MethodsCore
PPI Script Documentation
5/8/2013

Table of Contents

Introduction

        The following documentation explains how to use MethodsCore scripts to perform Psychophysiologic (PPI) analysis with SPM8. The batch system consists of three files: a central Matlab script and two user specified files. PPI_mc_central.m is the central Matlab script where the batch job is built for SPM8 and is referred as the central file. It should NEVER be edited. PPI_mc_template.m is a template M-file and will be referred as the template file. The variable values within the template file can be edited by the user. These options are used in the central file to help build the batch job for SPM8. FirstLevel_mc_PPI.m is a sample template file for building first level PPI models after you've used PPI_mc_template to create the regressors. You should edit this sample file to match your experiment. Explanation of the user specified files for the MethodsCore second level batch is split into <u>basic</u> and <u>advanced</u>. The basic section describes the required options to fill in the three user specified files. The advanced section describes in further detail optional parameters and how they affect the batch system. If you have any questions about how to use these scripts please contact MethodsCoreHelp@umich.edu.

Visual Tutorials
There are a series of video tutorials available online. They demonstrate how to set up a number of common designs using these scripts.

```
1 Introduction              http://youtu.be/2mMAVMteVDc?hd=1
2 PPI Overview              http://youtu.be/Szta0NZEskY?hd=1
3 Creating Regressors       http://youtu.be/RZgTeR4H6G8?hd=1
4 Running PPI Models        http://youtu.be/HWcrRQTq99A?hd=1
```

Basic

PPI_mc_template.m

PPI_mc_template is a template script that will allow you to quickly and easily set up VOI extraction and PPI regressor generation for a list of subjects. Some of the variables in the script are the same as used in the Methods Core FirstLevel script, and will only be briefly discussed here. Below is an overview of the basic options from the template script.

```matlab
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% The folder that contains your subject folders
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
Exp = '/data/testdata/PPI/';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Path where your logfiles will be stored
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
LogTemplate = '[Exp]/Logs';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% The list of subjects to process
%%% The format is 'subjectfolder',subject number in masterfile,[runs to
include]
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
SubjDir = {
     'subject01',1,[1 2];
     'subject02',2,[2];
     'subject03',3,[1 2];

};

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% A list of run folders where the script can find the images to use
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
RunDir = {
     'run_01/';
     'run_02/';
};

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%  Path where your images are located
%%%
%%%  Variables you can use in your template are:
%%%      Exp       = path to your experiment directory
%%%      iSubject  = index for subject
%%%      Subject   = name of subject from SubjDir
%%%      Run       = name of run from RunDir
%%%       *        = wildcard (can only be placed in final part of template)
%%% Examples:
%%% ImageTemplate = '[Exp]/Subjects/[Subject]/func/run_0[iRun]/';
%%% ImageTemplate = '[Exp]/Subjects/[Subject]/TASK/func/[Run]/'
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ImageTemplate = '[Exp]/Subjects/[Subject]/func/[Run]/';
```

```matlab
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% List of conditions in your model
%%% NOTE: These names MUST match the condition names used in your original
%%% first level model.  In the event of missing conditions, the script will
%%% attempt to determine which conditions are present in each subjects
%%% model based on condition name.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ConditionName = {
    'cond1';
    'cond2';
    'cond3';
};

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Path where the original First Level model resides.  This model will be
%%% used to extract the VOI data to calculate the PPI regressors.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ModelTemplate = '[Exp]/FirstLevel/[Subject]/MV/SPM.mat';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% ContrastNum is the index of the contrast you're using to identify
%%% your active voxels.  If you're planning on extracting from all voxels
%%% in your ROI (unthresholded), then this number can be any valid contrast
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ContrastNum = 1;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% ContrastThresh is the p-value threshold to use on ContrastNum to
%%% identify super-threshold voxels for the extraction.  If you'd like to
%%% include all voxels in your ROI (unthresholded) this should be set to 1
%%% Similarly, ContrastExtent is a minimum cluster size extent threshold.
%%% When extracting unthresholded data, this should be 0.
%%% ContrastCorrection sets the correction level of the contrast threshold.
%%% Allowed values are 'none' and 'FWE'.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ContrastThresh = 1;
ContrastExtent = 0;
ContrastCorrection = 'none';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% PPIType is the type of the analysis to perform. Valid settings are:
%%%   'standard'   this is a standard SPM PPI (contrast of conditions)
%%%   'gPPI'              this is a generalized PPI (each condition separate)
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
PPIType = 'standard';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% ROIs is a list of different ROIs that you would like to extract from
%%% and create PPI regressors.  Each one will be saved in a different
%%% CSV file in OutputTemplate based on the first field below. The second
%%% field is either the path to an ROI image file (for images) or coordinates
%%% of the center of your ROI (for sphere or cluster). The next field is
%%% blank for images or clusters, but should be the radius of your ROI for
%%% spheres.
%%% The final field defines your contrast of conditions (in standard mode)
%%% by using values of 0, 1, and -1.  In gPPI mode, this field should
%%% contain only 0s and 1s and determines which conditions to include.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ROIs = {
    'vmPFC',[8 42 -12],[5],[1 0 -1];
};
```

Exp: Your main experiment directory.

LogTemplate: A folder to hold the information logs and archived script copies.

SubjDir: Identical to the SubjDir variable in the FirstLevel_mc_template script (and others). This variable holds the subject folder, subject number, and which runs to include.

RunDir: Identical to the RunDir variable in the FirstLevel_mc_template script. This holds the list of folder names for the runs in your experiment.

ImageTemplate: Identical to the ImageTemplate variable in the FirstLevel_mc_template script. This is the path to your functional image data. This is where the PPI regressor CSV files will be written out.

ConditionName: This holds a list of the conditions of interest in your model.
> **NOTE: These conditions names must match the condition names used in your original model.**

ModelTemplate: The path to your original first level model. This is the model the script will use to extract VOI data to calculate the PPI regressors.

ContrastNum: The contrast number to use to threshold the results for VOI extraction. If you'd like to extract unthresholded data (i.e. all voxels in your VOI regardless of significance), set this to any valid contrast and set the ContrastThresh to 1.

ContrastThesh: The P-value threshold to use for VOI extraction. To extract unthresholded data, set this to 1.
ContrastExtent: The extent threshold to use for VOI extraction. To extract unthresholded data, set this to 0.
ContrastCorrection: The correction method for ContrastThresh (either 'none' or 'FWE'). To extract unthresholded data set this to 'none'.

PPIType: This sets the type of PPI analysis that you'd like to perform. It can either be 'standard' or 'gPPI'. A standard PPI analysis is the type of analysis that SPM is built to perform normally where you specify a contrast of conditions and use that to build your PPI regressor. A gPPI model is a Generalized PPI (McLaren, et. al. 2012, "A generalized form of context-dependent psychophysiological interactions") where each task condition has its own PPI regressor and effects are investigated by contrasting these different regressor columns. For more information on how the models differ and how their regressors are constructed, refer to the second video tutorial above.

ROIs: This is a cell array that specifies the different ROIs that you are going to use to create PPI regressors. Each line is a single ROI, so if you are planning on conducting multiple PPI analyses, you can enter more than one ROI here to loop over them for your subjects. The first value is a string with a descriptive name for the ROI. This will be the name of the CSV file output containing your PPI regressors. The second element is either a string path to a mask image for your ROI, or a 3 element vector with the MNI coordinates for the center of a sphere. The next element is the radius of the sphere (or blank [] for an image). The final element is the PPI weights vector. There should be as many values here as you have conditions in your model. If you are performing a standard PPI, there should be 0s, 1s, and -1s here to define the contrast of conditions that you're interested in. If you are performing a generalized PPI there should only be 0s and 1s indicating the conditions that you want to create separate PPI regressors for.

After running this script, each subject will have a CSV file for each of your ROIs in each run folder from RunDir. The contents of this CSV file will depend on whether you were running a standard or generalized PPI. In a standard PPI, these files will always have 3 columns. The first column is the seed ROI timecourse. The second column is the psychological regressor for your contrast of conditions of interest, and the final column is the interaction regressor.

For a generalized PPI, the number of columns will be twice the number of conditions plus one. Again the first column is your seed ROI. Then each pair of columns after that is the psychological regressor and interaction for one of the conditions from your model. If you had any 0 weighted conditions in your PPI weight vector for an ROI, that condition will be skipped and will not have a psychological regressor or interaction present in the CSV file. If a given psychological condition is absent during a run for some subject, there will be a column of 0's present for both the psychological regressor and interaction regressor in the CSV file for that run. This is to allow the FirstLevel script to know when conditions have been skipped so that it can properly replicate and scale your PPI contrast vectors in the next step.

FirstLevel_mc_PPI.m

This script is just a copy of the FirstLevel_mc_template.m script from the Methods Core FirstLevel folder, but it has had a few small changes performed to make it ready for PPI analyses. The ConditionName variable has been left blank. This is because for our first level PPIs we won't include any conditions, we will only include user-specified regressors. Consequently, most of the variables dealing with the MasterData file and conditions do not need to change. These include SubjColumn, RunColumn, CondColumn, TimColumn, DurColumn, and ParList. The exception is that MasterTemplate still needs to point to a valid MasterData file – but you can just point it to the original version used from your original first level analysis.

You will need to add a pointer to your CSV files containing your PPI regressors in RegFileTemplates. This is done by adding a line to RegFileTemplates that includes a string path template as the first element, and a number as the second. The number is the number of columns that you want to use from the regressor file. To automatically use all columns, you can just set

this to Inf. Additionally, there is a variable called RegDerivatives that you can use to automatically calculate and include first derivatives for any of your regressor files. You just add the index of the regressor file to RegDerivatives to have them included. In the example below, we've indicated a 2 here, so that first derivatives will be calculated for the second row of RegFileTemplates – in this case our motion paramters.

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%   Location of user specified regressor files. To use these make sure
%%%   column 2 of RegOp is set to 1 above.
%%%
%%%   Variables you can use in your template are:
%%%        Exp       = path to your experiment directory
%%%        Subject   = folder name of current subject
%%%        Run       = folder name of current run
%%%        *         = wildcard (can only be placed in final part of template)
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
RegFileTemplates = {
    '[Exp]/Subjects/[Subject]/func/[Run]/vmPFC.csv',Inf;
    '[Exp]/Subjects/[Subject]/func/[Run]/mcflirt*.dat',Inf;
    '[Exp]/Subjects/[Subject]/func/[Run]/fdOutliers.csv',Inf;
    '[Exp]/Subjects/[Subject]/func/[Run]/frameOutliers.csv',Inf;
};

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Indices from RegFileTemplates for which regressor files should have
%%% automatic first derivatives calculated and also included
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
RegDerivatives = [2];
```

Finally we need to deal with contrasts on the PPI regressors. This will be relatively painless, as long as your PPI CSV file is the first element of your RegFileTemplates array. The FirstLevel central script will automatically add 0s as necessary to make sure all regressor columns of the design matrix have a value for every contrast, so we only need to specify up to the regressors that we actually care about contrasting. If our PPI CSV file was the first element in the RegFileTemplates, this is simplified as we don't need to include a lot of extra 0s for other regressor files.

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% List of contrasts to add to the estimated model
%% Format is 'ContrastName' [Cond1 Param1..N]..[CondN Param1..N] [Reg1..RegN]
%% You need to properly balance/weight your contrasts below as if it was just
%% one run/session
%% The script will handle balancing it across runs
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ContrastList = {
    'PPIC1vC3'         [0 0 1];
 };
```

Notice that I don't need to include any 0s after my column of interest because the script will automatically add those to fill up the contrast. Also notice that we do not have any of the typical condition contrast values between our contrast name and regressor columns. This is because we have not included any conditions in our model, only user-specified regressors.

In the case of a generalized PPI, your contrast will look a bit different. In this example I have three conditions, so I have three pairs of Psychological and PPI regressor. To create my PPI contrast of interest I subtract the condition 3 PPI from the condition 1 PPI.

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% List of contrasts to add to the estimated model
%% Format is 'ContrastName' [Cond1 Param1..N]..[CondN Param1..N] [Reg1..RegN]
%% You need to properly balance/weight your contrasts below as if it was just
%% one run/session
%% The script will handle balancing it across runs
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ContrastList = {
    'PPIC1vC3'         [0 0 1 0 0 0 -1];
};
```

Advanced

The advanced section describes additional options avaible for the user specified files.

PPI_mc_template.m

The advanced options for the template file are displayed in the below frame.

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% EOIAdjust is an F-contrast index in your model that you would like to
%%% use to adjust the extracted data.  What this means is that contributions
%%% to your signal from effects that are NOT included in the chosen F-
contrast
%%% will be removed from your signal.  Set to 0 to skip adjustment.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
EOIAdjust = 0;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% SPM Default Values for First Level analysis
%%% this is set up as a cell array where each row corresponds to a default
%%% value in SPM.  The first element is a string with the name of the
%%% default field (without defaults. at the beginning).  You can view
%%% spm_defaults.m for a list of possible fields to set.  The second
%%% element is the value you want to set for that default.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
spmdefaults = {
};
```

There are only two options in the PPI_mc_template advanced section.

EOIAdjust: When extracting VOIs in SPM, the program gives you the option of adjusting for an F-contrast for effects of interest. What this means is that effects that are not modeled in your F-contrast (i.e. effects of no interest) will have their variance removed from the time series that is extracted for use in your PPI analysis. If you have created such an F-contrast in your original first level model, you can set the contrast number here so SPM adjusts your VOI output. If you don't want to do this (or don't have any F-contrasts in your model) this should be set to 0.

spmdefaults: This is the standard defaults variable used in Methods Core Matlab scripts to allow setting of any SPM default values that you need to set for your analysis.