

Dynamic Causal Modelling for Resting State fMRI

Guide to practical demonstration

stemX, IBA

Adeel Razi

(Adapted from Chapter 38, SPM12 Manual written by Adeel Razi)

Data used for this example can be downloaded from (<https://drive.google.com/drive/folders/12E-V8QQ0nop1iiSgJj-3h8-662YH2WDV>). This data consist of a few exemplar subjects from the full dataset available from ABIDE database (<http://preprocessed-connectomes-project.org/abide/>) to interrogate the information integration in *default mode network*. (DMN) – a distinct brain system that is activated when an individual engages in introspection like mindwandering or daydreaming. The DMN comprises part of the medial prefrontal cortex (mPFC), posterior cingulate cortex (PCC) and parts of inferior parietal lobe and superior frontal regions.

The archive contains the smoothed, spatially normalised, realigned, slice-time corrected images in the directory `func'. The directory `struc' contains a spatially normalised T1 structural image. For detailed preprocessing steps, please refer to the above ABIDE webpage.

Defining the GLM

First, we need to set up the GLM analysis and extract our time series from our regions of interest (ROIs). For resting state fMRI because there is no task so first we need to generate SPM.mat so that we can extract the time series. This can be done by following the steps below.

Let's specify a batch that will specify the GLM and estimate it.

1. The exemplar subject we used is a healthy control, subject ID: 0051057. The directory you have downloaded should include:

- (a) A directory named 'func', which includes the preprocessed fMRI volumes (176 *.nii files).
- (b) A directory named 'struc', which includes a normalised T1 structural volume
2. A directory named 'glm',
3. In Matlab type

```
>> cd glm
```

```
>> spm fmri
```

4. From the main SPM window, click on the Batch button.
5. From the SPM menu at the top of the Batch Editor, select "Stats > fMRI model specification".
6. Click Directory and choose the GLM directory that you made above.

7. Units for design [scans]
8. Interscan interval [2]
9. Click Data & Design, Choose New "Subject/Session"
10. Click Scans and choose all the functional scans xxxx.nii. There should be 176 *.nii files.
11. Set the 'Masking Threshold' to a small number ('-inf') instead of 0.8.
11. From the SPM menu at the top of the Batch Editor, select "Stats > model estimation".
12. For Select SPM.mat, click on the Dependency button and choose the proposed item (the output from the previous module).
13. You should now be able to press the Run green arrow at the top of the Batch Editor window. This will specify and estimate the GLM.

Extracting the time Series:

Once you have specified and estimated the GLM, here is now a step-by-step example for extracting the PCC time series:

1. From the main SPM window, click on the Batch button.
2. From the SPM menu at the top of the Batch Editor, select "Util > Volume of interest"
3. Select the SPM.mat file (generated during the previous section).
4. Adjust data: NaN
5. Which session: 1
6. Name of VOI: PCC
7. Select 'Region(s) of Interest' > Sphere
8. Centre: [0 -52 26]
9. VOI radius(mm): e.g. 8 mm
10. Select 'Movement of Centre' > Fixed
11. Select 'Region(s) of Interest' > Mask Image
12. Image file: select mask.nii (in glm folder)
- 13: Expression: i1 & i2
- 14: Now you should be able to press the green arrow button. This would extract the PCC time series and save this as VOI_PCC_1.mat in the working directory.

SPM now computes the first principal component of the time series from all voxels included in the sphere. The result is stored (together with the original time series) in a file named VOI_PCC_1.mat in the working directory (the "1" refers to session 1). Do the same for the rest

of the VOIs: mPFC ([3 54 -2]), LIPC ([-50 -63 32]) and RIPC ([48 -69 35]). The DCM graph is shown in Figure 1.

Specify and Estimate the DCM:

1. Press the large Dynamic Causal Modelling button.
2. Choose specify.
3. Select the SPM.mat file you just created when specifying the GLM.
4. Name for DCM_???.mat: e.g. DMN.
5. Select all VOIs in order VOI_PCC_1, VOI_mPFC_1, VOI_LIPC_1 and VOI_RIPC_1
6. Specify slice timings for each area. The default values are set to the last slice of the data, which was the default in the original DCM version. For sequential (as opposed to interleaved) data, this modelling option allows to use DCM in combination with any TR (slice timing differences). Here, we proceed with the default values.
7. Enter 0.04 for “Echo Time, TE[s]”.
8. Define the fully connected model. Your connectivity matrix should look like the one in **Fig. 2.**

A polite “Thank you” completes the model specification process. A file called DCM_DMN.mat will have been generated.

You can now estimate the model parameters, either by pressing the DCM button again and choosing estimate (cross spectra), or by typing

```
>> spm_dcm_fmri_csd('DCM_DMN');
```

from the Matlab command line.

Once this is completed, you can review the results as follows:

1. Press the DCM button.
2. Choose review.
3. Select DCM_DMN

By clicking “review...” you can now select from multiple options, e.g. you can revisit the fit of the model (“Cross-spectra (BOLD)”), shown in **Fig 3** or look at the parameter estimates for the endogenous coupling (“Coupling (A)”) as shown in **Fig 4**.

Of course, you can also explore the model results at the level of the Matlab command line by loading the model and inspecting the parameter estimates directly. These can be found in DCM.Ep.A (endogenous coupling), DCM.Ep.a (neuronal parameters).

Figure 1

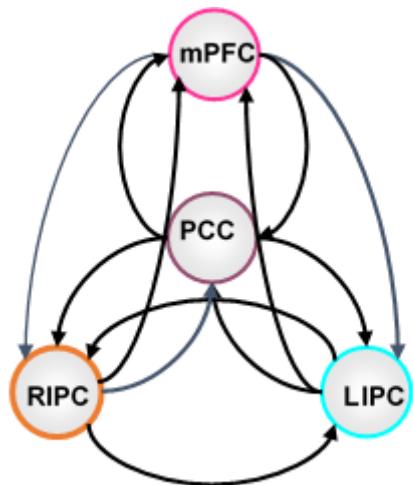


Figure 2

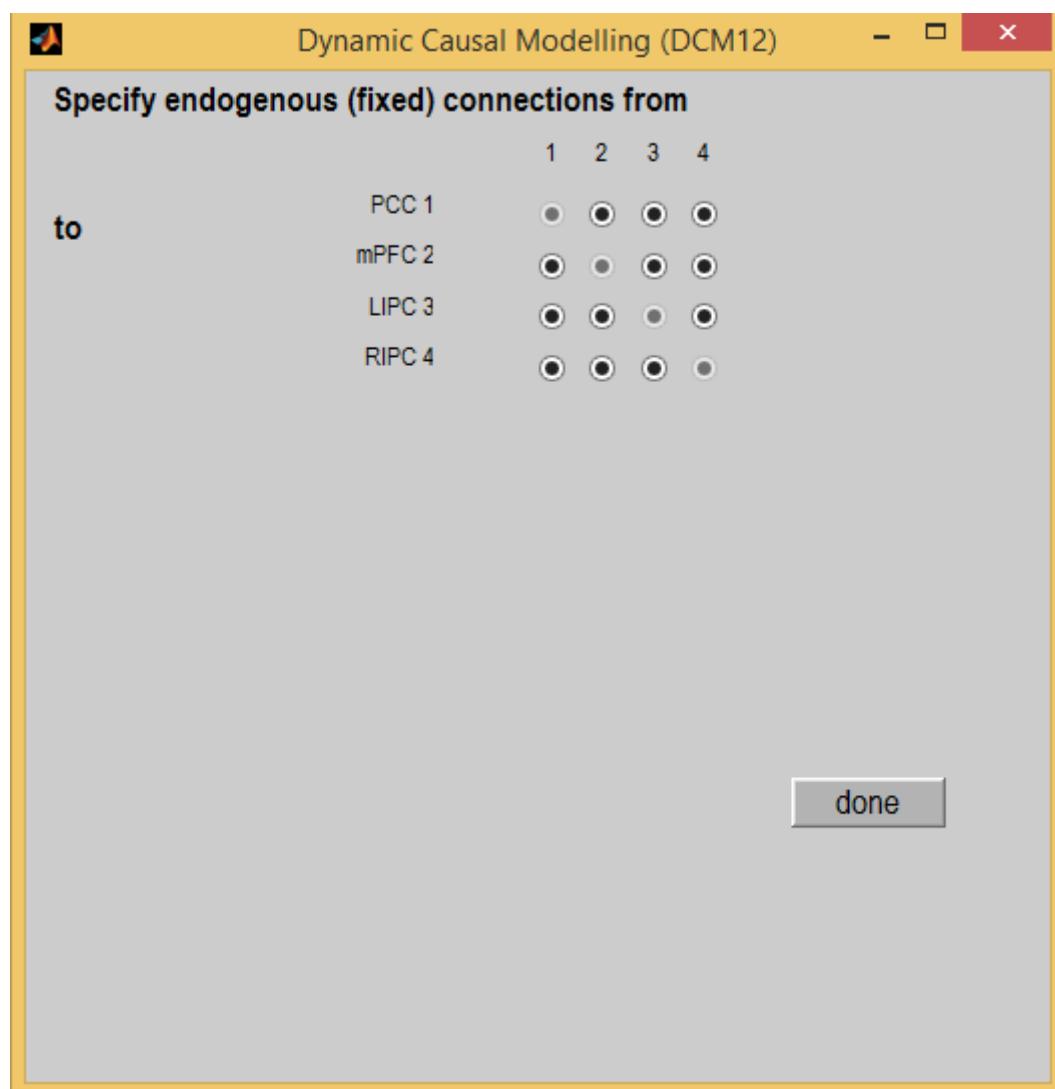


Figure 3

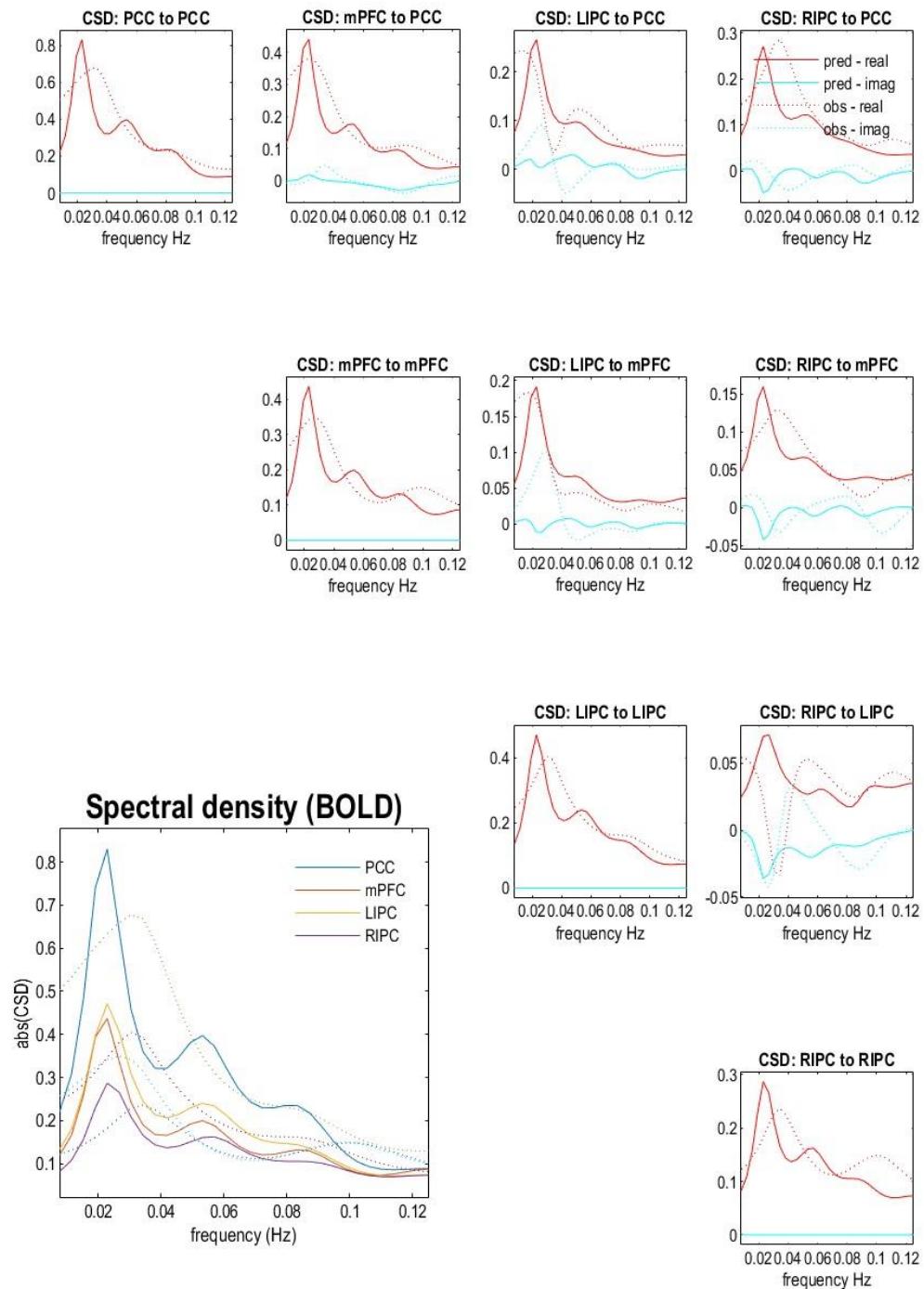


Figure 4

