Dear experts,

We compared the data in the files ('~.dtseries.nii') proccessed respectively from the **fmriprep pipeline** and the **ciftify pipeline**, and found that the differences is intolerable. However, we had difficulties to further explore the causes. Following is the important details of our investigation.

1. We first preprocessed data by fmriprep20.2.1:

```
fmriprep-docker $bids_fold $out_dir participant --participant-label core0
--fs-license-file $license_file \
 --output-spaces anat MNI152NLin6Asym:res-2 fsLR \
 --use-aroma --cifti-output 91k \
 -w $work_dir
```

Because we set on '--cifti-otput', fmriprep will produced .dtseries.nii file for each run, like '~space-fsLR_den-91k_bold.dtseries.nii'.

2. For some reasons in my project, we use ciftify to transfer outputs of fmriprep into HCP format:

```
ciftify_recon_all --surf-reg MSMSulc --resample-to-T1w32k $subject
ciftify_subject_fmri --surf-reg MSMSulc --ciftify-work-dir $cftifyworkdir
$func_file $subject $out_name
```

The second command takes input of the '~space-T1w_desc-prepro_bold.nii.gz' in fmriprep outputs, and produce the '~Atlas_s0.dtseries.nii'.

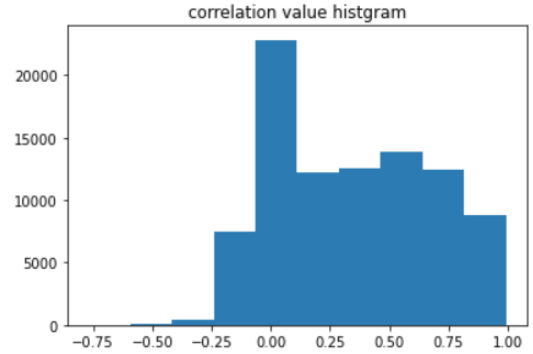
3. We then compare the time-series data in two .dtseries.nii. :

3.1 For each position(cortical vertex or subcortical voxel) in brain image, compute correlation of time series from two files.

```
import os
import nibabel as nib
import numpy as np
from os.path import join as pjoin

# load data
ciftify_file = 'ses-COCO_task-retinotopy_run-1_Atlas_s0.dtseries.nii'
fmriprep_file = 'sub-core02_ses-LOC_task-retinotopy_run-1_space-fsLR_den-
91k_bold.dtseries.nii'
ciftify_data = nib.load(ciftify_file).get_fdata()
```

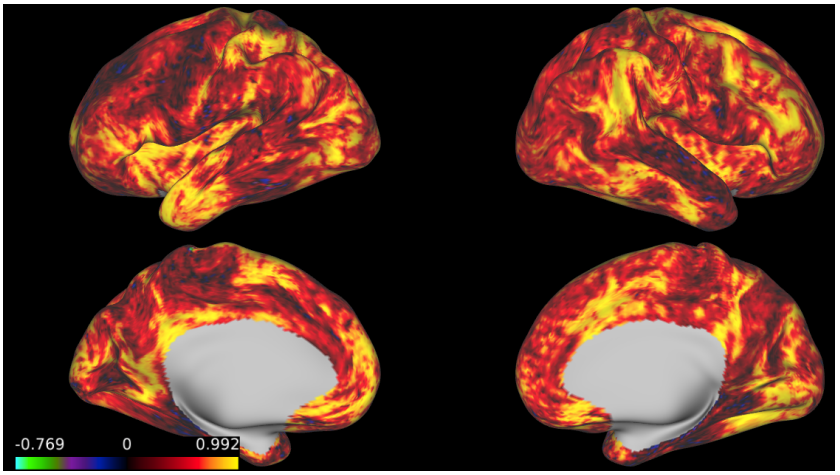
```
fmriprep_data = nib.load(fmriprep_file).get_fdata()

# compute correlation
r = np.zeros(91282)
for _ in range(91282):
    r[_] = np.corrcoef(fmriprep_data[:,_],ciftify_data[:,_])[0,1]
```

The mean of r is around 0.34 for a randomly selected scan, and we repeat the similar result on another scan. Combined with the histogram of r, indicating that there are even thousands of negative values, we were very astonished and curious about the cause of this probelm.

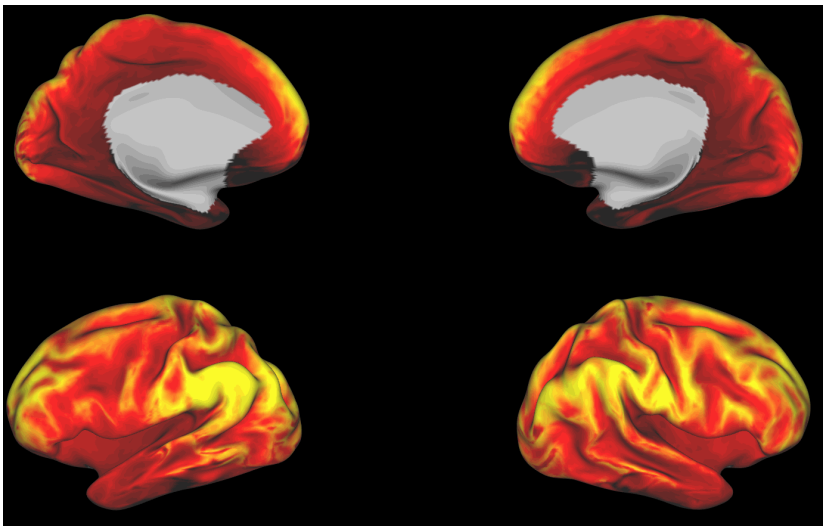


3.2 visulization

We tried to visulize two dtseries and the r-map, but find little cue on the cause.



r map on a inflated template



visualization at TR=0, two time-series data flash on the inflated template

4. some additional analysis

We thought that one plausible reason may lies on the the usage of '--use-aroma' in fmriprep. For this possibility, we check the log to determine how fmriprep generate .dtseries.nii, but the log information is unclear about it. However, we rerun fmriprep without aroma, and the comparison remain the same conclusion.

We are planning to use traditional analysis like funtional localizer to continue the comparison as a validation of outputs from two pipelines.

If anyone has already known some hint on this problem, please contact us! Thank you for reading.

Best regards