**Pipeline**

1. Convert MRIs from DICOM to NIFTI using dcm2niix via shell script (convert2nii.sh).
2. Run Freesurfer RECON –all via shell script (reconall.sh).
3. Use docker to align atlases (Wang, etc.) to subject-specific grey-matter meshes:
   1. Run additional FreeSurfer routines to register subject-specific meshes to average template (prep4docker.sh)
   2. Run docker routine (run\_docker\_serial.sh)
   3. Run Wang/Glasser label conversion on cluster (to\_labels.sh)
4. Create preprocessed fieldtrip data structure:
   1. N.B. must include head loc channels in data matrix
   2. Data should \*not\* be planar gradient transformed
   3. Example script MEGpreprocessing4mne\_induced.m
5. Write data to mne-compatible file (read\_fieldtrip.py).
6. Create high density head shape model via mne (head\_shape\_model.sh):
   1. Can give error for each subject when decimating high-density models to intermediate density, but this is fine – only high density required.
7. Make head meshes via fieldtrip (all\_meshes.m, which calls make\_mesh.m).
8. Make transformation matrix by coregistering MEG headloc fiducials to head models: (first set fiducial locations to head model for each participant session using set\_fiducials.py; then make and save transformation matrices using run\_make\_trans.py).
9. Run LCMV source reconstruction (lcmv\_peter.py).
10. Aggregate within ROIs (sr\_agg\_parallel.py).
    1. This will save .hdf file source estimates separately for ‘paired’ (each distinct cluster for each hemisphere), ‘averaged’ (mean per cluster across hemispheres) or ‘lateralized’ (difference across hempispheres) estimates, aggregated within spatial clusters that are specified in pymeg/aggregate\_sr.