**Introduction to the One-step General Registration and Extraction (OGRE) Pipeline**

[**https://github.com/PhilipLab/OGRE-pipeline**](https://github.com/PhilipLab/OGRE-pipeline)

**Last update: July 11, 2024**

* **Added IntendedFor: metadata to OGREdcm2niix.sh**

The goal of this project is to create an off-the-shelf mac preprocessing pipeline (with registration and motion correction combined via one-step resampling) with outputs immediately analyzable with FSL FEAT. If you have questions or suggestions to improve this document, please contact [bphilip@wustl.edu](mailto:bphilip@wustl.edu).

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# 1) Creating required files

OGRE uses csv files to describe which scans were performed in which order (see sections 1A, 1B).

You will also need to create fsf files for your FSL analysis (section 1C), and optionally specify these fsf files' locations (section 1D).

To maintain flexibility, file names are never required to be any particular pattern; instead, OGRE learns their names when you pass the names as inputs to OGRE scripts. We recommend filenames that are recognizable to BIDS format (e.g. “sub-XXXX\_scanlist.csv”).

Future versions of OGRE will be able to draw this information from BIDS .json files.

## 1A. Create scanlist.csv

The “scanlist.csv” links the dicom names to nifti file outputs, and also is used by the rest of OGRE to identify file names and locations. **If you ever move your nifti files, make sure to update scanlist.csv so it remains correct**.

You can create “scanlist.csv” manually. An example is in **OGRE-pipeline/examples/sub-2025\_scanlist.csv**, and reproduced here:

7,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/anat/sub-2025\_T1w

8,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/fmap/sub-2025\_acq-draw\_dir-AP\_epi

9,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/fmap/sub-2025\_acq-draw\_dir-PA\_epi

10,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawRH\_run-1\_sbref

11,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawRH\_run-1\_bold

13,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawLH\_run-1\_sbref

14,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawLH\_run-1\_bold

19,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawRH\_run-2\_sbref

20,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawRH\_run-2\_bold

22,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawLH\_run-2\_sbref

23,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawLH\_run-2\_bold

31,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/fmap/sub-2025\_acq-draw\_run-3\_dir-AP\_epi

32,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/fmap/sub-2025\_acq-draw\_run-3\_dir-PA\_epi

33,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawRH\_run-3\_sbref

34,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawRH\_run-3\_bold

36,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawLH\_run-3\_sbref

37,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-drawLH\_run-3\_bold

39,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/fmap/sub-2025\_acq-dbsi\_dir-PA\_epi

40,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/dwi/sub-2025\_acq-dbsi\_dwi

41,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-rest\_run-1\_sbref

42,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-rest\_run-1\_bold

44,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-rest\_run-2\_sbref

45,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-rest\_run-2\_bold

47,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-rest\_run-3\_sbref

48,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/func/sub-2025\_task-rest\_run-3\_bold

50,/Users/Shared/10\_Connectivity/raw\_data/sub-2025/anat/sub-2025\_T2w

In this example, the dicom names were just single numbers (e.g. “7”). If multiple field maps exist (highlighted), OGRE will apply the most recent one to a given func scan.

* Future versions of OGRE will use BIDS metadata, if available, to determine which fieldmap applies to which scan. This will supersede the “most recent” default behavior.

For automatic generation of scanlists, we have included **pdf2scanlist.py** which is designed to take a XNAT screenshot pdf and compare it to the “protocol.csv” (see below) to create a “scanlist.csv”.

**% pdf2scanlist.py /Users/Shared/10\_Connectivity/raw\_data/sub-2025/sub-2025\_CNDA.pdf -p /Users/mcavoy/repo/NRL-misc/10\_Connectivity\_protocol.csv**

When using pdf2scanlist.py, review your pdf’s and scanlists to ensure that no scans have been omitted (e.g. due to page breaks).

## 1B. Create protocol.csv (OPTIONAL)

The “protocol.csv“ defines the data that was acquired in the scanner, and is only required if you intend to use **pdf2scanlist.py**. If you are creating your scanlist.csv files manually, “protocol.csv” is not needed.

Consider the example for study “10\_Connectivity“:

t1\_mpr\_1mm\_p2\_pos50, overwrite, anat, T1w

SpinEchoFieldMap2\_AP, append, fmap, dir-AP\_epi

SpinEchoFieldMap2\_PA, append, fmap, dir-PA\_epi

CMRR\_fMRI\_TASK\_R1\_AP\_3mm\_488meas\_SBRef, overwrite, func, task-drawRH\_run-1\_sbref

CMRR\_fMRI\_TASK\_R1\_AP\_3mm\_488meas, overwrite, func, task-drawRH\_run-1\_bold

CMRR\_fMRI\_TASK\_R2\_AP\_3mm\_488meas\_SBRef, overwrite, func, task-drawLH\_run-1\_sbref

CMRR\_fMRI\_TASK\_R2\_AP\_3mm\_488meas, overwrite, func, task-drawLH\_run-1\_bold

CMRR\_fMRI\_TASK\_R3\_AP\_3mm\_488meas\_SBRef, overwrite, func, task-drawRH\_run-2\_sbref

CMRR\_fMRI\_TASK\_R3\_AP\_3mm\_488meas, overwrite, func, task-drawRH\_run-2\_bold

CMRR\_fMRI\_TASK\_R4\_AP\_3mm\_488meas\_SBRef, overwrite, func, task-drawLH\_run-2\_sbref

CMRR\_fMRI\_TASK\_R4\_AP\_3mm\_488meas, overwrite, func, task-drawLH\_run-2\_bold

CMRR\_fMRI\_TASK\_R5\_AP\_3mm\_488meas\_SBRef, overwrite, func, task-drawRH\_run-3\_sbref

CMRR\_fMRI\_TASK\_R5\_AP\_3mm\_488meas, overwrite, func, task-drawRH\_run-3\_bold

CMRR\_fMRI\_TASK\_R6\_AP\_3mm\_488meas\_SBRef, overwrite, func, task-drawLH\_run-3\_sbref

CMRR\_fMRI\_TASK\_R6\_AP\_3mm\_488meas, overwrite, func, task-drawLH\_run-3\_bold

ep2ddbsi\_b0\_PE=PA, overwrite, fmap, acq-dbsi\_dir-PA\_epi

ep2ddbsi\_19\_2mm\_iso\_LowBW\_2av, overwrite, dwi, acq-dbsi\_dwi

CMRR\_fMRI\_REST\_R1\_AP\_3mm\_550meas\_SBRef, overwrite, func, task-rest\_run-1\_sbref

CMRR\_fMRI\_REST\_R1\_AP\_3mm\_550meas, overwrite, func, task-rest\_run-1\_bold

CMRR\_fMRI\_REST\_R2\_AP\_3mm\_550meas\_SBRef, overwrite, func, task-rest\_run-2\_sbref

CMRR\_fMRI\_REST\_R2\_AP\_3mm\_550meas, overwrite, func, task-rest\_run-2\_bold

CMRR\_fMRI\_REST\_R3\_AP\_3mm\_550meas\_SBRef, overwrite, func, task-rest\_run-3\_sbref

CMRR\_fMRI\_REST\_R3\_AP\_3mm\_550meas, overwrite, func, task-rest\_run-3\_bold

t2\_spc\_sag\_p2\_iso1.0, overwrite, anat, T2w

Each item contains 4 fields:

1. Scan name. As received from scanner.
2. Write mode: can be *append* or *overwrite*
   1. *Append*: retains all scans with this name. See highlighted lines in examples.
   2. *Overwrite*: if there are multiple scans with this exact name, keeps last one only.
3. Bids directory: specify a subdirectory for BIDS compliance. E.g. *anat*, *fmap*, *func*, *dwi*
4. Output root: add this to end of filename to produce BIDS-compliant nifti

## 1C. Create .fsf files for FSL FEAT analysis

This document assumes you are already familiar with FSL. FSL documentation is available [here](https://fsl.fmrib.ox.ac.uk/fsl/docs/#/).

*If this is your first time running OGRE, we recommend saving this until after you've successfully run the functional pipeline. That* way you will have the pipeline outputs on hand. (You are never required to create your .fsf files in advance; you will run your FEAT analysis at the end of the functional pipeline.)

To use FSL FEAT on data preprocessed by OGRE, you will use FEAT's “statistics” option (rather than “full analysis”), to skip preprocessing and registration.

Confirm in your first-level .fsf files: “set fmri(analysis) 2”

In addition, FEAT will always try to run SUSAN spatial smoothing, even if you turn off preprocessing. Therefore, you must also set the spatial smoothing kernel to 0 in your first-level analyses. You can do this in the GUI "Preprocessing" tab if you temporarily switch back to "full analysis," but the important check is:

Confirm in your first-level .fsf files: “set fmri(smooth) 0”

*Alternatively, you could perform your spatial smoothing (if any) in FEAT instead of OGRE. We find that logistically cumbersome, but it's functionally identical - FSL and OGRE use the same tools. The critical part is to avoid accidentally smoothing your data more times than you intended!*

You will also need to select the appropriate OGRE output as your input to first-level FEAT. The correct file is:

If no smoothing: **sub-2025\_task-drawLH\_run-1\_OGRE-preproc\_bold.nii.gz**  
 If using SUSAN smoothing (from -f option): **sub-2025\_task-drawLH\_run-1\_OGRE-preproc\_susan-#mm\_hptf-%s\_bold.nii.gz**

*(Where # is your SUSAN smoothing FWHM, and % is your temporal cutoff)*

Otherwise, create your .fsf files as normal for your study design. Example first- and second-level .fsf's are included in OGRE-pipeline/examples.

Note that if you wish to include motion parameters in your model, you will need to do so via the "additional confound EVs" option. A text file of standard MCFLIRT motion parameters can be found in OGRE output at e.g:

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.3.1/sub-2025\_task-drawLH\_run-1\_bold/MotionCorrection/sub-2025\_task-drawLH\_run-1\_bold\_mc.par**

## 1D. Create locator.txt files to let OGRE identify your .fsf files (OPTIONAL)

These files will allow OGRE to automatically run your first- and second-level FSL analyses (and the necessary adapter). They will make your life easier, but they are not necessary.

For each subject, create a .txt file with the full paths of all first-level analyses. The paths can be separated by commas, spaces, tabs and/or newlines. See **OGRE-pipeline/examples/sub-2025\_locatorOne.txt**

If you want OGRE to also autorun your second-level analyses, create a second separate .txt file with their paths. Same format; see **OGRE-pipeline/examples/sub-2025\_locatorTwo.txt**

# 2. Convert dicoms to niftis

OGREdcm2niix.sh uses Chris Rorden’s dcm2niix to perform the dicom to nifti conversion automatically on an entire scanlist.csv.

**% OGREdcm2niix.sh /Users/Shared/10\_Connectivity/raw\_data/sub-2025/sub-2025\_scanlist.csv \**

**-i /Volumes/NRLbackup/10\_Connectivity/dicom/sub-2025**

In the above example, the “scanlist.csv“ created in section 1A is used to convert the dicoms located at **/Volumes/NRLbackup/10\_Connectivity/dicom/sub-2025** as specified by the -i option.

If nifti files are not created, check **/Users/Shared/10\_Connectivity/raw\_data/sub-2025/sub-2025\_dcm2niix.sh.txt**. If it says “input folder invalid“ this may be a permissions error, run chmod -R 775 or 777 on the subject directory.

**% chmod -R 775 /Users/Shared/10\_Connectivity/raw\_data/sub-2025**

Note that this step is “required” in the sense that nifti files are required for OGRE. You may be able to use preexisting nifti files, though OGREdcm2niix.sh will ensure the creation of nifti files that match your scanlist.csv.

For compatibility with non-OGRE software, OGREdcm2niix.sh adds the "IntendedFor" field in each .json to link your scans to the most recent fieldmap in the scanlist (if any). As noted in 1A, OGRE does not (yet) call this field.

# 3. Pipeline operation common principles

The main OGRE scripts are “OGRExxxSETUP” scripts that will take in a scanlist.csv and other arguments to create a subject-specific .sh scripts. **The real processing happens when you run the subject-specific scripts**.

The setup scripts will, by default, work in **[Project]/derivatives/preprocessed/sub-XXXX/** . The subject-specific scripts (and their interim outputs) will appear in a "pipeline7.4.1" subdirectory, and final outputs will appear in separate BIDS subdirectories (e.g. "func").

Subject-specific scripts will always be accompanied by a “\_fileout.sh” variant. The difference is that the “\_fileout.sh” version will send its output to a text file instead of the command line.

Default output location for setup scripts is **[Project]/derivatives/preprocessed/sub-XXXX/** . The subject-specific scripts (and their interim outputs) appear in a "pipeline7.4.1" directory therein, and final outputs will appear in separate BIDS directories therein (e.g. "func").

To automatically execute the \_fileout.sh at the moment when you create it via a SETUP script, use the -A argument when calling the SETUP script.

A convenient way to set up the structural and functional pipelines together is via the -b “batchscript” option:

**% OGREstructpipeSETUP.sh /Users/Shared/10\_Connectivity/raw\_data/sub-2025/sub-2025\_scanlist.csv [arguments] -b**

**% OGREfMRIpipeSETUP.py /Users/Shared/10\_Connectivity/raw\_data/sub-2025/sub-2025\_scanlist.csv [arguments] -b**

This will create:

**% /Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_OGREbatch\_fileout.sh**

which is identical to running the subject-specific struct script, followed by the subject-specific func script.

In the description of each pipeline it mentions "uses [scantype] (if available)." OGRE will find & use these optional files if they are included in scanlist.csv.

*Do not execute the functional pipeline's subject-specific scripts until the structural pipeline has completed.*

# 4. Structural pipeline

The structural pipeline is modified from Glasser's HCP v3.27 pipelines (Glasser 2013 Neuroimage), and uses the T1 (required) and T2 (if available) to extract, segment and parcellate the brain and apply motion correction along with the registration to the MNI atlas via FSL and Freesurfer.

Basic usage is with “scanlist.csv“ as the sole argument,

**% export OGREDIR=/path/to/OGRE-pipeline**

**% OGREstructpipeSETUP.sh /Users/Shared/10\_Connectivity/raw\_data/sub-2025/sub-2025\_scanlist.csv**

This will create the scripts

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_OGREstruct.sh**

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_OGREstruct\_fileout.sh**

As described in the Common Principles, the processing happens when you run the "struct.sh" script (for output to command line) or "struct\_fileout.sh" (for output to a text file).

*We recommend the argument "-erosion 0" if you are applying spatial smoothing to your data, so that HCP-based tools do not remove outside-brain voxels that contain data due to smoothing.* Future versions of OGRE will dynamically select a better default value, but this will require a combined setup script for struct/func because the structural default will be based on functional settings (voxel size, spatial smoothing).

The structural setup script will also copy your scanlist.csv file to:

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/original\_scanlist\_filename**

# 5. Functional pipeline

The functional pipeline uses the outputs of the structural pipeline along with the SBRef images (if available) and field maps (if available) to preprocess the BOLD time series. The implementation follows that of the structural pipeline with additional options for spatial smoothing **-f**, high pass filtering **-p**, and first-level **-o** and second-level **-t** feat analyses. For example,

**% pipedir=/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1**

**% OGREfMRIpipeSETUP.py /Users/Shared/10\_Connectivity/raw\_data/sub-2025/sub-2025\_scanlist.csv -f 6 -p 60 -o ${pipedir}/sub-2025\_locatorOne.txt -t ${pipedir}/sub-2025\_locatorTwo.txt**

(Note that OGREfMRIpipeSETUP is a .py python script, rather than a .sh bash script.)

This will create the scripts

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_OGREfMRIvol.sh**

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_OGREfMRIvol\_fileout.sh**

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_bidscp.sh**

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_FEATADAPTER.sh** (if -o set)

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_cleanup.sh**

The main processing happens when you run the "fMRIvol.sh" script (for output to command line) or "fMRIvol\_fileout.sh" (for output to a text file).

The **-o** and **-t** arguments to SETUP are used to run your FEAT analyses as part of a single step. Each one takes as input a “locator.txt” file described in previous section. If you specify **-o**, the script will run the functional pipeline, copy the outputs to bids directories, smooth and filter, run all your first level FSL analyses, then run the FEATADAPTER (see below). If you also specify **-t**, it will then run your second-level analyses.

*If this is your first time running OGRE, we recommend omitting -o and -t. Then you can use the outputs to set up your .fsf files, and thereafter run the FEAT adapter as described in step 7.*

Normally you will not need to invoke “bidscp.sh” or “FEATADAPTER.sh”, these are both automatically executed by “fMRIvol.sh.”

“bidscp.sh“ copies the OGRE pipeline outputs in “pipedir“ to the appropriate BIDS directories, e.g.

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/anat**

**/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/func**

Spatial smoothing (**-f**) and temporal filtering (**-p**), if any, are applied at this stage to the final BIDS outputs.

The "cleanup.sh" script is described under 9. Cleanup.

# 6. FEAT first-level analysis

With the output of the functional scripts, you are ready to run first-level FEAT analysis (as described in section 2D). The OGRE output to use as an input to FEAT is:

/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-XXXX/func/xyz where xyz is, for example:  
 If no smoothing: **sub-2025\_task-drawLH\_run-1\_OGRE-preproc\_bold.nii.gz**  
 If using SUSAN smoothing (from -f option): **sub-2025\_task-drawLH\_run-1\_OGRE-preproc\_susan-#mm\_hptf-%s\_bold.nii.gz**

*(Where # is your SUSAN smoothing FWHM, and % is your temporal cutoff)*

To set yourself up for the next step, all your FEAT work should go in, for example:

**/Users/Shared/10\_Connectivity/derivatives/analysis/sub-2025/sub-2025\_model-OGRE**

If you used the **-o** option in the functional analysis, it will automatically run FEAT using .fsf files you specified.

# 7. FEAT adapter

One additional step is needed between first-level FEAT analysis and higher-level FEAT analyses. The first-level results will lack registration information, because FEAT does not (yet) know about all the registration work completed by OGRE. The “FEATADAPTER.sh” script will copy the appropriate transformations and matrices to create a “reg“ directory inside each first-level FEAT output directories. All of this is automatically performed by “fMRIvol.sh” if you set -o, but you have the power to run it later or manually.

% **sub-2025\_FEATADAPTER.sh**

As noted above, FEATADAPTER.sh script is automatically created as part of the functional pipeline. To recreate FEATADAPTER.sh without running any other analysis, use the **-F** option:

**% OGREfMRIpipeSETUP.py /Users/Shared/10\_Connectivity/raw\_data/sub-2025/sub-2025\_scanlist.csv -o ${pipedir}/sub-2025\_locatorOne.txt -t {pipedir}/sub-2025\_locatorTwo.txt -F**

This will create a sub-XXXX\_FEATADAPTER\_fileout.sh and sub-XXXX\_FEATADAPTER.sh; run either of those (as always, fileout doesn't lock up your terminal window).

You may find it useful to run the adapter manually on individual .feat directories. The script that does the work here is **OGRE-pipeline/lib/OGREmakeregdir.sh**, which is documented and ready for independent use on an individual .feat directory:

% **OGREmakeregdir.sh -f [path]/sub-2025\_task-drawLH\_run-1.feat**

This is the same as running FEATADAPTER on a list of directories. All FEATADAPTER does is look through your locator.txt to identify your .feat directories and run **OGREmakeregdir.sh** on each of them.

# 8. FEAT higher-level analysis

Now you can run a normal higher-level analysis on your first-level FEAT outputs. (Or maybe you already did with **-t**.) Go forth and get your results!

# 9. Cleanup

If you are satisfied that you know which files you need, you can save disk space by deleting everything except the final BIDS-format outputs via "sub-XXXX\_cleanup.sh", e.g.:

% **/Users/Shared/10\_Connectivity/derivatives/preprocessed/sub-2025/pipeline7.4.1/sub-2025\_cleanup.sh**

would delete all OGRE subdirectories in the parent directory **derivatives/preprocessed/sub-2025/pipeline7.4.1**. Individual files in the parent directory and non-OGRE subdirectories are retained.

The only reason to retain pipeline7.4.1 files is if you want to use them in your analyses. (If so, you should of course copy out any useful files before you run “cleanup.sh”). The files in pipeline7.4.1 will not help with future processing. If you need to rerun a struct script, you are starting that analysis from scratch and should delete all existing outputs first. If you need to rerun a func script, it will overwrite any previous func outputs.

# 10. OGRE outputs

OGRE's primary outputs are BIDS-compatible, created when *sub-XXXX\_bidscp.sh* copies the OGRE pipeline's outputs from the *pipeline7.4.1* working directory to the bids output directories (specified originally in scanlist.csv and maintained in raw\_data).

Let *parent* = derivatives/preprocessed/sub-XXXX

Let *runname* = everything between the subject ID and the suffix in scanlist.csv (e.g. “task-X\_run-Y”)

BOLDs:

From *parent*/pipeline7.4.1/MNINonLinear/Results*/runname*/sub-XXXX\_*runname*\_bold.nii.gz

To *parent*/func/sub-XXXX\_*runname*\_OGRE-preproc\_bold.nii.gz

Brain masks:

From *parent*/pipeline7.4.1/MNINonLinear/Results/*runname*/brainmask\_fs.2.nii.gz

To *parent*/func/sub-XXXX\_*runname*\_OGRE-preproc\_res-2\_label-brain\_mask.nii.gz

Structurals:

T1 and T2 weighted whole head images

From *parent*/pipeline7.4.1/MNINonLinear/TXw\_restore.nii.gz

To *parent*/anat/sub-XXXX\_OGRE-preproc\_desc-restore\_TXw.nii.gz

T1 and T2 weighted brain-only images *(not BIDS-compliant, instead in filename format required by FSL)*

From *parent*/pipeline7.4.1/MNINonLinear/TXw\_restore\_brain.nii.gz

To *parent*/anat/sub-XXXX\_OGRE-preproc\_desc-restore\_TXw\_brain.nii.gz

Regressors:

MCFLIRT motion outputs (xyz translation, xyz rotation)

From: *parent***/**pipeline7.4.1/sub-XXXX\_*runname*\_bold/MotionCorrection/sub-XXXX\_runname\_bold\_mc.par

To: *parent*/regressors/sub-XXXX\_*runname*\_bold\_mc.par

Extended motion parameters (xyz translation, xyz rotation, derivative of xyz transl, derivative of xyz rot)

From: *parent***/**pipeline7.4.1/sub-XXXX\_*runname*\_bold/Movement\_Regressors.txt

To: *parent*/regressors/sub-XXXX\_task-*runname*\_bold\_mc-withderiv.txt

Detrended (zero mean, zero slope) extended motion parameters

From: *parent***/**pipeline7.4.1/sub-XXXX\_task-*runname*\_bold/Movement\_Regressors\_dt.txt

To: *parent*/regressors/sub-XXXX\_task-*runname*\_bold\_mc-withdetrendderiv.txt

fsl\_motion\_outliers output confound file [fsl\_motion\_outliers -o] (if any)

In: *parent*/regressors/sub-XXXX\_task-*runname*\_bold\_fmospikes.txt

fsl\_motion\_outliers metric values [fsl\_motion\_outliers -s] (if any)

In: *parent*/regressors/sub-XXXX\_task-*runname*\_bold\_fmovalues.txt

Combined MCFLIRT motion outputs (.par above) + fsl\_motion\_outliers output (if any). If you didn't call fsl\_motion\_outliers, this is identical to the .par output.

In: *parent*/regressors/sub-XXXX\_task-*runname*\_bold\_confoundevs.txt

Future versions of the OGRE manual will detail the files in the pipeline7.4.1 working directory.

# 11. Troubleshooting

Some issues and solutions we have encountered...

1. If the file locations specified in scanlist.csv are not in the same project directory as your raw\_data directory, OGREfMRIpipeSetup.py may crash.
   1. Resolve this with the **-d** argument to OGREfMRIpipeSetup.py to explicitly set your file locations
2. If python scripts don't work, try the following:

**% cd OGRE-pipeline/lib/PY**

**% bash setup.sh**

1. If you need to update/recreate metadata, use:

**% OGRE-pipeline/scripts/scanlist2json.py**

1. If your "scanlist.csv" is ever incorrect, everything will crash. Therefore, if you move files/directories, you should update "scanlist.csv."
   1. When you run the struct pipeline, it copies your current scanlist to the pipeline7.4.1 directory. Beware of versioning errors if you update one copy but use the other.

# 12. Update Plans

This is the current list of planned updates & improvements to OGRE. Expect it to constantly change.

1. More user-friendly handling of motion parameters, including optional calling of fsl\_motion\_outliers
2. More user-friendly handling of the "FEAT adapter"
3. A single setup script, for ease-of-use and to dynamically select structural brain size (erosion) based on functional smoothing arguments
4. Produce BIDS-compliant .json metadata alongside output files
5. Reading optional BIDS metadata to match scans with appropriate fieldmaps
6. Full documentation of files in pipeline7.4.1 working directory