

sMRI Data Preprocessing

fMRIPrep structural MRI Preprocessing Pipeline

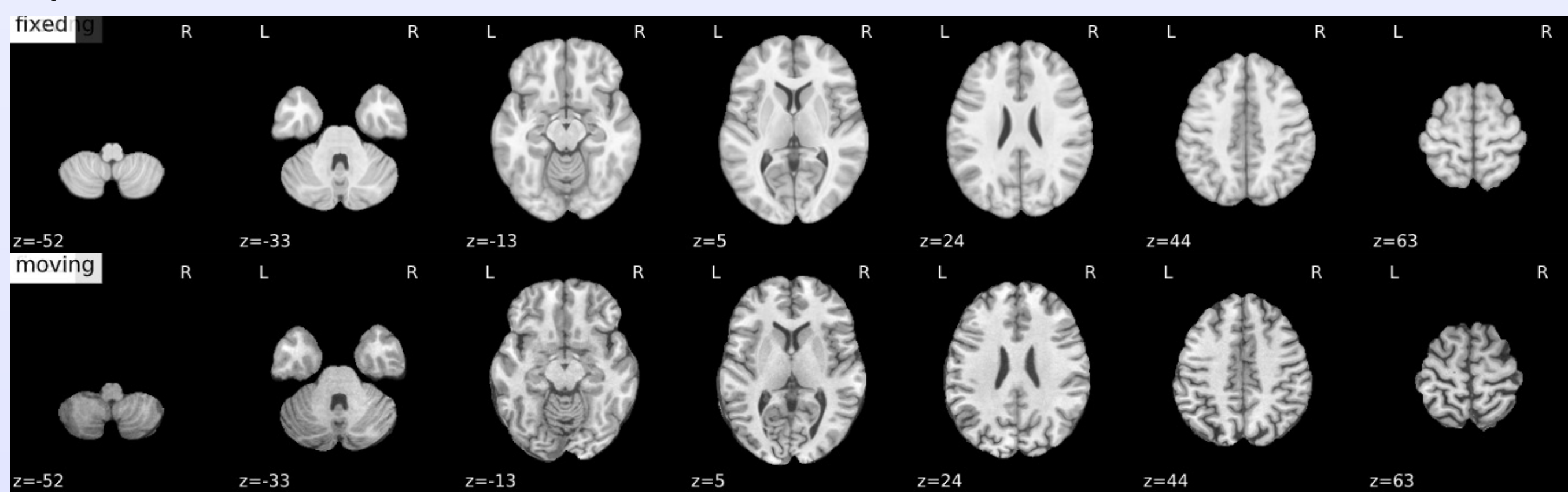
- Input: BIDS format, at least one T1w structural image
- Output: derivatives ready for analysis and visual quality assessment report for each subject



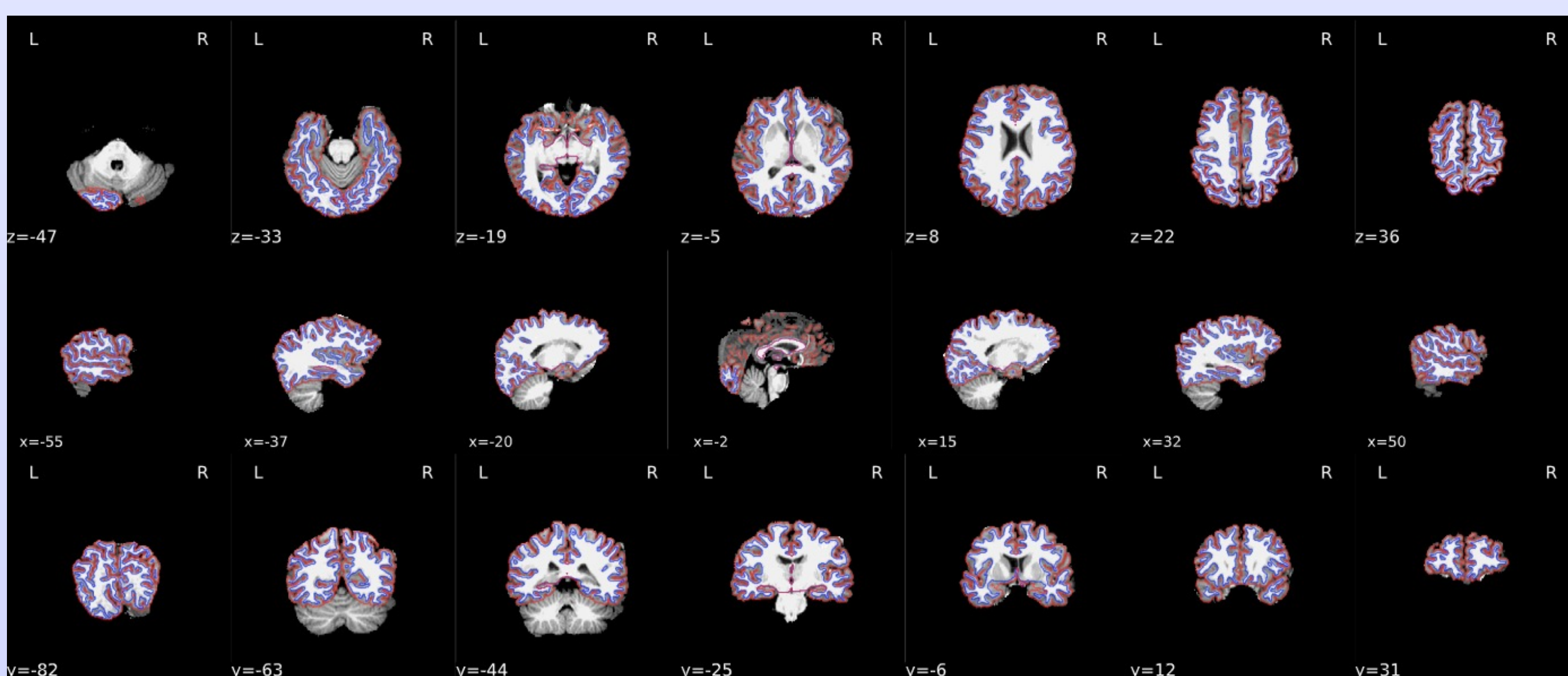
Brain Extraction & Segmentation



Spatial Normalization

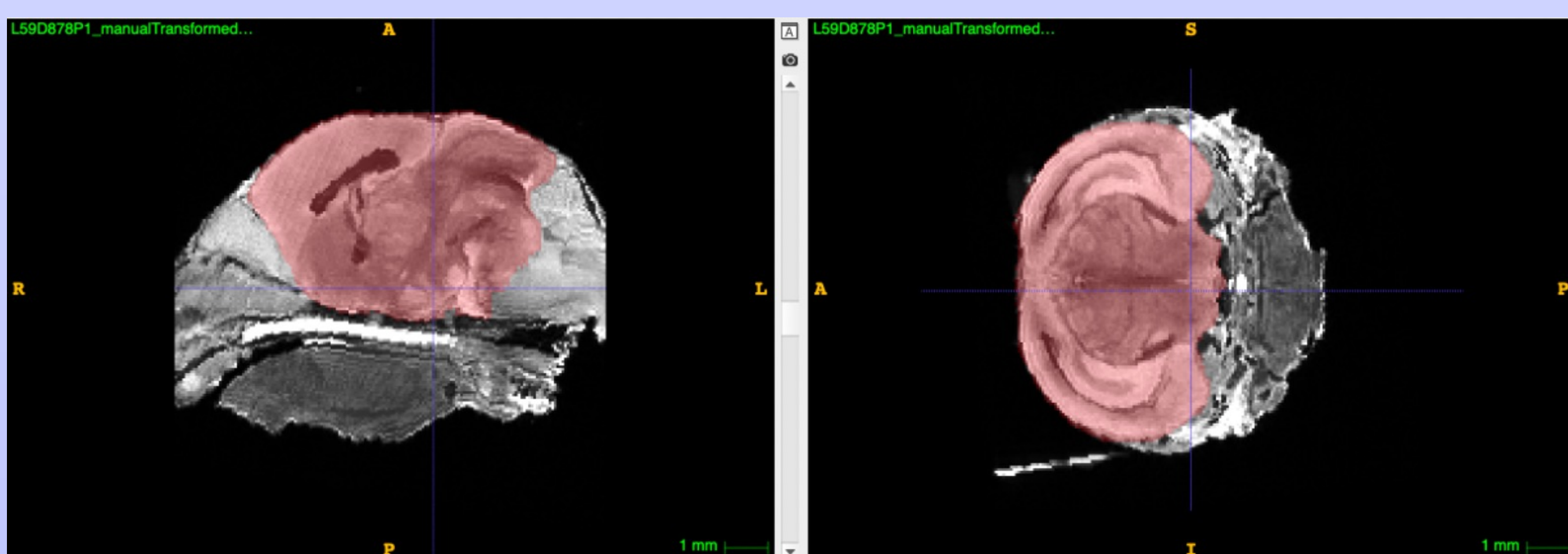


Surface Reconstruction



Brain Mask Refinement

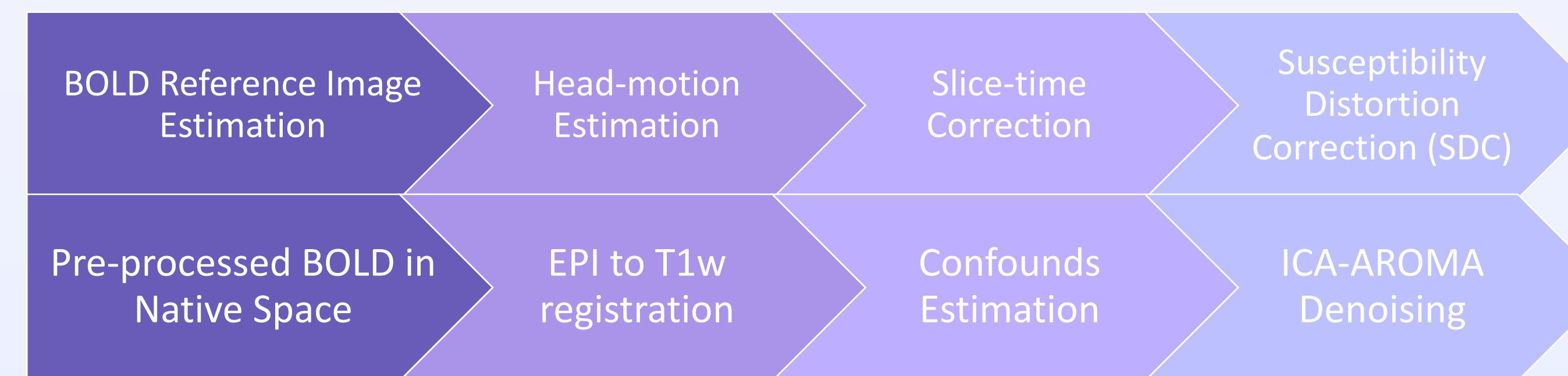
- ITK-SNAP
- Manual Refinement



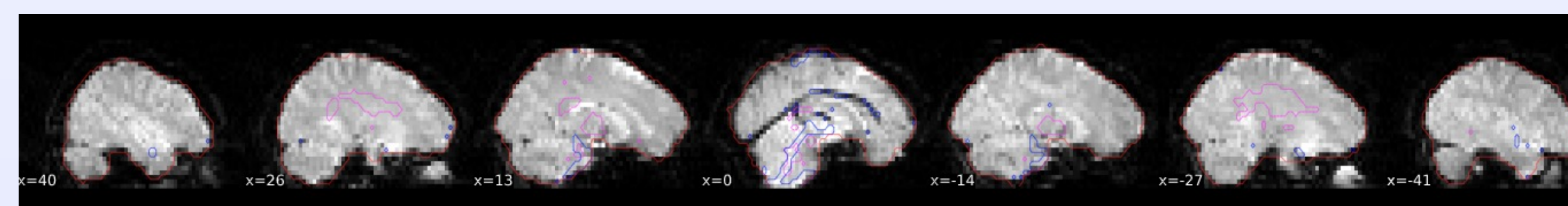
fMRI Data Preprocessing

fMRIPrep functional MRI Preprocessing Pipeline

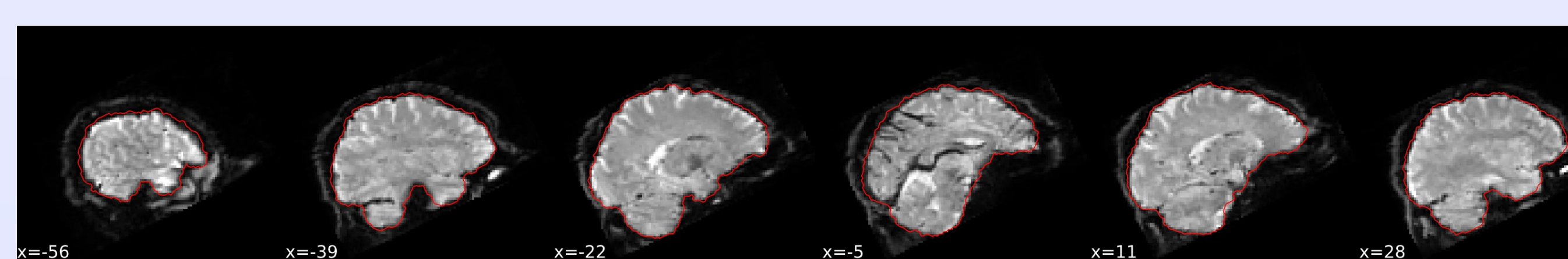
- Input: BIDS format, at least one T1w structural image, BOLD series
- Output: derivatives ready for analysis and visual quality assessment report for each subject



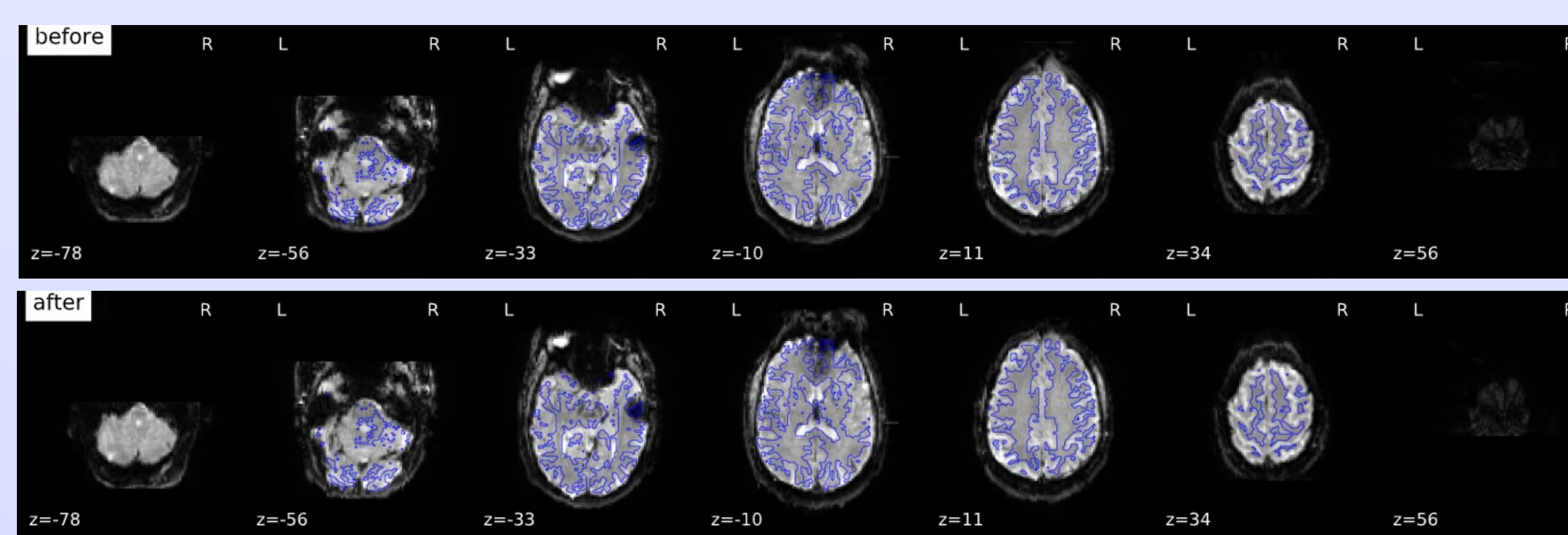
BOLD Reference Image Estimation



Calculation of a brain mask from BOLD series



Before vs After susceptibility-derived distortion correction

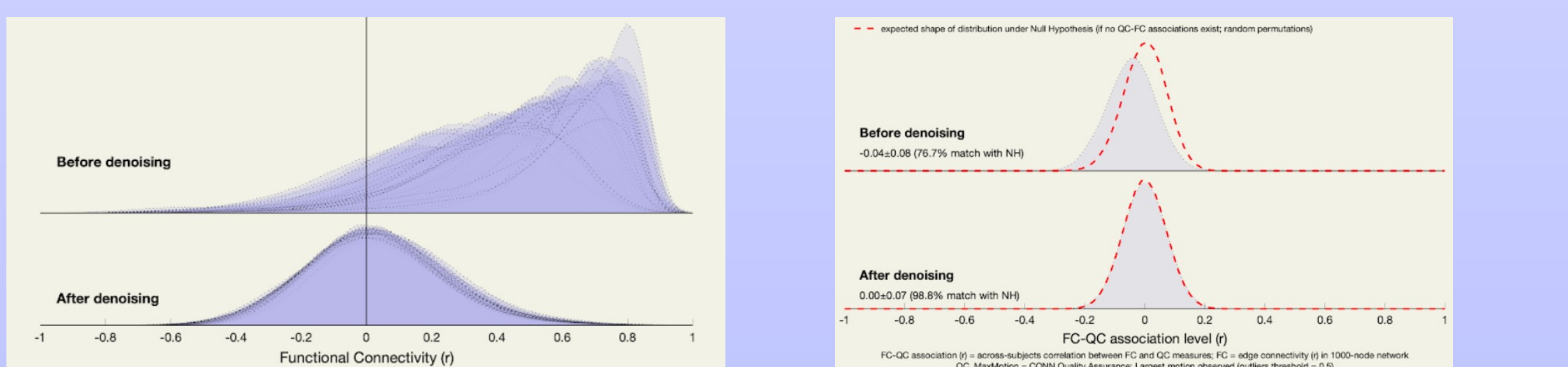


CONN Toolbox Denoising Pipeline

- Input: preprocessed data
- Output: denoised data
- fMRI Denoising Pipeline



Distributions of FC Values and QC-FC Associations



Command-Line Arguments

The fMRIPrep workflow takes as principal input the path of the dataset that is to be processed. The exact command to run fMRIPrep depends on the Installation method. The common parts of the command follow the BIDS-Apps definition.

```
fmriprep [-h] [--skip_bids_validation]
[--participant-label PARTICIPANT_LABEL [PARTICIPANT_LABEL ...]]
[-t TASK_ID] [--echo-idx ECHO_IDX] [--bids-filter-file FILE]
[-d [PATH ...]] [--bids-database-dir PATH] [--nprocs NPROCS]
[--omp-nthreads OMP_NTHREADS] [--mem MEMORY_MB] [--low-mem]
[--use-plugin FILE] [--sloppy] [--anat-only]
[--level {minimal,resampling,full}] [--boilerplate-only]
[--reports-only]
[--ignore {fieldmaps,slicetiming,sbref,t2w,flair,fmap-jacobian}
[{fieldmaps,slicetiming,sbref,t2w,flair,fmap-jacobian} ...]]
[--output-spaces [OUTPUT_SPACES ...]] [--longitudinal]
[--bold2t1w-init {register,header}] [--bold2t1w-dof {6,9,12}]
[--force-bbr] [--force-no-bbr]
[--slice-time-ref SLICE_TIME_REF] [--dummy-scans DUMMY_SCANS]
[--random-seed _RANDOM_SEED]
[--me-t2s-fit-method {curvefit,loglin}]
[--output-layout {bids,legacy}] [--me-output-echos]
[--medial-surface-nan] [--project-goodvoxels]
[--md-only-boilerplate] [--cifti-output [{91k,170k}]]
[--no-msm] [--use-aroma]
[--aroma-melodic-dimensionality AROMA_MELODIC_DIM]
[--error-on-aroma-warnings] [--return-all-components]
[--fd-spike-threshold REGRESSORS_FD_TH]
[--dvars-spike-threshold REGRESSORS_DVARS_TH]
[--skull-strip-template SKULL_STRIP_TEMPLATE]
[--skull-strip-fixed-seed]
[--skull-strip-t1w {auto,skip,force}] [--fmap-bspline]
[--fmap-no-demean] [--use-syn-sdc [{warn,error}]]
[--force-syn] [--fs-license-file FILE]
[--fs-subjects-dir PATH] [--no-submm-recon] [--fs-no-reconall]
[--track-carbon] [--country-code COUNTRY_CODE] [--version]
[-v] [-w WORK_DIR] [--clean-workdir] [--resource-monitor]
[--config-file FILE] [--write-graph] [--stop-on-first-crash]
[--notrack]
[--debug {compcor,fieldmaps,pdb,all}] [{compcor,fieldmaps,pdb,all} ...]]
bids_dir output_dir {participant}
```

Acknowledgments

1. Esteban, O., Markiewicz, C. J., Blair, R. W., Moodie, C. A., Isik, A. I., Erramuzpe, A., Kent, J. D., Goncalves, M., DuPre, E., Snyder, M., Oya, H., Ghosh, S. S., Wright, J., Durnez, J., Poldrack, R. A., & Gorgolewski, K. J. (2019). fMRIPrep: a robust preprocessing pipeline for functional MRI. *Nature Methods*, 16(1), 111–116. <https://doi.org/10.1038/s41592-018-0235-4>
2. Nieto-Castanon, A. (2020). Handbook of functional connectivity Magnetic Resonance Imaging methods in CONN. Boston, MA: Hilbert Press