

# Brain Connectivity Summer School, Quebec, 15-16 May 2017

## Welcome to NeuroPype

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# NeuroType

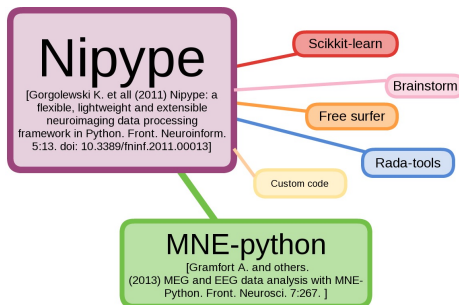
**NeuroType** is an **open-source** multi-modal brain data analysis kit which provides **Python-based pipelines** for advanced **multi-thread processing** of fMRI, MEG and EEG data, with a focus on **connectivity and graph analyses**.

NeuroType is based on **Nipype** framework, a tool developed in fMRI field, which facilitates data analyses by wrapping many commonly-used neuro-imaging software into a **common python framework**

# NeuroType packages

NeuroType includes three different packages:

- **neurotype\_ephy** includes pipelines for **electrophysiology data analysis**
- **neurotype\_graph** allows to study **functional connectivity** exploiting **graph-theoretical metrics** including also **modular partitions**
- **neurotype\_cli** is a command line interface for neurotype\_ephy package

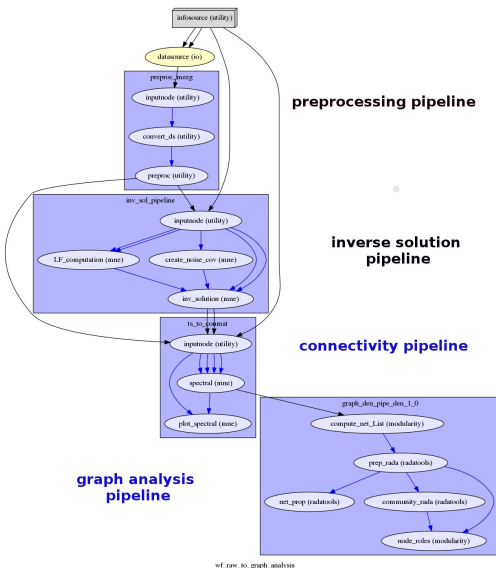


# NeuroPyne: from raw MEG/EEG to graph properties



- NeuroPyne provides a very common and fast framework to develop **workflows** for advanced data analyses
- Each **pipeline** could be used stand-alone or as **lego** of a bigger workflow
- Pipelines are defined by **nodes**
  - ▶ wrapping of existing software
  - ▶ wrapping of function defined by the user

# Workflow example



From MEG raw data to spectral connectivity and graph theoretical analysis in source space

# Nipype



frontiers  
in Neuroinformatics



< Articles

## ORIGINAL RESEARCH ARTICLE

Front. Neuroinform., 22 August 2011 | <https://doi.org/10.3389/fninf.2011.00013>

# Nipype: a flexible, lightweight and extensible neuroimaging data processing framework in Python

Krzysztof Gorgolewski<sup>1\*</sup>, Christopher D. Burns<sup>2</sup>, Cindee Madison<sup>3</sup>, Dav Clark<sup>3</sup>, Yaroslav O. Halchenko<sup>4</sup>, Michael L. Waskom<sup>5,6</sup> and Satrajit S. Ghosh<sup>7</sup>

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<sup>5</sup> Department of Brain and Cognitive Sciences, Massachusetts Institute of Technology, Cambridge, MA, USA

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Current neuroimaging software offer users an incredible opportunity to analyze their data in different ways, with different underlying assumptions. Several sophisticated software packages (e.g., AFNI, BrainVoyager, FSL, FreeSurfer, Nipy, R, SPM) are used to process and analyze large and often diverse (highly multi-dimensional) data. However, this heterogeneous collection of specialized applications creates several issues that hinder replicable, efficient, and optimal use of neuroimaging analysis approaches: (1) No uniform access to neuroimaging analysis software and usage information; (2)

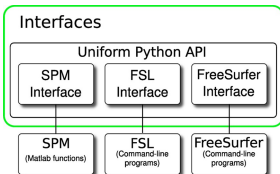
# Nipype

- The workflow design is based on the **Nipype framework**
- Nipype (Neuroimaging in Python: Pipelines and Interfaces) is an open-source, community developed, **Python based** software package that easily interfaces with existing software for efficient analysis of neuroimaging data and **rapid comparative development of algorithms**.
- Nipype provides **Interfaces** to existing neuroimaging software with uniform semantics and facilitates interactions between these packages using **Workflow**



## Nipype: Neuroimaging in Python Pipelines and Interfaces

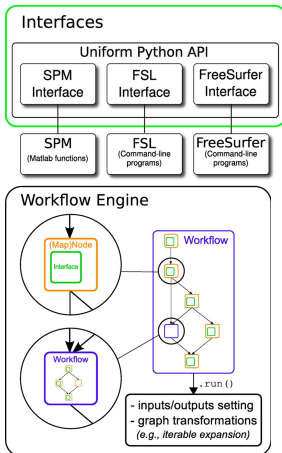
# Nipype: 3 main components



**Interfaces to external tools** that provide a unified way for setting inputs, executing and retrieving outputs



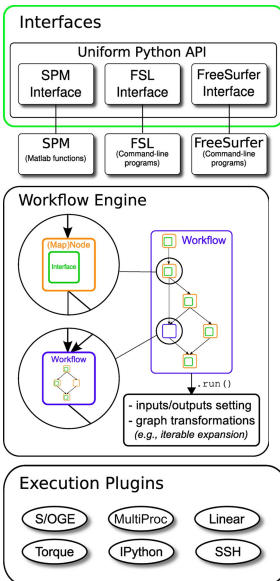
# Nipype: 3 main components



**Interfaces to external tools** that provide a unified way for setting inputs, executing and retrieving outputs

a **workflow engine** that allows **to create analysis pipelines** by connecting inputs and outputs of interfaces as a directed acyclic graph (DAG)

# Nipype: 3 main components

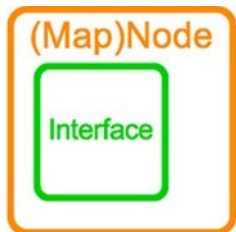


**Interfaces to external tools** that provide a unified way for setting inputs, executing and retrieving outputs

a **workflow engine** that allows **to create analysis pipelines** by connecting inputs and outputs of interfaces as a directed acyclic graph (DAG)

**plug-ins** that **execute workflows** either locally or in a distributed processing environment

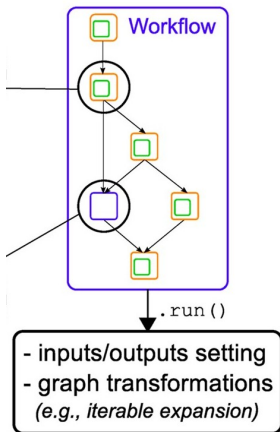
# Interfaces and Nodes



To be used in a Workflow the Interfaces are encapsulated in **Node objects**

- each Node is characterized by its unique name and has a least one input and one output
- the Nodes execute the underlying Interface in their own **uniquely named directories**
  - ▶ mechanism to isolate and track the outputs resulting from the Interface execution

# Workflow



Interfaces encapsulated into Nodes can be connected together within a **Workflow**

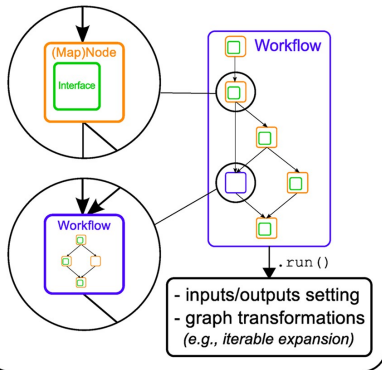
- by connecting the outputs of some Node to inputs of another one, the user implicitly specifies dependencies
- to run the Workflow one simply call its `.run()` method

The **workflow engine**

- validates that each Node has a unique name
- checks if all mandatory inputs are set
- checks if all dependencies are satisfied

# Workflow and Nodes

## Workflow Engine



- Node provides also a easy way to implement functions defined by the user
- **Workflow** themselves **can be a Node** of the Workflow graph

# Summary

## Main steps to **develop a workflow in nipype framework**

- create a **Workflow** object
- create **Nodes** object
- define the **connections** between the Nodes
- **run** the Workflow object!



# NeuroPyne Packages

## NeuroPyne online tutorial

neuropyne

Search docs

neuropyne\_ephy  
neuropyne\_cli  
neuropyne\_graph  
Examples  
CINQ

Docs » NeuroPyne documentation [View page source](#)

### NeuroPyne documentation

NeuroPyne is an open-source multi-modal brain data analysis kit which provides **Python-based pipelines** for advanced multi-thread processing of fMRI, MEG and EEG data, with a focus on connectivity and graph analyses. NeuroPyne is based on [Nipype](#), a tool developed in fMRI field, which facilitates data analyses by wrapping many commonly-used neuro-imaging software into a common python framework.

NeuroPyne project includes three different packages:

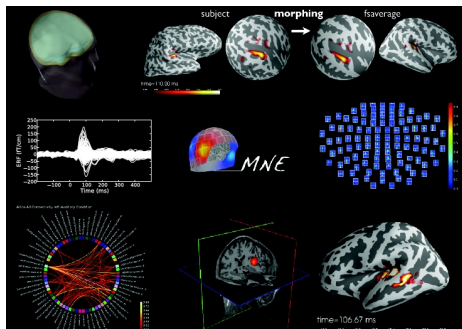
- [neuropyne\\_ephy](#) based on [MNE python](#) includes pipelines for electrophysiology analysis
- [neuropyne\\_cli](#) is a command line interface for neuropyne\_ephy package
- [neuropyne\\_graph](#) based on [radatools](#) includes pipelines for graph theoretical analysis of neuroimaging data

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# NeuroPype-ephy

**NeuroPype-ephy** is a package based on **MNE-python** software <http://martinos.org/mne/> and includes pipelines for **electrophysiology** data analysis. Current implementations allow for

- MEG/EEG data import
- MEG/EEG data pre-processing and cleaning by an automatic removal of eyes and heart related artefacts
- sensor or **source-level** connectivity analyses

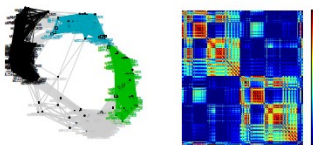
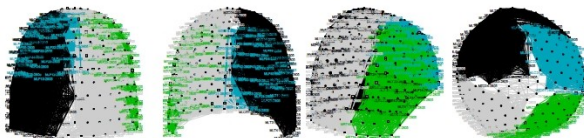




# NeuroPyne-graph

**NeuroPyne-graph** is a package based on **radatools** software <http://deim.urv.cat/~sergio.gomez/radatools.php> and includes pipelines for **graph theoretical analysis of neuroimaging data**. Current implementations allow to construct pipelines

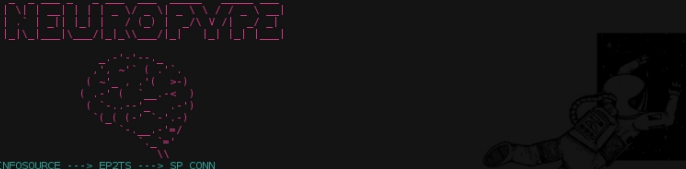
- from nifti 4D (after preprocessing) to connectivity matrices
- from connectivity matrices to graph analysis
- from integer matrices (normally cocompartmentation matrices) to graph analysis



# NeuroType-cli

## Command line interface for neurotype\_ephy

```
/media/dmalt/DATAS/motorprobe/data
> neurotype -p MultiProc -n 4 ep2ts conn -b 16 25 -m imcoh -m plv -s 1000 input ./*/*/CONTROL_RH/*.fif
```



**Key idea:** Use globbing to improve flexibility of the pipeline

- Flexible input
- Connect nodes on the go
- Same pattern for launching remotely
- Works on clusters
- **help** pages for each option and command

# NeuroType doors

Can I use NeuroType on



# NeuroType doors

Can I use NeuroType on

- raw MEG, EEG data?



# NeuroType doors

Can I use NeuroType on

- raw MEG, EEG data? **YES**



# NeuroType doors

Can I use NeuroType on



- raw MEG, EEG data? **YES**
- time series of data in sensor or source space?

# NeuroType doors

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- raw MEG, EEG data? **YES**
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# NeuroType doors

Can I use NeuroType on



- raw MEG, EEG data? **YES**
- time series of data in sensor or source space? **YES**
- connectivity matrices?



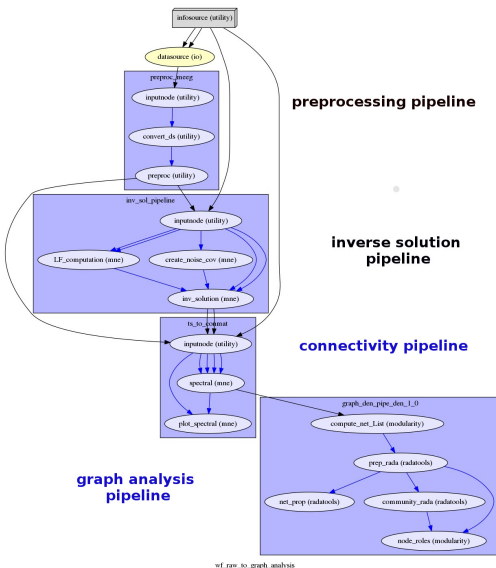
# NeuroType doors

Can I use NeuroType on



- raw MEG, EEG data? **YES**
- time series of data in sensor or source space? **YES**
- connectivity matrices? **YES**

# Workflow example

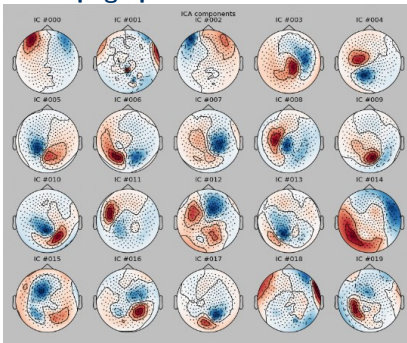


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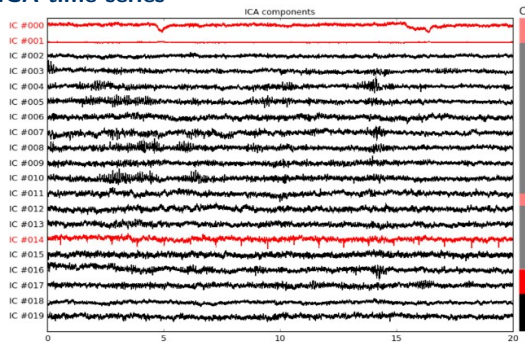
wf\_raw\_to\_graph\_analysis

# Visualization - preprocessing

## ICA topographies

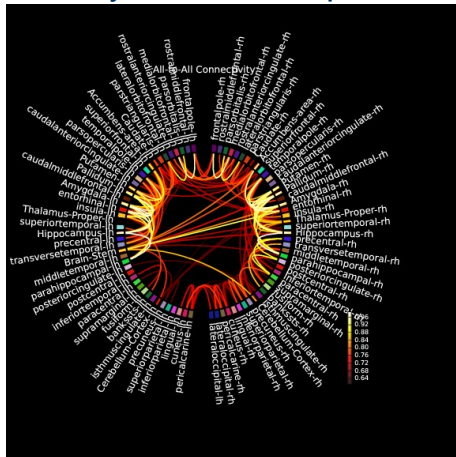


## ICA time series

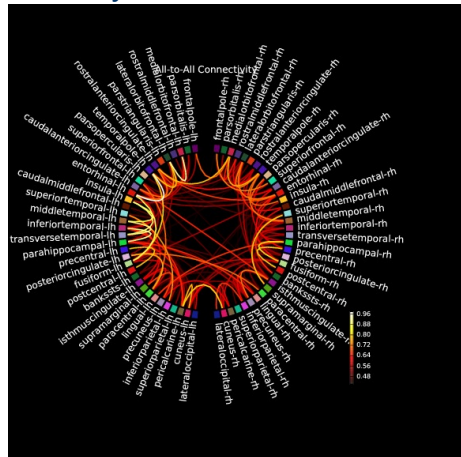


# Visualization - connectivity on source space

## connectivity on mixed source space



## connectivity on cortical surface



### graph - MEG data



# Advantages and strengths

- **Multi-threading**
- **Caching**
- Access to numerous **python-wrappers** for image analysis
- **Multimodal analyses**
- **open-source and free**



# NeuroPype Team and collaborators

Karim Jerbi



Dmitrii Altukhov



David Meunier



Annalisa Pascarella



## CoCo lab users and collaborators



# Reference

Bullmore E, Sporns O (2009) [Complex brain networks: graph theoretical analysis of structural and functional systems](#), Nat Rev Neurosci 10:186-198

Gorgolewski K, Burns CD, Madison C, Clark D, Halchenko YO, Waskom ML, Ghosh SS (2011) [Nipype: a flexible, lightweight and extensible neuroimaging data processing framework in Python](#), Front. Neuroinform. 5:13. doi:10.3389/fninf.2011.00013

Gramfort A, Luessi M, Larson E, Engemann D A, Strohmeier D, Brodbeck C, Parkkonen L and Hämäläinen M (2014), [MNE software for processing MEG and EEG data](#), Neuroimage, 86, 446-460

Gramfort A, Luessi M, Larson E, Engemann D A, Strohmeier D, Brodbeck C, Goj R, Jas M, Brooks T, Parkkonen L and Hämäläinen M (2013), [MEG and EEG data analysis with MNE-Python](#), Frontiers in Neuroscience