BIDS: Tools and Services

CHRIS GORGOLEWSKI
@CHRISFILOG
tool_cmd /bids_dataset /output
BIDS Apps

Gorgolewski et al. 2017
Self-contained!
Simple parallelization scheme – map/reduce
## Available BIDS Apps

<table>
<thead>
<tr>
<th>App</th>
<th>Version</th>
<th>Issues</th>
<th>Build Status</th>
<th>Pull Requests</th>
<th>Docker Pulls</th>
<th>Size</th>
<th>Layers</th>
</tr>
</thead>
<tbody>
<tr>
<td>bids/example</td>
<td>0.0.6</td>
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<td>passing</td>
<td>0</td>
<td>202</td>
<td>1.5GB</td>
<td>24</td>
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<td>38 layers</td>
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<td>3.4GB</td>
<td>56 layers</td>
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</table>
MRIQC: group anatomical report

Summary
- Date and time: 2017-02-05, 12:27.
- MRIQC version: 0.9.0-rc2.

The individual reports show the calculated IQMs and metadata in the summary, and a series of image mosaics and plots designed for the visual assessment of images.

MRIQC: individual anatomical report

Summary
- Subject ID: 51296.
- Date and time: 2017-02-05, 03:44.
- MRIQC version: 0.9.0-rc2.

Data points in the scatter plots of the group report can be clicked to open the corresponding individual report. This feature is particularly useful to identify low-quality datasets visually.

mriqc.nimh.nih.gov

- Crowdsourced database of MR QC metrics
- Over QC metrics from over 40,000 unique BOLD scans
- Publicly available
Is tSNR lower for higher multi band factors?
Is tSNR lower for higher multi band factors?
FMRIPREP: Robust preprocessing

Esteban et al. (2018, biorxiv)
<table>
<thead>
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<th>Scn</th>
<th>S</th>
<th>T</th>
<th>R</th>
<th>Mod</th>
<th>Part. IDs</th>
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<td>1 T1w, 3 BOLD</td>
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<td>01, 02, 07, 08</td>
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</tbody>
</table>

Robustness tested on 60 OpenfMRI datasets.
Robustness

high quality results
Distortion correction without fieldmaps
The glass box software design principles

1. Write educational documentation
2. Verify/visualize assumptions
3. Guide dissemination of the results
EPI to T1w registration

> fnriprep.workflows.bold.registration.init_bold_reg_wf

**Functional Reports for Task: rest**

**Summary**
- Slice timing correction: Not applied
- Susceptibility distortion correction: Symmetric normalization (SyN) - not applied
- Registration: FreeSurfer boundary-based registration (bbregister)
- Functional series resampled to spaces: template, fsaverage5
- Confounds collected: Global signals, DVARS, Framewise displacement, Motion parameters

Results of performing SyN-based SDC on the EPI

Animation showing EPI to T1w registration (FreeSurfer bbregister)

Transparency: documentation and reports

With Freesurfer:
- Susceptibility Distortion Correction: none
- With AROMA:
  - Skullstrip template: OASIS
  - With slicetime correction:

Results included in this manuscript come from preprocessing performed using FMRIprep version latest [1], a Nipype [2,3] based tool. Each T1w (T1-weighted) volume was corrected for INU (intensity non-uniformity) using 'NipypeFieldCorrection' v2.1.0 [4] and skull-stripped using 'antsBrainCorrection.sh' v2.1.0 (using the OASIS template). Brain surfaces were reconstructed using 'recon-all' from FreeSurfer v6.0.0 [5], and the brain mask estimated previously was refined with a custom variation of the method to reconcile ANTs-derived and FreeSurfer-derived segmentations of the cortical gray-matter of Mindboggle [20]. Spatial normalization to the ICBM 152 Nonlinear Asymmetrical template version 2009c [6] was performed through nonlinear registration with the 'antsRegistration' tool of ANTs v2.1.0 [7], using brain-extracted versions of both T1w volume and template. Brain tissue segmentation of cerebrospinal fluid (CSF), white matter (WM) and gray-matter (GM) was performed on the brain-extracted T1w using 'fsl' [16] (FSL v5.0.9).

Functional data was slice time corrected using 'mantsify' from AFNI v16.2.07 [10] and motion corrected using 'realign' (FSL v5.0.9 [8]). This was followed by co-registration to the corresponding T1w using boundary-based registration [15] with 9 degrees of freedom, using 'bbregister' (FreeSurfer v6.0.0). Motion correcting transformations, BOLD-to-T1w transformation and T1w-to-template (MNI) warp were concatenated and applied in a single step using 'antsApplyTransforms' (ANTS v2.1.0) using Lanczos interpolation.
This is my attempt at adding ICA_AROMA functionality to fmriprep. Almost 100% certain it doesn't work as is.

I have ICA_AROMA completing it's own transforms since it appears the template space could be something something different than ICA AROMA is expecting, in addition, ICA_AROMA requires a affine fsl matrix and fnirt fsl warp to pass in so ANTs is off the table (afaik).

I may continue editing/working on this, but first I wanted feedback if this is a worthwhile endeavour or if it's better to hi-jack the original code from ICA-AROMA to make it flexibly fit in the fmriprep workflows (as was done with compcor).

Thanks!
James
FMRIPrep: a robust preprocessing pipeline for functional MRI

Oscar Esteban, Christopher J. Markiewicz, Ross W. Blair, Craig A. Moodie, A. Ilkay Isik, Asier Erramuzpe, James D. Kent, Mathias Goncalves, Elizabeth DuPre, Madeleine Snyder, Hiroyuki Oya, Satrajit S. Ghosh, Jesse Wright, Joke Durnez, Russell A. Poldrack, Krzysztof J. Gorgolewski

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Contributed equally to this work

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https://doi.org/10.1101/306951

send us your feedback
FitLins - Fitting Linear Models to BIDS Datasets

FitLins is a tool for estimating linear models, defined by the BIDS Model specification proposal, to BIDS-formatted datasets.

This software is in alpha stage, and should be considered unstable. Users are welcome to test the software, and open issues.

The CLI follows the BIDS-Apps convention:

Usage:

```
fitlins <bids_root> <out_dir> <analysis_level> [--model <model_name>]
```

See the output of `fitlins --help` for all valid options:

```
usage: fitlins [-h] [-v]
               [--participant-label PARTICIPANT_LABEL [PARTICIPANT_LABEL ...]]
               [-m MODEL] [-p PREPROC_DIR] [--space {MNI152NLin2009cAsym}]
               [--debug]
               bids_dir output_dir {run,session,participant,dataset}
```

https://github.com/poldracklab/fitlins
OpenNEURO

a free online platform for sharing and analysis of neuroimaging data
Access to data!
Your dataset is not a valid BIDS dataset. Fix the 1 Error and select your folder again.

By aleph4@gmail.com - 2 days ago

Are the T1 anat images available for this dataset? That is needed for preprocessing with fmriprep.

By neggink@princeton.edu - Dataset Uploader - 22 minutes ago

I am in contact with the researcher and will get T1s as soon as possible.

ds000009_R2.0.1
34/856 files complete

sub-29_task-stopsignal_run-01_bold.nii.gz...
sub-29_dwi.nii.gz...
sub-29_T1w.json
Architecture
Reproducibility

data snapshots + software containers == reproducibility