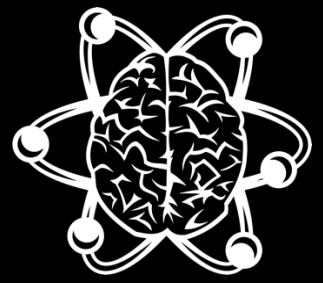
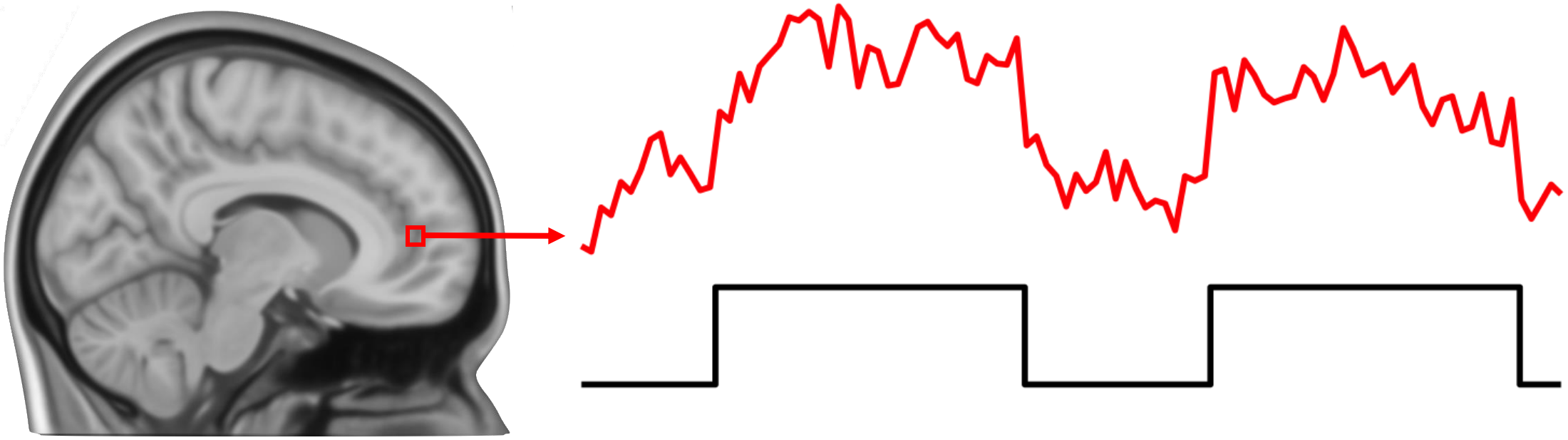


Practical framework for preprocessing fMRI data

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

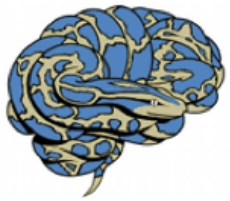
- **Motion correction**: Compensates for head movements by realigning the images to a common reference.
- **Co-registration**: Aligns images from different modalities into a common coordinate system.
- **Normalization**: Transforms individual brain images into a standard space enabling comparisons across 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



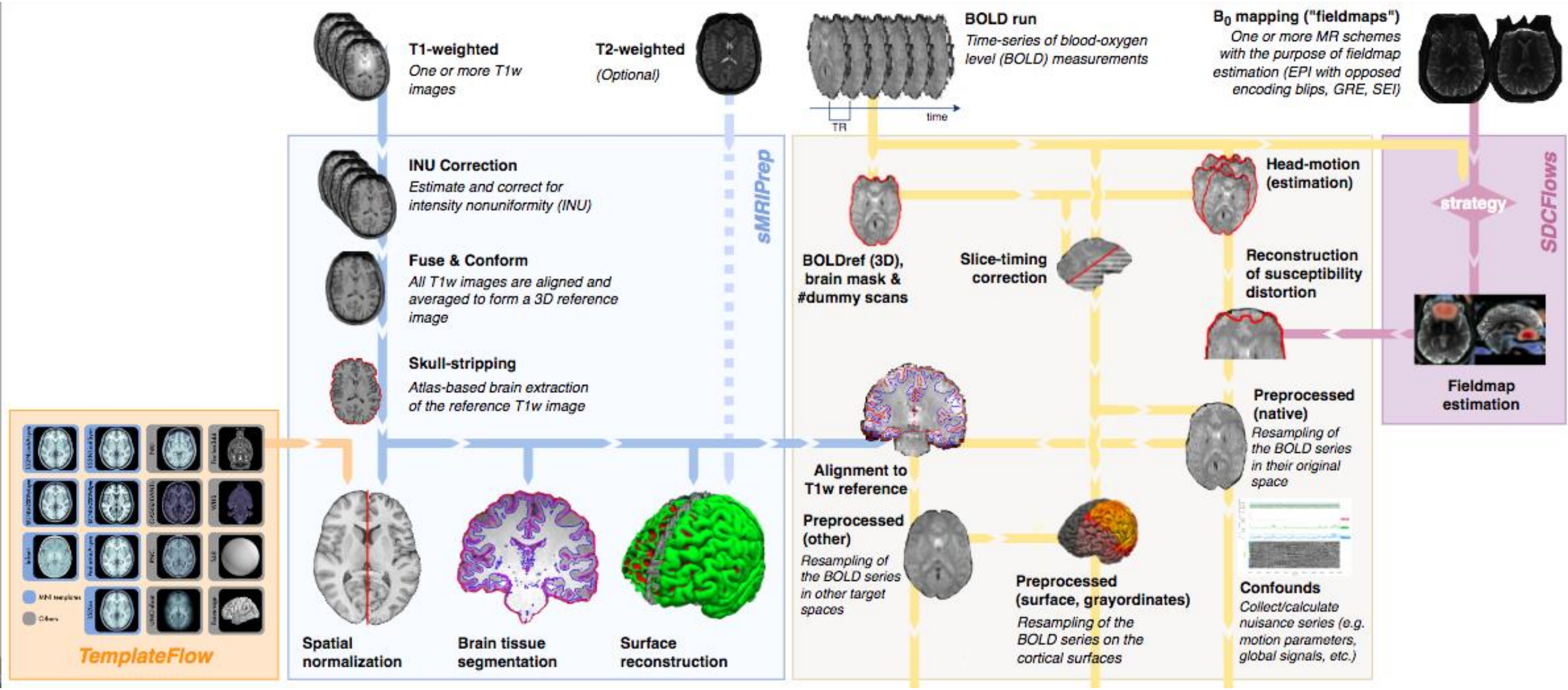
Nipype:
Neuroimaging in Python
Pipelines and Interfaces

fMRIPrep: a robust preprocessing pipeline for functional MRI

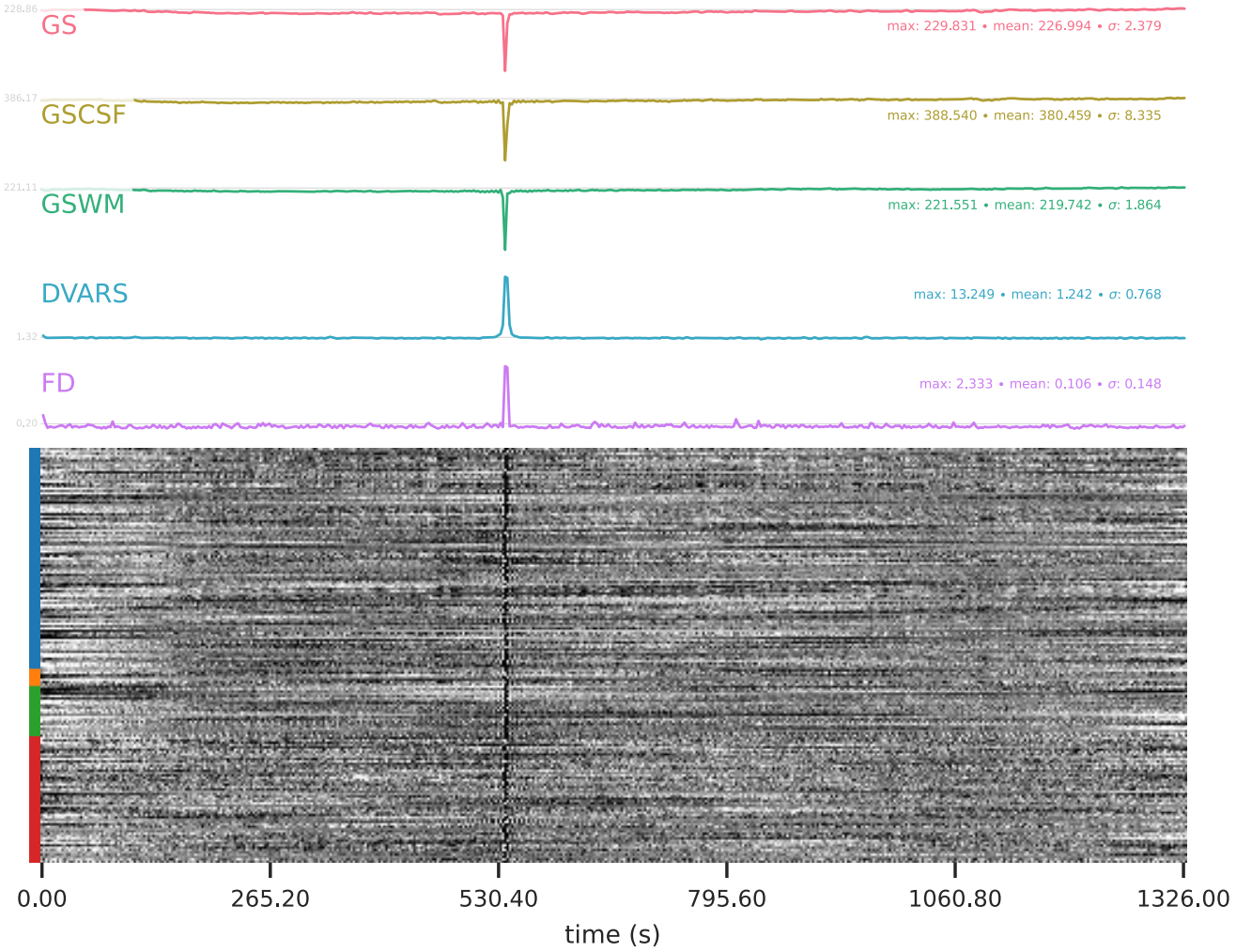
Oscar Esteban[1*], Christopher J. Markiewicz[1], Ross W. Blair[1], Craig A. Moodie[1], A. Ilkay Isik[2], Asier Erramuzpe[3], James D. Kent[4], Mathias Goncalves[5], Elizabeth DuPre[6], Madeleine Snyder[7], Hiroyuki Oya[8], Satrajit S. Ghosh[5,9], Jessey Wright[1], Joke Durnez[1], Russell A. Poldrack[1,10] 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.

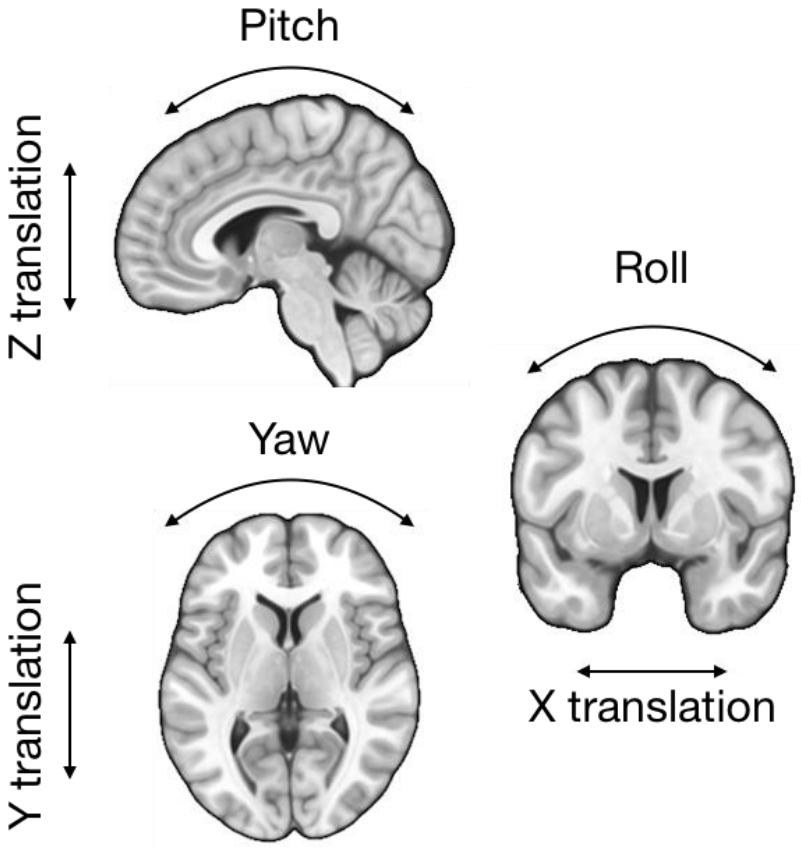
Preprocessing task	Included with fMRIPrep
Anatomical T1-weighted brain extraction	antsBrainExtraction.sh (ANTs)
Anatomical surface reconstruction	recon-all (FreeSurfer)
Head-motion estimation (and correction)	MCFLIRT (FSL)
Susceptibility-derived distortion estimation (and unwarping)	3dqwarp (AFNI)
Slice-timing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

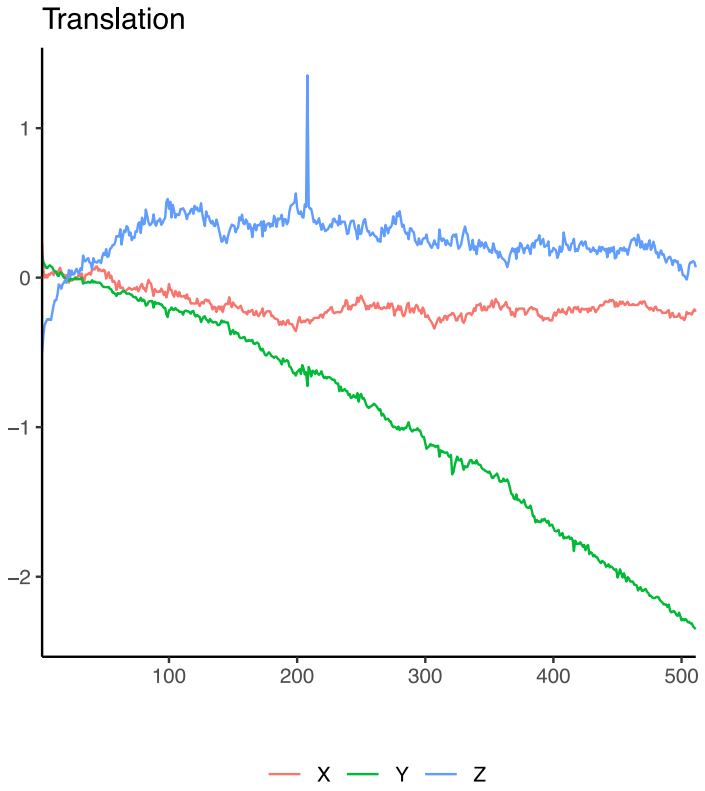

T1-weighted
One or more T1w images
T2-weighted
(Optional)
BOLD run
Time-series of blood-oxygen level (BOLD) measurements
TR
time
B0 mapping ("fieldmaps")
One or more MR schemes with the purpose of fieldmap estimation (EPI with opposed encoding blips, GRE, SEI)
sMRIPrep
INU Correction
Estimate and correct for intensity nonuniformity (INU)
Fuse & Conform
All T1w images are aligned and averaged to form a 3D reference image
Skull-stripping
Atlas-based brain extraction of the reference T1w image
BOLDref (3D), brain mask & #dummy scans
Slice-timing correction
Head-motion (estimation)
Reconstruction of susceptibility distortion
SDCFlows
strategy
Fieldmap estimation
Alignment to T1w reference
Preprocessed (native)
Resampling of the BOLD series in their original space
Preprocessed (other)
Resampling of the BOLD series in other target spaces
Preprocessed (surface, grayordinates)
Resampling of the BOLD series on the cortical surfaces
Confounds
Collect/calculate nuisance series (e.g. motion parameters, global signals, etc.)
Spatial normalization
Brain tissue segmentation
Surface reconstruction
MNI templates
Others
TemplateFlow

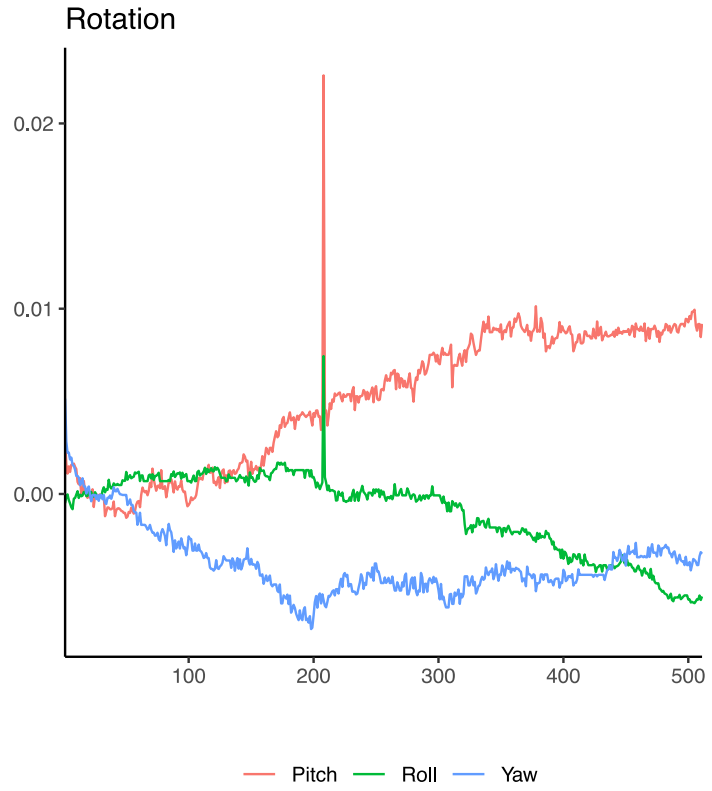
Head Motion


228.86
GS
max: 229.831 • mean: 226.994 • σ: 2.379
386.17
GSCSF
max: 388.540 • mean: 380.459 • σ: 8.335
221.11
GSWM
max: 221.551 • mean: 219.742 • σ: 1.864
DVARS
max: 13.249 • mean: 1.242 • σ: 0.768
1.32
FD
max: 2.333 • mean: 0.106 • σ: 0.148
0.20
0.00
265.20
530.40
795.60
1060.80
1326.00
time (s)

Head Motion


Pitch
Z translation
Roll
Yaw
Y translation
X translation


Translation
1
0
−1
−2
100
200
300
400
500
X
Y
Z


Rotation
0.02
0.01
0.00
100
200
300
400
500
Pitch
Roll
Yaw

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)

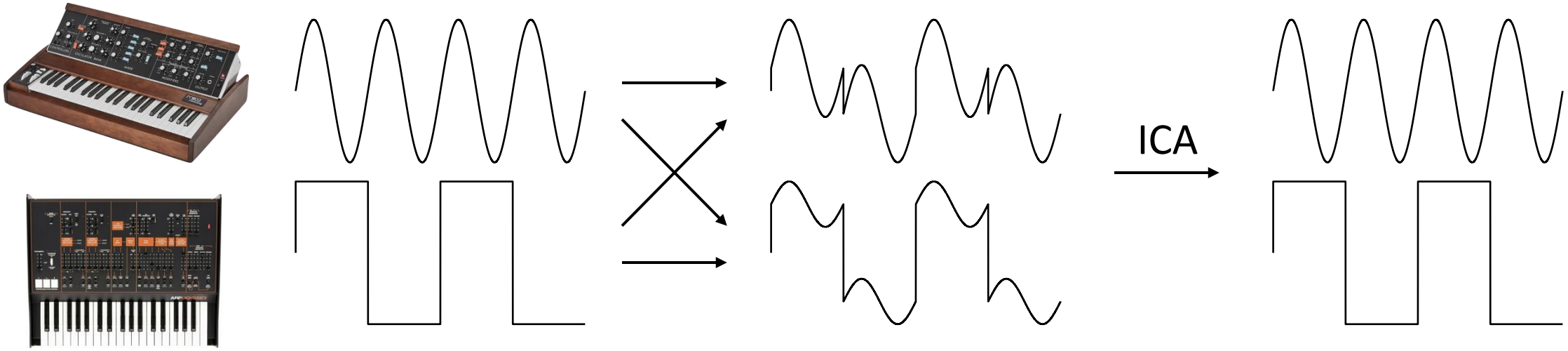
Frame 1 vs. frame 200 without motion correction

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

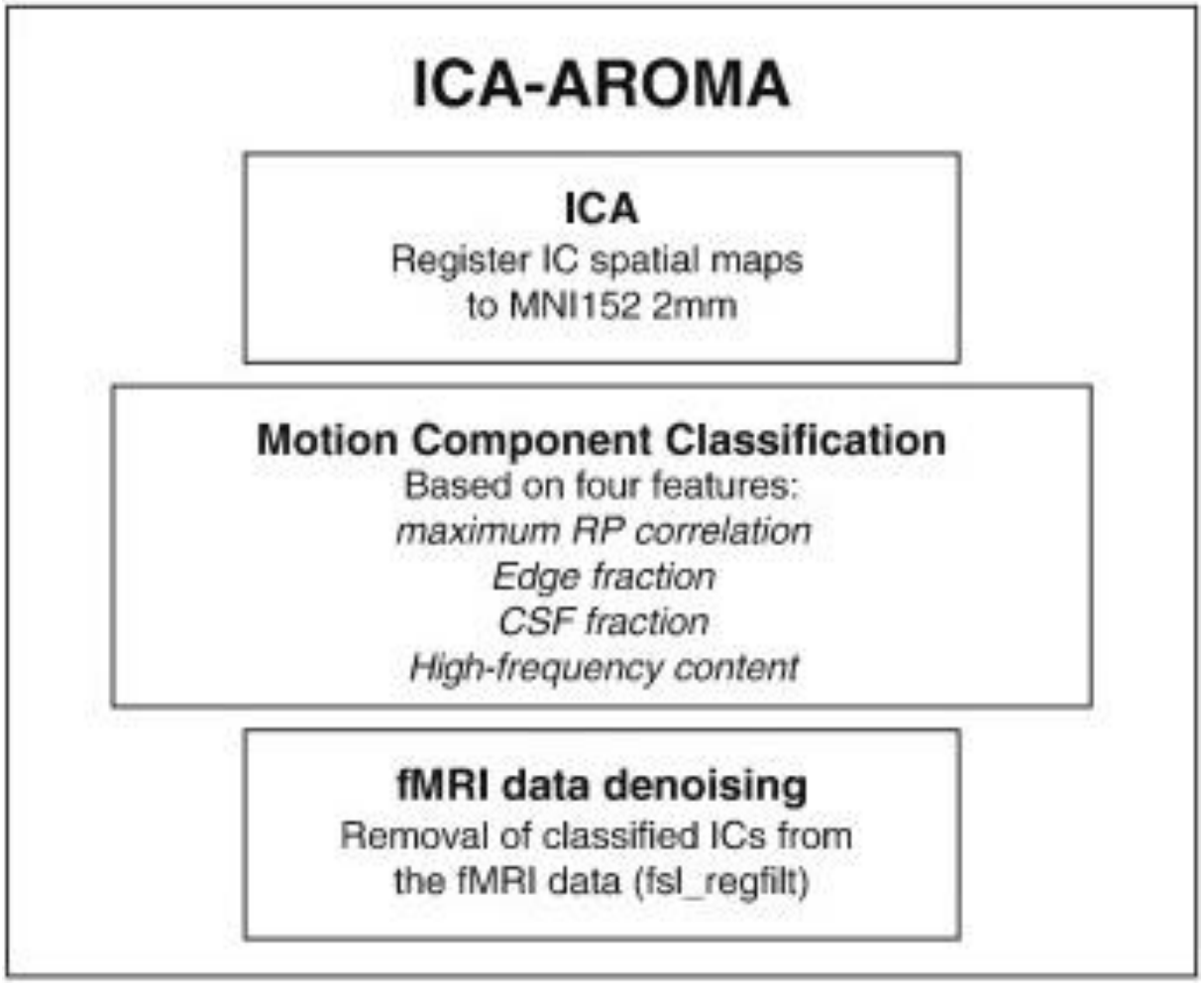
ICA-AROMA Denoising

- **I**CA-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



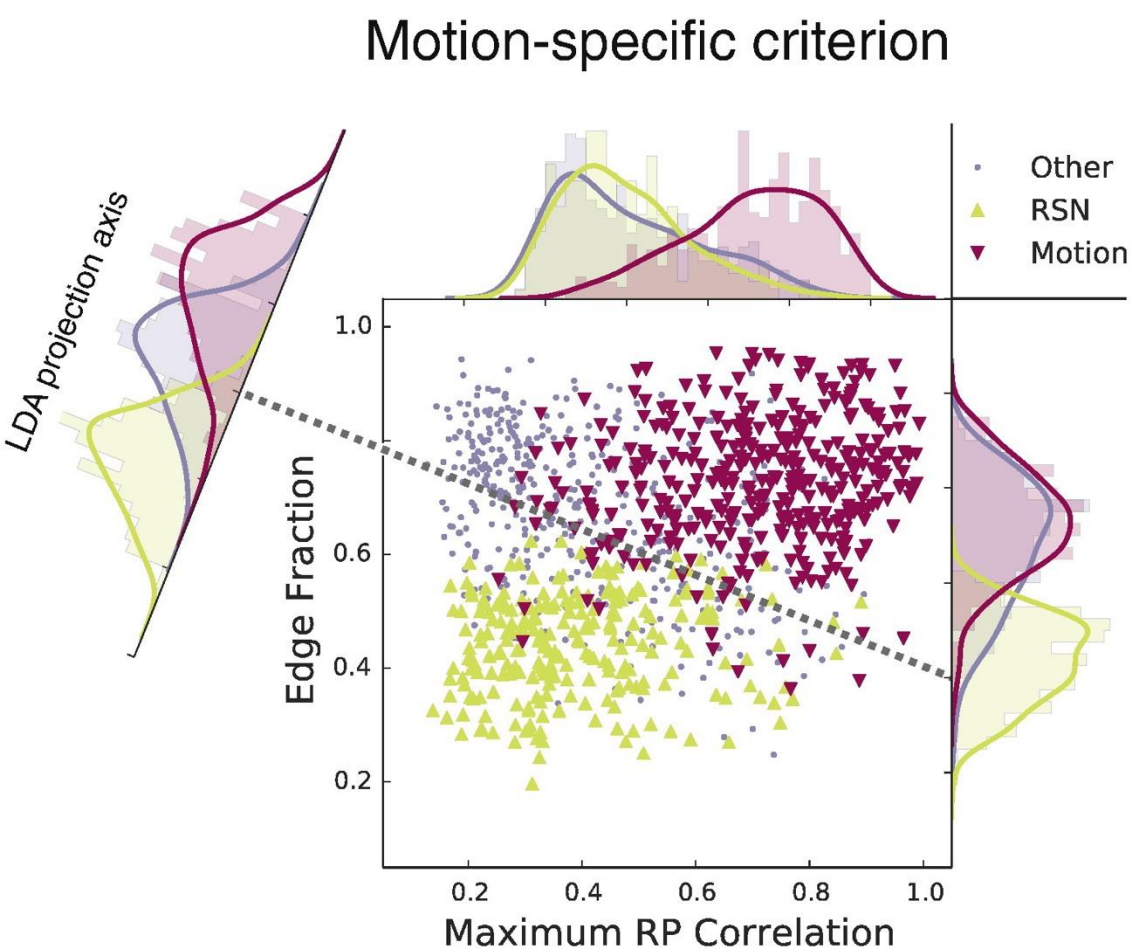
ICA-AROMA Denoising

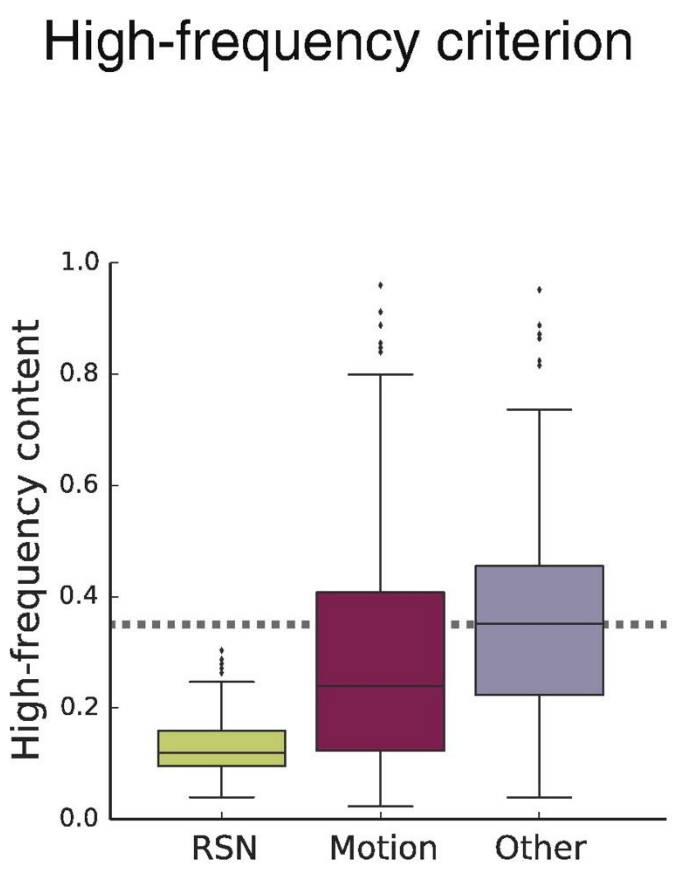


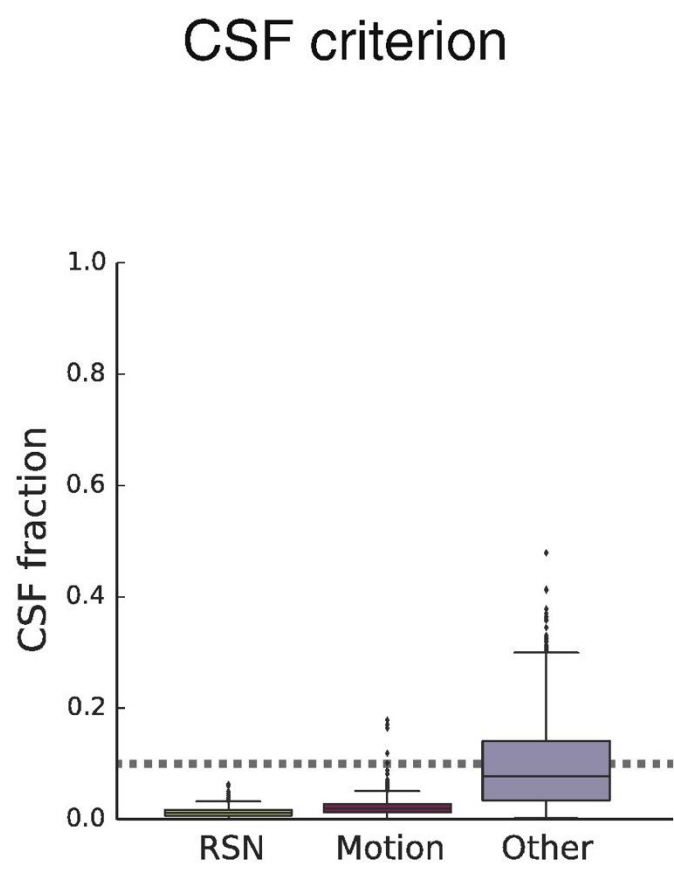
Pruim et al., 2015

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.

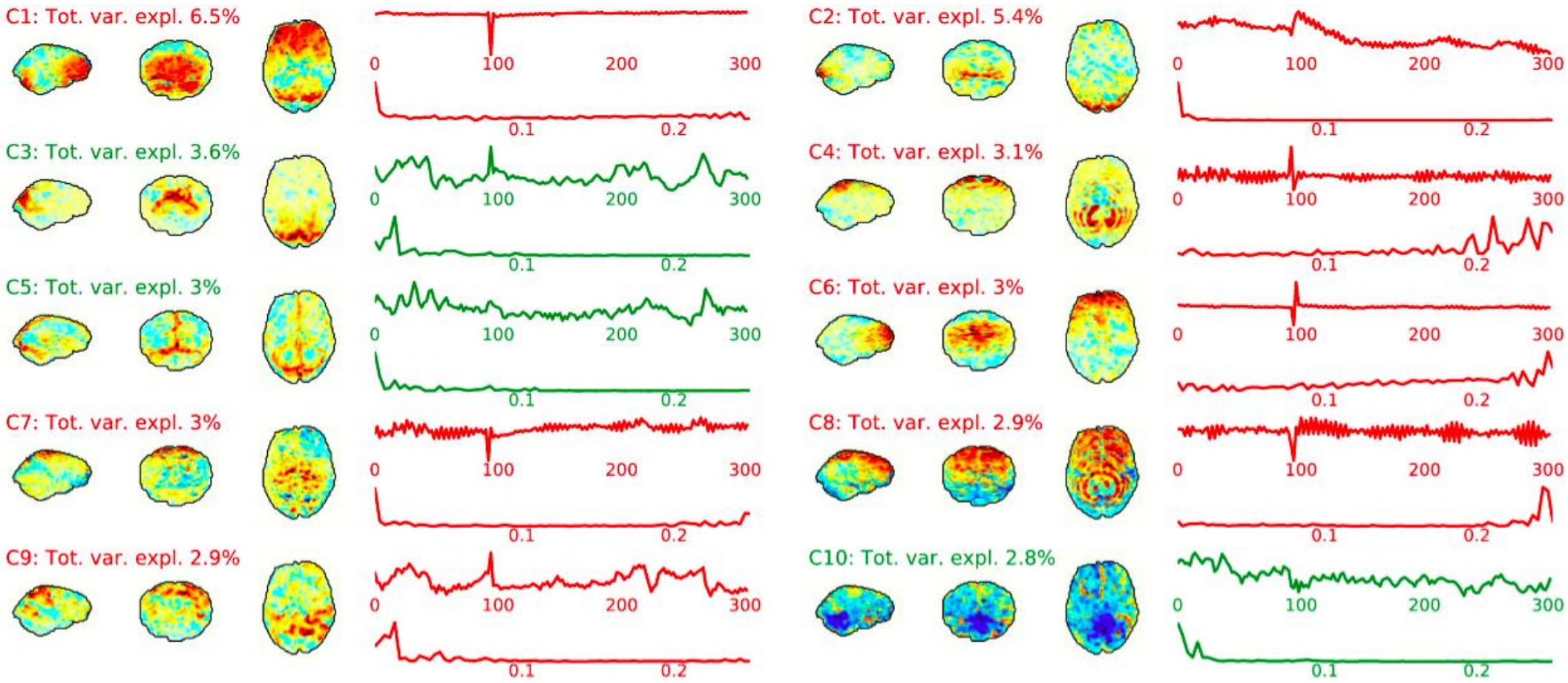






Pruim et al., 2015

ICA-AROMA Denoising



ICA-AROMA Denoising

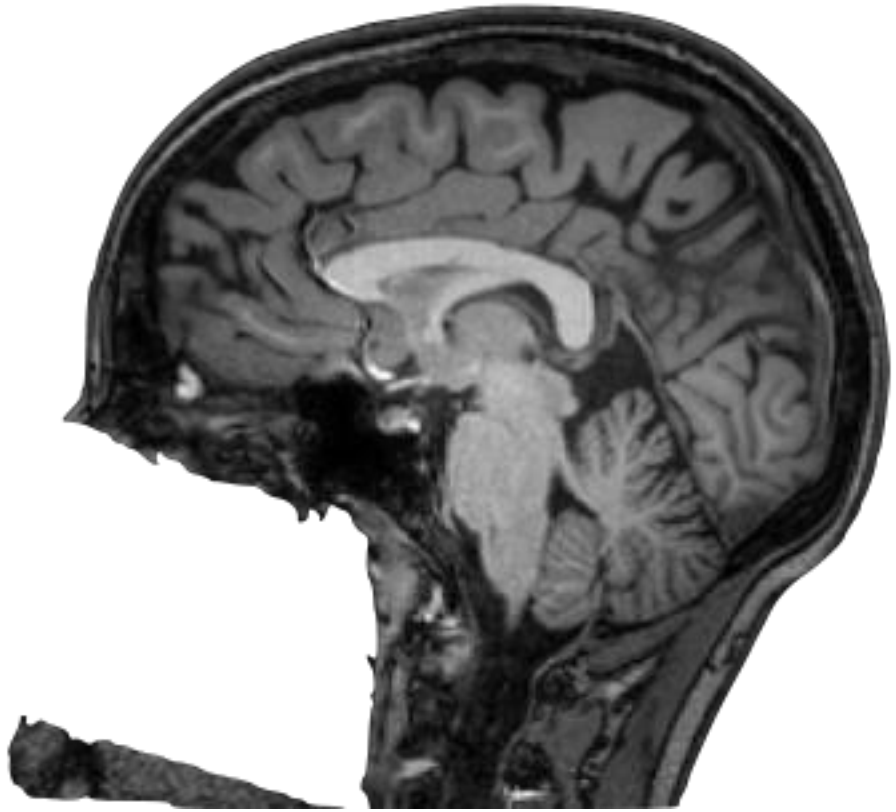
Non-aggressive ICA AROMA denoising aims to remove only the most obvious sources of noise and preserve as much of the signal as possible.

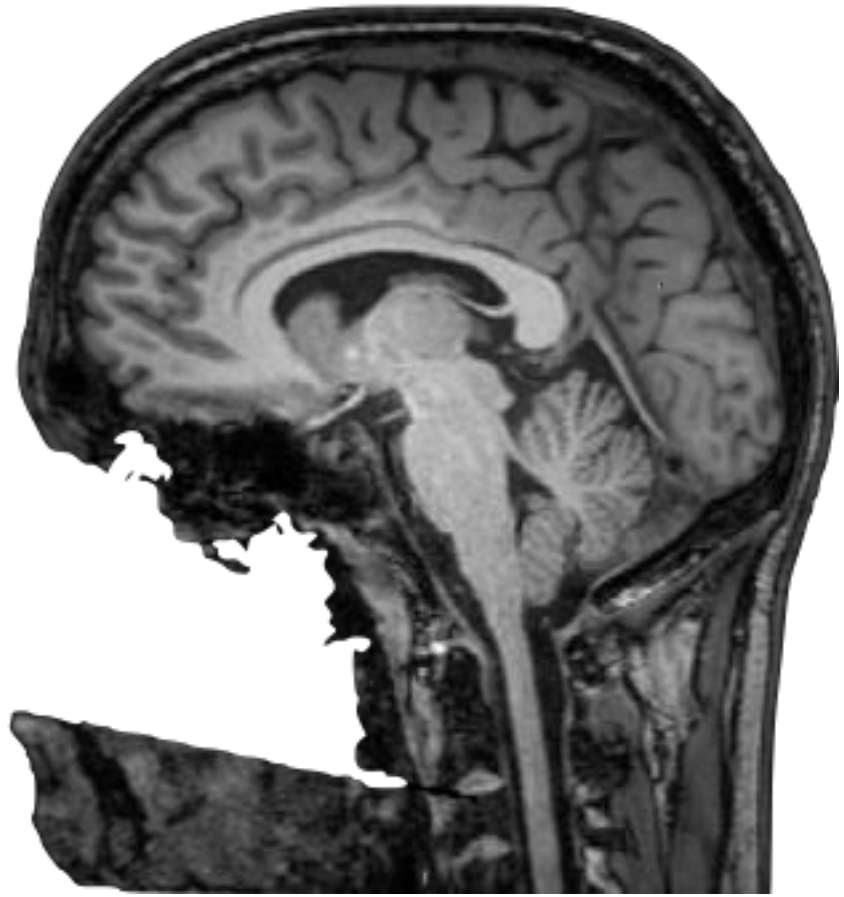
Aggressive ICA AROMA denoising removes all independent components identified as noise, including those that may contain some signal.

Spatial Normalization

*

*Avants et al., 2014



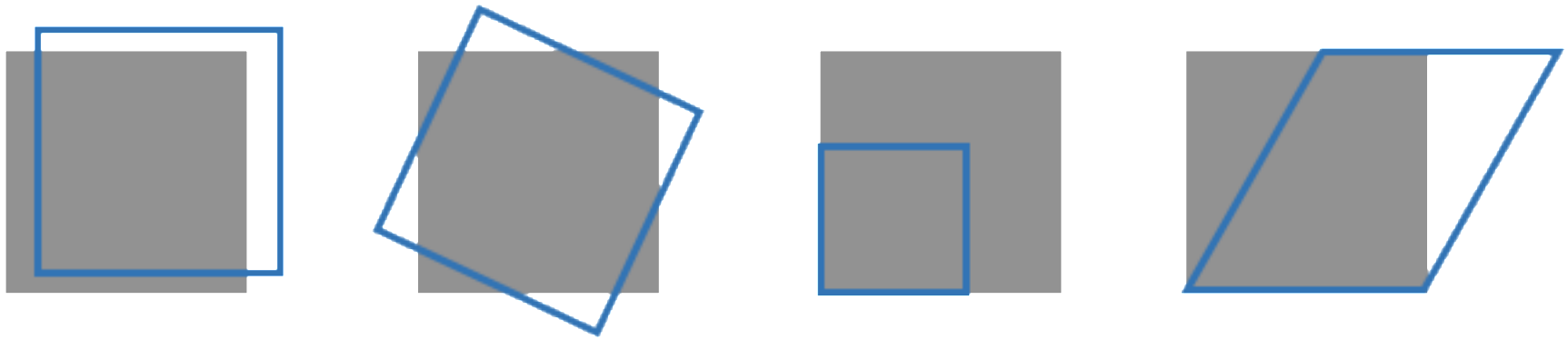


Spatial Normalization

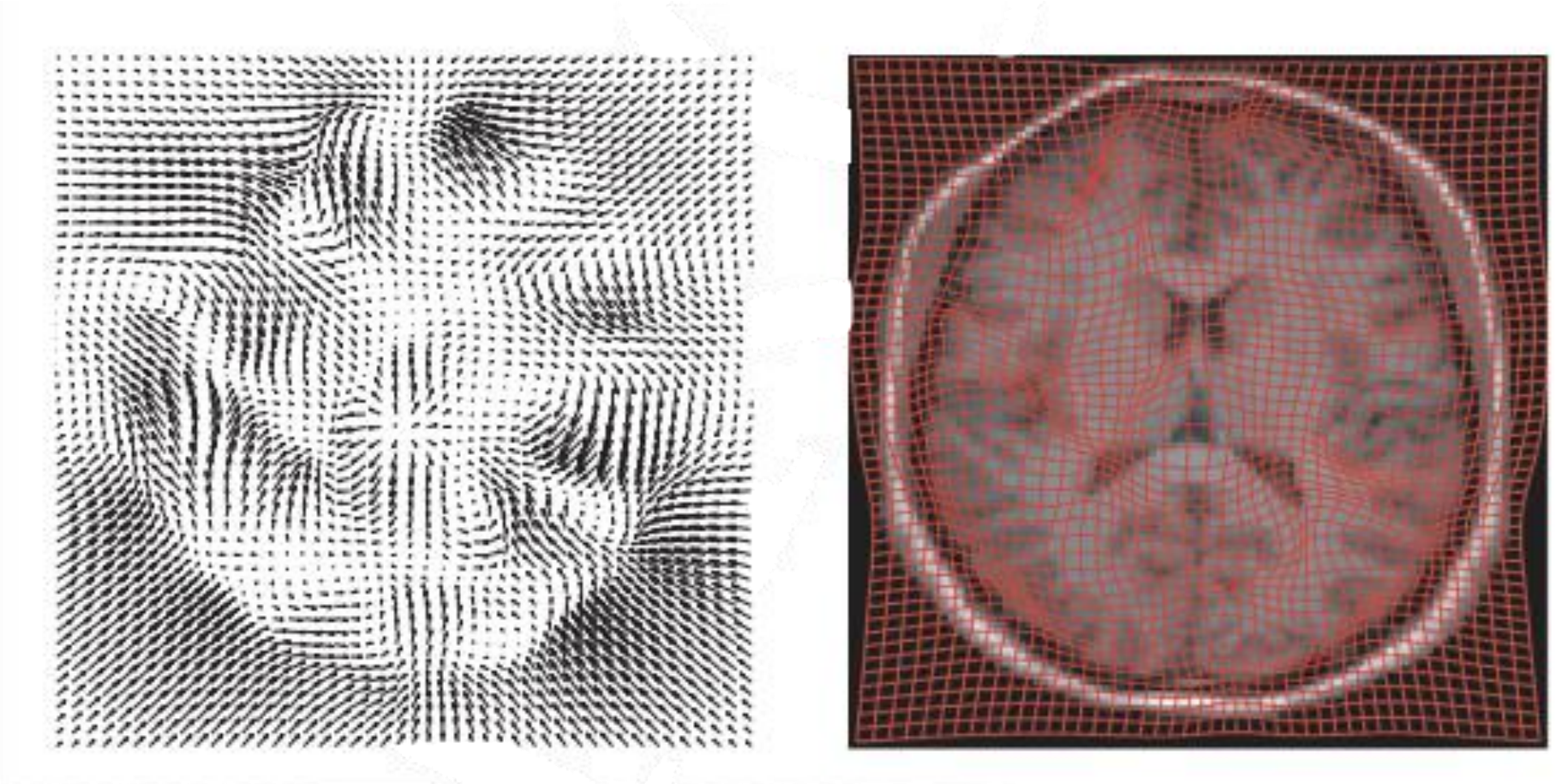
- **Objective**: Adjusting the images so that corresponding voxels represent approximately the same brain region across subjects.
  - Enables group-level statistical analysis.
  - Reduction in spatial resolution and alignment errors.
- The **MNI** (Montreal Neurological Institute) space is the most commonly 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



Poldrack, 2011

Spatial Normalization in fMRIprep

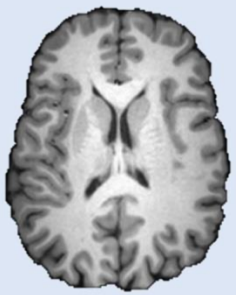
- By default, fMRIPrep uses Advanced Normalization tools (ANTs) (Avants et al., 2009) for registration with MNI152NLin2009cAsym as the reference.
- Performs nonlinear registration with mutual-information as the similarity metric (cost function).
- ANTs' Symmetric Normalization (SyN) algorithm that has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

Spatial Normalization

Native space

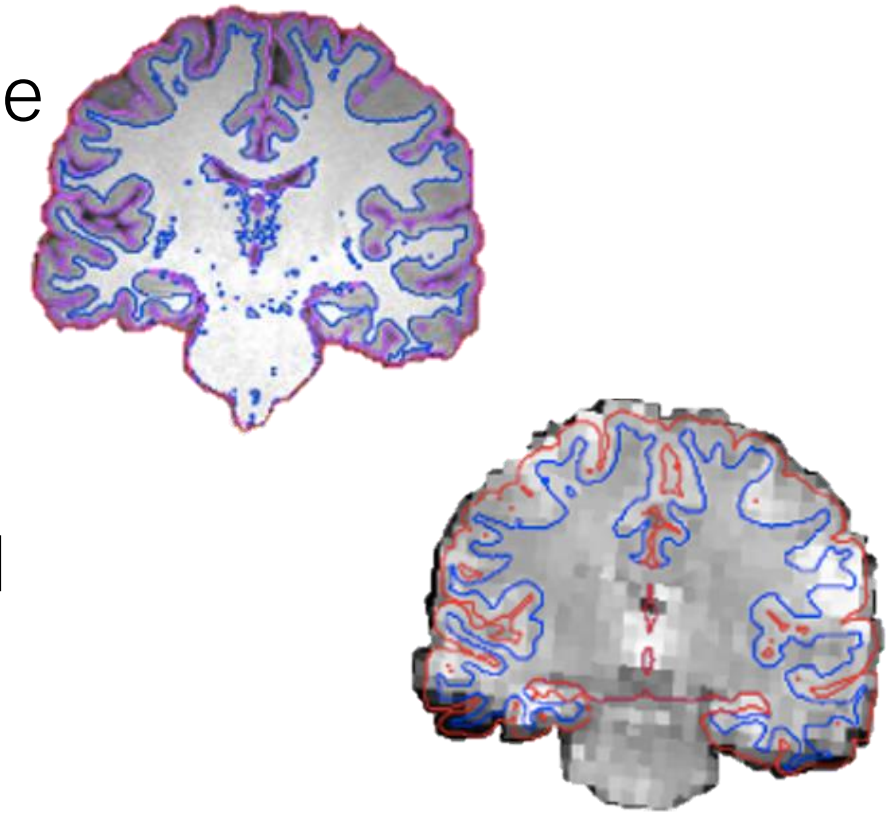
Subject 1

Subject 2



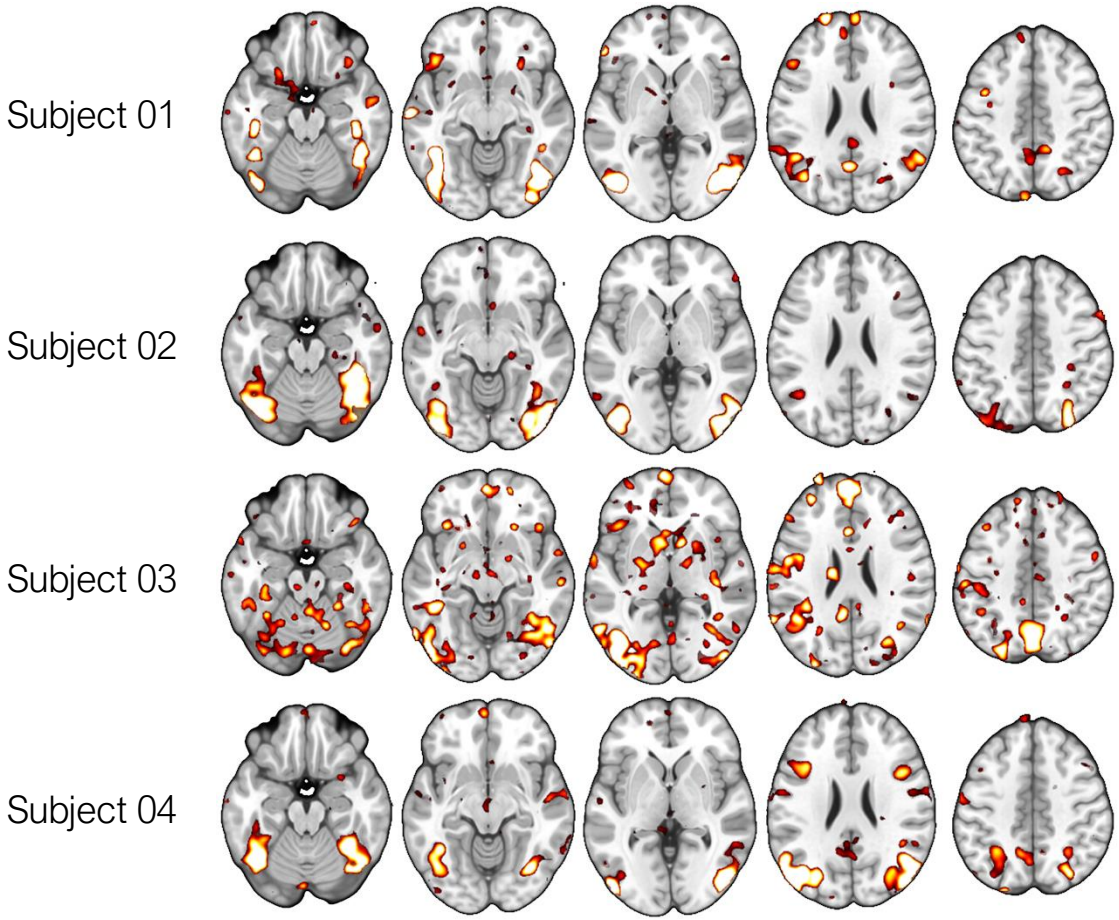
Co-registration

- 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

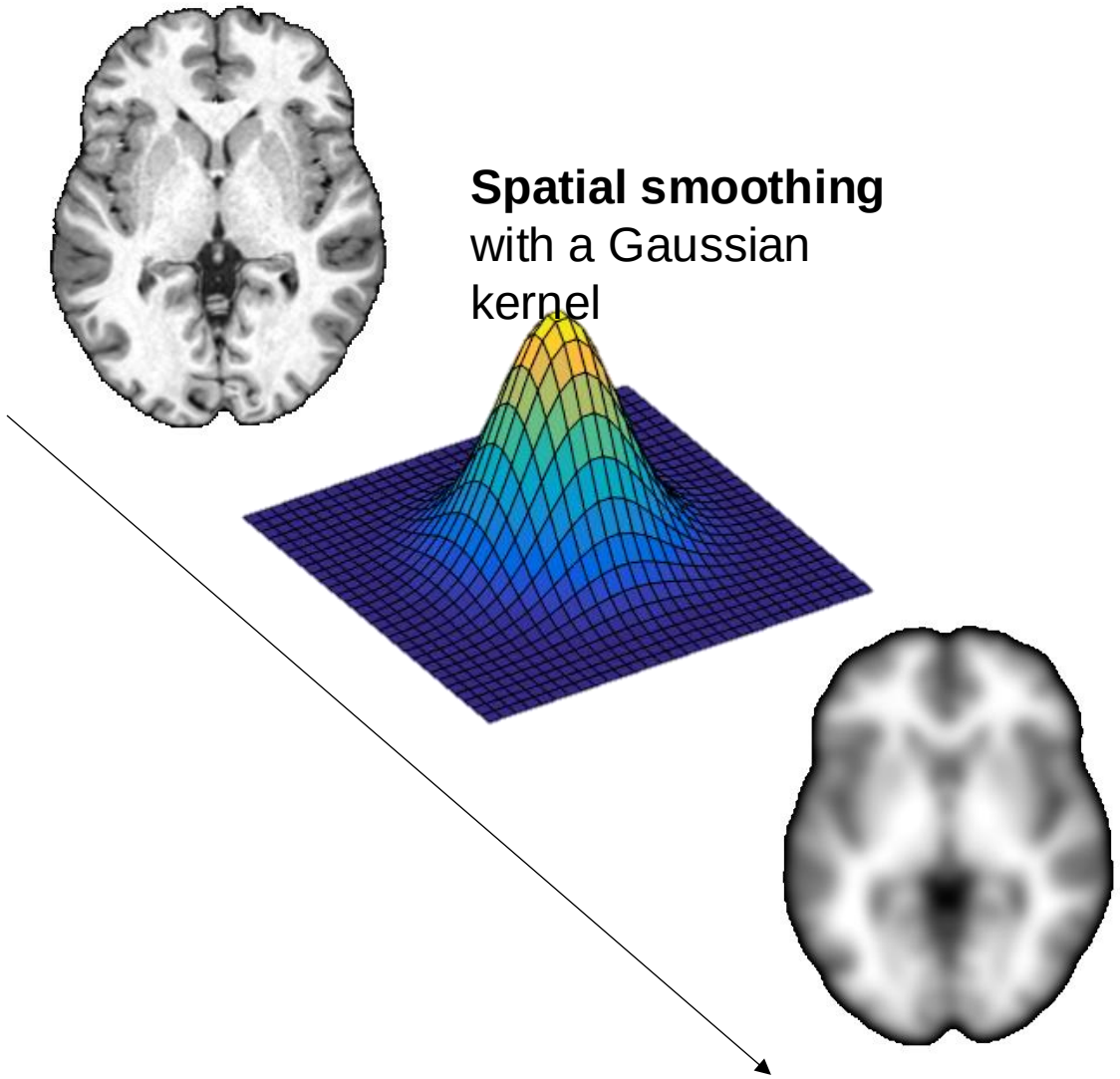
Possible benefits:

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

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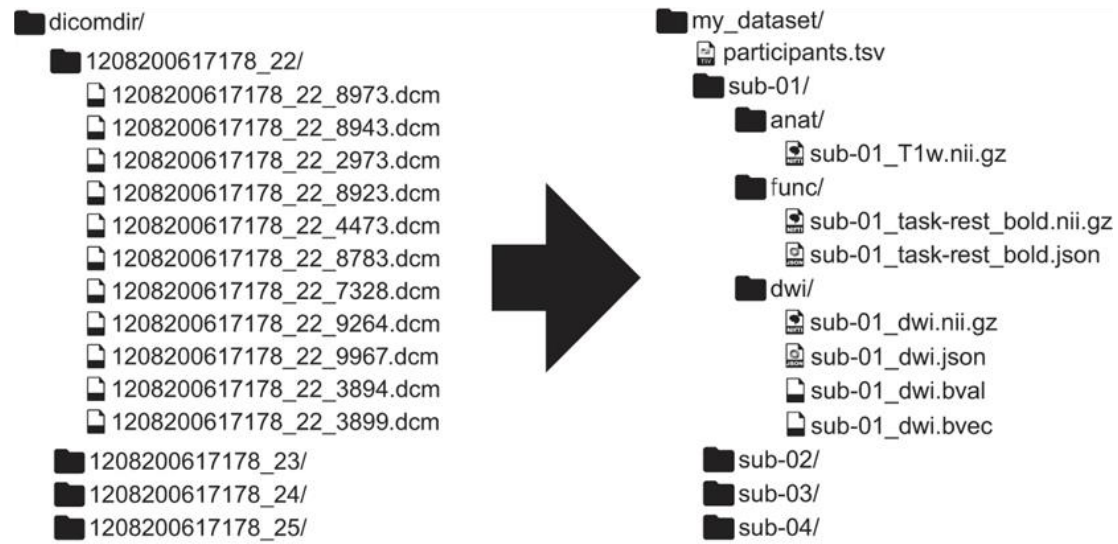
The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments

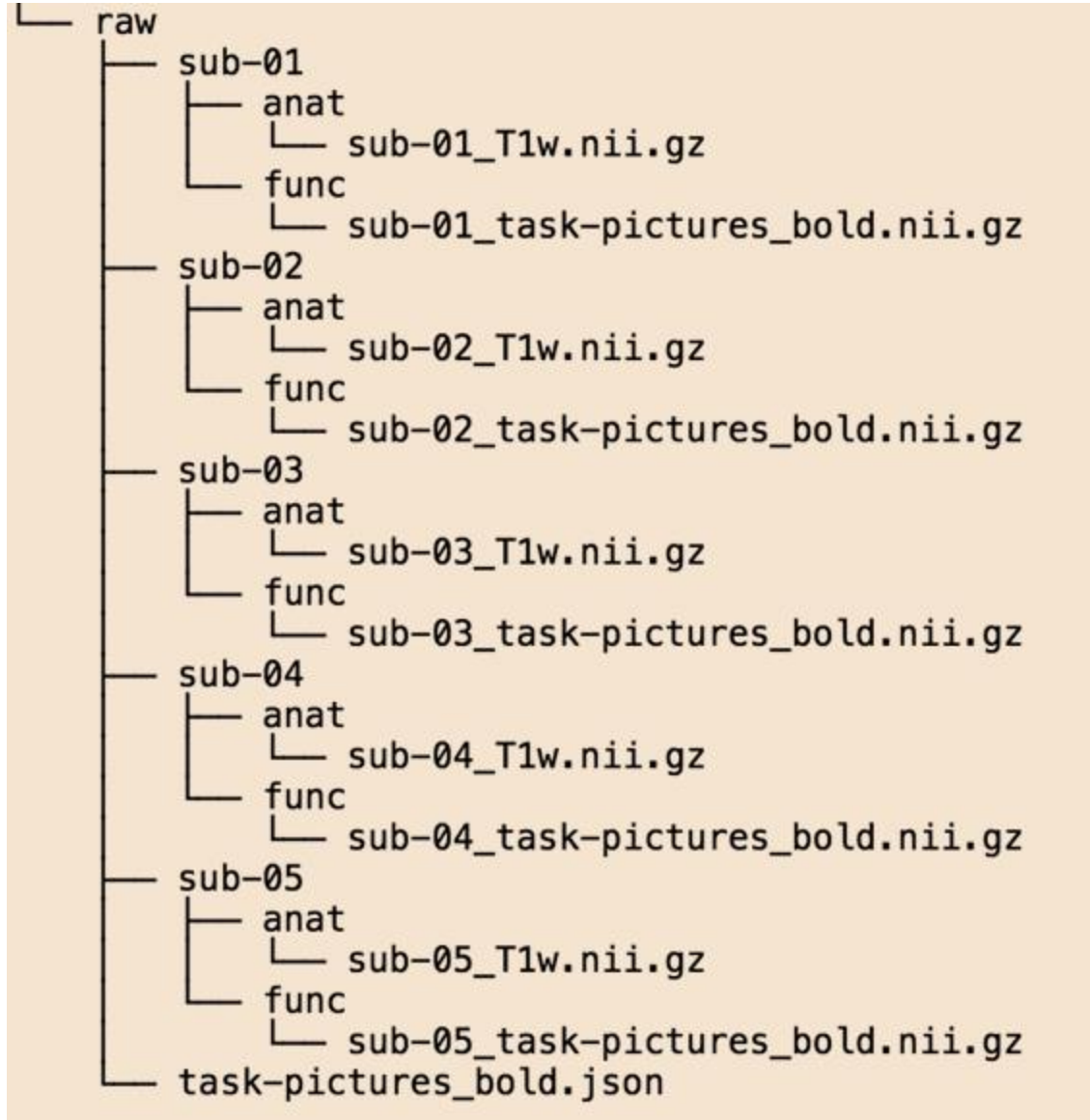
Krzysztof J. Gorgolewski[1], Tibor Auer[2], Vince D. Calhoun[3,4], R. Cameron Craddock[5,6], Samir Das[7], Eugene P. Duff[8], Guillaume Flandin[9], Satrajit S. Ghosh[10,11], Tristan Glatard[7,12], Yaroslav O. Halchenko[13], Daniel A. Handwerker[14], Michael Hanke[15,16], David Keator[17], Xiangrui Li[18], Zachary Michael[19], Camille Maumet[20], B. Nolan Nichols[21,22], Thomas E. Nichols[20,23], John Pellman[6], Jean-Baptiste Poline[24], Ariel Rokem[25], Gunnar Schaefer[1,26], Vanessa Sochat[27], William Triplett[1], Jessica A. Turner[3,28], Gaël Varoquaux[29] & Russell A. Poldrack[1]

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.

BIDS
BRAIN IMAGING DATA STRUCTURE



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
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├── 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)

```
fmriprep-docker /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
```

fmriprep-docker <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 derivates

```
./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
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```
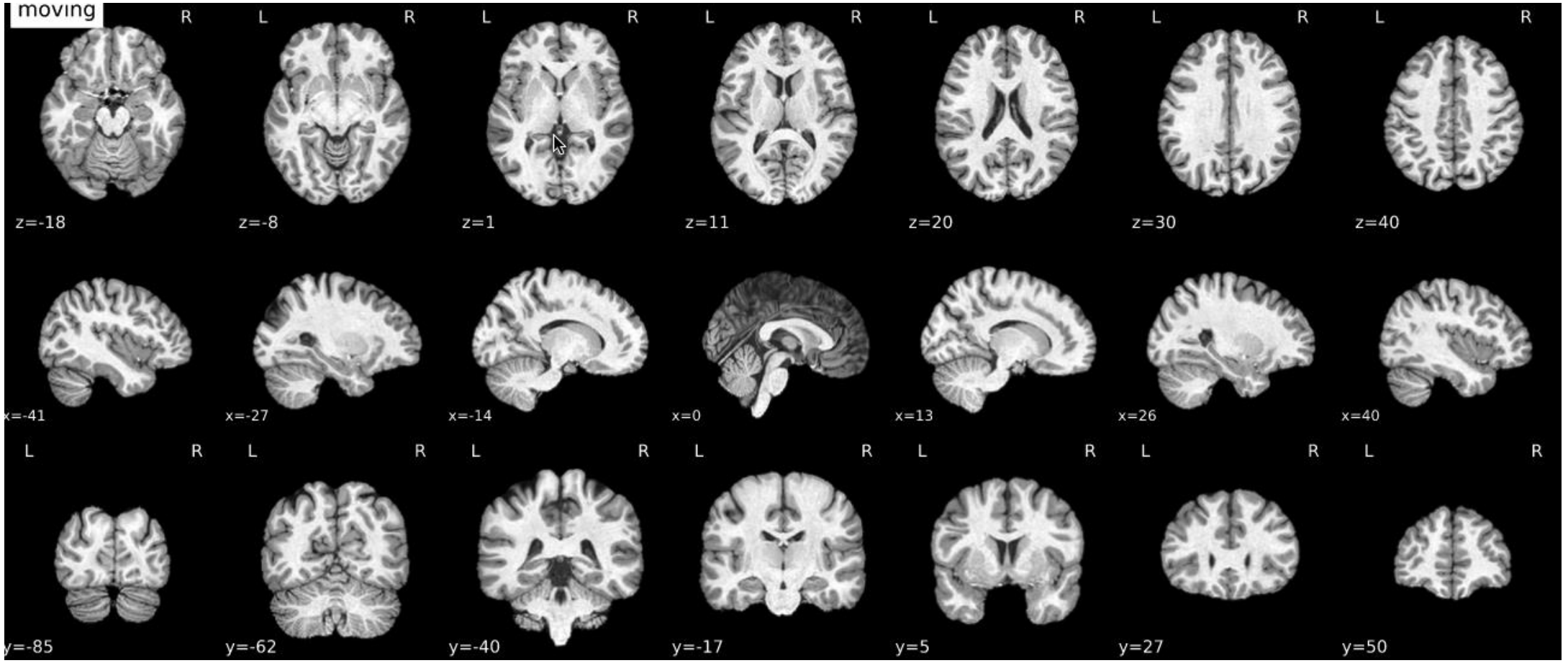
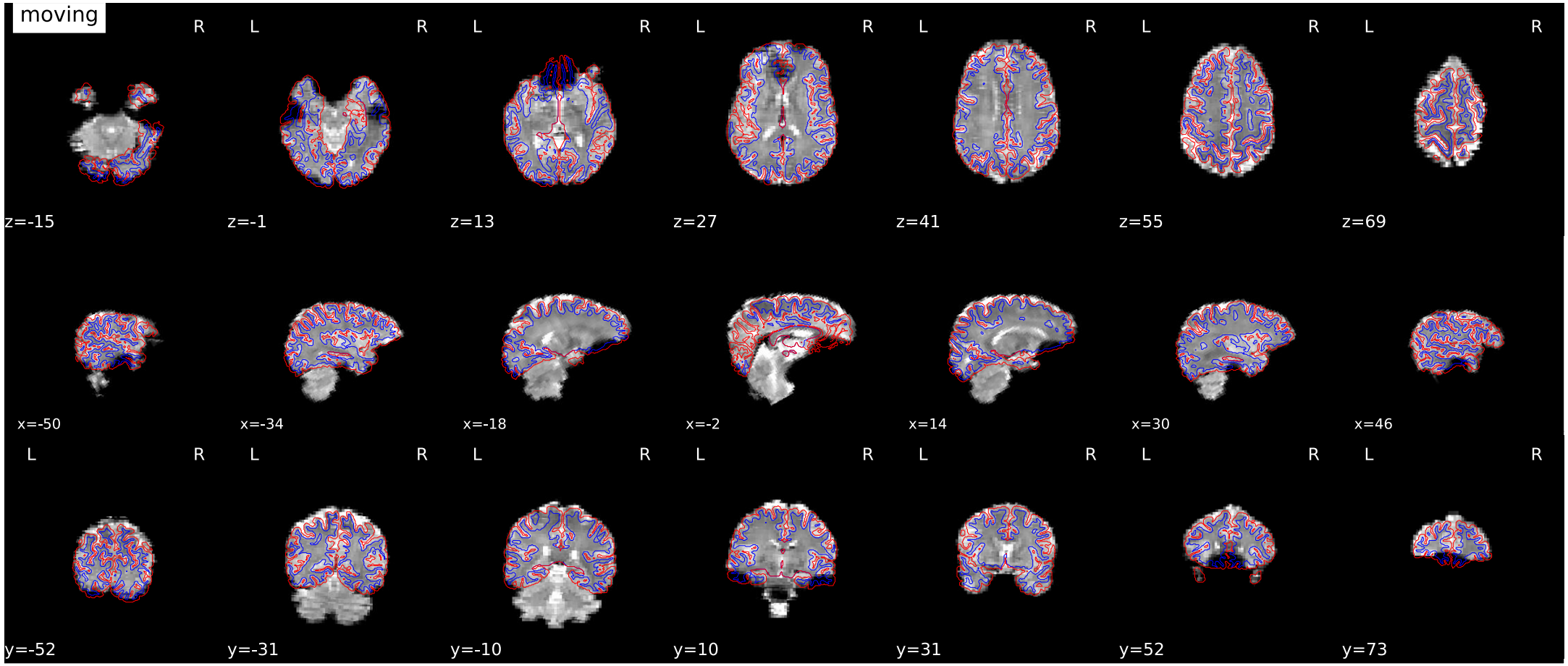

QA: T1 Normalization



QA: Co-registration



https://fmriprep.org/

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