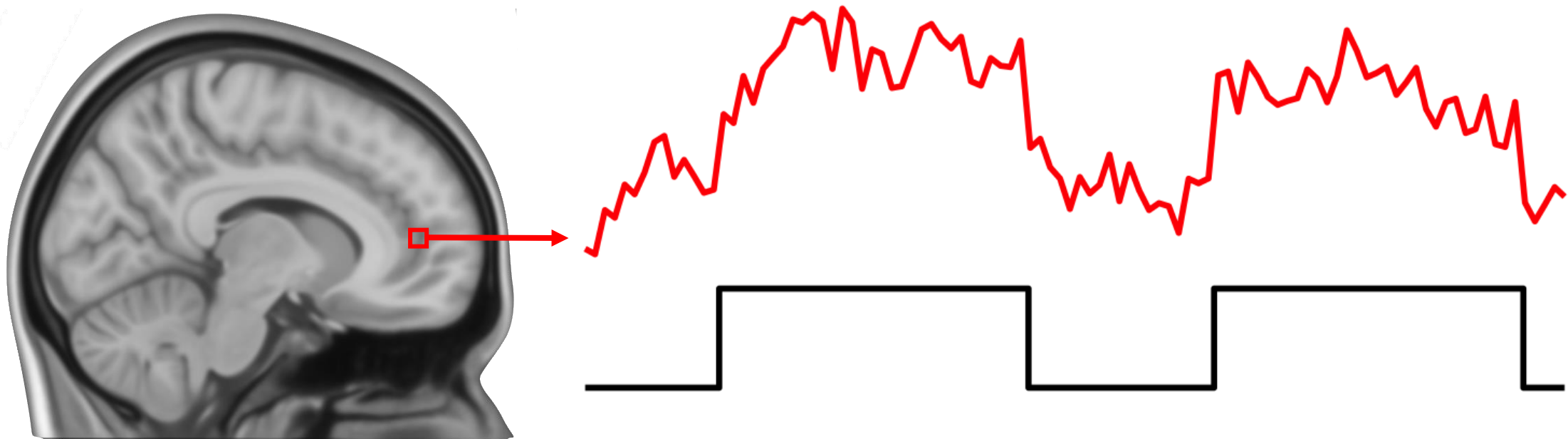


Practical framework for preprocessing fMRI data

Turku PET Centre Brain Imaging Course 2024

Vesa Putkinen, Turku PET Centre





Preparing your data for statistical analysis

- I. Dealing with artifacts
- II. Spatial normalization

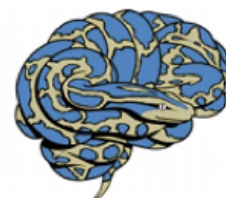
- **Motion correction:** Compensates for head movements by realigning the images to a common reference.
- **Co-registration:** Aligns images from different modalities into a common coordinate system.
- **Normalization:** Transforms individual brain images into a standard space enabling comparisons across subjects.
- **Smoothing:** Applies smoothing techniques to enhance signal-to-noise ratio by averaging neighboring voxel values.

fMRIPrep

nature|methods

ARTICLES

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



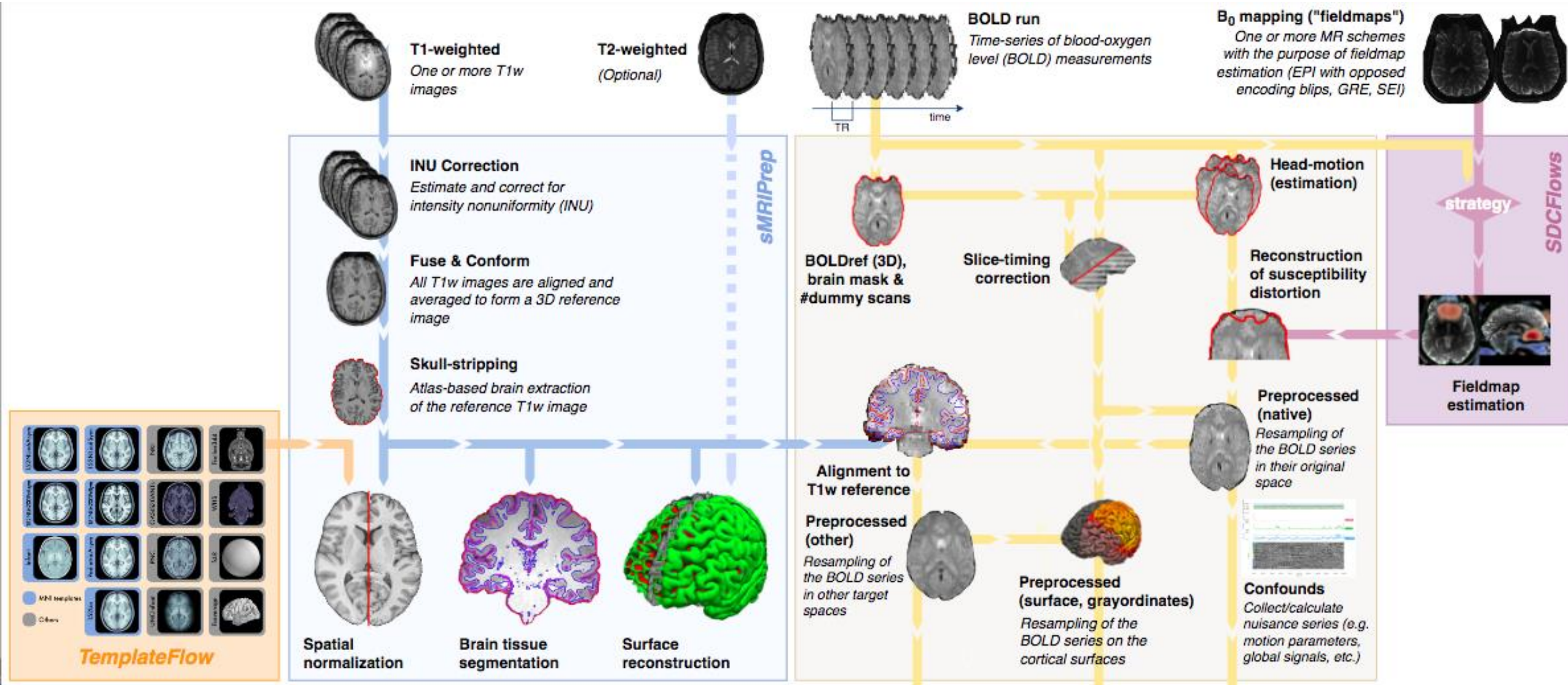
Nipype:
Neuroimaging in Python
Pipelines and Interfaces

fMRIPrep: a robust preprocessing pipeline for functional MRI

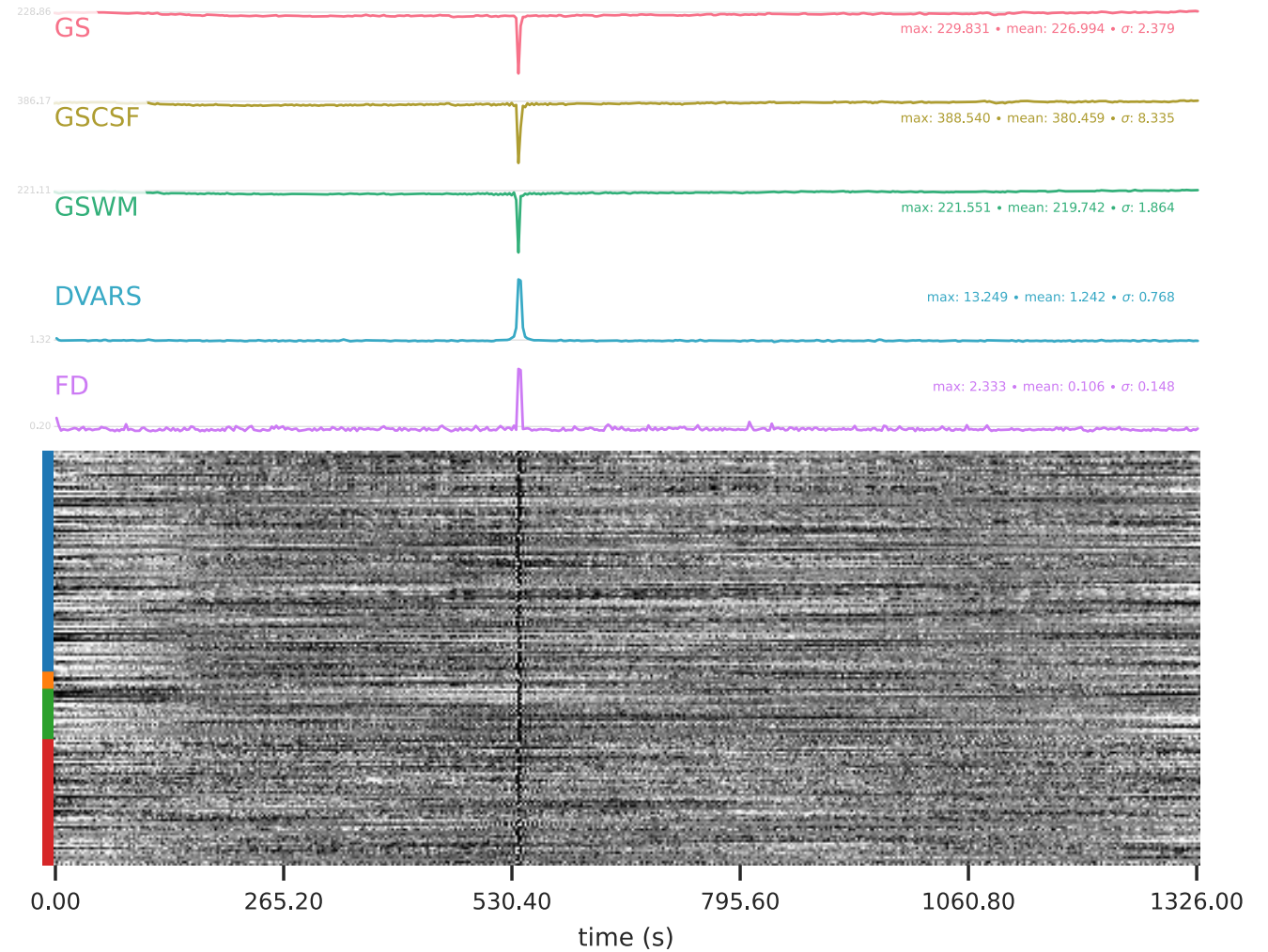
Oscar Esteban^{1*}, Christopher J. Markiewicz¹, Ross W. Blair¹, Craig A. Moodie¹, A. Ilkay Isik², Asier Erramuzpe³, James D. Kent⁴, Mathias Goncalves⁵, Elizabeth DuPre⁶, Madeleine Snyder⁷, Hiroyuki Oya⁸, Satrajit S. Ghosh^{5,9}, Jessey Wright¹, Joke Durnez¹, Russell A. Poldrack^{1,10} and Krzysztof J. 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.

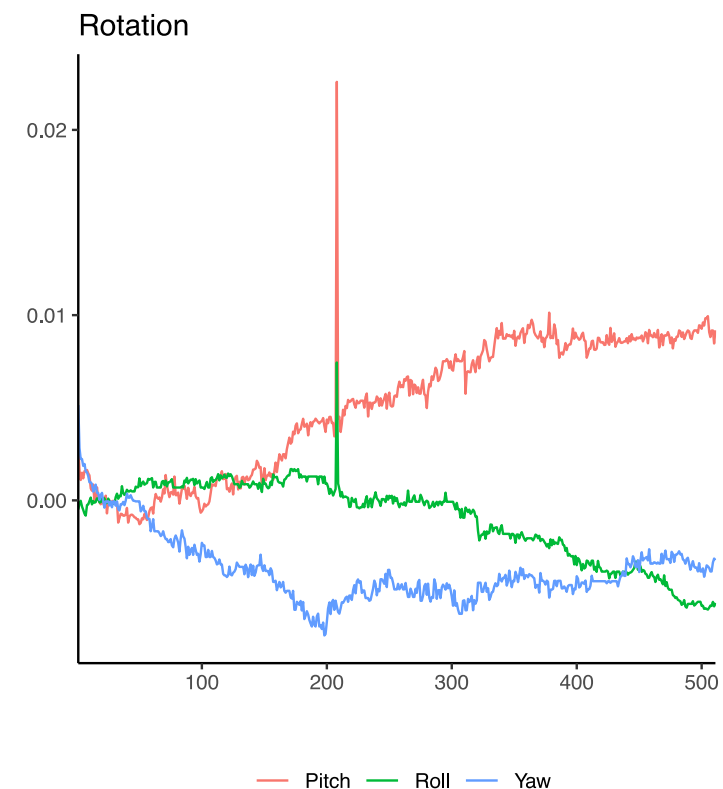
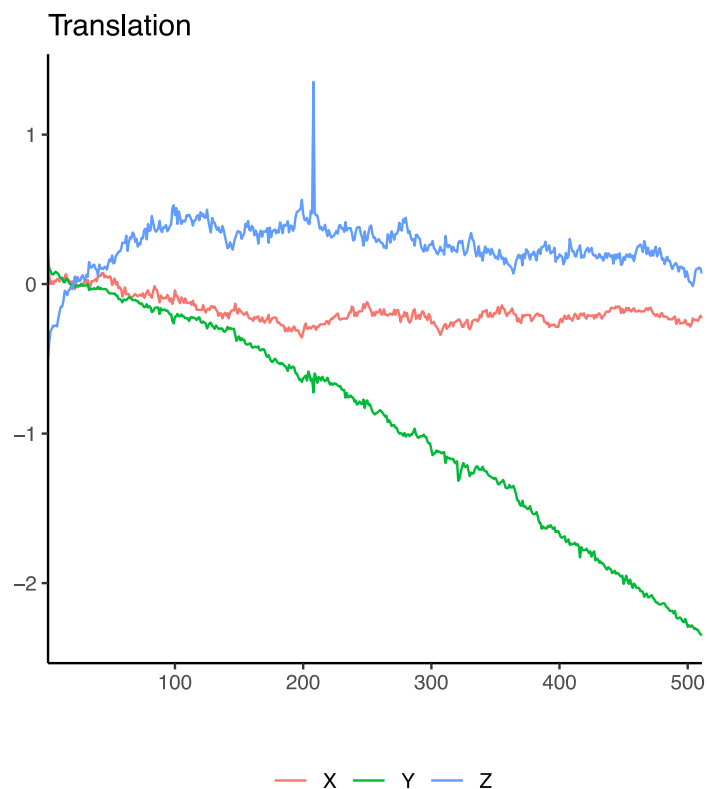
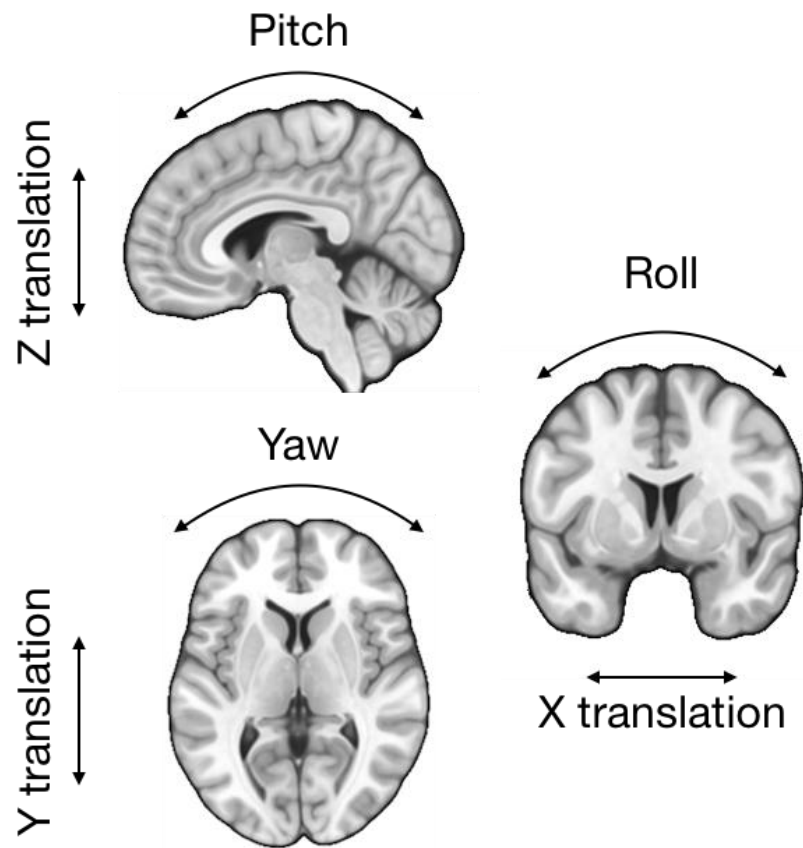
Preprocessing task	Included with fMRIPrep
Anatomical T1-weighted brain extraction	antsBrainExtraction.sh (ANTs)
Anatomical surface reconstruction	recon-all (FreeSurfer)
Head-motion estimation (and correction)	MCFLIRT (FSL)
Susceptibility-derived distortion estimation (and unwarping)	3dqwarp (AFNI)
Slice-timing 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

- **Head Motion Estimation:** fMRIPrep uses FSL's MCFLIRT* tool to estimate for head motion.
- **Head Motion Correction:**
 - **Reference Volume Selection:** A volume is chosen as the reference for alignment (often the first one).
 - **Frame Alignment:** Each frame is registered to the reference volume using linear transformations and a cost function.
- **Objective:** To optimally realign all volumes to the reference volume, minimizing motion-related artifacts.

*Motion Correction Using Linear Image Registration Tool (Jenkinson et al., 2002)

Frame 1 vs. frame 200 without motion correction



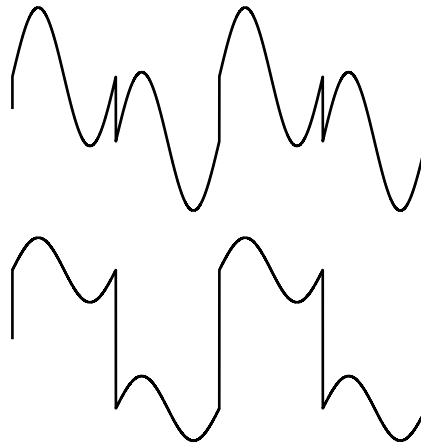
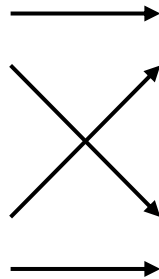
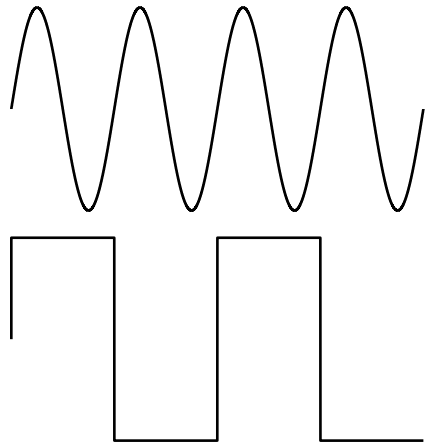
Frame 1 vs. frame 200 with motion correction with FSL's mcflirt



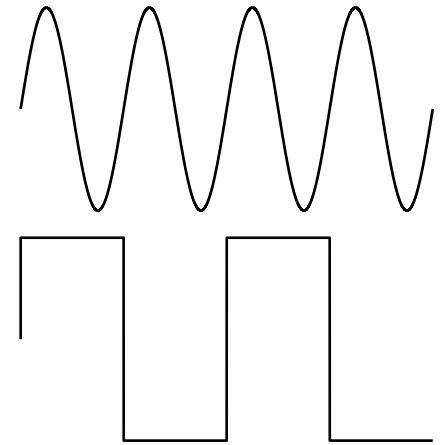
ICA-AROMA Denoising

- 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.

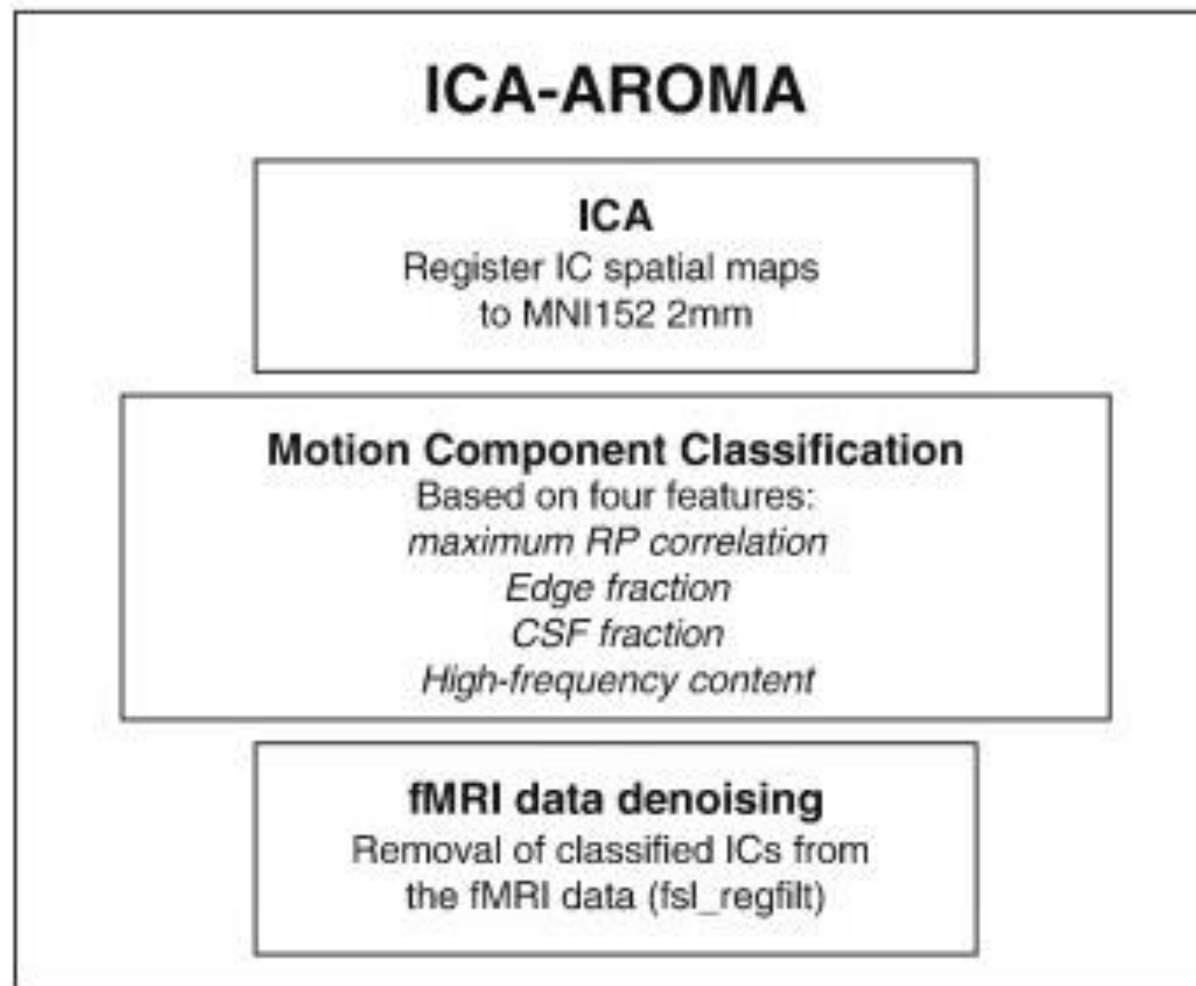
Independent component analysis



ICA

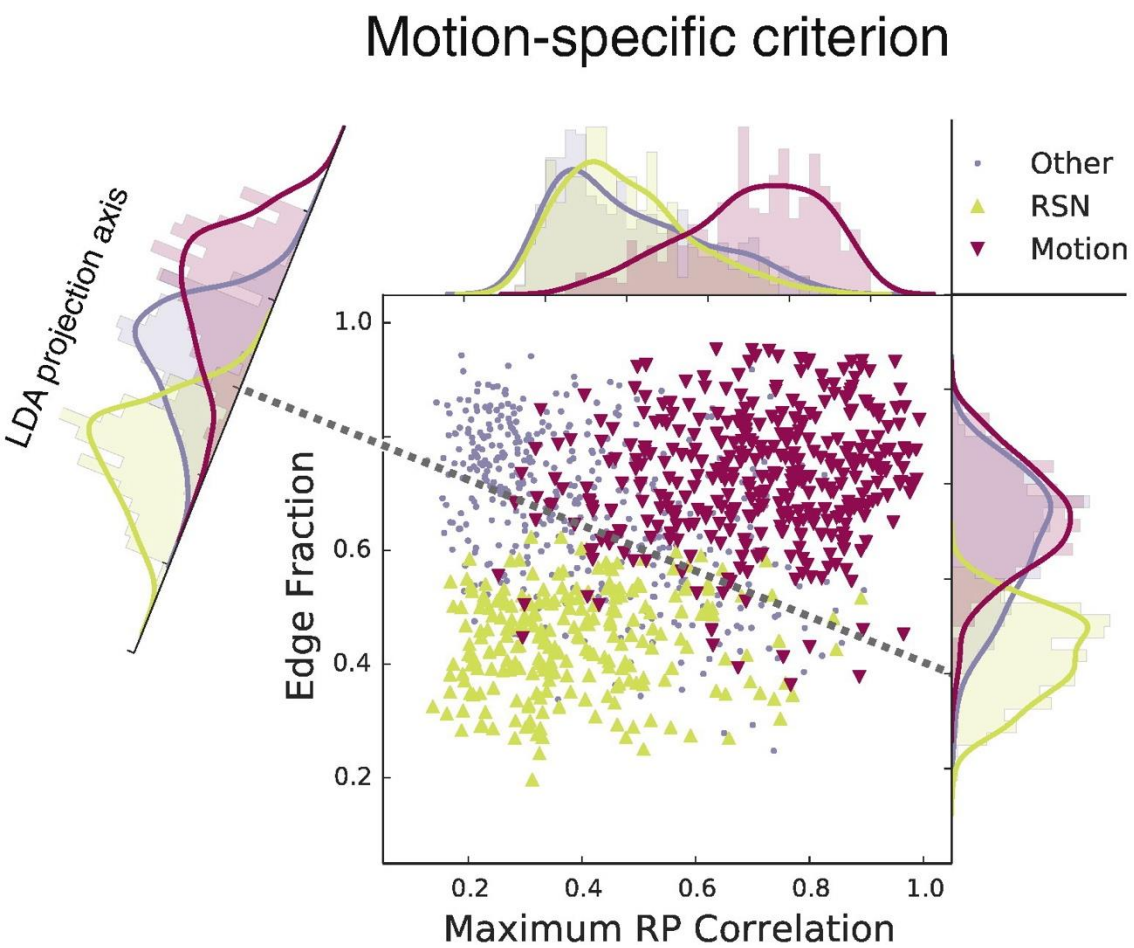


ICA-AROMA Denoising

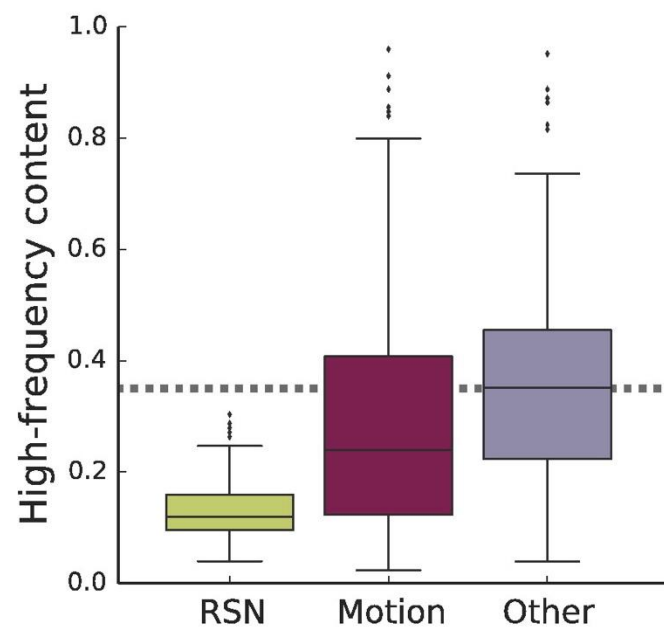


ICA-AROMA Denoising

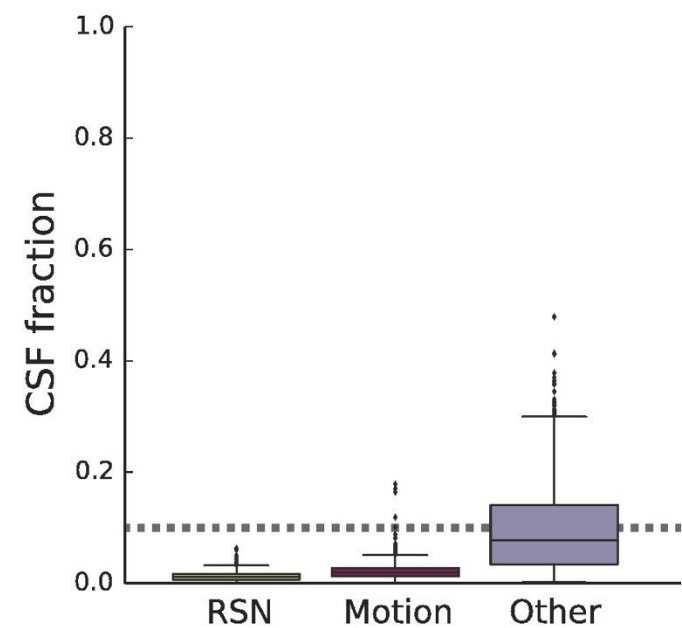
- **High-frequency content:** BOLD-related IC time-series are typically dominated by low-frequencies.
- **Maximum correlation with realignment parameters (RP):** Time-series of ICs representing motion artifact should correlate with RPs.
- **Edge fraction:** Head motion can cause strong variation in voxels situated close to the edge of the brain.
- **CSF fraction:** Same is true for other intensity edges such as ventricle borders.



High-frequency criterion

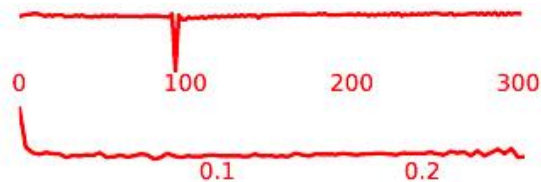
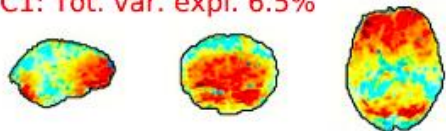


CSF criterion

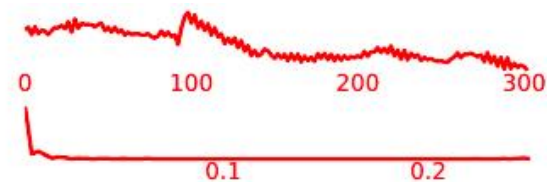
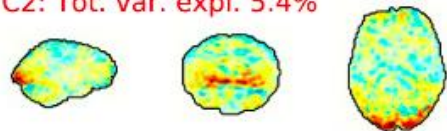


ICA-AROMA Denoising

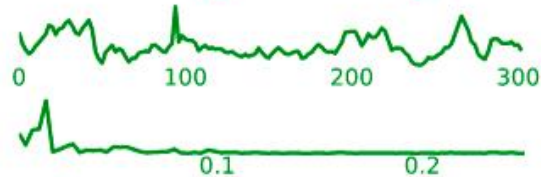
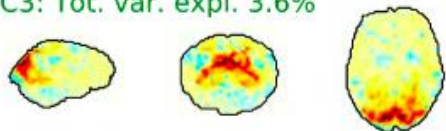
C1: Tot. var. expl. 6.5%



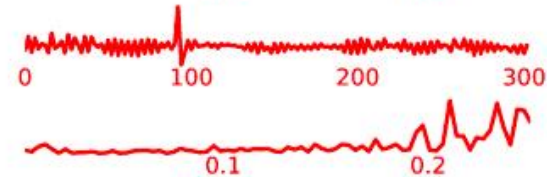
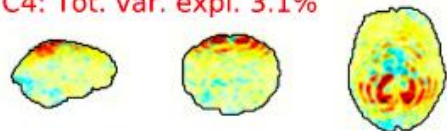
C2: Tot. var. expl. 5.4%



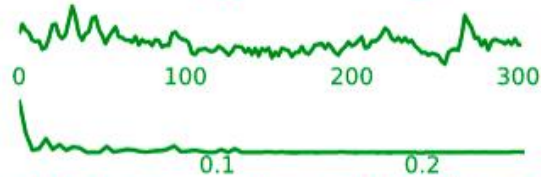
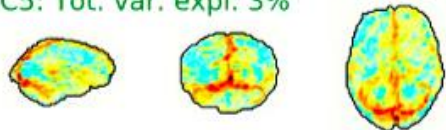
C3: Tot. var. expl. 3.6%



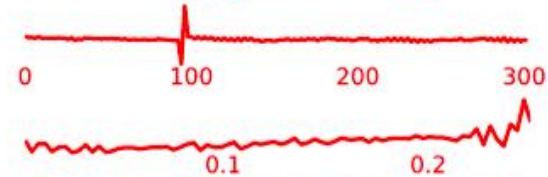
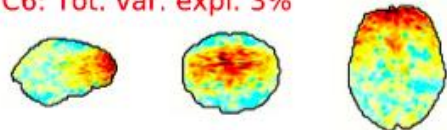
C4: Tot. var. expl. 3.1%



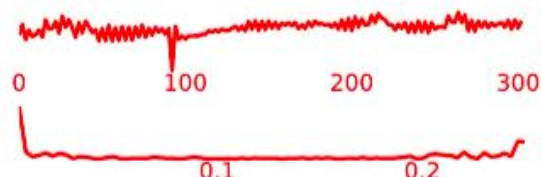
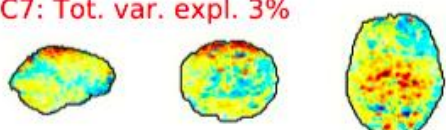
C5: Tot. var. expl. 3%



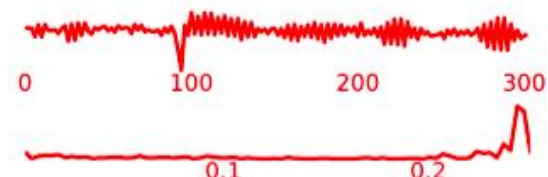
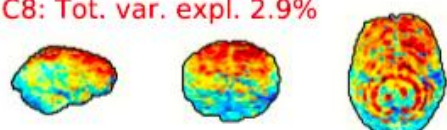
C6: Tot. var. expl. 3%



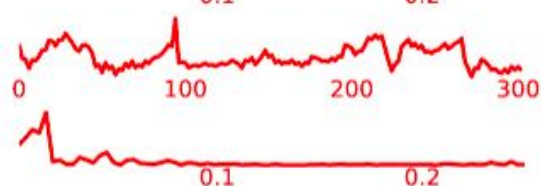
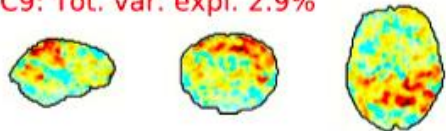
C7: Tot. var. expl. 3%



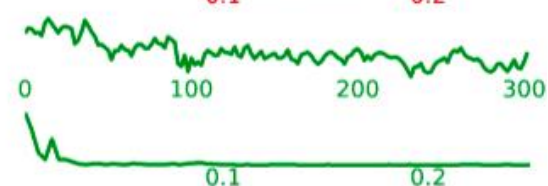
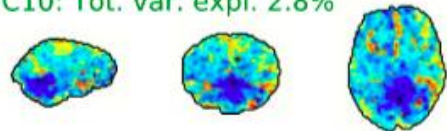
C8: Tot. var. expl. 2.9%



C9: Tot. var. expl. 2.9%



C10: Tot. var. expl. 2.8%



ICA-AROMA Denoising



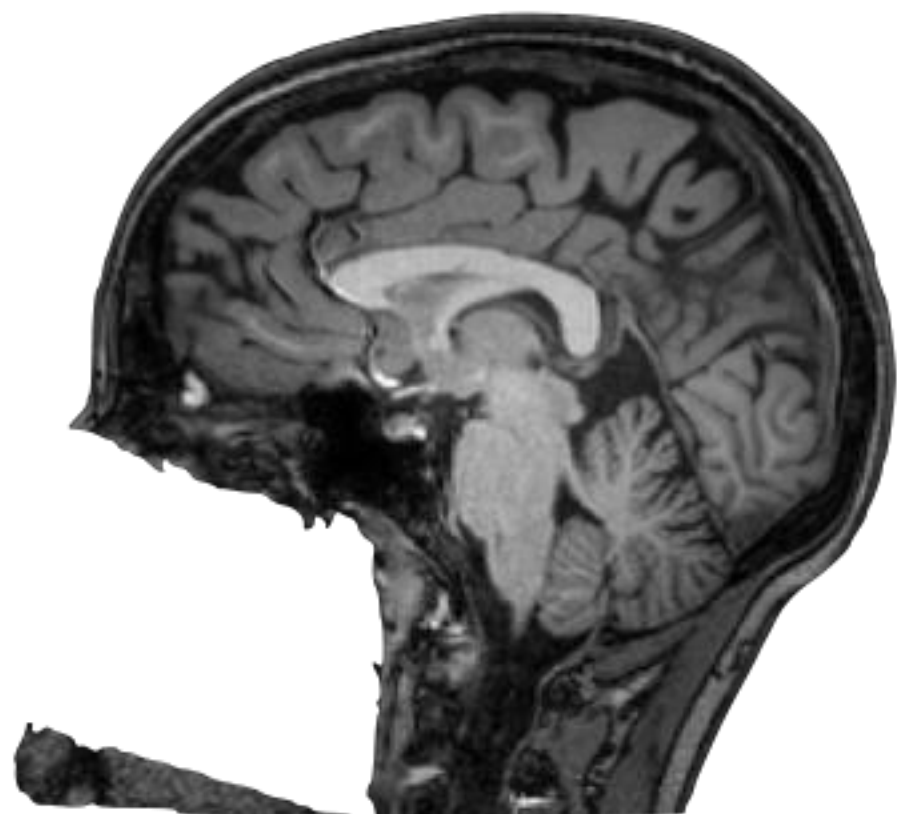
Non-aggressive ICA AROMA denoising aims to remove only the most obvious sources of noise and preserve as much of the signal as possible.



Aggressive ICA AROMA denoising removes all independent components identified as noise, including those that may contain some signal.

Spatial Normalization



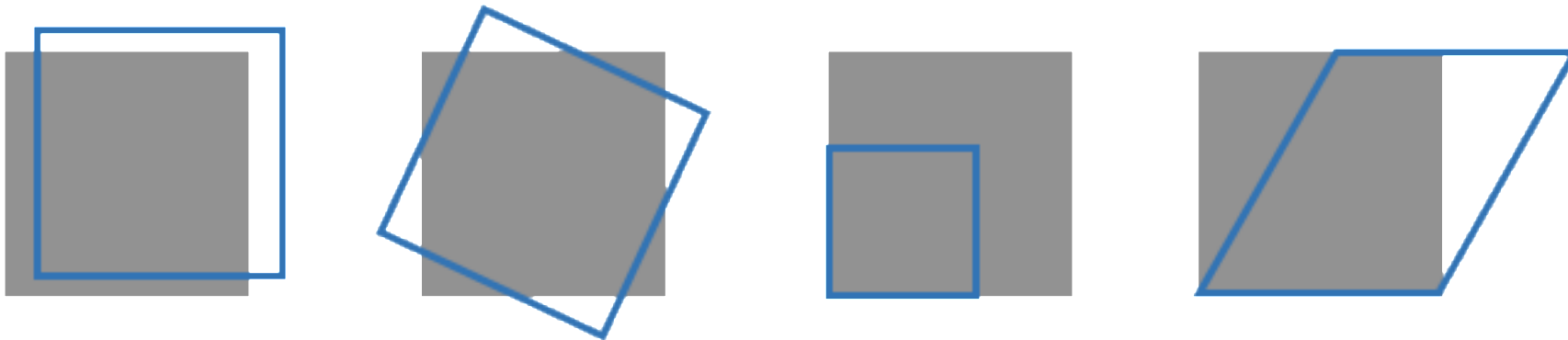


Spatial Normalization

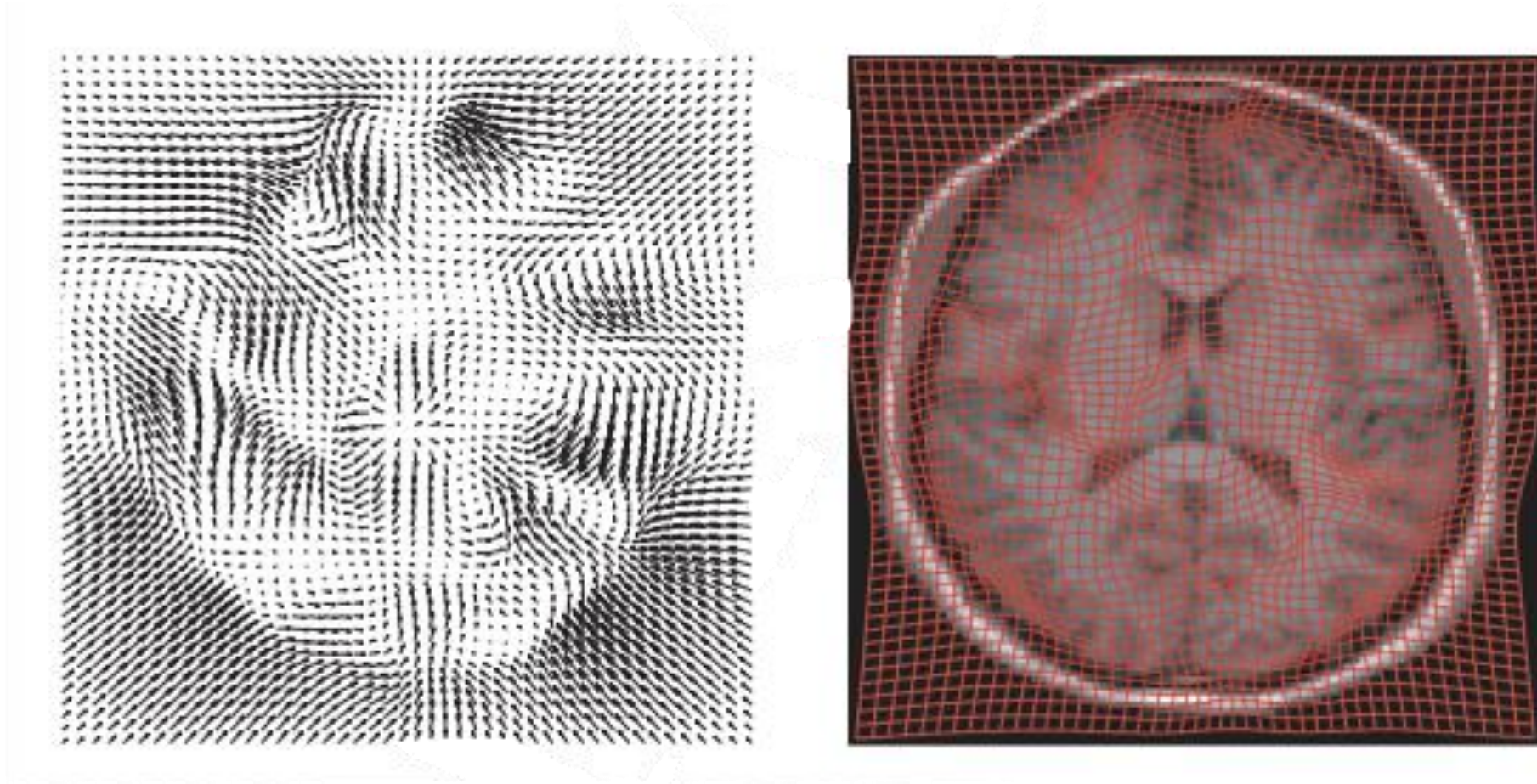
- **Objective:** Adjusting the images so that corresponding voxels represent approximately the same brain region across subjects.
 - Enables group-level statistical analysis.
 - Reduction in spatial resolution and alignment errors.
- The **MNI** (Montreal Neurological Institute) space is the most commonly used standard space.
 - Derived from the average of several co-registered brain volumes to be used as a template for automated registration processes.

Spatial Normalization: Affine transforms

- **Translation:** Moving an object in a particular direction by a certain distance.
- **Rotation:** Turning an object around a fixed point by a certain angle.
- **Scaling:** Changing the size of an object uniformly in all dimensions
- **Shear:** Distorting an object by stretching or skewing it along one or more axes while keeping other axes fixed.



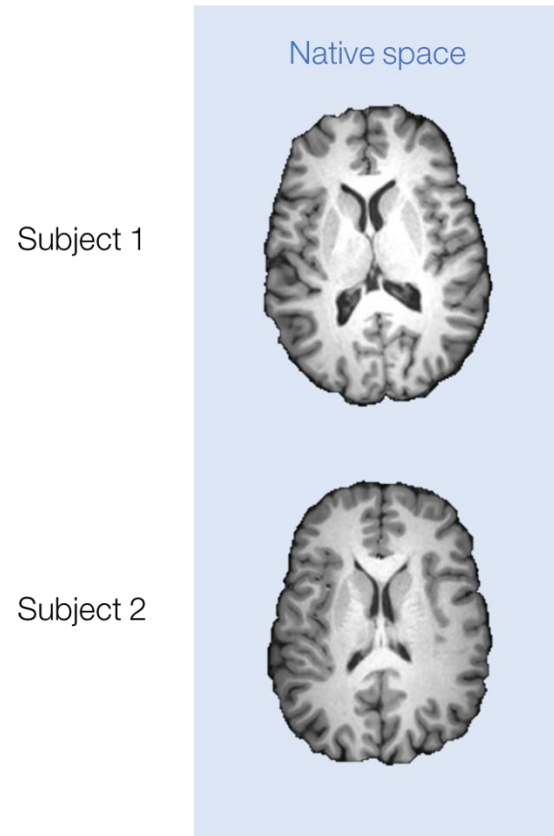
Spatial Normalization: diffeomorphism



Spatial Normalization in fMRIPrep

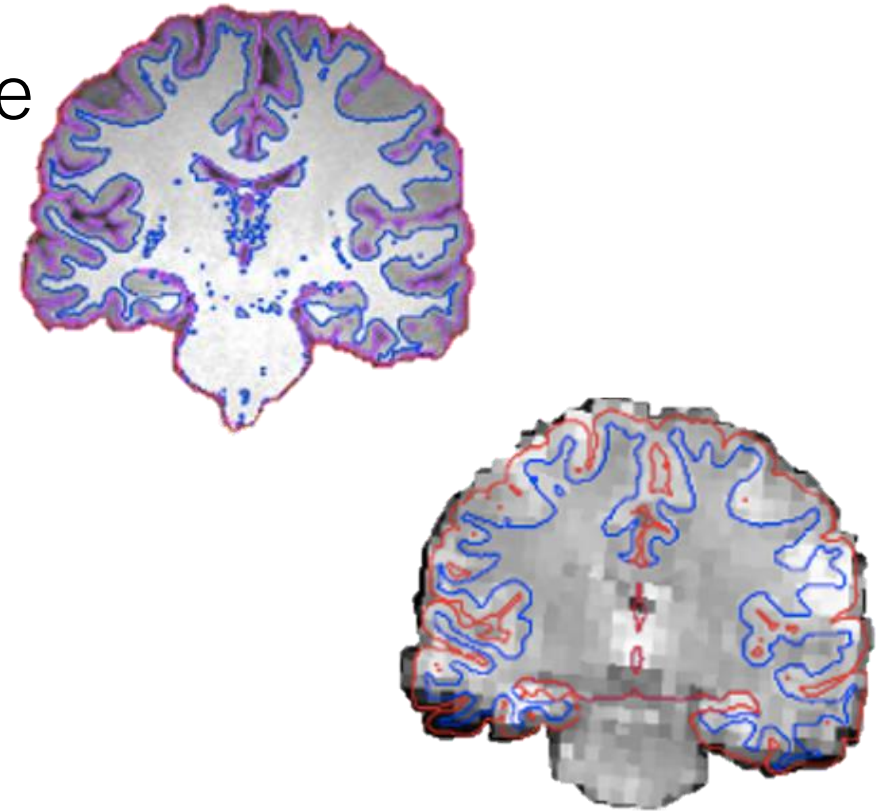
- By default, fMRIPrep uses Advanced Normalization tools (ANTs) (Avants et al., 2009) for registration with MNI152NLin2009cAsym as the reference.
- Performs nonlinear registration with mutual-information as the similarity metric (cost function).
- ANTs' Symmetric Normalization (SyN) algorithm that has performed very well in comparison studies (e.g. Klein et al., 2009)

Spatial Normalization



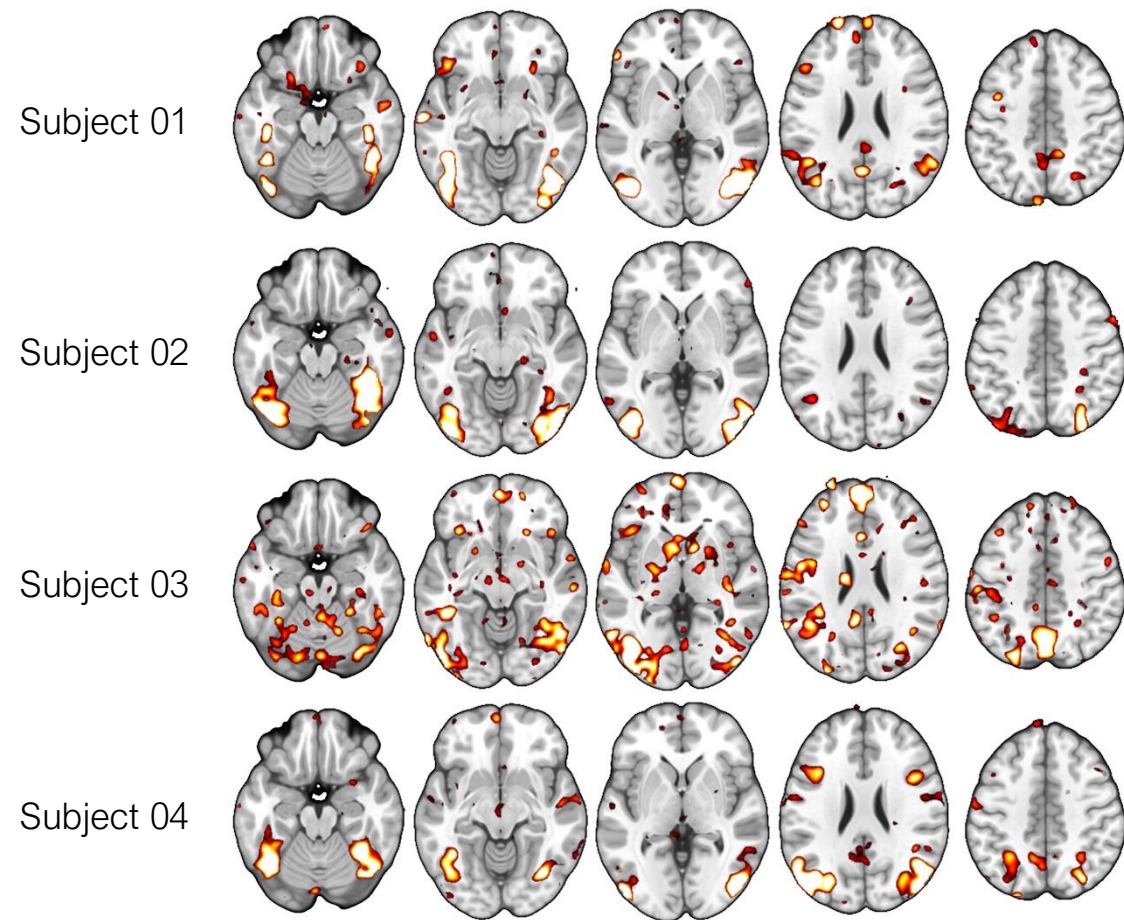
Co-registration

- 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

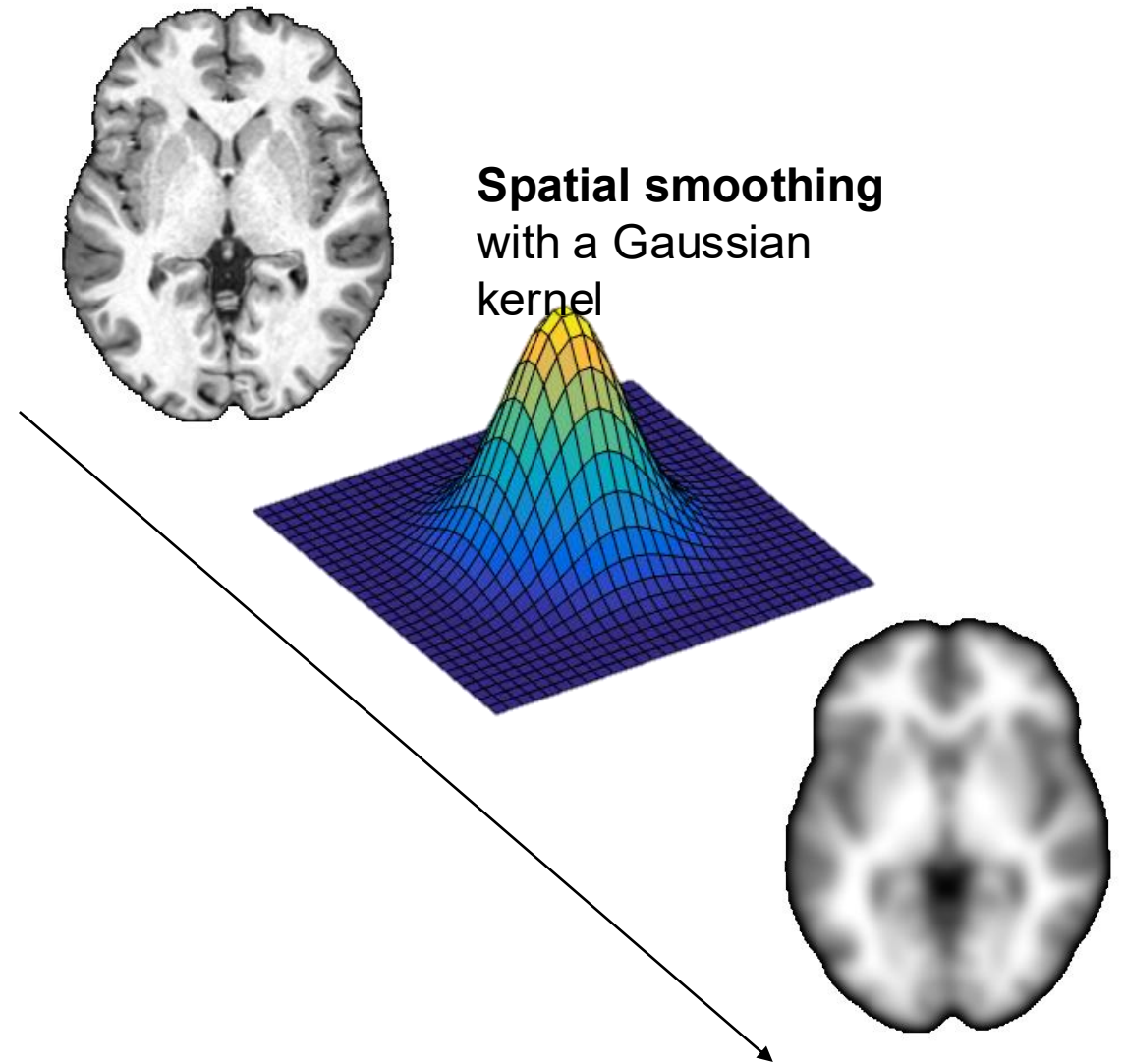


Spatial Smoothing

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)



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

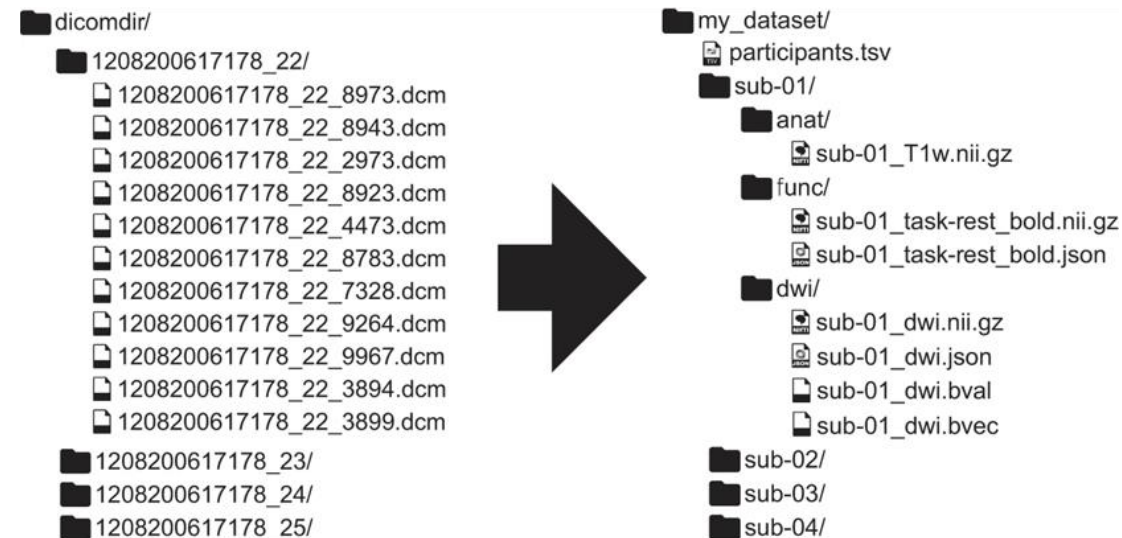
Krzysztof J. Gorgolewski¹, Tibor Auer², Vince D. Calhoun^{3,4}, R. Cameron Craddock^{5,6}, Samir Das⁷, Eugene P. Duff⁸, Guillaume Flandin⁹, Satrajit S. Ghosh^{10,11}, Tristan Glatard^{7,12}, Yaroslav O. Halchenko¹³, Daniel A. Handwerker¹⁴, Michael Hanke^{15,16}, David Keator¹⁷, Xiangrui Li¹⁸, Zachary 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
```

BIDS

- There are many tools available for converting your fMRI (and other) data to BIDS format
 - A list of some them can be found at <https://bids.neuroimaging.io/benefits>
 - Mostly Python-based
- You may want to check out the BIDS started kit
 - <https://bids-standard.github.io/bids-starter-kit/>

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

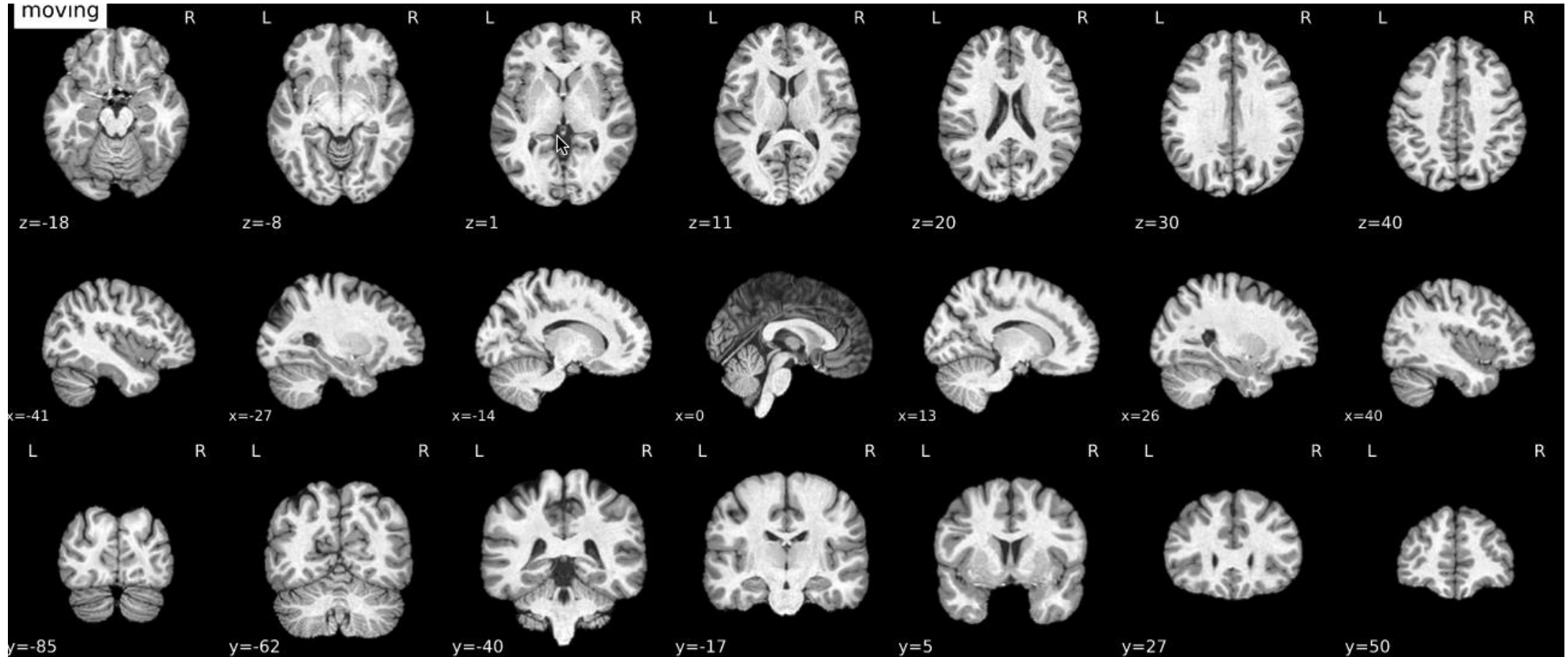
--participant-label: participant identifier

fMRIPrep Outputs

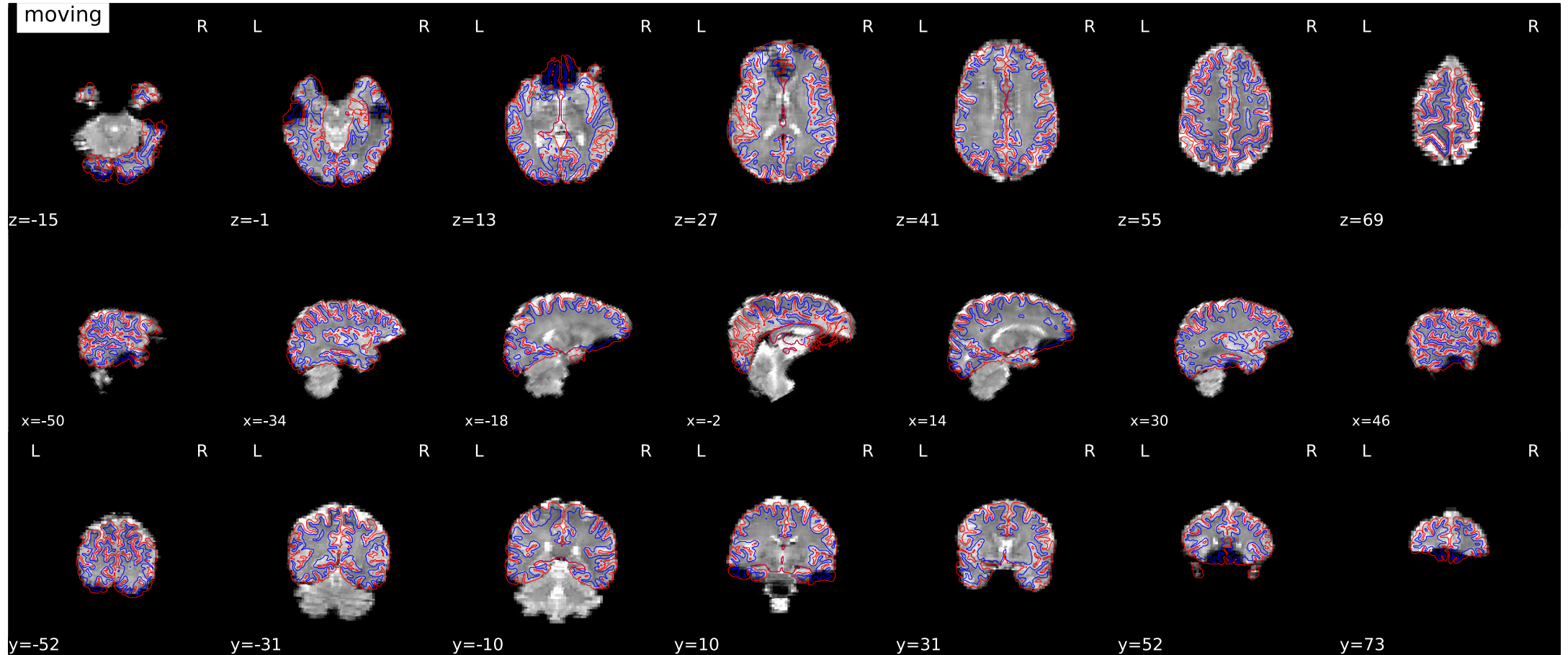
fRMIPrep derivatives

```
./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



<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.