Preprocessing with fMRIPrep

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Preparing your data for statistical analysis

- I. Dealing with artifacts
- II. Spatial normalization

fMRIPrep

nature methods

ARTICLES



Nipype: Neuroimaging in Python Pipelines and Interfaces

fMRIPrep: a robust preprocessing pipeline for functional MRI

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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	MELODIC (FSL), ICA-AROMA



MNI templotes

Cites

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 linear 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

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



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Spatial Normalization

- The goal is to deform the images so that a given voxel refers (roughly) to the same region across subjects.
- Allows group-level statistics
 - However, loss of spatial resolution & misalignment errors.
- The most commonly used standard space is the MNI (Montreal Neurological Institute) space.
 - Average of several co-registered brain volumes developed to be used for template in automated registration.

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.
- ANTs' SYN algorithm that has performed very well in comparison studies (e.g. Klein et al., 2009)

Spatial Normalization

Subject 1



Native space

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

Subject 01

Subject 02

Subject 03

Subject 04



Spatial Smoothing

Possible benefits:

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

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

SUBJECT CATEGORIES » Data publication and

» Research data

archiving

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

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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 guality 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.



dicomdir/ my dataset/ participants.tsv 1208200617178 22/ sub-01/ 1208200617178_22_8973.dcm anat/ 1208200617178 22 8943.dcm sub-01 T1w.nii.az 1208200617178 22 2973.dcm func/ 1208200617178 22 8923.dcm sub-01 task-rest bold.nii.gz 1208200617178 22 4473.dcm sub-01_task-rest_bold.json 1208200617178 22 8783.dcm dwi/ 1208200617178 22 7328.dcm 1208200617178 22 9264.dcm sub-01 dwi.nii.gz 1208200617178 22 9967.dcm sub-01 dwi.json 1208200617178 22 3894.dcm sub-01 dwi.bval 1208200617178 22 3899.dcm sub-01 dwi.bvec sub-02/ 1208200617178 23/ sub-03/ 1208200617178 24/ sub-04/ 1208200617178 25/

https://bids.neuroimaging.io/



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
- ---- sub-014_task-pictures_space-MNI152NLin2009cAsym_desc-smoothAROMAnonaggr_bold.nii.gz

QA: T1 Normalization



QA: Co-registration



https://fmriprep.org/

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