BPM^{e} Toolbox

Biological Parametric Mapping - Extended

The BPM Random Regressors Toolbox is provided as an overlay on the WFU Biological Parametric Mapping Toolbox release 1.5d as modified by the robust extension package. All indications of license terms apply only to the changes made to the code from its original developers.

Please cite the following reference for the BPM software:

- Ramon Casanova, Ryali Srikanth, Aaron Baer, Paul J. Laurienti, Jonathan H. Burdette, Satoru Hayasaka, Lynn Flowers, Frank Wood and Joseph A. Maldjian. "Biological parametric mapping: A statistical toolbox for multimodality brain image analysis." *NeuroImage* Volume 34, Issue 1, 1 January 2007, Pages 137-143 PMC1994117

Please cite the following reference for the Robust and Non-Parametric BPM additions:

- X. Yang, L. Beason-Held, S. M. Resnick, and B. A. Landman, "Biological parametric mapping with robust and non-parametric statistics," Neuroimage, vol. 57, pp. 423-30, Jul 15 2011. PMID21569856

Please cite the following reference for the Model II and Regression Calibration Extensions:

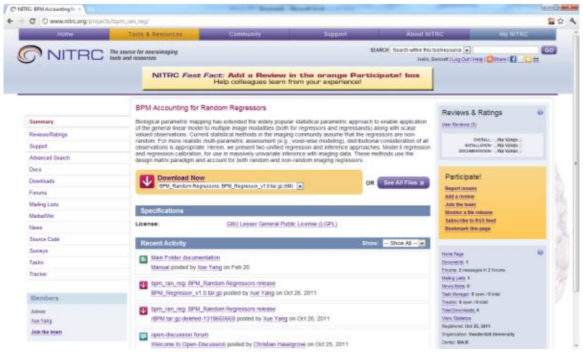
- X. Yang, C. B. Lauzon, C. Crainiceanu, B. Caffo, S. M. Resnick, and B. A. Landman, "Accounting for Random Regressors: A Unified Approach to Multi-modality Imaging," in MICCAI 2011 Workshop of Multi-Modal Methods, Toronto, Canada, 2011. URL

REVISION HISTORY

- 3.0 BPM^{e} 2012/2/28 – All toolboxes combined into a single package of extensions
- 2.1 rbpm 2011/06/08
- 2.0 rbpm/bnpm 2011/04/07
- 1.0 rpbm/bnpm 2011/01/03

INSTALLATION

- Download the latest version of the toolbox from http://www.nitrc.org/projects/rbpm/ (click on the red arrow)



NITRC *Fast Fact:* Add a Review in the orange Participate! box
Help colleagues learn from your experience!

BPM Accounting for Random Regressors

Biological parametric mapping has extended the widely popular statistical parametric approach to enable application of the general linear model to multiple image modalities (both for regressors and regressands) along with scalar valued observations. Current statistical methods in the imaging community assume that the regressors are non-random. For more realistic multi-parametric assessment (e.g., voxel-wise modeling), distributional consideration of all observations is appropriate. Herein, we present two unified regression and inference approaches. Model II regression and regression calibration, for use in massively univariate inference with imaging data. These methods use the design matrix paradigm and account for both random and non-random imaging regressors.

License: GNU Lesser General Public License (LGPL)

Main Folder documentation
Manual posted by Xue Yang on Feb 20

bpm_ran_reg: BPM_Random Regressors release
BPM_Regressor_v1.0.tar.gz posted by Xue Yang on Oct 26, 2011

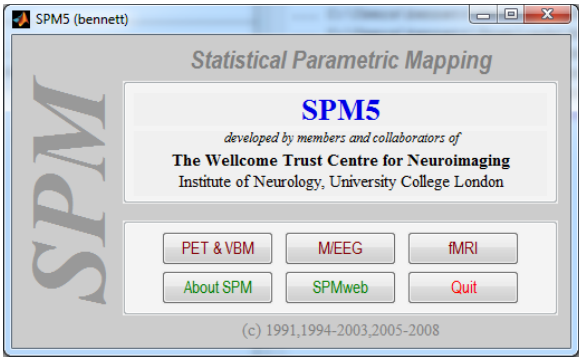
bpm_ran_reg: BPM_Random Regressors release
rBPM.tar.gz-deleted-1319660669 posted by Xue Yang on Oct 26, 2011

open-discussion forum
Welcome to Open-Discussion posted by Christian Haselgrove on Oct 25, 2011

- Decompress and extract the bundle to a location accessible by Matlab. We tested Matlab 7.12 (R2011a and b).
- Add the extracted directory and subdirectories to your Matlab path:
    - `addpath('<full path to directory')`
- To initialize the BPM toolbox, run:
    - `wfu_startup`

```
Adding WFU toolboxes to path
... <path>\BPM_Regressor\wfu_bpm
... <path>\BPM_Regressor\wfu_insertion_tool
... <path>\BPM_Regressor\wfu_utilities
... <path>\BPM_Regressor\wfu_pickatlas
... <path>\BPM_Regressor\random_reg
```

- We currently fully support the SPM5 software with all updates applied. Please see the Wake Forest website for details to enable partial support for SPM8 (http://fmri.wfubmc.edu/software/Bpm). SPM5 availability via SPM Central has been intermittent (http://www.fil.ion.ucl.ac.uk/spm/software/). Archived copies of the complete package may be downloaded via SourceForge at http://sourceforge.net/projects/spm5/files/.
- Check to ensure that SPM5 is installed and operational. Type:
    - `spm`



Statistical Parametric Mapping

SPM5

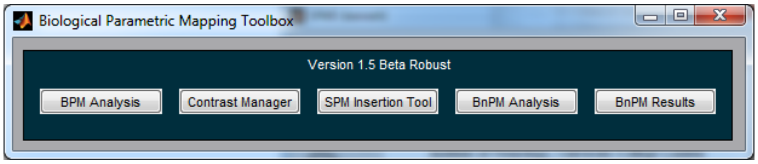
developed by members and collaborators of

The Wellcome Trust Centre for Neuroimaging

Institute of Neurology, University College London

(c) 1991,1994-2003,2005-2008

- Close the SPM window and verify that the BPM toolbox will start. Type
    - `wfu_bpm`



ROBUST BPM (rBPM) - DEMONSTRATION

SIMULATION DATA

Download and extract the BPMe_3.0.zip file, all sample images are in the folder “sampledata”.

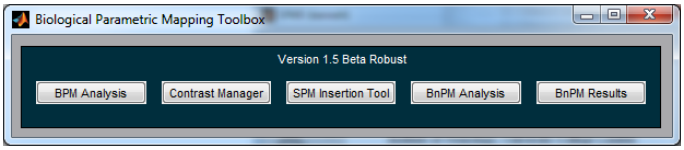
For without outlier example, the dependent modality images are listed in file simulation_y.flist and one imaging covariate images are listed in file simulation_gm.flist.

For with outlier example, the dependent modality images are listed in file simulation_y_shift.flist and one imaging covariate images are listed in file simulation_gm_shift.flist.

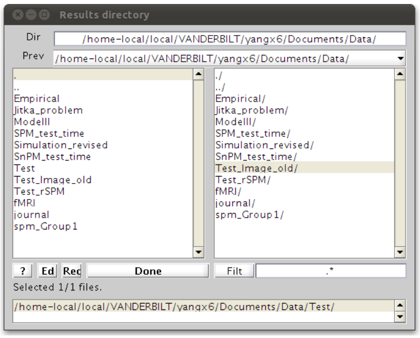
These data repeat Figure 4 in *X. Yang, L. Beason-Held, S. M. Resnick, and B. A. Landman, "Biological parametric mapping with robust and non-parametric statistics," Neuroimage, vol. 57, pp. 423-30, Jul 15 2011.* PMID21569856.

ANALYSIS

- Open BPM, type wfu_bpm



- Estimation: Click “BPM Analysis” button.
- Choose result directory, click “Done”.



Dir /home-local/local/VANDERBILT/yangx6/Documents/Data/

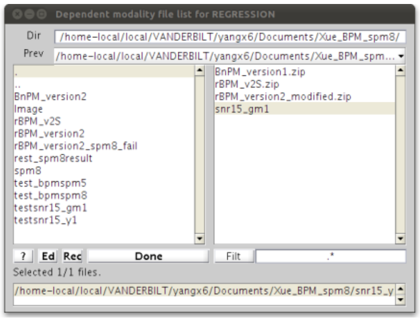
Prev /home-local/local/VANDERBILT/yangx6/Documents/Data/

.*

Selected 1/1 files.

/home-local/local/VANDERBILT/yangx6/Documents/Data/Test/

- In the pull-down manual of “Select type of analysis”, choose “Regression”.
- Choose the file listing dependent modality images, press “Done”. (snr15_y1.flist)



Dependent modality file list for REGRESSION

Dir: /home-local/local/VANDERBILT/yangx6/Documents/Xue_BPM_spm8/

Prev: /home-local/local/VANDERBILT/yangx6/Documents/Xue_BPM_spm...

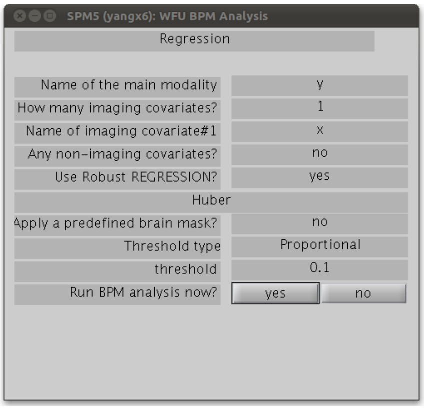
```
.
..
BnPM_version2
Image
rBPM_v2S
rBPM_version2
rBPM_version2_spm8_fail
rest_spm8result
spm8
test_bpmspm5
test_bpmspm8
testsnr15_gm1
testsnr15_y1
```

```
BnPM_version1.zip
rBPM_v2S.zip
rBPM_version2_modified.zip
snr15_gm1
```

Selected 1/1 files.

/home-local/local/VANDERBILT/yangx6/Documents/Xue_BPM_spm8/snr15_y

- Write down the name for the dependent modality (e.g., “y”).
- Write down the number of imaging covariates (“1” here).
- Write down the name for the imaging covariates.
- Choose the file containing the imaging covariate images, press “Done”.
- Select if any non-imaging covariates (e.g., sex, age). If the answer is yes, the value of these covariates should be written in a file with one column for each covariate, select this file, press “Done”.
- Select if use robust regression. If yes, select the weight function for the robust regression. If no, it will perform traditional BPM analysis.
- Select if apply a predefined brain mask. If no, select the threshold type and write down the threshold value.
- Choose “yes” to run rBPM analysis, “no” to cancel.

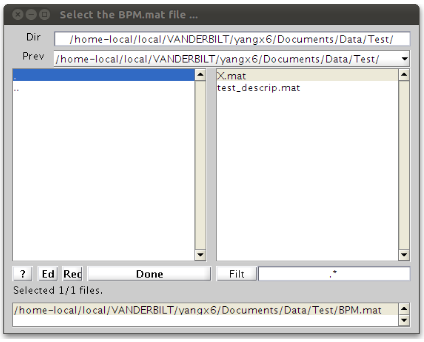


SPM5 (yangx6): WFU BPM Analysis

Regression

Name of the main modality	y
How many imaging covariates?	1
Name of imaging covariate#1	x
Any non-imaging covariates?	no
Use Robust REGRESSION?	yes
Huber	
Apply a predefined brain mask?	no
Threshold type	Proportional
threshold	0.1
Run BPM analysis now?	yes no

- Inference: after rBPM Analysis is done, click “Contrast Manager” button.
- Choose the BPM.mat file in the result directory.



Select the BPM.mat file ...

Dir: /home-local/local/VANDERBILT/yangx6/Documents/Data/Test/

Prev: /home-local/local/VANDERBILT/yangx6/Documents/Data/Test/

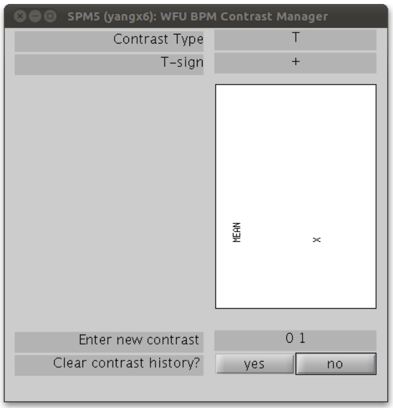
```
.
..
```

```
X.mat
test_descrip.mat
```

Selected 1/1 files.

/home-local/local/VANDERBILT/yangx6/Documents/Data/Test/BPM.mat

- Select T-test or F-test. If select T-test, choose positive or negative sign.
- Enter contrast for each covariate with space between them.



Contrast Type T

T-sign +

Enter new contrast 0 1

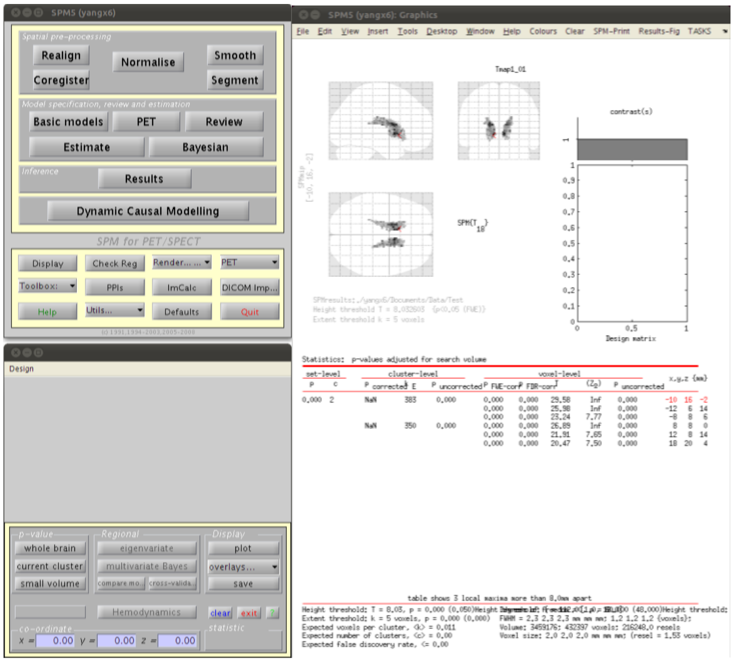
VISUALIZATION

- In the BPM toolbox, click “SPM Insertion Tool” button.
- Choose the BPM.mat file in the result directory, press “Done”.
- Type the name of the name of the map title, press enter.
- Open SPM (Type “spm”).
- Click “PET & VBM” button.
- Click “Results” in the pop up toolbox.
- Choose the SPM.mat file in the directory, press “Done”.
- In the SPM contrast manager, choose the map build by BPM.

001 {T} : Tmap1_01

Selected 1 contrast, press "Done" when finished.

- The result is displayed in SPM graphics.



NON-PARAMETRIC BPM (BnPM)- DEMONSTRATION

Note: BnPM require computer cluster access.

SIMULATION DATA

Download and extract the BPMe_3.0.zip file, all sample images are in the folder “sampledata”.

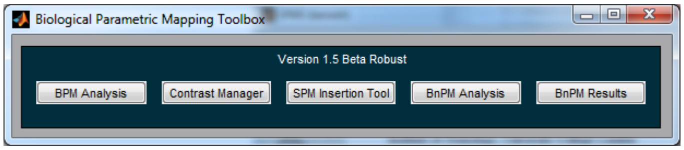
For without outlier example, the dependent modality images are listed in file simulation_y.flist and one imaging covariate images are listed in file simulation_gm.flist.

For with outlier example, the dependent modality images are listed in file simulation_y_shift.flist and one imaging covariate images are listed in file simulation_gm_shift.flist.

These data repeat Figure 4 in *X. Yang, L. Beason-Held, S. M. Resnick, and B. A. Landman, "Biological parametric mapping with robust and non-parametric statistics," Neuroimage, vol. 57, pp. 423-30, Jul 15 2011.* PMID21569856.

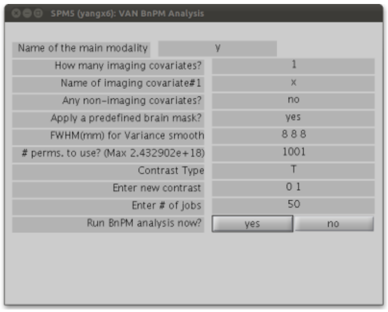
ANALYSIS

- Open BPM, type wfu_bpm



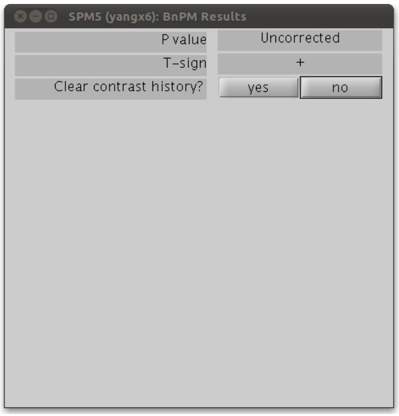
- Estimation: Click “BnPM Analysis” button.
- Choose result directory, click “Done”.
- Choose the file listing dependent modality images, press “Done”. (snr15_y1.flist)
- Write down the name for the dependent modality (e.g., “y”).
- Write down the number of imaging covariates (“1” here).

- Write down the name for the imaging covariates.
- Choose the file containing the imaging covariate images, press “Done”.
- Select if any non-imaging covariates (e.g., sex, age). If the answer is yes, the value of these covariates should be written in a file with one column for each covariate, select this file, press “Done”.
- Select if apply a predefined brain mask. If no, select the threshold type and write down the threshold value.
- Enter FWHM (mm) for variance smooth. One value for each dimension with space between them (We type ‘8 8 8’ here).
- Choose if use approximate permutation test. If yes, enter the number of permutations. This number cannot be larger than the max permutations.
- Select T-test or F-test.
- Enter the number of sub-jobs.
- Select a pbs template to execute qsub. Please refer to the “computer cluster” section for more details.
- Choose “yes” to run BnPM analysis.



Name of the main modality	y
How many imaging covariates?	1
Name of imaging covariate#1	x
Any non-imaging covariates?	no
Apply a predefined brain mask?	yes
FWHM(mm) for Variance smooth	8 8 8
# perms. to use? (Max 2.432902e+18)	1001
Contrast Type	T
Enter new contrast	0 1
Enter # of jobs	50
Run BnPM analysis now?	yes no

- Inference: after all BnPM sub-jobs are done, click “BnPM Results” button.
- Select the BnPMstr.mat file in the result directory.
- Choose uncorrected or corrected p-value.
- If T-test is used in the estimation, choose the sign of the T-test.

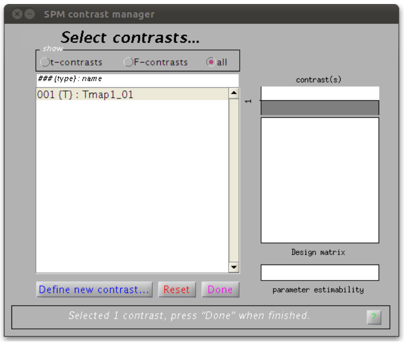


P value	Uncorrected
T-sign	+
Clear contrast history?	yes no

VISUALIZATION

- In the BPM toolbox, click “SPM Insertion Tool” button.
- Choose the BPM.mat file in the result directory, press “Done”.
- Type the name of the name of the map title, press enter.
- Open SPM (Type “spm”).
- Click “PET & VBM” button.

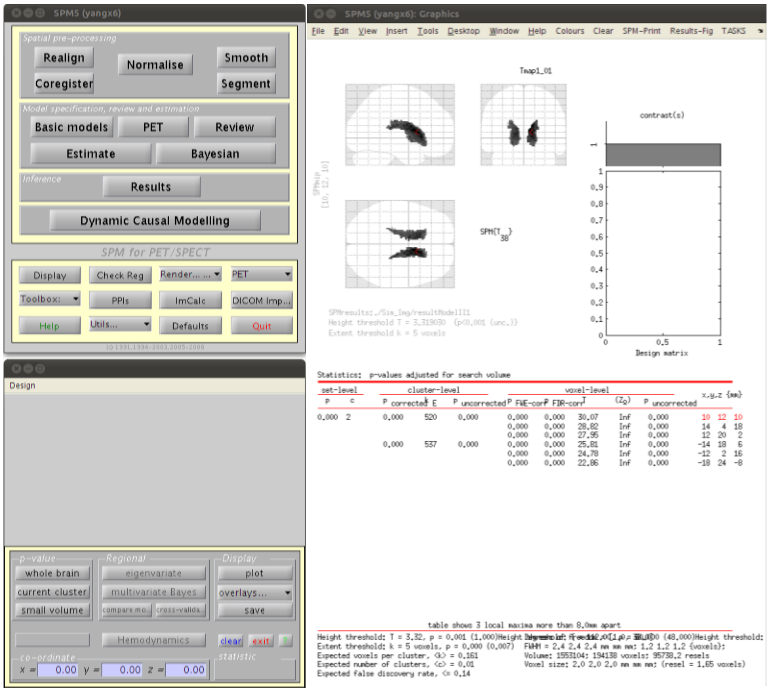
- Click “Results” in the pop up toolbox.
- Choose the SPM.mat file in the directory, press “Done”.
- In the SPM contrast manager, choose the map build by BPM.



001 {T} : Tmap1_01

Selected 1 contrast, press "Done" when finished.

- The result is displayed in SPM graphics.



```
SPMresults: ./Sim_Img/resultModelII1
Height threshold T = 3.319030  {p<0.001 (unc.)}
Extent threshold k = 5 voxels
```

```
Statistics:  p-values adjusted for search volume

 set-level       cluster-level                 voxel-level                          x,y,z {mm}
 p     c    p corrected  k E  p uncorrected p FWE-corr p FDR-corr  T    (Z≡)  p uncorrected

0.000  2      0.000      520     0.000      0.000    0.000   30.07   Inf   0.000     10  12  10
                                            0.000    0.000   28.82   Inf   0.000     14   4  18
                                            0.000    0.000   27.95   Inf   0.000     12  20   2
              0.000      537     0.000      0.000    0.000   25.81   Inf   0.000    -14  18   6
                                            0.000    0.000   24.78   Inf   0.000    -12   2  16
                                            0.000    0.000   22.86   Inf   0.000    -18  24  -8

                     table shows 3 local maxima more than 8.0mm apart
Height threshold: T = 3.32, p = 0.001 (1.000)Height [illegible] (48.000)Height threshold:
Extent threshold: k = 5 voxels, p = 0.000 (0.007)  FWHM = 2.4 2.4 2.4 mm mm mm; 1.2 1.2 1.2 {voxels};
Expected voxels per cluster, <k> = 0.161           Volume: 1553104; 194138 voxels; 95738.2 resels
Expected number of clusters, <c> = 0.01            Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 1.65 voxels)
Expected false discovery rate, <= 0.14
```

MODEL II REGRESSION (BPM^e)- DEMONSTRATION

SIMULATION DATA

Download and extract the BPMe_3.0.zip file, all sample images are in the folder “sampledata”.

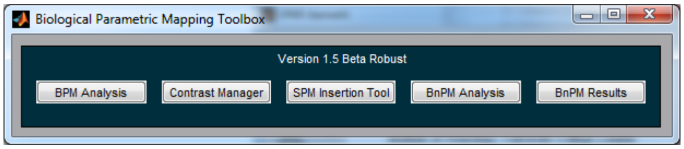
The dependent modality images are listed in file regressand.flist

One imaging covariate images are listed in file GM1.flist.

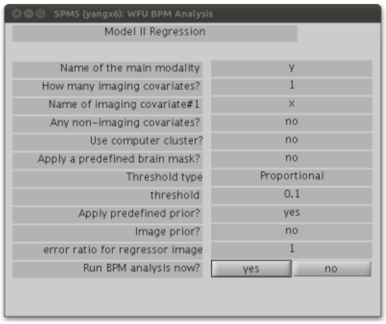
These data is subset of the dataset for Figure 5 in *X. Yang, C. B. Lauzon, C. Crainiceanu, B. Caffo, S. M. Resnick, and B. A. Landman, "Accounting for Random Regressors: A Unified Approach to Multi-modality Imaging," in MICCAI 2011 Workshop of Multi-Modal Methods, Toronto, Canada, 2011.* URL.

ANALYSIS

- Open BPM, type wfu_bpm



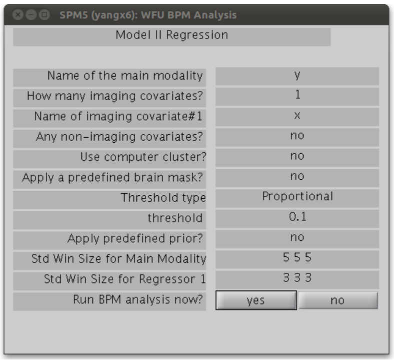
- Estimation: Click “BPM Analysis” button.
- Choose result directory, click “Done”.
- In the pull-down manual of “Select type of analysis”, choose “Model II Regression”.
- Choose the file listing dependent modality images, press “Done”. (regressand.flist)
- Write down the name for the dependent modality (e.g., “y”).
- Write down the number of imaging covariates (“1” here).
- Write down the name for the imaging covariates.
- Choose the file containing the imaging covariate images, press “Done”.
- Select if any non-imaging covariates (e.g., sex, age). If the answer is yes, the value of these covariates should be written in a file with one column for each covariate, select this file, press “Done”.
- Select if use computer cluster. Analysis of typical size images need to use computer cluster to complete estimation in a reasonable time. If not use computer cluster:
    - Select if apply a predefined brain mask. If no, select the threshold type and write down the threshold value.
    - Choose if apply a predefined prior. If yes, select an image prior or type the error ratio for each imaging covariate.



Model II Regression

Name of the main modality	y
How many imaging covariates?	1
Name of imaging covariate#1	x
Any non-imaging covariates?	no
Use computer cluster?	no
Apply a predefined brain mask?	no
Threshold type	Proportional
threshold	0.1
Apply predefined prior?	yes
Image prior?	no
error ratio for regressor image	1
Run BPM analysis now?	yes no

    - If not applying predefined prior, write down the window size for the main modality and the regressor images with one value for each dimension.



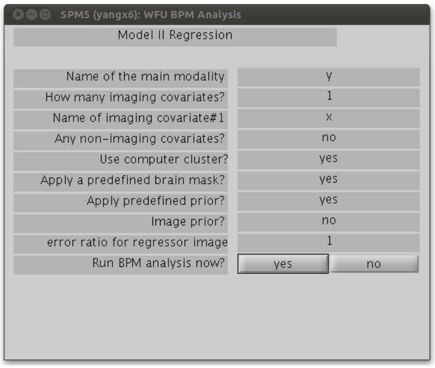
Model II Regression

Name of the main modality	y
How many imaging covariates?	1
Name of imaging covariate#1	x
Any non-imaging covariates?	no
Use computer cluster?	no
Apply a predefined brain mask?	no
Threshold type	Proportional
threshold	0.1
Apply predefined prior?	no
Std Win Size for Main Modality	5 5 5
Std Win Size for Regressor 1	3 3 3
Run BPM analysis now?	yes no

    - Press “yes” to run model II regression analysis, “no” to cancel.

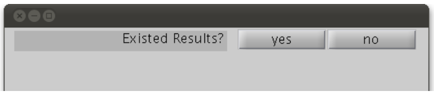
- If use computer cluster

- Enter your email address for the computer cluster.
- Select a .pbs template file to execute qsub. Please refer to the "computer cluster" section for more details.
- Select if apply a predefined brain mask. If no, select the threshold type and write down the threshold value.
- Choose if apply a predefined prior. If yes, select an image prior or type the error ratio for each imaging covariate.

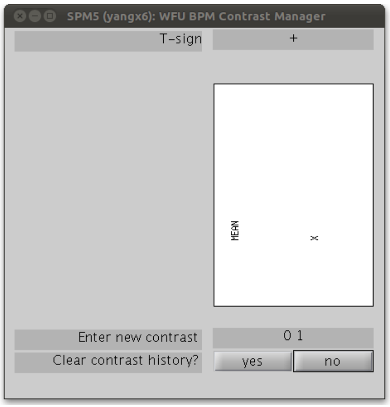


Name of the main modality	y
How many imaging covariates?	1
Name of imaging covariate#1	x
Any non-imaging covariates?	no
Use computer cluster?	yes
Apply a predefined brain mask?	yes
Apply predefined prior?	yes
Image prior?	no
error ratio for regressor image	1
Run BPM analysis now?	yes no

- If not applying predefined prior, write down the window size for the main modality and the regressor images with one value for each dimension.
- Press "yes" to run model II regression analysis, it will ask if results are existed first.
- Choose "no" to submit jobs to computer cluster nodes. It will ask to select the spm toolbox folder and the bpm toolbox folder. The window will pop up again when all jobs are finished and the user can choose "yes" to combine all results together.



- Inference: after model II regression estimation is done, click "Contrast Manager" button.
- Choose the BPM.mat file in the result directory.
- Select positive or negative sign for T-test. (This version only support T-test for Model II regression)
- Enter contrast for each covariate with space between them.

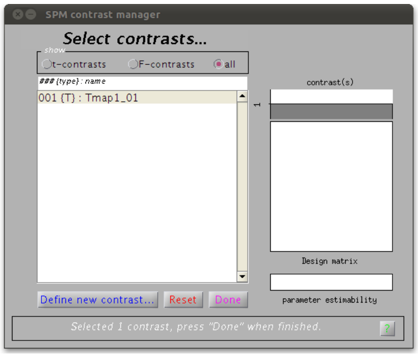


T-sign	+
Enter new contrast	0 1
Clear contrast history?	yes no

VISUALIZATION

- In the BPM toolbox, click "SPM Insertion Tool" button.
- Choose the BPM.mat file in the result directory, press "Done".

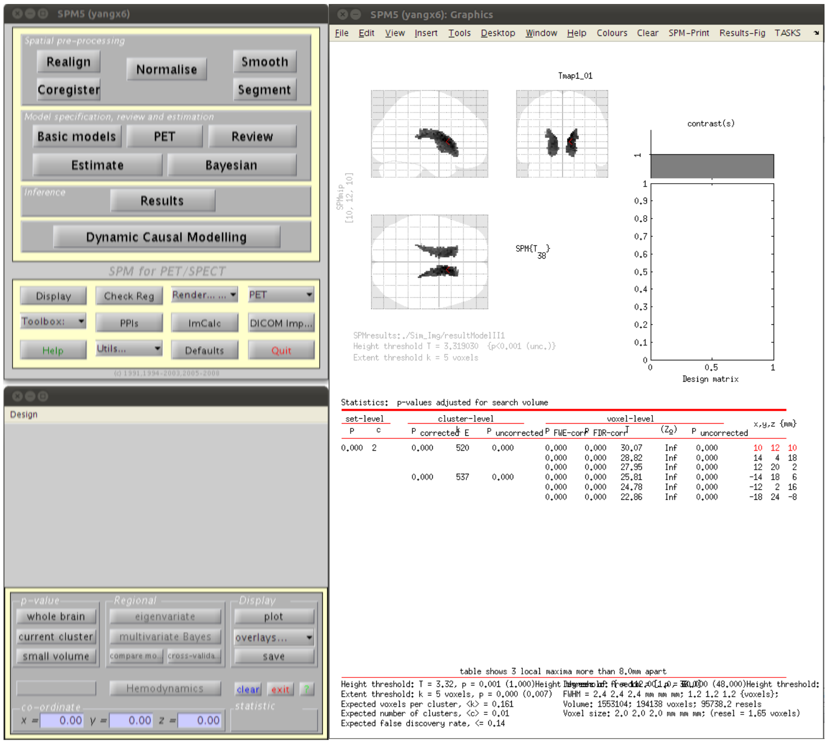
- Type the name of the name of the map title, press enter.
- Open SPM (Type “spm”).
- Click “PET & VBM” button.
- Click “Results” in the pop up toolbox.
- Choose the SPM.mat file in the directory, press “Done”.
- In the SPM contrast manager, choose the map build by BPM.



001 {T} : Tmap1_01

Selected 1 contrast, press "Done" when finished.

- The result is displayed in SPM graphics.



```
SPMresults:./Sim_Img/resultModelII1
Height threshold T = 3.319030  {p<0.001 (unc.)}
Extent threshold k = 5 voxels

Statistics:  p-values adjusted for search volume
set-level        cluster-level                         voxel-level                              x,y,z {mm}
 P     c     P corrected k E   P uncorrected P FWE-corr P FDR-corr T    (Zo)   P uncorrected

0.000  2     0.000      520      0.000       0.000      0.000    30.07   Inf    0.000        10  12  10
                                             0.000      0.000    28.82   Inf    0.000        14   4  18
                                             0.000      0.000    27.95   Inf    0.000        12  20   2
             0.000      537      0.000       0.000      0.000    25.81   Inf    0.000       -14  18   6
                                             0.000      0.000    24.78   Inf    0.000       -12   2  16
                                             0.000      0.000    22.86   Inf    0.000       -18  24  -8

                     table shows 3 local maxima more than 8.0mm apart
Height threshold: T = 3.32, p = 0.001 (1.000)Height threshold: ... (48.000)Height threshold:
Extent threshold: k = 5 voxels, p = 0.000 (0.007)   FWHM = 2.4 2.4 2.4 mm mm mm; 1.2 1.2 1.2 {voxels};
Expected voxels per cluster, <k> = 0.161            Volume: 1553104; 194138 voxels; 95738.2 resels
Expected number of clusters, <c> = 0.01             Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 1.65 voxels)
Expected false discovery rate, <= 0.14
```

REGRESSION CALIBRATION (BPM^{e})- DEMONSTRATION

SIMULATION DATA

Download and extract the BPMe_3.0.zip file, all sample images are in the folder “sampledata”.

The dependent modality images are listed in file regressand.flist

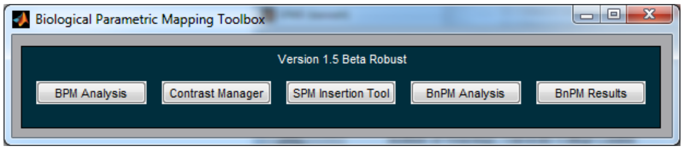
One imaging covariate images are listed in file GM1.flist.

The replicated measurements of the imaging covariate images are listed in file GM2.flist.

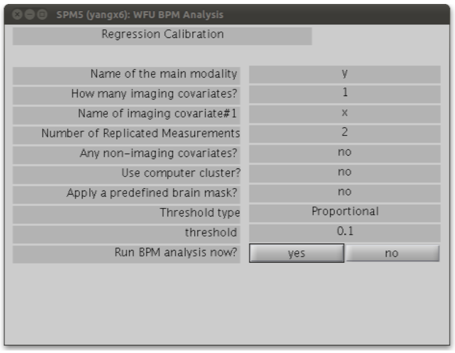
These data is subset of the dataset for Figure 5 in *X. Yang, C. B. Lauzon, C. Crainiceanu, B. Caffo, S. M. Resnick, and B. A. Landman, "Accounting for Random Regressors: A Unified Approach to Multi-modality Imaging," in MICCAI 2011 Workshop of Multi-Modal Methods, Toronto, Canada, 2011.* URL.

ANALYSIS

- Open BPM, type wfu_bpm

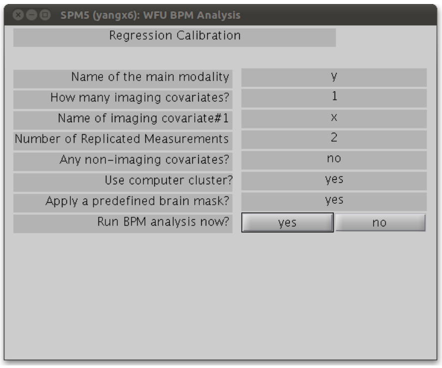


- Estimation: Click “BPM Analysis” button.
- Choose result directory, click “Done”.
- In the pull-down manual of “Select type of analysis”, choose “Regression Calibration”.
- Choose the file listing dependent modality images, press “Done”. (regressand.flist)
- Write down the name for the dependent modality (e.g., “y”).
- Write down the number of imaging covariates (“1” here).
- Write down the name for the imaging covariates.
- Enter number of replicated measurements for the imaging covariates. (“2” here)
- Choose the file containing the imaging covariate images, press “Done”. One measurement by a time.
- Select if any non-imaging covariates (e.g., sex, age). If the answer is yes, the value of these covariates should be written in a file with one column for each covariate, select this file, press “Done”.
- Select if use computer cluster. Analysis of typical size images need to use computer cluster to complete estimation in a reasonable time. If not use computer cluster
    - Select if apply a predefined brain mask. If no, select the threshold type and write down the threshold value.
    - Press “yes” to run regression calibration, “no” to cancel.



Name of the main modality	y
How many imaging covariates?	1
Name of imaging covariate#1	x
Number of Replicated Measurements	2
Any non-imaging covariates?	no
Use computer cluster?	no
Apply a predefined brain mask?	no
Threshold type	Proportional
threshold	0.1
Run BPM analysis now?	yes / no

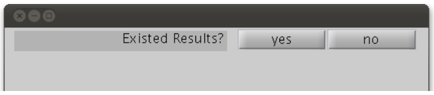
- If use computer cluster,
    - Enter your email address for the computer cluster.
    - Select a .pbs template file to execute qsub. Please refer to the “computer cluster” section for more details.
    - Select if apply a predefined brain mask. If no, select the threshold type and write down the threshold value.



Regression Calibration

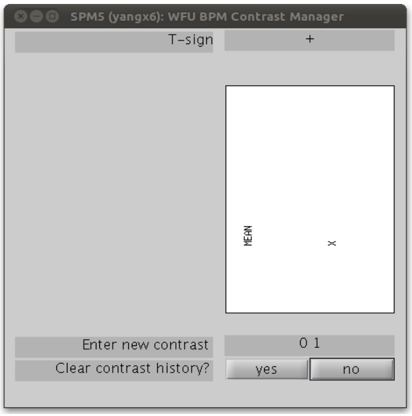
Name of the main modality: y
How many imaging covariates?: 1
Name of imaging covariate#1: x
Number of Replicated Measurements: 2
Any non-imaging covariates?: no
Use computer cluster?: yes
Apply a predefined brain mask?: yes
Run BPM analysis now?

    - Press "yes" to run model II regression analysis, it will ask if results are existed first.
    - Choose "no" to submit jobs to computer cluster nodes. It will ask to select the spm toolbox folder and the bpm toolbox folder. The window will pop up again when all jobs are finished and the user can choose "yes" to combine all results together.



Existed Results?

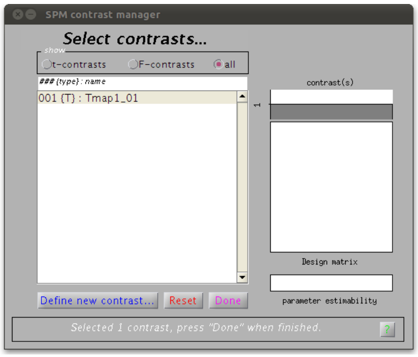
- Inference: after regression calibration estimation is done, click "Contrast Manager" button.
- Choose the BPM.mat file in the result directory.
- Enter contrast for each covariate with space between them.
  Select positive or negative sign for T-test. (This version only support T-test for Model II regression)



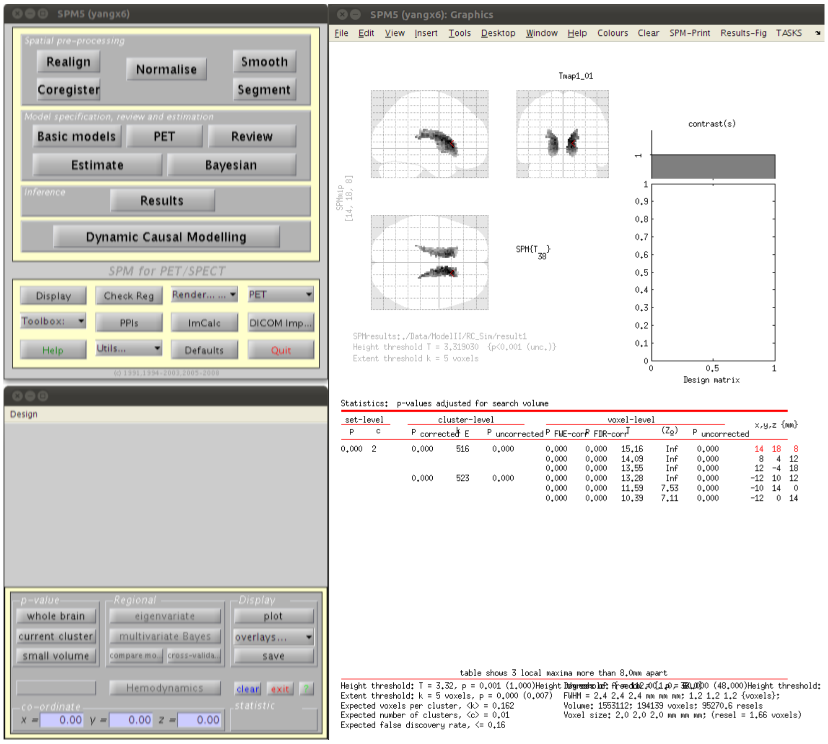
T-sign: +
Enter new contrast: 0 1
Clear contrast history?

VISUALIZATION

- In the BPM toolbox, click "SPM Insertion Tool" button.
- Choose the BPM.mat file in the result directory, press "Done".
- Type the name of the name of the map title, press enter.
- Open SPM (Type "spm").
- Click "PET & VBM" button.
- Click "Results" in the pop up toolbox.
- Choose the SPM.mat file in the directory, press "Done".
- In the SPM contrast manager, choose the map build by BPM.



- The result is displayed in SPM graphics.



```
SPMresults:./Data/ModelII/RC_Sim/result1
Height threshold T = 3.319030  {p<0.001 (unc.)}
Extent threshold k = 5 voxels

Statistics:  p-values adjusted for search volume
set-level      cluster-level                        voxel-level
 P    c   P corrected  kE  P uncorrected  P FWE-corr  P FDR-corr   T     (Zo)  P uncorrected   x,y,z {mm}

0.000  2    0.000     516    0.000        0.000       0.000     15.16   Inf    0.000        14  18   8
                                          0.000       0.000     14.09   Inf    0.000         8   4  12
                                          0.000       0.000     13.55   Inf    0.000        12  -4  18
            0.000     523    0.000        0.000       0.000     13.28   Inf    0.000       -12  10  12
                                          0.000       0.000     11.59   7.53   0.000       -10  14   0
                                          0.000       0.000     10.39   7.11   0.000       -12   0  14

                  table shows 3 local maxima more than 8.0mm apart
Height threshold: T = 3.32, p = 0.001 (1.000)Height Degrees of freedom = [1.0, 38.0]00 (48.000)Height threshold:
Extent threshold: k = 5 voxels, p = 0.000 (0.007)   FWHM = 2.4 2.4 2.4 mm mm mm; 1.2 1.2 1.2 {voxels};
Expected voxels per cluster, <k> = 0.162            Volume: 1553112; 194139 voxels; 95270.6 resels
Expected number of clusters, <c> = 0.01             Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 1.66 voxels)
Expected false discovery rate, <= 0.16
```

COMPUTER CLUSTER

- When mention "computer cluster access" in the manual, it means that
    - `the user has a qsub based cluster,`
    - `matlab is present on all nodes,`
    - `the file system access is shared across all nodes.`
- User needs to select a pbs template file for generating pbs files for each job. The pbs template file should not include the matlab command line. e.g., a pbs template:

```
#!/bin/bash
#PBS -M xue.yang@vanderbilt.edu
#PBS -l nodes=1:ppn=1:x86
#PBS -l walltime=01:00:00
#PBS -l mem=2000mb
#PBS -o xue-cluster.txt
#PBS -j oe
```

The corresponding submitted pbs file for one job is

```
#!/bin/bash
#PBS -M xue.yang@vanderbilt.edu
#PBS -l nodes=1:ppn=1:x86
#PBS -l walltime=1:00:00
#PBS -l mem=2000mb
#PBS -o xue-cluster.txt
#PBS -j oe
matlab -nodesktop < /gpfs21/scratch/yangx6/Sim_Img/resultModelII1/Slice1/modII_slice1.m >matlab.output
touch /gpfs21/scratch/yangx6/Sim_Img/resultModelII1/Slice1job58669.done
```