

## PPI Instructions

### 1) **SELECT VOIS from original single subject data (SPM.mat)**

1. Go to ROI, Rt mouse click to get Local Max
2. Press VOI
3. Name the region [reg]
4. Adjust data for [effects of interest]
5. VOI definition [sphere]
6. VOI radius(mm) [\*\*]

This saves the relevant info in VOI\_reg\_1.mat in the working directory

### **PPI analysis, say we're interested in contrast A-B**

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#### 1) **Create PPI structure**

1. Press PPI, select the **previous** SPM.mat file
2. Analysis type ? [PsychoPhysiologic interaction]
3. Select VOI\_reg\_1.mat
4. Include Cond1 [No], Cond2 [No] ...
5. Include CondB [Yes], contrast weight [-1]
6. Include ConDA [Yes], contrast weight [1]
7. Name of PPI [Regx(A-B)]

This creates the file PPI\_regx(A-B).mat. It contains the variable PPI.ppi which you can use a user-defined regressor in a new analysis

#### 2) **Create a new directory**

1. Copy over PPI\_regx(A-B).mat
2. At the matlab prompt load in your PPI\*.mat info  
>> load PPI\_regx(A-B)
3. Press the 'fMRI' button
4. Specify [design]
5. ISI[secs] = []
6. scans per session []
7. Specify design in [scans]
8. Select basis set [hrf]
10. model interactions (Volterra) [No]...
11. **Number of conditions** [0]
12. **User specified** [3]
13. **regressor 1** [PPI.ppi]
14. **regressor 2** [PPI.P]
15. **regressor 2** [PPI.Y]
16. name of [interaction]
26. name of [A-B]
27. name of [reg]

Now

1. Press 'fMRI'
2. Specify [data]
3. Select the **newly created SPM.mat**

4. Assign the scans from the 'functional' directory
5. Remove global effects [none]
6. High-pass filter [specify]
7. Cut-off period(secs) [128]
8. Correct for serial correlations [AR(1)]

SPM will now update your SPM.mat file.

We can now estimate the model by pressing the 'ESTIMATE' button. Then select the SPM.mat file that has just been updated.

SPM will now compute the hyperparameters and parameters and update the SPM.mat file once again.

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To interrogate the results press 'RESULTS'.

1. Select the SPM.mat file
2. **Create and select a [1 0 0 0] t-contrast**
3. Mask with other contrasts [No]
4. Title for comparison [**interaction**]
5. p value adjustment to control [none]
6. p value [0.01]

The resulting SPM shows areas showing differential connectivity to REG due to the ConDA vs. CondB conditions.

### PPI DATA STRUCTURE:

```
function PPI = spm_peb_ppi(SPM)
% Bold deconvolution to create physio- or psycho-physiologic
interactions
% FORMAT PPI = spm_peb_ppi(SPM);
%
% SPM      - Structure containing generic details about the analysis
%
% PPI.ppi   = (PSY*xn or xn1*xn2) convolved with the HRF
% PPI.Y     = Original BOLD eigenvariate. Use as covariate of no
interest.
% PPI.P     = PSY convolved with HRF for psychophysiological
interactions,
%           or in the case of physiophysiological interactions contains
%           the eigenvariate of the second region.
% PPI.name  = Name of PPI
% PPI.xY    = Original VOI information
% PPI.xn    = Deconvolved neural signal(s)
% PPI.U.u   = Psychological variable or input function (PPIs only)
% PPI.U.w   = Contrast weights for psychological variable (PPIs only)
% PPI.U.name = Names of psychological conditions (PPIs only)
```