FMRIPrep: a robust preprocessing pipeline for functional MRI

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Preprocessing of functional MRI (fMRI) involves numerous steps to clean and standardize data before statistical analysis. Generally, researchers create *ad hoc* preprocessing workflows for each new dataset, building upon a large inventory of tools available for each step. The complexity of these workflows has snowballed with rapid advances in MR data acquisition and image processing techniques. We introduce *fMRIPrep*, an analysis-agnostic tool that addresses the challenge of robust and reproducible preprocessing for task-based and resting fMRI data. *FMRIPrep* automatically adapts a best-in-breed workflow to the idiosyncrasies of virtually any dataset, ensuring high-quality preprocessing with no 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 comprising participants from 54 different studies in the OpenfMRI repository. We review the distinctive features of *fMRIPrep* in a qualitative comparison to other preprocessing workflows. We demonstrate that *fMRIPrep* achieves higher spatial accuracy as it introduces less uncontrolled spatial smoothness than commonly used preprocessing tools. *FMRIPrep* has the potential to transform fMRI research by equipping neuroscientists with a high-quality, robust, easy-to-use and transparent preprocessing workflow which can help ensure the validity of inference and the interpretability of their results.

Functional magnetic resonance imaging (fMRI) is a commonly used technique to map human brain activity[1]. However, the blood-oxygen-level dependent (BOLD) signal measured by fMRI is typically mixed with many non-neural sources of variability[2]. Preprocessing identifies the nuisance sources and reduces their effect on the data[3]. Other major preprocessing steps[4] deal with particular imaging artifacts and the anatomical location of signals. For instance, slice-timing[5] correction (STC), head-motion correction (HMC), and susceptibility distortion correction (SDC) address particular artifacts; while co-registration, and spatial normalization are concerned with signal location (see Online Methods, sec. Preprocessing of fMRI in a nutshell, for a summary). Extracting a signal that is most faithful to the underlying neural activity is crucial to ensure the validity of inference and interpretability of results[6]. Faulty preprocessing may lead to the interpretation of noise patterns as signals of interest. For example, Power et al. demonstrated that unaccounted-for head-motion can generate spurious and systematic correlations in resting-state fMRI[7], which would be interpreted as functional connectivity. An illustration of failed spatial normalization familiar to most researchers is finding significant activation outside of the brain. Other preprocessing

choices may result in the removal of signal originating from brain activity. The ongoing debate on the need for regressing out global signals[2,8,9] reflects just such concerns. Thus, a primary goal of preprocessing is to reduce sources of Type I errors without inducing excessive Type II errors.

Workflows for preprocessing fMRI produce two broad classes of outputs: *preprocessed* data (as opposed to *raw*, original data) and measurements of experimental *confounds* for use in later modeling. Preprocessed data generally include new fMRI time-series after the application of retrospective signal correction and filtering algorithms. In addition, these data are typically resampled onto a target space appropriate for analysis, such as a standardized anatomical reference. The *confounds* are additional time-series such as physiological recordings and estimated noise sources that are useful for analysis (e.g. they can be applied as nuisance regressors). Some commonly used confounds include: motion parameters, framewise displacement (FD[7]), spatial standard deviation of the data after temporal differencing (DVARS[7]), global signals, etc. Preprocessing may include further steps for denoising and estimation of confounds. For instance, dimensionality reduction methods based on principal components analysis (PCA) or independent components analysis (ICA), such as component-based noise correction (*CompCor*[10]) or automatic removal of motion artifacts (ICA-AROMA[11]).

The neuroimaging community is well equipped with tools that implement the majority of the individual steps of preprocessing described so far. These tools are readily available within software packages including AFNI[12], ANTs[13], FreeSurfer[14], FSL[15], Nilearn[16], or SPM[17]. Despite the wealth of accessible software and multiple attempts to outline best practices for preprocessing[2,4,6,18], the large variety of data acquisition protocols have led to the use of *ad hoc* pipelines customized for nearly every study; for example, Carp[19] found 223 unique analysis workflows across 241 fMRI studies. Thus, current preprocessing workflows offer a poor trade-off between the quality of results and robust, consistent performance on datasets other than those that they were built for. Alternatively, researchers can adopt the acquisition protocols defined by large neuroimaging consortia like the Human Connectome Project (HCP[20]) or the UK Biobank[21], which then allows the use of their preprocessing pipelines[22,23] developed for those studies. Since these pipelines are optimized for particular data acquisition protocols, they are not applicable to datasets acquired using different protocols. In practice, the neuroimaging community lacks a preprocessing workflow that reliably provides high-quality and consistent results on arbitrary datasets.

Here we introduce *fMRIPrep*, a preprocessing workflow for task-based and resting-state fMRI. *FMRIPrep* is built around four driving principles: 1) **robustness** to the idiosyncrasies of the input dataset; 2) **quality** of preprocessing outcomes; 3) **transparency** to encourage the scrutiny of preprocessing results for quality, and to facilitate accurate communication of the methods; and 4) **ease-of-use** with the minimization of manual intervention. *FMRIPrep* is robust by virtue of a flexible, self-adapting architecture that combines tools from existing neuroimaging analysis packages. Tools for each processing operation are selected through an evidence-driven and community-informed optimization process. Here we also report a comprehensive evaluation of the workflow on a large and heterogeneous subsample of the OpenfMRI repository, to quantify robustness and quality of the results. This evaluation leverages the comprehensive visual reports generated by *fMRIPrep*, which facilitate assessment and curation of the results. These reports contribute to the "glass-box" philosophy with which the software was developed; rather than hiding a complex set of operations within a monolithic black box, *fMRIPrep* exposes interim results at multiple steps to encourage active engagement by the scientist.

RESULTS

FMRIPrep is a robust and convenient tool for researchers and clinicians to prepare both task-based and resting-state fMRI data for analysis. Its outputs enable a broad range of applications, including within-subject analysis using functional localizers, voxel-based analysis, surface-based analysis, task-based group analysis, resting-state connectivity analysis, and many others. In the following, we describe the overall architecture, software engineering principles, and a comprehensive validation of the tool.

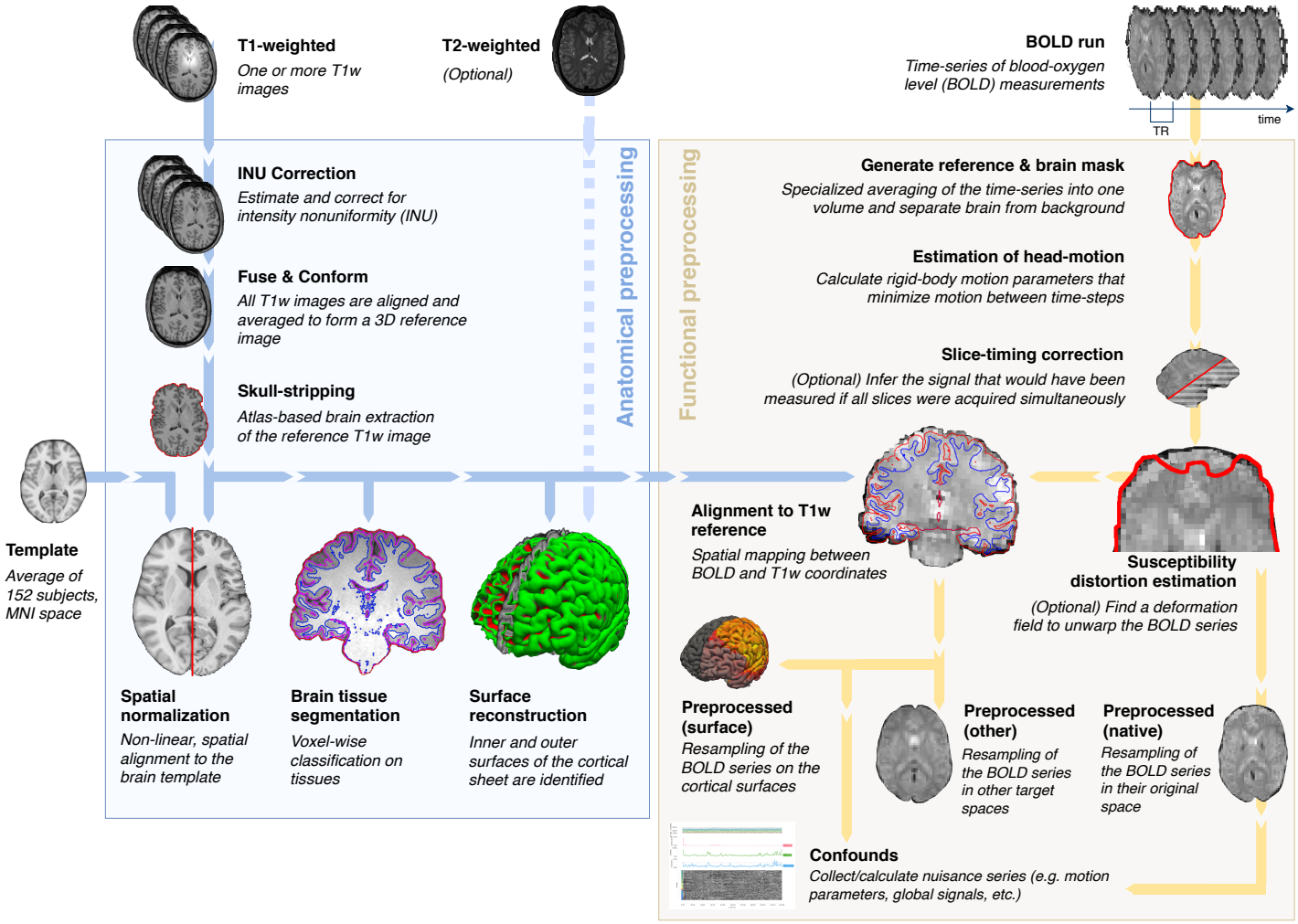


Figure 1. *FMRIPrep* is an fMRI preprocessing tool that adapts to the input dataset. Leveraging the Brain Imaging Data Structure (BIDS[24]), the software self-adjusts automatically, configuring the optimal workflow for the given input dataset. Thus, no manual intervention is required to locate the required inputs (one T1-weighted image and one BOLD series), read acquisition parameters (such as the repetition time –TR– and the slice acquisition-times) or find additional acquisitions intended for specific preprocessing steps (like field maps and other alternatives for the estimation of the susceptibility distortion). Outputs are easy to navigate due to compliance with the BIDS Extension Proposal for derived data (see Online Methods, *Figure S4*).

A modular design allows for a flexible, adaptive workflow

The foundation of *fMRIPrep* is presented in *Figure 1*. The workflow is composed of sub-workflows that are dynamically assembled into different configurations depending on the input data. These building blocks combine tools from widely-used, open-source neuroimaging packages (see *Table 1* for a summary). *Nipype*[25] is used to stage the workflows and to deal with execution details (such as resource management). As presented in *Figure 1*, the workflow comprises two major blocks, separated into anatomical and functional MRI processing streams.

Automatically understanding the input dataset. The Brain Imaging Data Structure (BIDS[24]) allows *fMRIPrep* to precisely identify the structure of the input data and gather all the available metadata (e.g. imaging parameters). Online Methods, sec. The BIDS ecosystem describes how BIDS enables workflow flexibility. *FMRIPrep* reliably adapts to dataset irregularities such as missing acquisitions or runs through a set of heuristics. For instance, if only one participant of a sample lacks field-mapping acquisitions, *fMRIPrep* will by-pass the correction step for that one participant.

Table 1. State-of-the-art neuroimaging offers a large catalog of readily available software tools. *FMRIPrep* integrates best-in-breed tools for each of the preprocessing tasks that its workflow covers, except for steps implemented as part of the development of *fMRIPrep* (*in-house* implementations). Tasks listed on the first column are described in detail in Online Methods, sec. Preprocessing of fMRI in a nutshell.

Preprocessing task	*fMRIPrep* includes	Alternatives (not included within *fMRIPrep*)
Anatomical T1w brain-extraction	`antsBrainExtraction.sh` (ANTs)	`bet` (FSL), `3dSkullstrip` (AFNI), MRTOOL (SPM Plug-in)
Anatomical surface reconstruction	`recon-all` (FreeSurfer)	CIVET, BrainSuite, Computational Anatomy (SPM Plug-in)
Head-motion estimation (and correction)	`mcflirt` (FSL)	`3dvolreg` (AFNI), `spm_realign` (SPM), `cross_realign_4dfp` (4dfp), `antsBrainRegistration` (ANTs)
Susceptibility-derived distortion estimation (and unwarping)	`3dqwarp` (AFNI)	`fugue` and `topup` (FSL), FieldMap and HySCO (SPM Plug-ins)
Slice-timing correction	`3dTshift` (AFNI)	`slicetimer` (FSL), `spm_slice_timing` (SPM), `interp_4dfp` (4dfp)
Intra-subject registration	`bbregister` (FreeSurfer), `flirt` (FSL)	`3dvolreg` (AFNI), `antsRegistration` (ANTs), Coregister (SPM GUI)
Spatial normalization (inter-subject co-registration)	`antsRegistration` (ANTs)	`@auto_tlrc` (AFNI), `fnirt` (FSL), Normalize (SPM GUI)
Surface sampling	`mri_vol2surf` (FreeSurfer)	MNE, Nilearn
Subspace projection denoising (ICA, PCA, etc)	`melodic` (FSL), ICA-AROMA	Nilearn, LMGS (SPM Plug-in)
Confounds	*in-house* implementation	`fsl_motion_outliers` (FSL), TAPAS PhysIO (SPM Plug-in)
Detection of nonsteady-states	*in-house* implementation	*Ad hoc* implementations, manual setting

Preprocessing anatomical images. The T1-weighted (T1w) image is corrected for intensity non-uniformity (INU) using `N4BiasFieldCorrection`[26] (ANTs), and skull-stripped using `antsBrainExtraction.sh` (ANTs). Skull-stripping is performed through coregistration to a template, with two options available: the OASIS template[27] (default) or the NKI template[28]. Using visual inspection, we have found that this approach outperforms other common approaches, which is consistent with previous reports[22]. When several T1w volumes are found, the INU-corrected versions are first fused into a reference T1w map of the subject with `mri_robust_template`[29] (FreeSurfer). Brain surfaces are reconstructed from the subject's T1w reference (and T2-weighted images if available) using `recon-all`[30] (FreeSurfer). The brain mask estimated previously is refined with a custom variation of a method (originally introduced in Mindboggle[31]) to reconcile ANTs-derived and FreeSurfer-derived segmentations of the cortical gray matter (GM). Both surface reconstruction and subsequent mask refinement are optional and can be disabled to save run time when surface-based analysis is not needed. Spatial normalization to the ICBM 152 Nonlinear Asymmetrical template[32] (version 2009c) is performed through nonlinear registration with `antsRegistration`[33] (ANTs), using brain-extracted versions of both the T1w reference and the standard template. ANTs was selected due to its superior performance in terms of volumetric group level overlap[34]. Brain tissues –cerebrospinal fluid (CSF), white matter (WM) and GM– are segmented from the reference, brain-extracted T1w using `fast`[35] (FSL).

Preprocessing functional runs. For every BOLD run found in the dataset, a reference volume and its skull-stripped version are generated using an in-house methodology (reported in Online Methods, sec. Particular processing elements of *fMRIPrep*). Then, head-motion parameters (volume-to-reference transform matrices, and corresponding rotation and translation parameters) are estimated using `mcflirt`[36] (FSL). Among several alternatives (see ***Table 1***), `mcflirt` is used because its results are comparable to other tools[37] and it stores the estimated parameters in a format that facilitates the composition of spatial transforms to achieve one-step interpolation (see below). If slice timing information is available, BOLD runs are (optionally) slice time corrected using `3dTshift` (AFNI[12]). When field map information is

available, or the experimental "fieldmap-less" correction is requested (see Highlights of *fMRIPrep* within the neuroimaging context), SDC is performed using the appropriate methods (see Online Methods, ***Figure S3***). This is followed by co-registration to the corresponding T1w reference using boundary-based registration[38] with nine degrees of freedom (to minimize remaining distortions). If surface reconstruction is selected, *fMRIPrep* uses `bbregister` (FreeSurfer). Otherwise, the boundary based coregistration implemented in `flirt` (FSL) is applied. In our experience, `bbregister` yields the better results[38] due to the high resolution and the topological correctness of the GM/WM surfaces driving registration. To support a large variety of output spaces for the results (e.g. the native space of BOLD runs, the corresponding T1w, FreeSurfer's *fsaverage* spaces, the template used as target in the spatial normalization step, etc.), the transformations between spaces can be combined. For example, to generate preprocessed BOLD runs in template space (e.g. MNI), the following transforms are concatenated: head-motion parameters, the warping to reverse susceptibility-distortions (if calculated), BOLD-to-T1w, and T1w-to-template mappings. The BOLD signal is also sampled onto the corresponding participant's surfaces using `mri_vol2surf` (FreeSurfer), when surface reconstruction is being performed. Thus, these sampled surfaces can easily be transformed onto different output spaces available by concatenating transforms calculated throughout *fMRIPrep* and internal mappings between spaces calculated with `recon-all`. The composition of transforms allows for a single-interpolation resampling of volumes using `antsApplyTransforms` (ANTs). Lanczos interpolation is applied to minimize the smoothing effects of linear or Gaussian kernels[39]. Optionally, ICA-AROMA can be performed and corresponding "non-aggressively" denoised runs are then produced. When ICA-AROMA is enabled, the time-series are first smoothed and then denoised, following the description of the original method[11].

Extraction of nuisance time-series. To avoid restricting *fMRIPrep*'s outputs to particular analysis types, the tool does not perform any temporal denoising by default. Nonetheless, it provides researchers with a diverse set of confound estimates that could be used for explicit nuisance regression or as part of higher-level models. This lends itself to decoupling preprocessing and behavioral modeling as well as evaluating robustness of final results across different denoising schemes. A set of physiological noise regressors are extracted for the purpose of performing component-based noise correction (*CompCor*[10]). Principal components are estimated after high-pass filtering the BOLD time-series (using a discrete cosine filter with 128s cut-off) for the two CompCor variants: temporal (tCompCor) and anatomical (aCompCor). Six tCompCor components are then calculated from the top 5% variable voxels within a mask covering the subcortical regions. This subcortical mask is obtained by heavily eroding the brain mask, which ensures it does not include cortical GM regions. For aCompCor, six components are calculated within the intersection of the aforementioned mask and the union of CSF and WM masks calculated in T1w space, after their projection to the native space of each functional run (using the inverse BOLD-to-T1w transformation). Framewise displacement[40] and DVARS are calculated for each functional run, both using their implementations in Nipype (following the definitions by Power et al.[7]). Three global signals are extracted within the CSF, the WM, and the whole-brain masks using Nilearn[16]. If ICA-AROMA[11] is requested, the "aggressive" noise-regressors are collected and placed within the corresponding confounds files. Since the non-aggressive cleaning with ICA-AROMA is performed after extraction of other nuisance signals, the "aggressive" regressors can be used to orthogonalize those other nuisance signals to avoid the risk of re-introducing nuisance signal within regression. In addition, a "non-aggressive" version of preprocessed data is also provided since this variant of ICA-AROMA denoising cannot be performed using only nuisance regressors.

Visual reports ease quality control and maximize transparency

Users can assess the quality of preprocessing with an individual report generated per participant. ***Figure 2*** shows an example of such reports and describes their structure. Reports contain dynamic and static mosaic views of images at different quality control points along the preprocessing pipeline. Many visual elements of the reports, as well as some of the figures in this manuscript are generated using Nilearn[16]. Only a web browser is required to open the reports on any platform, since they are

written in hypertext markup language (HTML). HTML also enables the trivial integration within online neuroimaging services such as OpenNeuro.org, and maximizes shareability between peers. These reports effectively minimize the amount of time required for assessing the quality of the results. They also help understand the internals of processing by visually reporting the full provenance of data throughout the workflow. As an additional transparency enhancement, reports are accompanied by a *citation boilerplate* (see Online Methods, ***Box S1***) that follows the guidelines for reporting fMRI studies by Poldrack et al.[41]. Meant for its inclusion within the methodological section of papers using *fMRIPrep*, the boilerplate provides a literate description of the processing that includes software versions of all tools involved in the particular workflow and gives due credit to all authors of all of the individual pieces of software used within *fMRIPrep*.

Highlights of *fMRIPrep* within the neuroimaging context

FMRIPrep is not the first preprocessing pipeline for fMRI data. The most widely used neuroimaging packages generally provide workflows, such as `afni_proc.py` (AFNI) or `feat` (FSL). Other alternatives include C-PAC[42] (configurable pipeline for the analysis of connectomes), HCP Pipelines[22] or the Batch Editor of SPM. In this section, we highlight some additional features beyond robustness and quality that will likely incline scientists to find in *fMRIPrep* the best fit for their fMRI preprocessing needs.

Analysis-agnostic: *fMRIPrep* supports a wide range of existing, higher-level analysis and modeling. Alternative workflows are not *agnostic* to currently-available analysis options because they prescribe particular methodologies to analyze the preprocessed data. Important limitations to compatibility with downstream analysis derive from the coordinates space of the outputs and the regular (volume) vs. irregular (surface) sampling of the BOLD signal. For example, HCP Pipelines supports surface-based analyses on subject or template space. Conversely, C-PAC and `feat` are volume-based only. Although `afni_proc.py` is volume-based by default, pre-reconstructed surfaces can be manually set for sampling the BOLD signal prior to analysis. *FMRIPrep* allows a multiplicity of output spaces including subject-space and atlases for both volume-based and surface-based analyses. While *fMRIPrep* avoids including processing steps that may limit further analysis (e.g. spatial smoothing), other tools are designed to perform preprocessing that supports specific analysis pipelines. For instance, C-PAC performs several processing steps towards the connectivity analysis of resting-state fMRI.

Susceptibility distortion correction (SDC) in the absence of field maps. Many legacy and current human fMRI protocols lack the MR field maps necessary to perform standard methods for SDC. *FMRIPrep* adapts the "fieldmap-less" correction method for diffusion echo-planar imaging (EPI) images introduced by Wang et al.[43]. They propose using the same-subject T1w reference as the *undistorted* target in a nonlinear registration scheme. To maximize the similarity between the T2* contrast of the EPI scan and the reference T1w, the intensities of the latter are inverted. To regularize the optimization of the deformation field only displacements along the phase-encoding (PE) direction are allowed, and the magnitude of the displacements is modulated using priors. To our knowledge, no other existing pipeline applies "fieldmap-less" SDC to the BOLD images.

***FMRIPrep* is thoroughly documented, community-driven, and developed with high-standards of software engineering.** Preprocessing pipelines are generally well documented, however the extreme flexibility of *fMRIPrep* makes its proper documentation substantially more challenging. As for other large scientific software communities, *fMRIPrep* contributors pledge to keep the documentation thorough and updated along coding iterations. Packages also differ on the involvement of the community: while *fMRIPrep* includes researchers in the decision making process and invites their suggestions and contributions, other packages have a more closed model where the feedback from users is more limited (e.g. a mailing list). In contrast to other pipelines, *fMRIPrep* is community-driven. This paradigm allows the fast adoption of cutting-edge advances on fMRI preprocessing, tend to render existing workflows (including *fMRIPrep*) obsolete. For example, while *fMRIPrep* initially performed STC before HMC, we adapted the tool to

Summary

Reports start with an overview of the dataset, as identified using BIDS.

Anatomical processing

Several panels allow for quality control of the anatomical workflow. Brain tissue segmentation, spatial normalization and surface reconstruction (if requested) can be inspected using these visualization panels.

Fieldmaps processing

When the dataset contains any of the supported alternatives to estimate the deformation map corresponding to susceptibility distortions, these panels help assess these images were correctly processed.

Functional processing

Each BOLD run across the different tasks and sessions will be presented at different quality control points.

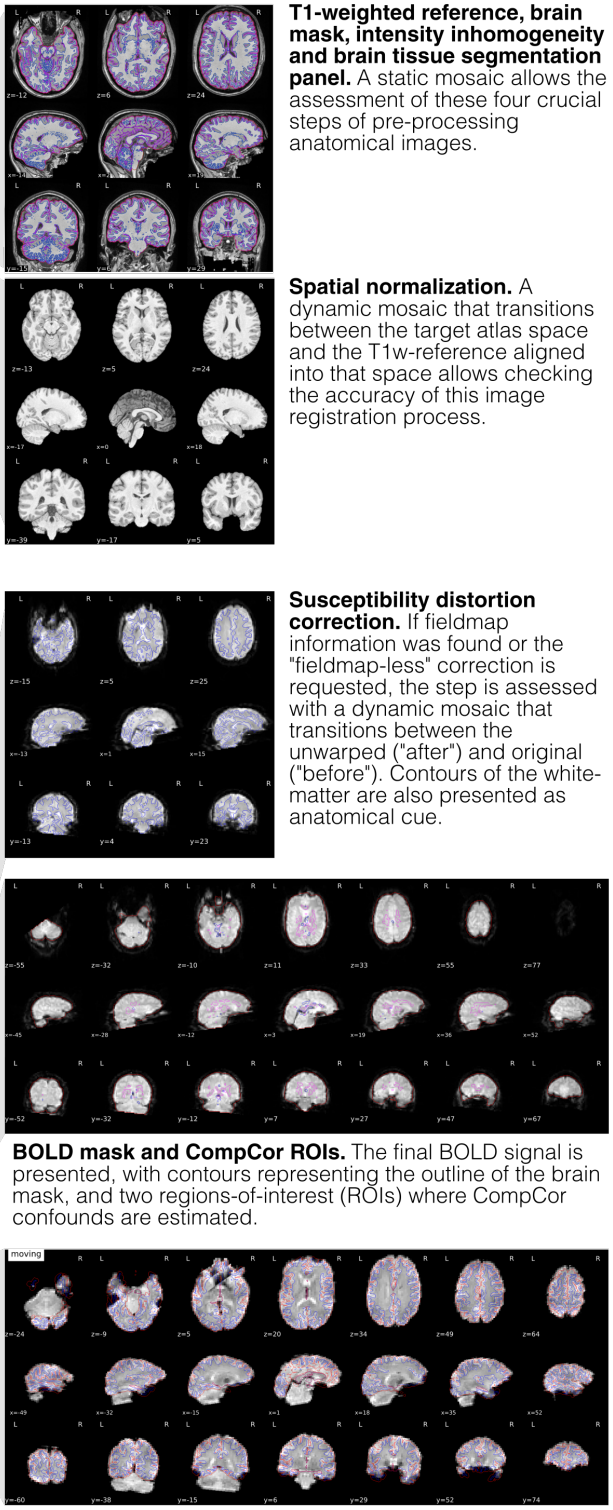
First, when fieldmaps were found, some mosaics will show the alignment of those maps to the BOLD reference. The block ends with a dynamic plot showing how images are unwarped.

The report also shows processing in native BOLD space plotting the brain mask calculated from the functional MR signal and the regions-of-interest (ROIs) where the CompCor confounds are calculated.

Finally, the alignment between same-subject T1-weighted and that specific BOLD run is presented.

Errors

FMRIPrep is explicit about errors, and any problems encountered along the processing will be listed at the end of the report, with collapsible panels containing the specific detail of each error.



T1-weighted reference, brain mask, intensity inhomogeneity and brain tissue segmentation panel. A static mosaic allows the assessment of these four crucial steps of pre-processing anatomical images.

Spatial normalization. A dynamic mosaic that transitions between the target atlas space and the T1w-reference aligned into that space allows checking the accuracy of this image registration process.

Susceptibility distortion correction. If fieldmap information was found or the "fieldmap-less" correction is requested, the step is assessed with a dynamic mosaic that transitions between the unwarped ("after") and original ("before"). Contours of the white-matter are also presented as anatomical cue.

BOLD mask and CompCor ROIs. The final BOLD signal is presented, with contours representing the outline of the brain mask, and two regions-of-interest (ROIs) where CompCor confounds are estimated.

Alignment of BOLD and the T1w reference. The correct alignment to the anatomical reference is assessed with a dynamic mosaic that renders the reconstructed surfaces over the BOLD reference.

Figure 2. The visual reports ease quality control and help understand the processing flow. The reports enhance the transparency of the tool, because they reflect the multiple steps that the workflow performs, and how these elements are intertwined.

the recent recommendations of Power et al.[18] upon a user's request*. This model has allowed the user base to grow rapidly and enabled substantial third-party contributions to be included in the software, such as the support for processing datasets without anatomical information. The open-source nature of *fMRIPrep* has permitted frequent code reviews that are effective in enhancing the software's quality and reliability[44]. Online Methods, sec. Community-centered, peer-reviewed development, and adoption of fMRIPrep describes how the community interacts, discusses the code review process, and underscores how the modular design of *fMRIPrep* successfully facilitates contributions from peers. Finally, *fMRIPrep* undergoes continuous integration testing (see Online Methods, ***Figure S5***), a technique that has recently been proposed as a means to ensure reproducibility of analyses in computational sciences[45,46].

Ensuring reproducibility with hard versioning and containers. For enhanced reproducibility, *fMRIPrep* fully supports execution via the Docker (https://docker.com) and Singularity[47] container platforms. Container images are generated and uploaded to a public repository for each new version of *fMRIPrep*. This helps address the widespread lack of reporting of specific software versions and the large variability of software versions, which threaten the reproducibility of fMRI analyses[19]. These containers are released with a fixed set of software versions for *fMRIPrep* and all its dependencies, maximizing run-to-run reproducibility in an easy way. Except for C-PAC, alternative pipelines do not provide official support for containers. The adoption of the BIDS-Apps[45] container model makes *fMRIPrep* amenable to a multiplicity of infrastructures and platforms: PC, high-performance computing (HPC), Cloud, etc.

FMRIPrep yields high-quality results on a diverse set of input data

Figure 3 presents the validation framework that we applied to iteratively maximize the robustness of the tool and validate the quality of the results. The validation framework implements a testing plan elaborated prior the release of the version 1.0 of the software (see Online Methods, sec. Evaluation of *fMRIPrep*). The plan is divided in two validation phases in which different data samples and validation procedures are applied. ***Table 2*** describes the data samples used on each phase and emphasizes how these data are collected from a large number of different, unrelated studies. In Phase I, we ran *fMRIPrep* on a manually selected sample of participants that are potentially challenging to the tool's robustness, exercising the adaptiveness to the input data. Phase II focused on the visual assessment of the quality of preprocessing results on a large and heterogeneous sample.

Validation Phase I – Fault-discovery testing. We tested *fMRIPrep* on a set of 30 datasets from OpenfMRI (see ***Table 2***). Included participants were manually selected for their low quality as visually assessed by two experts using MRIQC[105] (the assessment protocol is further described in in Online Methods, sec. Evaluation of *fMRIPrep*). Data showing substandard quality are known to likely degrade the outcomes of image processing[105], and therefore they are helpful to test software reliability. Phase I concluded with the release of *fMRIPrep* version 1.0 on December 6, 2017.

Validation Phase II – Quality assurance and reliability testing. We extended the evaluation data up to 54 datasets from OpenfMRI (see ***Table 2***). Participants were selected randomly as described in Online Methods, sec. Evaluation of *fMRIPrep*. Validation Phase II integrated a protocol for the screening of results into the software testing (***Figure 3***). As shown in ***Figure 4***, this effectively contributed to substantive improvements on the quality of results. Three raters (authors CJM, KJG and OE) evaluated the 213 visual reports at six quality control points throughout the pipeline, and also assigned an overall score to each participant. Their ratings are made available with the corresponding reports for scrutiny. The scoring scale has three levels: 1 ("poor"), 2 ("acceptable") and 3 ("excellent"). A special rating of 0 ("unusable") is assigned to critical failures that hamper any further processing beyond the quality control checkpoint. Further details on how these quality categories were assigned are given in Online Methods, sec. Iterative quality and robustness assurance. After Phase II, 50 datasets out of the total 54 were rated above the "acceptable" average quality level. The remaining 4 datasets were all above the "poor" level and in or nearby the "acceptable" rating. ***Figure 4*** illustrates the quality of results, while Online Methods,

*https://neurostars.org/t/obtaining-movement-estimates-before-slice-time-correction/1007

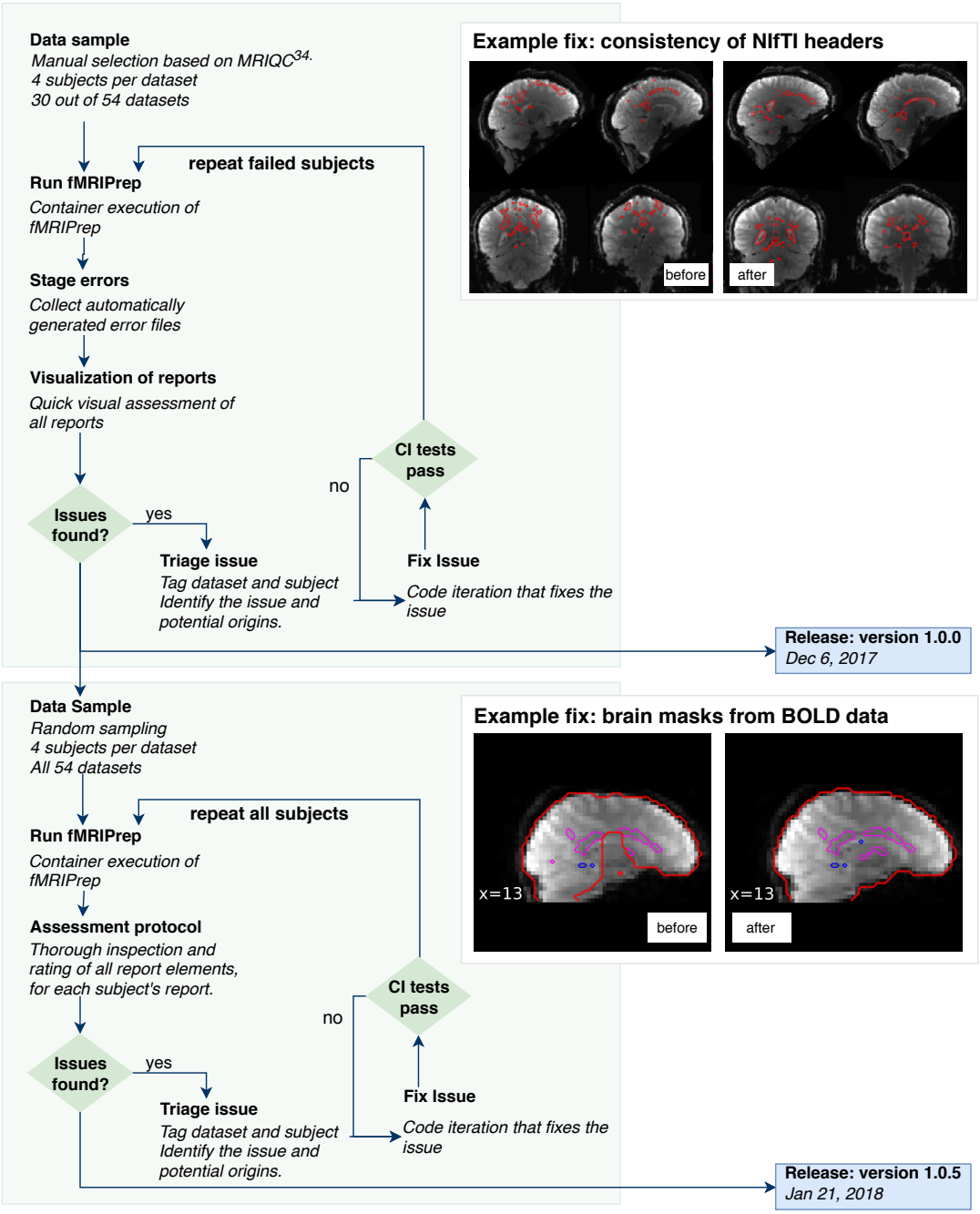


Figure 3. Combining visual assessment within the software testing flow. We complement well-established techniques for software integration testing with manual assessment of the outputs. The evaluation framework is designed with two subsequent testing phases. Phase I focuses on fault-discovery and visual reports are used to better understand the issues found. The top box (Example fix 1) shows an example of defect identified and solved during this testing cycle. After addressing a total of 21 issues affecting 7 datasets, and the release of *fMRIPrep* version 1.0.0, the next testing stage is initiated. Phase II focuses on increasing the overall quality of results as evaluated visually by experts. Following an inspection protocol, reports from 213 participants belonging to 58 different studies were individually assessed. We found 12 additional issues affecting 11 datasets that have been addressed with the release of *fMRIPrep* version 1.0.3 on January 3, 2018. The bottom box (Example fix 2) illustrates one of these issues, which produced errors in the brain extraction process from BOLD data. In Online Methods, sec. Iterative quality and robustness assurance, both examples and the corresponding solutions are described in detail.

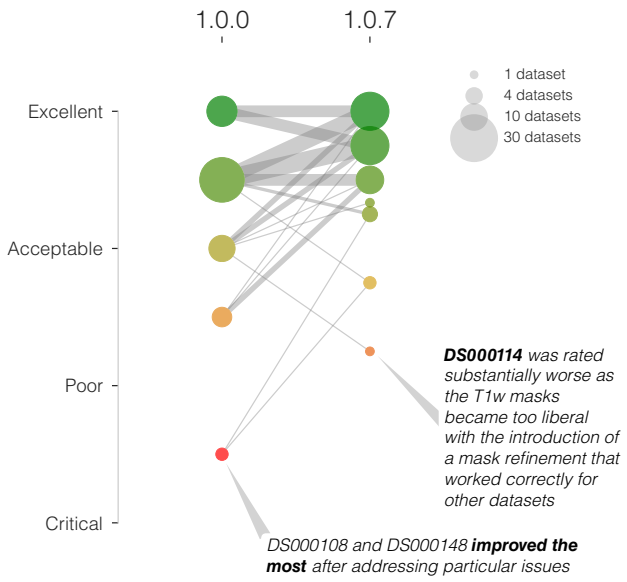


Figure 4. Integrating visual assessment into the software testing framework effectively increases the quality of results. In an early assessment of quality using *fMRIPrep* version 1.0.0, the overall rating of two datasets was below the "poor" category and four below the "acceptable" level (left column of colored circles). After addressing some outstanding issues detected by the early assessment, the overall quality of processing is substantially improved (right column of circles), and no datasets are below the "poor" quality level. Only two datasets are rated below the "acceptable" level in the second assessment (using *fMRIPrep* version 1.0.7).

Figure S6 shows the individual evolution of every dataset at each of the seven quality control points. Phase II concluded with the release of *fMRIPrep* version 1.0.8 on February 22, 2018.

FMRIPrep improves spatial precision through reduced smoothing

We investigate whether the focus on robustness against data irregularity comes at a cost in quality of the preprocessing outcomes by comparing it to the commonly used FSL `feat` workflow. Using all the scans of the "stopsignal" task in DS000030 (N=257 participants) from OpenfMRI, we ran *fMRIPrep* and a standard `feat` workflow. We chose `feat` because DS000030 had successfully been preprocessed and analyzed with FSL tools previously[55]. Smoothing is intentionally excluded from both preprocessing routes with the aim to apply it early within a common (identical) analysis workflow. We calculated standard deviation maps in MNI space[106] for the temporal average map of the "stopsignal" task derived from preprocessing with both alternatives. Visual inspection of these variability maps (*Figure 5*) reveals a higher anatomical accuracy of *fMRIPrep* over `feat`, likely reflecting the combined effects of a more precise spatial normalization scheme and the application of "fieldmap-less" SDC. *FMRIPrep* outcomes are particularly better aligned with the underlying anatomy in regions typically warped by susceptibility distortions such as the orbitofrontal lobe, as demonstrated by close-ups in Online Methods, *Figure S7*.

We also compared preprocessing done with *fMRIPrep* and FSL's `feat` in two common fMRI analyses. First, we performed within subject statistical analysis using `feat` –the same tool provides preprocessing and first-level analysis– on both sets of preprocessed data. Second, we perform a group statistical analysis using ordinary least squares (OLS) mixed modeling (`flame`[107], FSL). In both experiments, we applied identical analysis workflows and settings to both preprocessing alternatives. Using AFNI's `3dFWHMx`, we estimated the smoothness of data right after preprocessing (unsmoothed), and after an initial smoothing step of 5.0mm (full-width half-minimum, FWHM) of the common analysis workflow. As visually suggested by *Figure 5*, we indeed found that `feat` produces smoother data (*Figure 6*A). Although preprocessed data were resampled to an isotropic voxel size of 2.0×2.0×2.0 [mm], the smoothness estimation (before the prescribed smoothing step) for *fMRIPrep* was below 4.0mm, very close to the original resolution of

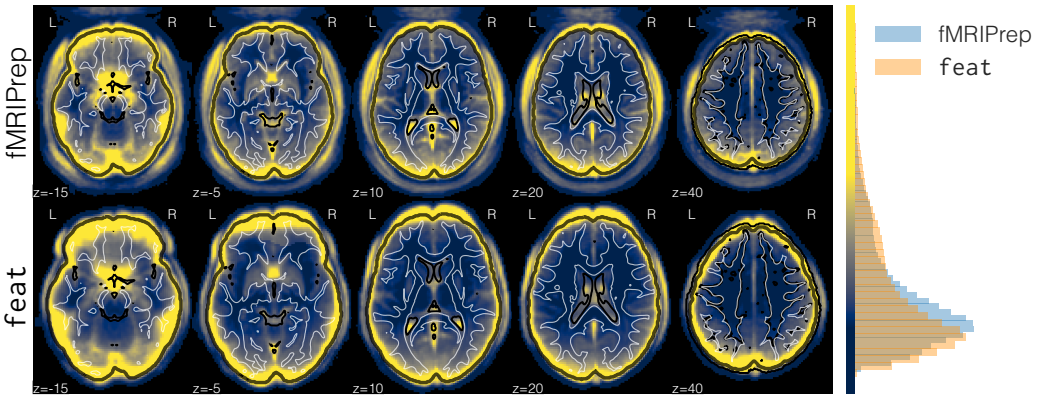


Figure 5. Maps of between-subjects variability of the averaged BOLD time-series resampled into MNI space. We preprocessed DS000030 (N=257) with *fMRIPrep* and FSL `feat`. This figure shows greater between-subject variability of the averaged BOLD series obtained with `feat`, in MNI space. The top box of the panel shows these maps at different axial planes of the image grid, with reference contours from the MNI atlas. The map summarizing `feat`-derived results displays greater variability around the brain outline (represented with a black contour). This effect is generally associated with a lower performance of spatial normalization[106]. The histogram at the right side plots the normalized frequency of variability (arbitrary units) for both maps, within the brain mask. The color bar maps the bins of the histogram to the corresponding colors that are used in the left panel. The heavier tail of `feat` in the distribution of variability is compensated in the case of *fMRIPrep* by the peak in voxel-counts located at a higher variability than that of `feat`. Such peak in *fMRIPrep*'s distribution corresponds to variability in cortical gray matter regions. See Online Methods, ***Figure S7*** for close-ups into regions affected by susceptibility-derived distortions.

3.0×3.0×4.0 [mm] of these data. The first-level analysis showed that the thresholded activation count maps for the go vs. successful stop contrast in the "stopsignal" task were very similar (***Figure 6***B). It can be seen that the results from both pipelines identified activation in the same regions. However, since data preprocessed with `feat` are smoother, the results from *fMRIPrep* are more local and better aligned with the cortical sheet.

To investigate the implications of either pipeline on the group analysis use-case, we run the same OLS modeling on two disjoint subsets of randomly selected subjects. We calculate several metrics of spatial agreement on the resulting maps of (uncorrected) p-statistical values, and also after binarizing these maps with a threshold chosen to control for the false discovery rate at 5%. The overlap of statistical maps, as well as Pearson's correlation, were tightly related to the smoothing of the input data. In Online Methods, sec. Comparison to FSL `feat` we report the group-level analysis in full. We ran two variants of the analysis: with a prescribed smoothing of 5.0mm FWHM, and without the smoothing step. These results showed that, at the group-level analysis, *fMRIPrep* and `feat` perform equivalently.

DISCUSSION

FMRIPrep is an fMRI preprocessing workflow developed to excel at four aspects of scientific software: *robustness* to data idiosyncrasies, high *quality* and consistency of results, maximal *transparency*, and *ease-of-use*. We describe how using the Brain Imaging Data Structure (BIDS[24]) along with a flexible design allows the workflow to self-adapt to the idiosyncrasy of inputs (sec. A modular design allows for a flexible, adaptive workflow). The workflow (briefly summarized in ***Figure 1***) integrates state-of-art tools from widely used neuroimaging software packages at each preprocessing step (see ***Table 1***). Some other relevant facets of *fMRIPrep* and how they relate to existing alternative pipelines are presented in sec. Highlights of *fMRIPrep* within the neuroimaging context. We stress that *fMRIPrep* is developed with the best software engineering principles, which are fundamental to ensure software reliability. The pipeline is easy to use for researchers and clinicians without extensive computer engineering experience, and produces comprehensive visual reports (***Figure 2***).

In sec. *FMRIPrep* yields high-quality results on a diverse set of input data, we demonstrate the

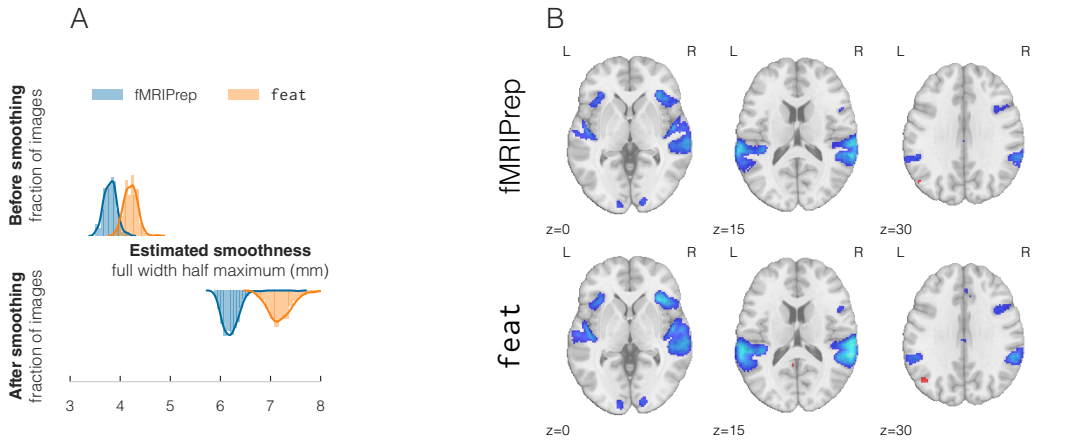


Figure 6. A | Estimating the spatial smoothness of data before and after the initial smoothing step of the analysis workflow confirmed that results of preprocessing with `feat` are intrinsically smoother. Therefore, *fMRIPrep* affords the researcher finer control over the smoothness of their analysis. **B** | Thresholded activation count maps for the go vs. successful stop contrast in the "stopsignal" task after preprocessing using either *fMRIPrep* or FSL's `feat`, with identical single subject statistical modeling. Both tools obtained similar activation maps, with *fMRIPrep* results being slightly better aligned with the underlying anatomy.

robustness of *fMRIPrep* on a representative collection of data from datasets associated with different studies (***Table 2***). We then interrogate the quality of those results with the individual inspection of the corresponding visual reports by experts (sec. Visual reports ease quality control and maximize transparency and the corresponding summary in ***Figure 4***). A comparison to FSL's `feat` (sec. *FMRIPrep* improves spatial precision through reduced smoothing) demonstrates that *fMRIPrep* achieves higher spatial accuracy and introduces less uncontrolled smoothness (Figures 5, 6). Group *p*-statistical maps only differed on their smoothness (sharper for the case of *fMRIPrep*). The fact that first-level and second-level analyses resulted in small differences between *fMRIPrep* and our *ad hoc* implementation of a `feat`-based workflow indicates that the individual preprocessing steps perform similarly when they are fine-tuned to the input data. That justifies the need for *fMRIPrep*, which autonomously adapts the workflow to the data without error-prone manual intervention. To a limited extent, that also mitigates some concerns and theoretical risks arisen from the analytical degrees-of-freedom [19] available to researchers. *FMRIPrep* stands out amongst pipelines because it automates the adaptation to the input dataset without compromising the quality of results.

One limitation of this work is the use of visual (the reports) and semi-visual (e.g. ***Figure 5*** and ***Figure 6***) assessments for the quality of preprocessing outcomes. Although some frameworks have been proposed for the quantitative evaluation of preprocessing on task-based (such as NPAIRS [108]) and resting-state [109] fMRI, they impose a set of assumptions on the test data and the workflow being assessed that severely limit their suitability. The modular design of *fMRIPrep* defines an interface to each processing step, which will permit the programmatic evaluation of the many possible combinations of software tools and processing steps. That will also enable the use of quantitative testing frameworks to pursue the minimization of Type I errors without the cost of increasing Type II errors.

The range of possible applications for *fMRIPrep* also presents some boundaries. For instance, very narrow field-of-view (FoV) images oftentimes do not contain enough information for standard image registration methods to work correctly. Reduced FoV datasets from OpenfMRI were excluded from the evaluation since they are not yet fully supported by *fMRIPrep*. Extending *fMRIPrep*'s support for these particular images is already a future line of the development road-map. *FMRIPrep* may also under-perform for particular populations (e.g. infants) or when brains show nonstandard structures, such as tumors, resected regions or lesions. Nonetheless, *fMRIPrep*'s modular architecture makes it straightforward to

extend the tool to support specific populations or new species by providing appropriate atlases of those brains. This future line of work would be particularly interesting in order to adapt the workflow to data collected from rodents and nonhuman primates. By contrast, *fMRIPrep* performed robustly on data from a simultaneous MRI/electrocorticography (ECoG) study, which is extremely challenging to analyze due to the massive BOLD signal drop-out near the implanted cortical electrodes (see Online Methods, ***Figure S11***). Likewise, *fMRIPrep* successfully preprocessed multiple multi-band datasets.

Approximately 80% of the analysis pipelines investigated by Carp[19] were implemented using either AFNI[12], FSL[15], or SPM[17]. *Ad hoc* pipelines adapt the basic workflows provided by these tools to the particular dataset at hand. Although workflow frameworks like Nipype[110] ease the integration of tools from different packages, these pipelines are typically restricted to just one of these alternatives (AFNI, FSL or SPM). Otherwise, scientists can adopt the acquisition protocols and associated preprocessing software of large consortia like the Human Connectome Project (HCP) or the UK Biobank. The *off-the-shelf* applicability of these workflows is contravened by important limitations on the experimental design. Therefore, researchers typically opt to recode their custom preprocessing workflows with nearly every new study[19]. That practice entails a "pipeline debt", which requires the investment on proper software engineering to ensure an acceptable correctness and stability of the results (e.g. continuous integration testing) and reproducibility (e.g. versioning, packaging, containerization, etc.). A trivial example of this risk would be the leakage of *magic numbers* that are hard-coded in the source (i.e. a crucial imaging parameter that inadvertently changed from one study to the next one). Until *fMRIPrep*, an analysis-agnostic approach that builds upon existing software instruments and optimizes preprocessing for robustness to data idiosyncrasies, quality of outcomes, ease-of-use, and transparency, was lacking.

The rapid increase in volume and diversity of data, as well as the evolution of available techniques for processing and analysis, presents an opportunity for significantly advancing research in neuroscience. The drawback resides in the need for progressively complex analysis workflows that rely on decreasingly interpretable models of the data. Such context encourages "black-box" solutions that efficiently perform a valuable service but do not provide insights into how the tool has transformed the data into the expected outputs. Black-boxes obscure important steps in the inductive process mediating between experimental measurements and reported findings. This way of moving forward risks producing a future generation of cognitive neuroscientists who have become experts in using sophisticated computational methods, but have little to no working knowledge of how data were transformed through processing. Transparency is often identified as a treatment for these problems. *FMRIPrep* ascribes to "glass-box" principles, which are defined in opposition to the many different facets or levels at which black-box solutions are opaque.

The visual reports that *fMRIPrep* generates are a crucial aspect of the glass-box. Their quality control checkpoints represent the logical flow of preprocessing, allowing scientists to critically inspect and better understand the underlying mechanisms of the workflow. A second transparency element is the citation boilerplate that formalizes all details of the workflow and provides the versions of all involved tools along with references to corresponding scientific literature. A third asset for transparency is the thorough documentation which delivers additional details on each of the building blocks that are represented in the visual reports and described in the boilerplate. Further, *fMRIPrep* is open-source since its inception: users have access to all the incremental additions to the tool through the history of the version-control system. The use of GitHub (https://github.com/poldracklab/fmriprep) grants access to the discussions held during development, allowing the retrieval of how and why the main design decisions were made. GitHub also provides an excellent platform to foster the community and provides useful tools such as source browsing, code review, bug tracking and reporting, submission of new features and bug fixes through pull-requests, etc. The modular design of *fMRIPrep* enhances its flexibility and helps transparency, as the main features of the software are more easily accessible to potential collaborators. In combination to some coding style and contribution guidelines, this modularity has enabled multiple contributions by peers and the creation of a rapidly growing community that would be difficult to nurture behind closed doors. A number of existing tools have implemented elements of "glass-box" philosophy (for example visual reports in FEAT, documentation in C-PAC, open source community of Nilearn), but the complete package (visual reports, educational documentation, reporting templates, collaborative open source community) is still

rare among scientific software. *FMRIPrep*'s transparent and accessible development and reporting aims to better equip fMRI practitioners to perform reliable, reproducible, statistical analyses with a high-standard, consistent, and adaptive preprocessing instrument.

CONCLUSION

Despite efforts to achieve high-quality preprocessing of idiosyncratic fMRI datasets, doing so reliably has remained an open problem. *FMRIPrep* is an analysis-agnostic, preprocessing workflow that yields consistent results across a wide range of input datasets. *FMRIPrep* is built on top of the best neuroimaging tools selected from various software packages. These tools are integrated into workflows that can be dynamically combined to compose a full preprocessing workflow adapted to the input data. The optimal workflow for the input dataset is constructed at runtime, blending a set of heuristics with the Brain Imaging Data Structure (BIDS) to read the inputs. *FMRIPrep* excels in four design goals: robustness, high-quality of results, transparency and ease-of-use. To validate and demonstrate these features, we integrate the individual screening of preprocessing results with continuous integration techniques of software testing. The process is aided by comprehensive, portable reports that inform the scientist about the workflow, ease the quality control of results and maximize the shareability of research outcomes. We highlight the aspects that justify the development of *fMRIPrep* with respect to currently available preprocessing workflows. We quantitatively demonstrate that *fMRIPrep* does not introduce uncontrolled smoothing as compared to one alternative software. *FMRIPrep* aims to better equip fMRI practitioners to perform reliable, reproducible statistical analyses with a high-standard, transparent, and verifiable instrument.

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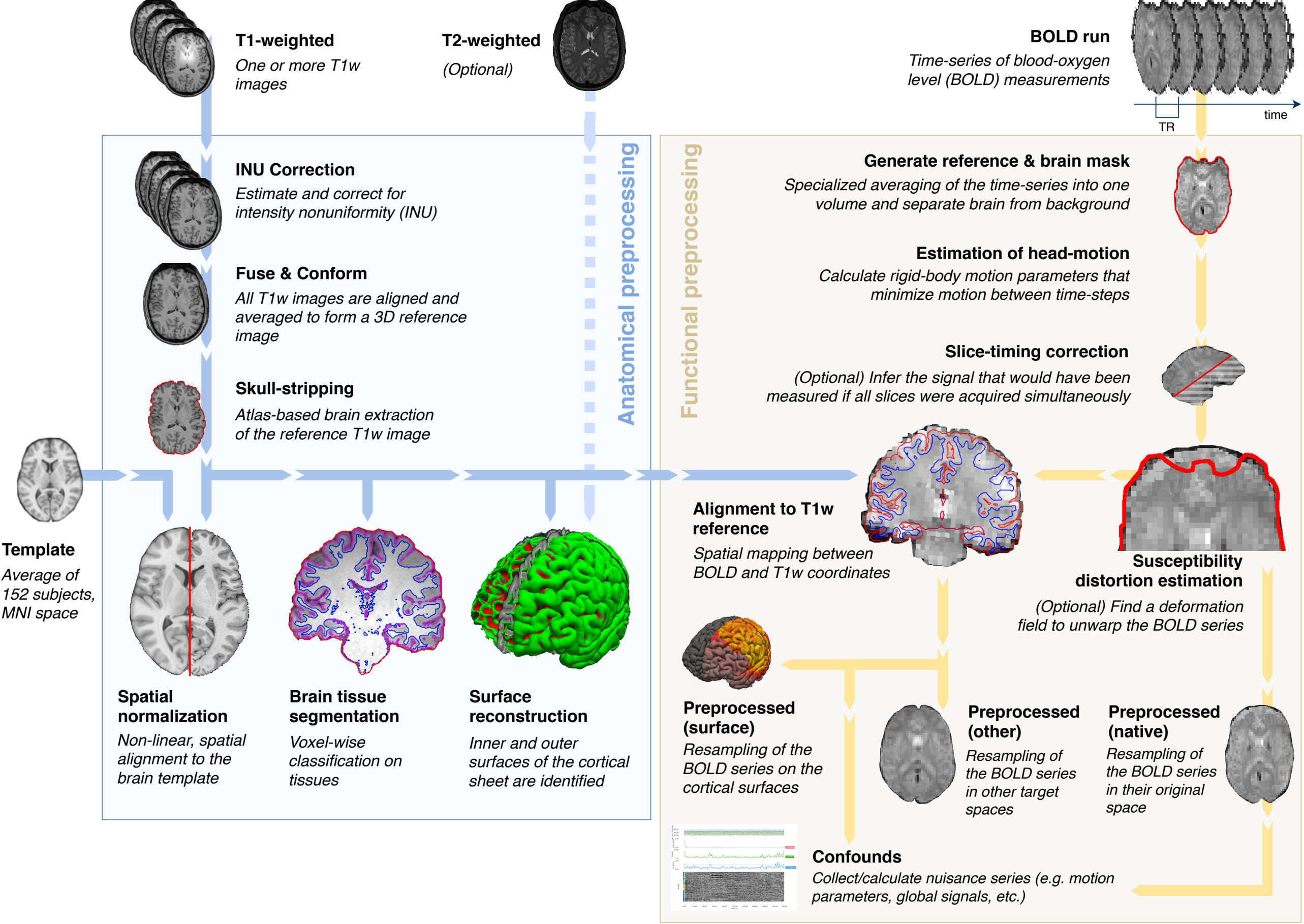
Table 2. Data from OpenfMRI used in evaluation. S: number of sessions; T: number of tasks; R: number of BOLD runs; Modalities: number of runs for each modality, per subject (FM indicates acquisitions for susceptibility distortion correction); Part. IDs (phase): participant identifiers included in testing phase; N: total of unique participants; TR: repetition time (s); #TR: length of time-series (volumes); Resolution: voxel size of BOLD series (mm).

DS000XXX	Scanner	S	T	R	Modalities	Part. IDs (Phase I)	Part. IDs (Phase II)	N	TR	#TR	Resolution
001 [48]	SIEMENS	1	1	21	1 T1w, 3 BOLD	02, 03, 09, 15	01, 02, 07, 08	7	2.0	6300	3.12×3.12×4.00
002 [49]	SIEMENS	1	3	48	1 T1w, 6 BOLD	01, 11, 14, 15	02, 03, 04, 10	8	2.0	9510	3.12×3.12×5.00
003 [50]	SIEMENS	1	1	6	1 T1w, 1 BOLD	03, 07, 09, 11	02, 09, 10, 11	6	2.0	956	3.12×3.12×4.00
005 [51]	SIEMENS	1	1	21	1 T1w, 3 BOLD	01, 03, 06, 14	01, 04, 05, 15	7	2.0	5040	3.12×3.12×4.00
007 [52]	SIEMENS	1	3	46	1 T1w, 5 BOLD	09, 11, 18, 20	03, 04, 08, 12	8	2.0	8205	3.12×3.12×4.00
008 [53]	SIEMENS	1	2	38	1 T1w, 5 BOLD	04, 09, 12, 14	10, 12, 13, 15	7	2.0	6808	3.12×3.12×4.39
009	SIEMENS	1	4	48	1 T1w, 6 BOLD	01, 03, 09, 10	17, 18, 21, 23	8	2.0	10528	3.00×3.00×4.00
011 [54]	SIEMENS	1	4	41	1 T1w, 5 BOLD	01, 03, 06, 08	03, 09, 11, 14	7	2.0	8041	3.12×3.12×5.00
017	SIEMENS	2	2	48	4 T1w, 9 BOLD	2, 4, 7, 8	2, 5, 7, 8	5	2.0	8736	3.12×3.12×4.00
030 [55,56]	SIEMENS	1	8	30	1 T1w, 7 BOLD		10[440,638,668,855]	4	2.2	6254	3.00×3.00×4.00
031 [57]	SIEMENS	107	9	191	29 T1w, 18 T2w, 46 FM, 191 BOLD		01	1	1.2	79017	2.55×2.55×2.54
051 [58]	SIEMENS	1	1	54	2 T1w, 7 BOLD	03, 04, 05, 13	02, 04, 06, 09	7	2.0	10800	3.12×3.12×6.00
052 [59]	SIEMENS	1	2	28	2 T1w, 4 BOLD	06, 08, 12, 14	05, 10, 12, 13	7	2.0	6300	3.12×3.12×6.00
053	SIEMENS	1	3	32	1 T1w, 8 BOLD		002, 003, 005, 006	4	1.2	10712	2.40×2.40×2.40
101	SIEMENS	1	1	16	1 T1w, 2 BOLD	06, 08, 16, 19	05, 11, 17, 20	8	2.0	2416	3.00×3.00×4.00
102 [60–62]	SIEMENS	1	1	16	1 T1w, 2 BOLD	05, 19, 22, 23	08, 10, 16, 20	8	2.0	2336	3.00×3.00×4.00
105 [63,64]	GE	1	1	71	1 T1w, 11 BOLD	1, 2, 3, 6	1, 4, 5, 6	6	2.5	8591	3.50×3.75×3.75
107 [65]	SIEMENS	1	1	14	1 T1w, 2 BOLD	02, 05, 20, 29	05, 36, 39, 47	7	3.0	2315	3.00×3.00×3.00
108 [66]	GE	1	1	41	1 T1w, 5 BOLD	01, 03, 07, 17	03, 10, 24, 26	7	2.0	7860	3.44×3.44×4.50
109 [67]	SIEMENS	1	1	12	1 T1w, 2 BOLD	02, 10, 39, 47	02, 11, 15, 39	6	2.0	2148	3.00×3.00×3.54
110 [68]	GE	1	1	80	1 T1w, 10 BOLD	07, 09, 17, 18	01, 02, 03, 06	8	2.0	14880	3.44×3.44×4.01
114 [69]	GE	2	5	70	2 T1w, 10 BOLD	01, 05, 07, 08	02, 03, 04, 07	7	5.0	10626	4.00×4.00×4.00
115 [70,71]	SIEMENS	1	3	24	1 T1w, 3 BOLD	31, 68, 77, 78	04, 33, 67, 79	8	2.5	3288	4.00×4.00×4.00
116 [72–75]	PHILIPS	1	2	36	1 T1w, 6 BOLD	02, 08, 10, 15	08, 12, 15, 17	6	2.0	6120	3.00×3.00×4.00
119 [76]	SIEMENS	1	1	31	1 T1w, 3 BOLD	10, 51, 59, 74	11, 26, 56, 58	8	1.5	7564	3.12×3.12×4.00
120 [77]	SIEMENS	1	1	11	1 T1w, 2 BOLD		04, 05, 08, 24	4	1.5	2376	3.12×3.12×4.00
121 [78]	SIEMENS	1	1	28	1 T1w, 4 BOLD	01, 04, 05, 20	01, 18, 22, 26	7	1.5	5656	3.12×3.12×4.00
133 [79]	PHILIPS	2	1	24	2 T1w, 6 BOLD		06, 21, 22, 23	4	1.7	3480	4.00×4.00×4.00
140 [80]	PHILIPS	1	1	36	1 T1w, 9 BOLD		05, 27, 32, 33	4	2.0	7380	2.80×2.80×3.00
148	GE	1	1	12	1 T1w, 1 T2w, 3 BOLD		09, 26, 28, 33	4	1.8	3162	3.00×3.00×3.00
157 [81]	PHILIPS	1	1	4	1 T1w, 1 BOLD		04, 21, 23, 28	4	1.6	1485	4.00×4.00×3.99
158 [82]	SIEMENS	1	1	4	1 T1w, 1 BOLD		064, 081, 122, 149	4	2.0	1240	3.00×3.00×3.30
164 [83]	SIEMENS	1	1	4	1 T1w, 1 BOLD		006, 012, 019, 027	4	1.5	1480	3.50×3.50×3.50
168 [84]	SIEMENS	1	1	4	1 T1w, 1 BOLD		08, 27, 30, 49	4	2.5	2112	3.00×3.00×3.00
170 [85–87]	GE	1	4	48	1 T1w, 12 BOLD		1700, 1708, 1710, 1713	4	3.0	2160	3.44×3.44×3.40
171 [88]	SIEMENS	1	2	20	1 T1w, 5 BOLD		control0[4,8,14], mdd03	4	3.0	2066	2.90×2.90×3.00
177 [89]	SIEMENS	1	1	4	1 T1w, 1 BOLD		04, 07, 10, 11	4	3.0	920	3.00×3.00×3.00
200 [90]	SIEMENS	1	1	4	1 T1w, 1 BOLD		2004, 2011, 2012, 2014	4	2.5	480	3.28×3.28×4.29
205 [91]	SIEMENS	1	2	12	1 T1w, 3 BOLD		01, 05, 06, 07	4	2.2	4103	3.00×3.00×3.00
208 [92]	SIEMENS	1	1	4	1 T1w, 1 BOLD		27, 45, 56, 69	4	2.5	1200	3.44×3.44×3.00
212 [93,94]	SIEMENS	1	2	40	1 T1w, 10 BOLD		07, 13, 20, 29	4	3.0	5808	3.12×3.12×4.00
213 [95]	SIEMENS	1	1	4	1 T1w, 1 BOLD		06, 10, 12, 13	4	2.0	1120	3.00×3.00×3.99
214 [96]	SIEMENS	1	1	4	1 T1w, 1 BOLD		EESS0[06,31,33,34]	4	1.6	1364	3.44×3.44×5.00
216 [97]	GE	1	1	16	1 T1w, 4 BOLD (ME)		01, 02, 03, 04	4	3.5	2688	3.00×3.00×3.00
218 [98]	PHILIPS	1	1	12	1 T1w, 3 BOLD		02, 07, 12, 17	4	1.5	6709	2.88×3.00×2.88
219 [98]	PHILIPS	1	1	14	1 T1w, 3 BOLD		04, 09, 10, 12	4	1.5	7807	2.88×3.00×2.88
220 [99]	PHILIPS, SIEMENS	3	1	12	3 T1w, 3 BOLD		tbi[03,05,06,10]	4	2.0	1728	3.00×3.00×4.00
221	SIEMENS	2	1	15	1 MP2RAGE, 9 FM, 3 BOLD		010[016,064,125,251]	4	2.5	9855	2.30×2.30×2.30
224 [100]	SIEMENS	12	6	399	4 T1w, 4 T2w, 10 FM, 79 BOLD	MSC[05,06,08,09]	MSC[05,08,09,10]	5	2.2	88528	4.00×4.00×4.00
228	SIEMENS	1	1	4	1 T1w, 1 BOLD		pixar[001,017,103,132]	4	2.0	672	3.06×3.06×3.29
229 [101]	SIEMENS	1	1	12	1 T1w, 3 BOLD		02, 05, 07, 10	4	2.0	4680	3.44×3.44×3.00
231 [102]	SIEMENS	1	1	12	1 T1w, 3 BOLD		01, 02, 03, 09	4	2.0	4548	2.02×2.02×2.00
233 [103]	PHILIPS	1	2	80	2 T1w, 10 BOLD	rid0000[12,24,36,41]	rid0000[01,17,31,32]	8	2.0	15680	3.00×3.00×3.00
237 [104]	SIEMENS	1	1	41	1 T1w, 5 BOLD	03, 08, 11, 12	01, 03, 04, 06	7	1.0	19844	3.00×3.00×3.00
243 [40]	SIEMENS	1	1	13	1 T1w, 1 BOLD	012, 032, 042, 071	023, 066, 089, 094	8	2.5	2884	4.00×4.00×4.00
Total				2176		120	202	304		551769	


T1-weighted
One or more T1w images
T2-weighted
(Optional)
BOLD run
Time-series of blood-oxygen level (BOLD) measurements
time
TR
Anatomical preprocessing
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
Template
Average of 152 subjects, MNI space
Spatial normalization
Non-linear, spatial alignment to the brain template
Brain tissue segmentation
Voxel-wise classification on tissues
Surface reconstruction
Inner and outer surfaces of the cortical sheet are identified
Functional preprocessing
Generate reference & brain mask
Specialized averaging of the time-series into one volume and separate brain from background
Estimation of head-motion
Calculate rigid-body motion parameters that minimize motion between time-steps
Slice-timing correction
(Optional) Infer the signal that would have been measured if all slices were acquired simultaneously
Alignment to T1w reference
Spatial mapping between BOLD and T1w coordinates
Susceptibility distortion estimation
(Optional) Find a deformation field to unwarp the BOLD series
Preprocessed (surface)
Resampling of the BOLD series on the cortical surfaces
Preprocessed (other)
Resampling of the BOLD series in other target spaces
Preprocessed (native)
Resampling of the BOLD series in their original space
Confounds
Collect/calculate nuisance series (e.g. motion parameters, global signals, etc.)

Summary

Reports start with an overview of the dataset, as identified using BIDS.

Anatomical processing

Several panels allow for quality control of the anatomical workflow. Brain tissue segmentation, spatial normalization and surface reconstruction (if requested) can be inspected using these visualization panels.

Fieldmaps processing

When the dataset contains any of the supported alternatives to estimate the deformation map corresponding to susceptibility distortions, these panels help assess these images were correctly processed.

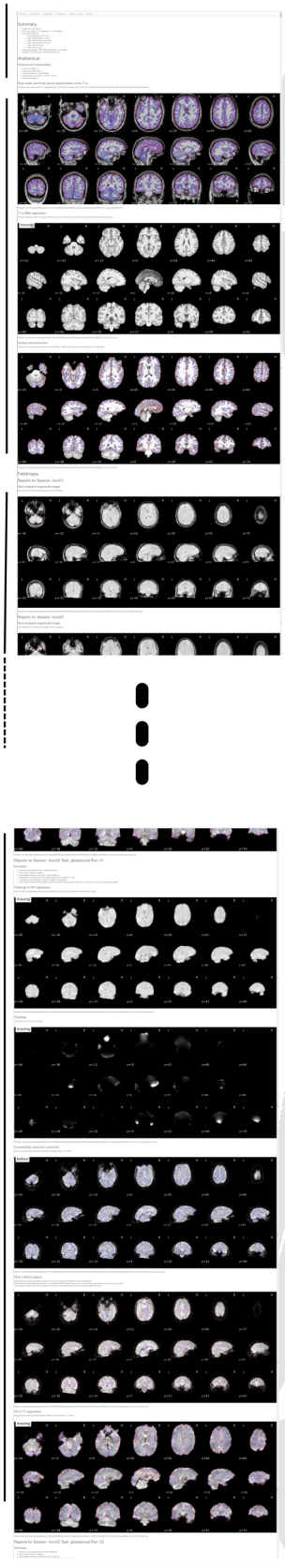
Functional processing

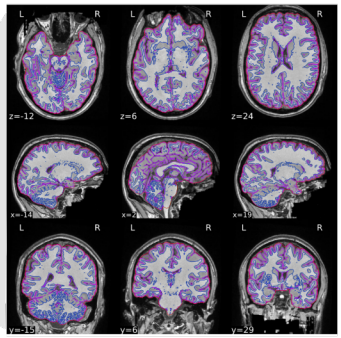
Each BOLD run across the different tasks and sessions will be presented at different quality control points.

First, when fieldmaps were found, some mosaics will show the alignment of those maps to the BOLD reference. The block ends with a dynamic plot showing how images are unwarped.

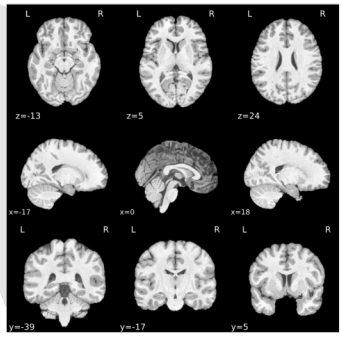
The report also shows processing in native BOLD space plotting the brain mask calculated from the functional MR signal and the regions-of-interest (ROIs) where the CompCor confounds are calculated.

Finally, the alignment between same-subject T1-weighted and that specific BOLD run is presented.

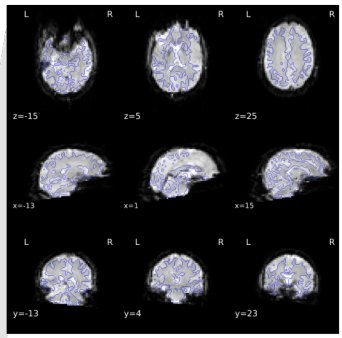




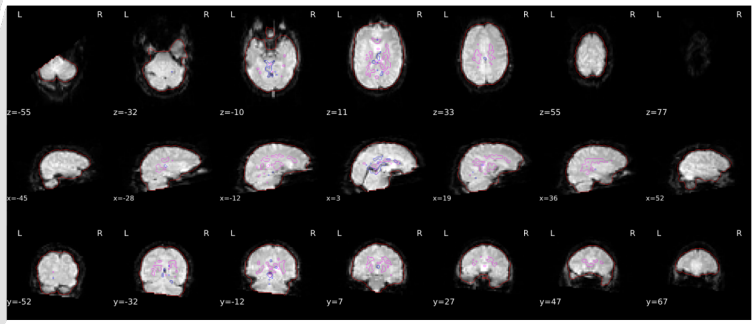
T1-weighted reference, brain mask, intensity inhomogeneity and brain tissue segmentation panel. A static mosaic allows the assessment of these four crucial steps of pre-processing anatomical images.



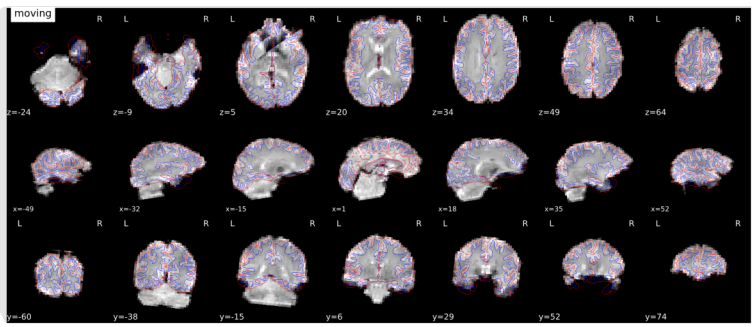
Spatial normalization. A dynamic mosaic that transitions between the target atlas space and the T1w-reference aligned into that space allows checking the accuracy of this image registration process.



Susceptibility distortion correction. If fieldmap information was found or the "fieldmap-less" correction is requested, the step is assessed with a dynamic mosaic that transitions between the unwarped ("after") and original ("before"). Contours of the white-matter are also presented as anatomical cue.



BOLD mask and CompCor ROIs. The final BOLD signal is presented, with contours representing the outline of the brain mask, and two regions-of-interest (ROIs) where CompCor confounds are estimated.



Alignment of BOLD and the T1w reference. The correct alignment to the anatomical reference is assessed with a dynamic mosaic that renders the reconstructed surfaces over the BOLD reference.

Errors

FMRIPrep is explicit about errors, and any problems encountered along the processing will be listed at the end of the report, with collapsible panels containing the specific detail of each error.

Data sample
Manual selection based on MRIQC[34].
4 subjects per dataset
30 out of 54 datasets

repeat failed subjects

Run fMRIPrep
Container execution of fMRIPrep

Stage errors
Collect automatically generated error files

Visualization of reports
Quick visual assessment of all reports

Issues found?

yes

Triage issue
Tag dataset and subject
Identify the issue and potential origins.

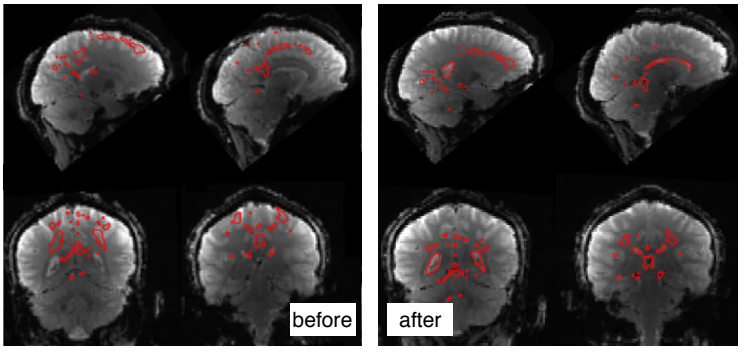
Fix Issue
Code iteration that fixes the issue

CI tests pass

no

Release: version 1.0.0
Dec 6, 2017

Example fix: consistency of NIfTI headers



Data Sample
Random sampling
4 subjects per dataset
All 54 datasets

repeat all subjects

Run fMRIPrep
Container execution of fMRIPrep

Assessment protocol
Thorough inspection and rating of all report elements, for each subject's report.

Issues found?

yes

Triage issue
Tag dataset and subject
Identify the issue and potential origins.

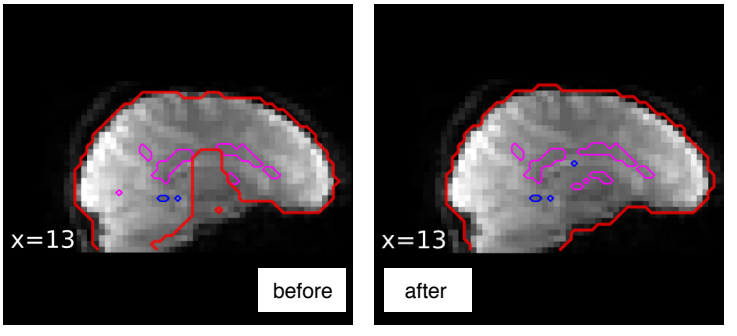
Fix Issue
Code iteration that fixes the issue

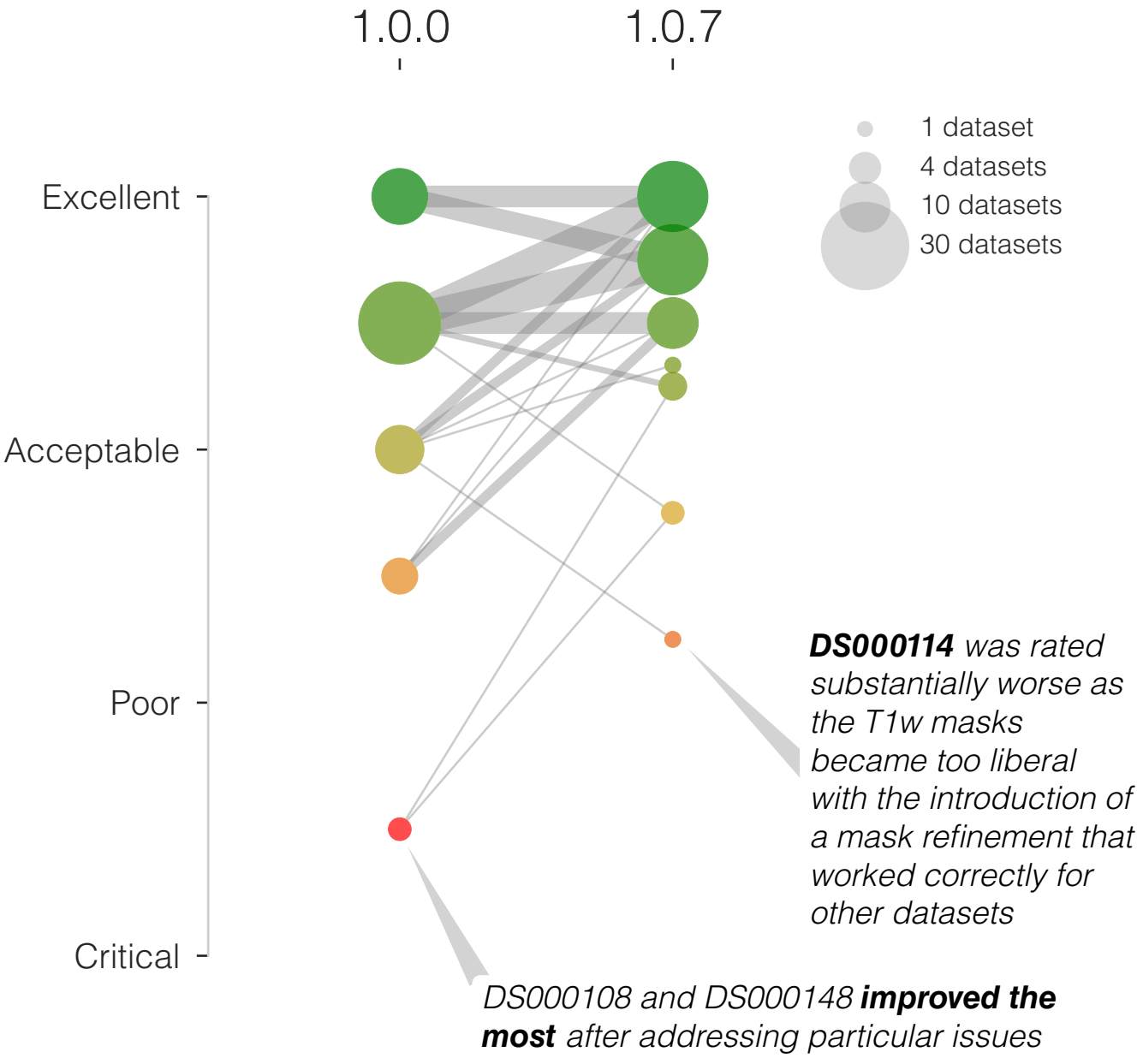
CI tests pass

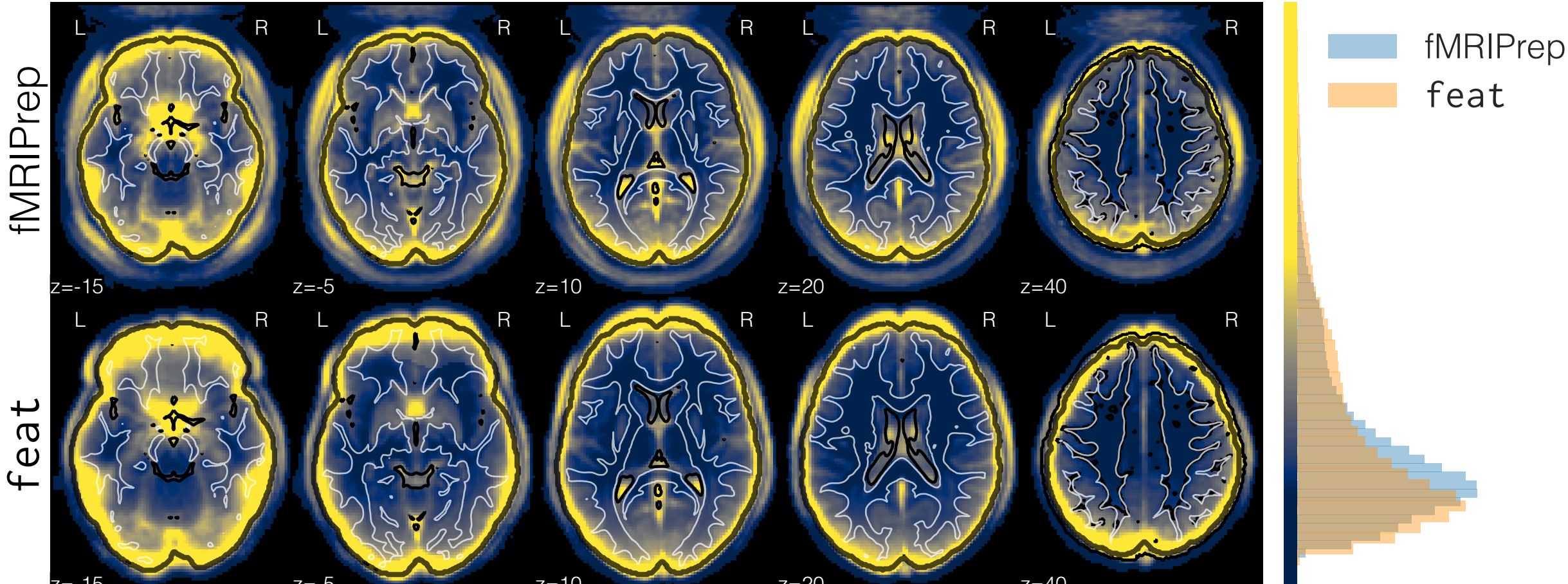
no

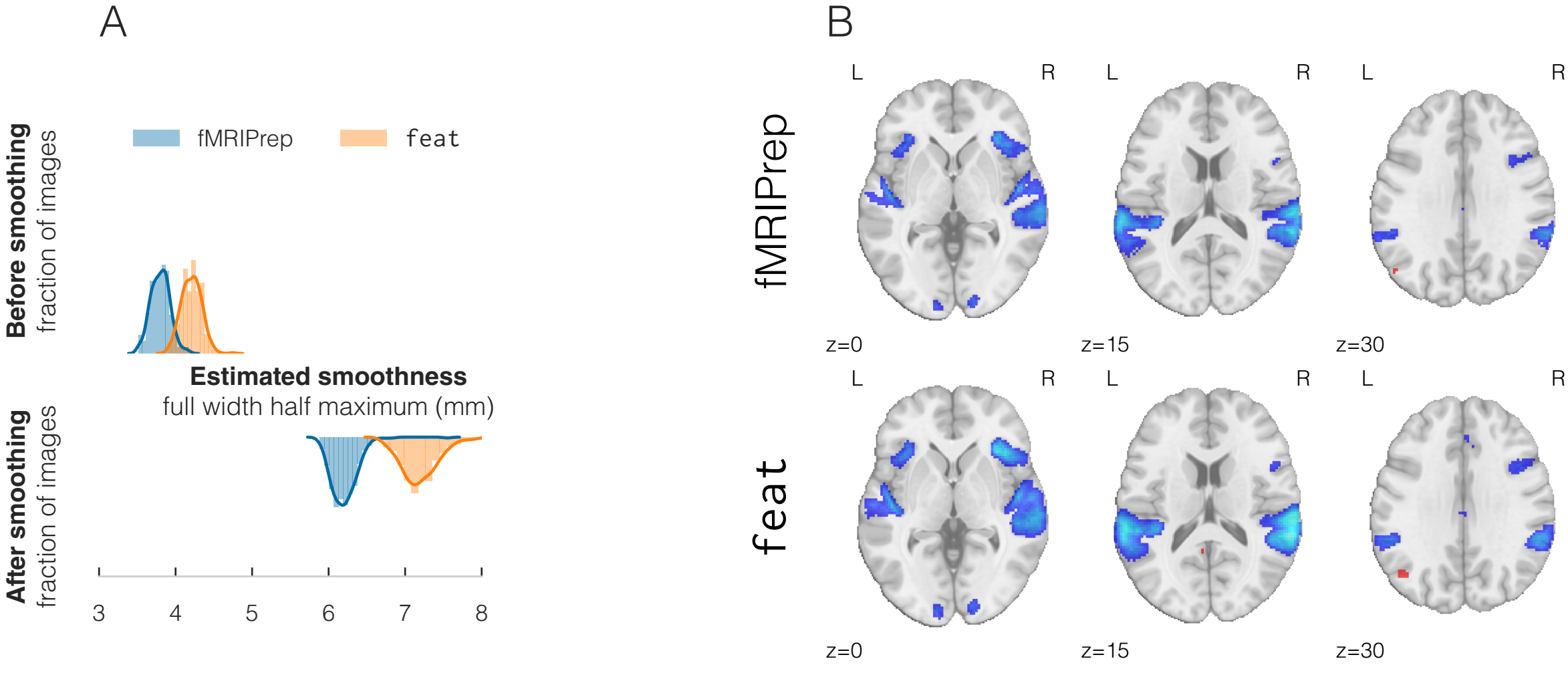
Release: version 1.0.5
Jan 21, 2018

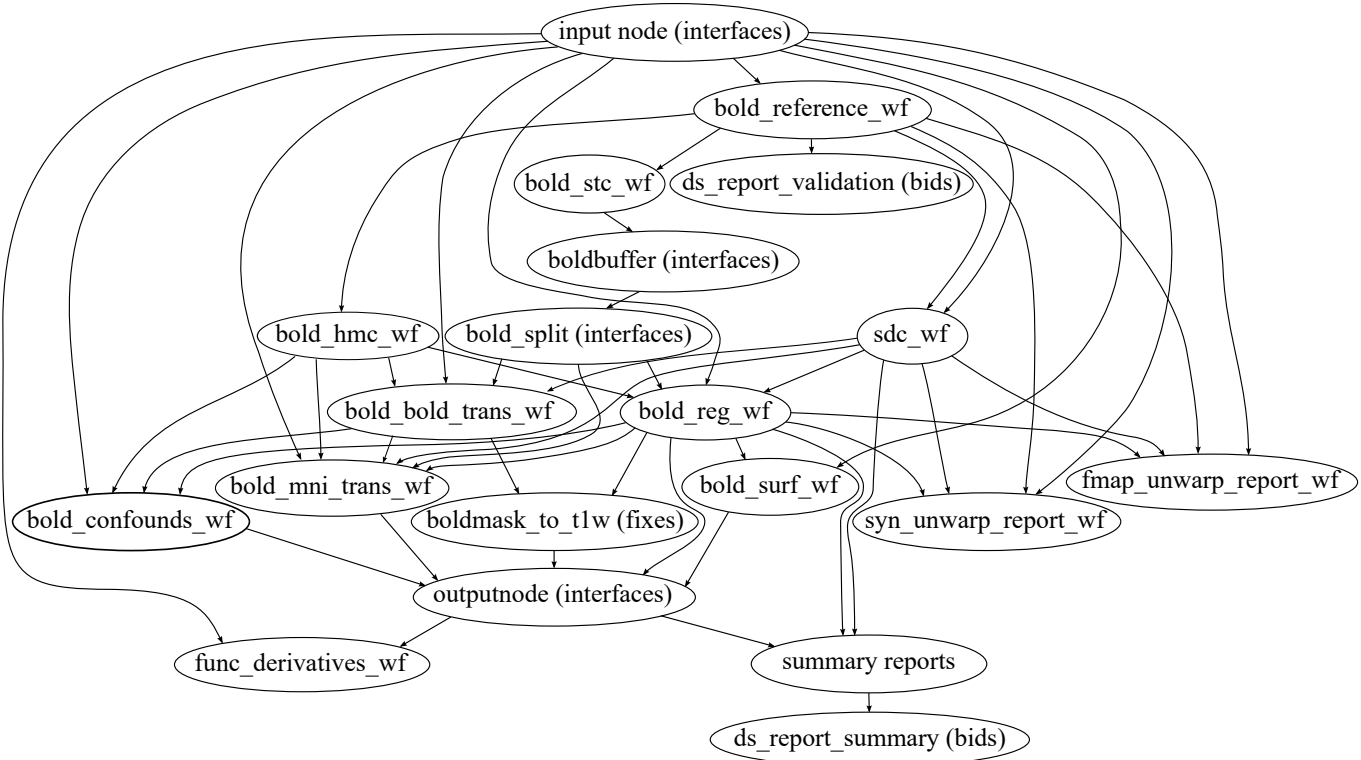
Example fix: brain masks from BOLD data

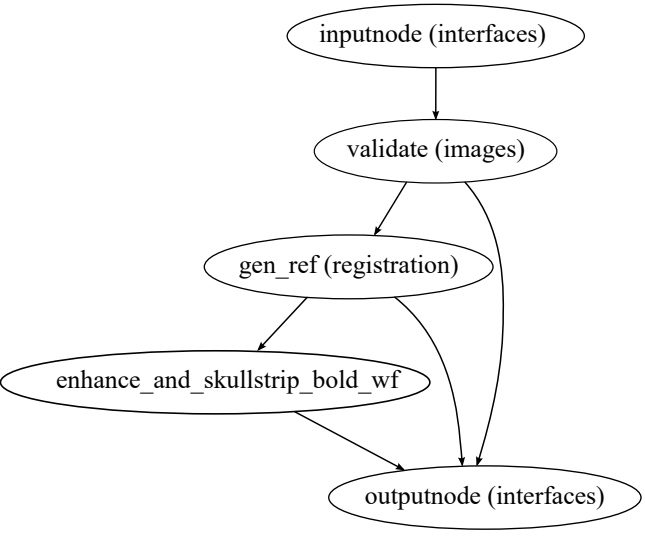


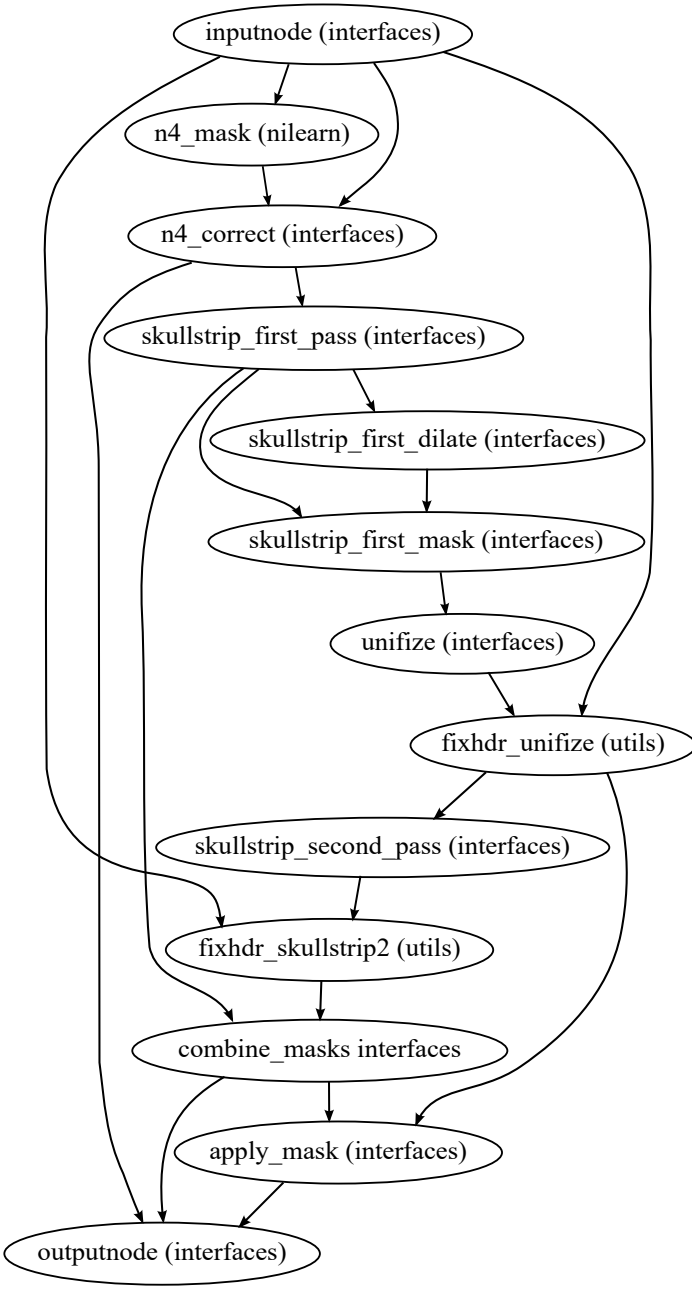

1.0.0
1.0.7
1 dataset
4 datasets
10 datasets
30 datasets
Excellent
Acceptable
Poor
Critical
DS000114 was rated substantially worse as the T1w masks became too liberal with the introduction of a mask refinement that worked correctly for other datasets
DS000108 and DS000148 improved the most after addressing particular issues


fMRIPrep
feat
L
R
z=-15
z=-5
z=10
z=20
z=40
fMRIPrep
feat


A
fMRIPrep
feat
Before smoothing
fraction of images
Estimated smoothness
full width half maximum (mm)
After smoothing
fraction of images
3
4
5
6
7
8
B
fMRIPrep
feat
L
R
z=0
z=15
z=30

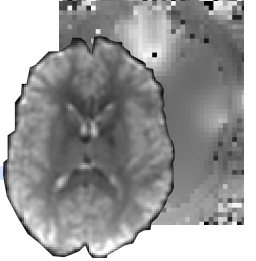

input node (interfaces)
bold_reference_wf
bold_stc_wf
ds_report_validation (bids)
boldbuffer (interfaces)
bold_hmc_wf
bold_split (interfaces)
sdc_wf
bold_bold_trans_wf
bold_reg_wf
bold_mni_trans_wf
bold_surf_wf
fmap_unwarp_report_wf
bold_confounds_wf
boldmask_to_t1w (fixes)
syn_unwarp_report_wf
outputnode (interfaces)
func_derivatives_wf
summary reports
ds_report_summary (bids)


inputnode (interfaces)
validate (images)
gen_ref (registration)
enhance_and_skullstrip_bold_wf
outputnode (interfaces)


inputnode (interfaces)
n4_mask (nilearn)
n4_correct (interfaces)
skullstrip_first_pass (interfaces)
skullstrip_first_dilate (interfaces)
skullstrip_first_mask (interfaces)
unifize (interfaces)
fixhdr_unifize (utils)
skullstrip_second_pass (interfaces)
fixhdr_skullstrip2 (utils)
combine_masks interfaces
apply_mask (interfaces)
outputnode (interfaces)

Original BOLD image

BOLD data acquired with EPI schemes typically present nonlinear distortions along the phase-encoding (PE) axis.



Additional acquisitions

Extra acquisitions are generally included within the imaging protocol to inform the susceptibility distortion correction (SDC) process.

Additional acquisitions with alternative PE directions available?

Yes

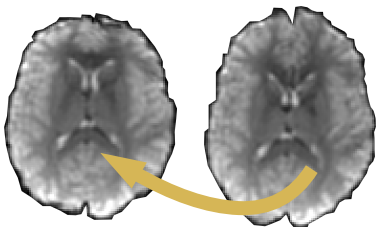
Field-map acquisition available?

Yes

"Fieldmap-less" correction enabled?

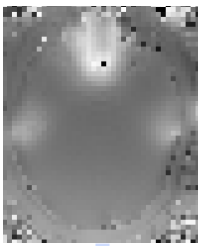
"PE-Polar" SDC

A highly constrained nonlinear registration process is used to map images with opposing realizations of distortion in an intermediate, undistorted reference.



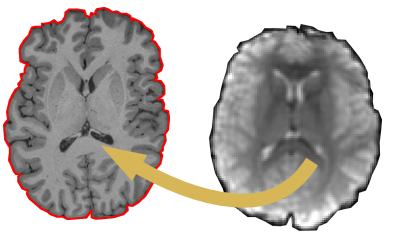
Direct field map estimation

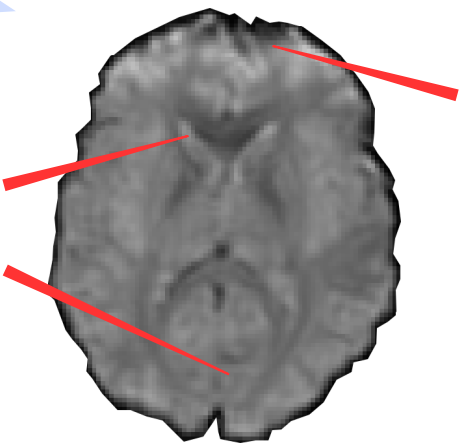
Certain MR schemes allow for the estimation of a field inhomogeneity map, that can then be used to calculate the displacement along the PE each voxel has suffered.



"Fieldmap-less" SDC

The T1w image can be used as "anatomically unwarped" reference. The intensities of the T1w image are inverted to maximize the similarity to the T2 contrast of BOLD images.*





Low-frequency distortion

SDC compensates for the small displacements across the brain caused by the low-frequency component of the map of field inhomogeneity

Drop-out

Regions where higher frequency components of the field map are present are not, generally, recoverable. As a result, signal is lost and a considerable amount of distortion may remain.

```
derivatives/
└ fmriprep/
  ├ sub-E82
  ├ sub-E83/
  │ ├ anat/
  │ │ ├ sub-E83_T1w_brainmask.nii.gz
  │ │ ├ sub-E83_T1w_class-CSF_probtissue.nii.gz
  │ │ ├ sub-E83_T1w_class-GM_probtissue.nii.gz
  │ │ ├ sub-E83_T1w_class-WM_probtissue.nii.gz
  │ │ ├ sub-E83_T1w_dtissue.nii.gz
  │ │ ├ sub-E83_T1w_preproc.nii.gz
  │ │ ...
  │ │ └ sub-E83_T1w_space-MNI152NLin2009cAsym_preproc.nii.gz
  │ └ func/
  │   ├ sub-E83_task-machinegame_run-01_bold_confounds.tsv
  │   ├ sub-E83_task-machinegame_run-01_bold_space-MNI152NLin2009cAsym_brainmask.nii.gz
  │   ├ sub-E83_task-machinegame_run-01_bold_space-MNI152NLin2009cAsym_preproc.nii.gz
  │   ├ sub-E83_task-machinegame_run-02_bold_confounds.tsv
  │   ├ sub-E83_task-machinegame_run-02_bold_space-MNI152NLin2009cAsym_brainmask.nii.gz
  │   └ sub-E83_task-machinegame_run-02_bold_space-MNI152NLin2009cAsym_preproc.nii.gz
  ├ sub-E82.html
  └ sub-E83.html
```

One folder containing derivatives per subject

First derivatives of the T1-weighted image: Include the brain mask, tissue probability maps for CSF, GM and WM, a brain tissue segmentation and the T1w preprocessed (includes merging T1w images from sessions, INU correction, etc).

T1w derivatives in additional target spaces (e.g. MNI152NLin2009cAsym)

BOLD derivatives: for task "Machine Game" and run 01

BOLD derivatives: for task "Machine Game" and run 02

One visual report per subject

SUCCEEDED

Rerun

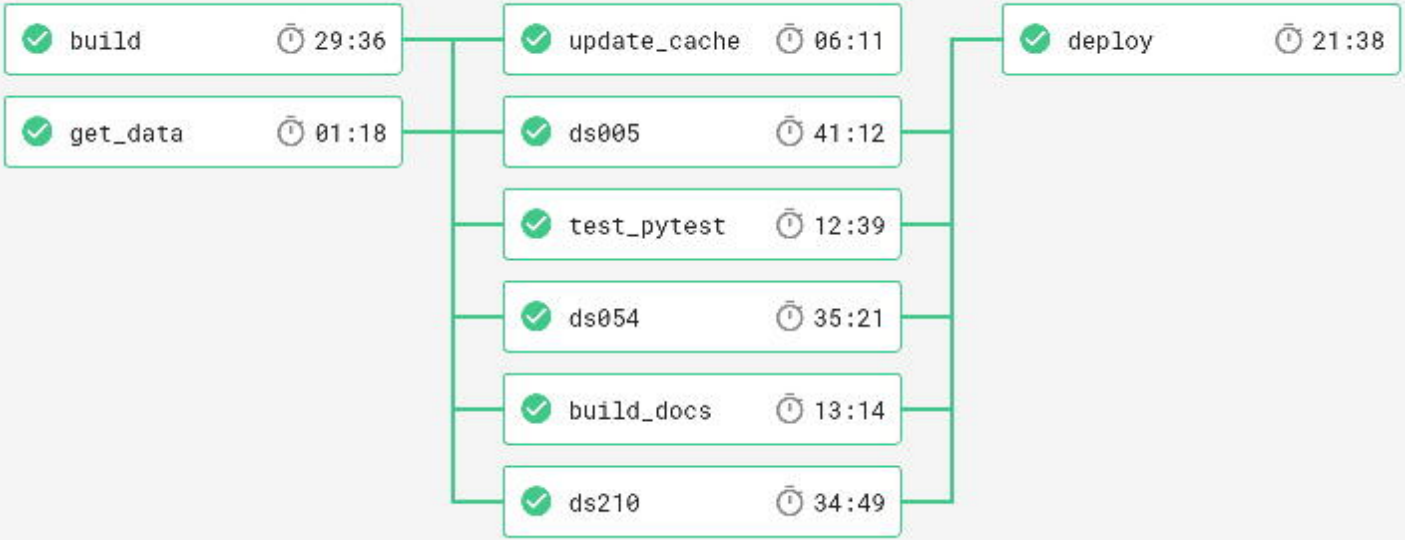
1.0.11 (tag) / build_test_deploy

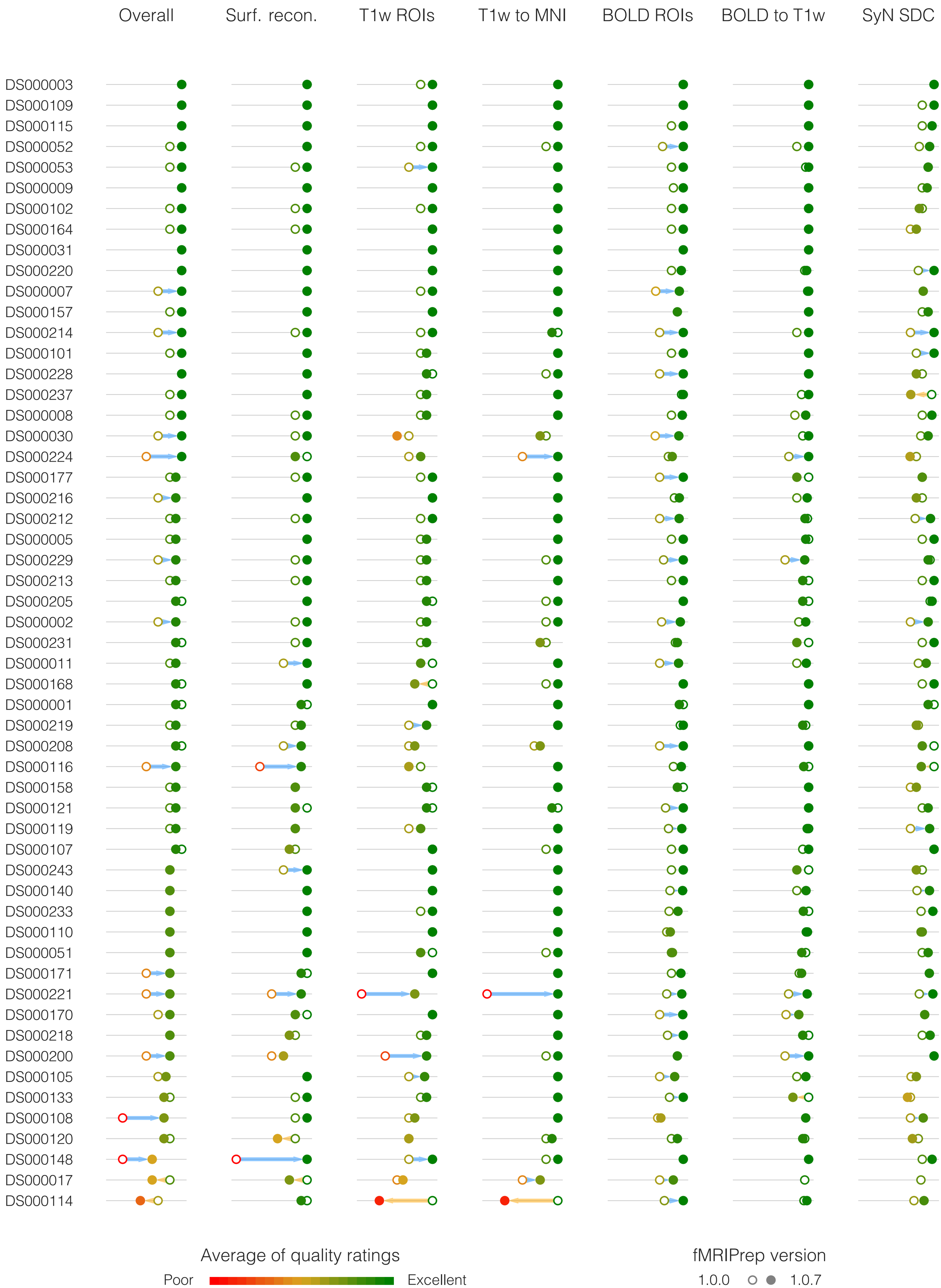
1 day ago

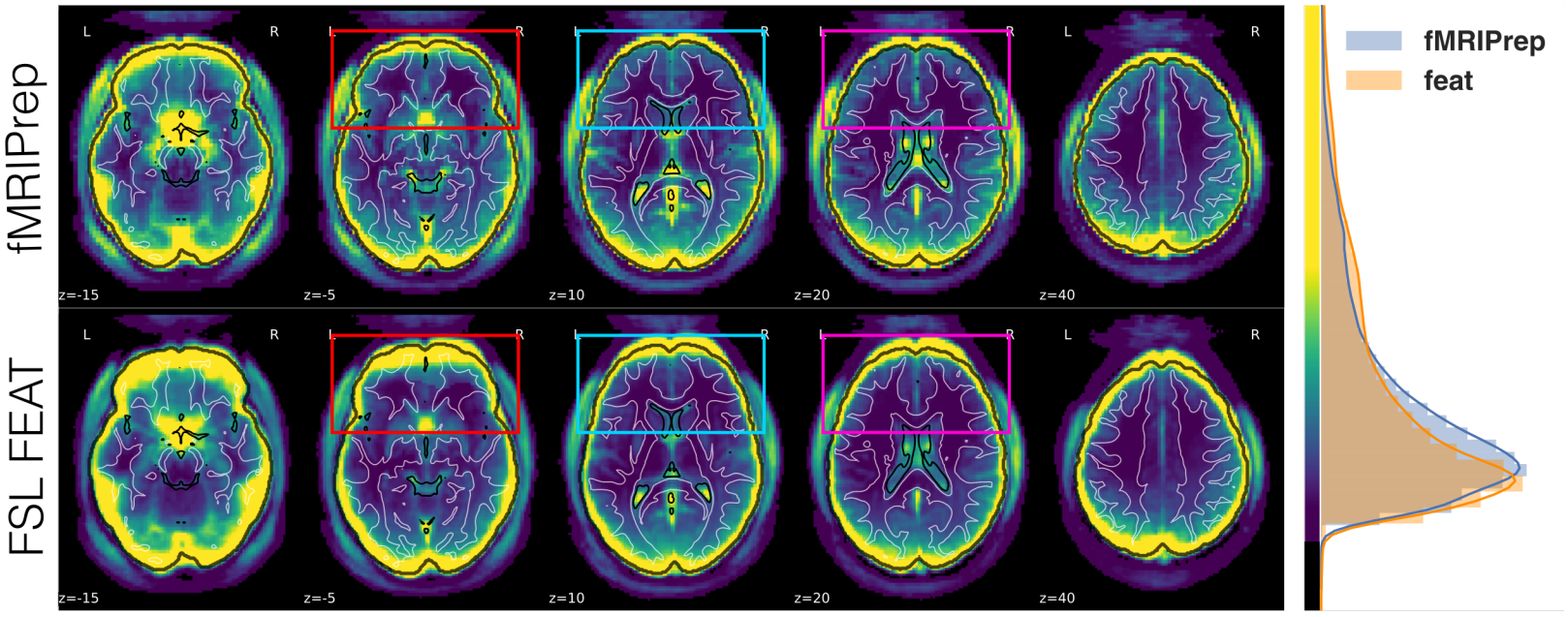
2:12:10

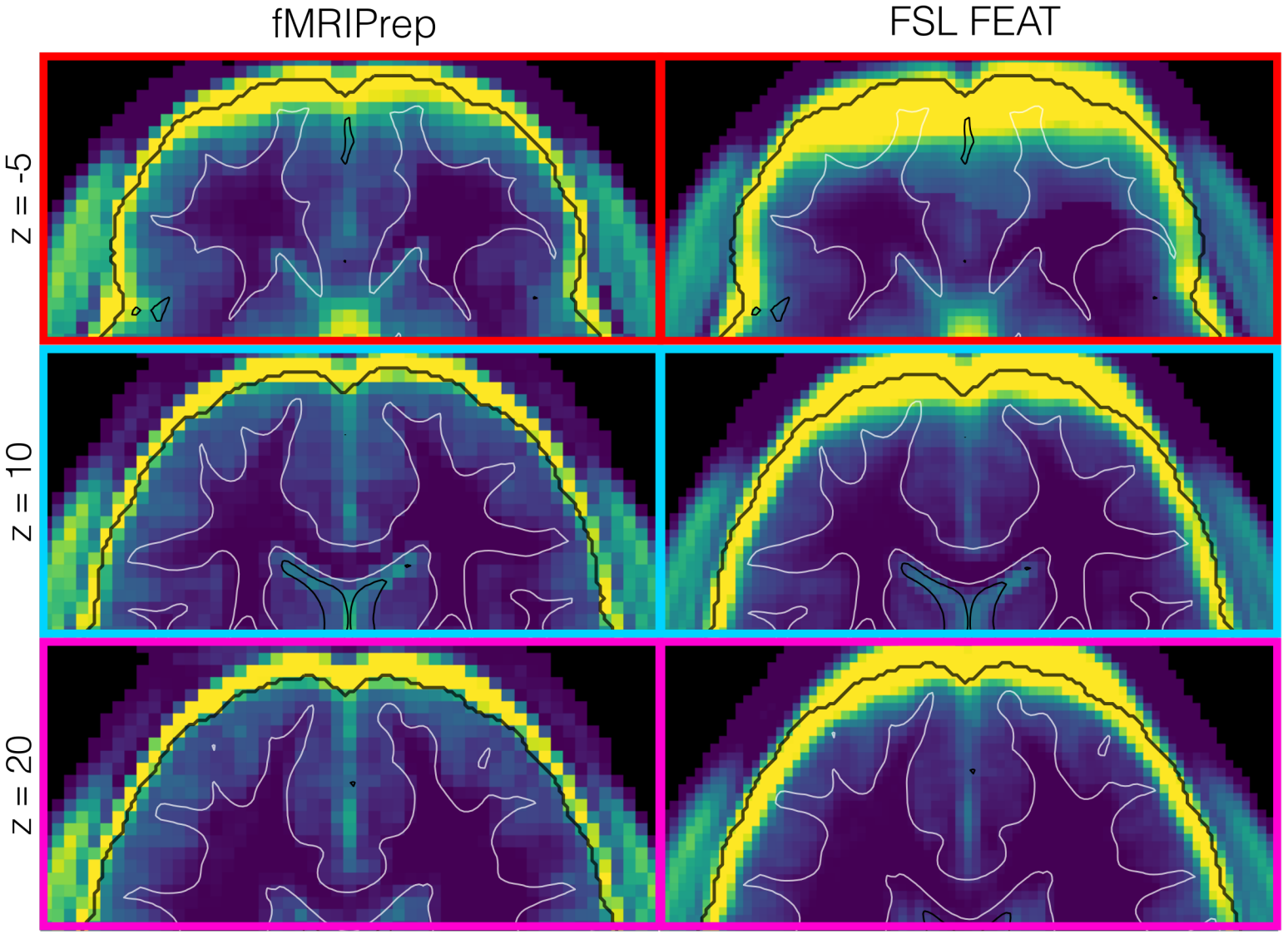
744de95

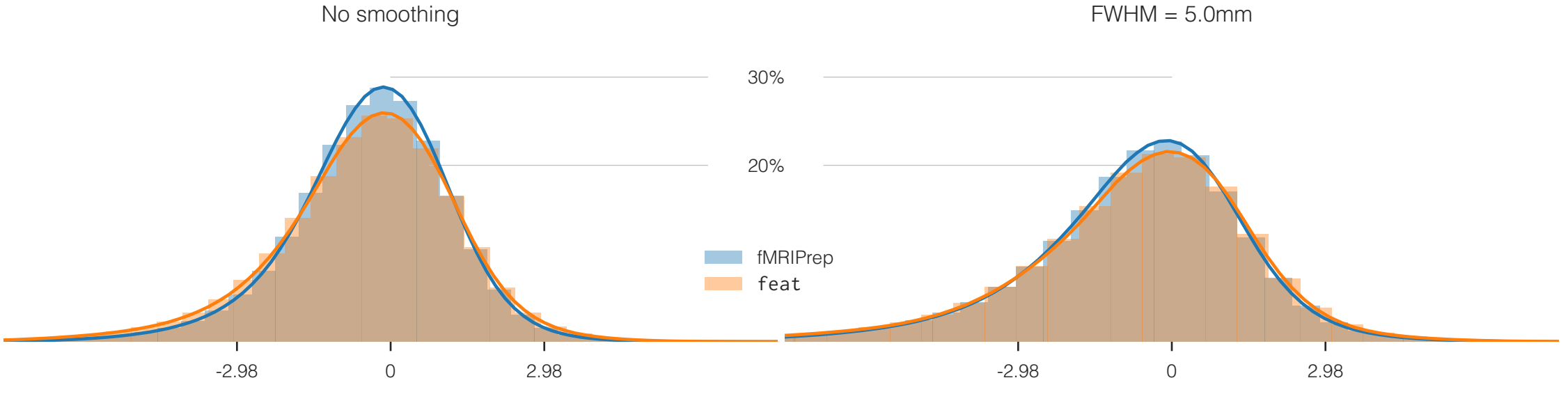
9 jobs in this workflow



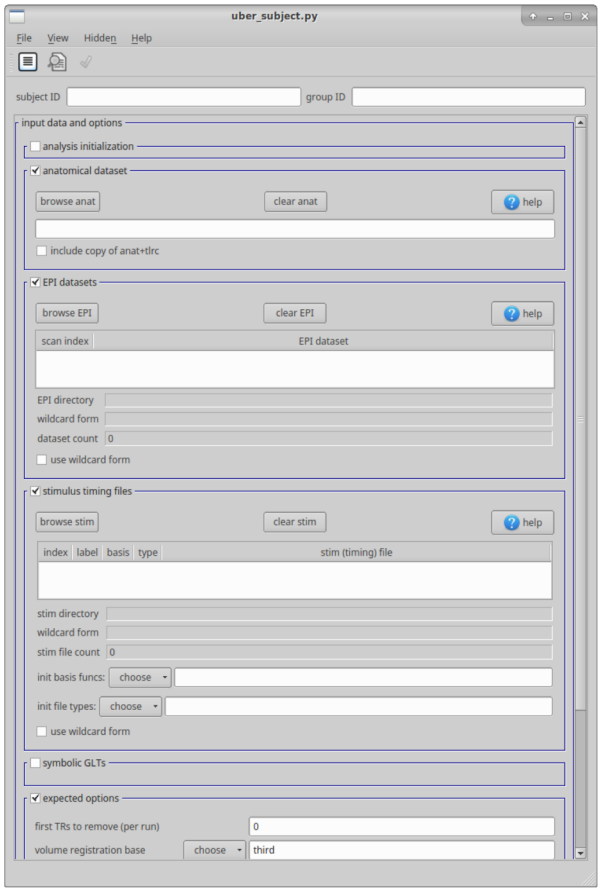

Overall
Surf. recon.
T1w ROIs
T1w to MNI
BOLD ROIs
BOLD to T1w
SyN SDC
DS000003
DS000109
DS000115
DS000052
DS000053
DS000009
DS000102
DS000164
DS000031
DS000220
DS000007
DS000157
DS000214
DS000101
DS000228
DS000237
DS000008
DS000030
DS000224
DS000177
DS000216
DS000212
DS000005
DS000229
DS000213
DS000205
DS000002
DS000231
DS000011
DS000168
DS000001
DS000219
DS000208
DS000116
DS000158
DS000121
DS000119
DS000107
DS000243
DS000140
DS000233
DS000110
DS000051
DS000171
DS000221
DS000170
DS000218
DS000200
DS000105
DS000133
DS000108
DS000120
DS000148
DS000017
DS000114
Average of quality ratings
Poor
Excellent
fMRIPrep version
1.0.0
1.0.7


fMRIPrep
FSL FEAT
L
R
z=-15
z=-5
z=10
z=20
z=40
fMRIPrep
feat

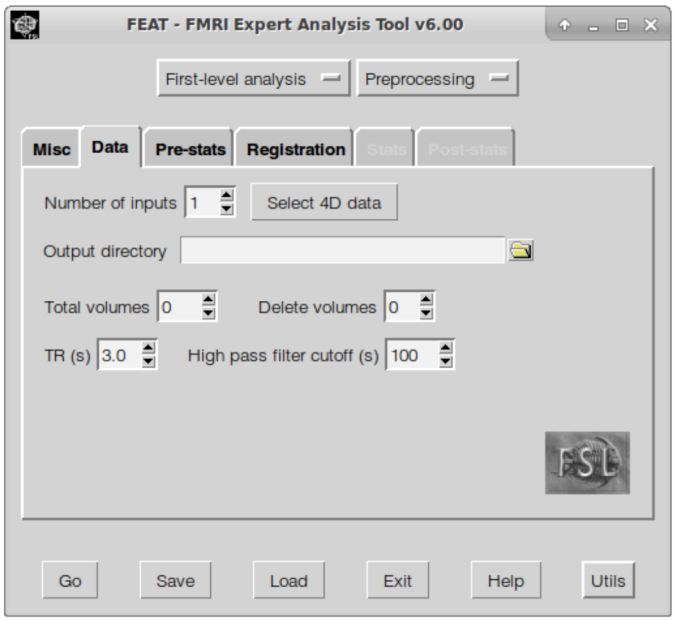

fMRIPrep
FSL FEAT
z = -5
z = 10
z = 20


No smoothing
FWHM = 5.0mm
30%
20%
fMRIPrep
feat
-2.98
0
2.98
-2.98
0
2.98

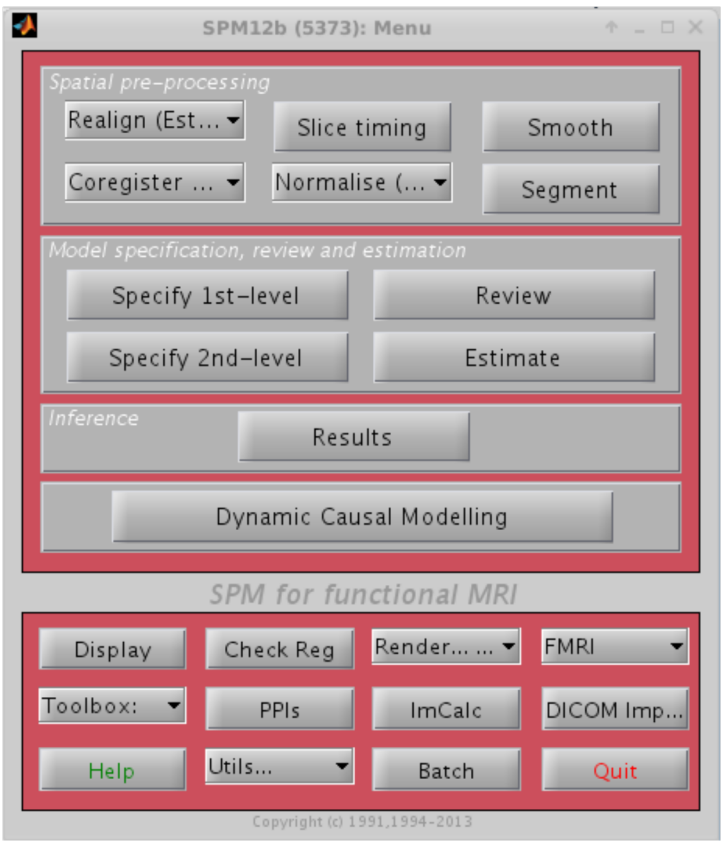
a


uber_subject.py
File View Hidden Help
subject ID
group ID
input data and options
analysis initialization
anatomical dataset
browse anat
clear anat
help
include copy of anat+tlrc
EPI datasets
browse EPI
clear EPI
help
scan index
EPI dataset
EPI directory
wildcard form
dataset count 0
use wildcard form
stimulus timing files
browse stim
clear stim
help
index label basis type
stim (timing) file
stim directory
wildcard form
stim file count 0
init basis funcs: choose
init file types: choose
use wildcard form
symbolic GLTs
expected options
first TRs to remove (per run) 0
volume registration base choose third

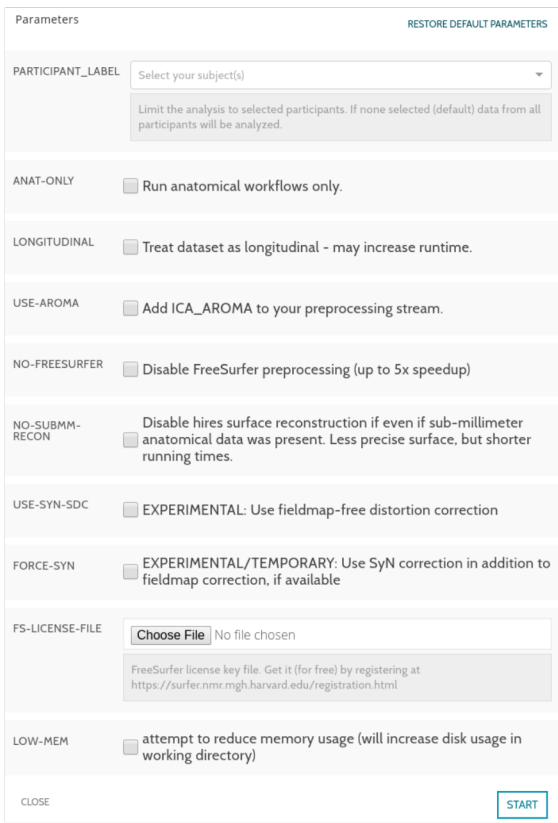
b


FEAT - FMRI Expert Analysis Tool v6.00
First-level analysis
Preprocessing
Misc
Data
Pre-stats
Registration
Stats
Post-stats
Number of inputs 1
Select 4D data
Output directory
Total volumes 0
Delete volumes 0
TR (s) 3.0
High pass filter cutoff (s) 100
FSL
Go
Save
Load
Exit
Help
Utils

c


SPM12b (5373): Menu
Spatial pre-processing
Realign (Est...
Slice timing
Smooth
Coregister ...
Normalise (...
Segment
Model specification, review and estimation
Specify 1st-level
Review
Specify 2nd-level
Estimate
Inference
Results
Dynamic Causal Modelling
SPM for functional MRI
Display
Check Reg
Render... ...
FMRI
Toolbox:
PPIs
ImCalc
DICOM Imp...
Help
Utils...
Batch
Quit
Copyright (c) 1991,1994-2013

d


Parameters
RESTORE DEFAULT PARAMETERS
PARTICIPANT_LABEL
Select your subject(s)
Limit the analysis to selected participants. If none selected (default) data from all participants will be analyzed.
ANAT-ONLY
Run anatomical workflows only.
LONGITUDINAL
Treat dataset as longitudinal - may increase runtime.
USE-AROMA
Add ICA_AROMA to your preprocessing stream.
NO-FREESURFER
Disable FreeSurfer preprocessing (up to 5x speedup)
NO-SUBMM-RECON
Disable hires surface reconstruction if even if sub-millimeter anatomical data was present. Less precise surface, but shorter running times.
USE-SYN-SDC
EXPERIMENTAL: Use fieldmap-free distortion correction
FORCE-SYN
EXPERIMENTAL/TEMPORARY: Use SyN correction in addition to fieldmap correction, if available
FS-LICENSE-FILE
Choose File
No file chosen
FreeSurfer license key file. Get it (for free) by registering at https://surfer.nmr.mgh.harvard.edu/registration.html
LOW-MEM
attempt to reduce memory usage (will increase disk usage in working directory)
CLOSE
START

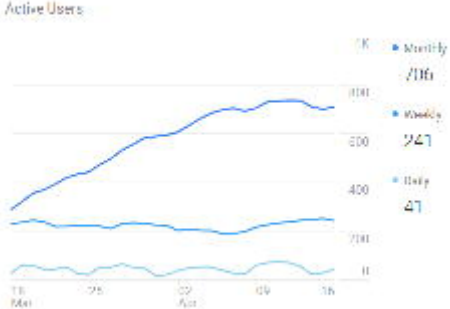
What pages do your users visit?

Page	Pageviews	Page Value
/en/latest/	[illegible]	$0.00
/en/latest/usage.html	753	$0.00
/en/latest/installation.html	[illegible]	$0.00
/en/latest/workflows.html	647	$0.00
/en/latest/outputs.html	245	$0.00
/en/latest/changes.html	206	$0.00
/en/latest/cli.html	185	$0.00
/en/latest/api/index.html	162	$0.00
/en/latest/config.html	139	$0.00
/en/latest/index.html	139	$0.00

Last 30 days

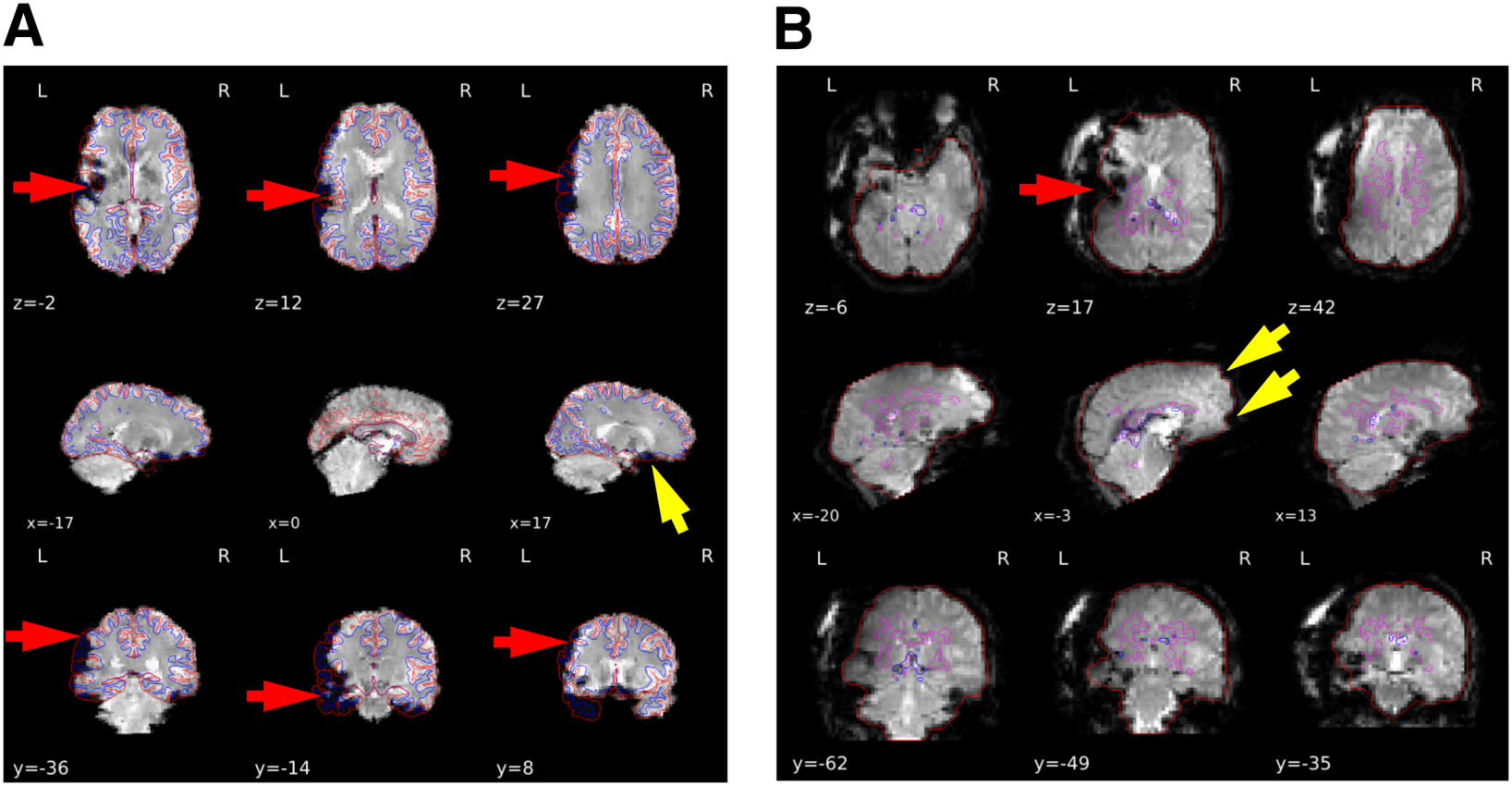
PAGES REPORT >

How are your active users trending over time?



Last 30 days

ACTIVE USERS REPORT >


A
L
R
z=-2
z=12
z=27
x=-17
x=0
x=17
y=-36
y=-14
y=8
B
z=-6
z=17
z=42
x=-20
x=-3
x=13
y=-62
y=-49
y=-35