

# Macapype

An open multi-software framework for  
non-human primate anatomical MRI processing

**David Meunier, Bastien Cagna, Kep Kee Loh,**  
Régis Trapeau, Julien Sein, Sylvain Takerkart, Olivier Coulon,  
Pascal Belin

*Presentation RMN Centre IRM Cerimed,  
10/09/2020*



# History

## How it all started:

- starting from the local hackathon on monkey MRI processing
- different teams working with macaques were having different approach on PNH MRI processing

## A common framework:

- each approach may be optimal for different set of acquisitions
- how to compare them (bash scripts, matlab code, etc)?
  - > develop a common framework to share the knowledge
  - > make Marseille great again!

MACAPYPE



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# Outline

**Kepkee** will introduce the rationale of PNH MRI processing and the *PRIME-RE* initiative

**David** and **Bastien** will present *macapype*, a tool dedicated to build PNH MRI pipelines 3

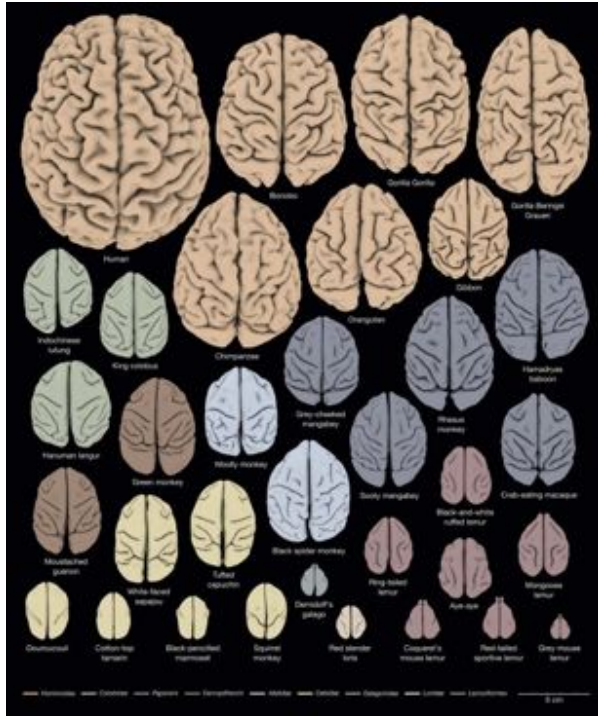
MACAPYPE



Kep Kee

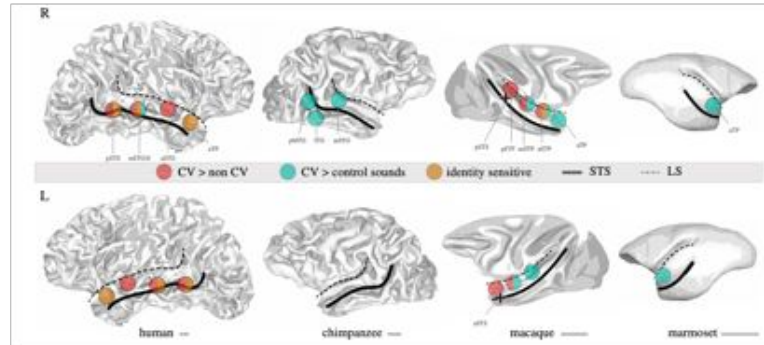
# Nonhuman Primate (NHP) /Comparative MRI

Using MRI to study NHP brains, and compare them with humans..



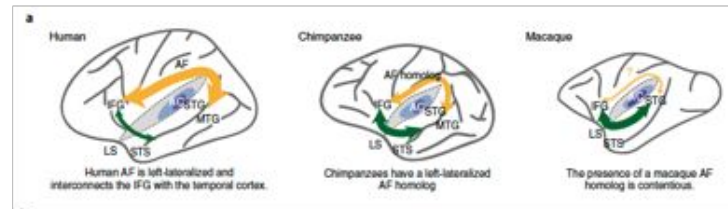
Heuer et al, 2019, Cortex

To understand the homologies...



Primate Voice Areas (Bodin et Belin, 2019)

To understand the specialisations...



Evolution of Frontal-Temporal connections (Balezeau et al, 2020)

# Nonhuman Primate (NHP) /Comparative MRI

Using MRI to study NHP brains, and compare them with humans..

## Key Advantages

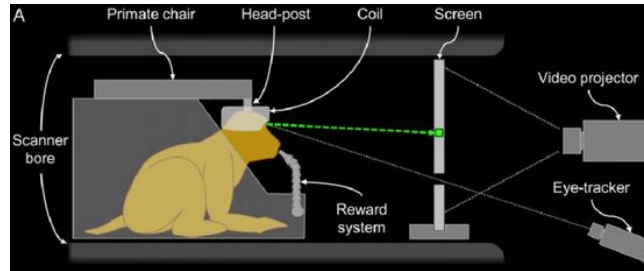
- *Less invasive...*
- Repeatability \*\*\*\*\*
- Equivalent measurements  
across individuals and  
species
- Multimodal - gives a  
complete picture of the  
brain.. (DTI, rs-fMRI,  
sMRI...)
- Digital – data-sharing,  
public databases, big data..

# Nonhuman Primate (NHP) /Comparative MRI

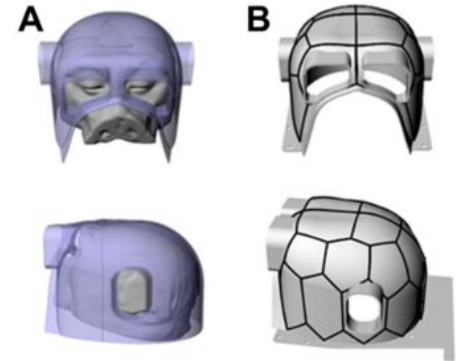
Using MRI to study NHP brains, and compare them with humans..

## Key Advantages

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- **Repeatable \*\*\*\*\***
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*Cottureau et al 2017*



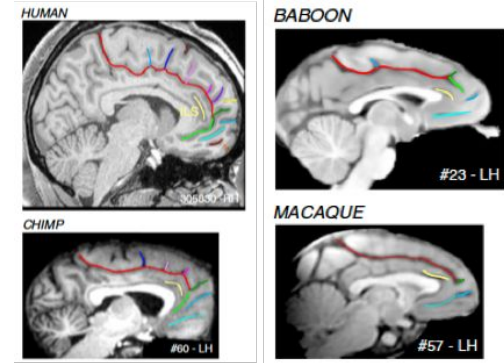
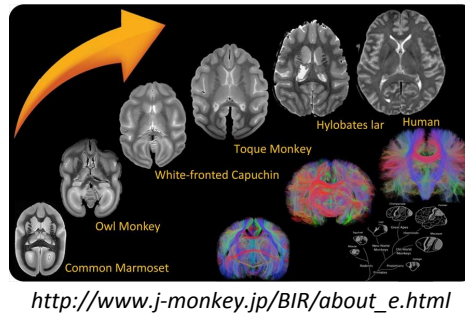
*Autio et al 2020*

# Nonhuman Primate (NHP) /Comparative MRI

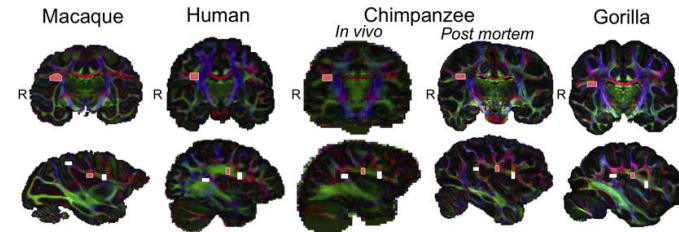
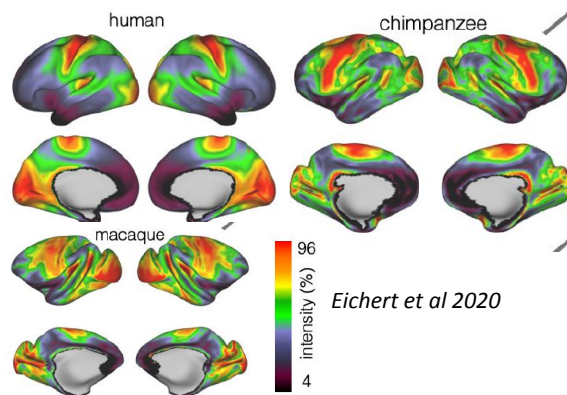
Using MRI to study NHP brains, and compare them with humans..

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- Repeatable \*\*\*\*\*
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- Multimodal - gives a complete picture of the brain.. (DTI, rs-fMRI, sMRI...)
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Amiez et al 2019



Roumazeilles et al 2020



# NHP MRI – An emergent and “open” field



[http://fcon\\_1000.projects.nitrc.org/indi/indiPRIME.html](http://fcon_1000.projects.nitrc.org/indi/indiPRIME.html)

## An Open Resource for Non-human Primate Imaging

Milham et al., 2018, *Neuron* 100, 61–74

October 10, 2018 © 2018 The Authors. Published by Elsevier Inc.

<https://doi.org/10.1016/j.neuron.2018.08.039>

## Accelerating the Evolution of Nonhuman Primate Neuroimaging

The PRIMatE Data Exchange (PRIME-DE) Global Collaboration Workshop and Consortium\*\*

\*Correspondence: [michael.milham@childmind.org](mailto:michael.milham@childmind.org) or [chris.petkov@ncl.ac.uk](mailto:chris.petkov@ncl.ac.uk)

<https://doi.org/10.1016/j.neuron.2019.12.023>

600 *Neuron* 105, February 19, 2020 © 2019 Elsevier Inc.

# NHP MRI – An emergent and “open” field



<https://prime-re.github.io/>

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Cold  
Spring  
Harbor  
Laboratory

bioRxiv

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### A collaborative resource platform for non-human primate neuroimaging

Adam Messinger, Nikoloz Sirmipilatze, Katja Heuer, Kep Kee Loh, Rogier B. Mars, Julien Sein, Ting Xu, Daniel Glen, Benjamin Jung, Jakob Seidlitz, Paul Taylor, Roberto Toro, Eduardo A. Garza-Villarreal, Caleb Sponheim, Xindi Wang, R. Austin Benn, Bastien Cagna, Rakshit Dadarwal, Henry C. Evrard, Pamela Garcia-Saldivar, Steven Giavasis, Renée Hartig, Claude Lepage, Cirong Liu, Piotr Majka, Hugo Merchant, Michael P. Milham, Marcello G.P. Rosa, Jordy Tasserie, Lynn Uhrig, Daniel S. Margulies, P. Christiaan Klink

doi: <https://doi.org/10.1101/2020.07.31.230185>

Neuroimage, *under review*

# NHP MRI – An emergent and “open” field



Comparative MRI  
Consortium  
(no logo yet...)

<https://prime-re.github.io/>

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<sup>\*</sup>Correspondence: [michael.milham@childmind.org](mailto:michael.milham@childmind.org) or [chris.petkov@ncl.ac.uk](mailto:chris.petkov@ncl.ac.uk)

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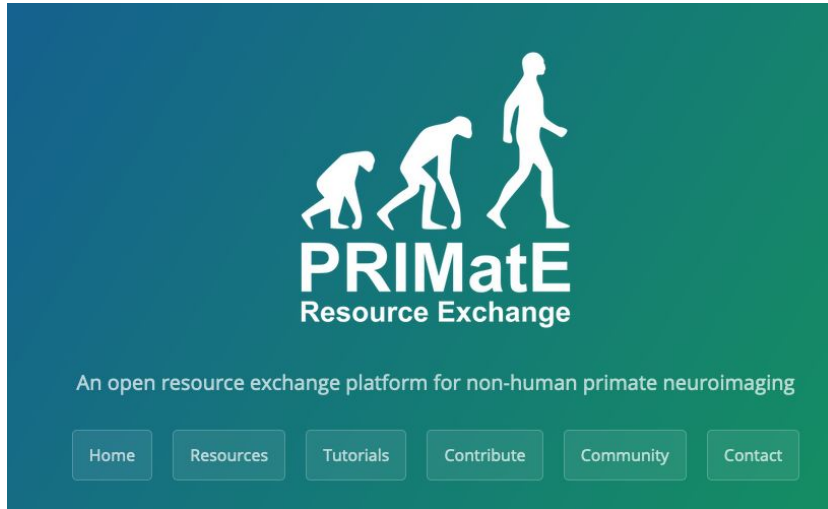
Neuroimage, *under review*

## Imaging the primate brain evolution: the next frontier?

Patrick Friedrich<sup>1,2</sup>, Stephanie J. Forkell<sup>1-3</sup>, Céline Amiez<sup>15</sup>, Joshua H. Balsters<sup>9</sup>, Olivier Coulon<sup>16-17</sup>, Lingzhong Fan<sup>19-20</sup>, Alexandros Goulas<sup>13</sup>, Fadila Hadj-Bouziane<sup>22</sup>, Erin E. Hecht<sup>14</sup>, Katja Heuer<sup>23,24</sup>, Tianzi Jiang<sup>19-21</sup>, Robert D. Latzman<sup>10</sup>, Xiaojin Liu<sup>4-5</sup>, Kep Kee Loh<sup>16-17</sup>, Kaustubh R. Patil<sup>4-5</sup>, Alizée Lopez-Persem<sup>6, 18</sup>, Emmanuel Procyk<sup>15</sup>, Jerome Sallet<sup>15,18</sup>, Roberto Toro<sup>23,25</sup>, Sam Vickery<sup>4-5</sup>, Susanne Weis<sup>4-5</sup>, Charlie Wilson<sup>15</sup>, Ting Xu<sup>1</sup>, Valerio Zerbi<sup>12</sup>, Simon B. Eickhoff<sup>4-5\*</sup>, Daniel Margulies<sup>1,6\*</sup>, Rogier B. Mars<sup>7,8\*</sup>, Michel Thiebaut de Schotten<sup>1,2\*</sup>

Neuroimage, *under review*

# Getting started on NHP MRI (processing)!



<https://prime-re.github.io/>



## A Primer on NHP-MRI

### PRIME-RE wiki for the Perplexed and Frustrated...

Initial contributions: Kep Kee Loh, Julien Sein, Ting Xu, & Rogier Mars  
Further contributions: Chris Klink

This is **not** meant as a definitive guide. We welcome the community to keep complementing, improving, and correcting this wiki. However, we have chosen to not make the wiki completely open to the public. You can request writing access of submit an update proposal by filing [an issue](#)

Together, we can make this the information you wish you had when you started out with NHP-MRI.

<https://github.com/PRIME-RE/prime-re.github.io/wiki>

Pages 9

[Back to PRIME-RE](#)

### Wiki

[Wiki start page](#)

- [A. Why the interest in NHP neuroimaging?](#)
- [B. What makes NHP MRI challenging?](#)
- [C. Typical data analysis challenges](#)
- [D. Structural data processing steps and PRIME-RE tools](#)
- [E. Functional data processing steps and PRIME-RE tools](#)
- [F. Diffusion data processing steps and PRIME-RE tools](#)
- [G. Cross-species comparisons and PRIME-RE tools](#)

Clone this wiki locally

<https://github.com/PRIME-RE/prime-re.github.io/wiki>

# NHP MRI processing – *same same, but different..*

Typical human anatomical pipeline

Dicom2nii

Reorientation/denoising/  
bias-correction

Skull-stripping

Tissue Segmentation

Normalise to standard  
space (MNI)

Registration with  
functional/DTI

# NHP MRI processing – *same same, but different.*



Typical human anatomical pipeline

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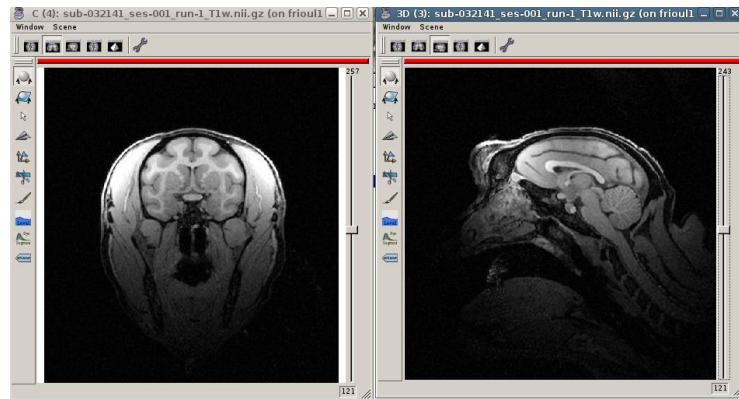
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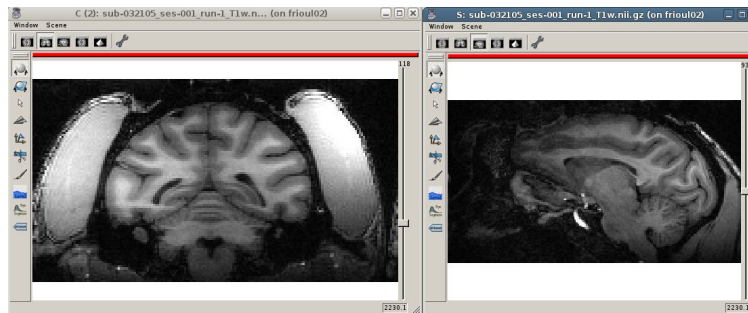
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*pretty-good* T1  
(uc davis dataset)



*quite-good* T1  
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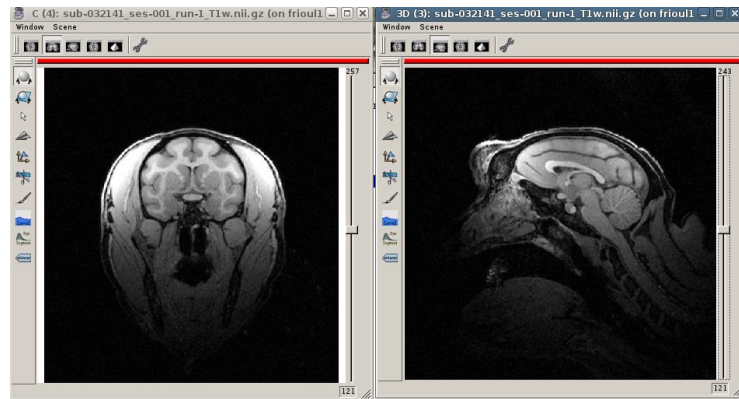
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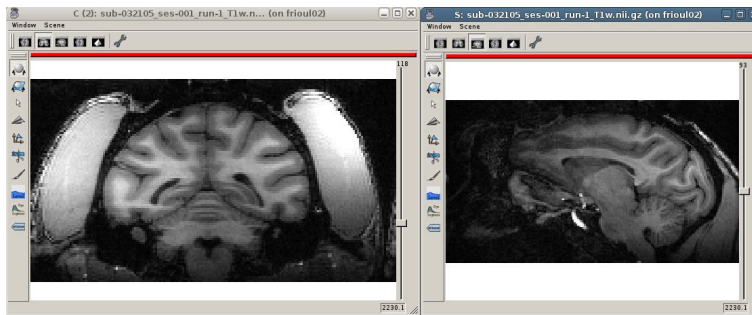
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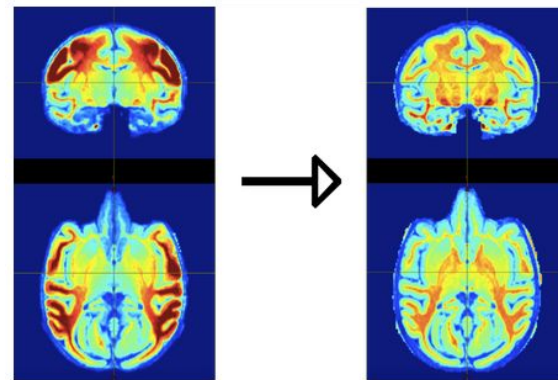
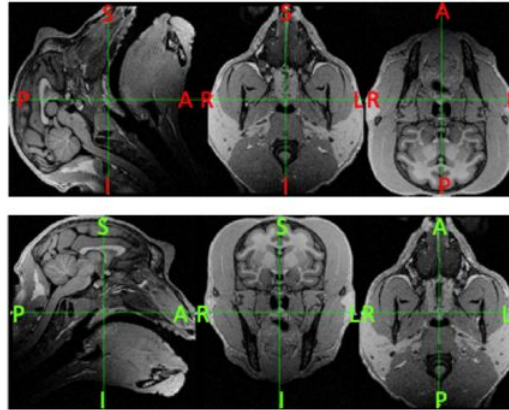
*pretty-good* T1  
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*quite-good* T1  
(newcastle dataset)

# NHP MRI data processing – *Key challenges...*

1. *Non-classic orientations*
2. *Non-head/brain parts*
3. *Bias-correction*
4. *Denoising*
5. *Registration*
6. *Segmentation*





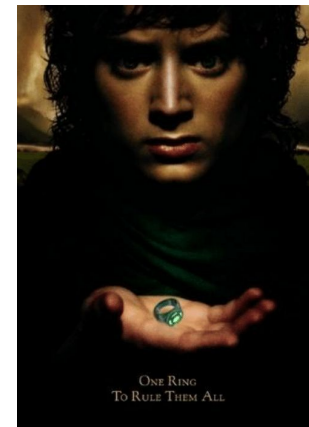
# NHP MRI data processing – *Solutions*

1. Data Preparation	
Reorientation	FSL: <code>fslreorient2std, fslswapdim + fslreorient</code> Freesurfer: <code>mri_convert -sphinx, mri_convert --in_orientation</code> <a href="#">Jip analysis toolkit</a> <a href="#">Web-based Reorient Tool</a>
Deoblique	AFNI: <code>3drefit -deoblique</code> (for changing header information)
Cropping	FSL: <code>fslroi, FSLeyes</code> AFNI: <code>@clip_volume</code> FreeSurfer: <code>mri_convert --slice-crop</code>
Denoising	Adaptive non-local means filter denoising in ANTs ( <code>ImageDenoise</code> ), SPM or <a href="#">Matlab package</a>
Averaging multiple images	Linear Registration tools: FSL-FLIRT, AFNI-3dVolReg, <code>3dAllineate</code> , SPM Register, etc. Image averaging: <code>fslnmats</code> , SPM <code>Imcalc</code> , etc.

2. Bias-Correction	
T1xT2 bias field correction (HCP Method)	Can be implemented using standard image calculation software such as <code>fslnmats</code> based on procedures described in Rilling et al. (2011) A module for this bias-correction is also available in Macapype ( <code>correct_bias.py</code> ).
<code>N3, N4BiasFieldCorrection</code>	Available in ANTs, MINC, Freesurfer packages. One could also consider <code>N3biascorrection</code> which works better in some cases.
FSL-Fast	FSL
CMTK-mrbias	<a href="#">Find it here</a>
3. Brain Extraction	
Template-based	AntsBrainExtraction (ANTs), <a href="#">Atlasbrex</a>
Non Template-based	FSL-BET (can also be used with a template), <a href="#">bet_macaque.sh</a>
Deep Learning Model	<a href="#">U-NET</a>
Manual corrections	ITK-SNAP, Slicer, <a href="#">BrainBox</a>

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4. Brain Segmentation	
Template-based	AntsAtroposN4 script, Atropos (ANTs), SPM Segment
Non Template-based	FSL-Fast (can be used with templates)
Manual segmentations/corrections	ITK-SNAP, BrainBox
5. Templates and Atlases	
	<a href="#">See PRIME-RE</a>

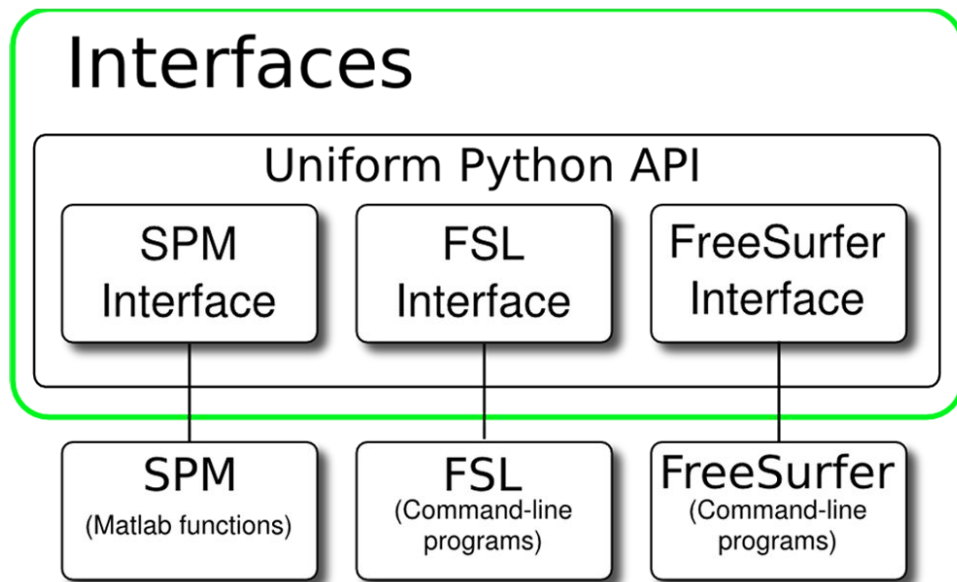
- ***Involves a “mix-n-match” of available neuroimaging tools and codes.***
- ***Need to adapt to various acquisitions.***
- ***No one single pipeline to rule them all..***



David

# What is macatype?

## Nipype-based framework:



Nipype wraps the most used softwares in Neuroimaging

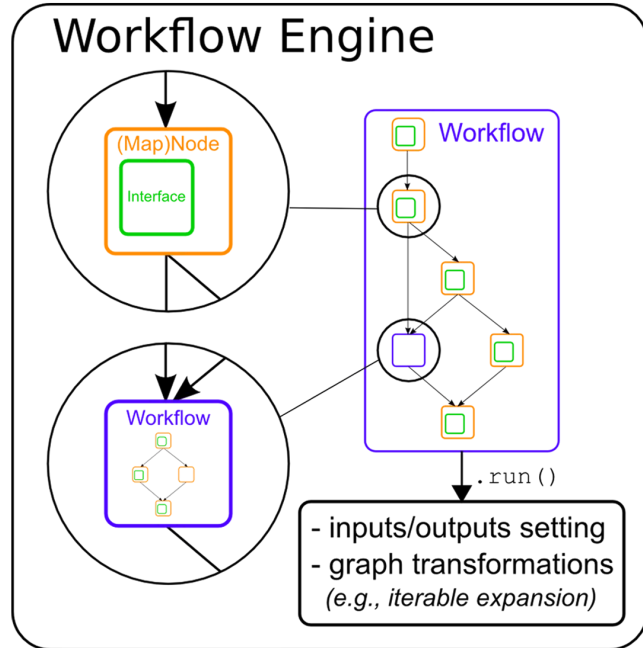
i.e. FSL/SPM/AFNI/ANTS

(Quick self ad):  
*neuropython* for EEG/MEG (ephypype)  
and functional connectivity / graph  
analysis (graphpype)

# What is macapype?

## Nipype-based framework:

- Notion of pipeline/nodes: design of sequences that can be easily re-used, or re-combined



Based on the notion of workflow

A workflow is a sequence of nodes  
Each node is a step in the full processing

it can call another program (interface/  
wrapper) or be written by the user (in python)

A node in the workflow can be a workflow itself  
(by convention, called a pipeline)

# Functionalities

## Wraps of specific NHP tools

- AtlasBREGX:
  - a specific tool for brain extraction,
  - multiple fine-grain parameters for contrast differences

# Functionalities

## Wraps of specific NHP tools

- AtlasBREX:
  - a specific tool for brain extraction,
  - multiple fine-grain parameters for contrast differences
- NMTSubjectAlign:
  - Advanced tools for normalisation to NMT template
  - also works for normalisation to other templates

# Functionalities

## Wraps of specific NHP tools

- AtroposN4: Ants based tools for segmentation

# Functionalities

## Wraps of specific NHP tools

- AtroposN4: Ants based tools for segmentation
- Shell-based tools by Regis Trapeau:
  - IterREG, T1xT2BiasCorrection, T1xT2BET, etc.)



# General scheme of the pipelines

## Split in 3 big categories

- Data preparation
- Brain extraction
- Segmentation

## 2 types of input data

- T1/T2 available
- T1 only (~ work in progress ?)

# General scheme of the pipelines

- Data preparation
  - short (using the T1xT2BET by Regis),
  - long single (average same modality images, then crop and N4debias)
  - long multi (crop and N4debias before average same modality images)

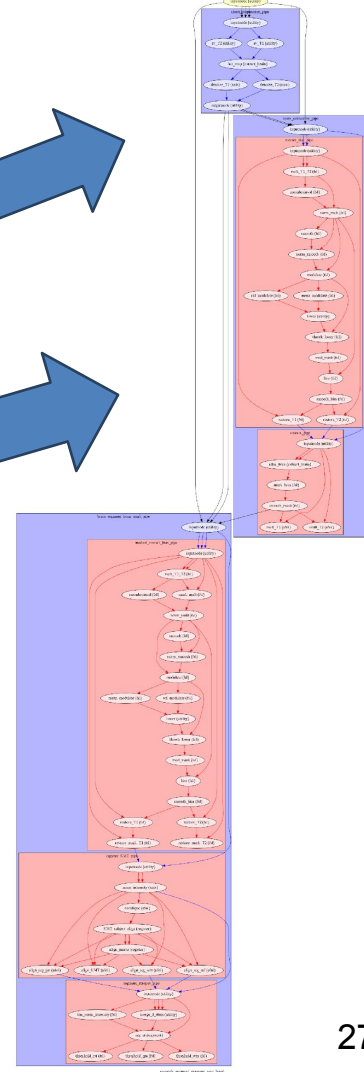
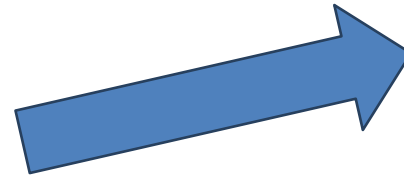
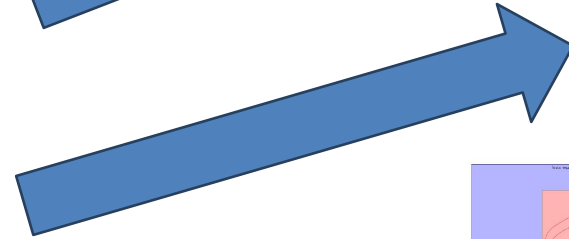
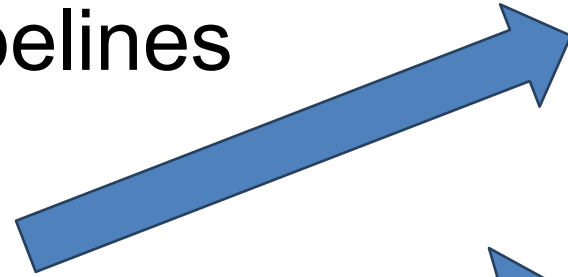
# Wrapped pipelines

Pipeline by Kepkee: ANTS-based T1\*T2

data preparation

brain extraction

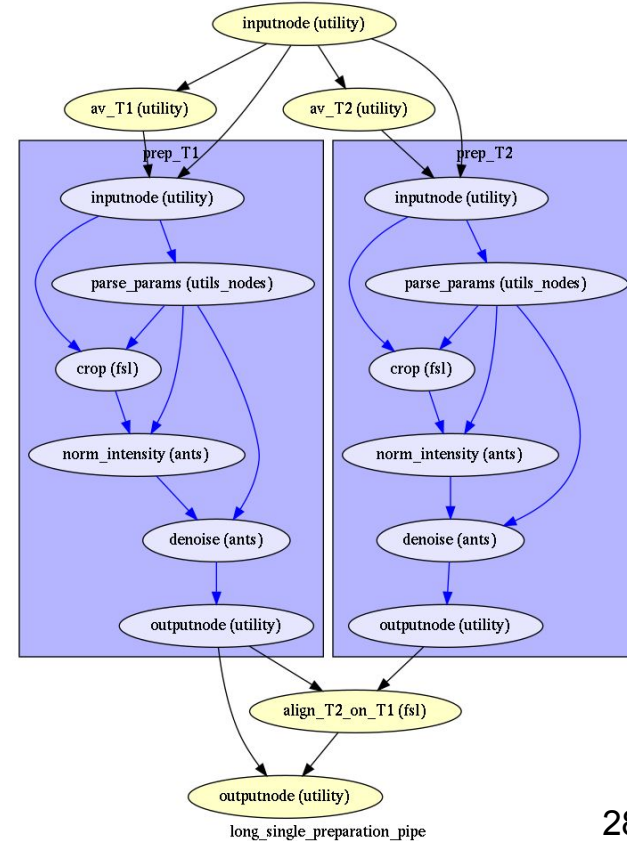
brain segmentation



# Wrapped pipelines

## Pipeline by Kepkee: ANTS-based T1\*T2

- data preparation (long single)
  - average same modality images,
  - crop
  - N4debias
  - denoise
  - then align T2 on T1



# Wrapped pipelines

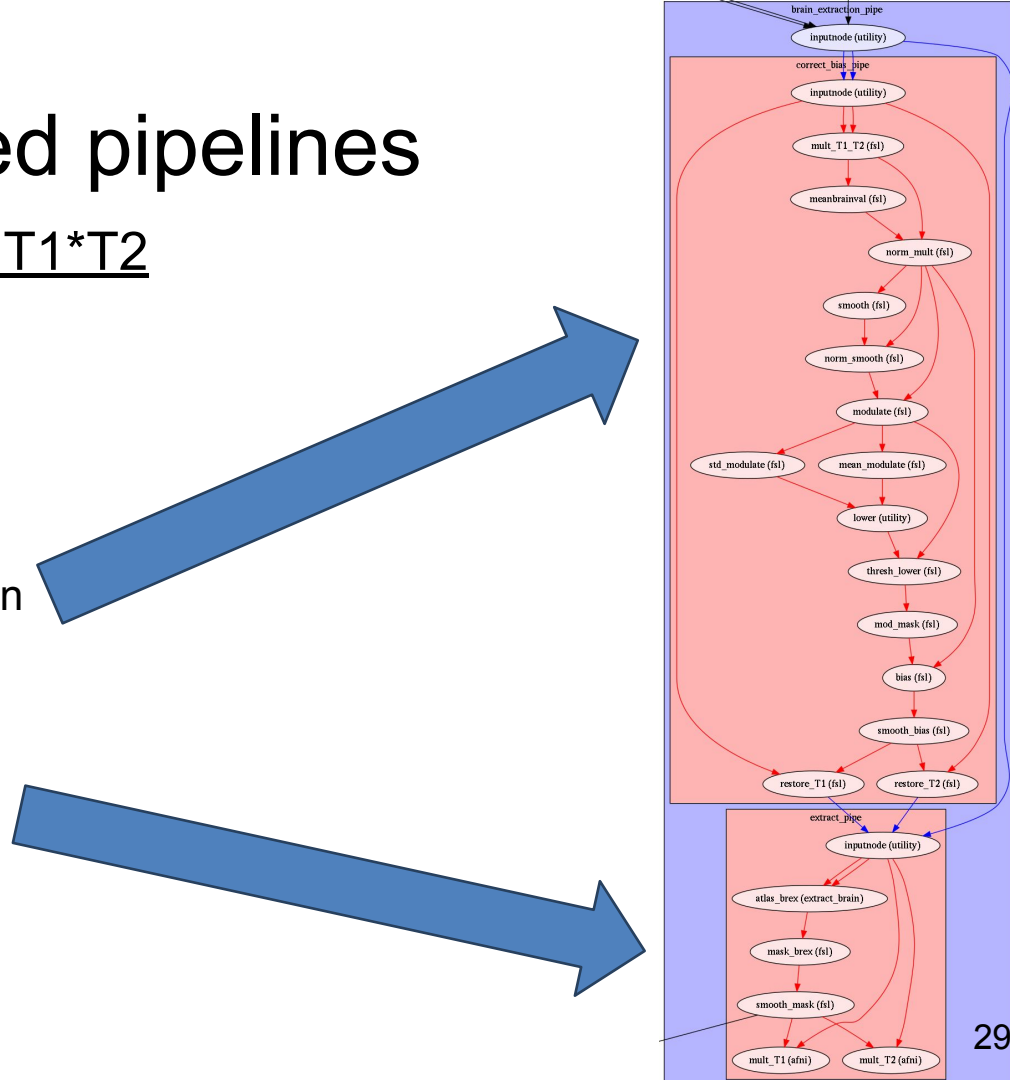
## Pipeline by Kepkee: ANTS-based T1\*T2

Brain extraction:

**! Local know-how !**

first T1\*T2BiasCorrection  
(sub-pipeline)

AtlasBRES



# Wrapped pipelines

## Pipeline by Kepkee: ANTS-based T1\*T2

- Brain segmentation

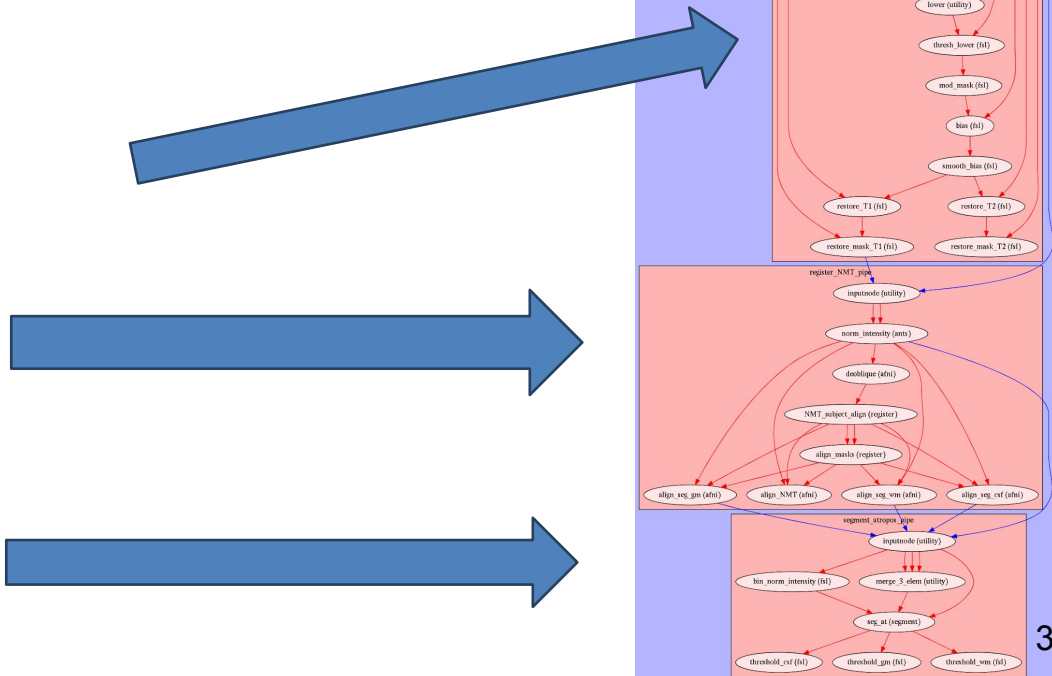
! Local know-how !

T1\*T2 bias correction  
on masked T1 (i.e. brain only)

! Local know-how !

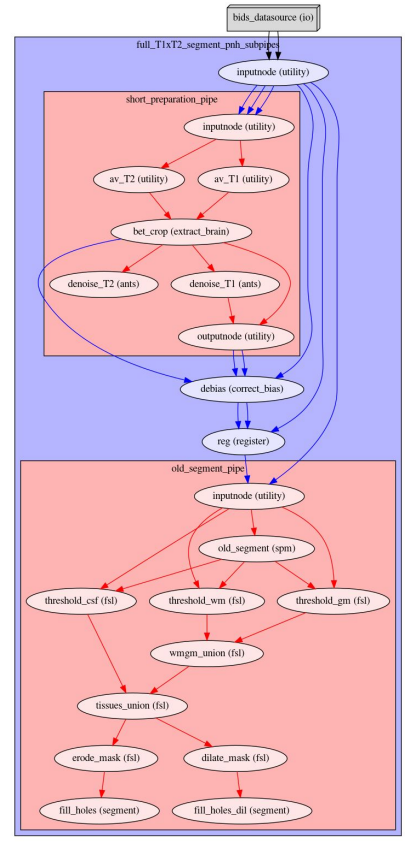
Normalisation of the NMT  
template to native space

AtroposN4 (ANTS)



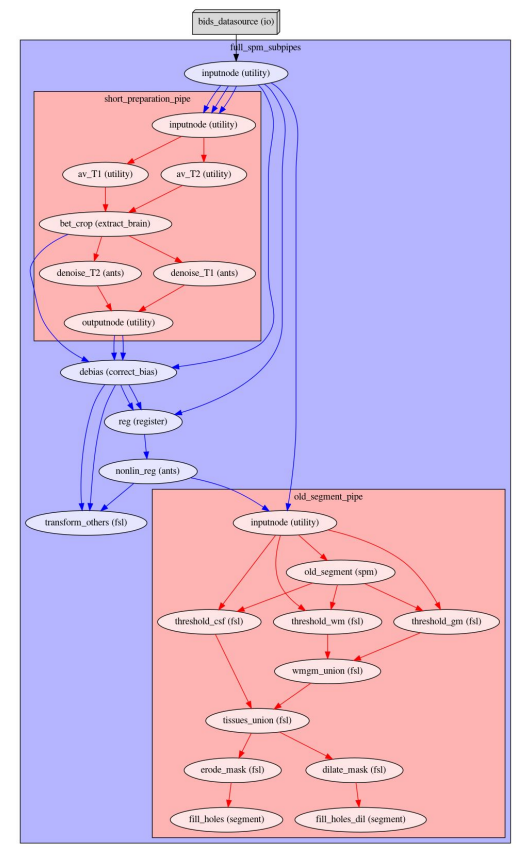
# Bastien

## T1w + T2w



test\_pipeline\_single\_spm

## Only T1w



test\_pipeline\_single\_spm\_1



# How to use Macapype ?

- Anaconda cloud

```
conda install -c macatools macapype
```

- PIP

```
pip install macapype
```

- Github (source code)

```
git clone https://github.com/Macatools/macapype.git
cd macapype
python setup.py install
```

macatools / packages / macapype 0.1.1

Pipeline for anatomic processing for macaque

Conda Files Labels Badges

- License: BSD 3
- Home: The package home page
- Documentation: <https://macatools.github.io/macapype/>
- 3 total downloads
- Last upload: 13 days and 20 hours ago

Installers

conda install

To install this package with conda run:

```
conda install -c macatools macapype
```



Go to file Add file Code

Clone with HTTPS Use SSH

Use Git or checkout with SVN using the web URL.

<https://github.com/Macatools/macapype>

Download ZIP

About

PNH segmentation pipelines based on nlype

[macatools.github.io/macapype/](https://macatools.github.io/macapype/)

python nlype mri-segmentation

primate afni ants spm12 fsl

mri mri-analysis brain-extraction

brain-segmentation

Readme

Ready to use workflow:

```
python segment_pnh.py -data /path/to/my/bids/data -out /path/to/output/directory  
-soft SPM_t1 -params params_segment_macaque_spm_based.json -subjects Elouk Apache  
-acq 0p4mm -indiv_params indiv_params_segment_macaque_spm_based.json
```

BIDS directory

Output directory

Pipeline to use  
(SPM, SPM\_T1 or ANTS)

JSON parameters  
file (opt.)

JSON file for individual  
parameters (opt.)

Subjects names

Acquisition name (opt.)

Ready to use workflow:

```
python segment_pnh.py -data /path/to/my/bids/data -out /path/to/output/directory  
-soft SPM_t1 -params params_segment_macaque_spm_based.json -subjects Elouk Apache -acq  
Op4mm -indiv_params indiv_params_segment_macaque_spm_based.json
```

```
1 {  
2   "general":  
3   {  
4     "template_name": "inial19"  
5   },  
6   "short_preparation_pipe":  
7   {  
8     "bet_crop":  
9     {  
10      "m": true,  
11      "aT2": true,  
12      "c": 10,  
13      "n": 2  
14    }  
15  },  
16  "debias":  
17  {  
18    "s": 4  
19  },  
20  "reg":  
21  {  
22    "n": 2,  
23    "m": "ref",  
24    "dof": 12  
25  },  
26  "..."
```

```
1 {  
2   "sub-Apache":  
3   {  
4     "ses-01":  
5     {  
6       "threshold_gm":  
7       {  
8         "thresh": 0.05  
9       },  
10      "threshold_wm":  
11      {  
12        "thresh": 0.05  
13      },  
14      "threshold_csf":  
15      {  
16        "thresh": 0.05  
17      }  
18    }  
19  }  
20 }
```

New python script:

```
1 #!/usr/bin/env python3
2
3 from macapype.nodes.correct_bias import T1xT2BiasFieldCorrection
4
5
6 correction = T1xT2BiasFieldCorrection()
7 correction.inputs.t1 = "/path/to/the/T1w.nii"
8 correction.inputs.t2 = "/path/to/the/T2w.nii"
9 correction.run()
10
```

New nipype workflow:

```
8
9 # Init a new workflow
10 wf = pe.Workflow(name="Preprocessing_workflow")
11 wf.base_dir = process_path
12
13 # List matching file from the BIDS directory
14 datasource = create_datasource(
15     data_path, task, subjects, sessions, acquisitions)
16
17 # **** Preprocessing part ****
18 correct_bias = pe.Node(T1xT2BiasFieldCorrection(), name="bias_correction")
19 wf.connect(datasource, 'T1', correct_bias, 't1')
20 wf.connect(datasource, 'T2', correct_bias, 't2')
21
22 wf.config['execution'] = {'remove_unnecessary_outputs': 'false'}
23 wf.write_graph(graph2use="colored")
24
25 # Run the pipeline
26 wf.run()
27
```

Idiosyncratic, Heterogeneous APIs

## Execution Plugins

S/OGE

MultiProc

Linear

Torque

IPython

SSH

### Several running strategies:

- Simple processing
- Multicores processing
- Others parallel processing

```
wf.run()
```

```
wf.run(plugin='MultiProc', plugin_args={'n_procs' : 8})
```

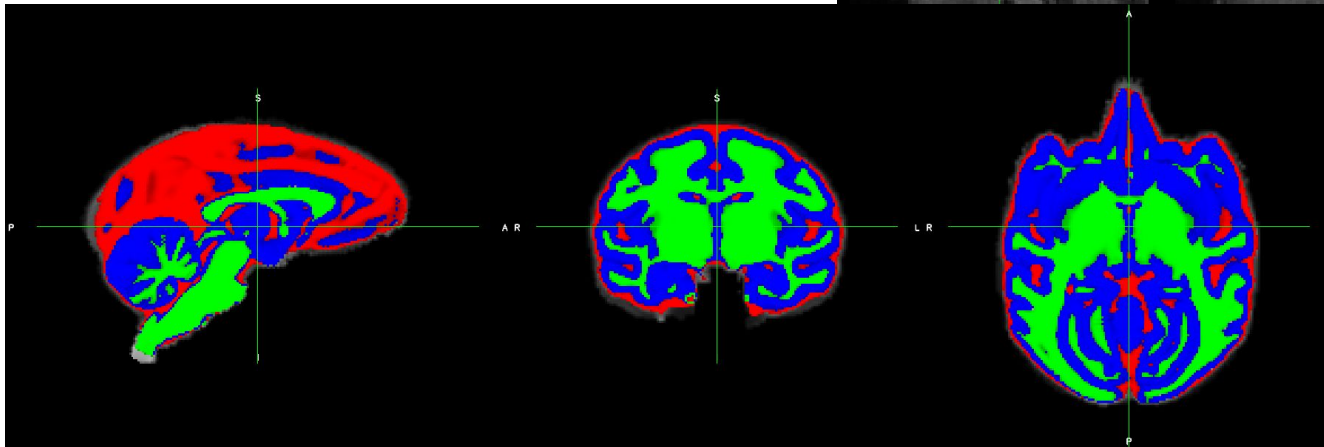
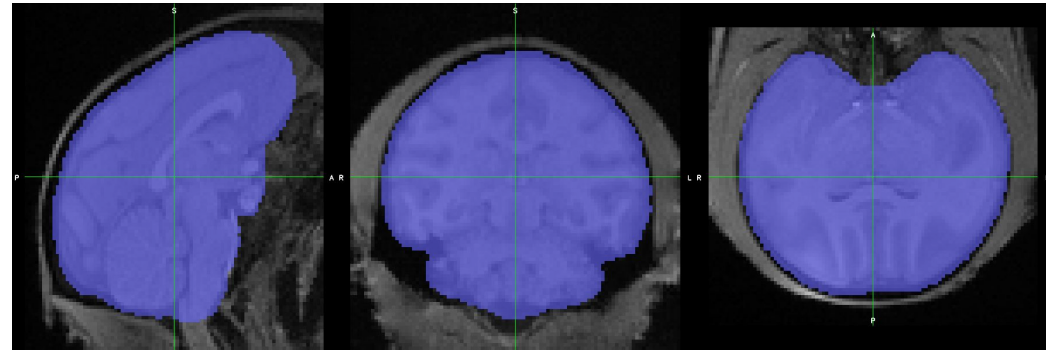
```
wf.run(plugin='SGE', plugin_args=dict(qsub_args='-q long -l sps=1'))
```

### Caching:

Re-run the pipeline = starting where it has stopped

Earlier tests on macaque:

- iterative FLIRT/FNIRT
- OldSegment SPM

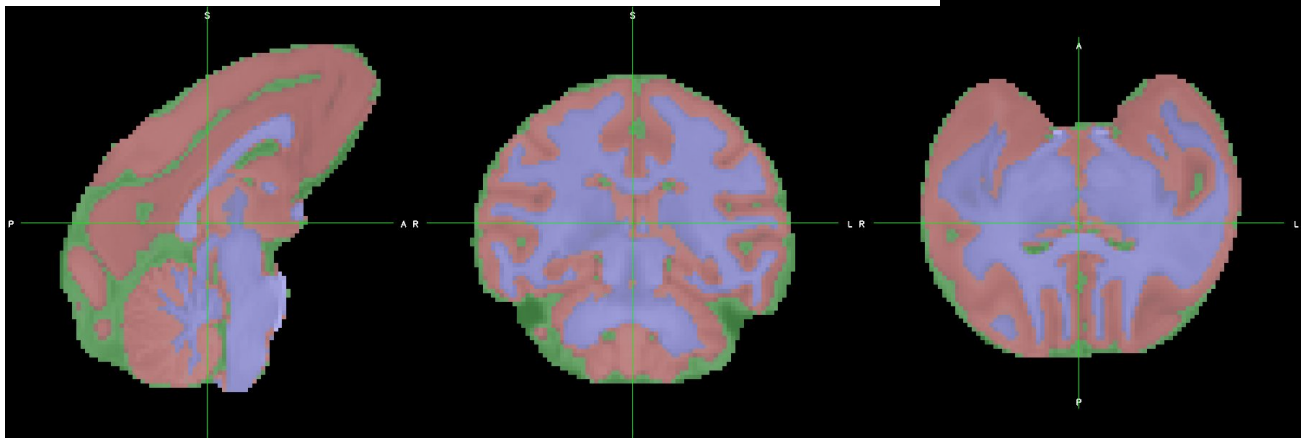
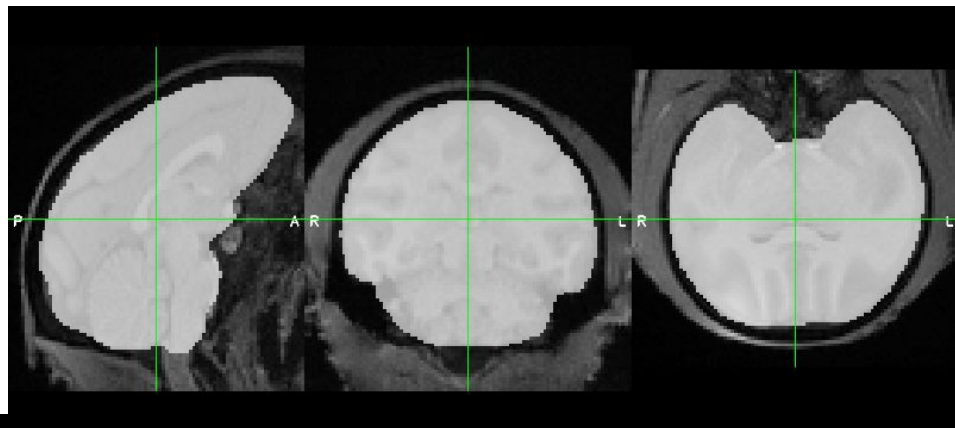


Data courtesy of Regis Trapeau/Pascal Belin. For more information, see

[https://macatools.github.io/macapy/auto\\_examples/plot\\_segment\\_macaque\\_spm\\_based.html](https://macatools.github.io/macapy/auto_examples/plot_segment_macaque_spm_based.html)

Macaque (same dataset):

- atlasbrex
- ANTS atropos

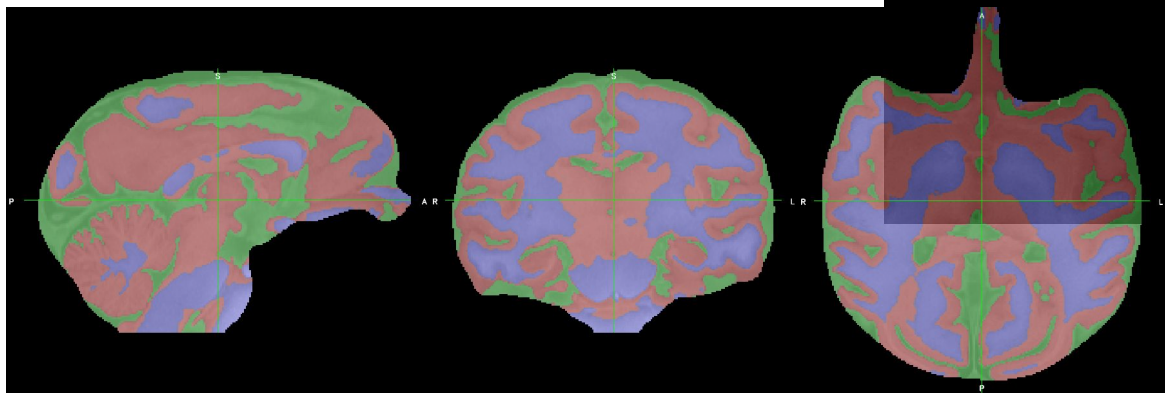
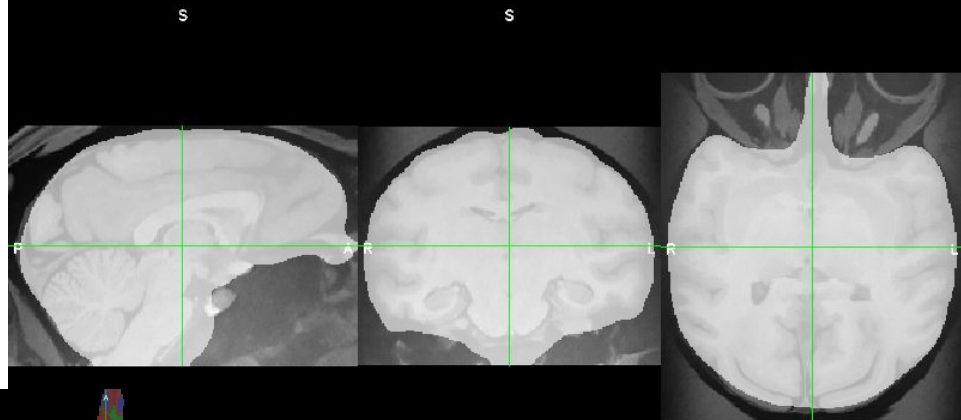


Data courtesy of Regis Trapeau/Pascal Belin. For more information, see

[https://macatools.github.io/macapype/auto\\_examples/plot\\_segment\\_macaque\\_ants\\_based.html](https://macatools.github.io/macapype/auto_examples/plot_segment_macaque_ants_based.html)

infant baboon (same dataset):

- atlasbrex (using adult template)
- ANTS atropos

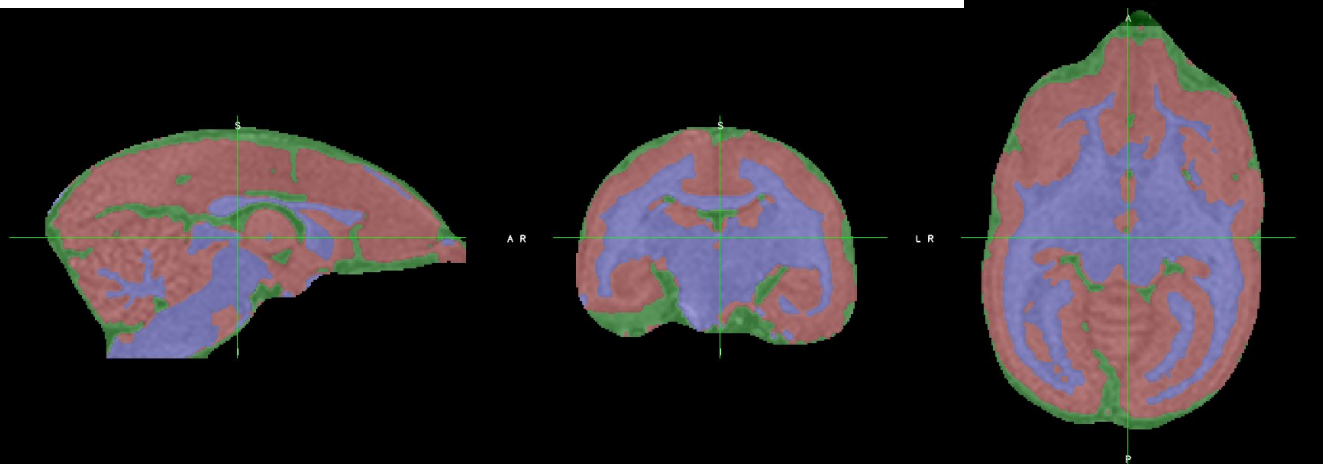
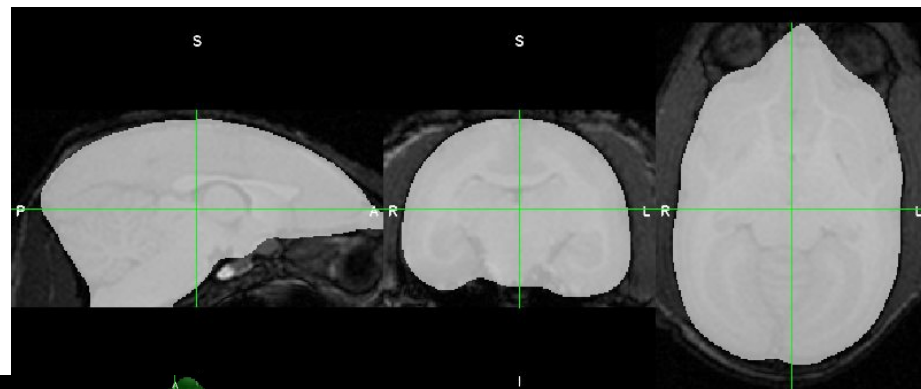


Data courtesy of Yannick Becker/Adrien Meguerditchian (ERC GestImage). For more information, see [https://macatools.github.io/macapype/auto\\_examples/plot\\_segment\\_baboon\\_ants\\_based.html](https://macatools.github.io/macapype/auto_examples/plot_segment_baboon_ants_based.html)



Also tried on marmoset (from cerimed 3T):

- atlas brex (different settings)
- ANTS atropos



Data courtesy of Thomas Brochier/Frederic Chavane (Marmobrain project). For more information, see [https://macatools.github.io/macapype/auto\\_examples/plot\\_segment\\_marmo\\_ants\\_based.html](https://macatools.github.io/macapype/auto_examples/plot_segment_marmo_ants_based.html)

<https://macatools.github.io/macapype>

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Macapype

Ressources

Forum macapype\_users

Installation

Docker

Workflows

Tutorial

Examples

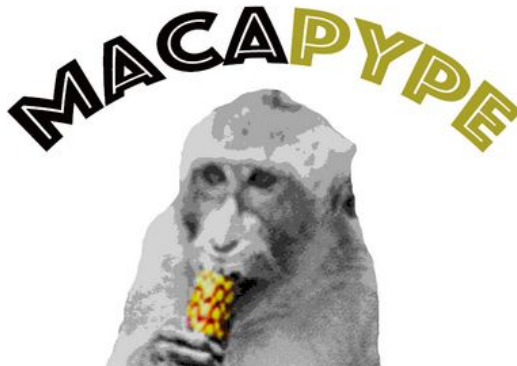
Contributing

Table of contents

## Macapype

Macapype is an open-source multi-modal brain data analysis kit which provides **Python-based pipelines** for advanced multi-thread processing of MRI anatomical data of PNH brain images. Neuropycon 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.

API, describing the different pipelines and nodes, can be found [here](#)



- **Test it!**
- Install Macapype
- Input your data to the segmentation workflow
- Wait and see what append!
- Use mattermost channel to get some help or report bugs or failures  
[https://framateam.org/signup\\_user\\_complete/?id=ebtxf45nmiyqmkm8e6oh9qjsoe](https://framateam.org/signup_user_complete/?id=ebtxf45nmiyqmkm8e6oh9qjsoe)
- **Be part of the development**
- Fork the github repository
- Create a new branch
- Modify the package (adding new features or pipelines)
- Submit a pull request

# Thanks for your attention !

Further information?

*david.meunier AT univ-amu.fr*



This is the “unofficial logo”,  
let us know what you think...

# Macapype links:

Official Repo: <https://github.com/Macatools/macapype>

Documentation: <https://macatools.github.io/macapype/index.html>

PYPI : <https://pypi.org/project/macapype/>

Docker hub: <https://hub.docker.com/r/macatools/macapype>

# Useful links:

PRIME-RE: <https://github.com/PRIME-RE/prime-re.github.io/wiki>

PRIME-DE: [http://fcon\\_1000.projects.nitrc.org/indi/indiPRIME.html](http://fcon_1000.projects.nitrc.org/indi/indiPRIME.html)

# References

Nipype :Gorgolewski, K et al. (2011). Nipype: a flexible, lightweight and extensible neuroimaging data processing framework in Python. Front. Neuroinform.5:13.

BIDS : Gorgolewski, K et al. (2016). The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments. Sci Data.3:160044.

AtlasBRESX : Lohmeier, J et al. (2019). AtlasBRESX: Automated template-derived brain extraction in animal MRI. Sci Rep. 9(1):12219

NMT template and scripts : Seidlitz J et al. (2018). A population MRI brain template and analysis tools for the macaque. Neuroimage 170:121-131