How to make ROI files

Ver. 1.0

2012/08/07

<u>*Introduction*</u>

This manual explains how to make ROI (Region Of Interest) files that you can use in your analysis through the Brain Decoder Toolbox (BDTB).

You need the following tools to make ROI files.
You can obtain them from the following sources.

- ・SPM (ver.5 is assumed)
   http://www.fil.ion.ucl.ac.uk/spm/

- ・WFU PickAtlas (ver.2.4 is assumed)
   http://fmri.wfubmc.edu/software/PickAtlas
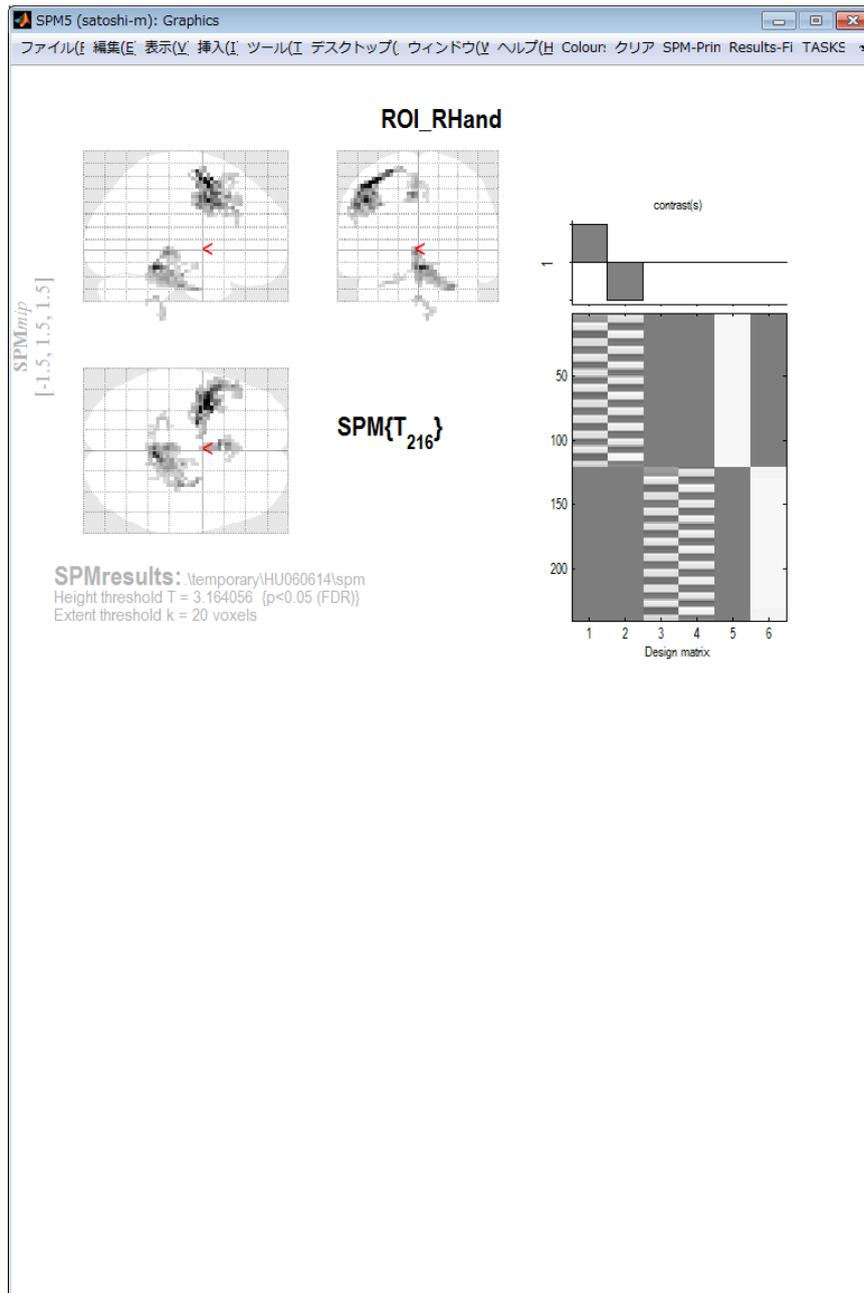
- ・MRIcro
   http://www.cabiatl.com/mricro/

This manual explains only how to make ROI files.
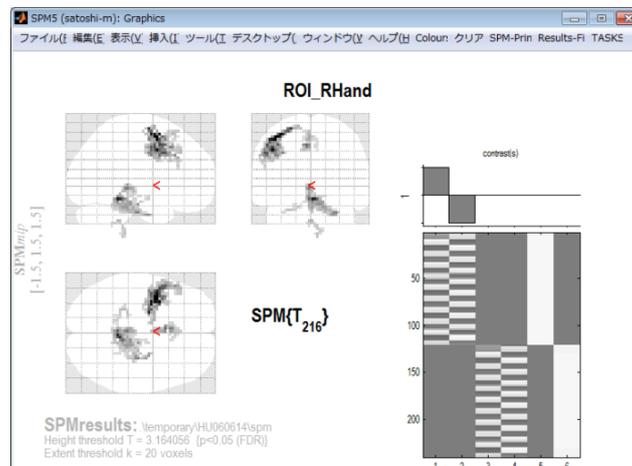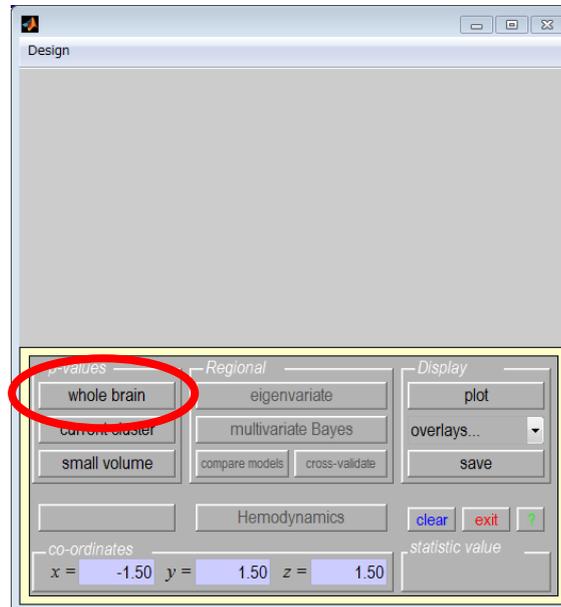Please refer to the each tool's manual for detailed information about it.

Functional ROI

> The ROI is defined as the area that is active during a ROI session.

1. Perform a ROI session analysis using SPM
2. Show the results of the analysis in the "Graphics" window.

3. Click the "whole brain" button, and information about voxels will be shown in the Graphics window.

ROI_RHand

$SPM\{T_{216}\}$

SPMresults: \temporary\HU060614\spm
Height threshold T = 3.164056 {p<0.05 (FDR)}
Extent threshold k = 20 voxels

Statistics: *p-values adjusted for search volume*

set-level		cluster-level			voxel-level					mm mm mm		
p	c	$p_{corrected}$	k_E	$p_{uncorrected}$	$p_{FWE-corr}$	$p_{FDR-corr}$	T	$(Z_=)$	$p_{uncorrected}$			
0.000	5	0.000	298	0.000	0.000	0.000	22.92	Inf	0.000	-41	5	53
					0.000	0.000	21.78	Inf	0.000	-35	8	59
					0.000	0.000	21.12	Inf	0.000	-35	-2	59
		0.000	287	0.000	0.000	0.000	19.63	Inf	0.000	2	-41	-14
					0.000	0.000	12.04	Inf	0.000	-2	-29	-2
					0.000	0.000	11.17	Inf	0.000	29	-17	-29
		0.000	59	0.000	0.000	0.000	13.24	Inf	0.000	-5	14	47
					0.000	0.000	7.67	7.21	0.000	-2	5	56
					0.152	0.000	4.66	4.54	0.000	-2	32	44
		0.000	29	0.000	0.000	0.000	7.04	6.67	0.000	2	-41	-38
					0.000	0.000	6.13	5.88	0.000	8	-32	-53
		0.000	28	0.000	0.000	0.000	7.04	6.67	0.000	-2	23	59
					0.977	0.002	4.22	4.13	0.000	5	23	44

table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 3.16, p = 0.001 (1.000) {p<0.05 (FDR)}
Extent threshold: k = 20 voxels, p = 0.000 (0.000)
Expected voxels per cluster, <k> = 0.287
Expected number of clusters, <c> = 0.00
Expected false discovery rate, <= 0.05

Degrees of freedom = [1.0, 216.0]
FWHM = 4.5 4.0 3.9 mm mm mm; 1.5 1.3 1.3 {voxels};
Volume: 1464318 = 54234 voxels = 17913.7 resels
Voxel size: 3.0 3.0 3.0 mm mm mm; (resel = 2.59 voxels)

4. Select the group of voxels that you want to use as a ROI by clicking the "mm mm mm" column.

Then the font color of the coordinate value will change to red, and a red arrow will appear in the brain image.
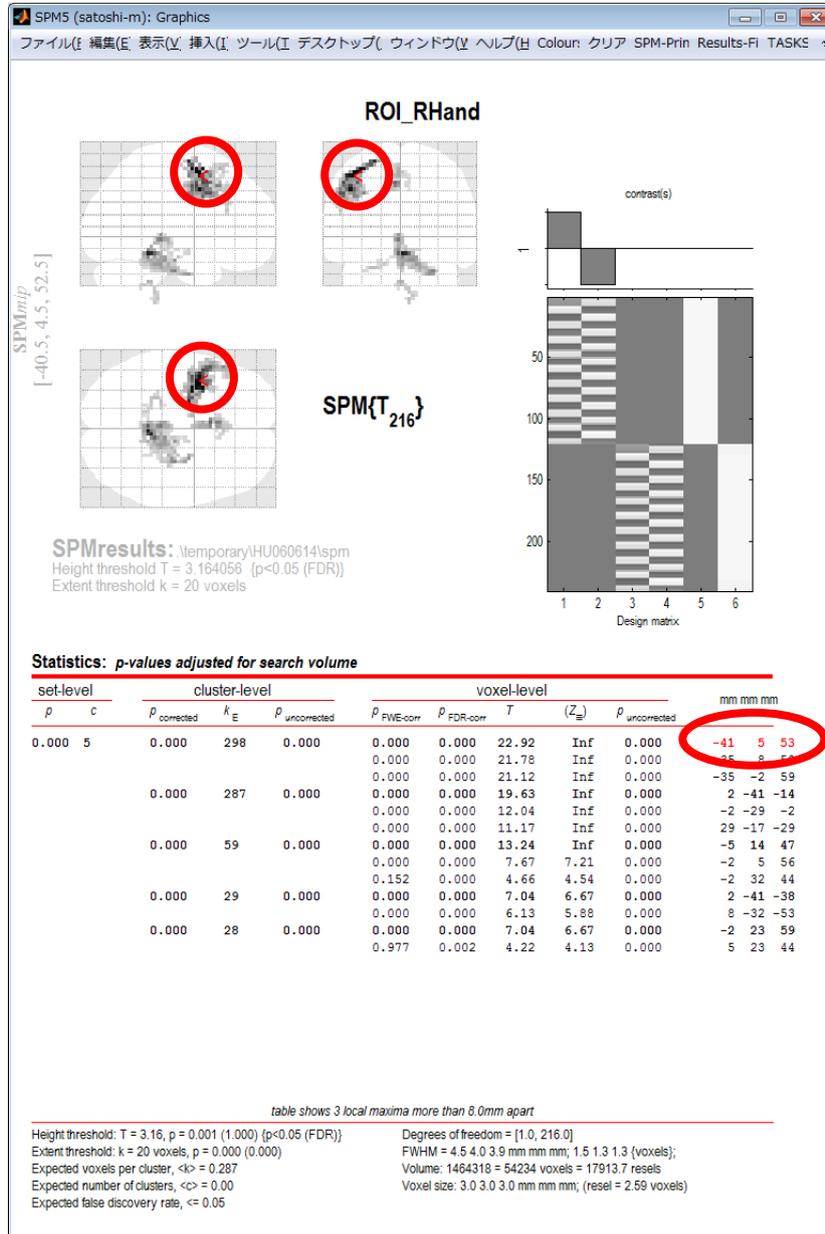
5. On the MATLAB command window, input and run the following code.

```
>> [x, i] = spm_XYZreg( 'NearestXYZ' , ans, xSPM.XYZmm);     ①
>> A = spm_clusters(xSPM.XYZ);                                 ②
>> C = find(A==A(i));                                          ③
>> roi = xSPM.XYZmm(:, C);                                     ④
>> roi(4,:) = xSPM.Z(:, C);                                    ⑤
```

> The brief explanation of the above procedure:
> The variable "ans" contains the coordinate value that is selected in 4.
> In ①, get the cluster ID that includes the coordinate value.
> In ②, get the cluster ID list of each voxel.
> In ③, get the index of the selected group of voxels.
> In ④, get the coordinate values of the group of voxels.
> In ⑤, get the intensity of the group of voxels.
> Finally, the data is put into a 4(x,y,z,intensity) x number of voxels format
>   and saved into the variable "roi".
> (Please refer to the help of each function for more detailed information)

6. Save variable "roi".

    In BDTB, the default names of ROI files are "VOX_*".

Structural ROI

The ROIs are defined according to the brain structure.

1. Run "WFU PickAtlas".
   a. On the MATLAB command window, input
      >> wfu_pickatlas
   b. Run SPM, and select "wfupickatlas" from "Toolbox:".
2. Make a ROI and save it as an image file on WFU PickAtlas.
3. Convert the ROI image file based on the standard-brain into that based on the individual-brain.
   (Please skip this process when your analysis is based on standard-brain)
   i. Normalize individual data (ex. 3D) by SPM.
       This process is needed only to get the parameter file for ROI image file conversion. Don't normalize the data that you'll analyze.
   ii. Run SPM, and select "TASKS" – "Util" – "Deformations" from the menu bar in the "Graphics" window.
   iii. Select "New "Inverse"" at "Deformations" – "Composition" in the "Graphics" window.
   iv. Select "New "Imported _sn.mat"" at "Deformations" – "Composition" – "Inverse" – "Composition".
   v. Specify the "*_sn.mat" file (ex. 3D_sn.mat), that was created in the normalizing process (i), at "Deformations" – "Composition" – "Inverse" –"Composition" – "Imported _sn.mat".
   vi. Specify the individual brain image file (ex. 3D.img), that was used in the normalizing process (i), at "Deformations" – "Composition" – "Inverse" – "Image to base inverse on".
   vii. Specify the ROI image file, that was created in 2., at "Deformations" – "Apply to".
   viii. Click the "Run" button, and the converted ROI file is created.
4. Perform a ROI session analysis using SPM
5. Select "yes" at "ROI Analysis", this parameter appears between "mask with other contrast(s)" and "title for comparison" in "Result" process.
   If the parameter doesn't appear, please make sure the directory of WFU PickAtlas is on the MATLAB path.
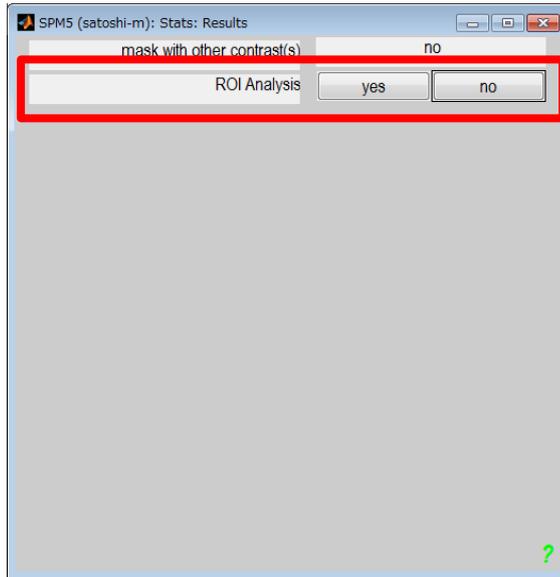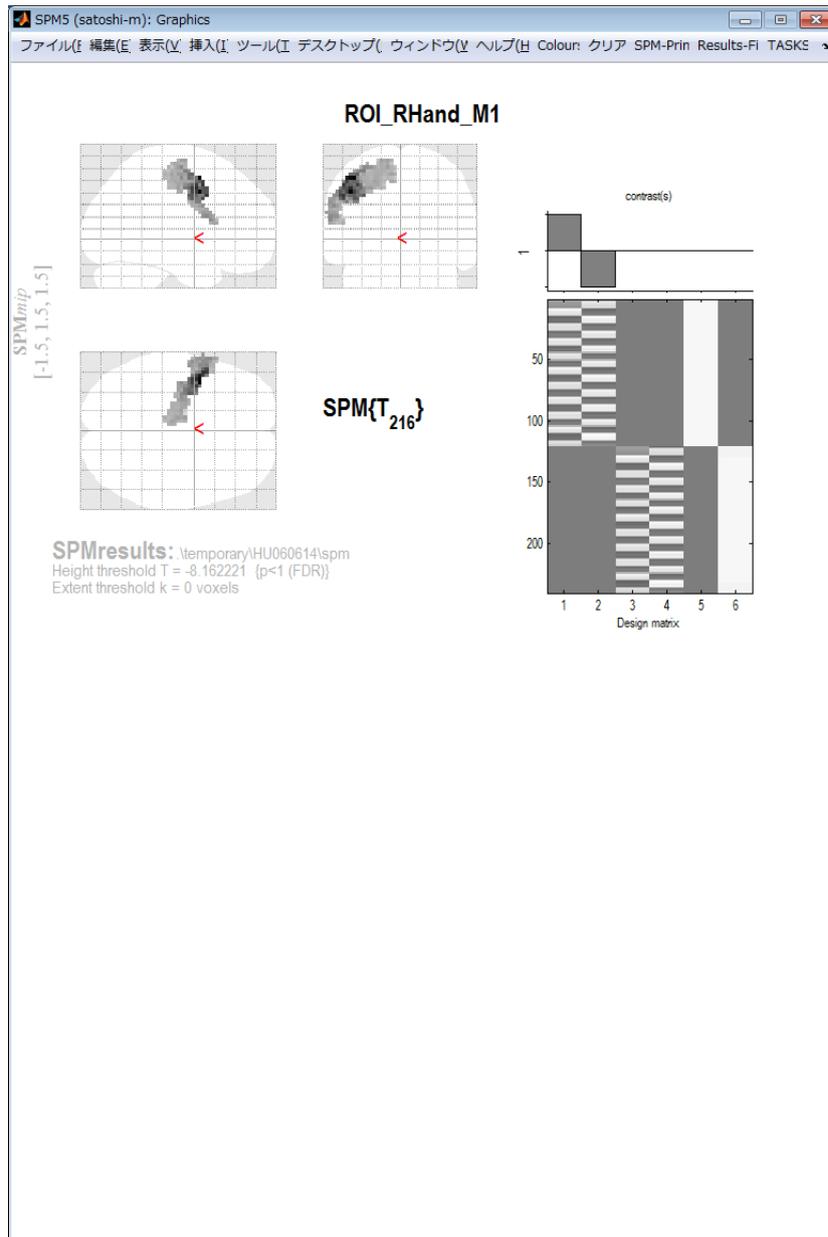
6. Select "Saved File" at "ROI analysis from".
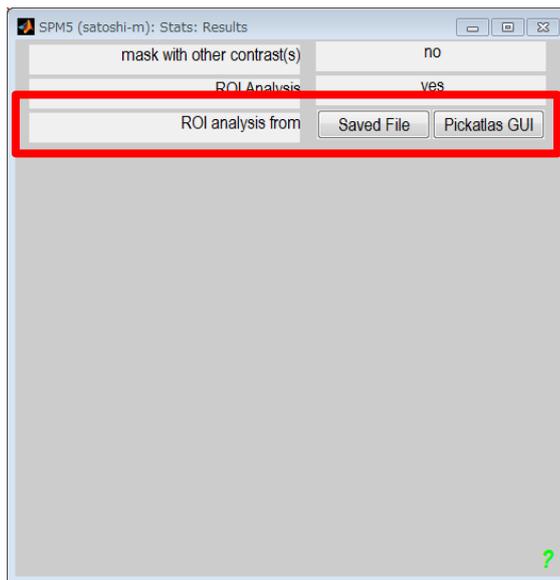
7. Specify ROI image file that you created (and normalized).

8. Show the result in "Graphics" window.

9. Make ROI file by the same method of <u>3.~ in Functional ROI</u>.

Hand-made ROI

Specify the area on the brain image manually, and save it as ROI.

1. Open the brain image that you'll analyze with "MRIcro".
2. Specify the area that you want to use as a ROI with the "Region of Interest" tool.
3. Select "ROI" – "Export ROI as Analyze image…" at the menu bar, and save the area as a ROI image file.
4. The Analyze format image file is created, so use it as the mask in the same way as 5.~ in Structural ROI.

History

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