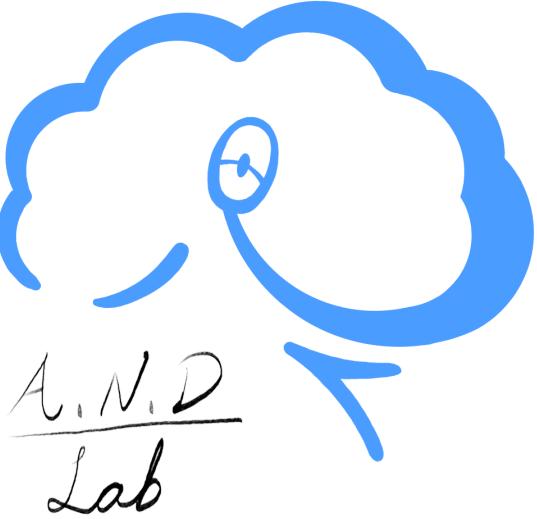




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fMRIPrep Tutorial: A practical guide

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Contents

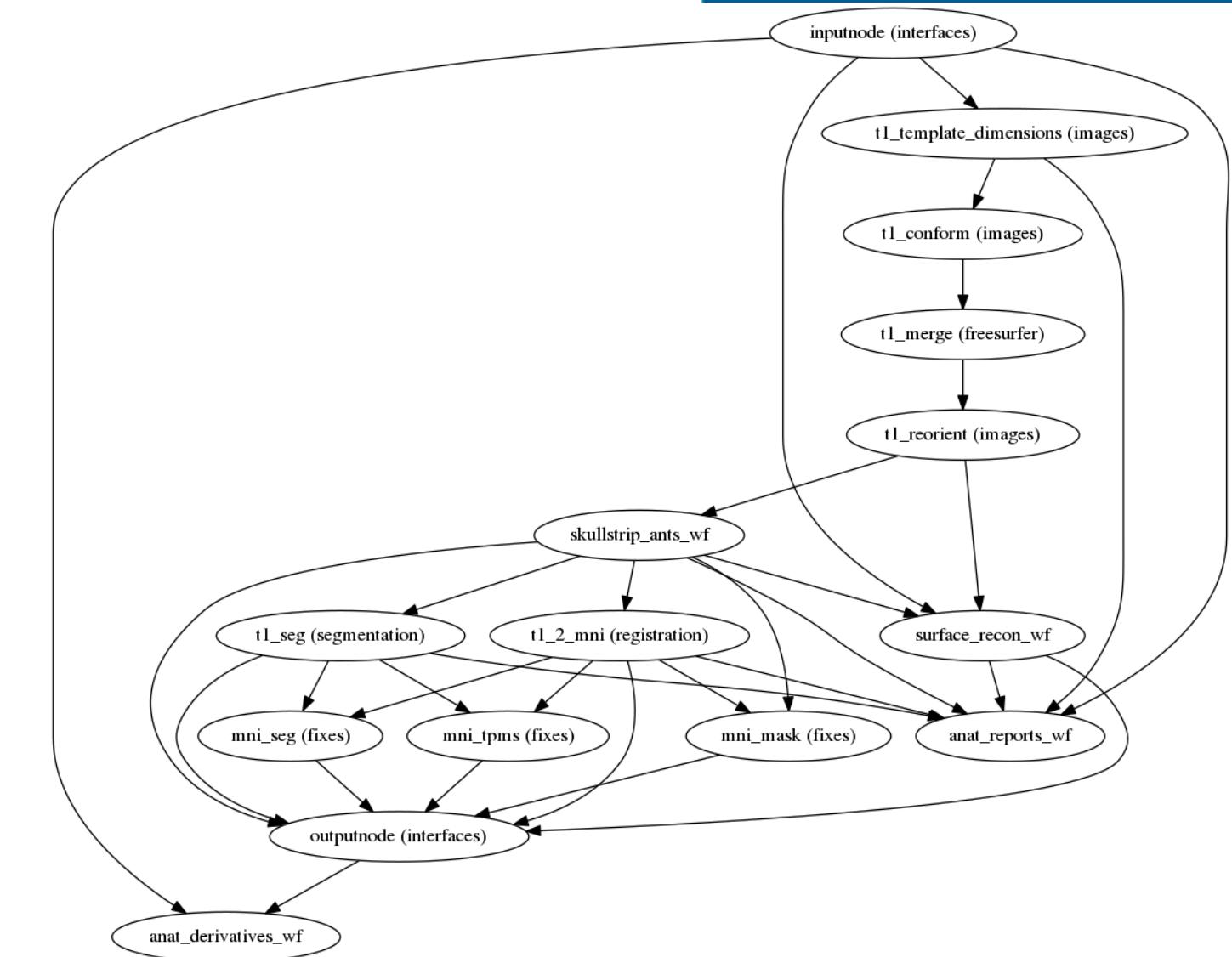
- 1. What is fMRIPrep? Why should I use it?**
- 2. How do I use it?**
- 3. Inputs and outputs of fMRIPrep**
- 4. Code Walk-through**



Introducing fMRIPrep

What is fMRIPrep and why was it created?

- Open-source Nipype-based pipeline promotes use of transparent, reproducible workflows
- Developed by the Poldrack laboratory for the Stanford Center for Reproducible Neuroscience



Why should I use fMRIPrep?

- Increasingly recognized as the standard for fMRI preprocessing
- Used by researchers at peer institutions including Stanford, Harvard and MIT., etc
- Version-controlled: To understand what analyses you have conducted, the audience simply needs to know the fMRIPrep version you ran

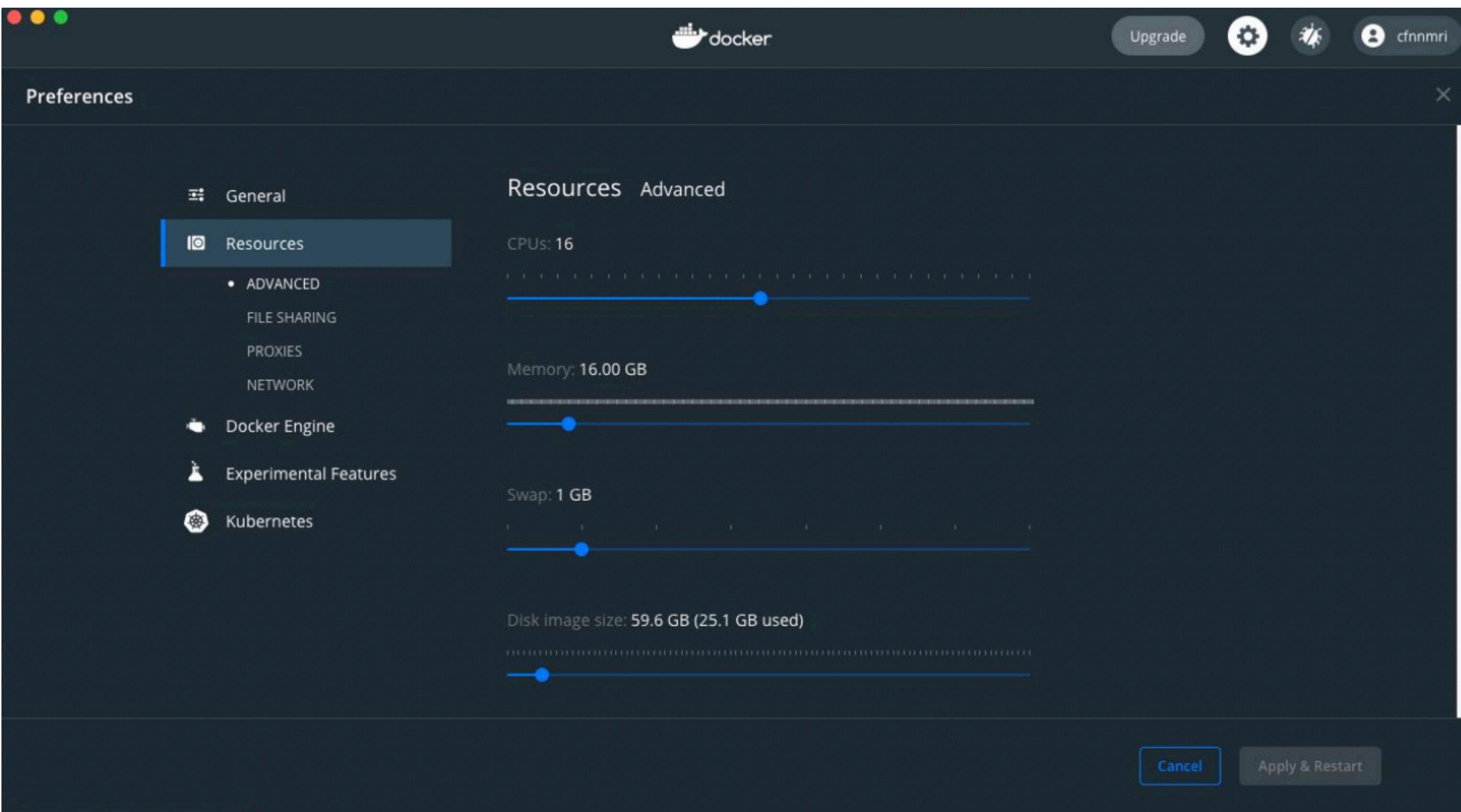
Tips: fMRIPrep doesn't perform Masking and Smoothing



How do I use it?- Run fMRIprep locally with docker

Docker install and set-up

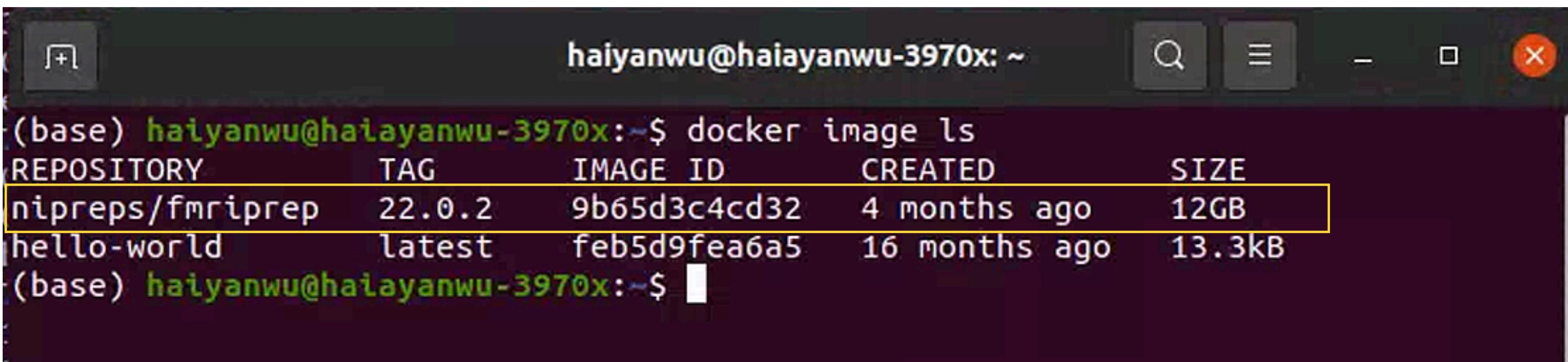
- Install docker on your computer: <https://www.docker.com/get-started/>
- Once docker installs, open the application
- In settings -> Resources: Change Memory to be 16.00 GB



How do I use it?- Run fMRIPrep locally with docker

Add fMRIPrep to docker

- You need to pull the latest fMRIPrep image to your docker application
- In the terminal, type < [docker pull nipreps/fmriprep:xx.x.x](https://www.nipreps.org/apps/docker/) >
- To check the images in docker, type < [docker image ls](https://www.nipreps.org/apps/docker/) >
- To delete the images in docker, type < [docker rm -f IMAGE ID](https://www.nipreps.org/apps/docker/) >
- <https://www.nipreps.org/apps/docker/>
- <https://github.com/nipreps/fmriprep/issues/673>



```
haiyanwu@haiayanwu-3970x: ~
(base) haiyanwu@haiayanwu-3970x:~$ docker image ls
REPOSITORY          TAG      IMAGE ID      CREATED       SIZE
nipreps/fmriprep   22.0.2   9b65d3c4cd32  4 months ago  12GB
hello-world         latest   feb5d9fea6a5  16 months ago  13.3kB
(base) haiyanwu@haiayanwu-3970x:~$
```



How do I use it?- Run fMRIPrep locally with docker

Install fmriprep-docker wrapper

- The fmriprep-docker is a wrapper program that helps to run the docker engine. The script re-directs the command-line inputs into a normal < docker run > command that docker will use to run fMRIPrep
- To install: < [pip install fmriprep-docker](#) > in the terminal
- To upgrade: < [pip install —upgrade fmriprep-docker](#) > in the terminal
- Check the latest version: < [fmriprep-docker --version](#) >
- Command not found: <https://neurostars.org/t/fmriprep-docker-command/4105?page=4>; <https://zhuanlan.zhihu.com/p/267140961>; https://blog.csdn.net/Yal_insist/article/details/124807896

The screenshot shows two terminal windows. The left window displays the configuration of the `.bashrc` file. It includes commands to export the PATH, specify the Docker container path, and source the updated configuration. The right window shows the execution of the `fMRIPrep` command within a Docker container.

```
vim ~/.bashrc
把下面的代码粘贴到最下面

(base) haiyanwu@haiyanwu:~/data:ro -v
export PATH="/home/username/.local/bin:$PATH"
###冒号后面的路径是你fmriprep-docker通过 pip 安装 所在的路径。
退出vim
###使环境生效
source ~/.bashrc

10.11 -it -v /home/haiy
1.1 /data /out particip
l be removed in a futur
```



How do I use it?- Run fMRIPrep locally with docker

Freesurfer License

- fMRIprep runs on Freesurfer version 6.0.0
- Download Freesurfer license: [https://surfer.nmr.mgh.harvard.edu/fswiki/
License](https://surfer.nmr.mgh.harvard.edu/fswiki/License)

fMRIPrep usage

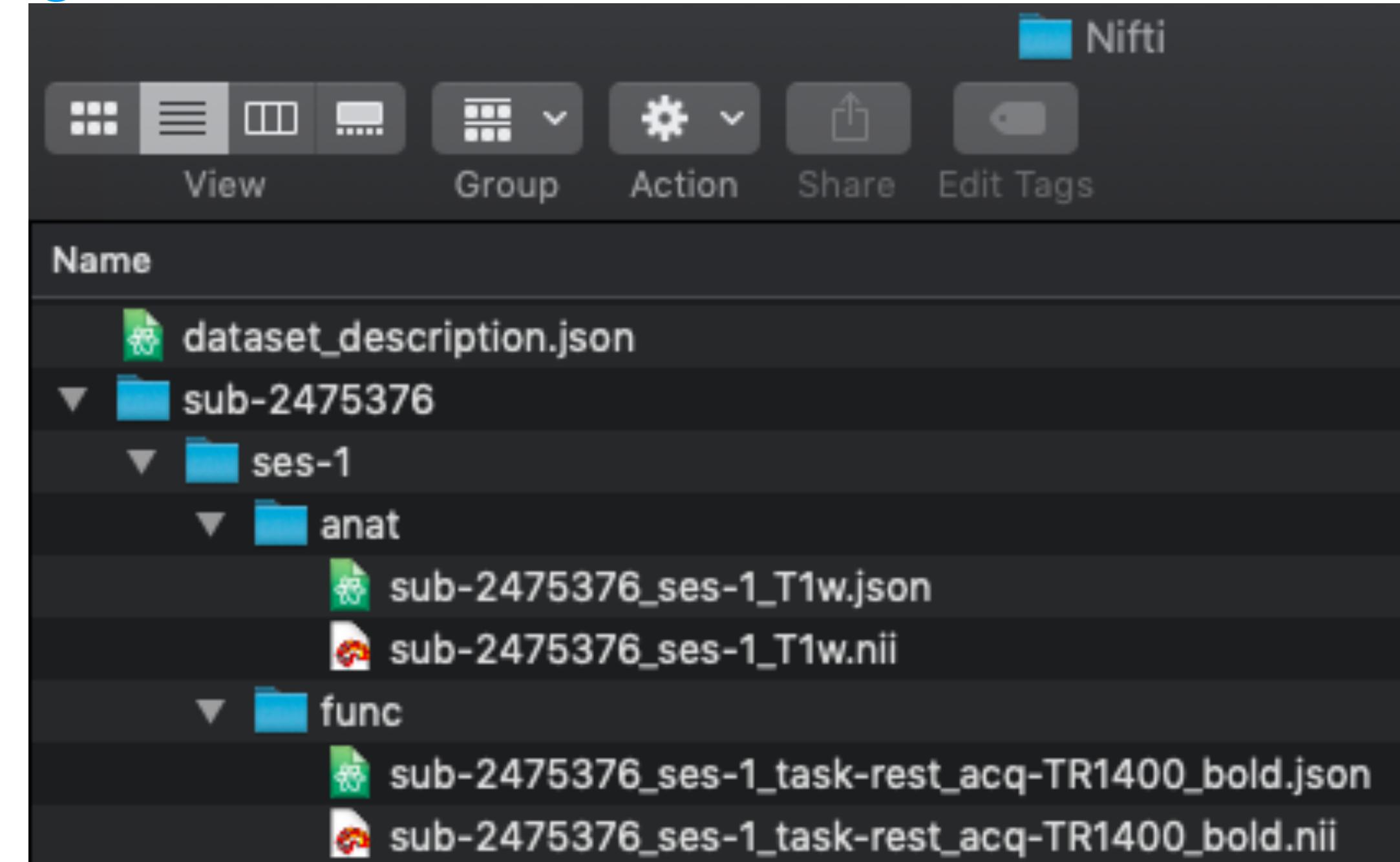
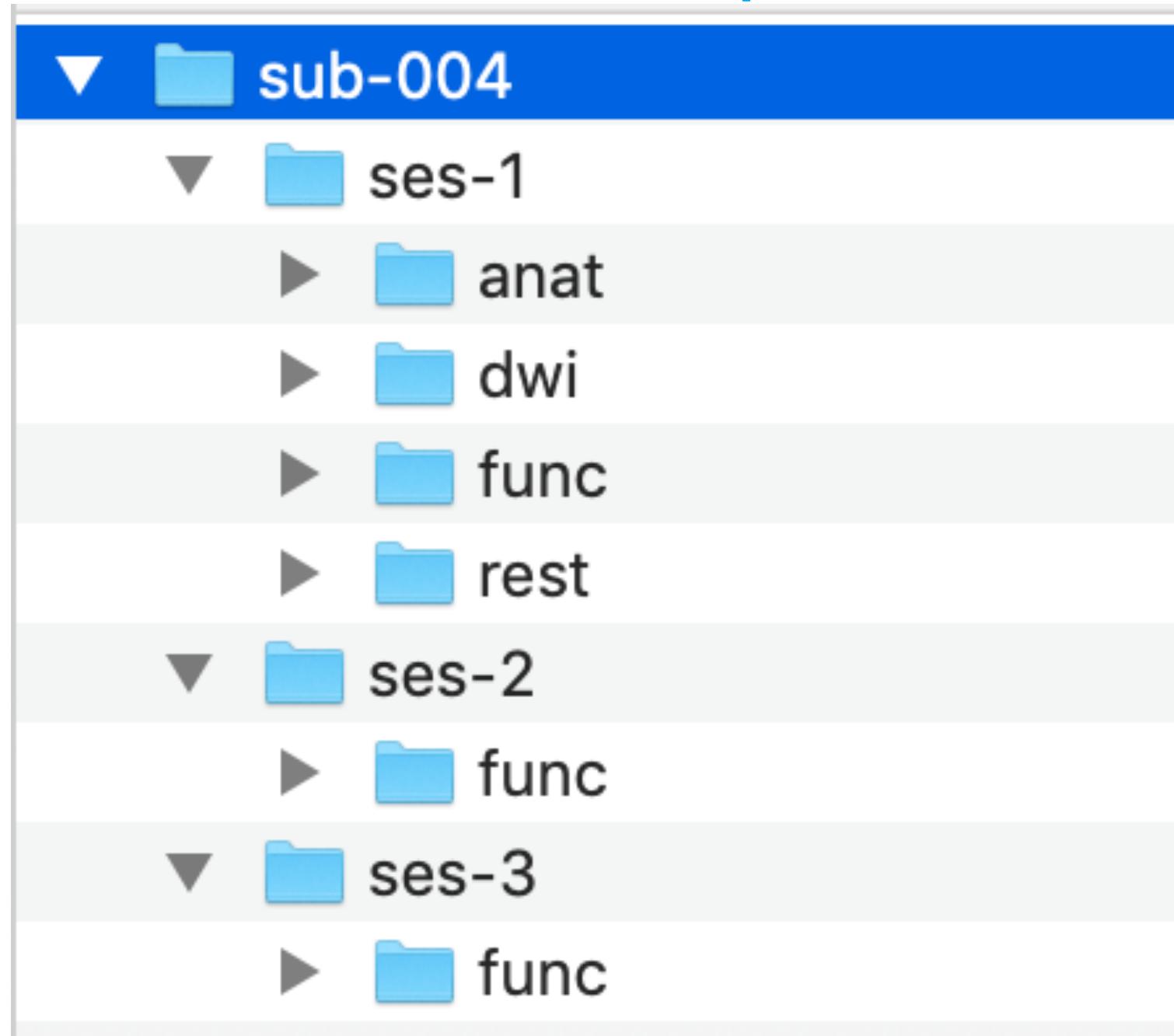
```
usage: sudo /root/.local/bin/fmriprep-docker ${PROJECT_DIR}/bidsdata \
          ${PROJECT_DIR}/outputdata \
          --participant-label $i \
          --fs-license-file ${PROJECT_DIR}/freesurfer.txt \
          --fs-no-reconall `#skip the recon-all process of freesurfer, use this if you
                           only want volume analysis` \
          --stop-on-first-crash
          #--anat-only #if you only want to do the anatomical analysis \
          #--skip_bids_validation #not suggested \
          #--skull-strip-t1w skip #run this line if you have already stripped skull \
```



Inputs of fMRIPrep

BIDS(Brain Imaging Data Structure)

- Data that come off the scanner are converted to NIFTI and JSON files, organized into a specific directory schema, and labeled following a precise naming convention.
- Input dataset must include at least **one T1w structural image** and (unless disabled) **a BOLD series**
- BIDS validator: <https://bids-standard.github.io/bids-validator/>



Inputs of fMRIPrep

How to convert my data to BIDS? An automated solution

step1: Initialize script and create the dataset_description file

```
#!/bin/bash

set -e
###Defining pathways
toplvl=/Users/franklinfeingold/Desktop/NKI_script
dcmdir=/Users/franklinfeingold/Desktop/NKI_script/Dicom
dcm2niidir=/Users/franklinfeingold/Desktop/dcm2niix_3-Jan-2018_mac
#Create nifti directory
mkdir ${toplvl}/Nifti
niidir=${toplvl}/Nifti
```

Then we can generate the dataset_description.json file.

```
###Create dataset_description.json
jo -p "Name"="NKI-Rockland Sample - Multiband Imaging Test-Retest Pilot Dataset" "BIDSVersion"="1.0.2" >>
${niidir}/dataset_description.json
```



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- <https://reproducibility.stanford.edu/bids-tutorial-series-part-1b/>

Inputs of fMRIPrep

How to convert my data to BIDS? An automated solution

step2: Create anatomical folders, convert dicoms and rename

```
####Anatomical Organization#####
##Convert T1w files to BIDS
if [ -d ${dcmdir}/ses-1/anat ];then
    echo "processing anatomical images of $j"
    mkdir -p ${niidir}/sub-${subj}/ses-1/anat
    dcm2niix -z n -b y -o ${niidir}/sub-${subj}/ses-1/anat -f ${subj}_%f_%p ${dcmdir}/ses-1/anat
    cd ${niidir}/sub-${subj}/ses-1/anat
    mv *.json sub-${subj}_ses-1_T1w.json
    mv *.nii sub-${subj}_ses-1_T1w.nii
fi
done
```

`dcm2niix -z y -f %p_%t_%s -o /path/output /path/to/dicom/folder` will save data as gzip compressed, with the filename based on the protocol name (%p) acquisition time (%t) and DICOM series number (%s), with all files saved to the folder "output".

For more help see help: <code>dcm2niix -h</code> https://github.com/rordenlab/dcm2niix



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Inputs of fMRIPrep

How to convert my data to BIDS? An automated solution

step3: Create functional folders, convert dicoms and rename

```
####Functional Organization#####
#Create subject folder
mkdir -n ${niidir}/sub-${subj}/ses-1_ses-2/func
###Convert task-related files to BIDS
for session in {1,2,3,4}; do
if [ -d ${dcmdir}/ses-${session}/func ];then
echo "processing task-related functional images of $subj"
#
mkdir -p ${niidir}/sub-${subj}/ses-${session}/func
dcm2niix -z n -b y -o ${niidir}/sub-${subj}/ses-${session}/func -f ${subj}_%f_%p ${dcmdir}/ses-${session}/func
cd ${niidir}/sub-${subj}/ses-${session}/func
mv *.json sub-${subj}_ses-${session}_task-ua_bold.json
mv *.nii sub-${subj}_ses-${session}_task-ua_bold.nii
fi
$done
done
else
${dcm2niidir}/dcm2niix -o ${niidir}/sub-${subj} -f ${subj}_${direcs}_%p ${dcmdir}/${subj}/${direcs}
fi
done
```



Inputs of fMRIPrep

How to convert my data to BIDS? An automated solution

step4: Self-validation

- Check all func jsons for required fields: 'RepetitionTime', 'VolumeTiming' or 'SliceTiming', and 'TaskName'

```
#Does TaskName exist?  
taskexist=$(cat ${funcjson} | jq '.TaskName')  
if [ "$taskexist" == "null" ]; then  
jsonname="${funcjson%.*}"  
taskfield=$(echo $jsonname | cut -d '_' -f2 | cut -d '-' -f2)  
jq '. |= . + {"TaskName":'"${taskfield}"'}' ${funcjson} > tasknameadd.json  
rm ${funcjson}  
mv tasknameadd.json ${funcjson}  
echo "TaskName was added to ${jsonname} and matches the tasklabel in the filename"  
else  
Taskquotevalue=$(jq '.TaskName' ${funcjson})  
Taskvalue=$(echo $Taskquotevalue | cut -d '"' -f2)  
jsonname="${funcjson%.*}"  
taskfield=$(echo $jsonname | cut -d '_' -f2 | cut -d '-' -f2)  
if [ $Taskvalue == $taskfield ]; then  
echo "TaskName is present and matches the tasklabel in the filename"  
else  
echo "TaskName and tasklabel do not match"
```

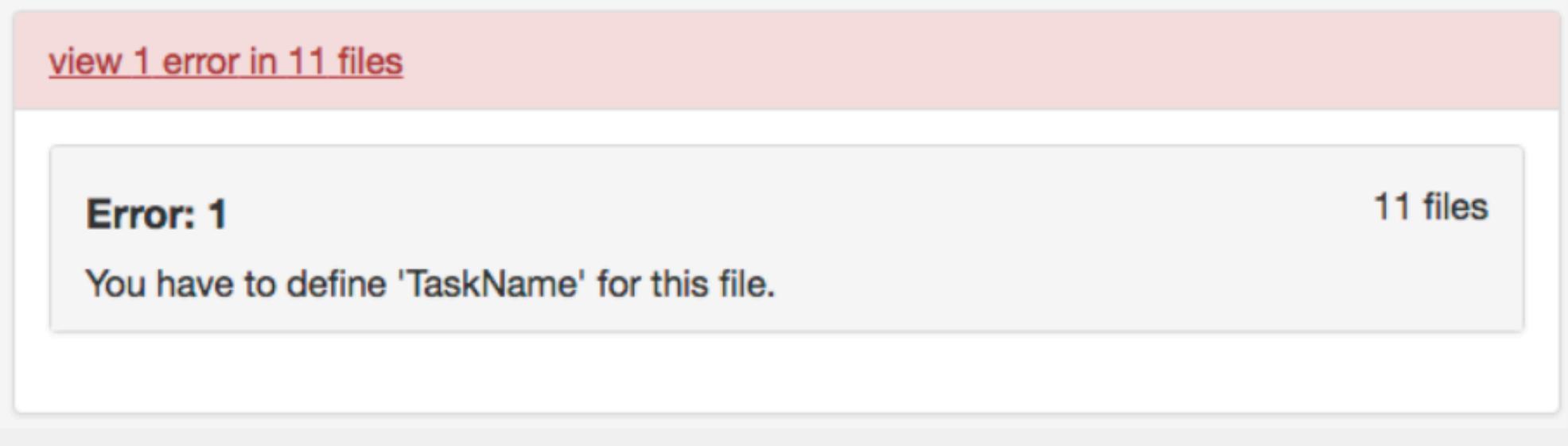


Inputs of fMRIPrep

How to convert my data to BIDS? BIDS validator

step5: BIDS validator

Step 11. At this point, one may try validating. However, one will receive the same error message from part A regarding defining TaskName in the task json files. The slice timing for multiband imaging was corrected in the version of dcm2niix implemented in the script.



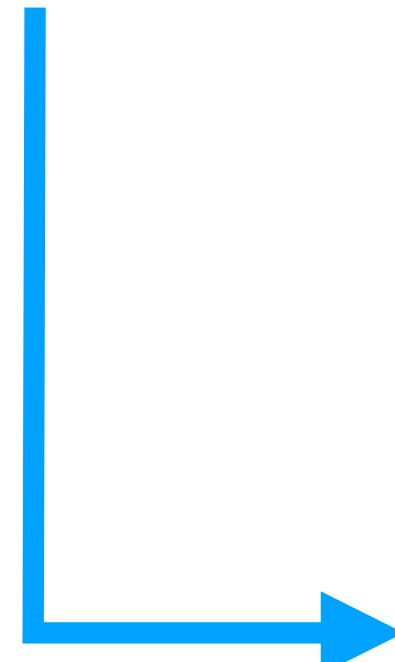
- BIDS validator: <https://bids-standard.github.io/bids-validator/>



Outputs of fMRIPrep

fMRIPrep derivatives

	dataset_description.json	494 bytes	19 Nov 2022
	sub-101.html	112.2 kB	18 Nov 2022
	sub-101	6 items	18 Nov 2022
		figures	33 items 18 Nov 2022
		log	1 item 18 Nov 2022
		ses-1	2 items 18 Nov 2022
		ses-2	1 item 18 Nov 2022
		ses-3	1 item 18 Nov 2022



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Outputs of fMRIPrep

Anatomical

```
(base) haiyanwu@haiayanwu-3970x:/media/haiyanwu/HDD4/fmriprep-workshop/fmriprep/sub-101/ses-1/anat$ ls
sub-101_ses-1_desc-brain_mask.json
sub-101_ses-1_desc-brain_mask.nii.gz
sub-101_ses-1_desc-preproc_T1w.json
sub-101_ses-1_desc-preproc_T1w.nii.gz
sub-101_ses-1_dseg.nii.gz
sub-101_ses-1_from-MNI152NLin2009cAsym_to-T1w_mode-image_xfm.h5
sub-101_ses-1_from-T1w_to-MNI152NLin2009cAsym_mode-image_xfm.h5
sub-101_ses-1_label-CSF_probseg.nii.gz
sub-101_ses-1_label-GM_probseg.nii.gz
sub-101_ses-1_label-WM_probseg.nii.gz
sub-101_ses-1_space-MNI152NLin2009cAsym_desc-brain_mask.json
sub-101_ses-1_space-MNI152NLin2009cAsym_desc-brain_mask.nii.gz
sub-101_ses-1_space-MNI152NLin2009cAsym_desc-preproc_T1w.json
sub-101_ses-1_space-MNI152NLin2009cAsym_desc-preproc_T1w.nii.gz
sub-101_ses-1_space-MNI152NLin2009cAsym_dseg.nii.gz
sub-101_ses-1_space-MNI152NLin2009cAsym_label-CSF_probseg.nii.gz
sub-101_ses-1_space-MNI152NLin2009cAsym_label-GM_probseg.nii.gz
```

Subject space preprocessed images

Transformation matrices (fields) from/to standard spaces

Subject space segmentation (grey, white, CSF)

Preprocessed images registered to MNI152NLin6Asym space
(Mask, T1w are used GLM & FC analysis)



Outputs of fMRIprep

Functional

```
(base) haiyanwu@haiyanwu-3970x:/media/haiyanwu/HDD4/fmriprep-workshop/fmriprep/sub-101/ses-1/func$ ls
sub-101_ses-1_task-ua_desc-confounds_timeseries.json      Confounds for latter regression
sub-101_ses-1_task-ua_desc-confounds_timeseries.tsv
sub-101_ses-1_task-ua_from-scanner_to-T1w_mode-image_xfm.txt Transformation matrix
sub-101_ses-1_task-ua_from-T1w_to-scanner_mode-image_xfm.txt
sub-101_ses-1_task-ua_space-MNI152NLin2009cAsym_boldref.nii.gz BOLD registered to
sub-101_ses-1_task-ua_space-MNI152NLin2009cAsym_desc-brain_mask.json MNI152NLin6Asym space
sub-101_ses-1_task-ua_space-MNI152NLin2009cAsym_desc-brain_mask.nii.gz (xxx_bold.nii.gz for latter analysis)
sub-101_ses-1_task-ua_space-MNI152NLin2009cAsym_desc-preproc_bold.json
```

```
regnames = {'trans_x','trans_y','trans_z','rot_x','rot_y','rot_z', 'global_signal',  
'framewise_displacement', 'a_comp_cor_00','a_comp_cor_01','a_comp_cor_02',  
'a_comp_cor_03','a_comp_cor_04','a_comp_cor_05',...  
'cosine00','cosine01','cosine02','cosine03'}; %18 regressors
```

Reference: <https://fmriprep.org/en/stable/outputs.html>



Outputs of fMRIprep

Summary

Summary Anatomical Functional ▾ About Methods Errors

Summary

- Subject ID: 101
- Structural images: 1 T1-weighted
- Functional series: 4
 - Task: ua (4 runs)
- Standard output spaces: MNI152NLin2009cAsym
- Non-standard output spaces:
- FreeSurfer reconstruction: Not run

Anatomical

Anatomical Conformation

- Input T1w images: 1
 - Output orientation: RAS
 - Output dimensions: 176x256x256
 - Output voxel size: 1mm x 1mm x 1mm
 - Discarded images: 0

Summary Anatomical **Functional** ▾ About Methods Errors

Reports for: session 1, task ua.

▼ Summary

- Original orientation: LAS
 - Repetition time (TR): 1s
 - Phase-encoding (PE) direction: Anterior-Posterior
 - Single-echo EPI sequence.
 - Slice timing correction: Applied
 - Susceptibility distortion correction: None
 - Registration: FSL `flirt` with boundary-based registration (BBR) metric - 6 dof
 - Non-steady-state volumes: 0

▼ Confounds collected

global_signal, global_signal_derivative1, global_signal_derivative1_power2, global_signal_power2, csf_wm, tcompcor, std_dvars, dvars, framewise_displacement, rmsd, t_comp_cor_00, t_comp_cor_0

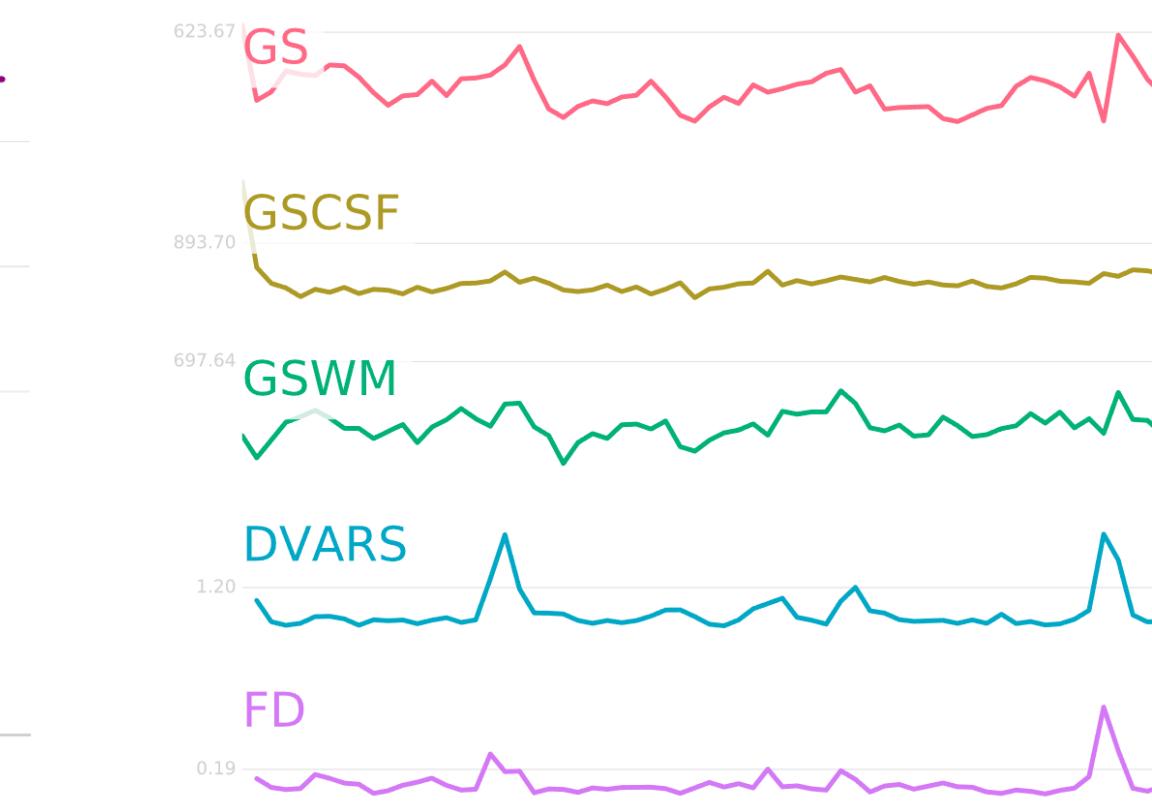
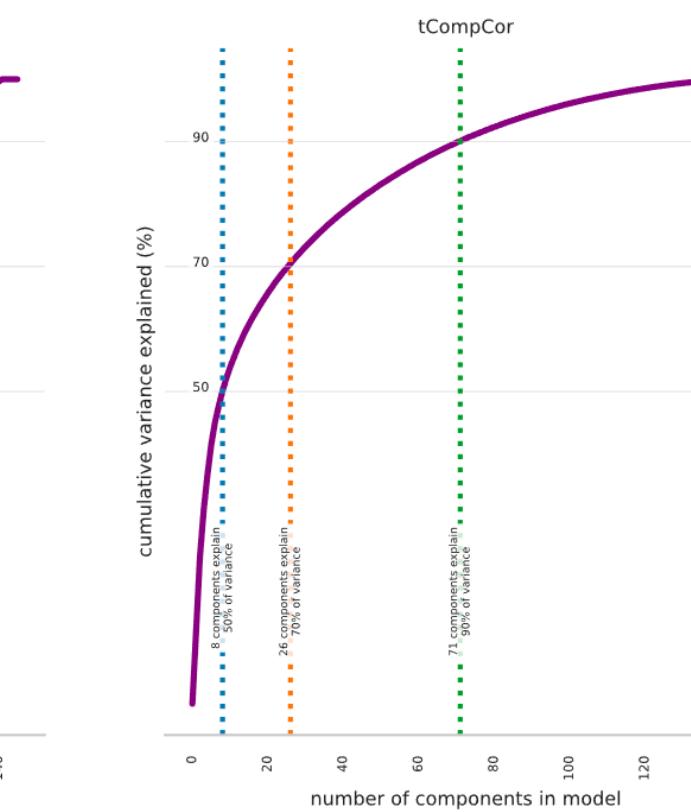
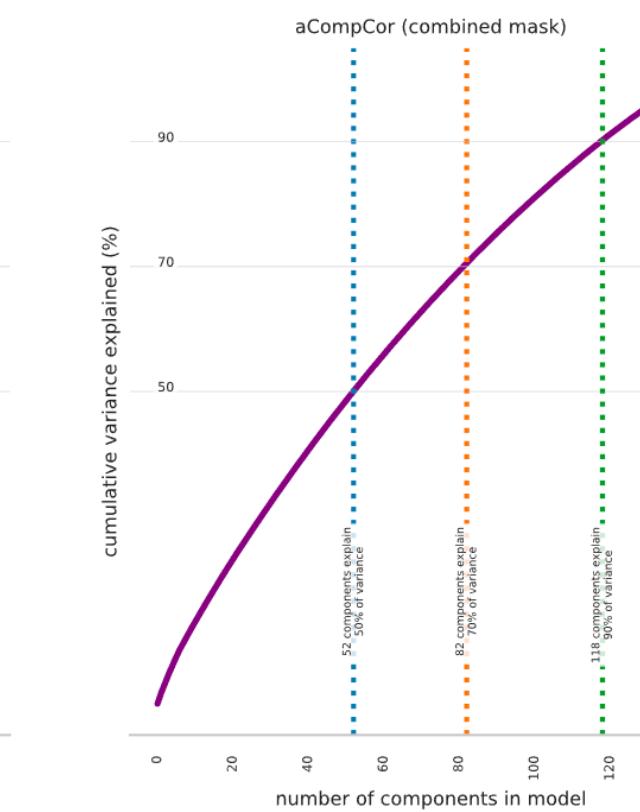
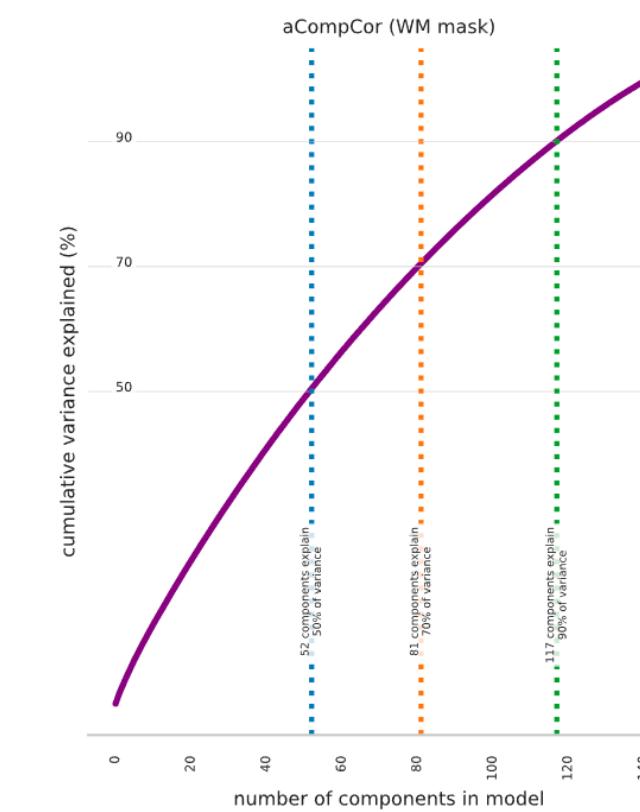
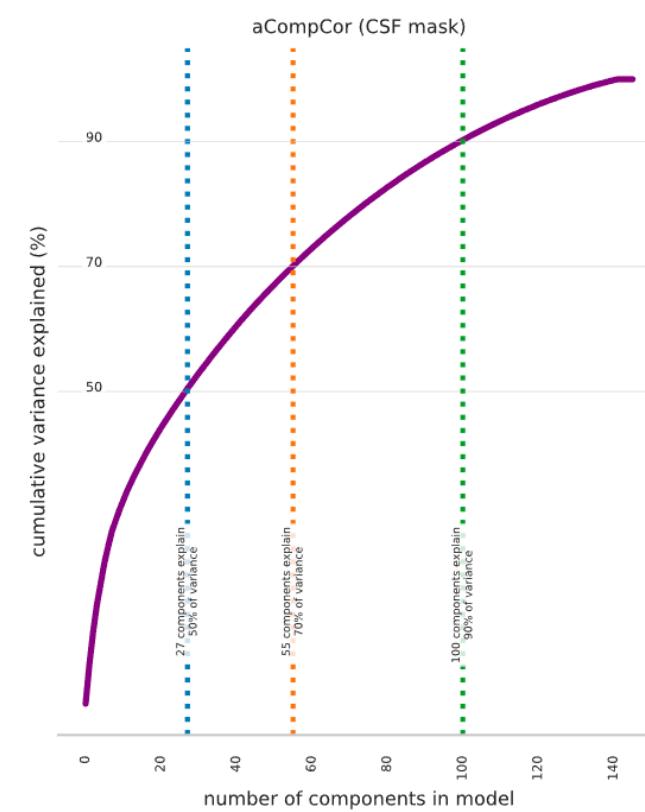
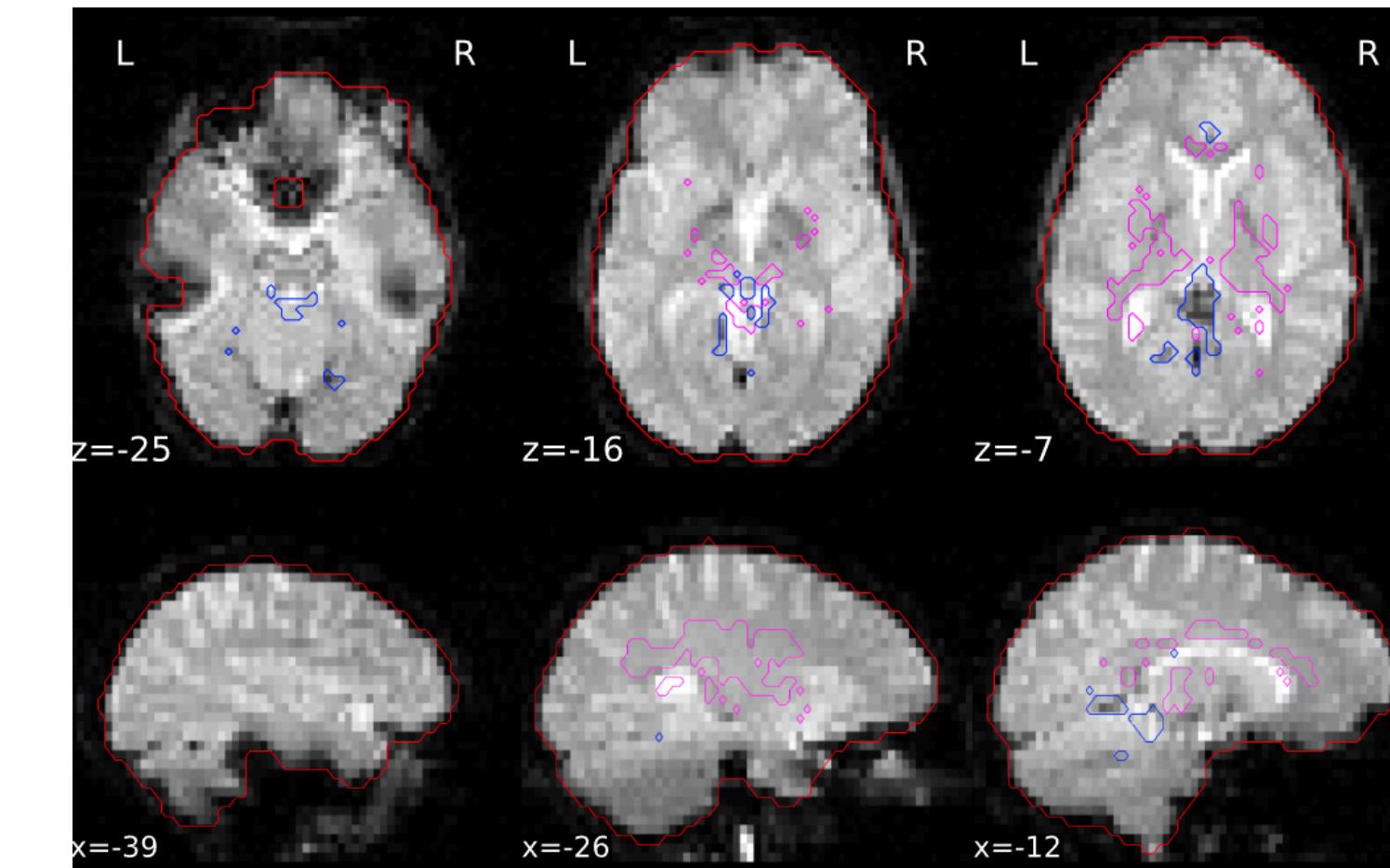
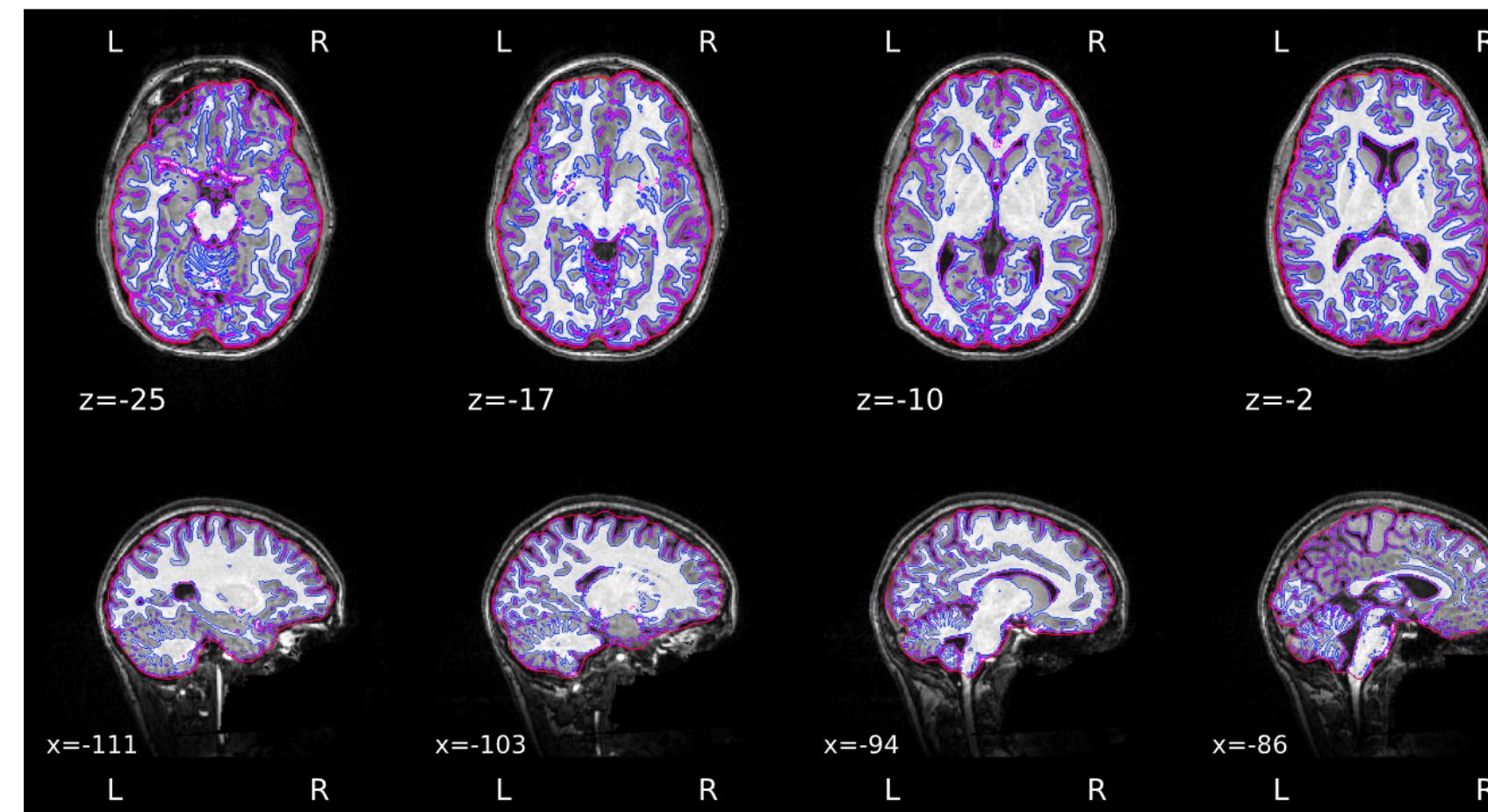


Outputs of fMRIPrep

The HTML report: Quality Assessment (QA) check

Brain mask and brain tissue segmentation of the T1w

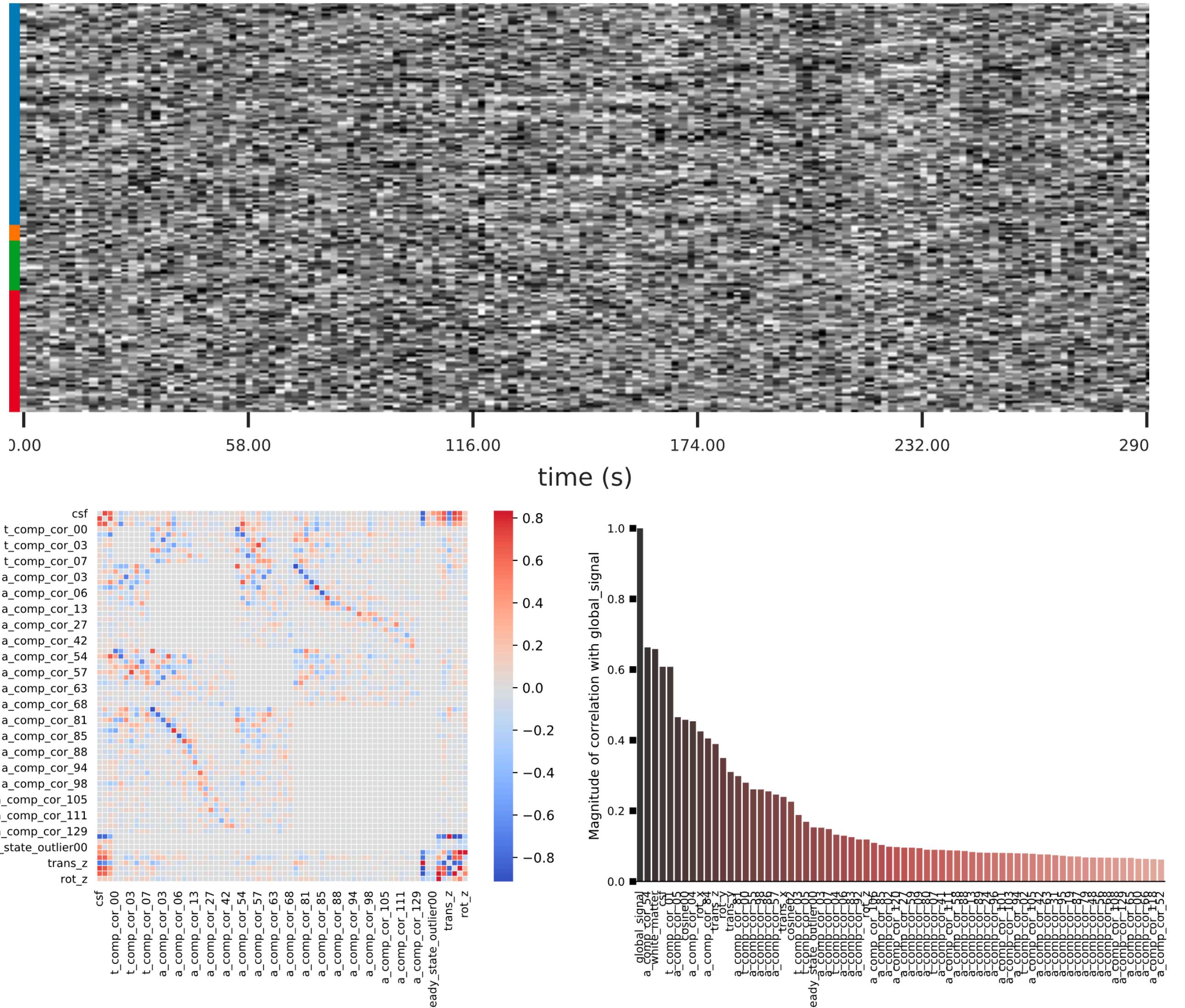
This panel shows the template T1-weighted image (if several T1w images were found), with contours delineating the detected brain mask and brain tissue segmentations.



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Outputs of fMRIPrep

The HTML report: Quality Assessment (QA) check



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Outputs of fMRIPrep

The HTML report: Methods + Citations

Methods

We kindly ask to report results preprocessed with this tool using the following boilerplate.

Bibliography

```
@article{fmriprep1,
  author = {Esteban, Oscar and Markiewicz, Christopher and Blair, Ross W and Moodie, Craig and Isik, Ayse Ilkay and Erramuzpe Aliaga, Asier and Kent, James and Goncalves, Mathias and DuPre, Elizabeth and Snyder, Matthew},
  title = {{fMRIPrep}: a robust preprocessing pipeline for functional {MRI}},
  year = {2018},
  doi = {10.1038/s41592-018-0235-4},
  journal = {Nature Methods}
}

@article{fmriprep2,
  author = {Esteban, Oscar and Blair, Ross and Markiewicz, Christopher J. and Berleant, Shoshana L. and Moodie, Craig and Ma, Feilong and Isik, Ayse Ilkay and Erramuzpe, Asier and Kent, James D. and Goncalves, Mathias and DuPre, Elizabeth and Snyder, Matthew},
  title = {fMRIPrep },
  year = 2018,
  doi = {10.5281/zenodo.852659},
  publisher = {Zenodo},
  journal = {Software}
}

@article{nipyper1,
  author = {Gorgolewski, K. and Burns, C. D. and Madison, C. and Clark, D. and Halchenko, Y. O. and Waskom, M. L. and Ghosh, S.},
  doi = {10.3389/fninf.2011.00013},
  journal = {Frontiers in Neuroinformatics},
  pages = 13,
  shorttitle = {Nipype},
  title = {Nipype: a flexible, lightweight and extensible neuroimaging data processing framework in Python},
  volume = 5,
  year = 2011
}

@article{nipyper2,
  author = {Gorgolewski, K. and Burns, C. D. and Madison, C. and Clark, D. and Halchenko, Y. O. and Waskom, M. L. and Ghosh, S.},
  title = {Nipype: a flexible, lightweight and extensible neuroimaging data processing framework in Python},
  volume = 5,
  year = 2011
}

registration with \texttt{antsRegistration} (ANTs 2.3.3), using
brain-extracted versions of both T1w reference and the T1w template. The
following template was selected for spatial normalization: \emph{ICBM
152 Nonlinear Asymmetrical template version 2009c}
{{}\citet{mni152nlin2009casym}, RRID:SCR\_008796; TemplateFlow ID:
```



Smoothing & Masking

Smoothing

```
# Define input and output files
=$subDir/ses-$run/func/sub-${sub}_ses-${run}_task-ua${run}_space-MNI152NLin2009cAsym_desc-preproc_bold.nii.gz
=$subDir/ses-$run/func/sub-${sub}_ses-${run}_preproc_smoothed6.nii.gz

# Run smoothing
fslmaths $inputFile -kernel gauss $sigma -fmean $outputFile
```



FWHM = $\sigma \sqrt{8 \ln(2)}$ = $\sigma \cdot 2.3548$
(Two or three times the size of your voxel)

Masking

```
# Define input, mask, and output files
=$subDir/ses-$run/func/sub-${sub}_ses-${run}_preproc_smoothed6.nii.gz
=$subDir/ses-$run/func/sub-${sub}_ses-${run}_task-ua${run}_space-MNI152NLin2009cAsym_desc-brain_mask.nii.gz
=$subDir/ses-$run/func/sub-${sub}_ses-${run}_preproc_smoothed6_masked.nii.gz

# Run masking
fslmaths $inputFile -mul $maskPath $outputFile
```



Resources

Websites

- fMRIPrep homepage: <https://fmriprep.org/en/stable/>
- fMRIPrep github: <https://github.com/nipreps/fmriprep>
- NeuroStars: <https://neurostars.org/>

Tutorials

- Stanford BIDS conversion tutorial: <https://reproducibility.stanford.edu/bids-tutorial-series-part-1b/>
- Stanford fMRIPrep tutorial: <https://reproducibility.stanford.edu/fmriprep-tutorial-running-the-docker-image/>
- Andy's book: https://andysbrainbook.readthedocs.io/en/latest/OpenScience/OS_fMRIPrep.html#fmriprep



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