**Study 1 & 2 CAMCAN**

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**E:/Study\_1\_and\_2 > CAMCAN > full\_run**

**1st\_level**

This contains a folder for each of the analyses but with the suffix 1 which indicates just a single participant is saved here (for modelling purposes):

**Hrf** (canonical model)

**Hrf\_td** (canonical with derivative)

**Fourier** (fourier set)

**Hrf\_td\_fourier** (canonical with derivative controlling for fourier set)

**Fourier\_hrf\_td** (fourier set controlling for canonical with derivatives)

There is also a subfolder called ‘1st\_level’ in which the same structure is found, only these are the full set of participants, and have been compressed to save space. Due to the sample size the sample split into four separate compressed files (first\_140, second\_140, third\_140, fourth\_140).

**2nd\_level**

Under the subfolder ‘conimages’ there is all data pertaining to the second level analysis. Within this there are five subfolders pertaining to each of the analyses with the suffix ‘conimages’ (such as ‘hrf\_conimages’ for the canonical model). This saved con images across each age group with relevant subfolders, but critically has a subfolder ‘1\_con’ which contains the output from the main second level analysis for study 2, looking across age groups. Within ‘1\_con’ there are beta, con, and SPM files for the analysis, with one factor of age and seven levels, however for flexible models there is a second factor of basis\_function with 3 or 7 levels. There is also a subfolder ‘baseline’ which contains a basic 2nd level analysis used to ascertain mean baseline signal across participants within each age group.

**2nd\_level\_group**

This contains data from the 2nd level analysis but for study 1, looking at all participants as one group irrespective of age. There is again a sub folder for each model, and within these there is also a mean baseline signal analysis.

*Note on Percentage Signal Change*

SPM automatically sets the mean signal over the brain to be 100. So when we have an amplitude of e.g. 0.2, this means both 0.2% of the mean signal, and an absolute value of 0.2. This is percentage change in signal, percentage of the mean signal. However GM has a higher signal than elsewhere, and so we need to ascertain local mean signal to adjust our percentage. To do this we take the final column in the design matrix which is mean signal. If this is 250, all we need to do is take our absolute signal 0.2, which is also 0.2%, divide by 250 and multiply by 100. What we are essentially doing is downscaling this % signal change by 2.5 as the baseline is 2.5 times higher than actually anticipated. To form this third column I run a 2nd level analysis just on the final beta values from the 1st level analysis. This is fine as the con image is the summation of all relevant betas, and I have only one beta.

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**Preprocessing and analysis scripts in order of application**

**Field map/realign/unwarp/coregistration**

Field mapping, realignment and unwarping, co-registering to T1 and segmentation was carried out in a single script:

/CAMCAN/full\_run/aFM\_realign\_coreg\_coreg\_segment\_V2.mat

The jobfile is located in:

/CAMCAN/full\_run/batch/Up\_to\_seg\_13May\_V2\_job.m

**Realignment outliers**

The realignment parameters are then checked, the file located in:

/CAMCAN/full\_run/pathways/rp\_pathways\_raw.txt

The script to do this is located in:

/CAMCAN/full\_run/b\_check\_rp\_files\_V2.m

**QA**

Next the signal is analysed for quality assurance:

/CAMCAN/full\_run/c1\_check\_nifti\_outliers.m

Participant data is taken from:

/CAMCAN/full\_run/pathways/epi\_files.txt

Files are saved in:

/CAMCAN/full\_run/checks/QA/range

Outputs include:

Results (key data)

a plot for each participant

stack\_rand (a list of all outliers and an equal number of randomly selected included participants, the order of which are randomised)

grand\_out (included ps)

grand\_in (outliers)

**QA continued**

The randomised list of outliers with included ps is carried forward via:

/CAMCAN/full\_run/c2\_check\_nifti\_outlier\_vs\_control.m

The outputs are saved in:

/CAMCAN/full\_run/checks/QA/range/outliers

And include:

Results (key parameters)

A plot for each participant

**Outlier removal**

Final outliers are removed via:

/CAMCAN/full\_run/d\_remove\_outliers.txt

An outliers folder is made in the raw data directories, and the relevant data shifted across

**Create Dartel Template**

The following folder creates a pathway for each included participant, in preparation for creation of the Dartel template:

/CAMCAN/full\_run/e\_Create\_rc\_paths.m

This uses:

/CAMCAN/full\_run/pathways/t1\_files\_out.txt

The resulting data is then copied and pasted into:

/CAMCAN/full\_run/e\_load\_rc1\_2\_job.m

Then the Dartel template is created using:

/CAMCAN/full\_run/f\_create\_dartel\_template\_noloop.m

**Dartel Normalisation**

Dartel normalisation then takes place via:

/CAMCAN/full\_run/ga\_dartel\_norm.m

Using the batch script:

/CAMCAN/full\_run/batch/part2\_dartel\_FM\_job.m

**Mask check (no. voxels)**

The 1st level analysis was then run preliminarily, after which the resulting masks were checked for the number of voxels containing signal:

/CAMCAN/full\_run/gb\_check\_mask.m

Using participant data from:

/CAMCAN/full\_run/con\_files\_list\_old.txt

**Standardised mask check**

An additional check was run looking at how well each participant meets a standardised mask:

/CAMCAN/full\_run/gc\_check\_norm\_via\_mask\_V3.m

Outputs were saved to:

/CAMCAN/full\_run/checks/check\_normalisation/first

Then upon second run they were saved to:

/CAMCAN/full\_run/checks/check\_normalisation

**Manual co-reg check**

To run manual checks on random slices the following script was used to speed the process:

/CAMCAN/full\_run/gcd\_check\_reg.m

**Fourier window**

The length of the fourier basis set window was established via:

/CAMCAN/full\_run/ab\_cross\_correlations.m

The necessary files were generated first iteratively via:

/CAMCAN/full\_run/checks/check\_cross\_correlations/basic\_fourier\_script.m

Outputs to:

/CAMCAN/full\_run/checks/check\_cross\_correlations

**1st level**

Next all 1st level analyses were run:

/CAMCAN/full\_run/h\_1st\_Level\_GammaTD.m

/CAMCAN/full\_run/i\_1st\_Level\_fourier.m

/CAMCAN/full\_run/j\_1st\_Level\_Gamma.m

/CAMCAN/full\_run/k\_1st\_Level\_GammaTD\_fourier.m

/CAMCAN/full\_run/l\_1st\_Level\_fourier\_hrfTD.m

**Move/rename con files**

For the 2nd level analysis we moved and rename con files via the following 4 scripts:

/CAMCAN/full\_run/m\_RenameConFiles\_for\_2ndAnalysis\_1st

/CAMCAN/full\_run/m\_RenameConFiles\_for\_2ndAnalysis\_2nd

/CAMCAN/full\_run/m\_RenameConFiles\_for\_2ndAnalysis\_3rd

/CAMCAN/full\_run/m\_RenameConFiles\_for\_2ndAnalysis\_4th

**Sort by age**

These are then split into their respective age groups:

/CAMCAN/full\_run/n\_split\_cons\_into\_age\_groups

Outputting to each mHRF within:

/CAMCAN/full\_run/2nd\_level/conimages

**Final list**

The final N list with some additional participant data was located in:

/CAMCAN/full\_run/pathways/demo\_finalN.mat

**2nd level – study 2**

For the 2nd level analysis looking at each age group separately the files are located in:

/CAMCAN/full\_run/2nd\_level/conimages/hrf\_conimages/1\_con

/CAMCAN/full\_run/2nd\_level/conimages/hrf\_td\_conimages/1\_con

/CAMCAN/full\_run/2nd\_level/conimages/fourier\_conimages/1\_con

/CAMCAN/full\_run/2nd\_level/conimages/fourier\_hrftd\_conimages/1\_con

/CAMCAN/full\_run/2nd\_level/conimages/hrftd\_fourier\_conimages/1\_con

**2nd level – study 1**

For the 2nd level analysis looking at all the age groups together, the scripts are located at:

/CAMCAN/full\_run/2nd\_level\_group/hrfc.m

/CAMCAN/full\_run/2nd\_level\_group /hrftd.m

/CAMCAN/full\_run/2nd\_level\_group /fourier.m

/CAMCAN/full\_run/2nd\_level\_group /fourier\_hrftd.m

/CAMCAN/full\_run/2nd\_level\_group /hrftd\_fourier.m

The baseline analyses were run via:

/MRIWork/MRIWork06/nr/matthew\_danvers/CAMCAN/full\_run/2nd\_level\_group /hrfc/baseline/baseline.m

/MRIWork/MRIWork06/nr/matthew\_danvers/CAMCAN/full\_run/2nd\_level\_group /hrftd/baseline/baseline.m

/MRIWork/MRIWork06/nr/matthew\_danvers/CAMCAN/full\_run/2nd\_level\_group /fourier/baseline/baseline.m

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**Results for study 1**

**Definition of GM and WM**

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/GM\_comparisons/GM\_vs\_WM/check\_GM\_WM\_values.m

This allows us to check how much overlap there is between GM and WM depending upon the threshold we set.

**Table 1**

Binarised ROI masks were in the following locations:

/CAMCAN/full\_run/2nd\_level/conimages/M1\_left\_bin.nii

/CAMCAN/full\_run/2nd\_level/conimages/A1\_bin.nii

/CAMCAN/full\_run/2nd\_level/conimages/V1\_bin.nii

/CAMCAN/full\_run/2nd\_level/conimages/cer\_bin.nii

/CAMCAN/full\_run/2nd\_level/conimages/Fp1\_bin.nii

Binarised F maps were in the following locations:

/CAMCAN/full\_run/2nd\_level\_group/hrfc

/CAMCAN/full\_run/2nd\_level\_group/hrftd

/CAMCAN/full\_run/2nd\_level\_group/fourier

/CAMCAN/full\_run/2nd\_level\_group/fourier\_hrftd

/CAMCAN/full\_run/2nd\_level\_group/hrftd\_fourier

They were called the following with prefixes of ‘h\_’, ‘htd\_’, ‘f\_’, ‘fh\_’, or ‘hf\_’ depending on the model:

m1\_bin.nii

a1\_bin.nii

v1\_bin.nii

cer\_bin.nii

fp1\_bin.nii

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| mHRF | ROI | F\_vol | ROI\_vol | % |
| HRFc | M1 | 6118.875 | 10040 | 60.94 |
|  | A1 | 6969.375 | 7059 | 98.73 |
|  | V1 | 25029 | 32662 | 76.63 |
|  | Cer | 64418.63 | 180343 | 35.72 |
|  | Fp1 | 4357.125 | 28001 | 15.56 |
|  | all | 891594 |  |  |
| HRFtd | M1 | 9470.25 | 10040 | 94.33 |
|  | A1 | 6969.375 | 7059 | 98.73 |
|  | V1 | 25180.88 | 32662 | 77.10 |
|  | Cer | 82042.88 | 180343 | 45.49 |
|  | Fp1 | 5076 | 28001 | 18.13 |
|  | all | 1329993 |  |  |
| Fourier | M1 | 9470.25 | 10040 | 94.33 |
|  | A1 | 6969.375 | 7059 | 98.73 |
|  | V1 | 25180.88 | 32662 | 77.10 |
|  | Cer | 82650.38 | 180343 | 45.83 |
|  | Fp1 | 5089.5 | 28001 | 18.18 |
|  | All | 1324603 |  |  |
| Fourier(H) | M1 | 5862.375 | 10040 | 58.39 |
|  | A1 | 5929.875 | 7059 | 84.00 |
|  | V1 | 18511.88 | 32662 | 56.68 |
|  | Cer | 18461.25 | 180343 | 10.24 |
|  | Fp1 | 283.5 | 28001 | 1.01 |
|  | All | 488473.9 |  |  |
| HRFtd(F) | M1 | 7462.125 | 10040 | 74.32 |
|  | A1 | 6969.375 | 7059 | 98.73 |
|  | V1 | 23331.38 | 32662 | 71.43 |
|  | Cer | 30634.88 | 180343 | 16.99 |
|  | Fp1 | 0 | 28001 | 0.00 |
|  | All | 602734.5 |  |  |

These comparisons worked by volume as they overlapped in MNI space, although the voxels do not match as ROI masks had 1mm voxels (151 x 188 x 154) and F masks had 1.5mm voxels (121 x 145 x 121). Therefore these comparisons only worked in FSLstats, and would not work in Matlab.

**Table 1 cont**

The five relevant scripts are in:

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/gm\_wm\_other

The outputs are with the scripts, containing the list of how many voxels resided within GM, WM or other.

F masks were in:

/CAMCAN/full\_run/2nd\_level\_group /hrfc/h\_all.nii

/CAMCAN/full\_run/2nd\_level\_group /hrftd/htd\_all.nii

/CAMCAN/full\_run/2nd\_level\_group /fourier/f\_all.nii

/CAMCAN/full\_run/2nd\_level\_group /fourier\_hrftd/fh\_all.nii

/CAMCAN/full\_run/2nd\_level\_group /hrftd\_fourier/hf\_all.nii

The GM and WM templates matched the number of voxels in the F masks (121 x 145 x 121) but had smaller voxels (1mm vs 1.5mm). Therefore these could be compared voxel for voxel within matlab, but not volume for volume.

**Table 1 cont**

The binned F masks over the whole brain are located below:

/CAMCAN/full\_run/2nd\_level\_group /hrfc/h\_all\_bin.nii

/CAMCAN/full\_run/2nd\_level\_group /hrftd/htd\_all\_bin.nii

/CAMCAN/full\_run/2nd\_level\_group /fourier/f\_all\_bin.nii

/CAMCAN/full\_run/2nd\_level\_group /fourier\_hrftd/fh\_all\_bin.nii

/CAMCAN/full\_run/2nd\_level\_group /hrftd\_fourier/hf\_all\_bin.nii

F masks were 121 x 145 x 121 (1.5mm)

**SVA/RA (single voxel analysis/regional analysis)**

Here there is an hrfc, hrftd and fourier folder within:

/CAMCAN/full\_run/2nd\_level/conimages/SVA

In each there is a find\_peaks.m script to be run independently, then in the SVA file there is a plot\_functions.m script. Saved as figure1.jpg

The beta values are taken from the alternative 2nd level analysis.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | HRFc | | HRFtd | | Fourier | |
|  | PL | FWHM | PL | FWHM | PL | FWHM |
| M1 | 5.17 | 5.26 | 4.31 | 3.30 | 4.53 | 3.40 |
| A1 | 5.17 | 5.26 | 4.06 | 3.33 | 4.29 | 3.59 |
| V1 | 5.17 | 5.26 | 4.19 | 3.38 | 4.41 | 3.57 |
| Cer | 5.17 | 5.26 | 4.31 | 3.67 | 4.53 | 3.71 |
| pfc | 5.17 | 5.26 | 7.14 | 6.79 | 7.59 | 9.63 |

Next the analysis across ROIs is located in:

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/visualisation/ROIs

The script is called:

a\_plot\_all\_Voxels\_fourier.m

Then run:

Separate\_into\_ROIs.mat producing ROI\_list.mat

This is then saved as ROI\_analysis and ROI\_analysis\_out (outliers removed) within:

Study\_1\_and\_2/Study\_1/SPSS

**Whole GM Analysis**

The following 3 scripts were used to analyse all significant voxels that fell within grey matter, across the 3 mHRFs, everything done at the alternative 2nd level of analysis:

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/a\_plot\_all\_Voxels\_hrfc\_TPM\_v3

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/a\_plot\_all\_Voxels\_hrftd\_TPM\_v3

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/a\_plot\_all\_Voxels\_fourier\_TPM\_v3

The results of these are found in the files:

GM\_fourier\_v6.mat

GM\_HRFtd\_v6.mat

GM\_HRFc\_v6.mat

Figure 2 is then plotted using:

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/GM\_comparisons/plot\_histograms\_GM\_v3.m

Next the flexible models are compared to the canonical, using:

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/GM\_comparisons/compare\_to\_canonical\_NO\_OUTREM\_all\_bimodal.m

This outputs 3 files, c2c\_results\_NO\_REM\_all, c2c\_range\_NO\_REM\_all and saved in the c2c folder, results.

Then we compare the flexible models to one another:

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/GM\_comparisons/ create\_ANOVA\_data\_NO\_OUTREM\_all\_bimodal.m

This outputs multiple files:

GM\_pos\_NOREM\_all: positive only data

GM\_neg\_NOREM\_all: negative only data

Fourier\_NOREM\_all: all fourier data

Hrftd\_NOREM\_all: all HRFtd data

GM\_results\_four\_hrftd\_comparison\_NOREM\_all: initial information about final results

All of this was done using the alternative second level analyses.

We then plot the WMPSR tests Group\_plot\_NOREM\_all\_bimodal.m and save in /CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/GM\_comparisons/create\_ANOVA as all\_differences.jpg

We run general comparisons to canonical plot\_histograms\_GM\_v3

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Htd pl+ | F pl+ | Htd pl- | F pl- | Htd f2+ | F fw+ | Htd fw- | F fw- |
| Z | 260.47 | 260.40 | 171.72 | 171.49 | 259.99 | 259.99 | 171.68 | 171.46 |

**Simulation**

This is located in:

/CAMCAN/full\_run/2nd\_level/conimages/simulation

There are 5 functions to be modelled: HRFc.mat, short\_pos.mat, long\_pos.mat, sublong.mat and short\_fwhm.mat

The first three were created using Create\_data.m, short\_fwhm using Create\_more\_data.m, and sublong using Create\_sublong.m

Also the basis functions are saved here as HFtd.mat and fourier.mat

I then run the tests in:

/CAMCAN/full\_run/2nd\_level/conimages/simulation/lin\_reg

This contains summary\_table\_four.m, summary\_table\_HRFtd.m and summary\_table\_HRFc.m.

I then call all this information for HRFtd and Fourier independently using the scripts, and this creates figure 3 as well as bringing forward all key data under the variable names four\_table.mat and HRFtd\_table.mat.

The actual analyses are saved under:

Study\_1\_and\_2/Study\_1/SPSS

The data in the folder simulation is Fourier\_simulation and HRFtd\_simulation and Fourier\_simulation\_noHanning, with outputs in HRFc\_sim\_out, HRFtd\_sim\_out, fourier\_noHan\_output and fourier\_sim\_output

There is also final check using a run which is based on the actual timing of the study events

The script is called longer\_run.m, and then SPSS files fourier\_full, fourier\_full\_output, hrftd\_full, and hrftd\_full\_output.

**Logistic Regression**

This data is held within:

Study\_1\_and\_2/Study\_1/SPSS

With a script logistic\_regression and output file logistic\_regression\_output

**Appendices**

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/plot\_summed\_functions\_v2.m

Save the output as Appendix\_A.jpg

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/total\_data\_v3.m

This outputs AppendixN\_v3.mat

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/visualisation/cerebellar\_and\_aPFC\_coordinates

The script is called aPFC\_check\_FH.m and the output is total\_pfc\_FH.mat

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/visualisation/cerebellar\_and\_aPFC\_coordinates

The script is called cerebellar\_aPFC\_check.m and the outputs are called appendix.jpg, cerebellum.mat and aPFC.mat

**Peak Latency and FWHM via fourier**

The script is called:

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/visualisation/create\_fourier\_mask.m

This saves two files:

pl.nii and fwhm.nii

**Not included in the paper**

I ran through all coordinates in which the Fourier basis set finds significance and HRFc does not (within grey matter), then plot a random selection:

/CAMCAN/full\_run/2nd\_level/conimages/all\_voxels/version\_3/visualisation/fourier\_only.m

Output of the raw file saved as:

Total.mat

**Results for study 2**

This script found all the voxels which were significant across all age groups. Did not have to be in GM

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/parameter\_analysis\_accAGE3.m

The output files end with accAGE and are saved in:

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/check

I then create Figure 1 using:

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/create\_data\_GM.m

This script also totals the peak latency and FWHM data for Figure 4 a and b, with and without outliers:

data\_GM.mat

data\_GM\_plOUT.mat

data\_GM\_fwOUT.mat

I then run a separate script for the undershoot (Figure 4c), as this may have had some zero values (where an undershoot could not be found):

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/create\_data\_GM\_undershoot.m

This outputs:

data\_GM\_US.mat

data\_GM\_usOUT2.mat

**Age x NBR**

First level coordinates were checked to establish the prevalence of NBRs in each age group

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/1st\_level/investigate\_just\_age3.m

This outputted:

Age\_data\_all.mat

Age\_correlations\_all.mat

**Undershoot investigation**

The canonical function percentage beta weighting was calculated using the following script on lines 706-723:

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/create\_data\_GM\_undershoot.m

This is seen in the output file data\_GM\_US.mat in columns 25-27 (original betas are in 22-24). The percentage beta values are reassigned their positive or negative weighting once the percentage is calculated, but this does not affect the canonical as all values were positive.

The distributions of beta weightings can be found:

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/plot\_beta\_age\_comparison.m

**Number of Voxels**

The number of voxels within GM were investigated for each age group, within each model. The script is found in:

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/number\_of\_voxel/number\_of\_voxel\_masks.m

Outputs are in .mat and .nii formats, one for each age, within each model. These could then be analysed via fslstats.

**Visualisations**

Run using:

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/visualisation/visualisation.m

This calculated the voxels that showed significance within grey matter, across age groups. The file is saved as image.nii and is modified in SPM to align with the MNI brain.

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/visualisation/visualisation\_agediff.m

This calculated the mean peak latency and FWHM of the 3 oldest age groups, and 3 youngest, for the GM coordinates. It then subtracts young from old to make a difference mask, outputting peak\_lat.nii and fwhm.nii

/CAMCAN/full\_run/2nd\_level/conimages/age\_effects/parameter\_analysis/GM/visualisation/visualisation\_agediff\_US.m

This does the same for the undershoot coordinates, outputting undershoot.nii

**For the graphs and analysis in SPSS**

Study\_1\_and\_2/Study\_2/SPSS

This location houses the data for can\_weight, PL\_FW\_wholedata, US\_wholedata and an outlier version for each.

Study\_1\_and\_2/Study\_2/SPSS/extra

This location houses matlab files and the outputs, as well as the data in an excel spreadsheet

**L:/archive/matthew\_danvers/camCAN/raw\_data**

This folder contains all the pre-processed data for:

epi\_smt: EPI scans within this folder, broken down into four batches of participants

Anat.tar.gz: anatomical scans

Fmap\_smt.tar.gz: field maps