**Distorting anatomy to test MEG models and metrics**

README file for spm\_distort code on github.

1. **Download the data from figshare.com**

<https://doi.org/10.6084/m9.figshare.28675724>

Make directory rootdir

(in my case

rootdir='C:\Users\gbarnes\Documents\jimmytest\')

Unzip the data.zip from figshare.com into

rootdir (not rootdir\data)

There should be 3 subdirectories (‘mri’, ‘surf’, ‘meg’) in ‘data’ now. Need to unzip the files in the surf directory.

Format of directory structure should be :

rootdir \ data \ surf \ s01-synth

rootdir \ data \ mri \ s01

rootdir \ data \ meg \ s01

rootdir \ data \ surf \ s02-synth

rootdir \ data \ mri \ s02

rootdir \ data \ meg \ s02

etc

1. **Make sure you have an up to date version of SPM (code released March 2025).**
2. **Start matlab ( ideally later than version code developed in 9.11.0.1769968 (R2021b))**
3. **Edit** spm\_distort\_mesh\_example.m

**Edit lines 10-12 to put in your specific paths:**

addpath('D:\spm'); %% spm directory

addpath('D:\spm\_distort'); %% directory with distort code from github

rootdir='C:\Users\gbarnes\Documents\jimmyupload\'; %% where the downloaded data sits (as in point 1 above)

1. Run **spm\_distort\_mesh\_example**

The code takes a long time to run ~ 24 hours on typical PC. As it goes through a trajectory of 17 points and 8 random seeds. Can shorten this if you just set RandomSeeds=[3]. This is a trajectory that looks similar to the average. Can also take fewer points on trajectory.

Running with cross-validation will take longer still. But once surfaces are made, and lead-fields constructed it does have to be done again.

The output should look like this:

