 config\_view(*cmp.bidsappmanager.stages.parcellation.parcellation.ParcellationStage*  
     attribute), 151  
 config\_view(*cmp.bidsappmanager.stages.preprocessing.fmri\_preprocessing.FMRIPreprocessingStage*  
     attribute), 151  
 config\_view(*cmp.bidsappmanager.stages.preprocessing.preprocessing.PreprocessingStage*  
     attribute), 152  
 config\_view(*cmp.bidsappmanager.stages.registration.registration.RegistrationStage*  
     attribute), 153  
 config\_view(*cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationStage*  
     attribute), 154  
 ConfigQualityWindowHandler (class in *cmp.bidsappmanager.gui.handlers*), 133  
 configurator(*cmp.bidsappmanager.gui.principal.MainWindow* attribute), 136  
 configurator\_ui(*cmp.bidsappmanager.gui.principal.MainWindow* attribute), 136  
 connectivity\_metrics  
     (*cmp.bidsappmanager.stages.connectome.connectome.ConnectomeStage* attribute), 145  
 connectivity\_metrics  
     (*cmp.stages.connectome.connectome.ConnectomeConfig* attribute), 98  
 connectome(*cmp.bidsappmanager.pipelines.diffusion.diffusion.DiffusionPipeline* attribute), 143  
 connectome(*cmp.bidsappmanager.pipelines.functional.fMRI.fMRIPipeline* attribute), 144  
 ConnectomeConfig (class in *cmp.stages.connectome.connectome*), 98  
 ConnectomeConfig (class in *cmp.stages.connectome.fmri\_connectome*), 99  
 ConnectomeConfigUI (class in *cmp.bidsappmanager.stages.connectome.connectome*), 145  
 ConnectomeConfigUI (class in *cmp.bidsappmanager.stages.connectome.fmri\_connectome*), 146  
 ConnectomeStage (class in *cmp.stages.connectome.connectome*), 98  
 ConnectomeStage (class in *cmp.stages.connectome.fmri\_connectome*), 100  
 ConnectomeStageUI (class in *cmp.bidsappmanager.stages.connectome.connectome*), 145  
 ConnectomeStageUI (class in *cmp.bidsappmanager.stages.connectome.fmri\_connectome*), 146  
 ConnectomeStageUI (class in *cmp.bidsappmanager.stages.connectome.fmri\_connectome*), 146



ConstrainedSphericalDeconvolution, 192  
 contrast\_type(*cmp.stages.registration.registration.RegistrationConfig* attribute), 121  
 convert\_config\_ini\_2\_json() (in module *cmklib.config*), 213  
 convert\_list\_to\_tuple() (in module *cmklib.util*), 235  
 copyBrainMaskToFreesurfer, 171  
 copyFileToFreesurfer, 172  
 create\_ants\_workflow() (in module *cmp.stages.registration.registration.RegistrationStage* method), 122  
 create\_bregister\_workflow() (in module *cmp.stages.registration.registration.RegistrationStage* method), 122  
 create\_carbon\_footprint\_message() (in module *cmklib.carbonfootprint*), 211  
 create\_configparser\_from\_pipeline() (in module *cmklib.config*), 213  
 create\_datagrabber\_node() (in module *cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* method), 89  
 create\_datagrabber\_node() (in module *cmp.pipelines.diffusion.diffusion.DiffusionPipeline* method), 91  
 create\_datagrabber\_node() (in module *cmp.pipelines.functional.eeg.EEGPipeline* method), 94  
 create\_datagrabber\_node() (in module *cmp.pipelines.functional.fMRI.fMRIPipeline* method), 96  
 create\_datasinker\_node() (in module *cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* method), 89  
 create\_datasinker\_node() (in module *cmp.pipelines.diffusion.diffusion.DiffusionPipeline* method), 91  
 create\_datasinker\_node() (in module *cmp.pipelines.functional.fMRI.fMRIPipeline* method), 96  
 create\_dipy\_recon\_flow() (in module *cmp.stages.diffusion.reconstruction*), 106  
 create\_dipy\_tracking\_flow() (in module *cmp.stages.diffusion.tracking*), 108  
 create\_emissions\_tracker() (in module *cmklib.carbonfootprint*), 211  
 create\_endpoints\_array() (in module *cmklib.connectome*), 219  
 create\_field\_template\_dict() (in module *cmp.pipelines.diffusion.diffusion.DiffusionPipeline* method), 91  
 create\_flirt\_workflow() (in module *cmp.stages.registration.registration.RegistrationStage* method), 122  
 create\_html\_carbon\_footprint\_report() (in module *cmklib.carbonfootprint*), 211  
 create\_mrtrix\_recon\_flow() (in module *cmp.stages.diffusion.reconstruction*), 106  
 create\_mrtrix\_tracking\_flow() (in module *cmp.stages.diffusion.tracking*), 108  
 create\_pipeline\_flow() (in module *cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* method), 89  
 create\_pipeline\_flow() (in module *cmp.pipelines.diffusion.diffusion.DiffusionPipeline* method), 91  
 create\_pipeline\_flow() (in module *cmp.pipelines.functional.eeg.EEGPipeline* method), 94  
 create\_pipeline\_flow() (in module *cmp.pipelines.functional.fMRI.fMRIPipeline* method), 97  
 create\_roi() (in module *cmklib.parcellation*), 233  
 create\_stage\_flow() (in module *cmp.pipelines.common.Pipeline* method), 87  
 create\_subject\_configuration\_from\_ref() (in module *cmklib.config*), 213  
 create\_T1\_and\_Brain() (in module *cmklib.parcellation*), 233  
 create\_view(*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 139  
 create\_wm\_mask() (in module *cmklib.parcellation*), 233  
 create\_workflow() (in module *cmp.stages.connectome.connectome.ConnectomeStage* method), 98, 99  
 create\_workflow() (in module *cmp.stages.connectome.fmri\_connectome.ConnectomeStage* method), 100  
 create\_workflow() (in module *cmp.stages.diffusion.diffusion.DiffusionStage* method), 102, 103  
 create\_workflow() (in module *cmp.stages.eeg.inverse\_solution.EEGInverseSolutionStage* method), 109  
 create\_workflow() (in module *cmp.stages.eeg.loader.EEGLoaderStage* method), 110  
 create\_workflow() (in module *cmp.stages.eeg.preparer.EEGPreparerStage* method), 111  
 create\_workflow() (in module *cmp.stages.functional.functionalMRI.FunctionalMRIStage* method), 113  
 create\_workflow() (in module *cmp.stages.parcellation.parcellation.ParcellationStage* method), 114  
 create\_workflow() (in module *cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingStage* method), 116  
 create\_workflow() (in module *cmp.stages.preprocessing.preprocessing.PreprocessingStage* method), 118  
 create\_workflow() (in module *cmp.stages.registration.registration.RegistrationStage* method), 122, 123  
 create\_workflow() (in module *cmp.stages.segmentation.segmentation.SegmentationStage* method), 125

`create_workflow_custom()` (*cmp.stages.parcellation.parcellation.ParcellationStage* attribute), 115  
`create_workflow_custom()` (*cmp.stages.segmentation.segmentation.SegmentationStage* attribute), 125  
`CreateAcqpFile`, 175  
`CreateBEM`, 184  
`CreateBIDSStandardParcellationLabelIndexMappingFile`, 157  
`CreateCMPParcellationNodeDescriptionFilesFromBIDSFile`, 157  
`CreateCov`, 185  
`CreateFwd`, 185  
`CreateIndexFile`, 175  
`CreateMultipleCMPParcellationNodeDescriptionFilesFromBIDSFile`, 157  
`CreateRois`, 168  
`CreateSrc`, 186  
`creation_mode` (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 138  
`crop_and_move_datasets()` (in module *cmklib.parcellation*), 233  
`crop_and_move_WM_and_GM()` (in module *cmklib.parcellation*), 233  
`crop_at_gm_wmi` (*cmp.stages.diffusion.tracking.MRtrixTrackingConfig* attribute), 108  
`CSD`, 161  
`csf` (*cmp.stages.functional.functionalMRI.FunctionalMRIConfig* attribute), 112  
`custom_aparcaseg` (*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 125  
`custom_aparcaseg_group` (*cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationConfigUI* attribute), 154  
`custom_brainmask` (*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 124  
`custom_brainmask_group` (*cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationConfigUI* attribute), 153  
`custom_csf_mask` (*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 124  
`custom_csf_mask_group` (*cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationConfigUI* attribute), 153  
`custom_gm_mask` (*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 124  
`custom_gm_mask_group` (*cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationConfigUI* attribute), 153  
`custom_parcellation` (*cmp.stages.parcellation.parcellation.ParcellationConfig* attribute), 114  
`custom_parcellation_view` (*cmp.bidsappmanager.stages.parcellation.parcellation.ParcellationConfigUI* attribute), 101  
`custom_seg_wm_mask` (*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 124  
`custom_seg_wm_mask_group` (*cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationConfigUI* attribute), 153  
`CustomAparcasegBIDSFile` (class in *cmklib.bids.io*), 156  
`CustomBIDSFile` (class in *cmklib.bids.io*), 155  
`CustomBrainMaskBIDSFile` (class in *cmklib.bids.io*), 156  
`CustomCSFMaskBIDSFile` (class in *cmklib.bids.io*), 156  
`CustomGMMaskBIDSFile` (class in *cmklib.bids.io*), 156  
`CustomParcellationBIDSFile` (class in *cmklib.bids.io*), 156  
`CustomWMMaskBIDSFile` (class in *cmklib.bids.io*), 156  
`cuttoff_value` (*cmp.stages.diffusion.tracking.MRtrixTrackingConfig* attribute), 108

## D

`data_provenance_tracking` (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 129  
`datalad_dataset_path` (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 139  
`datalad_is_available` (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 129  
`datalad_update_environment` (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 129  
`dataset_view` (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 139  
`define_custom_mapping()` (*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* method), 89  
`define_custom_mapping()` (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline* method), 91  
`define_custom_mapping()` (*cmp.pipelines.functional.fMRI.fMRIPipeline* method), 97  
`define_inspect_outputs()` (*cmp.stages.connectome.connectome.ConnectomeStage* method), 99  
`define_inspect_outputs()` (*cmp.stages.connectome.fmri\_connectome.ConnectomeStage* method), 100  
`define_inspect_outputs()` (*cmp.stages.diffusion.diffusion.DiffusionStage* method), 100

method), 103

define\_inspect\_outputs()  
(cmp.stages.eeg.inverse\_solution.EEGInverseSolutionStage  
method), 109

define\_inspect\_outputs()  
(cmp.stages.eeg.loader.EEGLoaderStage  
method), 110

define\_inspect\_outputs()  
(cmp.stages.eeg.preparer.EEGPreparerStage  
method), 112

define\_inspect\_outputs()  
(cmp.stages.functional.functionalMRI.FunctionalMRIStage  
method), 113

define\_inspect\_outputs()  
(cmp.stages.parcellation.parcellation.ParcellationStage  
method), 115

define\_inspect\_outputs()  
(cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingStage  
method), 116

define\_inspect\_outputs()  
(cmp.stages.preprocessing.preprocessing.PreprocessingStage  
method), 118

define\_inspect\_outputs()  
(cmp.stages.registration.registration.RegistrationStage  
method), 123

define\_inspect\_outputs()  
(cmp.stages.segmentation.segmentation.SegmentationStage  
method), 125

denoising (cmp.stages.preprocessing.preprocessing.PreprocessingStage  
attribute), 117

denoising\_algo (cmp.stages.preprocessing.preprocessing.PreprocessingStage  
attribute), 117

desc (cmklib.bids.io.CustomBIDSFile attribute), 155

description (cmp.stages.preprocessing.preprocessing.PreprocessingStage  
attribute), 117

desired\_number\_of\_tracks  
(cmp.stages.diffusion.tracking.MRtrixTrackingConfig  
attribute), 107

Despike, 159

despiking (cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingStage  
attribute), 115

Detrending, 224

diffusion (cmp.bidsappmanager.pipelines.diffusion.diffusion.DiffusionPipeline  
attribute), 143

diffusion\_imaging\_model (cmp.project.ProjectInfo  
attribute), 81

diffusion\_imaging\_model  
(cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 101

diffusion\_imaging\_model  
(cmp.stages.registration.registration.RegistrationStage  
attribute), 119

diffusion\_imaging\_model\_editor  
(cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 101

diffusion\_imaging\_model\_select\_view  
(cmp.bidsappmanager.project.ProjectInfoUI  
attribute), 140

diffusion\_model (cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 102

diffusion\_model\_editor  
(cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 102

DiffusionConfig (class in  
cmp.stages.diffusion.diffusion), 101

DiffusionConfigUI (class in  
cmp.bidsappmanager.stages.diffusion.diffusion),  
147

DiffusionPipeline (class in  
cmp.pipelines.diffusion.diffusion), 90

DiffusionPipelineUI (class in  
cmp.bidsappmanager.pipelines.diffusion.diffusion),  
143

DiffusionStage (class in  
cmp.stages.diffusion.diffusion), 102

DiffusionStageUI (class in  
cmp.bidsappmanager.stages.diffusion.diffusion),  
147

dilate\_rois (cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 101

dilate\_stage\_kernel (cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 101

dilation\_radius (cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 101

dipyr\_noise\_model (cmp.stages.preprocessing.preprocessing.PreprocessingStage  
attribute), 117

dipy\_recon\_config (cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 102

Dipy\_recon\_configUI (class in  
cmp.bidsappmanager.stages.diffusion.reconstruction),  
148

dipy\_tracking\_config  
(cmp.stages.diffusion.diffusion.DiffusionConfig  
attribute), 102

Dipy\_tracking\_configUI (class in  
cmp.bidsappmanager.stages.diffusion.tracking),  
148

DipyReconConfig (class in  
cmp.stages.diffusion.reconstruction), 104

DipyTrackingConfig (class in  
cmp.stages.diffusion.tracking), 106

DirectionGetterTractography, 163

discard\_n\_volumes (cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingStage  
attribute), 115

DiscardTP, 225

dmri\_available (cmp.project.ProjectInfo attribute), 82

dmri\_available\_config (cmp.project.ProjectInfo attribute), 83



dmri\_bids\_acq(*cmp.pipelines.diffusion.diffusion.GlobalConfig* attribute), 93  
 dmri\_bids\_acq(*cmp.project.ProjectInfo* attribute), 81  
 dmri\_bids\_acq\_view(*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 139  
 dmri\_bids\_acqs(*cmp.project.ProjectInfo* attribute), 81  
 dmri\_config(*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow.registration.registration.RegistrationConfig* attribute), 128  
 dmri\_config\_error\_msg(*cmp.project.ProjectInfo* attribute), 83  
 dmri\_config\_error\_view(*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 139  
 dmri\_config\_to\_load(*cmp.project.ProjectInfo* attribute), 83  
 dmri\_custom\_last\_stage(*cmp.project.ProjectInfo* attribute), 83  
 dmri\_inputs\_checked(*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 128  
 dmri\_inputs\_checked(*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler* attribute), 133  
 dmri\_inputs\_checked(*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135  
 dmri\_inputs\_checked(*cmp.bidsappmanager.gui.qc.QualityInspectorWindow* attribute), 137  
 dmri\_load\_config\_json() (in module *cmtklib.config*), 213  
 dmri\_pipeline(*cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow* attribute), 131  
 dmri\_pipeline(*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler* attribute), 133  
 dmri\_pipeline(*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135  
 dmri\_pipeline(*cmp.bidsappmanager.gui.principal.MainWindow* attribute), 136  
 dmri\_pipeline(*cmp.bidsappmanager.gui.qc.QualityInspectorWindow* attribute), 137  
 dmri\_processed(*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler* attribute), 133  
 dmri\_processed(*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135  
 dmri\_run(*cmp.project.ProjectInfo* attribute), 82  
 dmri\_runs(*cmp.project.ProjectInfo* attribute), 82  
 dmri\_save\_config(*cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow* attribute), 131, 132  
 dmri\_save\_config() (in module *cmtklib.config*), 213  
 dmri\_select\_config\_to\_load(*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 140  
 dmri\_stage\_names(*cmp.project.ProjectInfo* attribute), 83  
 dmri\_warning\_view(*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 139  
 dmri\_warning\_view(*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 216  
 docker\_process(*cmp.bidsappmanager.gui.handlers.BIDSAppInterfaceWindow.registration.registration.RegistrationConfig* attribute), 132  
 DTIEstimateResponseSH, 162  
 DVARs\_thr(*cmp.stages.connectome.fmri\_connectome.ConnectomeConfig* attribute), 99  
 DWI2Tensor, 193  
 DWIBiasCorrect, 194  
 DWIDenoise, 195  
 E  
 Eddy, 175  
 eddy\_correct\_motion\_correction(*cmp.stages.preprocessing.preprocessing.PreprocessingConfig* attribute), 117  
 eddy\_correction\_algo(*cmp.stages.preprocessing.preprocessing.PreprocessingConfig* attribute), 117  
 eddy\_current\_and\_motion\_correction(*cmp.stages.preprocessing.preprocessing.PreprocessingConfig* attribute), 117  
 EddyOpenMP, 176  
 eeg\_available(*cmp.project.ProjectInfo* attribute), 82  
 eeg\_available\_config(*cmp.project.ProjectInfo* attribute), 84  
 eeg\_config\_error\_msg(*cmp.project.ProjectInfo* attribute), 84  
 eeg\_config\_to\_load(*cmp.project.ProjectInfo* attribute), 84  
 eeg\_custom\_last\_stage(*cmp.project.ProjectInfo* attribute), 84  
 eeg\_format(*cmp.stages.eeg.preparer.EEGPreparerConfig* attribute), 111  
 eeg\_load\_config\_json() (in module *cmtklib.config*), 214  
 eeg\_save\_config() (in module *cmtklib.config*), 214  
 eeg\_stage\_names(*cmp.project.ProjectInfo* attribute), 84  
 EEGInverseSolutionConfig (class in *cmp.stages.eeg.inverse\_solution*), 109  
 EEGInverseSolutionStage (class in *cmp.stages.eeg.inverse\_solution*), 109  
 EEGLoader, 168  
 EEGLoaderConfig (class in *cmp.stages.eeg.loader*), 110  
 EEGLoaderStage (class in *cmp.stages.eeg.loader*), 110  
 EEGPipeline (class in *cmp.pipelines.functional.eeg*), 93  
 EEGPreparerConfig (class in *cmp.stages.eeg.preparer*), 111

EEGPreparerStage (class in *cmp.stages.eeg.preparer*), 111

enabled (*cmp.stages.common.Stage* attribute), 126, 127

ENDC (*cmklib.util.BColors* attribute), 234

epochs (*cmp.stages.eeg.preparer.EEGPreparerConfig* attribute), 111

Erode, 196

erode\_mask() (in module *cmklib.parcellation*), 234

EstimateResponseForSH, 197

extension (*cmklib.bids.io.CustomBIDSFile* attribute), 155

extract() (in module *cmklib.parcellation*), 234

extract\_freesurfer\_subject\_dir() (in module *cmklib.util*), 235

extract\_reconall\_base\_dir() (in module *cmklib.util*), 235

ExtractFSLGrad, 198

ExtractHeaderVoxel2WorldMatrix, 182

ExtractImageVoxelSizes, 182

ExtractMRTrixGrad, 199

ExtractPVEsFrom5TT, 221

## F

fa\_thresh (*cmp.stages.diffusion.tracking.DipyTrackingConfig* attribute), 107

FAIL (*cmklib.util.BColors* attribute), 234

fast\_use\_priors (*cmp.stages.preprocessing.preprocessing.PreprocessingConfig* attribute), 117

FD\_thr (*cmp.stages.connectome.fmri\_connectome.ConnectomeConfig* attribute), 99

fill\_stages\_outputs() (*cmp.pipelines.common.Pipeline* method), 87

filter\_fibers() (in module *cmklib.diffusion*), 224

FilterTractogram, 199

flip\_table\_axis (*cmp.bidsappmanager.stages.diffusion.reconstruction.DipyReconConfig* attribute), 148

flip\_table\_axis (*cmp.bidsappmanager.stages.diffusion.reconstruction.MRTrixReconConfig* attribute), 148

flip\_table\_axis (*cmp.stages.diffusion.reconstruction.DipyReconConfig* attribute), 104

flip\_table\_axis (*cmp.stages.diffusion.reconstruction.MRTrixReconConfig* attribute), 105

FlipBvec, 221

FlipTable, 222

flirt\_args (*cmp.stages.registration.registration.RegistrationConfig* attribute), 120

fmri\_available (*cmp.project.ProjectInfo* attribute), 82

fmri\_available\_config (*cmp.project.ProjectInfo* attribute), 83

fmri\_config (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 128

fmri\_config\_error\_msg (*cmp.project.ProjectInfo* attribute), 83

fmri\_config\_error\_view (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 140

fmri\_config\_to\_load (*cmp.project.ProjectInfo* attribute), 83

fmri\_custom\_last\_stage (*cmp.project.ProjectInfo* attribute), 84

fmri\_inputs\_checked (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 128

fmri\_inputs\_checked (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler* attribute), 133

fmri\_inputs\_checked (*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135

fmri\_inputs\_checked (*cmp.bidsappmanager.gui.qc.QualityInspectorWindow* attribute), 137

fmri\_load\_config\_json() (in module *cmklib.config*), 214

fmri\_pipeline (*cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow* attribute), 131

fmri\_pipeline (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindow* attribute), 133

fmri\_pipeline (*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135

fmri\_pipeline (*cmp.bidsappmanager.gui.principal.MainWindow* attribute), 136

fmri\_pipeline (*cmp.bidsappmanager.gui.qc.QualityInspectorWindow* attribute), 137

fmri\_processed (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindow* attribute), 134

fmri\_processed (*cmp.bidsappmanager.gui.handlers.MainWindowHandler* attribute), 135

fmri\_run (*cmp.project.ProjectInfo* attribute), 82

fmri\_runs (*cmp.project.ProjectInfo* attribute), 82

fmri\_save\_config (*cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow* attribute), 131, 132

fmri\_save\_config() (in module *cmklib.config*), 214

fmri\_select\_config\_to\_load (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 140

fmri\_stage\_names (*cmp.project.ProjectInfo* attribute), 84

fmri\_warning\_view (*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 140

fMRIPipeline (class in *cmp.pipelines.functional.fMRI*), 95

fMRIPipelineUI (class in *cmp.bidsappmanager.pipelines.functional.fMRI*), 144

freesurfer\_args (*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 124

freesurfer\_subject\_id (*cmp.project.ProjectInfo* attribute), 82  
 freesurfer\_subject\_id (*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 124  
 freesurfer\_subjects\_dir (*cmp.project.ProjectInfo* attribute), 82  
 freesurfer\_subjects\_dir (*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 124  
 fs\_file (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterface* attribute), 128  
 fs\_subject\_id (*cmp.stages.registration.registration.RegistrationConfig* attribute), 122  
 fs\_subjects\_dir (*cmp.stages.registration.registration.RegistrationConfig* attribute), 122  
 fsl\_cost (*cmp.stages.registration.registration.RegistrationConfig* attribute), 121  
 FSLCreateHD, 177  
 functionalMRI (*cmp.bidsappmanager.pipelines.functionalMRI.fMRIPipeline* attribute), 144  
 FunctionalMRIConfig (class in *cmp.stages.functional.functionalMRI*), 112  
 FunctionalMRIConfigUI (class in *cmp.bidsappmanager.stages.functional.functionalMRI*), 149  
 FunctionalMRIStage (class in *cmp.stages.functional.functionalMRI*), 113  
 FunctionalMRIStageUI (class in *cmp.bidsappmanager.stages.functional.functionalMRI*), 149  
**G**  
 Generate5tt, 200  
 generate\_WM\_and\_GM\_mask() (in module *cmklib.parcellation*), 234  
 GenerateGMWMInterface, 200  
 get() (in module *cmp.parser*), 80  
 get\_anat\_process\_detail\_json() (in module *cmklib.config*), 214  
 get\_basename() (in module *cmklib.util*), 235  
 get\_dmri\_process\_detail\_json() (in module *cmklib.config*), 214  
 get\_docker\_wrapper\_parser() (in module *cmp.parser*), 80  
 get\_eeg\_process\_detail\_json() (in module *cmklib.config*), 215  
 get\_emission\_car\_miles\_equivalent() (in module *cmklib.carbonfootprint*), 211  
 get\_emission\_tv\_time\_equivalent() (in module *cmklib.carbonfootprint*), 212  
 get\_file() (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline* method), 92  
 get\_filename\_path() (*cmklib.bids.io.CustomBIDSFile* method), 155  
 get\_fmri\_process\_detail\_json() (in module *cmklib.config*), 215  
 get\_freesurfer\_parcellation() (in module *cmp.stages.diffusion.tracking*), 108  
 get\_freesurfer\_subject\_id() (in module *cmklib.util*), 235  
 get\_global\_conf() (in module *cmp.bidsappmanager.gui.globals*), 132  
 get\_hausanne2018\_parcellation\_annot() (in module *cmklib.data.parcellation.util*), 220  
 get\_hausanne2018\_parcellation\_mni\_coords() (in module *cmklib.data.parcellation.util*), 220  
 get\_native\_space\_files() (in module *cmklib.bids.utils*), 157  
 get\_native\_space\_no\_desc\_files() (in module *cmklib.bids.utils*), 158  
 get\_native\_space\_tsv\_sidecar\_files() (in module *cmklib.bids.utils*), 158  
 get\_nb\_of\_regions() (*cmklib.bids.io.CustomParcellationBIDSFile* method), 156  
 get\_parcellation() (in module *cmklib.parcellation*), 234  
 get\_pipeline\_dictionary\_outputs() (in module *cmklib.util*), 235  
 get\_process\_detail\_json() (in module *cmklib.config*), 215  
 get\_query\_dict() (*cmklib.bids.io.CustomBIDSFile* method), 155  
 get\_singularity\_wrapper\_parser() (in module *cmp.parser*), 81  
 get\_toolbox\_derivatives\_dir() (*cmklib.bids.io.CustomBIDSFile* method), 155  
 get\_wrapper\_parser() (in module *cmp.parser*), 81  
 global\_conf (*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* attribute), 89  
 global\_conf (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline* attribute), 92  
 global\_conf (*cmp.pipelines.functional.eeg.EEGPipeline* attribute), 94  
 global\_conf (*cmp.pipelines.functional.fMRI.fMRIPipeline* attribute), 97  
 global\_nuisance (*cmp.stages.functional.functionalMRI.FunctionalMRIC* attribute), 112  
 GlobalConfig (class in *cmp.pipelines.anatomical.anatomical*), 89  
 GlobalConfig (class in *cmp.pipelines.diffusion.diffusion*), 93  
 GlobalConfig (class in *cmp.pipelines.functional.eeg*), 95  
 GlobalConfig (class in *cmp.pipelines.functional.fMRI*), 95

`gmwmi_seeding(cmp.stages.preprocessing.preprocessing.FmriPreprocessingConfig)` (in module `cmp.bidsappmanager.project`), 141  
 attribute), 118  
`gmwmi_seeding(cmp.stages.registration.registration.RegistrationConfig)` (in module `cmp.project`), 85  
 attribute), 121  
`group_analysis_sconn()` (in module `cmtk-lib.connectome`), 219  
 method), 89  
`init_subject_derivatives_dirs()`  
 (in module `cmp.pipelines.anatomical.anatomical.AnatomicalPipeline`  
 method), 92  
 (in module `cmp.pipelines.diffusion.diffusion.DiffusionPipeline`  
 method), 92  
`init_subject_derivatives_dirs()`  
 (in module `cmp.pipelines.functional.eeg.EEGPipeline`  
 method), 94  
`init_subject_derivatives_dirs()`  
 (in module `cmp.pipelines.functional.fMRI.fMRIPipeline`  
 method), 97  
`input_folders(cmp.pipelines.anatomical.anatomical.AnatomicalPipeline`  
 attribute), 89  
`input_folders(cmp.pipelines.diffusion.diffusion.DiffusionPipeline`  
 attribute), 92  
`input_folders(cmp.pipelines.functional.eeg.EEGPipeline`  
 attribute), 95  
`input_folders(cmp.pipelines.functional.fMRI.fMRIPipeline`  
 attribute), 97  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.connectome.connectome.ConnectomeStageUI`  
 attribute), 146  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.connectome.fmri_connectome.ConnectomeStageUI`  
 attribute), 147  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.diffusion.diffusion.DiffusionStageUI`  
 attribute), 147  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.functional.functionalMRI.FunctionalMRIStageUI`  
 attribute), 149  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.parcellation.parcellation.ParcellationStageUI`  
 attribute), 150  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.preprocessing.fmri_preprocessing.PreprocessingStageUI`  
 attribute), 151  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.preprocessing.preprocessing.PreprocessingStageUI`  
 attribute), 152  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.registration.registration.RegistrationStageUI`  
 attribute), 153  
`inspect_output_button`  
 (in module `cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationStageUI`  
 attribute), 154  
`inspect_outputs(cmp.stages.common.Stage)` attribute), 126, 127  
`inspect_outputs_enum(cmp.stages.common.Stage)` attribute), 126



inspect\_outputs\_view (attribute), 104  
 (cmp.bidsappmanager.stages.connectome.connectome.LaplacianRegularization (attribute), 146  
 inspect\_outputs\_view (attribute), 104  
 (cmp.bidsappmanager.stages.connectome.fmri\_connectome.ProcessOneStagePipeline (attribute), 147  
 inspect\_outputs\_view length() (in module cmtklib.util), 236  
 (cmp.bidsappmanager.stages.diffusion.diffusion.DiffusionOfSubjects\_to\_be\_processed (attribute), 147  
 inspect\_outputs\_view (attribute), 128  
 (cmp.bidsappmanager.stages.functional.functional.MRIFunctionalMRISegDiffusion.reconstruction.DipyReconConfig (attribute), 150  
 inspect\_outputs\_view lmax\_order (cmp.stages.diffusion.reconstruction.MRtrixReconConfig (attribute), 150  
 (cmp.bidsappmanager.stages.parcellation.parcellation.ParcellationStageUI (attribute), 150  
 inspect\_outputs\_view load\_anat\_config\_file() (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandle (attribute), 151  
 (cmp.bidsappmanager.stages.preprocessing.fmri\_preprocessing.SinglePreprocessingStageUI (attribute), 151  
 inspect\_outputs\_view load\_and\_compute\_carbon\_footprint\_metrics() (in module cmtklib.carbonfootprint), 212  
 (cmp.bidsappmanager.stages.preprocessing.preprocessing.PreprocessingStageUI (attribute), 152  
 inspect\_outputs\_view load\_dataset() (cmp.bidsappmanager.gui.principal.MainWindow (attribute), 136, 137  
 (cmp.bidsappmanager.stages.registration.registration.RegistrationStageUI (attribute), 153  
 inspect\_outputs\_view load\_dmri\_config\_file() (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandle (attribute), 154  
 (cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationStageUI (attribute), 154  
 inspect\_outputs\_view load\_fmri\_config\_file() (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandle (attribute), 138  
 (cmp.bidsappmanager.project.ProjectInfoUI (attribute), 138  
 install\_datalad\_dataset\_via\_ssh load\_graphs() (in module cmtklib.bids.network), 156  
 (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandle (attribute), 117  
 (cmp.bidsappmanager.stages.preprocessing.preprocessing.PreprocessingStageUI (attribute), 117  
 interpolation load\_project\_config() (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandle (attribute), 134  
 (cmp.bidsappmanager.stages.eeg.inverse\_solution.EEGInverseSolutionEditor (attribute), 109  
 (cmp.bidsappmanager.stages.diffusion.reconstruction.DipyReconConfig (attribute), 104  
 invsol\_format local\_model (cmp.stages.diffusion.reconstruction.MRtrixReconConfig (attribute), 110  
 (cmp.bidsappmanager.stages.diffusion.reconstruction.MRtrixReconConfig (attribute), 106  
 invsol\_format local\_model\_editor (cmp.stages.diffusion.reconstruction.DipyReconConfig (attribute), 111  
 (cmp.bidsappmanager.stages.diffusion.reconstruction.DipyReconConfig (attribute), 104  
 is\_running() (cmp.stages.common.Stage method), 127  
 local\_model\_editor (cmp.stages.diffusion.reconstruction.MRtrixReconConfig (attribute), 105  
 is\_tool() (in module cmp.bidsappmanager.project), 141  
 log\_visualization (cmp.bidsappmanager.stages.connectome.connectome.ConnectomeConfig (attribute), 145  
 isavailable() (in module cmtklib.util), 236  
 log\_visualization (cmp.bidsappmanager.stages.connectome.fmri\_connectome.ConnectomeConfig (attribute), 146  
 ismember() (cmtklib.parcellation.CombineParcellations method), 229  
 log\_visualization (cmp.stages.connectome.connectome.ConnectomeConfig (attribute), 98  
 isotropic\_interpolation log\_visualization (cmp.stages.connectome.fmri\_connectome.ConnectomeConfig (attribute), 123  
 (cmp.stages.segmentation.segmentation.SegmentationConfig (attribute), 123  
 isotropic\_vox\_size (cmp.stages.segmentation.segmentation.SegmentationConfig (attribute), 123  
 (cmp.stages.segmentation.segmentation.SegmentationConfig (attribute), 123

## L

label (cmtklib.bids.io.CustomBIDSFile attribute), 155  
 laplacian\_regularization (cmp.stages.diffusion.reconstruction.DipyReconConfig (attribute), 136

## M

magn() (in module cmtklib.util), 236  
 MainWindow (class in cmp.bidsappmanager.gui.principal), 136

MainWindowHandler	(class in <code>cmp.bidsappmanager.gui.handlers</code> ), 134	<code>cmp.bidsappmanager.stages.diffusion.diffusion</code> , 147
make_isotropic	( <code>cmp.stages.segmentation.segmentation.SegmentConfig</code> attribute), 123	<code>cmp.bidsappmanager.stages.diffusion.reconstruction</code> , 148
manage_bidsapp_procs()	( <code>cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow</code> class method), 129	<code>cmp.bidsappmanager.stages.diffusion.tracking</code> , 149
manage_bidsapp_procs()	( <code>cmp.bidsappmanager.gui.handlers.BIDSAppInterfaceWindowHandler</code> class method), 132	<code>cmp.bidsappmanager.stages.functional</code> , 149
manager_group	( <code>cmp.bidsappmanager.gui.principal.MainWindow</code> attribute), 136	<code>cmp.bidsappmanager.stages.functional.functionalMRI</code> , 149
MAPMRI	, 165	<code>cmp.bidsappmanager.stages.parcellation</code> , 150
mapmri	( <code>cmp.stages.diffusion.reconstruction.DipyReconConfig</code> attribute), 104	<code>cmp.bidsappmanager.stages.parcellation.parcellation</code> , 150
MathsCommand	, 178	<code>cmp.bidsappmanager.stages.preprocessing</code> , 151
max_angle	( <code>cmp.stages.diffusion.tracking.DipyTrackingConfig</code> attribute), 107	<code>cmp.bidsappmanager.stages.preprocessing.fmri_preprocessing</code> , 151
mean_curvature()	(in module <code>cmtklib.util</code> ), 237	<code>cmp.bidsappmanager.stages.preprocessing.preprocessing</code> , 152
MNEInverseSolution	, 188	<code>cmp.bidsappmanager.stages.registration</code> , 152
modalities	( <code>cmp.pipelines.diffusion.diffusion.GlobalConfig</code> attribute), 93	<code>cmp.bidsappmanager.stages.registration.registration</code> , 152
module		<code>cmp.bidsappmanager.stages.segmentation</code> , 153
<code>cmp</code>	, 80	<code>cmp.bidsappmanager.stages.segmentation.segmentation</code> , 153
<code>cmp.bidsappmanager.gui</code>	, 127	<code>cmp.parser</code> , 80
<code>cmp.bidsappmanager.gui.bidsapp</code>	, 127	<code>cmp.pipelines.anatomical</code> , 88
<code>cmp.bidsappmanager.gui.config</code>	, 131	<code>cmp.pipelines.anatomical.anatomical</code> , 88
<code>cmp.bidsappmanager.gui.globals</code>	, 132	<code>cmp.pipelines.common</code> , 87
<code>cmp.bidsappmanager.gui.handlers</code>	, 132	<code>cmp.pipelines.diffusion</code> , 90
<code>cmp.bidsappmanager.gui.principal</code>	, 136	<code>cmp.pipelines.diffusion.diffusion</code> , 90
<code>cmp.bidsappmanager.gui.qc</code>	, 137	<code>cmp.pipelines.functional</code> , 93
<code>cmp.bidsappmanager.gui.traits</code>	, 138	<code>cmp.pipelines.functional.eeg</code> , 93
<code>cmp.bidsappmanager.pipelines.anatomical</code>	, 142	<code>cmp.pipelines.functional.fMRI</code> , 95
<code>cmp.bidsappmanager.pipelines.anatomical.anatomical</code>	, 142	<code>cmp.project</code> , 81
<code>cmp.bidsappmanager.pipelines.diffusion</code>	, 143	<code>cmp.stages</code> , 98
<code>cmp.bidsappmanager.pipelines.diffusion.diffusion</code>	, 143	<code>cmp.stages.common</code> , 126
<code>cmp.bidsappmanager.pipelines.functional</code>	, 144	<code>cmp.stages.connectome</code> , 98
<code>cmp.bidsappmanager.pipelines.functional.eeg</code>	, 144	<code>cmp.stages.connectome.connectome</code> , 98
<code>cmp.bidsappmanager.pipelines.functional.fMRI</code>	, 144	<code>cmp.stages.connectome.fmri_connectome</code> , 99
<code>cmp.bidsappmanager.project</code>	, 138	<code>cmp.stages.diffusion</code> , 101
<code>cmp.bidsappmanager.stages</code>	, 145	<code>cmp.stages.diffusion.diffusion</code> , 101
<code>cmp.bidsappmanager.stages.connectome</code>	, 145	<code>cmp.stages.diffusion.reconstruction</code> , 104
<code>cmp.bidsappmanager.stages.connectome.connectome</code>	, 145	<code>cmp.stages.diffusion.tracking</code> , 106
<code>cmp.bidsappmanager.stages.connectome.fmri_connectome</code>	, 146	<code>cmp.stages.eeg</code> , 109
<code>cmp.bidsappmanager.stages.diffusion</code>	, 147	<code>cmp.stages.eeg.inverse_solution</code> , 109
		<code>cmp.stages.eeg.loader</code> , 110
		<code>cmp.stages.eeg.preparer</code> , 111
		<code>cmp.stages.functional</code> , 112
		<code>cmp.stages.functional.functionalMRI</code> , 112
		<code>cmp.stages.parcellation</code> , 113
		<code>cmp.stages.parcellation.parcellation</code> , 113

cmp.stages.preprocessing, 115  
 cmp.stages.preprocessing.fmri\_preprocessing, 115  
 cmp.stages.preprocessing.preprocessing, 116  
 cmp.stages.registration, 119  
 cmp.stages.registration.registration, 119  
 cmp.stages.segmentation, 123  
 cmp.stages.segmentation.segmentation, 123  
 cmcklib, 154  
 cmcklib.bids, 154  
 cmcklib.bids.io, 154  
 cmcklib.bids.network, 156  
 cmcklib.bids.utils, 157  
 cmcklib.carbonfootprint, 211  
 cmcklib.config, 212  
 cmcklib.connectome, 216  
 cmcklib.data.parcellation.util, 220  
 cmcklib.diffusion, 221  
 cmcklib.eeg, 220  
 cmcklib.functionalMRI, 224  
 cmcklib.interfaces, 158  
 cmcklib.interfaces.afni, 158  
 cmcklib.interfaces.ants, 160  
 cmcklib.interfaces.dipy, 161  
 cmcklib.interfaces.eeg, 168  
 cmcklib.interfaces.freesurfer, 169  
 cmcklib.interfaces.fsl, 172  
 cmcklib.interfaces.misc, 182  
 cmcklib.interfaces.mne, 184  
 cmcklib.interfaces.mrtrix3, 189  
 cmcklib.interfaces.pycartool, 210  
 cmcklib.parcellation, 228  
 cmcklib.util, 234  
 motion(*cmp.stages.functional.functionalMRI.FunctionalMRIConfig* attribute), 112  
 motion\_correction(*cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingConfig* attribute), 116  
 MRConvert, 201  
 MRCrop, 203  
 MRThreshold, 203  
 MRTransform, 204  
 MRTrx3Base, 205  
 MRtrix\_mul, 206  
 mrtrix\_recon\_config(*cmp.stages.diffusion.diffusion.DiffusionConfig* attribute), 102  
 MRtrix\_recon\_configUI (class in *cmp.bidsappmanager.stages.diffusion.reconstruction*), 148  
 mrtrix\_tracking\_config(*cmp.stages.diffusion.diffusion.DiffusionConfig* attribute), 102  
 MRtrix\_tracking\_configUI (class in *cmp.bidsappmanager.stages.diffusion.tracking*), 149  
 MRtrixReconConfig (class in *cmp.stages.diffusion.reconstruction*), 105  
 MRtrixTrackingConfig (class in *cmp.stages.diffusion.tracking*), 107  
 MultipleANTsApplyTransforms, 160  
 MultiSelectAdapter (class in *cmp.bidsappmanager.gui.traits*), 138  

## N

 new\_project() (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindow* method), 134  
 no\_search(*cmp.stages.registration.registration.RegistrationConfig* attribute), 121  
 now(*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* attribute), 89  
 now(*cmp.pipelines.diffusion.diffusion.DiffusionPipeline* attribute), 92  
 now(*cmp.pipelines.functional.eeg.EEGPipeline* attribute), 95  
 now(*cmp.pipelines.functional.fMRI.fMRIPipeline* attribute), 97  
 NuisanceRegression, 225  
 number\_of\_cores(*cmp.pipelines.common.Pipeline* attribute), 87  
 number\_of\_parallel\_procs\_updated() (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* method), 129  
 number\_of\_participants\_processed\_in\_parallel(*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 128  
 number\_of\_seeds(*cmp.stages.diffusion.tracking.DipyTrackingConfig* attribute), 107  
 number\_of\_threads(*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 128  
 number\_of\_threads(*cmp.stages.segmentation.segmentation.SegmentationConfig* attribute), 125  
 number\_threads\_max(*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow* attribute), 128  

## O

 OKBLUE (*cmcklib.util.BColors* attribute), 235  
 OKGREEN (*cmcklib.util.BColors* attribute), 235  
 open\_view(*cmp.bidsappmanager.project.ProjectInfoUI* attribute), 140  
 ordered\_stage\_list(*cmp.pipelines.anatomical.anatomical.AnatomicalPipeline* attribute), 89  
 ordered\_stage\_list(*cmp.pipelines.diffusion.diffusion.DiffusionPipeline* attribute), 92  
 ordered\_stage\_list(*cmp.pipelines.functional.eeg.EEGPipeline* attribute), 95  
 ordered\_stage\_list(*cmp.pipelines.functional.fMRI.fMRIPipeline* attribute), 97

Orient, 179  
 output\_anat\_available (cmp.bidsappmanager.gui.qc.QualityInspectorWindow attribute), 137  
 output\_dir (cmp.bidsappmanager.gui.bidsapp.BIDSAppInspectorWindow attribute), 127  
 output\_dir (cmp.stages.common.Stage attribute), 126  
 output\_directory (cmp.project.ProjectInfo attribute), 81  
 output\_dmri\_available (cmp.bidsappmanager.gui.qc.QualityInspectorWindow attribute), 138  
 output\_fmri\_available (cmp.bidsappmanager.gui.qc.QualityInspectorWindow attribute), 138  
 output\_types (cmp.bidsappmanager.stages.connectome.connectome.ConnectomeConfig attribute), 145  
 output\_types (cmp.bidsappmanager.stages.connectome.fmri\_connectome.ConnectomeConfig attribute), 146  
 output\_types (cmp.stages.connectome.connectome.ConnectomeConfig attribute), 98  
 output\_types (cmp.stages.connectome.fmri\_connectome.ConnectomeConfig attribute), 99

## P

Parcellate, 230  
 ParcellateBrainstemStructures, 231  
 ParcellateHippocampalSubfields, 231  
 ParcellateThalamus, 232  
 parcellation (cmp.bidsappmanager.pipelines.anatomical.anatomical.AnatomicalPipeline attribute), 142  
 parcellation\_scheme (cmp.project.ProjectInfo attribute), 82  
 parcellation\_scheme (cmp.stages.parcellation.parcellation.ParcellationConfig attribute), 113  
 parcellation\_scheme\_editor (cmp.stages.parcellation.parcellation.ParcellationConfig attribute), 114  
 ParcellationConfig (class in cmp.stages.parcellation.parcellation), 113  
 ParcellationConfigUI (class in cmp.bidsappmanager.stages.parcellation.parcellation), 150  
 ParcellationStage (class in cmp.stages.parcellation.parcellation), 114  
 ParcellationStageUI (class in cmp.bidsappmanager.stages.parcellation.parcellation), 150  
 partial\_volume\_estimation (cmp.stages.preprocessing.preprocessing.PreprocessingConfig attribute), 117  
 Pipeline (class in cmp.pipelines.common), 87



method), 92

process() (cmp.pipelines.functional.eeg.EEGPipeline method), 95

process() (cmp.pipelines.functional.fMRI.fMRIPipeline method), 97

process\_type (cmp.pipelines.anatomical.anatomical.GlobalConfig attribute), 90

process\_type (cmp.pipelines.diffusion.diffusion.GlobalConfig attribute), 93

process\_type (cmp.pipelines.functional.eeg.GlobalConfig attribute), 95

process\_type (cmp.pipelines.functional.fMRI.GlobalConfig attribute), 95

processing\_tool\_editor (cmp.stages.diffusion.diffusion.DiffusionConfig attribute), 101

ProcessThread (class in cmp.pipelines.common), 87

ProgressThread (class in cmp.pipelines.common), 87

ProgressWindow (class in cmp.pipelines.common), 88

project\_info (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow attribute), 127

project\_info (cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow attribute), 131

project\_info (cmp.bidsappmanager.gui.principal.MainWindow attribute), 136

project\_info (cmp.bidsappmanager.gui.qc.QualityInspectorWindow attribute), 137

project\_loaded (cmp.bidsappmanager.gui.handlers.ConfigWindowHandler attribute), 133

project\_loaded (cmp.bidsappmanager.gui.handlers.MainWindowHandler attribute), 135

ProjectInfo (class in cmp.project), 81

ProjectInfoUI (class in cmp.bidsappmanager.project), 138

pw (cmp.pipelines.common.ProgressThread attribute), 87

**Q**

quality\_control (cmp.bidsappmanager.gui.principal.MainWindow attribute), 136

quality\_control\_ui (cmp.bidsappmanager.gui.principal.MainWindow attribute), 136

QualityInspectorWindow (class in cmp.bidsappmanager.gui.qc), 137

**R**

radial\_order (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 104

radial\_order\_values (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105

recon\_mode (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 104

recon\_mode (cmp.stages.diffusion.reconstruction.MRtrixReconConfig attribute), 106

recon\_processing\_tool (cmp.stages.diffusion.diffusion.DiffusionConfig attribute), 101

recon\_processing\_tool\_editor (cmp.stages.diffusion.diffusion.DiffusionConfig attribute), 101

refresh\_folder() (in module cmp.bidsappmanager.project), 141

refresh\_folder() (in module cmp.project), 85

registration (cmp.bidsappmanager.pipelines.diffusion.diffusion.DiffusionConfig attribute), 143

registration (cmp.bidsappmanager.pipelines.functional.fMRI.fMRIPipeline attribute), 144

registration\_mode (cmp.stages.registration.registration.RegistrationConfig attribute), 119

registration\_mode\_trait (cmp.stages.registration.registration.RegistrationConfig attribute), 119

RegistrationConfig (class in cmp.stages.registration.registration), 119

RegistrationConfigUI (class in cmp.bidsappmanager.stages.registration.registration), 152

RegistrationStage (class in cmp.stages.registration.registration), 122

RegistrationStageUI (class in cmp.bidsappmanager.stages.registration.registration), 122

QualityInspectorWindow (class in cmp.bidsappmanager.gui.qc), 137

RenameButton (cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingConfig attribute), 115

res (cmklib.bids.io.CustomBIDSFile attribute), 155

resampling (cmp.stages.preprocessing.preprocessing.PreprocessingConfig attribute), 117

return\_button\_style\_sheet() (in module cmklib.util), 237

RsfmriCmat, 217

run() (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow class method), 129

run() (cmp.pipelines.common.ProcessThread method), 87

run() (cmp.pipelines.common.ProgressThread method), 88

run\_anat\_pipeline (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow attribute), 128

run\_fmri\_pipeline (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow attribute), 128

run\_fmri\_pipeline (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow attribute), 128

run\_individual() (in module cmp.project), 85

**S**

save\_all\_config (cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow attribute), 131

save\_anat\_config\_file() (attribute), 105  
 (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler class method), 134  
 save\_configparser\_as\_json() (in module cmtklib.config), 215  
 save\_fmri\_config\_file() (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler class method), 134  
 save\_eeg\_connectome\_file() (in module cmtklib.eeg), 220  
 save\_fibers() (in module cmtklib.connectome), 219  
 save\_fmri\_config\_file() (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler class method), 134  
 Scrubbing, 227  
 SD (cmp.stages.diffusion.tracking.DipyTrackingConfig attribute), 106  
 SD (cmp.stages.diffusion.tracking.MRtrixTrackingConfig attribute), 107  
 seed\_density (cmp.stages.diffusion.tracking.DipyTrackingConfig attribute), 107  
 seed\_from\_gmwmi (cmp.stages.diffusion.tracking.DipyTrackingConfig attribute), 107  
 seed\_from\_gmwmi (cmp.stages.diffusion.tracking.MRtrixTrackingConfig attribute), 108  
 seg\_tool (cmp.stages.segmentation.segmentation.SegmentationConfig attribute), 123  
 segment\_brainstem (cmp.stages.parcellation.parcellation.ParcellationConfig attribute), 114  
 segment\_hippocampal\_subfields (cmp.stages.parcellation.parcellation.ParcellationConfig attribute), 114  
 segmentation (cmp.bidsappmanager.pipelines.anatomical\_stages.anatomical\_pipeline.Pipeline attribute), 142  
 SegmentationConfig (class in cmp.stages.segmentation.segmentation), 123  
 SegmentationConfigUI (class in cmp.bidsappmanager.stages.segmentation.segmentation), 153  
 SegmentationStage (class in cmp.stages.segmentation.segmentation), 125  
 SegmentationStageUI (class in cmp.bidsappmanager.stages.segmentation.segmentation), 154  
 select\_subject() (cmp.bidsappmanager.gui.qc.QualityInspector class method), 138  
 set\_pipeline\_attributes\_from\_config() (in module cmtklib.config), 215  
 sh\_order (cmp.stages.diffusion.tracking.DipyTrackingConfig attribute), 107  
 SHORE, 166  
 shore\_constrain\_e0 (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105  
 shore\_lambda\_n (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105  
 shore\_positive\_constraint (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105  
 shore\_radial\_order (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105  
 shore\_tau (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105  
 shore\_zeta\_tau (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105  
 show\_bidsapp\_window() (cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandler class method), 134  
 sift (cmp.stages.diffusion.tracking.MRtrixTrackingConfig attribute), 108  
 SIFT2, 206  
 single\_fib\_thr (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 104  
 single\_fib\_thr (cmp.stages.diffusion.reconstruction.MRtrixReconConfig attribute), 106  
 slice\_timing (cmp.stages.preprocessing.fmri\_preprocessing.PreprocessingConfig attribute), 115  
 small\_delta (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 105  
 ssh\_remote (cmp.bidsappmanager.project.ProjectInfoUI attribute), 138  
 SshUser (cmp.bidsappmanager.project.ProjectInfoUI attribute), 138  
 StageNames (cmp.bidsappmanager.project.ProjectInfoUI attribute), 138  
 stage\_names (cmp.pipelines.common.ProgressThread attribute), 88  
 stages (cmp.pipelines.common.ProgressThread attribute), 88  
 start\_bids\_app() (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterface class method), 130  
 start\_bids\_app() (cmp.bidsappmanager.gui.handlers.BIDSAppInterface class method), 132  
 start\_bidsapp (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow attribute), 129  
 start\_bidsapp\_participant\_level\_process() (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow method), 130  
 start\_bidsapp\_participant\_level\_process\_with\_datalad() (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow method), 130  
 start\_bidsapp\_process() (cmp.bidsappmanager.gui.handlers.BIDSAppInterfaceWindow class method), 132  
 step\_size (cmp.stages.diffusion.tracking.DipyTrackingConfig attribute), 107

stop\_bids\_app() (cmp.bidsappmanager.gui.handlers.BIDSAppInterfaceWindowHandler class method), 133  
 StreamlineTrack, 207  
 strip\_suffix() (in module cmp.stages.diffusion.diffusion), 103  
 subject (cmp.pipelines.anatomical.anatomical.GlobalConfig attribute), 90  
 subject (cmp.pipelines.common.Pipeline attribute), 87  
 subject (cmp.pipelines.diffusion.diffusion.GlobalConfig attribute), 93  
 subject (cmp.pipelines.functional.eeg.GlobalConfig attribute), 95  
 subject (cmp.project.ProjectInfo attribute), 81  
 subject (cmp.stages.connectome.connectome.ConnectomeConfig attribute), 98  
 subject (cmp.stages.connectome.fmri\_connectome.ConnectomeConfig attribute), 100  
 subject\_session (cmp.pipelines.anatomical.anatomical.GlobalConfig attribute), 90  
 subject\_session (cmp.pipelines.diffusion.diffusion.GlobalConfig attribute), 93  
 subject\_session (cmp.pipelines.functional.eeg.GlobalConfig attribute), 95  
 subject\_session (cmp.project.ProjectInfo attribute), 81  
 subject\_session\_view (cmp.bidsappmanager.project.ProjectInfoUI attribute), 139  
 subject\_sessions (cmp.project.ProjectInfo attribute), 81  
 subject\_view (cmp.bidsappmanager.project.ProjectInfoUI attribute), 139  
 subjects (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindowHandler attribute), 127  
 subjects (cmp.pipelines.anatomical.anatomical.GlobalConfig attribute), 90  
 subjects (cmp.pipelines.diffusion.diffusion.GlobalConfig attribute), 93  
 subjects (cmp.pipelines.functional.eeg.GlobalConfig attribute), 95  
 subjects (cmp.project.ProjectInfo attribute), 81  
 suffix (cmklib.bids.io.CustomBIDSFile attribute), 155  
 summary\_view\_button (cmp.bidsappmanager.project.ProjectInfoUI attribute), 139  
**T**  
 t1\_available (cmp.project.ProjectInfo attribute), 82  
 Tck2Trk, 222  
 Tensor2Vector, 209  
 TensorInformedEudXTractography, 167  
 Tkregister2, 170  
 toolbox\_derivatives\_dir (cmklib.bids.io.CustomBIDSFile attribute), 155  
 track\_carbon\_footprint (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindowHandler attribute), 116  
 tracking\_mode (cmp.stages.diffusion.tracking.DipyTrackingConfig attribute), 106  
 tracking\_mode (cmp.stages.diffusion.tracking.MRtrixTrackingConfig attribute), 107  
 tracking\_processing\_tool (cmp.stages.diffusion.diffusion.DiffusionConfig attribute), 101  
 tracking\_processing\_tool (cmp.stages.diffusion.reconstruction.DipyReconConfig attribute), 104  
 tracking\_processing\_tool\_editor (cmp.stages.diffusion.diffusion.DiffusionConfig attribute), 101  
 tracking\_tool (cmp.stages.preprocessing.preprocessing.PreprocessingConfig attribute), 118  
 tracking\_tool (cmp.stages.registration.registration.RegistrationConfig attribute), 121  
 traits\_view (cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindowHandler attribute), 129  
 traits\_view (cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow attribute), 132  
 traits\_view (cmp.bidsappmanager.gui.principal.MainWindow attribute), 137  
 traits\_view (cmp.bidsappmanager.gui.qc.QualityInspectorWindow attribute), 138  
 traits\_view (cmp.bidsappmanager.pipelines.anatomical.anatomical.AnatomicalConfig attribute), 142  
 traits\_view (cmp.bidsappmanager.pipelines.diffusion.diffusion.DiffusionConfig attribute), 143  
 traits\_view (cmp.bidsappmanager.pipelines.functional.fMRI.fMRIPipeline attribute), 144  
 traits\_view (cmp.bidsappmanager.project.ProjectInfoUI attribute), 139  
 traits\_view (cmp.bidsappmanager.stages.connectome.connectome.ConnectomeConfig attribute), 145  
 traits\_view (cmp.bidsappmanager.stages.connectome.fmri\_connectome.fMRIConnectomeConfig attribute), 146  
 traits\_view (cmp.bidsappmanager.stages.diffusion.diffusion.DiffusionConfig attribute), 147  
 traits\_view (cmp.bidsappmanager.stages.diffusion.reconstruction.DipyReconConfig attribute), 148  
 traits\_view (cmp.bidsappmanager.stages.diffusion.reconstruction.MRtrixReconConfig attribute), 148  
 traits\_view (cmp.bidsappmanager.stages.diffusion.tracking.Dipy\_tracking attribute), 149  
 traits\_view (cmp.bidsappmanager.stages.diffusion.tracking.MRtrix\_tracking attribute), 149  
 traits\_view (cmp.bidsappmanager.stages.functional.functionalMRI.FunctionalMRIConfig attribute), 149

traits\_view(*cmp.bidsappmanager.stages.parcellation.parcellation.ParcellationConfigUI*  
     *attribute*), 150      *update\_preprocessing\_act()*  
 traits\_view(*cmp.bidsappmanager.stages.preprocessing.fmri\_preprocessing.DiffusionConfigUI*, *DiffusionPipeline*  
     *attribute*), 151      *method*), 92  
 traits\_view(*cmp.bidsappmanager.stages.preprocessing.parcellation.ParcellationConfigUI*  
     *attribute*), 152      (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline*  
 traits\_view(*cmp.bidsappmanager.stages.registration.registration.RegistrationConfigUI*  
     *attribute*), 152      *update\_registration()*  
 traits\_view(*cmp.bidsappmanager.stages.segmentation.segmentation.SegmentationConfigUI*, *fMRI.fMRIPipeline*  
     *attribute*), 154      *method*), 97  
 U  
 UNDERLINE (*cmklib.util.BColors attribute*), 235  
 unicode2str() (in module *cmklib.util*), 237  
 update\_anat\_last\_processed() (in module *cmp.bidsappmanager.project*), 141  
 update\_anat\_last\_processed() (in module *cmp.project*), 86  
 update\_checksettings()  
     (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow*  
     *method*), 130  
 update\_diffusion\_imaging\_model()  
     (*cmp.bidsappmanager.gui.config.PipelineConfiguratorWindow*  
     *method*), 132  
 update\_diffusion\_imaging\_model()  
     (*cmp.bidsappmanager.gui.qc.QualityInspectorWindow*  
     *method*), 138  
 update\_dipy\_tracking\_SD()  
     (*cmp.stages.diffusion.diffusion.DiffusionConfig*  
     *method*), 102  
 update\_dipy\_tracking\_sh\_order()  
     (*cmp.stages.diffusion.diffusion.DiffusionConfig*  
     *method*), 102  
 update\_dmri\_last\_processed() (in module *cmp.bidsappmanager.project*), 141  
 update\_dmri\_last\_processed() (in module *cmp.project*), 86  
 update\_eeg\_last\_processed() (in module *cmp.project*), 86  
 update\_fmri\_last\_processed() (in module *cmp.bidsappmanager.project*), 141  
 update\_fmri\_last\_processed() (in module *cmp.project*), 86  
 update\_mrtrix\_tracking\_SD()  
     (*cmp.stages.diffusion.diffusion.DiffusionConfig*  
     *method*), 102  
 update\_nuisance\_requirements()  
     (*cmp.pipelines.functional.fMRI.fMRIPipeline*  
     *method*), 97  
 update\_outputs\_recon()  
     (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline*  
     *method*), 92  
 update\_outputs\_tracking()  
     (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline*  
     *method*), 97  
     (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow*  
     *method*), 130  
     (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow*  
     *method*), 130  
     (*cmp.bidsappmanager.gui.bidsapp.BIDSAppInterfaceWindow*  
     *method*), 130  
     (*cmp.pipelines.functional.fMRI.fMRIPipeline*  
     *method*), 97  
     (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandle*  
     *method*), 134  
     (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandle*  
     *method*), 134  
     (*cmp.bidsappmanager.gui.handlers.ConfigQualityWindowHandle*  
     *method*), 134  
     (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline*  
     *method*), 93  
     (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline*  
     *method*), 93  
     (*cmp.pipelines.diffusion.diffusion.DiffusionPipeline*  
     *method*), 93  
     UpdateGMWMInterfaceSeeding, 223  
     *use\_act* (*cmp.stages.diffusion.tracking.DipyTrackingConfig*  
         *attribute*), 107  
     *use\_act* (*cmp.stages.diffusion.tracking.MRtrixTrackingConfig*  
         *attribute*), 108  
     *use\_existing\_freesurfer\_data*  
         (*cmp.stages.segmentation.segmentation.SegmentationConfig*  
         *attribute*), 124  
     *use\_float\_precision*  
         (*cmp.stages.registration.registration.RegistrationConfig*  
         *attribute*), 119  
     *use\_fsl\_brain\_mask* (*cmp.stages.segmentation.segmentation.SegmentationConfig*  
         *attribute*), 124  
     *uses\_qform* (*cmp.stages.registration.registration.RegistrationConfig*  
         *attribute*), 121

## V

`view_mode(cmp.bidsappmanager.gui.principal.MainWindow  
attribute)`, [137](#)  
`view_mode(cmp.bidsappmanager.pipelines.anatomical.anatomical.AnatomicalPipelineUI  
attribute)`, [142](#)  
`view_mode(cmp.bidsappmanager.pipelines.diffusion.diffusion.DiffusionPipelineUI  
attribute)`, [143](#)  
`view_mode(cmp.bidsappmanager.pipelines.functional.fMRI.fMRIPipelineUI  
attribute)`, [144](#)

## W

`WARNING(cmtklib.util.BColors attribute)`, [235](#)  
`wm(cmp.stages.functional.functionalMRI.FunctionalMRIConfig  
attribute)`, [112](#)  
`write_derivative_description()` (in module `cmtk-  
lib.bids.utils`), [158](#)