

PPI in FSL

NITP Summer Course 2014

The difference-based PPI model is ok but is not ideal. It is tricky to interpret and requires careful attention to the regressor (centering). A more powerful approach – and more generalizable approach – was first proposed by Jeanette Mumford (SPM listserv/Friston personal communication), and more formally was covered by McLaren et al. (Neuroimage, 61(4):1277-86; doi: 10.1016/j.neuroimage.2012.03.068). To set up the generalized model here we will set up the PPI model one more time, but modeling separately each contributing condition and their interaction with the seed.

MODEL SETUP

We're working with similar data as previously but setting up a different model.

Go into ppi_a_vs_na_gPPI.feats and open the design.fsf file: **Feat design.fsf &**

The design has been set up for you but you're welcome to set it up following along.

- 1) Input 4D data is as previously: snff_convert.nii.gz file in outputs/
- 2) Output directory is your choice and all other parameters in the Data tab should be as before
- 3) Don't change Misc or Pre-Stats, or Post-stats or Registration
- 4) Go into Stats and open the model (click on **Full Model Setup**)
- 5) Increase #of original EVs to 5:
 - a. EV1 = "a" – this is a 1-column input (select "ev_a.txt" from /outputs/); keep temporal derivative and temporal filtering and double-gamma => this is just the "a" regressor
 - b. EV2 = "na" – this is a 1-column input (select "ev_na.txt" from /outputs/); same settings as for EV1
 - c. EV3 = "seed or phys" – this is the seed time series (select "seed_ts.txt" from /outputs/ as previously); no derivative here needed, but do apply filtering (no convolution)
 - d. EV4 = "PPIa" – this is the interaction b/w regressor "a" (EV1) and the seed (EV3); choose MIN centering for EV1 and MEAN centering for EV3; no additional processing
 - e. EV5 = "PPIna" – this is the interaction b/w regressor "na" (EV2) and the seed (EV3); choose MIN for EV2 and MEAN for EV3 as above
- 6) Now let's adjust contrasts; click on contrasts & f-tests:
 - a. Set up a total of 5 contrasts for: "a", "na", "seed", "PPIa", "PPIna" (place a 1 in the appropriate EV column)
 - b. Set up two more contrasts for PPIa-na (1 for PPIa, -1 for PPIna), and then PPIna-a (1 for PPIna, -1 PPIa)
 - c. Hint: final contrast matrix looks as follows:
 - i. [1 0 0 0 0]
 - ii. [0 1 0 0 0]
 - iii. [0 0 1 0 0]
 - iv. [0 0 0 1 0]
 - v. [0 0 0 1 -1]
 - vi. [0 0 0 -1 1]
- 7) View the design. Notice the different set up.
- 8) Normally you'd now say "go" but the results here have been run already. Note that the interaction terms are now in zstats 6 and 7 (for +/- comparisons).

PPI results

1) The results are in: ppi_a_vs_na_gPPI.feats

Look at the results in fslview. Open fslview: **fslview &**

Now open:

/ppi_a_vs_na_gPPI.feats/example_func.nii.gz - as background

/ppi_a_vs_na_gPPI.feats/stats/zstat6.nii.gz - as first overlay (PPIa-na - correlation in a > na)

/ppi_a_vs_na_gPPI.feats/stats/zstat7.nii.gz - as second overlay (PPIna-a - correlation in na > a)

you will also want to add the previous PPI result as a third overlay:

/ppi_a_vs_na.feats/stats/zstat3.nii.gz => old model

Notice if the same location (xyz: 17 11 17) shows a PPI effect in the new results. What is the zstat value? Do you see anything new/different relative to the other model (zstat3 above).

2) Take a look at zstat5 (PPIna) and zstat4 (PPIa) as well - these are the interactions between condition and the seed time course and should show you the correlations of the seed with other brain regions separately during each task. ***Do these make sense with respect to the interaction results? Is the correlation between the V1 seed and the MT stronger in the attend condition than in the non-attend condition?***