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

GRB. March 2025

README file for spm\_distort code on github (<https://github.com/barnesgr123/spm_distort/>).

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

<https://figshare.com/s/e3ff829753a76bcfda22>

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 directory ‘data’ now.

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 (currently (March 2025) in the development version of SPM). Note the ‘release’ version of SPM will not be updated until 2026.**

**This is the current development version of SPM :**

<https://github.com/spm/spm>

And should be in release version of SPM from March 2026 onwards.

1. **Start matlab**
2. **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\jimmytest\'; %% 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 not have to be done again.

The output should look like this:

