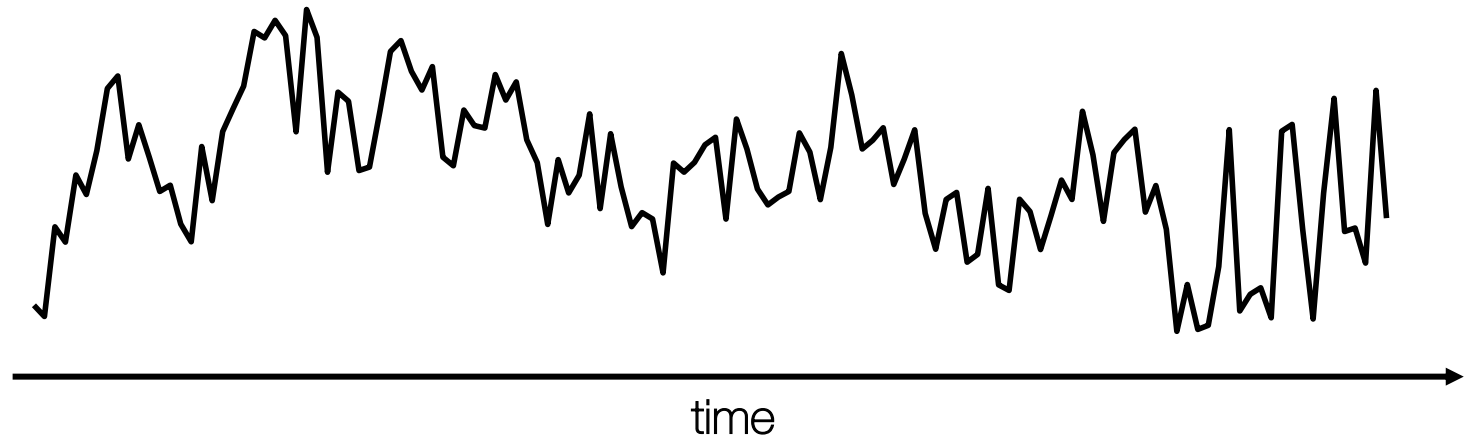
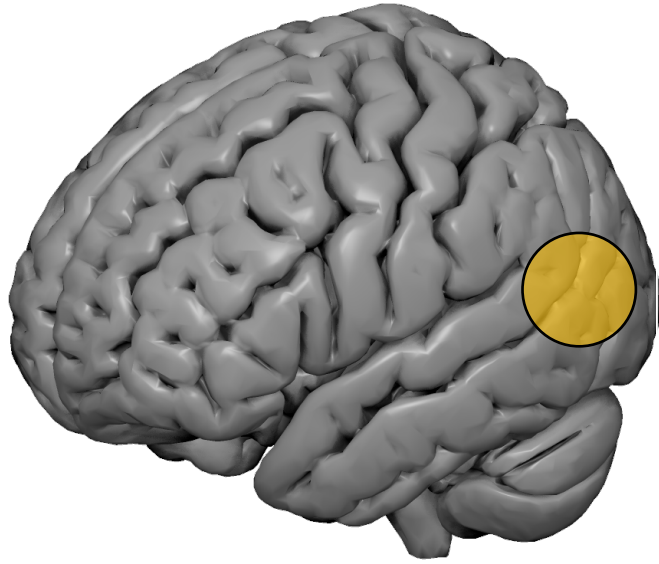


Preprocessing with fMRIPrep

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Turku PET Centre



Preparing your data for statistical analysis

- I. Dealing with artifacts
- II. Normalization

fMRIPrep

nature|methods









ARTICLES

<https://doi.org/10.1038/s41592-018-0235-4>



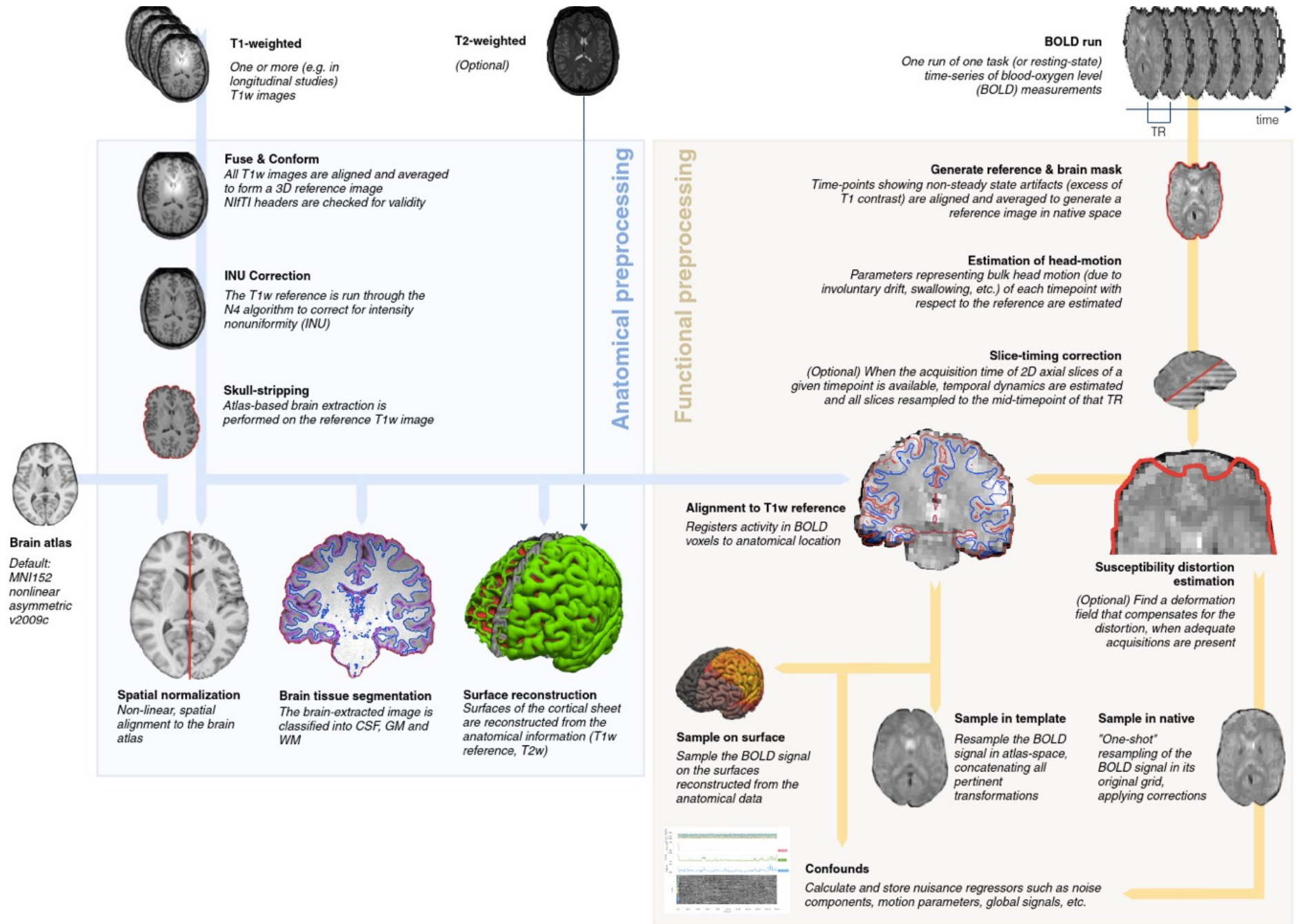
Nipype:
Neuroimaging in Python
Pipelines and Interfaces

fMRIPrep: a robust preprocessing pipeline for functional MRI

Oscar Esteban ^{1*}, Christopher J. Markiewicz ¹, Ross W. Blair¹, Craig A. Moodie ¹, A. Ilkay Isik ², Asier Erramuzpe ³, James D. Kent⁴, Mathias Goncalves⁵, Elizabeth DuPre ⁶, Madeleine Snyder⁷, Hiroyuki Oya⁸, Satrajit S. Ghosh ^{5,9}, Jessey Wright¹, Joke Durnez ¹, Russell A. Poldrack^{1,10} and Krzysztof J. Gorgolewski ^{1,10*}

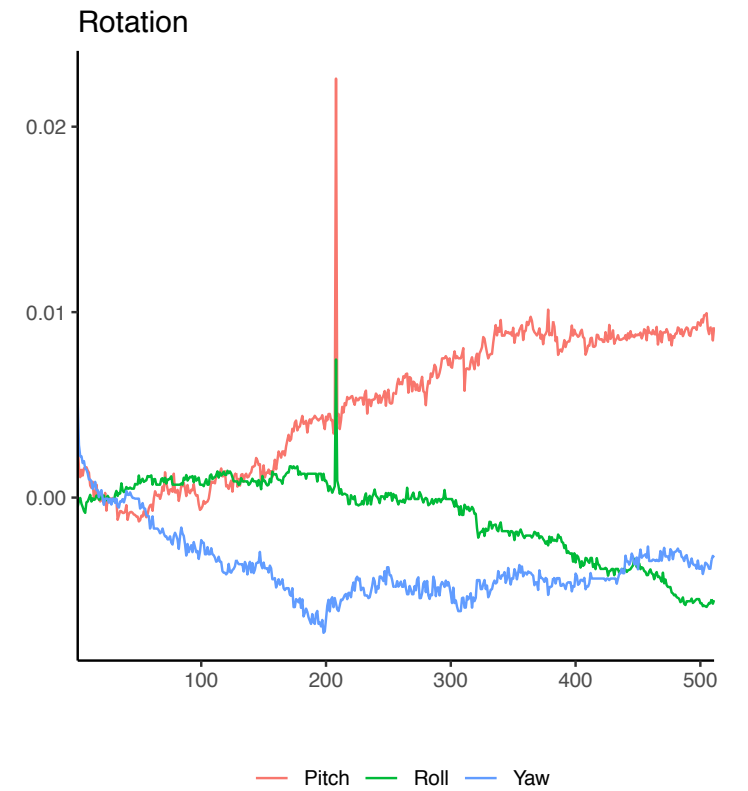
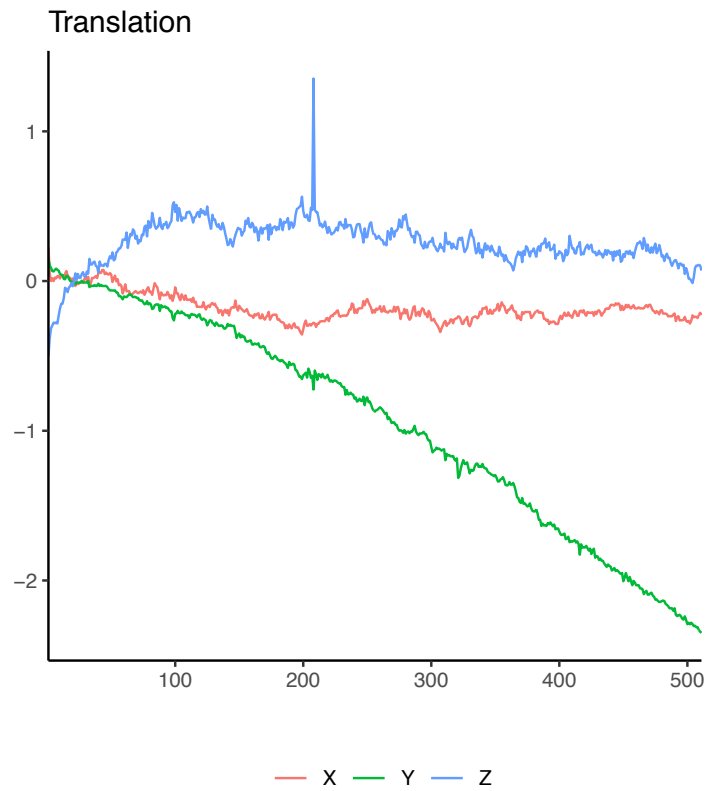
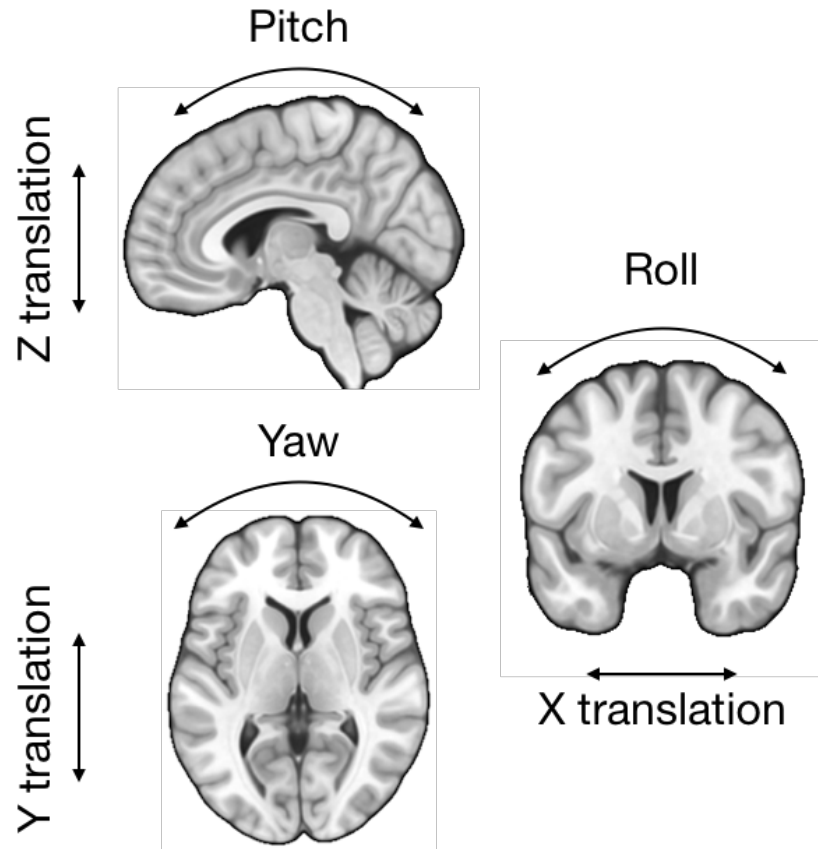
Preprocessing of functional magnetic resonance imaging (fMRI) involves numerous steps to clean and standardize the data before statistical analysis. Generally, researchers create ad hoc preprocessing workflows for each dataset, building upon a large inventory of available tools. The complexity of these workflows has snowballed with rapid advances in acquisition and processing. We introduce fMRIPrep, an analysis-agnostic tool that addresses the challenge of robust and reproducible preprocessing for fMRI data. fMRIPrep automatically adapts a best-in-breed workflow to the idiosyncrasies of virtually any dataset, ensuring high-quality preprocessing without manual intervention. By introducing visual assessment checkpoints into an iterative integration framework for software testing, we show that fMRIPrep robustly produces high-quality results on a diverse fMRI data collection. Additionally, fMRIPrep introduces less uncontrolled spatial smoothness than observed with commonly used preprocessing tools. fMRIPrep equips neuroscientists with an easy-to-use and transparent preprocessing workflow, which can help ensure the validity of inference and the interpretability of results.

Preprocessing task	Included with fMRIPrep
Anatomical T1-weighted brain extraction	antsBrainExtraction.sh (ANTs)
Anatomical surface reconstruction	recon-all (FreeSurfer)
Head-motion estimation (and correction)	MCFLIRT (FSL)
Susceptibility-derived distortion estimation (and unwarping)	3dqwarp (AFNI)
Slice-timing correction	3dTshift (AFNI)
Intrasubject registration	bbregister (FreeSurfer), FLIRT (FSL)
Spatial normalization (intersubject co-registration)	antsRegistration (ANTs)
Surface sampling	mri_vol2surf (FreeSurfer)
Subspace projection denoising (e.g., independent or principal component analysis)	MELODIC (FSL), ICA-AROMA



Head Motion

Head Motion



Head Motion

- fMRIPrep uses FSL's MCFLIRT to estimate head motion
- Motion correction:
 - I. Selection of a reference volume
 - II. Registration of each frame to the reference frame through rigid-body transformations
- The goal is to realign all volumes to the reference volume

Frame 1 vs. frame 200 without motion correction



Frame 1 vs. frame 200 with motion correction with FSL's mcflirt

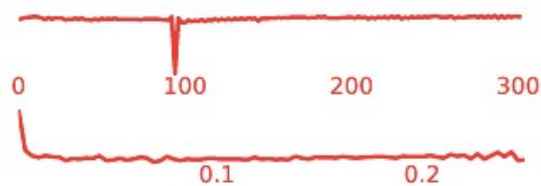
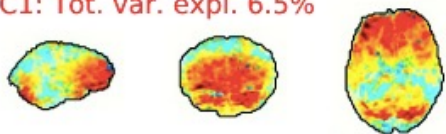


ICA-AROMA Denoising

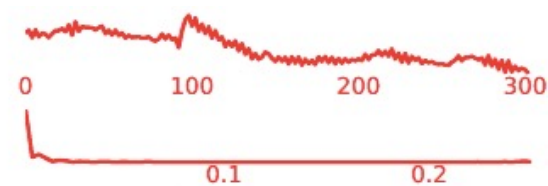
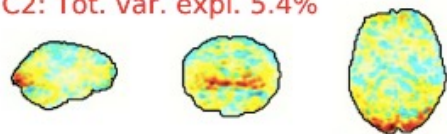
- ICA-AROMA can be used as a part of the preprocessing pipeline
 - ICA = Independent Component Analysis
 - AROMA = Automatic Removal of Motion Artifacts (Pruim et al., 2015).
- ICA decomposes the BOLD data into spatially independent component maps, and associated time-courses
- ICA-AROMA automatically identifies and removes motion-related independent components from the BOLD time series

ICA-AROMA Denoising

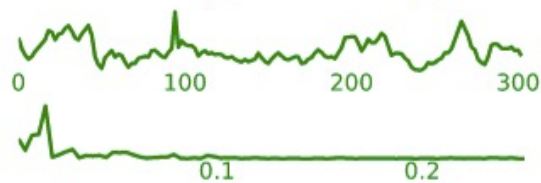
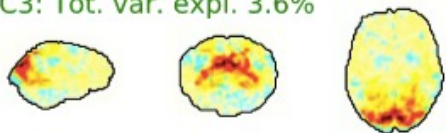
C1: Tot. var. expl. 6.5%



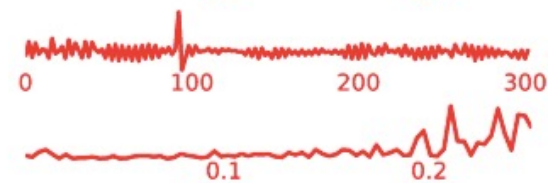
C2: Tot. var. expl. 5.4%



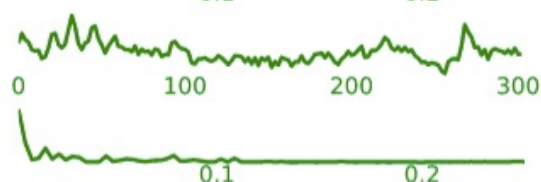
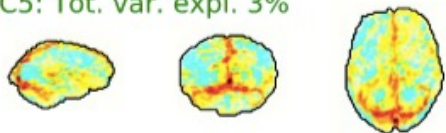
C3: Tot. var. expl. 3.6%



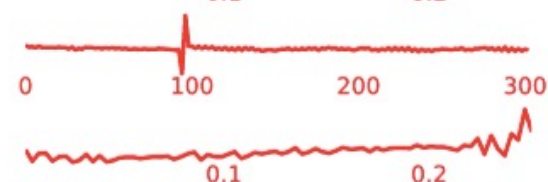
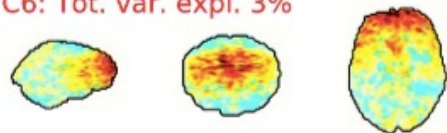
C4: Tot. var. expl. 3.1%



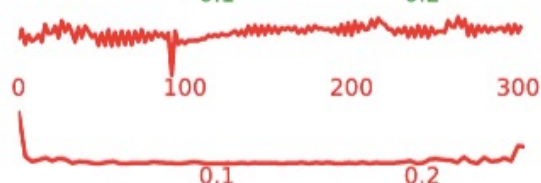
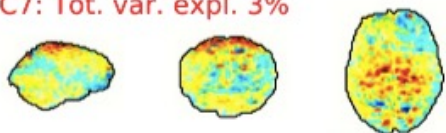
C5: Tot. var. expl. 3%



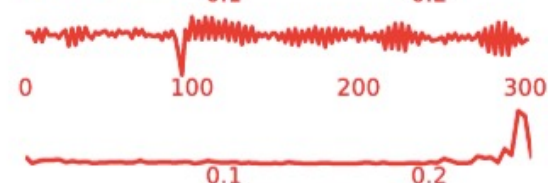
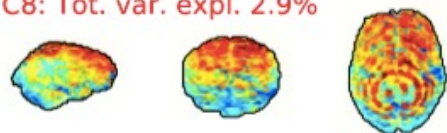
C6: Tot. var. expl. 3%



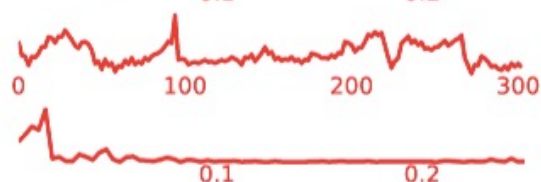
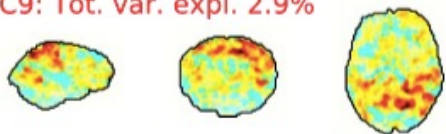
C7: Tot. var. expl. 3%



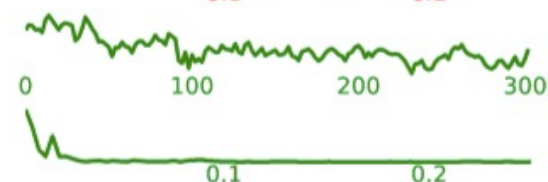
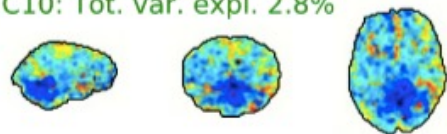
C8: Tot. var. expl. 2.9%



C9: Tot. var. expl. 2.9%



C10: Tot. var. expl. 2.8%



Spatial Normalization

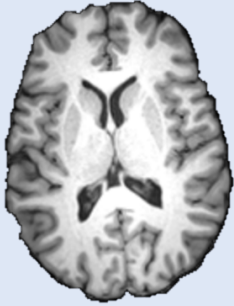
Spatial Normalization

- The goal is to deform the images so that a given voxel refers (roughly) to the same region across subjects.
- The most commonly used standard space is the **MNI** (Montreal Neurological Institute) space.
- By default, fMRIPrep uses (Advanced Normalization tools) ANTs nonlinear registration (Avants et al., 2009) with MNI152NLin2009cAsym as the reference.

Spatial Normalization

Native space

Subject 1

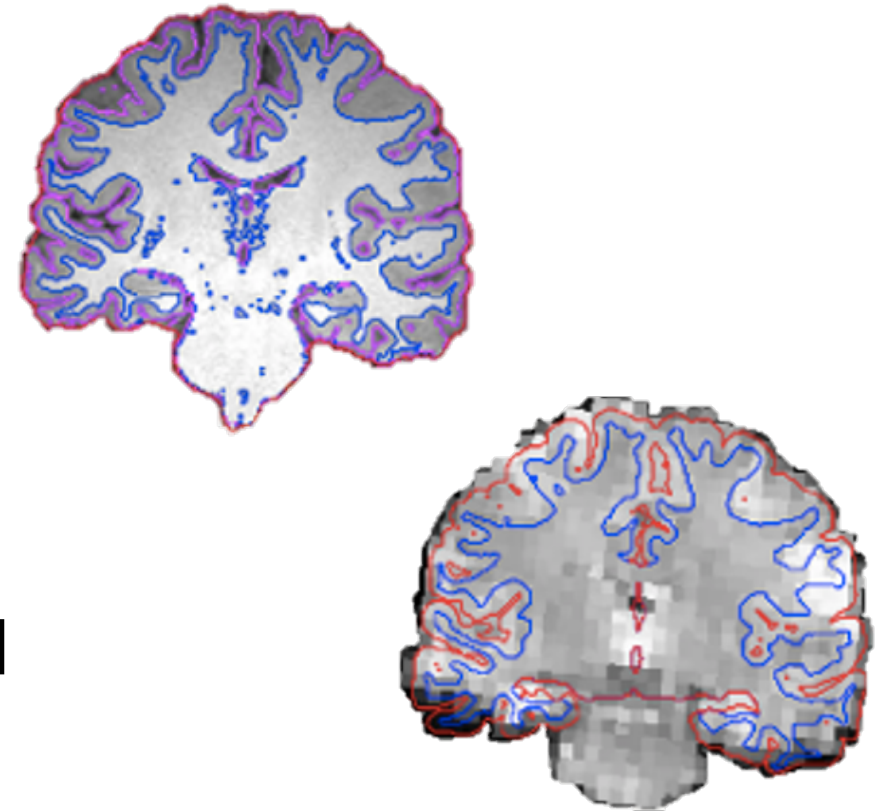


Subject 2



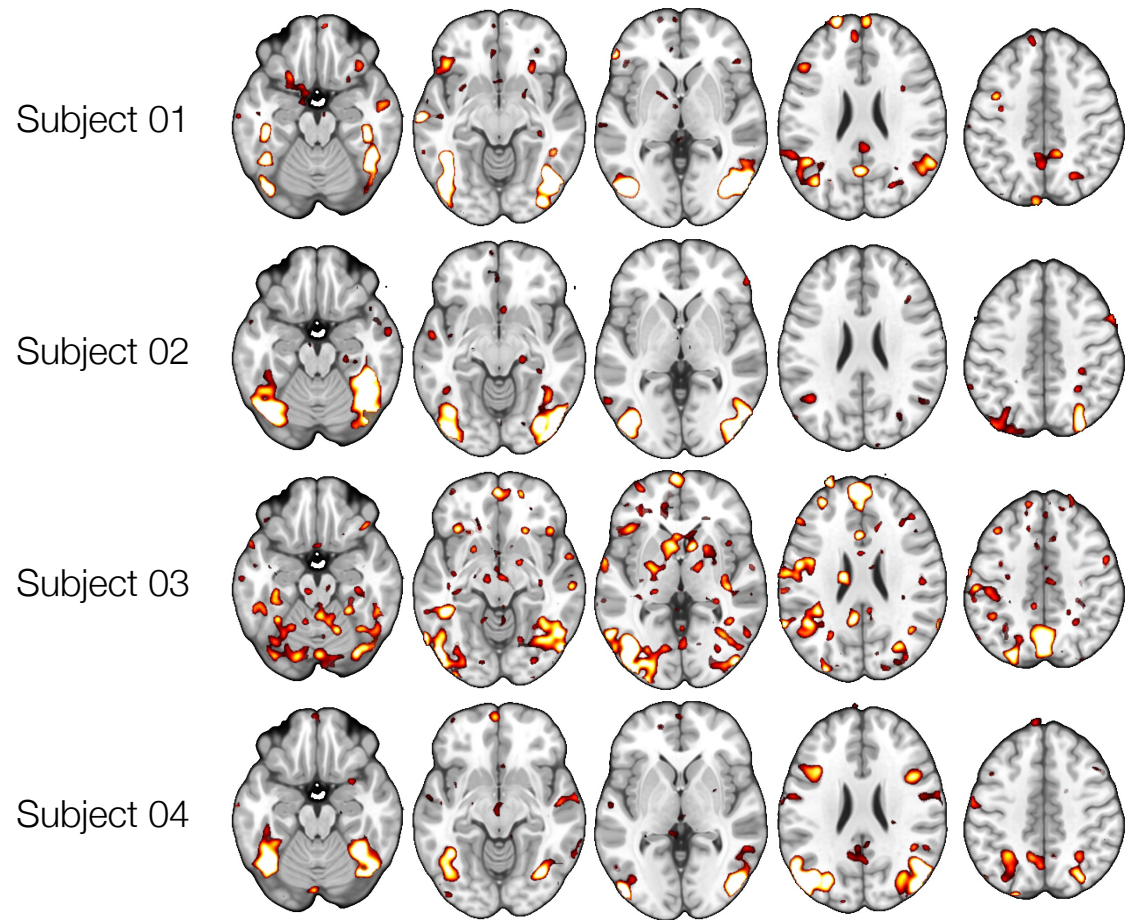
Co-registration

- Alignment of subject's fMRI data with the separately acquired anatomical image
- fMRIPrep uses Boundary Based Registration (BBR) (Greve & Fischl, 2009) for co-registration
- Gray/white matter boundary is obtained either by Freesurfer or FSL's FAST



1st level analysis

Subject-wise activation maps in standard space



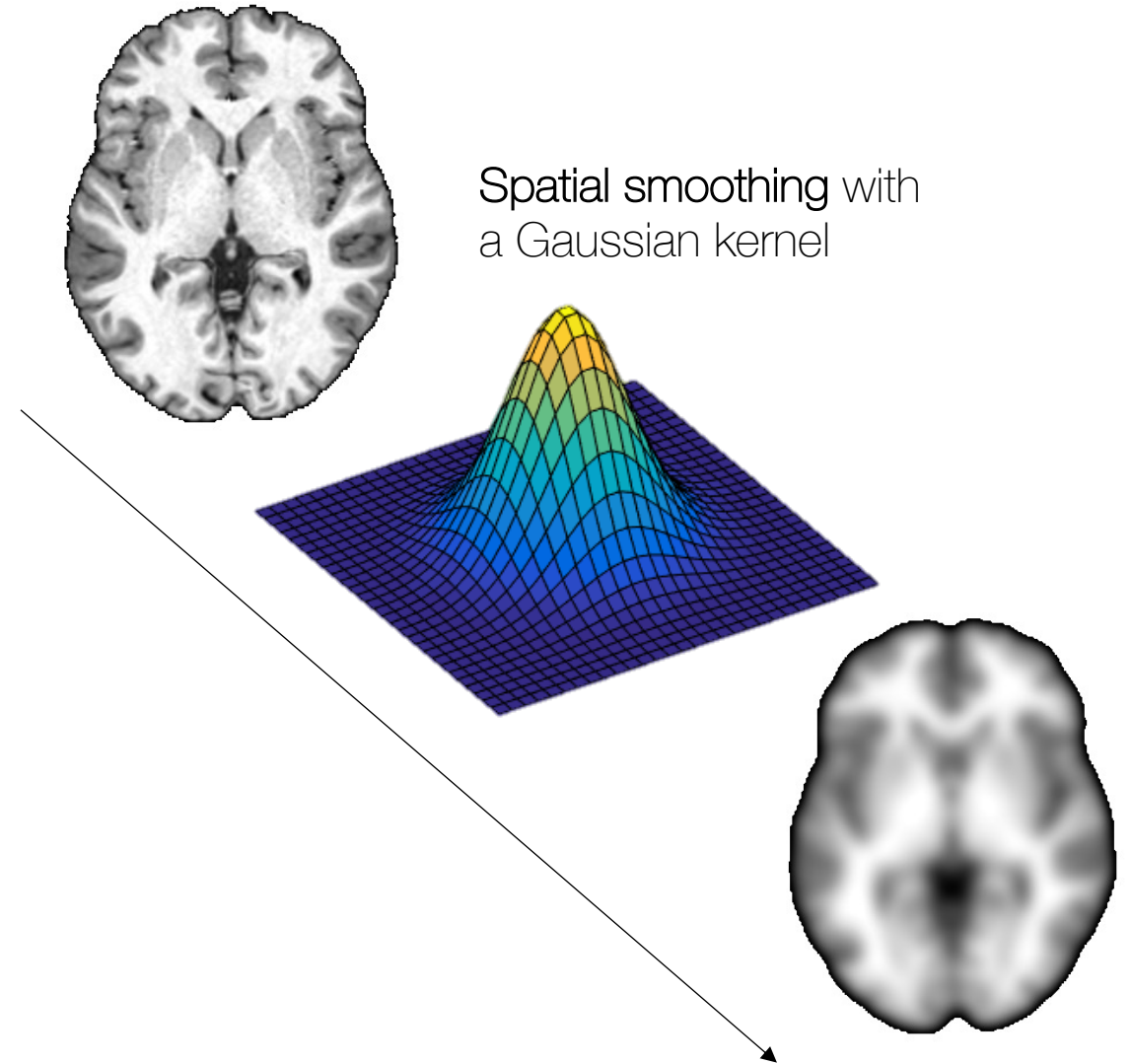
Spatial Smoothing

Spatial Smoothing

Possible benefits:

- I. Improved SNR
- II. more normally distributed data
- III. accomodation of intersubject-variability

By default, fMRIPrep does not perform spatial smoothing (however, smoothing is included in ICA-AROMA)

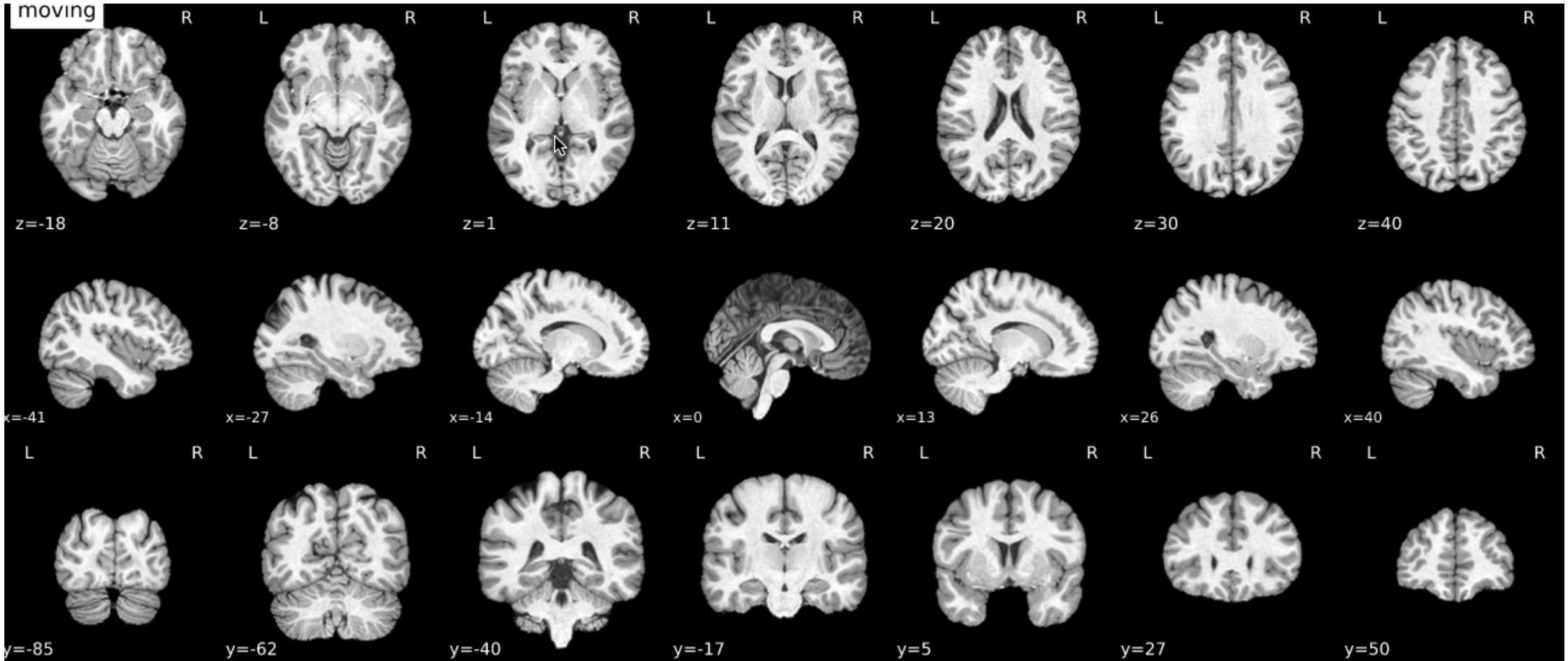


fMRIprep Outputs

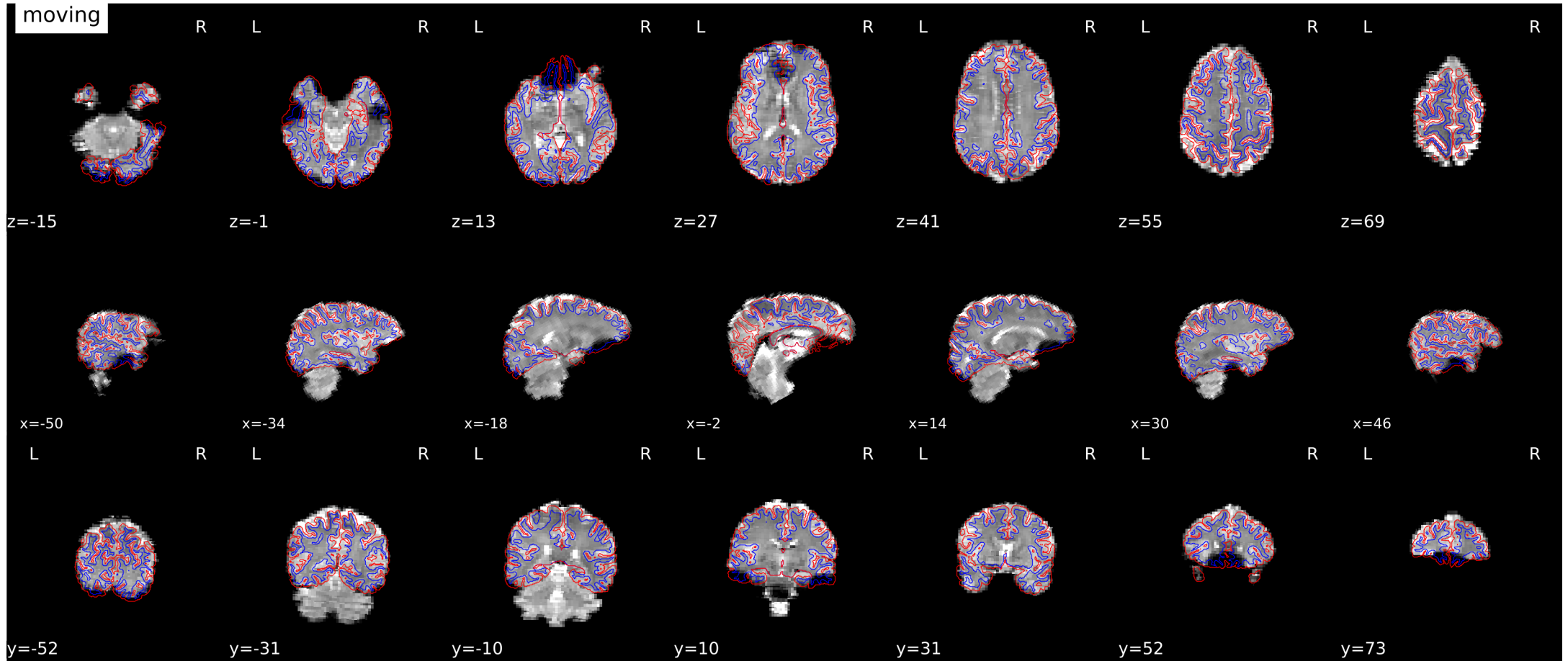
fRMIPrep derivatives

```
./func/  
— sub-014_task-pictures_AROMAnoiseICs.csv  
— sub-014_task-pictures_desc-confounds_regressors.tsv  
— sub-014_task-pictures_desc-MELODIC_mixing.tsv  
— sub-014_task-pictures_space-fsaverage5_hemi-L.func.gii  
— sub-014_task-pictures_space-fsaverage5_hemi-R.func.gii  
— sub-014_task-pictures_space-MNI152Nlin2009cAsym_boldref.nii.gz  
— sub-014_task-pictures_space-MNI152Nlin2009cAsym_desc-aparcaseg_dseg.nii.gz  
— sub-014_task-pictures_space-MNI152Nlin2009cAsym_desc-aseg_dseg.nii.gz  
— sub-014_task-pictures_space-MNI152Nlin2009cAsym_desc-brain_mask.nii.gz  
— sub-014_task-pictures_space-MNI152Nlin2009cAsym_desc-preproc_bold.nii.gz  
— sub-014_task-pictures_space-MNI152Nlin2009cAsym_desc-smoothAROMAnonaggr_bold.nii.gz
```

QA: T1 Normalization



QA: Co-registration



Running fMRIPrep

Running fMRIPrep

- Convert your images into NifTI format
- Save **metadata** to a task-specific JSON file
- Make **BIDS-compatible** folder structure
- Rename files in a **BIDS-compatible** manner

SCIENTIFIC DATA

OPEN

SUBJECT CATEGORIES

- » Data publication and archiving
- » Research data

The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments

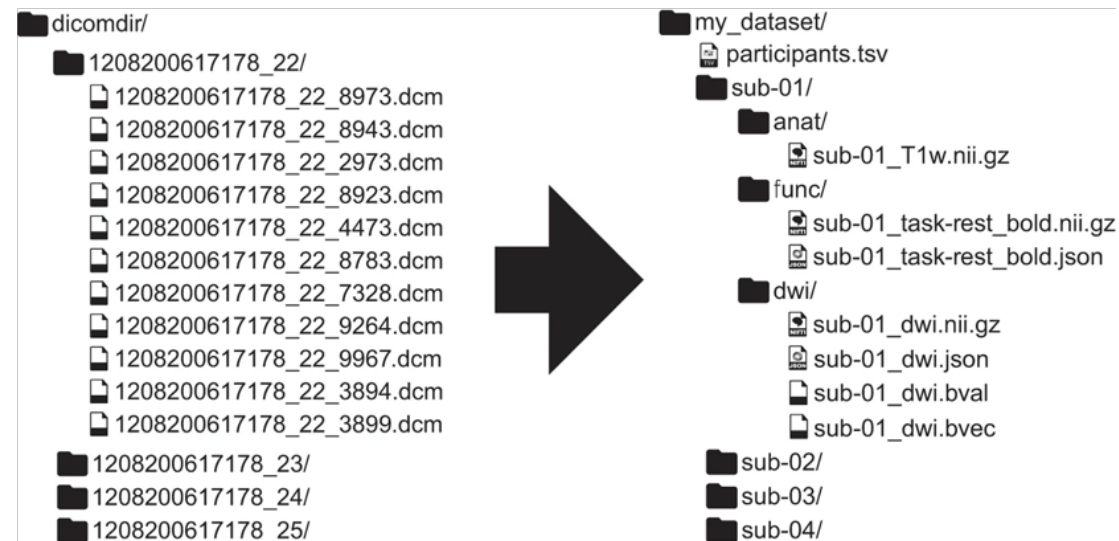
Krzysztof J. Gorgolewski¹, Tibor Auer², Vince D. Calhoun^{3,4}, R. Cameron Craddock^{5,6}, Samir Das⁷, Eugene P. Duff⁸, Guillaume Flandin⁹, Satrajit S. Ghosh^{10,11}, Tristan Glatard^{7,12}, Yaroslav O. Halchenko¹³, Daniel A. Handwerker¹⁴, Michael Hanke^{15,16}, David Keator¹⁷, Xiangrui Li¹⁸, Zachary Michael¹⁹, Camille Maumet²⁰, B. Nolan Nichols^{21,22}, Thomas E. Nichols^{20,23}, John Pellman⁶, Jean-Baptiste Poline²⁴, Ariel Rokem²⁵, Gunnar Schaefer^{1,26}, Vanessa Sochat²⁷, William Triplett¹, Jessica A. Turner^{3,28}, Gaël Varoquaux²⁹ & Russell A. Poldrack¹

Received: 18 December 2015

Accepted: 19 May 2016

Published: 21 June 2016

The development of magnetic resonance imaging (MRI) techniques has defined modern neuroimaging. Since its inception, tens of thousands of studies using techniques such as functional MRI and diffusion weighted imaging have allowed for the non-invasive study of the brain. Despite the fact that MRI is routinely used to obtain data for neuroscience research, there has been no widely adopted standard for organizing and describing the data collected in an imaging experiment. This renders sharing and reusing data (within or between labs) difficult if not impossible and unnecessarily complicates the application of automatic pipelines and quality assurance protocols. To solve this problem, we have developed the Brain Imaging Data Structure (BIDS), a standard for organizing and describing MRI datasets. The BIDS standard uses file formats compatible with existing software, unifies the majority of practices already common in the field, and captures the metadata necessary for most common data processing operations.



<https://bids.neuroimaging.io/>


```
└─ raw
   └─ sub-01
      └─ anat
         └─ sub-01_T1w.nii.gz
      └─ func
         └─ sub-01_task-pictures_bold.nii.gz
   └─ sub-02
      └─ anat
         └─ sub-02_T1w.nii.gz
      └─ func
         └─ sub-02_task-pictures_bold.nii.gz
   └─ sub-03
      └─ anat
         └─ sub-03_T1w.nii.gz
      └─ func
         └─ sub-03_task-pictures_bold.nii.gz
   └─ sub-04
      └─ anat
         └─ sub-04_T1w.nii.gz
      └─ func
         └─ sub-04_task-pictures_bold.nii.gz
   └─ sub-05
      └─ anat
         └─ sub-05_T1w.nii.gz
      └─ func
         └─ sub-05_task-pictures_bold.nii.gz
   └─ task-pictures_bold.json
```

Running fMRIprep from the command line (docker wrapper)

```
fmripredocker /scratch2/megafmri/preprocessing/raw /scratch2/megafmri/preprocessing/preprocessed  
participant -t pictures --use-aroma --fs-license-file /usr/local/freesurfer/license.txt -w /  
scratch2/megafmri/preprocessing/tmp --low-mem --nthreads 8 --participant-label sub-014
```

fmripredocker <bids_dir> <output_dir> participant

-t: task to be processed

--use-aroma: use ICA_AROMA to remove movement related components

--fs-license-file: path to FreeSurfer license key file. Get it from
<https://surfer.nmr.mgh.harvard.edu/registration.html>

-w: path where intermediate results are stored

--low-mem: reduce memory usage (will increase disk usage in working directory)

--nthreads: maximum number of threads across all processes

--participant-label: participant identifier

<https://fmriprep.org/>

References

- Esteban, et al (2020). Analysis of task-based functional MRI data preprocessed with fMRIPrep. *Nature Protocols*, 15(7), 2186–2202.
- Esteban, et al. (2019). FMRIprep: A robust preprocessing pipeline for functional MRI. *Nature Methods*, 16(1), 111.
- Gorgolewski, et al. (2016). The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments. *Scientific Data*, 3(1), 160044.
- Pruim, et al. (2015). ICA-AROMA: A robust ICA-based strategy for removing motion artifacts from fMRI data. *Neuroimage*, 112, 267-277.