# FMRIPREP

ROBUST.EASY.TRANSPARENT

# What is it?

fMRI data preprocessing tool

# Preprocessing?

denoising and normalization

# What it is not

- GLM
- DCM
- connectivity
- dynamics
- etc.

# Principles

- Easy to install and use
- Robust – works on any* data
- Transparent – “glass box”
  rather than “black box”

# Details

- T1w preprocessing
- EPI preprocessing
- Transformations

# T1w preprocessing

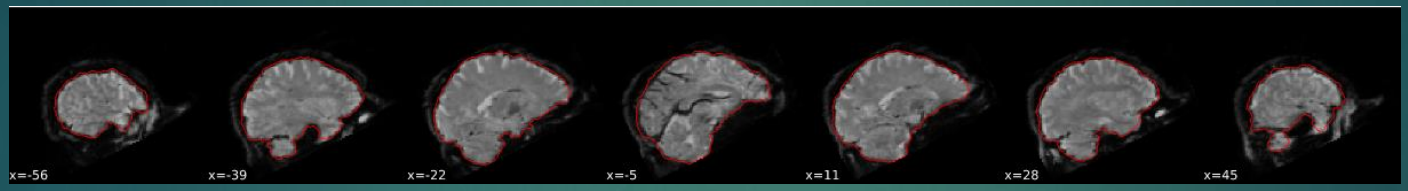
- N4 bias field correction (ANTs)
- Skull stripping (ANTs)


- 3 class tissue segmentation (FSL FAST)

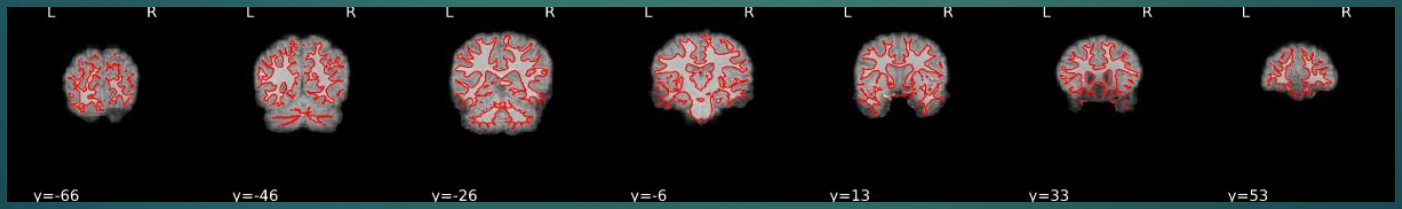

- Robust MNI coregistration (ANTs)

# EPI preprocessing

- Motion correction (FSL MCFLIRT)
- Skull stripping (nilearn)




- Coregistration to T1 (FreeSurfer bbregister)



# EPI preprocessing

- Confounds estimation (nipype)
  - DVARS
  - Framewise displacement
  - Global signal
  - Mean tissue signals
  - CompCor (temporal and anatomical)

# EPI transformations

- Combination of:
  - Motion correction affines
  - EPI -> T1 affine
  - T1 -> MNI affine
  - T1 -> MNI warp field
- Single interpolation step
- No upsampling (keeping original voxel size)

# Input

A BIDS formatted dataset

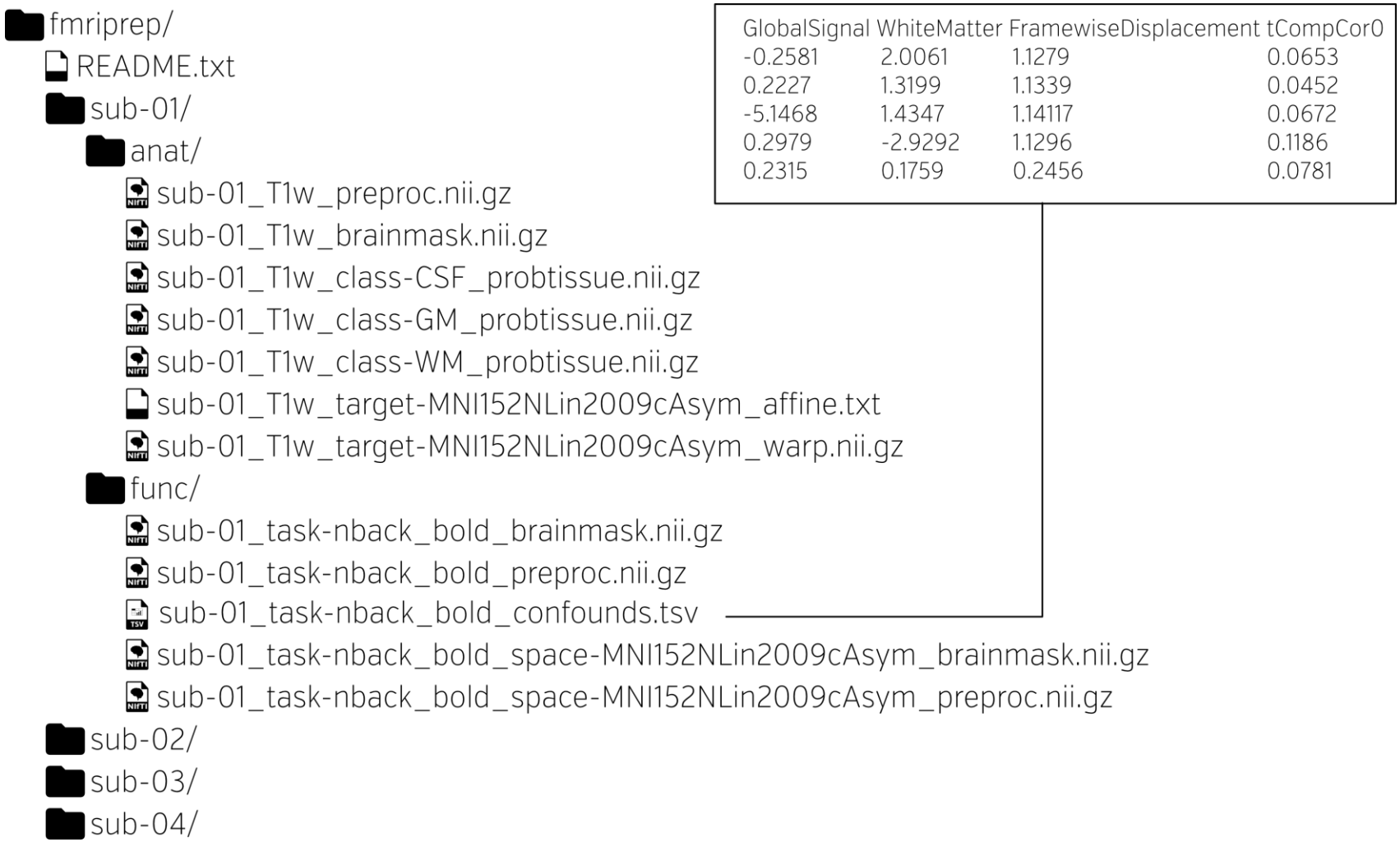
http://bids.neuroimaging.io

# Outputs

- T1w
  - Bias corrected volume
  - Brain mask
  - Tissue segmentation (+probability maps)
  - Affine and warp to MNI (both ways)

# Outputs

- EPI
  - Motion corrected images
  - Brain mask
  - Affine T1w
  - Tabular text file with all noise confounds
- All volumes in MNI and T1w space


fmriprep/
README.txt
sub-01/
anat/
sub-01_T1w_preproc.nii.gz
sub-01_T1w_brainmask.nii.gz
sub-01_T1w_class-CSF_probtissue.nii.gz
sub-01_T1w_class-GM_probtissue.nii.gz
sub-01_T1w_class-WM_probtissue.nii.gz
sub-01_T1w_target-MNI152NLin2009cAsym_affine.txt
sub-01_T1w_target-MNI152NLin2009cAsym_warp.nii.gz
func/
sub-01_task-nback_bold_brainmask.nii.gz
sub-01_task-nback_bold_preproc.nii.gz
sub-01_task-nback_bold_confounds.tsv
sub-01_task-nback_bold_space-MNI152NLin2009cAsym_brainmask.nii.gz
sub-01_task-nback_bold_space-MNI152NLin2009cAsym_preproc.nii.gz
sub-02/
sub-03/
sub-04/
GlobalSignal WhiteMatter FramewiseDisplacement tCompCor0
-0.2581 2.0061 1.1279 0.0653
0.2227 1.3199 1.1339 0.0452
-5.1468 1.4347 1.14117 0.0672
0.2979 -2.9292 1.1296 0.1186
0.2315 0.1759 0.2456 0.0781

# REPORTS

# Installation

- For single user machines (laptops desktops): Docker
  - Works on Mac, Windows and Linux
- For multi user compute clusters (Sherlock): Singularity
- Both options provide all of the required dependencies

# Docker

- Install: https://docs.docker.com/engine/installation/
- Run:

```
docker run --rm \
-v $HOME/ds005:/data:ro \
-v $HOME/ds005_preprocessed:/out \
poldracklab/fmriprep:latest /data /out participant
-w /out/work/
```

# Singularity

- Already installed on Sherlock
- Use our image or convert one from Docker
- Run:

```
fmriprep.img /data /out participant
-w /out/work/
```

- All data (and output folder) needs to be on $SCRATCH or $PI_SCRATCH or $HOME

# Command line options

- --participant_label – process only one participant (great for parallelization)
- --work-dir – folder where all intermediate results will be stored
- --skip-native – don't output EPI images in T1w space
- --nthreads – limit number of threads used
- --mem_mb – limit amount of memory used
  - (useful for big multiband datasets)
- --no-skull-strip-ants – use AFNI instead of ANTs for skullstripping
- --no-freesurfer – don't do surface reconstruction

# User support

- Questions:
  - https://neurostars.org
- Bug reports and feature requests:
  - https://github.com/poldracklab/fmriprep/issues
- Contributors guide:
  - http://fmriprep.readthedocs.io/en/latest/contributors.html

# Upcoming features

- Fieldmaps
  - TOPUP, spiral, and double TE difference
- Surface reconstruction using FreeSurfer
  - Surfaces and timecourses mapped to the surface
- Longitudinal analysis
- ICA Aroma
- Slice time correction

# Discussion

# General questions

- What setup do you use to analyze data?
  - Single user laptop/desktop?
  - Cluster (i.e. Sherlock)?
  - Cloud?
- What new features would you like?

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- Oscar Esteban
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