**fmriprep pipeline**

**Installation**

**(1) get free surfer license**

**(2) download docker**

**Note:** csic cluster already have docker installed

but one needs to get permission to run docker on the cluster

docker allows you to access containers, which are suits of programs needed to do a certain task. In our case, we can use docker to include all of the software packages needed for our analysis without having to download each of them separately.

**(3) python install fmriprep-docker**

on cluster

# install fmriprep docker into ~/.local/bin

pip3 install --user --upgrade fmriprep-docker

on own computer

# install fmriprep docker into ~/.local/bin

pip3 install --user --upgrade fmriprep-docker

# add fmriprep-docker path to PATH

echo 'export PATH=$PATH:~/.local/bin' >> ~/.bash\_profile

# make sure the shell looks there for programs to run

source ~/.bash\_profile

需要跑这两个代码吗 我的路径还没改

然后直接bash xx.sh就行

这个命令跟我之前用的也不太一样

Output里面在后续ICA作为input的文件是哪个

**Creating the script**

(1) create a derivatives folder and put the freesurfer license in it

~/dataset folder/derivates

e.g. /home/jran2/ABIDEI-KKI/derivaties

(2) create a code folder within the dataset folder

~/dataset folder/code [e.g. /home/jran2/ABIDEI-KKI/code]

(3) download fmriprep\_singleSubj.sh to the folder

https://github.com/andrewjahn/OpenScience\_Scripts/blob/master/fmriprep\_singleSubj.sh

make changes to the script accordingly, the changed script can be found in

/home/jran2/code/fmriprep\_singleSubj.sh

fmriprep arguments

https://fmriprep.org/en/stable/usage.html

In our case, we

(1) field map correction: without stating [—-ignore fieldmaps]

(2) slice time correction: without stating [—-ignore slicetiming]

(3) motion correction - image registration:

fsl flirt with boundary-based registration - 6 dof

Choices: rigid body(6 parameters) or 12-parameter affine?

Metrice to estimate motion (intensity based? boundary based?)

Method to realign image (interpolation scheme?)

(4) alignment

align functional data to the anatomical mri data (surface driven)

align T1-weighted structural image to a template, normalization to MNI space [--output-spaces MNI152NLin2009cAsym:res-2]

concatenate these two transformations, so we align functional data to the template space

No susceptibility distortion correction, no smoothing is applied. Disable freesurfer cortical reconstruction: —fs-no-reconall

**Running the script**

# log onto a computing node with good resources

qlogin

# submit the job

bash fmriprep\_singleSubj.sh

# check job status

qstat

**Interpreting the result**

**derivatives/sub-id/anat**

Anything with MN152NLin2009cAsym -> normalized to this template

Anything without the string is in raw or native space

**derivates/sub-id/func**

confounders

boldref: reference image used for registration and normalization

brain\_mask: estimated brain mask for this run

\_bold: preprocessed functional data up through normalization

**Html file in derivatives/sub-id.html**

Check the video for interpretation:

<https://www.youtube.com/watch?v=fQHEKSzFKDc&t=1s>

**Other information**

**TE**

The**echo time (TE)** refers to the time **between the application of the radio frequency excitation pulse and the peak of the signal induced in the coil**. It is measured in milliseconds. The amount of T2 relaxation is controlled by the TE.

**TR**

The **repetition time** **(TR)** is the time **from the application of an excitation pulse to the application of the next pulse**. It determines how much longitudinal magnetization recovers between each pulse. It is measured in milliseconds.

**T1-weighted images**

A T1-weighted image relies upon the longitudinal relaxation of a tissue’s net magnetization vector. Basically, spins aligned in an external field (B0) are put into the transverse plane by a radio frequency pulse. They then slide back toward the original equilibrium of B0. Not all tissues return back to equilibrium in the same amount of time, and a tissue's T1 reflects the amount of time taken for its protons' spins to realign with the main magnetic field (B0).

**Fat** quickly realigns its longitudinal magnetization with B0, and it therefore **appears bright** on a T1 weighted image. Conversely, **water** has much slower longitudinal magnetization realignment after a radio frequency pulse, and therefore, has less transverse magnetization after an RF pulse. Thus, water has low signal and **appears dark**.

T1 weighting tends to have short TE and TR times. Fat: bright; fluid: dark.

**T2-weighted images**

A T2WI relies upon the transverse relaxation (also known as "spin-spin" relaxation) of the net magnetization vector.

One way to think about T2 relaxation is as follows:

* after an RF excitation pulse, there is relaxation of the spins from the transverse plane toward the main longitudinal magnetic vector (B0) - this is T1 weighting
* at the same time, spins are decaying from their aligned precession in the transverse plane - differences in this decay are captured on T2 weighting
* T2 weight’s flip angle is less important than with T1 weighting
* T2 weighting tends to require long TE and TR times. Fat: intermediate-bright; fluid: bright.

**BIDS format**

The input dataset of fmriprep must be in a BIDS format, and it must include at least one T1w structural image and (unless disabled with a flag) a BOLD series. Validate bids format: https://bids-standard.github.io/bids-validator/

Might need to add “--bids-filter-file” to pass fMRIPrep a JSON file that describes a custom BIDS filter for selecting files with PyBIDS. The reason is that some folder has “session1” subfolder inside func. Details can be found here: https://fmriprep.org/en/21.0.2/faq.html#how-do-I-select-only-certain-files-to-be-input-to-fMRIPrep

**Preprocessing Pipeline**

https://www.youtube.com/watch?v=xLWES956JJE