

Robust Regression Toolbox help

This document is divided into several sections:

- A) Installation and requirements
- B) Getting started & graphic interface (GUI)
- C) Setup of data structure EXPT to use with robust regression
- D) Running robust regression
- E) Thresholding and visualizing results

About the toolbox:

The robust regression toolbox was created by Tor Wager, currently Assistant Professor at Columbia University.

If you use it, please see (and cite) the accompanying paper:

Wager, T. D., Keller, M. C., Lacey, S. C., & Jonides, J. (2005). Increased sensitivity in neuroimaging analyses using robust regression. *Neuroimage*, 26(1), 99-113.

A) Installation and requirements

You will need to download two SCNlab packages, each with several subdirectories, and place them on your Matlab path. You will also need SPM installed and on your Matlab path (most extensive testing: SPM2, but should work with SPM99/SPM2/SPM5).

The first SCNlab toolbox is the robust_toolbox folder.

The second is the SCN_Core_Support folder.

Optional: If you want to take full advantage of the results visualization of the SCNlab tools, you will also need the 3DheadUtility folder (not on the web currently; ask the authors if interested).

To install these, place them in a folder on your hard drive, and type

`>> pathtool`

at the Matlab command prompt.

Select each of the folders named above, and select “add with subfolders”

Use of SPM and other toolboxes

The robust regression toolbox is not an SPM toolbox per se. It uses SPM image manipulation (data I/O) functions, but does not rely on any SPM functions for statistics. It does, however, use the Matlab Statistics Toolbox, so you will need that as well.

B) Getting started & graphic interface

The robust regression toolbox uses a data structure with a specific format that stores information about image files and the second-level experimental design. This structure has a special variable name, EXPT. The toolbox contains tools to help you create this data structure automatically, but it's helpful if we first explain the structure of the information.

The main 2nd-level analysis function is called robfit.m.

Here is a list of the fields in EXPT required to ultimately run analyses with robfit:

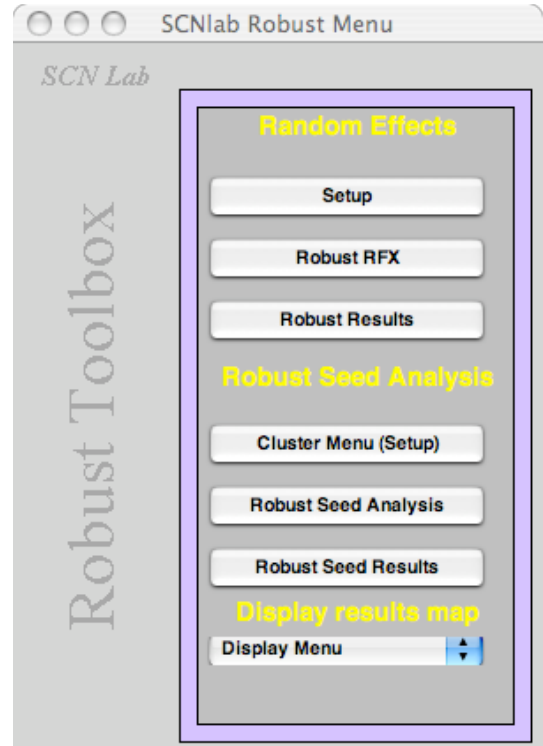
EXPT.subjects	List of subject directory names, in a cell array. {'subj1' 'subj2' ... etc.}
EXPT.SNPM.P	Cell array; each cell contains names of a set of images (one per subject) to be subjected to a group analysis. Each image list is a string matrix of image file names. Thus, images for multiple 2nd level analyses can be specified at once by entering images for each analysis into separate cells in EXPT.SNPM.P
EXPT.SNPM.connames	String matrix of names, whose rows correspond to names for the analyses. Each row (name) corresponds to the cell with the same index in EXPT.SNPM.P. E.g., ['Faces-Houses' 'Houses-Faces']
EXPT.SNPM.connums	A vector of integers numbering the analyses, and corresponding to cells in EXPT.SNPM.P. These numbers determine output directory names, which will be called: robust_0001 robust_0002 ...and so forth (one directory per 2nd-level analysis)
EXPT.mask	Name of mask image containing in-analysis voxels. This need not be in the same space as the images you're analyzing.

The graphic user interface (GUI) provides a way to organize and interact with the major functions. There are functions not included in the GUI.

Type **robust_toolbox_gui** to load the graphic interface. This has buttons that perform the major steps in the analysis. When it opens, the GUI will attempt to first use the EXPT variable in the workspace or, if it does not exist, load EXPT.mat, which contains the EXPT structure.

You can modify the EXPT structure in the workspace. Each time a GUI function is called (i.e., a button is pushed), the EXPT in the base workspace is loaded into the GUI workspace, so it will know about your updates.

You can save an EXPT structure created in the GUI or otherwise by typing “save EXPT EXPT”. This will save EXPT.mat in the current directory.



C) Setup of input data structure

Before running an analysis, you need to create an EXPT structure. There are several ways to do this.

- 1) Use the GUI and click Setup
 - a. This runs CreateExpt, and is the same as option 2.
- 2) Run the CreateExpt batch setup tool from the command line
 - a. See below for an example.
- 3) Add or modify fields in the EXPT variable manually
 - a. E.g., get images by using SPM's selection features:
EXPT.SNPM.P{1} = spm_get(); % for SPM2
EXPT.SNPM.P{1} = spm_select(); % for SPM5

Important note: An important feature of robfit.m is that will perform multiple regression at the second level, simultaneously testing the intercept (the analogue of the one-sample t-test for activation) and between-subjects covariates you may have entered into the model. You cannot add covariates using the GUI or CreateExpt, so you have to add them yourself to the EXPT structure after creating it with one of these tools. Each column in EXPT.cov is a between-subjects regressor. For example, say I'm interested in activation and correlations between activation and performance scores, controlling for drug

administration order. EXPT.cov(:,1) would contain a vector of N performance scores, one for each subject. EXPT.cov(:,2) would contain the admin order for each subject, coded as 1 or -1 (i.e., contrast coded).

For the intercept statistic values to be interpretable in terms of group (overall) activation, covariates must be centered, and this is done automatically within robfit. However, an important exception is in the case of contrast coded variables. Centering gives the equivalent of Type II sums of squares, whereas un-centered covariates gives the eq. of Type III SS of interest in most experimental designs. Therefore, if you have a nuisance variable with two levels, I recommend contrast coding with 1 or -1. In this case, robfit will recognize this and not center. If you dummy code, however, the regressor will be centered and you will get Type II SS.

The CreateExpt batch tool:

Following is an example of the commands I entered to set up an analysis, followed by the complete log of the session. To do this, I have each subject's images to be subjected to robust 2nd level analysis in a directory labeled with the subject's ID. The id's, and folder names, are 1001-1015. Within each directory, there are images whose names corresponds to a particular contrast of interest. A given contrast has the same name for all subjects.

Here's what I typed:

```
EXPT = CreateExpt('robfit');
1*
con*img
interaction
high-low
p-c_heat
p-c_warm
p-c_warm2
p-c_main_effect
```

Here's the full log:

```
>> EXPT = CreateExpt('robfit');

* ===== *
*                                     *
*          CreateExpt: batch data structure setup          *
*                                     *
*          Tor Wager, version July 2006                     *
*                                     *
* This function creates a data structure called EXPT that stores info *
* about your experimental designs and parameters. This structure can be *
* saved in a file called EXPT.mat and may be useful for reference.      *
* Many analysis toolboxes refer to various fields of EXPT to get filenames *
* and other info needed for analysis.                                *
* CreateExpt is a utility tool to help you set this up, but you can create *
* or edit any of the fields manually.                               *
*                                     *
* This process is sort of the 'weakest link' in the analyses at present *
* Please contact me if you run into bugs.                      *
*                                     *
* ===== *

Setting up analysis for: robfit
Required fields that CreateExpt will attempt to create are:
```

EXPT.subjects	List of subject directory names
EXPT.SNPM.P	Cell array; each cell is a string matrix of image file names, one per subject; one cell per contrast
EXPT.SNPM.connames	String matrix of names of each contrast, corresponding to cells in EXPT.SNPM.P
EXPT.SNPM.connums	Numbers of contrast images, corresponding to cells in EXPT.SNPM.P; determines output directory names
EXPT.mask	Name of mask image containing in-analysis voxels.

* ===== *

```

Creating field: EXPT.subjects.
Enter wildcard (e.g., 0*): 1*
Creating field: EXPT.SNPM.P.
Collect images for random effects.
Enter image wildcard (e.g., con*img: con*img
Finding con_H(P-C)-L(P-C)_activ.img images in subjects ., storing in tmp
1001.1002.1003.1004.1005.1006.1007.1008.1010.1011.1012.1013.1014.1015.1016.
Chk sorting. EXPT.tmp = sort_image_filenames([EXPT.tmp]);
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Saved images in: EXPT.SNPM.P{1}
Finding con_H-L_activ.img images in subjects ., storing in tmp
1001.1002.1003.1004.1005.1006.1007.1008.1010.1011.1012.1013.1014.1015.1016.
Chk sorting. EXPT.tmp = sort_image_filenames([EXPT.tmp]);
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Saved images in: EXPT.SNPM.P{2}
Finding con_P-C_Highheat_activ.img images in subjects ., storing in tmp
1001.1002.1003.1004.1005.1006.1007.1008.1010.1011.1012.1013.1014.1015.1016.
Chk sorting. EXPT.tmp = sort_image_filenames([EXPT.tmp]);
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Saved images in: EXPT.SNPM.P{3}
Finding con_P-C_Lowheat_activ.img images in subjects ., storing in tmp
1001.1002.1003.1004.1005.1006.1007.1008.1010.1011.1012.1013.1014.1015.1016.
Chk sorting. EXPT.tmp = sort_image_filenames([EXPT.tmp]);
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Saved images in: EXPT.SNPM.P{4}
Finding con_P-C_Warm_activ.img images in subjects ., storing in tmp
1001.1002.1003.1004.1005.1006.1007.1008.1010.1011.1012.1013.1014.1015.1016.
Chk sorting. EXPT.tmp = sort_image_filenames([EXPT.tmp]);
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Saved images in: EXPT.SNPM.P{5}
Finding con_P-C_activ.img images in subjects ., storing in tmp
1001.1002.1003.1004.1005.1006.1007.1008.1010.1011.1012.1013.1014.1015.1016.
Chk sorting. EXPT.tmp = sort_image_filenames([EXPT.tmp]);
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Saved images in: EXPT.SNPM.P{6}
Creating field: EXPT.SNPM.connames.
Add information about the contrast names.

```

Images in this contrast:

```

/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1001//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1002//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1003//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1004//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1005//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1006//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1007//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1008//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1010//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1011//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1012//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1013//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1014//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1015//con_H(P-C)-L(P-C)_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1016//con_H(P-C)-L(P-C)_activ.img
Enter contrast name for this set (avoid spaces/special chars): interaction

```

Images in this contrast:

```

/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1001//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1002//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1003//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1004//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1005//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1006//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1007//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1008//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1010//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1011//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1012//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1013//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1014//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1015//con_H-L_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1016//con_H-L_activ.img
Enter contrast name for this set (avoid spaces/special chars): high-low

```

Images in this contrast:

```

/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1001//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1002//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1003//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1004//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1005//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1006//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1007//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1008//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1010//con_P-C_Highheat_activ.img
/Users/tor/Documents/Tor_Documents/CurrentExperiments/Personal/Opioi
d_binding_placebo/Opioi
d_Placebo4/1011//con_P-C_Highheat_activ.img

```

Images in this contrast:

Images in this contrast:

Images in this contrast:

>>

```
'1001'  '1002'  '1003'  '1004'  '1005'  '1006'  '1007'  '1008'  '1010'  '1011'
```

Columns 11 through 15

```
'1012' '1013' '1014' '1015' '1016'
```

```
save EXPT EXPT
```

Now you have a file called EXPT.mat in the directory above individual subject directories. The individual dirs contain contrast images that you want to run random effects analyses on.

2) Now, you need to save the names of the contrast images you're interested in in EXPT. You should already have run the individual subject models in some other software (e.g., SPM) and created contrast images.

EXPT.SNPM.P is a cell array with one cell per random effects analysis. EXPT.SNPM.P{j} contains the names of contrast images for all subjects for contrast number j.

Option 1: Use `spm_get` and pick them manually

Option 2:

```
EXPT = getfunctnames2(EXPT,'con_P-C_Highheat*img','tmp');
```

```
tmp = str2mat(EXPT.tmp{:});
```

```
EXPT.SNPM.P{1} = tmp;
```

The above saves file names in the first cell of EXPT.SNPM.P

3) Now you need to add information about the contrast names. This goes in EXPT.SNPM.connames.

This is a string matrix with one row per contrast.

```
>> connames = {'contrast 1' 'contrast 2' 'contrast 3'}; connames = str2mat(connames{:})
```

```
connames =
```

```
contrast 1
```

```
contrast 2
```

```
contrast 3
```

```
EXPT.SNPM.connames = connames;
```

We also need an index number for each contrast. Robfit will run through each analysis in order, saving the results in a directory called robust000#, where # is the contrast number from EXPT.SNPM.connames.

4) You may want to add covariates (between subjects effects) – of interest or not. These go in EXPT.cov

One row per subject, one column per predictor.

Do not include an intercept here. It will be added to the front end of the design matrix, as the first predictor.

The output images, i.e., rob_tmap_0001.img, are numbered so that 0001 is the intercept (overall activation) and 0002 – 0000x are the maps for covariates 1 thru (x-1)

D) Running robust regression

5) Now we're ready to run.

```
save EXPT EXPT
```

```
EXPT = roffit(EXPT);
```

...or click on Robust RFX in the GUI.

Try help roffit for more options.

You can specify that you want to run only some contrasts in EXPT.SNPM.P. You can specify that you want to create OLS images side by side with robust images to compare. And you can specify a mask filename. The mask image should have 1's and 0's, with 1's in voxels you want to analyze.

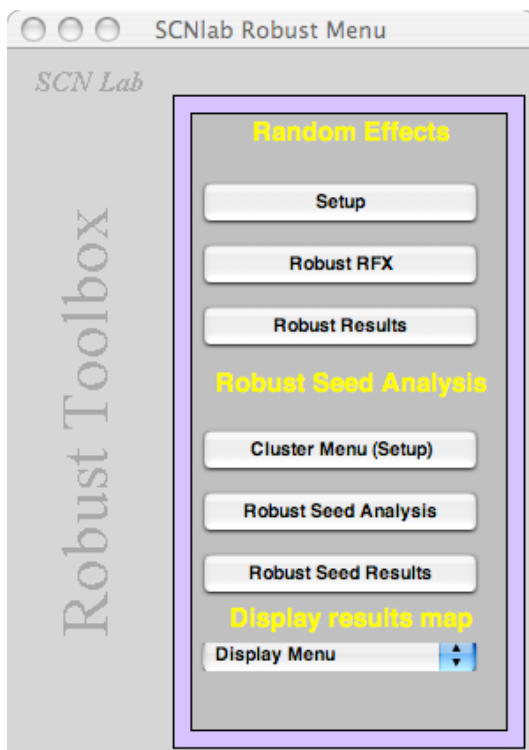
E) Thresholding and visualizing results

General info that you don't actually need to know to get results but that is useful if you want to use the programs flexibly:

Many thresholding and visualization tools in our lab use a clusters structure which saves information about a series of contiguous suprathreshold clusters. Coordinates, data, and other information can be attached. This structure is used in our lab to visualize and analyze 'blobs' and for ROI analysis. Clusters variables are usually named clusters or cl. Cl is a vector whose elements correspond to contiguous regions of voxels. Each element of a cl vector is a structure containing some of the info found in SPM.mat files, such as voxel and mm xyz coordinates and z-scores (though the z field is a bit of a misnomer, unfortunately, because it can contain t-scores or other values, depending on the application.) The tools below threshold robust p-value and/or t-value images and create cl structures, which are then saved and/or passed to visualization functions like cluster_orthviews.m and cluster_surf.m.

When you load the GUI, it also attempts to access a variable called "cl" in the base workspace.

You can use the GUI to display results.



Under the “Display Menu” at the bottom, there are several options. “Threshold/Display” is used to simply display a single image at a designated threshold. “Thresh/Disp With Scatterplots” is similar but allows for displaying correlations and/or further thresholding with another image. “Cluster tools menu” opens up the ROI toolbox GUI. “Intercept” and “Cov1” currently have no effect.

You can also run the results functions from the command line:

First, make sure the EXPT object is loaded, and go a robust*** results directory

There are two main ways to display results. Robust_results3 generates a filtered output image, and displays slice montages based on hard-coded thresholds.

Robust_results_threshold displays in the standard 3-view orthogonal display, and is very flexible.

For robust_results3, run robust_results3 to generate output for display or further analysis. A nice default is robust_results3(EXPT, .005, 10, 'resultnames', {'Contrast name', 'Covariate 1', 'Covariate 2', 'etc'})

This generates a filtered Analyze img at the threshold specified (here, .005) with a minimum cluster size of 10. (NB: instead of a numerical p-value, 'FDR' can also be specified for an automatically computed p-value based on a False Discovery Rate of .05).

robust_results3 also display two images per result (intercept/covs), an axial montage and a medial montage. These are automatically saved as PNG files based on the names you pass in. NB: The thresholds used in the display images are NOT related to the threshold you pass in for generating the filtered Analyze img. This will be fixed in the future.

For a more targeted look at the results, one that you can click around in, use robust_results_threshold. At its simplest, just run:

```
[clpos, clneg, dat, volInfo] = robust_results_threshold(.005, 10)
```

from inside a robust???? directory. But be sure to check the help of `robust_results_threshold`, as it has a lot of options, including the types of images to use (t, p, or raw), the types of thresholds (t, p, or raw), masks to apply, overlays to draw activations on, covariates, etc.