

The NiPreps ecosystem for reproducible neuroimaging

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The standard design (anti-)pattern for fMRI preprocessing

- Pick a single software package
 - Usually based on considerations other than performance



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- Pick a single software package
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- String together the tools from that package into a script to run the preprocessing workflow

```
#!/bin/bash

# Generate the subject list to make modifying this script
# to run just a subset of subjects easier.

for id in `seq -w 1 26` ; do
    subj="sub-$id"
    echo "====> Starting processing of $subj"
    echo
    cd $subj

    # If the brain mask doesn't exist, create it
    if [ ! -f anat/${subj}_T1w_brain_f02.nii.gz ] ; then
        echo "Skull-stripped brain not found, using bet with a fractional intensity thresh
        # Note: This fractional intensity appears to work well for most of the subjects in
        # Flanker dataset. You may want to change it if you modify this script for your own
        bet2 anat/${subj}_T1w.nii.gz \
            anat/${subj}_T1w_brain_f02.nii.gz -f 0.2
    fi

    # Copy the design files into the subject directory, and then
    # change "sub-08" to the current subject number
    cp ..../design_run1.fsf .
    cp ..../design_run2.fsf .

    # Note that we are using the | character to delimit the patterns
    # instead of the usual / character because there are / characters
    # in the pattern.
    sed -i '' "s|sub-08|${subj}|g" \
        design_run1.fsf
    sed -i '' "s|sub-08|${subj}|g" \
        design_run2.fsf

    # Now everything is set up to run feat
    echo "====> Starting feat for run 1"
    feat design_run1.fsf
    echo "====> Starting feat for run 2"
    feat design_run2.fsf
    echo

    # Go back to the directory containing all of the subjects, and repeat the loop
    cd ..
done
```

The standard design (anti-)pattern for fMRI preprocessing

- Pick a single software package
 - Usually based on considerations other than performance
- String together the tools from that package into a script to run the preprocessing workflow
 - Generally written by a student or postdoc with little software engineering experience
- Hope it keeps working over time...
- Trust that it does the right thing...

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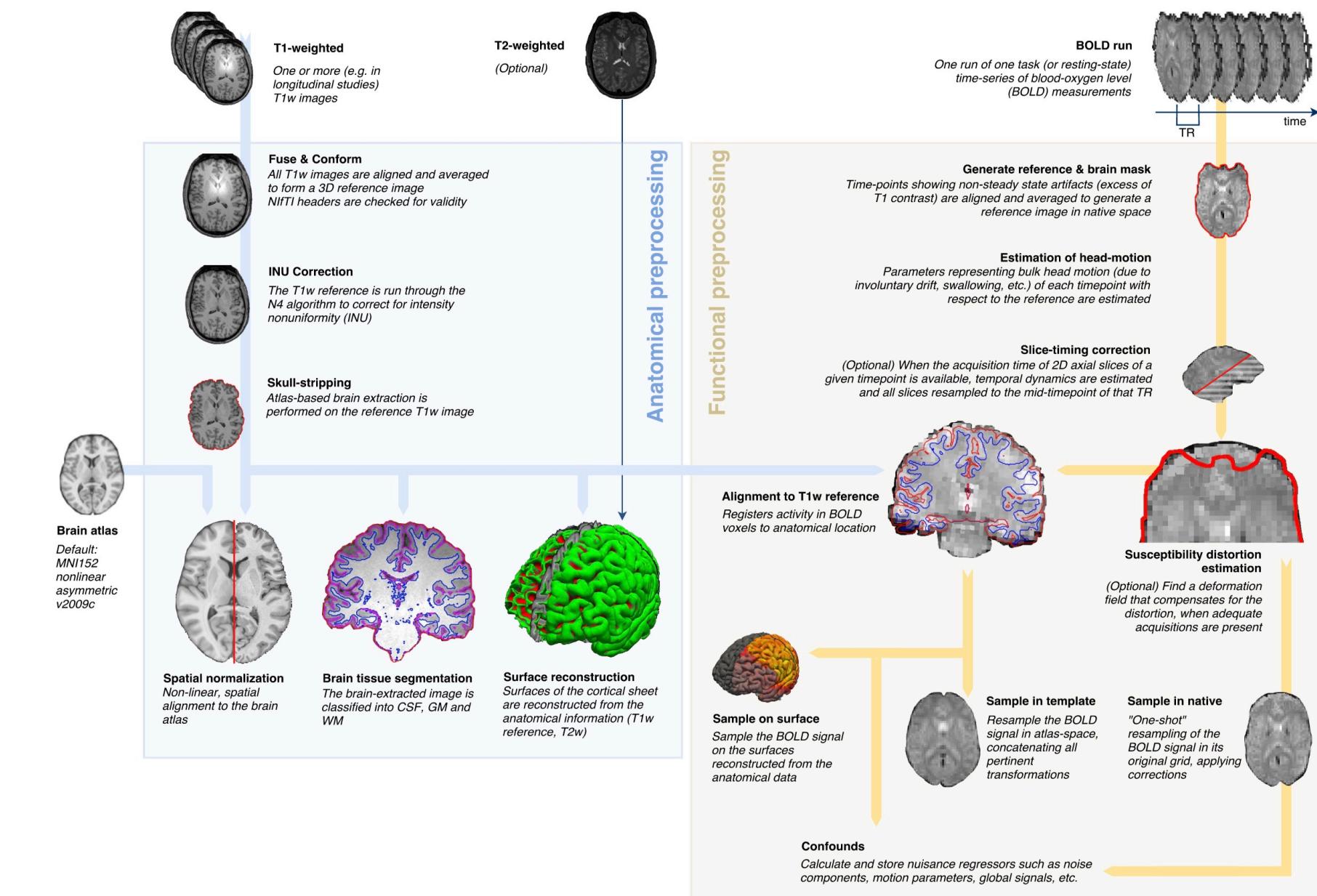
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Towards a new design pattern for preprocessing: fMRIPrep

- A robust workflow for preprocessing fMRI data

- Tested on a large number of fMRI datasets from OpenNeuro
- Adapt to each dataset and processes it in the best way possible
- Outputs to BIDS-Derivatives format
- Provides powerful visualizations :
 - to help identify problems
 - allowing glass-box access to training researchers
- Currently averaging ~5000 successful runs per week



Esteban et al., 2019, *Nature Methods*

RF1MH121867: NiPreps (NeuroImaging PREProcessing toolS)

*... the overarching **objective** of this project is to develop NiPreps, a software framework to perform standardized preprocessing of diverse neuroimaging data.*

- Aim 1: solidify the foundations of the NiPreps integration.
- Aim 2: enable integrative analysis approaches of heterogeneous data.
- Aim 3: accelerate the dissemination of NiPreps to the neuroscience community through hackathons and “docusprints”.



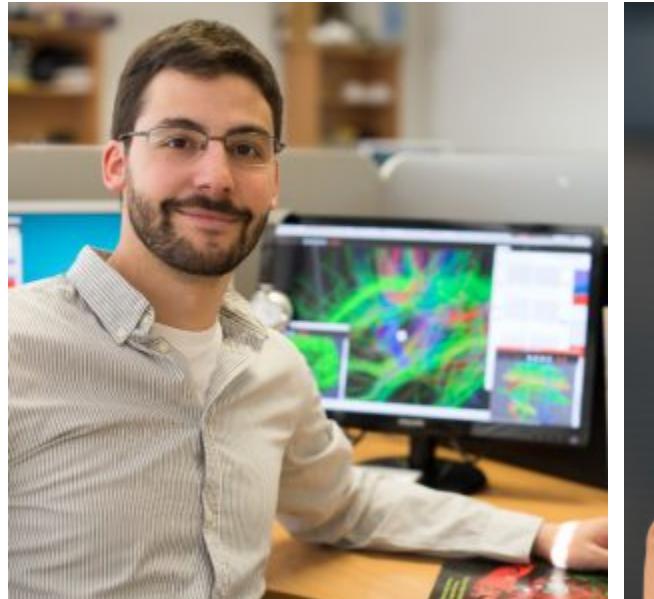
Why?

In developing fMRIPrep, we learned about critical aspects of neuroimaging workflows.
NiPreps is envisioned as a generalization of fMRIPrep.

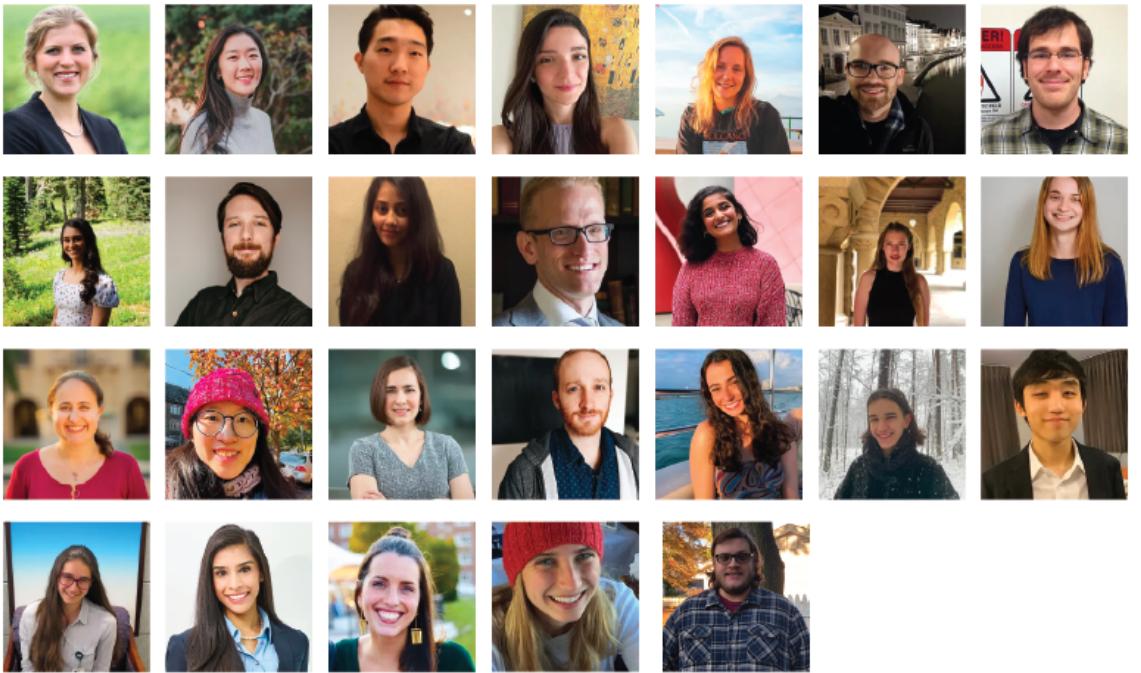
RF1MH121867: Sites



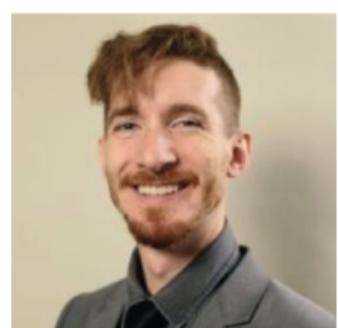
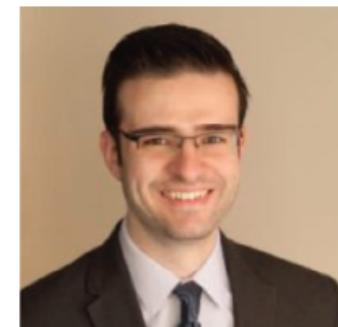
Poldracklab (Stanford)



Esteban Lab (CHUV Lausanne)



Satterthwaite Lab (Penn)



Milham Lab (Child Mind Inst)

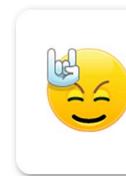
Ariel Rokem
Research Associate Professor
email: arokem@uw.edu
[Website](#)

Ezgi Yucel
Graduate student (with Ione Fine), started 2017

Teresa Gomez
Post-bacc student, started January 2022

McKenzie Hagen
Graduate student, started 2021

John Kruper
Post-bacc student, started July 2020



Rokem Lab (UW)

The NiPreps community

Welcome

NiPreps

- Home
- NiPreps > A total of 90 neuroimagers have already joined us. Becoming a member will give you access to additional forums for discussion, subscribing notifications for events and meetings, etc. You can request you are added to the organization by [creating a new issue here](#).
- BIDS-Apps
- Community

[Welcome](#)

[Membership](#)

[New features](#)

[Contributing](#)

[Code of Conduct](#)

[Licensing](#)

Developers >

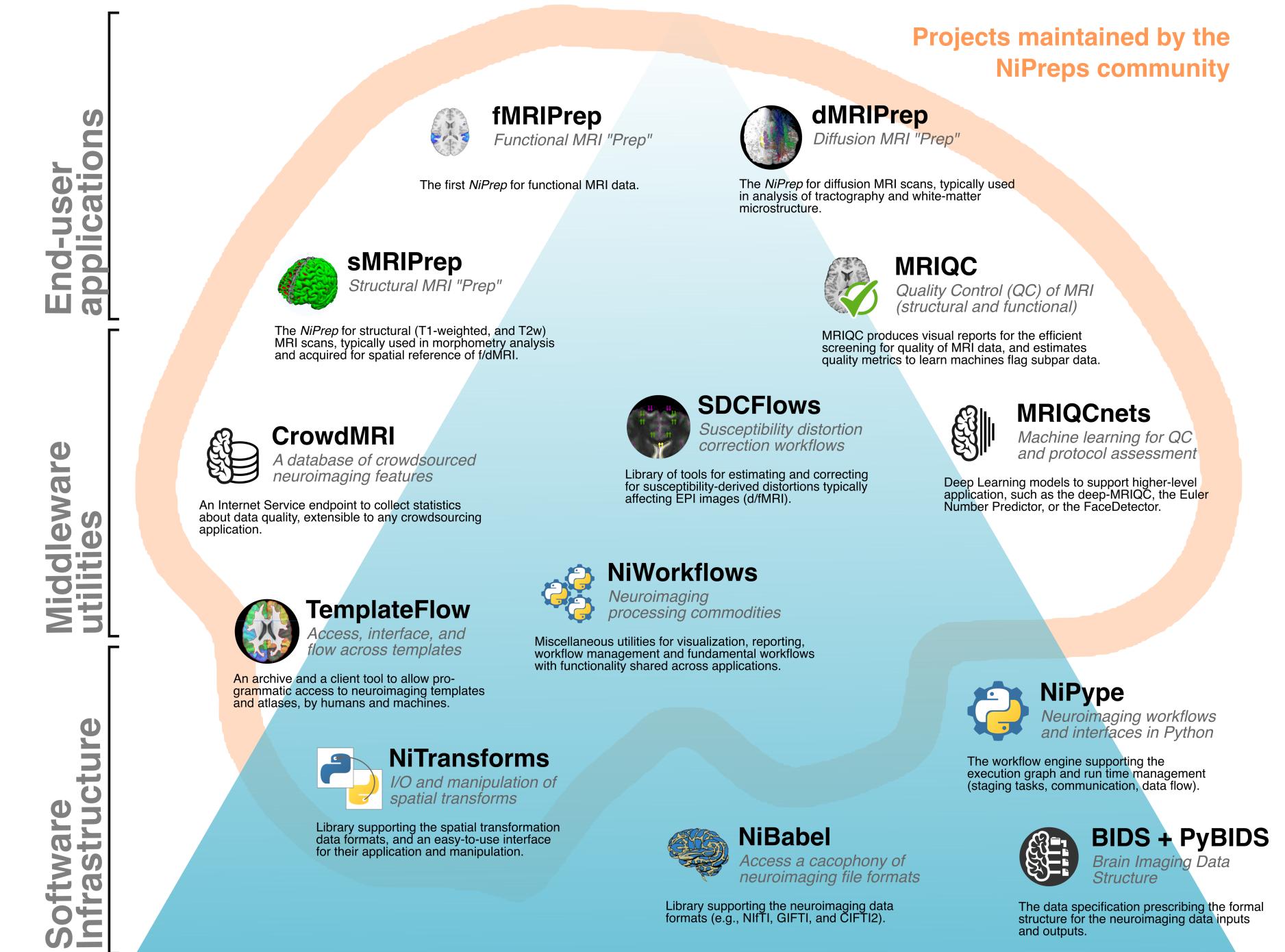


Current members of the GitHub organization

www.nipreps.org

Aim 1: Developing and refining reusable infrastructure/middleware components

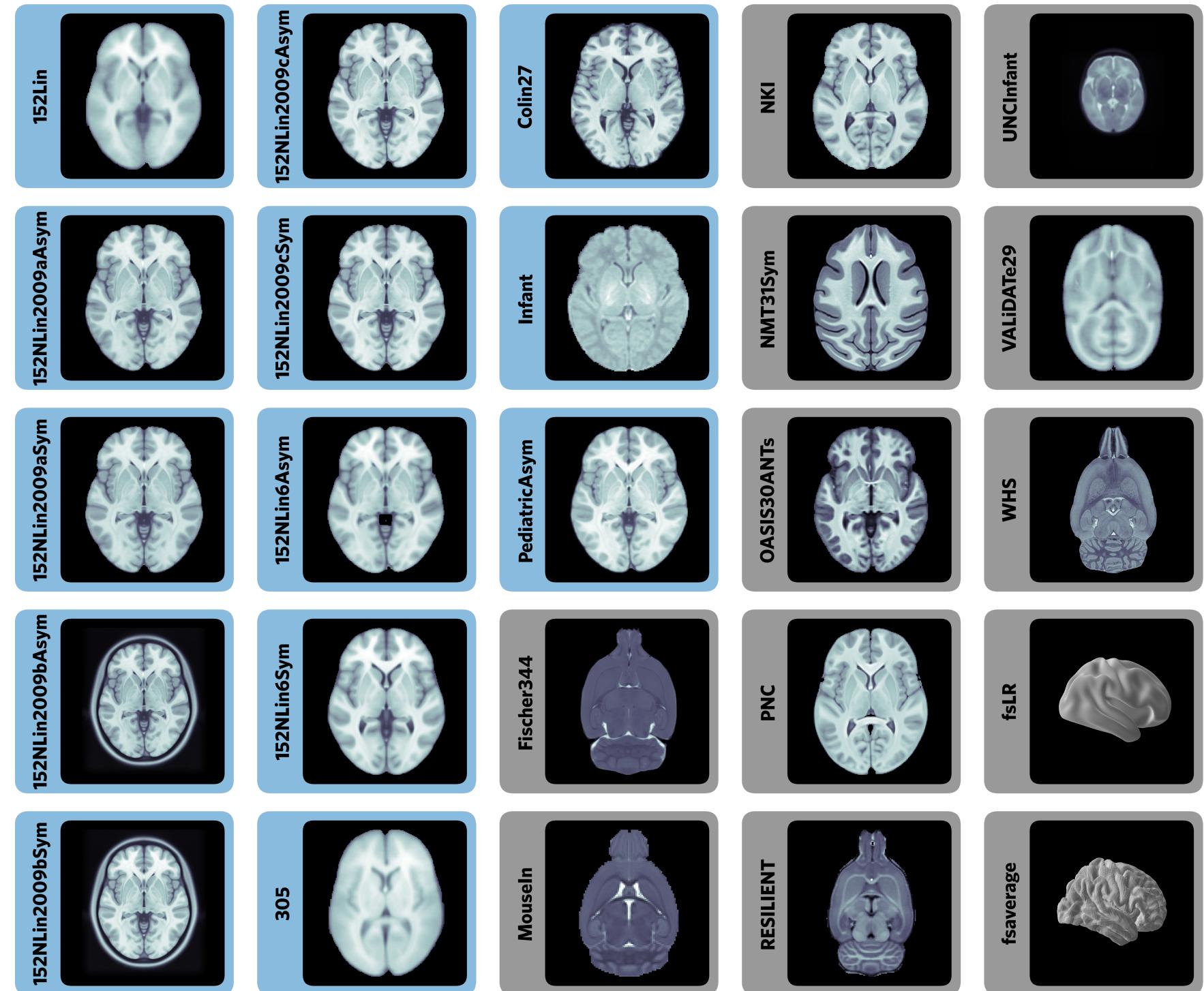
- *TemplateFlow*: FAIR Sharing and management of neuroimaging templates and atlases
- *SDCflows*: Integrating susceptibility distortion correction (SDC)
- *NiReports*: A modular visual reports system
- *NiTransforms*: Spatial transforms integration



TemplateFlow: FAIR sharing of neuroimaging templates and atlases

- Templates and atlases are commonly used in neuroimaging research
- There is significant lack of clarity in the use of these templates
 - There are numerous versions of the widely used “MNI template”
- Templateflow provides programmatic access to a database of templates and mappings between them
- Easy to use for humans and machines:

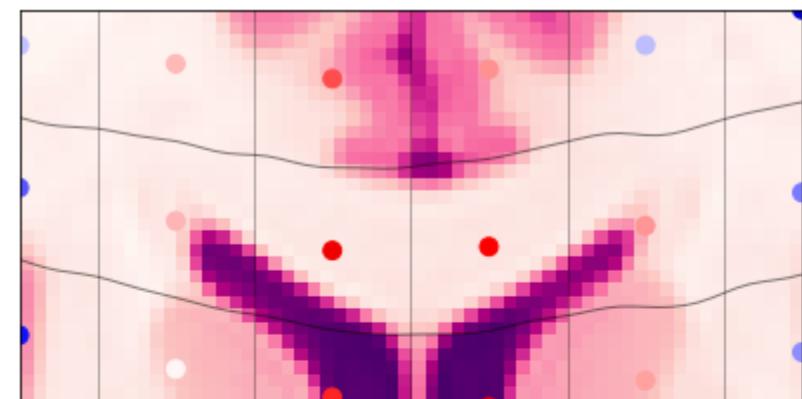
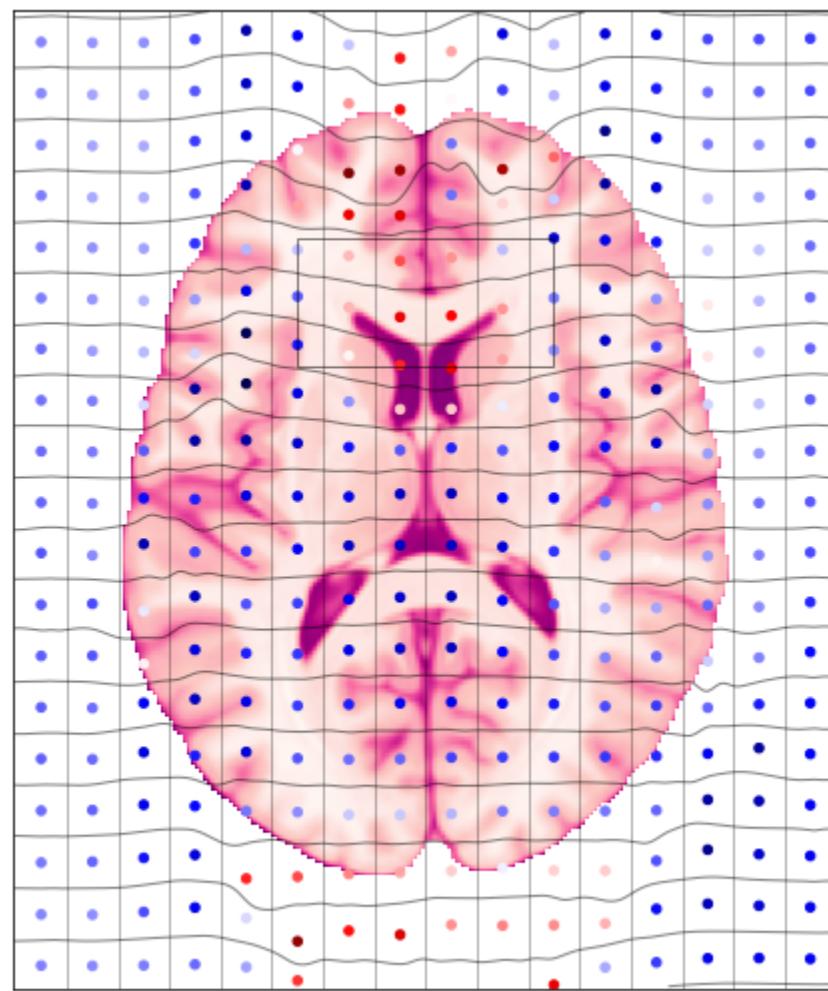
```
>>> from templateflow import api as tf
>>> tf.get("MNI152NLin2009cAsym",
...         suffix="T1w")
```



Ciric et al., 2022, *Nature Methods*

SDCFlows: Susceptibility Distortion Correction workflows

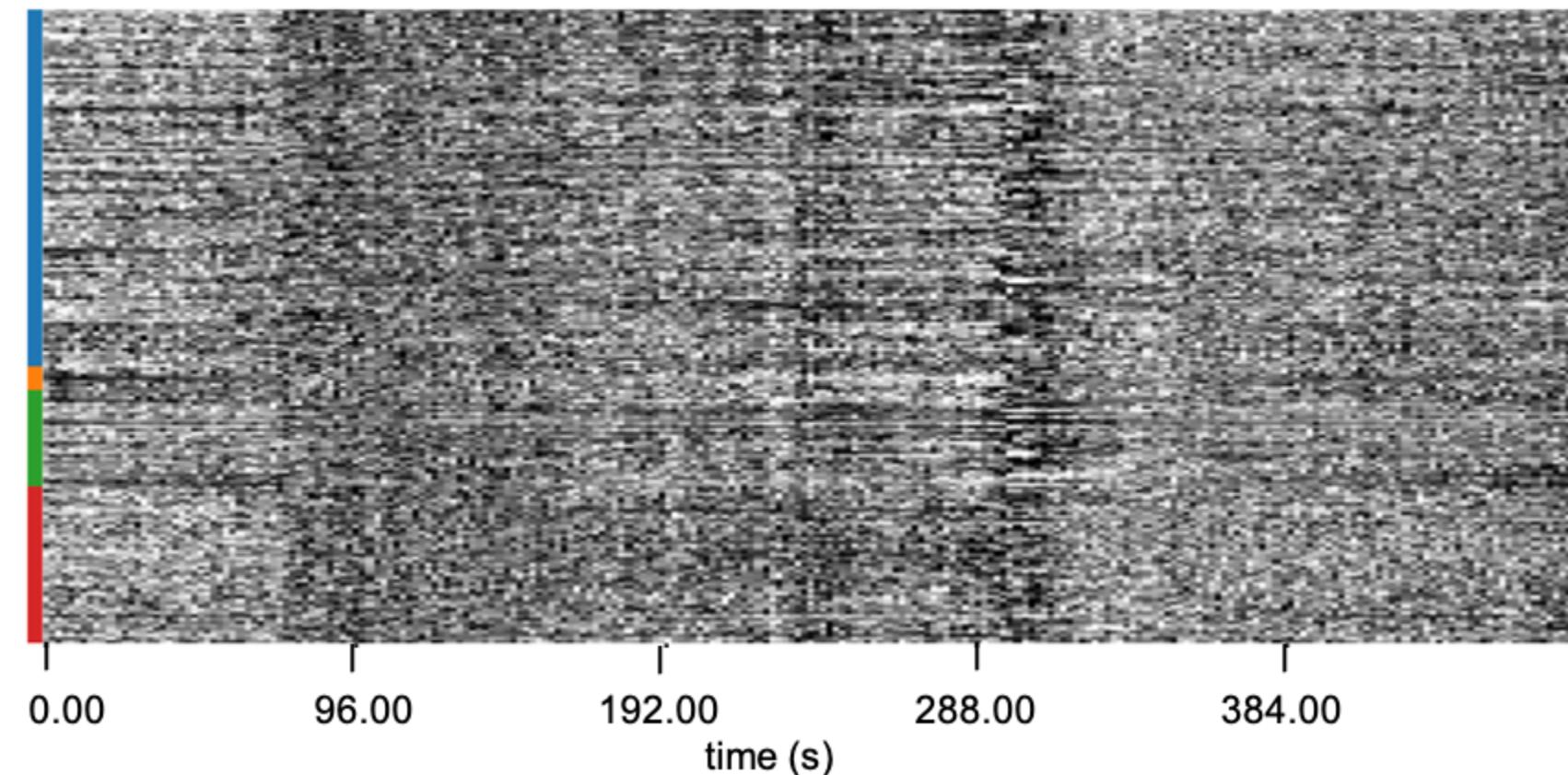
- SDCflows aims to provide a unified interface to susceptibility distortion correction methods
 - Defines a shared representation model (B-Spline) for the field map
 - “decouples” estimation and application steps (increasing modularity)
- Overhaul started early 2021 ([Esteban et al., OHBM 2021](#))
 - Faced many technical challenges
 - Requiring numerous bugfixes and “edge” cases
 - Developed new educational materials & Jupyter notebooks



Jupyter Notebook
on GitHub:
[nipreps/sdcflows](#)

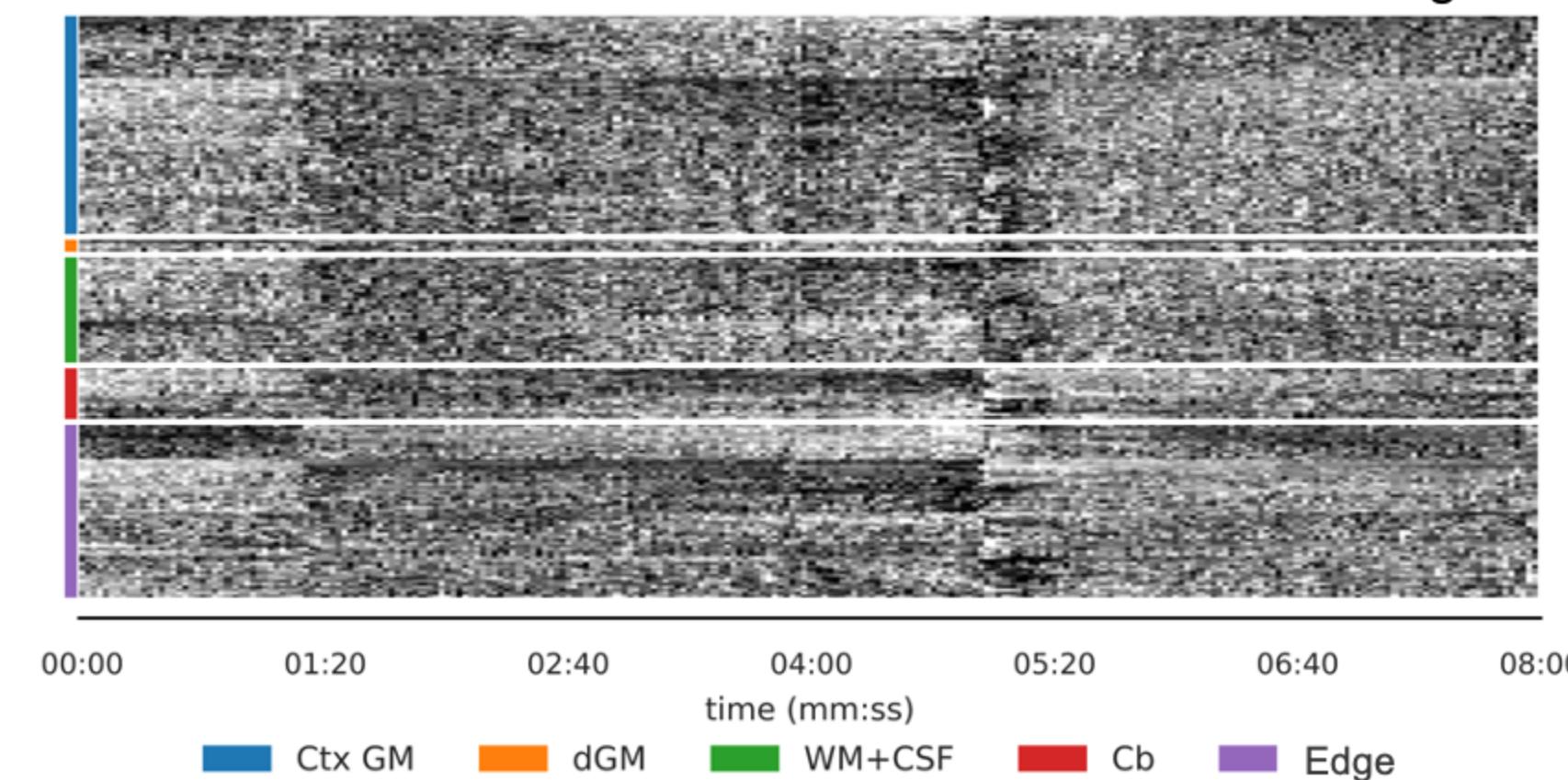
NiReports: New visualization tools from MRIQC

Old Design



Mixed Gambles Task^[21] subject 15 run 02

New Design



(Provins et al., ISMRM 2022)

- MRIQC is a quality control workflow for structural/functional MRI
- Developing a number of visualizations that will go into NiReports
 - Added visualization of voxels at the edge of the brain (“crown”)
 - Added hierarchical sorting of rows (voxels) to enhance patterns (Aquino et al. 2019)

Infrastructure: Architectural redesign

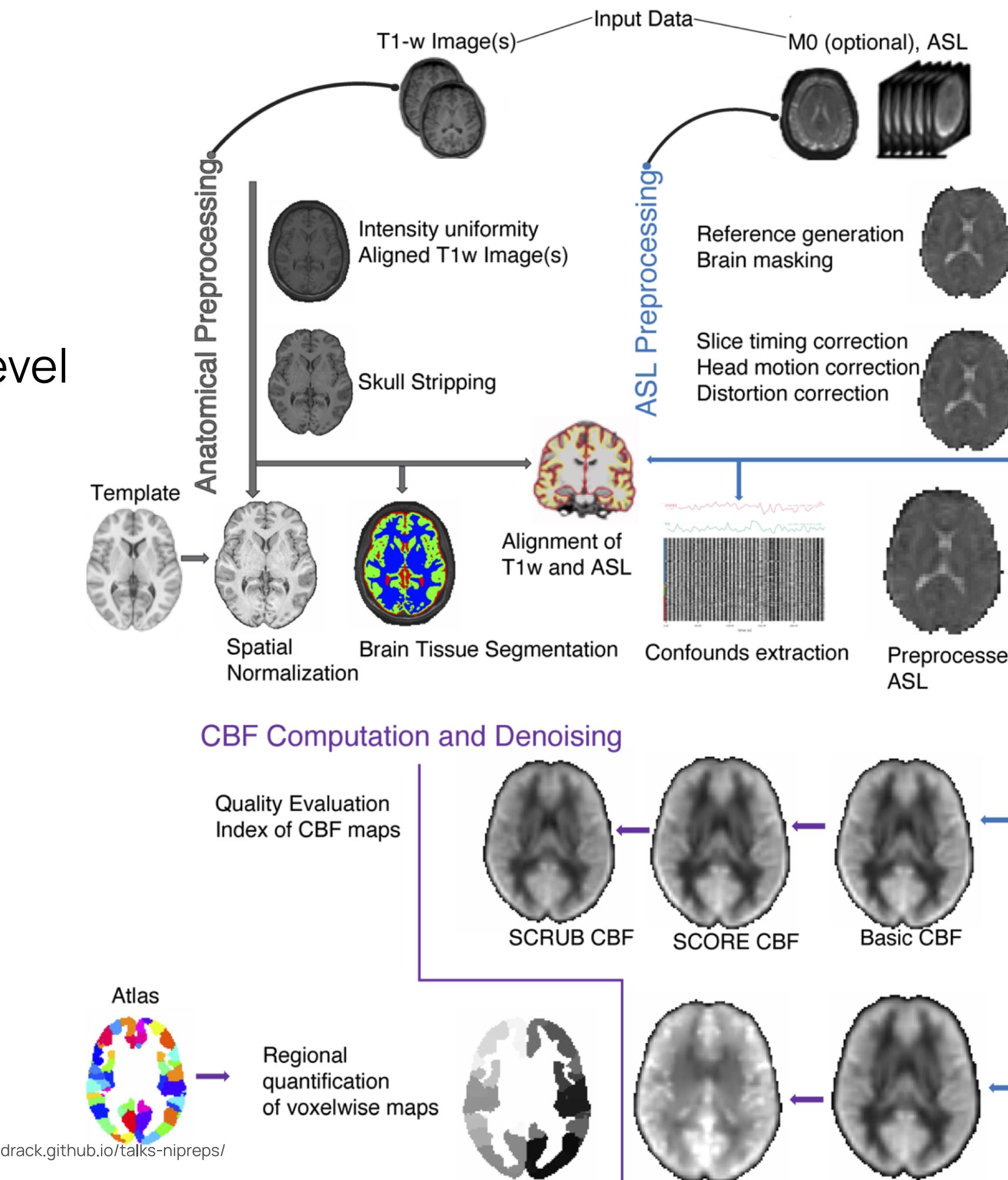
- Problem: fMRIPrep's “one size fits all” design has limitations for emerging use cases
 - Archiving preprocessing results requires balancing storage costs against possible use cases.
 - Including alternative algorithms requires custom code to integrate.
- Solution: Accept pre-computed derivatives and defer computationally cheap operations
 - E.g., Deep learning segmentations and masks can be accepted, skipping fMRIPrep defaults.
 - Multiple template registrations can be archived, analysts may resample BOLD series to different spaces on demand.
- This approach is implemented in SDCFlows and is being generalized to other components.

Aim 2: Expand the portfolio of end-user NiPreps

- ASLPrep
- dMRIPrep
- PETPrep
- fMRIPrep-infants (aka *NiBabies*)
- fMRIPrep-rodents (aka *NiRodents*)

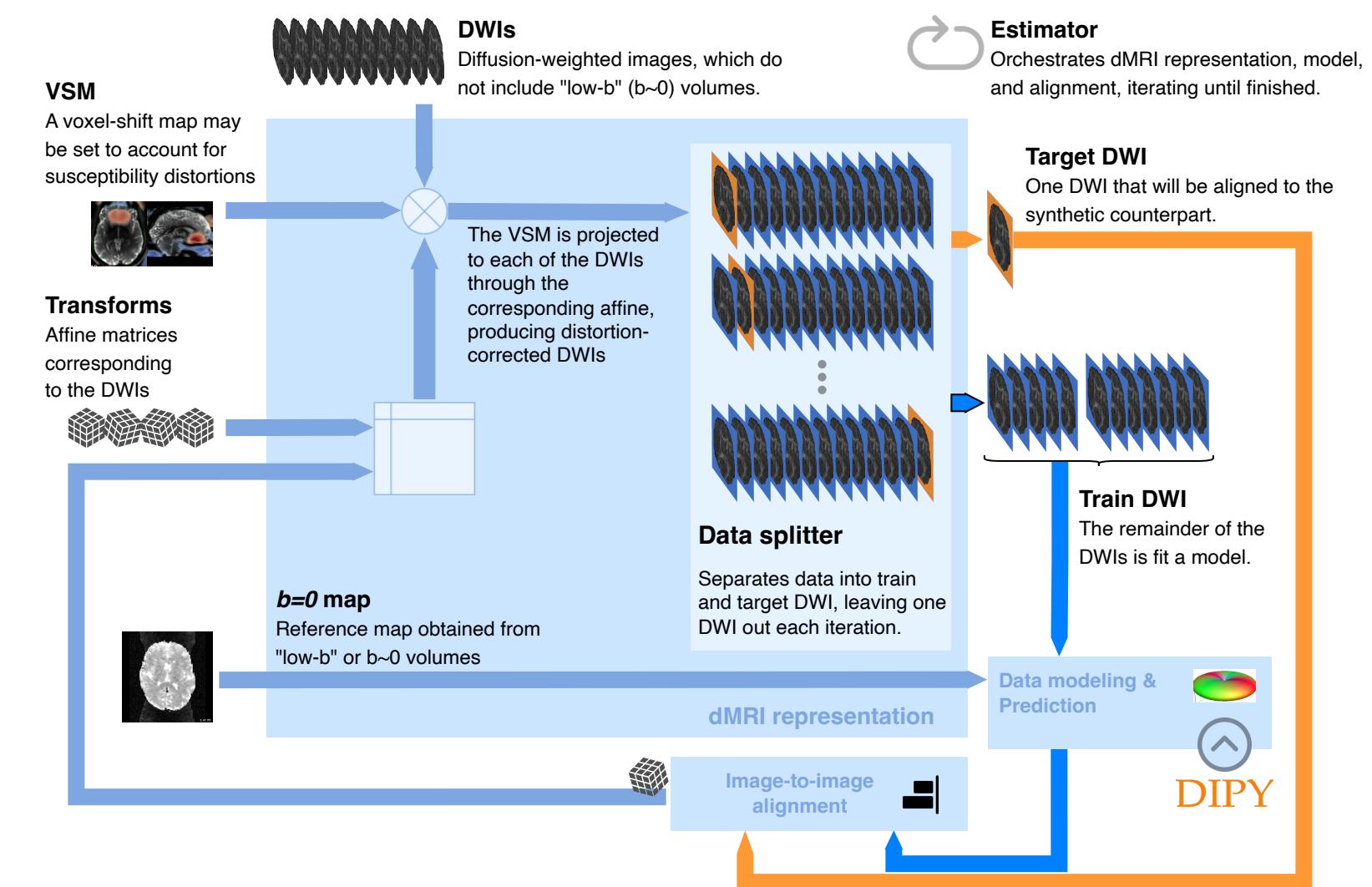
Workflows: ASLPrep (cerebral blood flow quantification)

- A robust workflow for preprocessing arterial spin labeling (ASL) data
 - Including cerebral blood flow (CBF) quantification
 - Provides quality evaluation for CBF maps
 - Provides CBF quantification at the regional level using atlases



Workflows: dMRIPrep (diffusion MRI)

- A workflow for preprocessing of diffusion MRI data
- Development currently focused on *eddy motion*
 - an algorithm to estimate head-motion (modality-agnostic) and modality-specific artifacts (eddy currents in the case of dMRI)

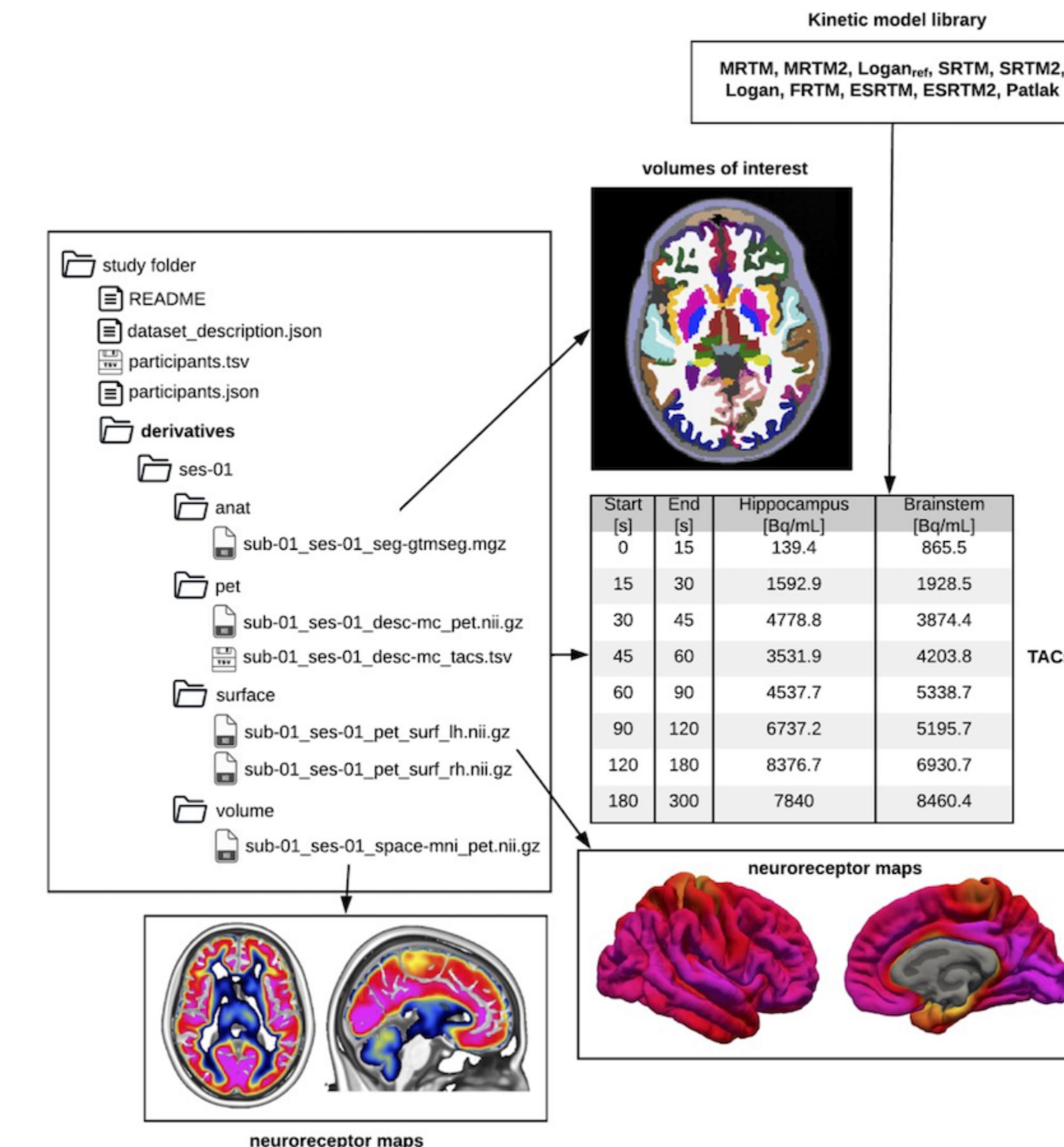


Preprint: Pisner et al., 2022.

Workflows: PETPrep (positron emission tomography)

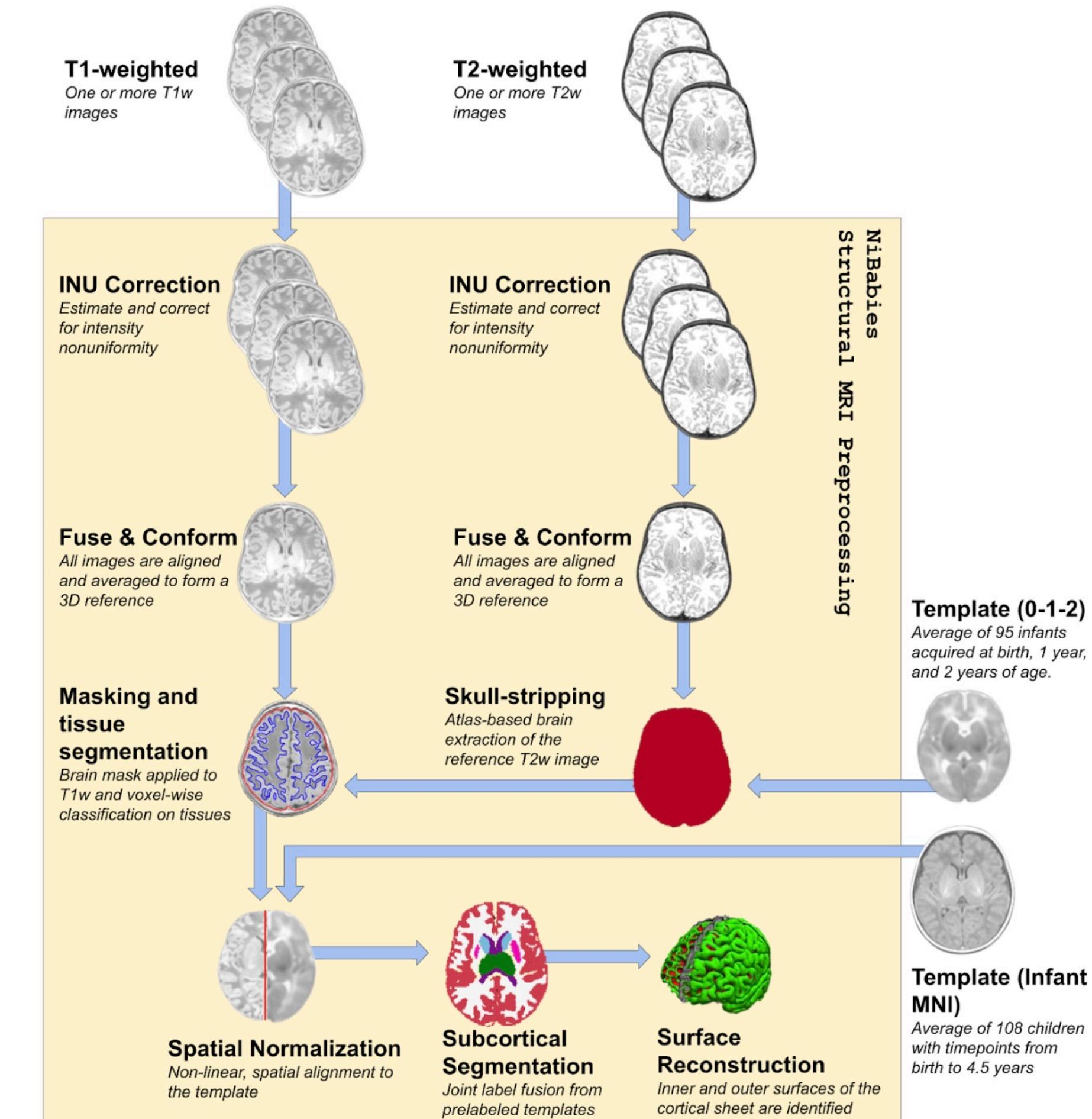
- A NiPreps workflow for PET preprocessing

- Successfully merged petsurfer into nipype (1.8.0)
- Incorporated nipype implementation of a robust head motion correction workflow (petprep_hmc)
- Developing a BIDS-Derivatives standard for PET derivatives
- Model-based head-motion correction leveraging *eddy motion* in progress



Workflows: fMRIPrep for infants

- Collaboration with Damien Fair & HBCD team
- **New developments**
 - Support for pre-computed derivatives (mask, segmentations).
 - Improved robustness and validity of CIFTI-2 outputs.
- **Upcoming developments**
 - Morphometric outputs (cortical thickness, curvature)
 - Improvements to susceptibility distortion correction versatility
 - T2 assisted surface generation

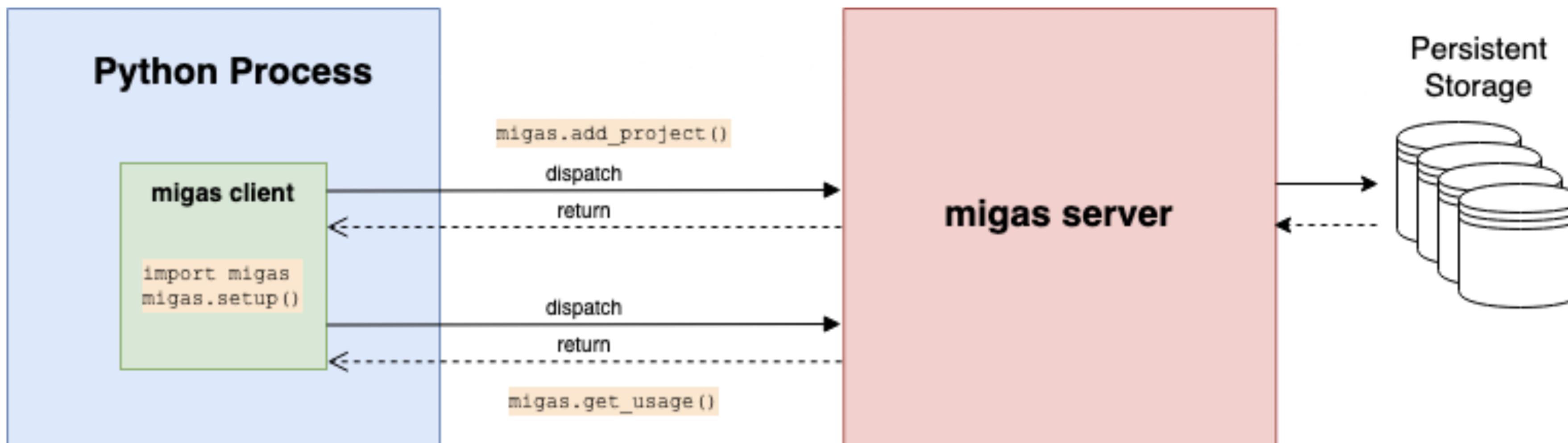


Aim 3: Consolidate the NiPreps community

- Project monitoring infrastructure: MIGAS
- Evaluation of cross-workflow reproducibility
- Hackathons and documentation
- Best practices and educational resources
- NMIND: Building common standards for software development

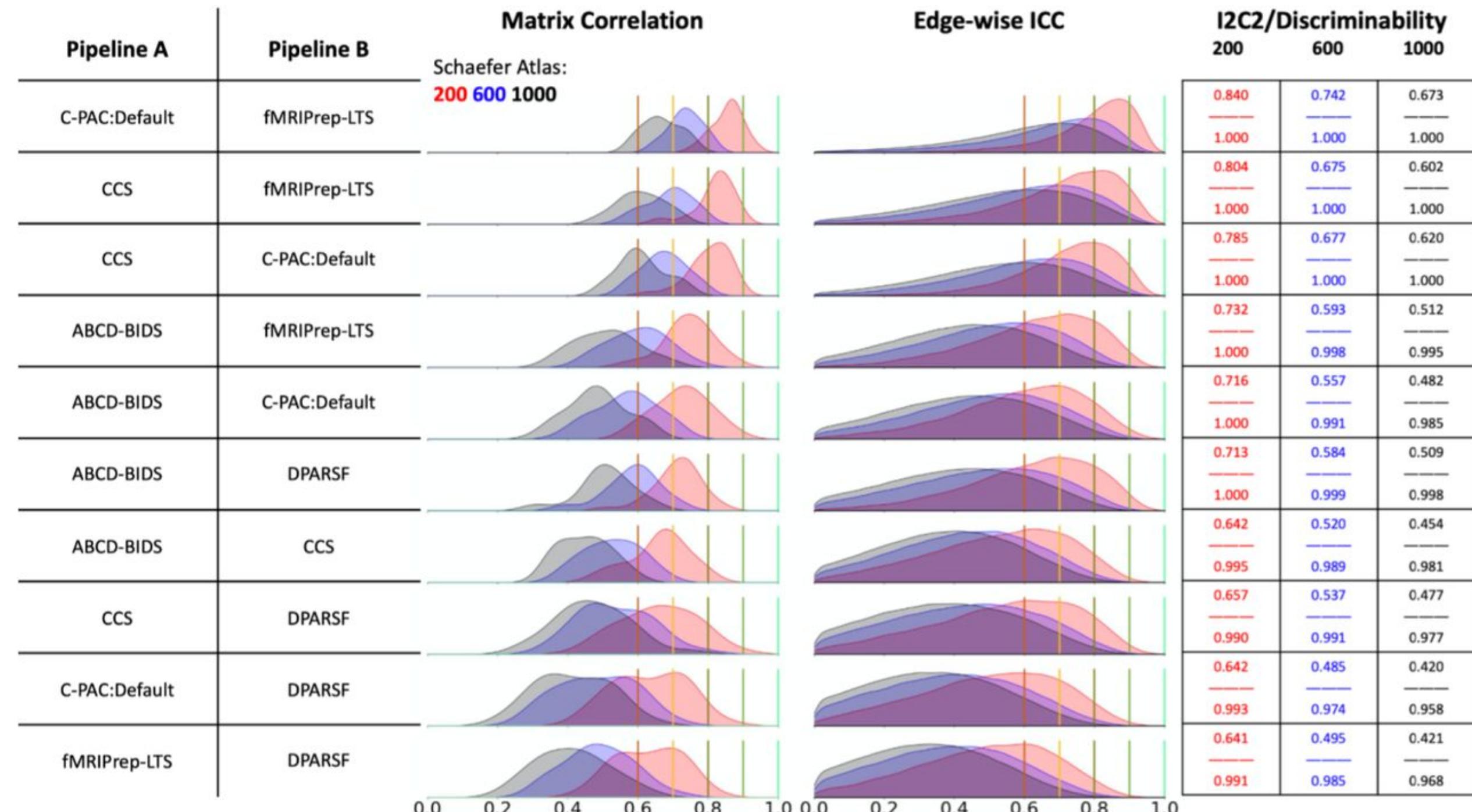
Project monitoring: MIGAS

- An open-source, customizable telemetry solution
- Allows collecting usage information, errors, and status throughout a process's lifetime
- Easy to deploy with various cloud providers (Heroku / GCP / AWS)
- Available as a Python package: <https://pypi.org/project/migas/>



Reproducibility: Cross-workflow evaluation

- CMI team developed a CPAC implementation of fMRIPrep
 - Able to achieve high levels of reproducibility in connectivity metrics between harmonized workflows
 - Helped identify causes of divergence, such as use of different versions of MNI template



Hackathons and documentation

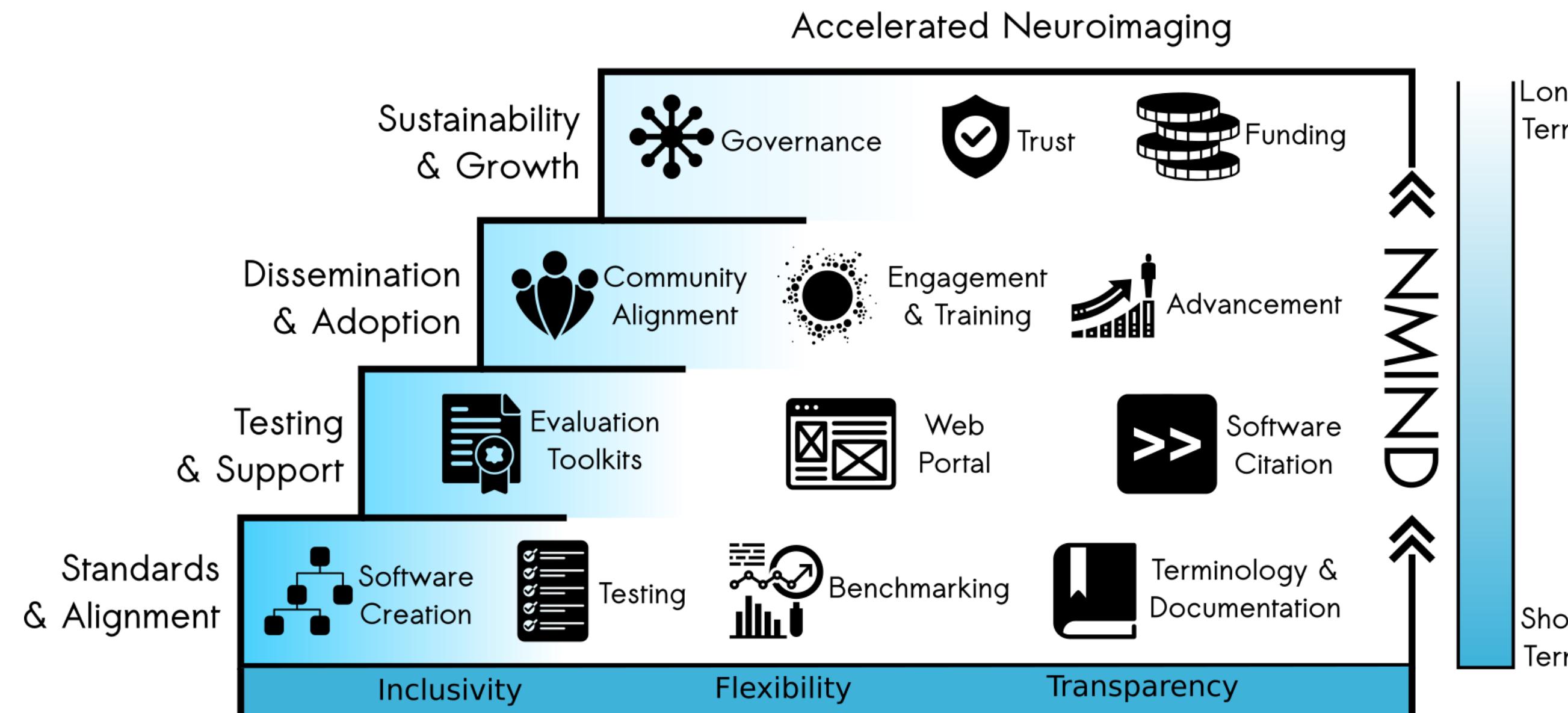
- Held a hackathon/documentation sprint in Glasgow following OHBM 2022
- Will participate in Brainhack Global 2022
- Planning to hold a hackathon/documentation sprint in Montreal in association with OHBM 2023

Best practices and educational resources

- Collaborative QC-Book (educational, ISMRM 2021): <https://nipreps.org/qc-book>
- MRIQC-SOPs (standard operating procedures)
 - A GitHub template-repository to create and maintain versioned SOPs documentation and checklists.
 - Example: <https://nipreps.org/mriqc-sops/>
- MRIQC Protocol report (Hagen et al., in preparation)
- Frontiers' research topic on QC of fMRI (Provins et al., under review)
- Biases introduced by defacing in QC (Provins et al., pre-registered report under review)

NMIND: Building common standards for software development

- NMIND: Nevermind, this Method Is Not Duplicated
 - *Alignment*: development and adoption of standards for critical software component
 - *Testing*: accessible and (semi-)automated mechanisms for evaluating standards compliance
 - *Engagement*: widespread promotion and adoption of the NMIND collaborative standards



Thank you!