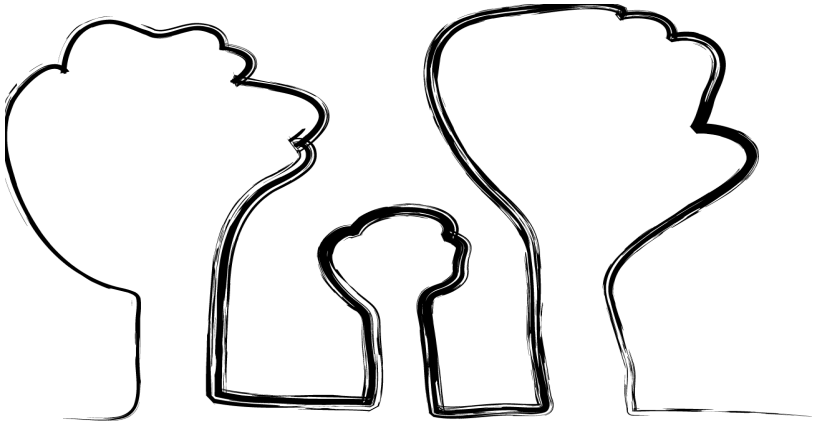
After what Tong has said and before what Fei is going to say…



HOW TO RUN PPI IN FSL?

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http://www.fmrib.ox.ac.uk/Members/joreilly/how-to-run-a-ppi-analysis-in-feat

Helder Filipe, Jul 7, 2011

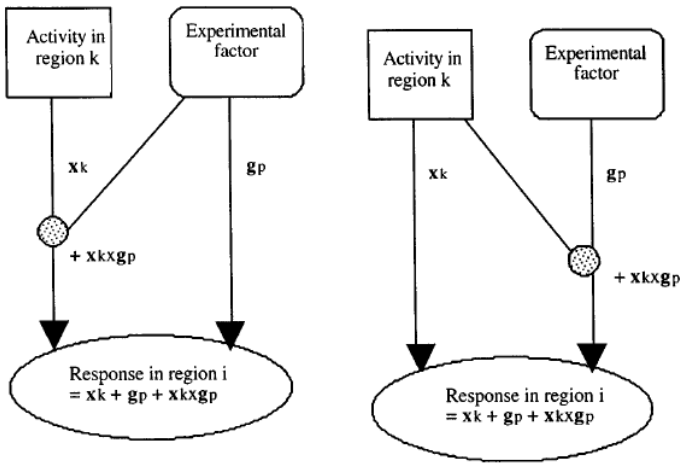
PPI measures how the contribution of one area to another changes according the experimental context

We regress the activity of REGION A on the activity of REGION B to explore the influence that the REGION B exerts over the REGION A.

The changes in this influence according to the context: a psychological interaction.

Friston et al., 1997
http://www.ncbi.nlm.nih.gov/pubmed/9344826

Two possible mechanisms: (i) a context chagce in the contribution of one area to another; or (ii) a modulation of responses in one area to the experimental task by a another area.



Friston et al., 1997

- Choose an ROI
- Extract the timecourse for that ROI
- Choose the contrast
- Run the analysis in FEAT, using filtered_func data. Do not run preprocessing.
- Set up the design
  - Basic design and contrasts
  - Group analysis

First, you need to choose your ROI

- ANATOMICAL
- FUNCTIONAL (GLM)
- MELODIC-DERIVED

You can draw your ROI

- **Anatomical region of interest**

Your options are:

- Draw a mask on individuals' structural scans with Fslview
- Draw a mask on the standard brain and transforming it into individual space using FLIRT or FNIRT
- Use an automated segmentation tool eg FIRST.

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You can use a functional ROI (1)

- On your group Feat results/ MELODIC component, draw a region of interest over the blob you are interested in.
  - Transform this into the functional space of each individual using FLIRT or FNIRT.
  - Check, for each individual, that your ROI is a sensible size and is contained within the brain and within the anatomical region of interest (if your ROI is near the surface and ends up lapping over the edge of the brain in some subjects, your timecourse data will be very noisy, so you really do need to check).

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You can use a functional ROI (2)

- OR, Go to each individual subject's Feat results and pick the peak voxel in the region of interest. Draw a small mask surrounding this peak voxel. This may be a more successful strategy when the functional regions are anatomically heterogeneous but functionally well defined, e.g. in the parietal cortex.

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Size matters.

- If you are defining ROIs individually (as in the second functional-ROI case, or some of the anatomical cases) you analysis will likely work better (have higher signal-to-noise) if you **keep the ROI small**.
  - This is because you are only taking one measurement from the whole ROI – so by enlarging the ROI to include voxels with a weaker effect you are actually 'watering down' the signal.
- On the other hand, if you are using a standard-space mask (as in the first functional-ROI strategy), you will want to make sure your ROI is **large enough to capture the individual activation peak** for each subject, despite inter-individual variations.

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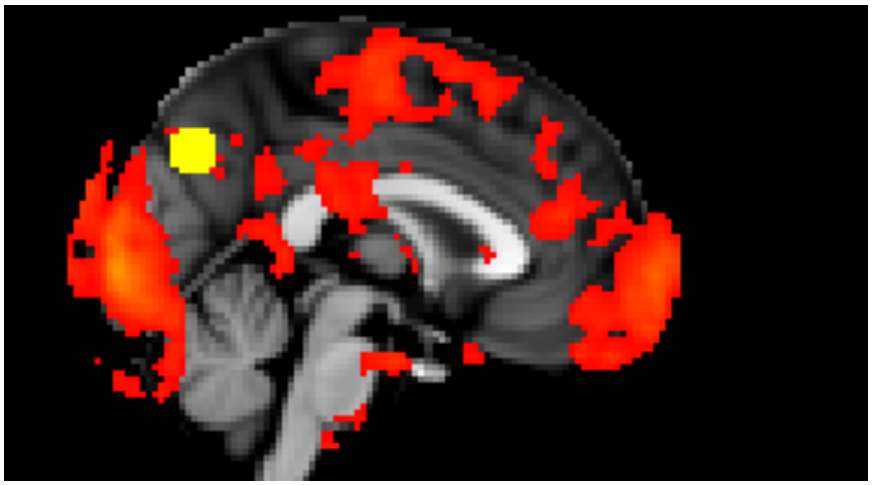
Eg. Posteromedial cortex maximum of MELODIC component (resting state) 17 subjects



Second, extract the time-course of the seed ROI

- Do this for each subject separately, using the fslmeants command.
- You should use **the filtered func data** from your initial analysis to extract the timecourse from - not the raw data as this will be noisy.
- **fslmeants -i filtered_func.nii.gz -o my_timecourse.txt -m your_roi_mask.nii.gz**

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The output is a column vector giving a value of raw signal at each time-point; there is one time-point per volume. The time-course is saved under a filename specified by you, for use later on.

```
10032.2
10021.1
9984.16
9950.34
9906.98
9931.94
9946.38
9922.89
9982.85
10000.8
9945.41
9983.45
10039.5
10029.3
9972.36
9961.7
9979.95
9892.44
9841.77
```

Third, you need to choose your task contrast

- PPI will look for voxels with increased connectivity to the SEED REGION in one condition to another.
- Ideally, you should include all the task variables (EVs) you included in your GLM model, even those which are not involved in generating your PPI regressor.

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Example of task contrasts

TWO CONDITIONS: TRAITS versus GENERAL INFORMATION

SELF1_1_run1_TRAITminusGENERAL_ppi.txt

3.029064	24.121818	-1
56.034139	24.119105	-1
104.037257	24.118459	1
152.040961	24.116960	1
200.042345	24.118011	1
248.043747	24.119175	-1
296.045015	24.120322	-1
344.046166	24.121277	1
392.047462	24.123035	1
440.048872	24.124032	1
488.050335	24.124842	-1
536.051493	24.109912	-1

Third, set up the design

3. Set up your Feat design

Go into Feat and load your data and set up your pre-processing as normal

If you are using the filtered_func from your GLM analysis as input, remember not to re-do any pre-processing steps such as BET, deleting volumes, or filtering.

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In the stats tab

You will need the following regressors:

EV1 is your psychological regressor (PSY). This will simply be your task regressor, convolved with an HRF;

EV2 is your physiological regressor (PHYS). This will be the time-course of your seed ROI:

- Basic shape is 'custom (1 entry per volume)' and the input file is the time-course from the seed region, which you generated earlier with fslmeants.
- Set **convolution** to **none** because this is BOLD data and has already been convolved by the brain!
- Switch off **temporal derivative** and **temporal filtering** groups at the second level as normal.

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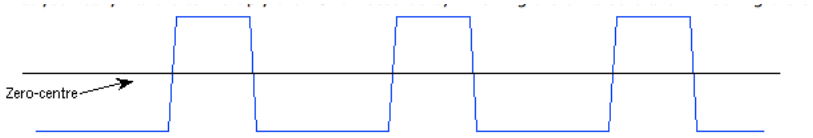
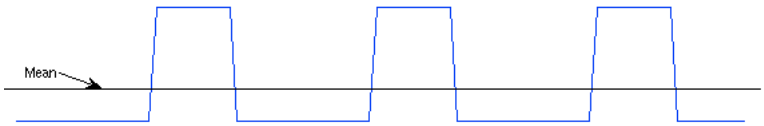
EV3 is PPI, which you generate here in the Feat GUI;

- **Basic shape** is 'interaction'
- **Between EVs**: select EV1 and EV2
- **Make zero -** these drop down boxes give you the choice of Min, Centre and Mean. You should choose

centre for your task (PSY) EV, Zero centering sets zero to be halfway between the highest and lowest points of the regressor.



mean for your ROI timecourse (PHYS) EV. This option literally subtracts the mean from the regressor.



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- **Orthogonalise**: You should probably not do this.
- Switch off **temporal derivative** and **temporal filtering**
- **Other task regressors**

As well as the three EVs described here, you should include all the task EVs you included in your original model.

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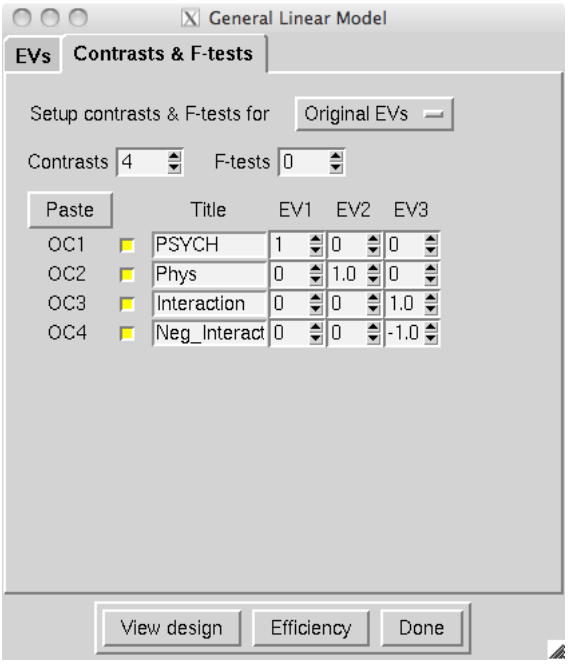
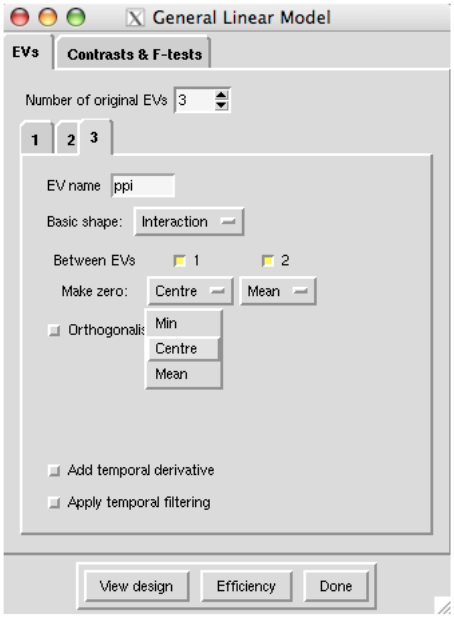
Set up the contrasts





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To run a group analysis

- You can then compare between groups at the second level as normal.

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- EXAMPLE
- file:///Users/helderaraujo/Documents/self_1/PPI/subject1/run1/trait_general_ic13_pmc.feat/report_poststats.html
- file:///Users/helderaraujo/Documents/self_1/PPI/subject1/trait_general_ic13_pmc.gfeat/cope3.feat/report.html

Full Tutorial

- http://www.fmrib.ox.ac.uk/Members/joreilly/what-is-ppi
- http://www.fmrib.ox.ac.uk/Members/joreilly/how-to-run-a-ppi-analysis-in-feat
- http://www.fmrib.ox.ac.uk/Members/joreilly/the-zero-ing-options-in-ppi