**MethodsCore**

**PPI Script Documentation**

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# 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 basic and advanced. 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](mailto: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/YNl3H8sXgwI?hd=1

2 PPI Overview http://youtu.be/Wo2-rTD81vo?hd=1

3 Creating Regressors http://youtu.be/TfdgtRzezYY?hd=1

4 Running PPI Models http://youtu.be/X-jkITWrado?hd=1

# Basic

## PPI\_mc\_template.m

SecondLevel\_mc\_template.m is an options file. The basic options for the template file are displayed in the below frame. The options are edited by changing the variable values. Each variable is heavily commented in the template file to explain its purpose.

%%%%%%%%%% Basic %%%%%%%%%%

%~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

%~~~~~~~~~~~~~~~~~~~~~~~~~~~ Basic Options ~~~~~~~~~~~~~~~~~~~~~~~~~~~

%~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The folder that contains your subject folders

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

Exp = '/data/SIM/ANOVA';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% Path where your logfiles will be stored

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

LogTemplate = '[Exp]/Logs';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The file name of the job file. The full path to the job file is

%%% needed if the template and job file are in different directories.

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

JobFileTemplate = 'jobfile.csv';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The file name of the scan file. The full path to the scan file is

%%% needed if the template and scan file are in different directories.

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

ScanFileTemplate = 'scanfile.csv';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The location to the subjects' first level analysis folders

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

FirstLevelTemplate = '[Exp]/Flexible/';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The model directory within each subject to find images.

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

ModelDir = 'Faces';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The directory where to output the results

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

OutputTemplate = '[Exp]/SecondLevel';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The filename prefix for images to use, which is typically 'con'

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

ContrastPrefix = 'con';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The file extension for the input images. Either 'img' or 'nii'

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

InputImgExt = 'img';

The whole path to the images to use in second level analysis is built by concatenating the following variables: /[FirstLevelTemplate]/[Subject]/[ModelDir]/[ContrastPrefix]. Here FirstLevelTemplate, ModelDir, and ContrastPrefix are specified in the template file.

**OutputName**: The name of the folder to place the test in (created inside other.OutputDir from the options file).

**PathCol**: The column number from the scan file that contains the subject folders for this test

# 

# 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.

%%%%%%%%%% Advanced %%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% Masking option: Only one of these options can appear in a template %%% file.

%%%

%%% opt.masking.tm.tm\_none = [] means no threshold masking

%%% opt.masking.tm.tma.athresh = N sets an absolute threshold mask

%%% equal to N

%%% opt.masking.tm.tmr.rthresh = N set a relative threshold mask equal %%% to N (N should be between 0 and 1 and %%% represent a percent value)

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

opt.masking.tm.tm\_none = [];

OR

opt.masking.tm.tma.athresh = N;

OR

opt.masking.tm.tmr.rthresh = N;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The option to specify whether an implicit mask is used;

%%% 1 = use, 0 = do not use

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

opt.masking.im = 1;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The file path to the explicit mask;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

opt.masking.em = '';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The variable that controls global calculation. This should always

%%% be set equal to [] for fMRI data

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

opt.globalc.g\_omit = [];

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% Global Normalization Option: Only one of these options can appear

%%% in a template file.

%%%

%%% opt.globalm.gmsca.gmsca\_no = [] uses no grand mean scaling

%%% opt.globalm.gmsca.gmsca\_yes.gmscv = N sets grand mean value to N

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

opt.globalm.gmsca.gmsca\_no = [];

OR

opt.globalm.gmsca.gmsca\_yes.gmscv = N;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% Global Normalization Options: Sets whether to use no normalization

%%% or proportional global normalization

%%% 1 = none, 2 = proportional global normalization

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

opt.globalm.glonorm = 1;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% ImColFlag controls how the ImCol column in the job file is

%%% interpreted. When set to 1, ImCol refers to the actual contrast

%%% image numbers. When set to 0, ImCol refers to the column in the

%%% scan file that holds the image number.

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

opt.other.ImColFlag = 1;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% SPM Default Values for Second 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.

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%% The main default that impacts second level analysis is the

%%% stats.fmri.ufp value. This value is an initial main effects

%%% F-threshold that is applied to the data during ReML estimation to

%%% select voxels which SPM uses to estimate non-sphericity. SPM's default

%%% value for this is an uncorrected p = 0.001. Sometimes a second level

%%% model will fail with the message "no significant voxels" which

%%% indicates that no voxels survived this initial main effects test. In

%%% order to get past this error and estimate the model anyway, you can try

%%% changing the fmri.ufp value to a more liberal p-value.

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

spmdefaults = {

'stats.fmri.ufp' 0.001

};