Talapas login

ssh [mmoss2@talapas-ln1.uoregon.edu](mailto:mmoss2@talapas-ln1.uoregon.edu" \t "_blank)

Get files from Talapas onto local

rsync -auxv --progress [mmoss2@Talapas-ln1.uoregon.edu](mailto:mmoss2@Talapas-ln1.uoregon.edu" \t "_blank):/projects/mayrlab/shared/SEQ201\_20180220\_102926/Series\_7\_Run1/MR.1.3.12.2.1107.5.2.19.45348.2018022010564579992861188.dcm /Users/Melissa/Desktop/dicoms\_seq/

Get files from local onto Talapas

rsync -r -auxv --progress /Users/melmo/Dropbox/P.SEQ\_fMRI/fMRI\_prep/ [mmoss2@Talapas-ln1.uoregon.edu](mailto:mmoss2@Talapas-ln1.uoregon.edu" \t "_blank):/projects/mayrlab/shared/SEQ\_prep/fMRI\_prep/

Access bash profile on Talapas

nano ~/.bash\_profile

Add paths for scripts/functions

export PATH="/projects/mayrlab/shared/softwares/dcm2niix-master/build/bin:$PATH"

Change permissions to write

chmod -R 770 /projects/mayrlab/shared/SEQ

Should use sbatch instead of sh when running scripts.

e.g., sbatch 01\_seq\_setup.sh 301 (to run the nifti setup for subject 301)