fMRIPrep

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What is fMRIPrep

- Preprocessing pipeline created by the Standard Center for Reproducible Neuroscience

- Designed to be robust, easy to use, and transparent

- Performs minimal processing: motion correction, fieldmap correction, normalization, bias field correction, and brain extraction

- Makes use of the best bits of popular software packages (e.g., ANTs, FSL, FreeSurfer, AFNI), as well as custom code

Reasons to use fMRIPrep

- Field-tested
- Reproducible
- Each step has been optimized
- Easy to use output
- Automatically generated reports for QC of each step

Reasons to not use fMRIPrep

- Data do not meet assumptions (e.g., narrow FOV)
- Need unlimited flexibility
- Have study population that does not conform to standard adult MNI templates (e.g., infants, NHP, rodent)

T1-weighted

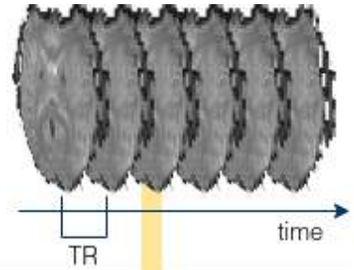
One or more (e.g. in longitudinal studies) T1w images

T2-weighted

(Optional)

BOLD run

One run of one task (or resting-state) time-series of blood-oxygen level (BOLD) measurements



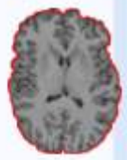
Anatomical preprocessing

Fuse & Conform

All T1w images are aligned and averaged to form a 3D reference image
NIfTI headers are checked for validity

INU Correction

The T1w reference is run through the N4 algorithm to correct for intensity nonuniformity (INU)

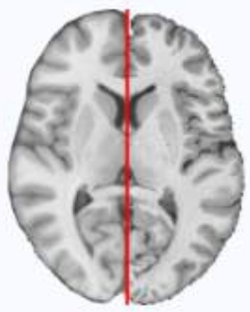


Skull-stripping

Atlas-based brain extraction is performed on the reference T1w image

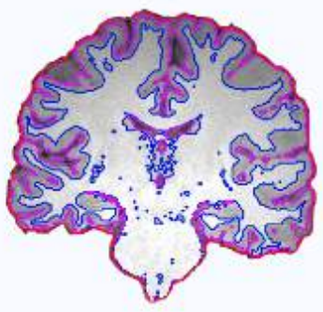
Brain atlas

Default: MNI152 nonlinear asymmetric v2009c



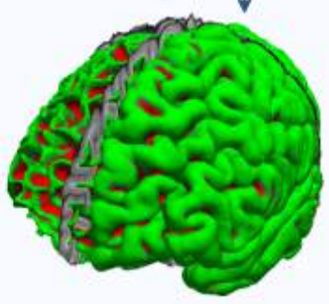
Spatial normalization

Non-linear, spatial alignment to the brain atlas



Brain tissue segmentation

The brain-extracted image is classified into CSF, GM and WM



Surface reconstruction

Surfaces of the cortical sheet are reconstructed from the anatomical information (T1w reference, T2w)

Functional preprocessing

Generate reference & brain mask

Time-points showing non-steady state artifacts (excess of T1 contrast) are aligned and averaged to generate a reference image in native space

Estimation of head-motion

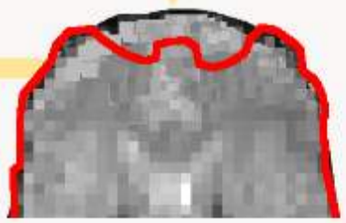
Parameters representing bulk head motion (due to involuntary drift, swallowing, etc.) of each timepoint with respect to the reference are estimated

Slice-timing correction

(Optional) When the acquisition time of 2D axial slices of a given timepoint is available, temporal dynamics are estimated and all slices resampled to the mid-timepoint of that TR

Alignment to T1w reference

Registers activity in BOLD voxels to anatomical location



Susceptibility distortion estimation

(Optional) Find a deformation field that compensates for the distortion, when adequate acquisitions are present

Sample on surface

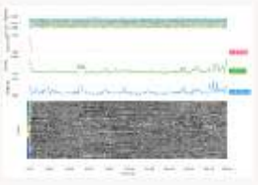
Sample the BOLD signal on the surfaces reconstructed from the anatomical data

Sample in template

Resample the BOLD signal in atlas-space, concatenating all pertinent transformations

Sample in native

"One-shot" resampling of the BOLD signal in its original grid, applying corrections



Confounds

Calculate and store nuisance regressors such as noise components, motion parameters, global signals, etc.

Options of interest

- ICA-AROMA
- FreeSurfer (including longitudinal)
- Anatomy only
- Fieldmap-less distortion correction
- Multi-echo EPI
- Multiple output spaces

Things fMRIPrep does not do

- Smoothing
- ICA-FIXX
- Denoising with user-specified confounds (e.g., in preparation for resting-state analyses)

What do I need to run fMRIPrep?

Minimum requirements

1. Data must be in BIDS format

2. Must have at least one T1w image

Quick review of BIDS (Brain Image Data Structure)

What is BIDS?

- BIDS is a system for naming and organizing ‘raw’ neuroimaging files
- BIDS is not a new file format

Stuff

What is BIDS?

- BIDS is a system for naming and organizing ‘raw’ neuroimaging files
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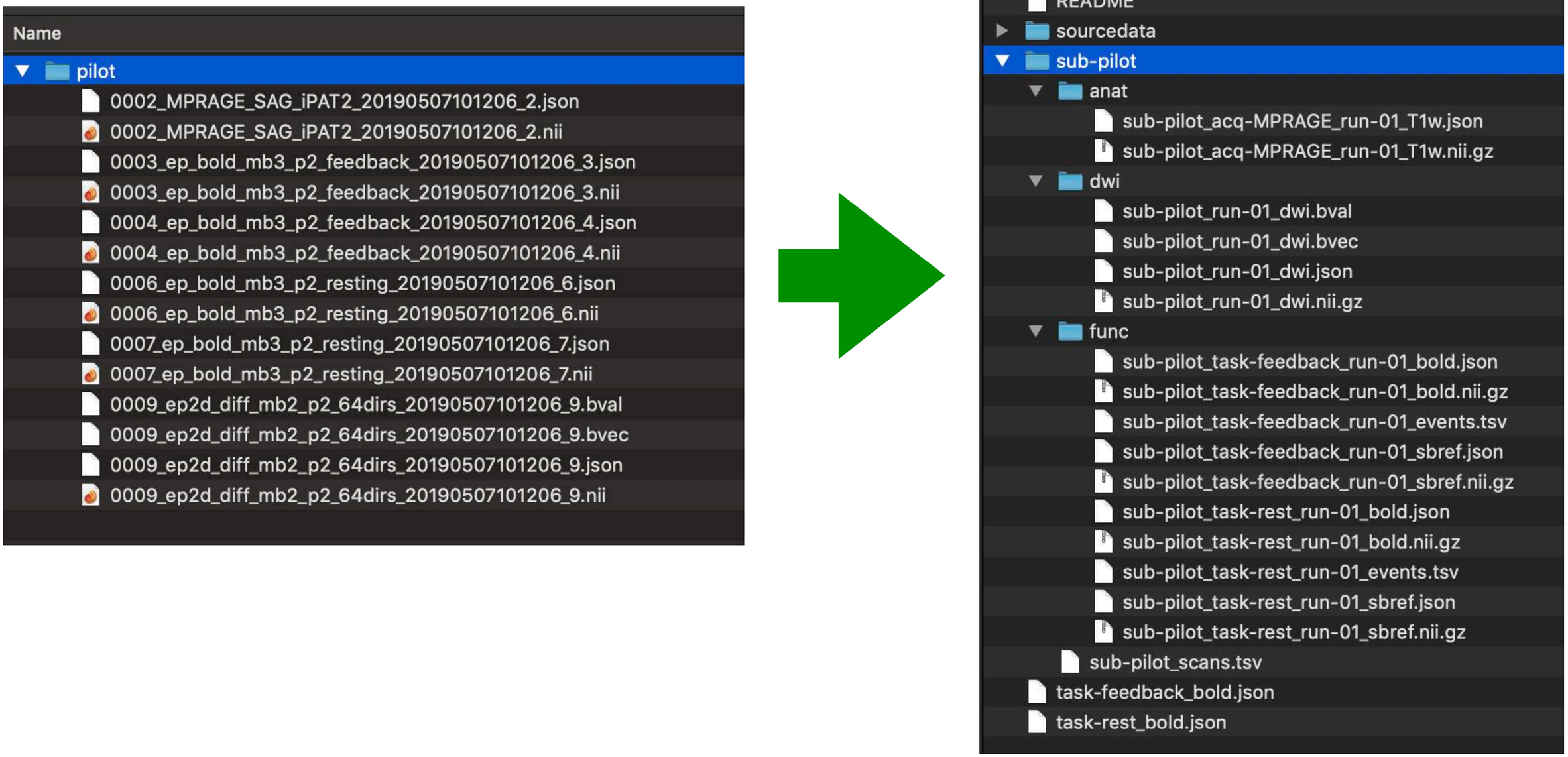
Animals

Household Items

Fruits and Vegetables

In practice for MRI data



How to run fMRIPrep?

Option 1: Docker

- fMRIPrep is a Docker container
- Can be run directly from Docker

```
docker run -ti --rm \
    -v filepath/to/data/dir:/data:ro \
    -v filepath/to/output/dir:/out \
    nipreps/fmriprep:latest \
    /data /out/out \
    participant
```

- Can be run using the fmriprep-docker wrapper script

```
pip install --user --upgrade fmriprep-docker

fmriprep-docker /path/to/data/dir /path/to/output/dir participant
RUNNING: docker run --rm -it -v /path/to/data/dir:/data:ro \
    -v /path/to_output/dir:/out nipreps/fmriprep:20.2.0 \
    /data /out participant
```

Option 2: Compute Canada

- Khan Lab has a set of wrapper scripts: neuroglia-helpers

```
git clone http://github.com/khanlab/neuroglia-helpers ~/neuroglia-helpers
```

- BIDS apps can be run using bidsBatch

```
bidsBatch fmriprep_20.2.0 ~/my-bids-dataset ~/my-bids-dataset/derivatives/fmriprep-v20.2.0 participant
```

Tips on running fMRIPrep

- Running time scales with number of functional runs
- If using Docker, it is recommended to only process one subject at a time
- If using Compute Canada, try and keep the job under 24 hours
- If time/memory is an issue, consider omitting FreeSurfer or looking into the threads and memory options for fMRIPrep

Where to get help?

1. fMRIPrep read the docs: https://fmriprep.org/en/stable/
2. Neurostars: https://neurostars.org/
3. fMRIPrep git page: https://github.com/nipreps/fmriprep

Output