

WFU_BPM Toolboxes

BETA VERSION 1.5d

The WFU Biological Parametric Mapping (BPM) Toolboxes have been developed to perform SPM analysis with imaging covariates.

REFERENCE

Ramon Casanova, Ryali Srikanth, Aaron Baer, Paul J. Laurienti, Jonathan H. Burdette, Satoru Hayasaka, Lynn Flowers, Frank Wood and Joseph A. Maldjian

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WFU_BPM SETUP

WFU Toolboxes Beta Release Distribution

The beta package is distributed with this directory structure:

```
wfu_toolboxes/
    wfu_startup.m
    wfu_bpm/
    wfu_compatibility/
    wfu_insertion_tool/
    WFU_PickAtlas/
    wfu_utilities/
wfu_bpm_data/
    bpm_img/
    bpm_results/
    bpm_simulated_data/
```

Requirements

SPM2 or SPM5
MATLAB version 6.5 or higher

Download, Extract, Select Toolboxes

For UNIX, download the compressed unix tar file, wfu_bpm_beta.tar.gz, and extract with:

```
gunzip wfu_bpm_beta.tar.gz
tar xvf wfu_bpm_beta.tar
```

For PC/WINDOWS, download and unzip the contents of the WINDOWS ZIP file, wfu_bpm_beta.zip.

Edit wfu_startup.m inside the wfu_toolboxes directory to select the WFU toolbox options for your site. Set each of the following parameters to 0 (for no) or 1 (for yes):

```
add_bpm
add_insertion_tool
add_utilities
add_compatibility
add_pickatlas
```

Add compatibility only if reconciliation with SPM-99 input is needed.

Running the WFU Toolboxes

(1) Once the SPM2 or SPM5 path is set in MATLAB and spm_defaults has been called, add the path of the wfu_toolboxes directory. For example, if located here:

```
c:\software\wfu_toolboxes
```

then issue this command:

```
addpath('c:\software\wfu_toolboxes');
```

(2) Add the paths for all the selected WFU toolboxes with:

```
wfu_startup;
```

(3) Run the toolbox of choice. To execute BPM:

```
wfu_bpm;
```

WFU_BPM EXAMPLES

The distribution includes example data and example results in the wfu_bpm_data directory. To preview the results that have already been generated with the example data sets, refer to the bpm_img subdirectory which contains JPEG images of screenshots from both WFU_BPM GUI selections and SPM/Results. To re-run the examples, follow the steps listed in the WFU_BPM_RESULTS section below.

WFU_BPM SIMULATED DATA

** Located in: wfu_bpm_data\bpm_simulated_data

SIMULATED DATA for BPM example input (anova, ancova, correlation)

Modality 1 = mod1 (fmri)

Modality 2 = mod2 (vbm)

Group 1 = grp1

Group 2 = grp2

Directories:

./mod1/grp1

./mod1/grp2

./mod2/grp1

./mod2/grp2

File lists (FLISTS):

fmri1.flist (mod1/grp1)

fmri2.flist (mod1/grp2)

vbm1.flist (mod2/grp1)

vbm2.flist (mod2/grp2)

SIMULATED DATA for BPM example input (regression)

Main Modality 1 = rmod1

Confound 1 = rmod2

Confound 2 = rmod3

Directories:

./rmod1

./rmod2

./rmod3

File lists (FLISTS):

reg_main_mod1.flist (rmod1/)

reg_conf1.flist (rmod2/)

reg_conf2_flist (rmod3/)

SIMULATED DATA ... FLISTS

The file list, or flist, is a text file listing file names used as input, one file name per line. If numeric, the first line in the flist specifies the number of file names to be read from the list that follows.

Typically the input data files may be scattered all over one or more disks, and the file names in the flist will include the full directory path of the file. It is best not to have blanks in the file name path.

For the convenience of this example that may be relocated anywhere on the user's disk, the leading "/" or "\" characters in the flist file name will be treated as a relative path to the data file names.

SIMULATED DATA ... RIGHT/LEFT

These data sets were generated by SPM2 from SPM-99 normalized input. The WFU_COMPATIBILITY functions were used to generate *.mat files in MATLAB 6.5 for all *.img and *.hdr outputs in ANALYZE format. These *.mat files indicate the orientation for SPM2 and SPM5 usage.

With or without the WFU_COMPATIBILITY functions, the BPM ancova results using this simulated data with the *.mat files will show a remaining activation on the LEFT.

MATLAB *.mat files may not be backwards compatible. If running with an earlier MATLAB version, the *.mat files could be unreadable. In that case, delete all the *.mat files in the wfu_bpm_data directory recursively before running BPM with the simulated data example files. Afterwards, if the SPM flag defaults.analyze.flip is set to 1, the ancova result will show the remaining activation on the RIGHT since the *.mat files, when present, indicate a flip.

WFU_BPM IMAGES

** Located in: wfu_bpm_data\bpm_img

IMAGES for RESULTS generated by wfu_bpm

These directories:

- ancova
- anovaFMRI
- anovaVBM
- correlation
- regression

contain these images:

- analysis
- contrast
- insertion
- spm_results

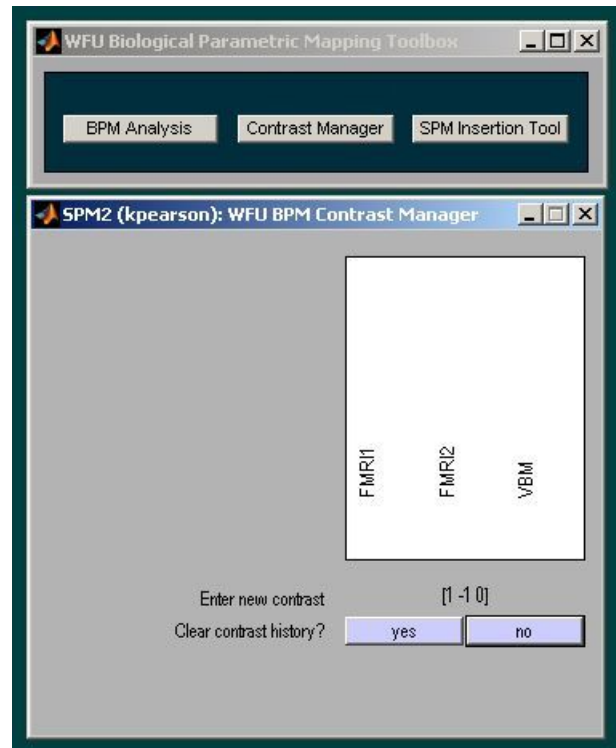
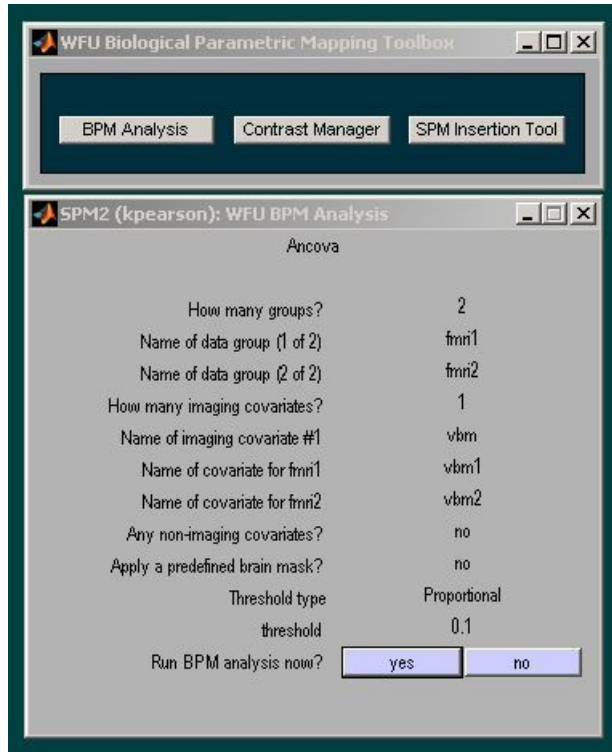
with the exception of correlation which has no contrast. The analysis, contrast, and insertion *.jpg files show the WFU BPM graphical user interface with default selections. The spm_results image within each directory shows the effect from:

- SPM
- choose SPM.mat
- press Results button
- answer Results questions

The top-level directory contains an example of the SPM Results Questions/Answers.

Screenshots of Step by Step ANCOVA example

- *BPM Analysis & Contrast Manager*



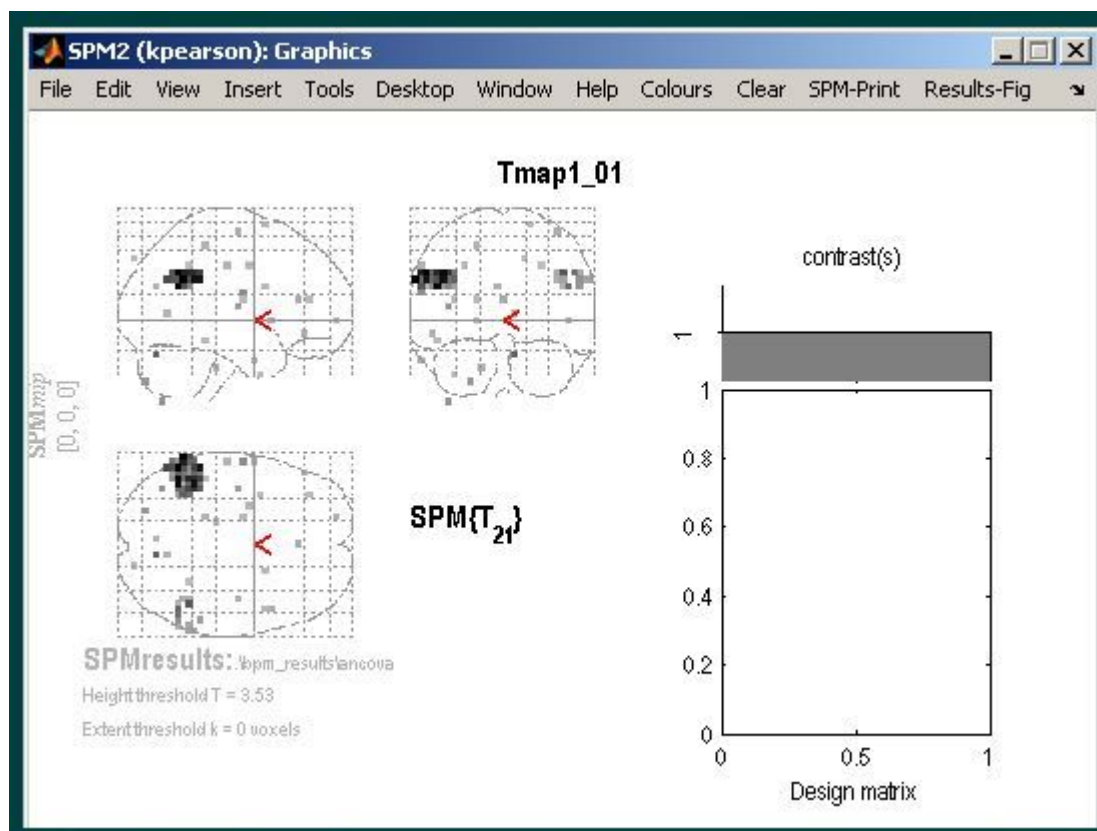
Screenshots of Step by Step ANCOVA example

- SPM Insertion Tool & SPM/Results Q/A



Screenshots of Step by Step ANCOVA example

- *SPM/Results*



WFU_BPM RESULTS

** Located in: wfu_bpm_data\bpm_results

RESULTS generated by wfu_bpm

The results directory specified for wfu_bpm must already exist before it is chosen by the SPM2 file selector. For the example simulated data, these results directories were created before running wfu_bpm:

- ancova
- anovaFMRI
- anovaVBM
- correlation
- regression

The results in this directory were generated with SPM2 running MATLAB 7.1 under the PC/Windows operating system.

BPM RESULTS -- versions, operating system, byte order

The SPM.mat files created by SPM2 do not display properly on an operating system with a different endian byte order.

The SPM.mat results in this directory, generated on PC/Windows, can be displayed correctly under Linux or PC/Windows. However, if using Solaris, the graph shows a gray mass covering the whole brain. This is an issue with SPM2 but may be resolved in SPM5.

Note that earlier MATLAB versions may not be able to read any of these *.mat files output by MATLAB 7.1.

BRAIN MASK

In all the steps listed below for generating the bpm_results output, no predefined brain mask is supplied. In this case, the BPM program creates one. The user should check the mask.img file so generated in the results directory to ensure its suitability. This mask represents the intersection of all individual masks from subjects in the main modality. For building the individual masks, the user may request either a proportional or absolute threshold. The proportional threshold is in relation to the absolute mean value of the signal. The absolute threshold is a fixed positive value input by the user.

NON-IMAGING COVARIATES

Non-imaging covariates can be specified in a single text file with one column for each non-imaging covariate involved in the analysis. A column contains values for each subject in the first group followed by values for each subject in the subsequent groups. The order of subject values for a group must correspond to the order of the subject images specified in the group f-list files. In the case of BPM multiple regression, each column will contain values for only one group.

```

*****
>>>> STEP BY STEP ANCOVA
*****
wfu_bpm

(1) BPM BUTTON1: BPM Analysis
Results directory                bpm_results\ancova
Select type of analysis         Ancova
How many groups                 2
Main group 1 file list          bpm_simulated_data\fmri1.flist
Name of data group (1 of 2)     fmri1
Main group 2 file list          bpm_simulated_data\fmri2.flist
Name of data group (2 of 2 )    fmri2
How many imaging covariates     1
Name of imaging covariate #1    vbm
Modality 2 group 1 file list     bpm_simulated_data\vbm1.flist
Name of covariate for fmri1     vbm1
Modality 2 group 2 file list     bpm_simulated_data\vbm2.flist
Name of covariate for fmri2     vbm2
Any non-imaging covariates      no
Apply a predefined brain mask    no
Threshold type                  Proportional
Threshold                       0.1
Run BPM analysis now            yes

(2) BPM BUTTON 2: Contrast Manager
Select the BPM.mat file         bpm_results\ancova\BPM.mat
Enter new contrast              [1 -1 0]
Reset contrast history          no

(3) BPM BUTTON 3: SPM Insertion Tool
Select the BPM.mat file         bpm_results\ancova\BPM.mat
map title                       Tmap1

(4) SPM: select fMRI time-series
Results
Select SPM.mat                  bpm_results\ancova\SPM.mat
Select contrasts                 Tmap1_01
mask with other contrast(s)     no
ROI Analysis                    no
title for comparison            Tmap1_01
p value adjustment to control   none
threshold {T or p value}       0.001
& extent threshold {voxels}    0

```

```

*****
>>>> STEP BY STEP ANOVA (fmri)
*****
wfu_bpm

(1) BPM Analysis
Results directory          bpm_results\anovaFMRI
Select type of analysis   Anova
How many groups           2
Group 1 file list         bpm_simulated_data\fmri1.flist
Name of data group (1 of 2) fmri1
Group 2 file list         bpm_simulated_data\fmri2.flist
Name of data group (2 of 2) fmri2
Apply a predefined brain mask no
Threshold type            Proportional
Threshold                  0.1
Run BPM analysis now      yes

(2) Contrast Manager
Select the BPM.mat file   bpm_results\anovaFMRI\BPM.mat
Enter new contrast        [1 -1]
Reset contrast history    no

(3) SPM Insertion Tool
Select the BPM.mat file   bpm_results\ancovaFMRI\BPM.mat
map title                 Tmap1

(4) SPM fMRI time-series
Results
Select SPM.mat            bpm_results\ancovaFMRI\SPM.mat
Select contrasts          Tmap1_01
mask with other contrast(s) no
ROI Analysis              no
title for comparison      Tmap1_01
p value adjustment to control none
threshold {T or p value} 0.001
& extent threshold {voxels} 0

.....
For ANOVA VBM, follow the same steps, selecting:
results directory:
    anovaVBM
with file lists:
    vbm1.flist
    vbm2.flist
and with data group names:
    vbm1
    vbm2
.....

```

```

*****
>>>> STEP BY STEP CORRELATION
*****
wfu_bpm

(1) BPM Analysis
Results directory          bpm_results\correlation
Select type of analysis   Correlation Analyses
Select type of Correlation Analysis Correlation
First file list for CORR  bpm_simulated_data\fmri1.flist
Second file list for CORR bpm_simulated_data\vbml.flist
Select type of Correlation Voxel-Voxel
Apply a predefined brain mask no
Threshold type            Proportional
Threshold                 0.1
Run BPM analysis now     yes

(2) Contrast Manager
SKIP THIS STEP FOR CORRELATION

(3) SPM Insertion Tool
Select type of analysis   Homologous Correlation Field
Select the BPM.mat file   bpm_results\correlation\BPM.mat
map title                 Corr_pos
map title                 Corr_neg

(4) SPM fMRI time-series
Results
Select SPM.mat            bpm_results\correlation\SPM.mat
Select contrasts          Corr_pos_01
mask with other contrast(s) no
ROI Analysis             no
title for comparison     Corr_pos_01
p value adjustment to control none
define threshold in terms of P-value
threshold {0<p<0.25,uncorrected} 0.001
& extent threshold {voxels}      0

```

```

*****
>>>> STEP BY STEP REGRESSION
*****
wfu_bpm

(1) BPM Analysis
Results directory          bpm_results\regression
Select type of analysis   Regression
Select dependent modality file list bpm_simulated_data\reg_main_mod.flist
Name of main modality     main
Number of imaging covariates 2
Name of imaging covariate #1 conf1
Name of imaging covariate #2 conf2
Select modality 2 file list bpm_simulated_data\reg_conf1.flist
Select modality 3 file list bpm_simulated_data\reg_conf2.flist
Any non-imaging covariates no
Apply a predefined brain mask no
Threshold type            Proportional
Threshold                 0.1
Run BPM analysis now     yes

(2) Contrast Manager
Select the BPM.mat file   bpm_results\regression\BPM.mat
Select the contrast type  F
Select the regressors     [1 0]
Reset contrast history    no

(3) SPM Insertion Tool
Select the BPM.mat file   bpm_results\regression\BPM.mat
map title                 Fmap1

(4) SPM fMRI time-series
Results
Select SPM.mat            bpm_results\regression\SPM.mat
Select contrasts          Fmap1_01
mask with other contrast(s) no
ROI Analysis             no
title for comparison     Fmap1_01
p value adjustment to control none
threshold {T or p value} 0.001
& extent threshold {voxels} 0

```