fmriPrep

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What is fmriPrep

- Data 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)



TR

emil

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

time-series of blood-oxygen level

(BOLD) measurements

Estimation of head-motion

Parameters representing bulk head motion (due to involuntary drift, swallowing, cto.) of cach 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 slipps resampled to the mid-timepoint of that TR

(Optional) Find a deformation

field that compensates for the distortion, when adequate acquisitions are present

> BOLD signal in its original grid, applying corrections

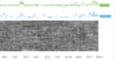


Alignment to T1w reference Registers activity in BOLD voxels to anatomical location



reconstructed from the anatomical data





Confounds Calculate and store nuisance regressors such as noise

components, motion parameters, global signals, etc.

Anatomical preprocessing preprocessin Functional

(Optional)

T2-weighted



Fuse & Conform All Ttw images are aligned and averaged to form a 3D reference image NIfTI headers are checked for velidity



INU Correction The T1w reference is run through the N4 algorithm to correct for intensity

conuniformity (INU)

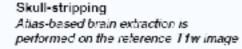
T1-weighted

T1w images

One or more (e.g. in

Iongitudinal studies)

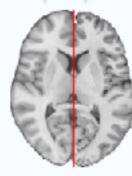




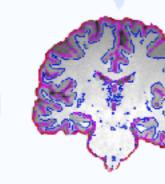


Brain atlas Detault: MNI152nonlinear asymmotrio

v20090

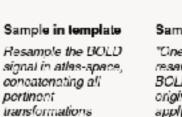


Spatial normalization Non-linear, spatial alignment to the brain atias

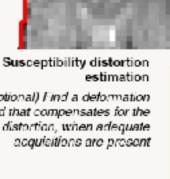


Brain tissue segmentation The brain-extracted image is classified into CSF, GM and WМ

Surface reconstruction Surfaces of the cortical sheet are reconstructed from the analomical information (T1w reterence, T2w)



Sample in native "One-shot" resampling of the



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)

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 \
    poldracklab/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 poldracklab/fmriprep:1.0.0 \
    /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
~/neuroglia-helpers/setup.sh

• BIDS apps can be run using bidsBatch

bidsBatch fmriprep_1.0.4 ~/my-bids-dataset ~/my-bids-dataset/derivatives/fmriprep-v1.0.4 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

Output