

# ConnectivityToolbox

## How-To (a sketch)

This is a tool that allows for seed-based connectivity analysis. The tool is inherently batch capable.

Things you will need for using:

- spm8Batch preprocessed data
- regions-of-interest (either coordinates or images)
- moderate comfort with editing matlab .m files

# ConnectivityToolbox

## How-To (a sketch)

This tool was developed by Robert Welsh with support from NIH R01NS052514 and released through UM-Psych Methods Core.

To utilize you will need to copy the template code to your working experimental directory and modify to your specific experimental conditions. This template is:

`...../MethodsCore/ConnTool/ConnTool_mc_batch_template.m`

The following pages will outline the changes you need to implement.

# Input

# Output

## ConnTool\_mc\_batch\_template

time-series  
data

realign.dat

WM\_ero

CSF\_ero

ROIS

```
#####
%% GENERAL OPTIONS
%% These options are shared among many of our scripts
#####

%% The folder that contains your subject folders
Exp = '/Volumes/ALS/ALS2008/';

%% Path where your images are located
%%
%% Variables you can use in your template are:
%% Exp = path to your experiment directory
%% iSubject = index for subject
%% Subject = name of subject from SubjDir (using iSubject as index of row)
%% iRun = index of run (listed in Column 3 of SubjDir)
%% Run = name of run from RunDir (using iRun as index of row)
%% * = wildcard (can only be placed in final part of template)
%% Examples:
%% ImageTemplate = '[Exp]/Subjects/[Subject]/func/run_0[iRun]';
%% ImageTemplate = '[Exp]/Subjects/[Subject]/TASK/func/[Run]';
ImageTemplate = '[Exp]/Subjects/[Subject]/connect/func/[Run]';

%% A list of run folders where the script can find functional images
RunDir = {
    'run_01';
};

%% The list of subjects to process
%% The format is 'subjectfolder', subject number in masterfile, [runs to include]
SubjDir = {
    '111129eb', 1, [1];
};
```

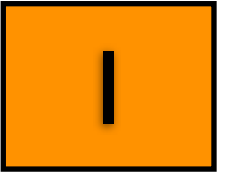
maps

images

With the script you specify input data, and control parameters for how the analysis will proceed, which in turn will produce output matrices or images.

Details on things to change in the script  
to execute a connectivity analysis





```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% GENERAL OPTIONS
%% These options are shared among many of our scripts
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% The folder that contains your subject folders
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
Exp = '/Volumes/ALS/ALS2008/';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Path where your images are located
%%
%% Variables you can use in your template are:
%%     Exp = path to your experiment directory
%%     iSubject = index for subject
%%     Subject = name of subject from SubjDir (using iSubject as index of row)
%%     iRun = index of run (listed in Column 3 of SubjDir)
%%     Run = name of run from RunDir (using iRun as index of row)
%%     * = wildcard (can only be placed in final part of template)
%% Examples:
%% ImageTemplate = '[Exp]/Subjects/[Subject]/func/run_0[iRun]';
%% ImageTemplate = '[Exp]/Subjects/[Subject]/TASK/func/[Run]';
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ImageTemplate = '[Exp]/Subjects/[Subject]/connect/func/[Run]';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% A list of run folders where the script can find functional images
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
RunDir = {
    'run_01';
};

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% The list of subjects to process
%% The format is 'subjectfolder',subject number in masterfile,[runs to include]
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
SubjDir = {
    '111129eb',1,[1];
};
```

Specify the top-level directory of your experiment.

Generic path to your time-series data.

List of runs for processing.

List of subjects and run numbers to use for each subject.

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% The TR your data was collected at
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
TR = 2;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% The file to extract the CSF and WM confounds from
%%
%% It usually the run file that is in MNI space but prior
%% to smoothing. The idea is that you don't want gray
%% smoothed into the CSF or WM regions.
%%
%% This can be the same file as the 'connectFile', but not ideal.
%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
confoundFile = 'w3mm_vbm8_ra8_run';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% The file to run the connectivity on
%%
%% This will be the smoothed and warped to MNI file.
%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
connectFile = 's5mm_w3mm_vbm8_ra8_run';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Image Type should be either 'nii' or 'img'
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
imagetype = 'nii';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Number of Functional scans per run
%% (if you have more than 1 run, there should be more than 1 value here)
%%
%% If you have subjects with varying number of time points you can pick
%% the smallest, that will edit them down so they all have the
%% same effective statistical power.
%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
NumScan = [240];

```

Sample period of your time-series data.

File name of your time-series data PRIOR to smoothing.

File name of your time-series data AFTER to smoothing.

Type of image file.

How many time-points to use for each run.

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% CONNECTIVITY OPTIONS
%% These options are only used for Connectivity
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Mode to run som_batch_mc_central in
%%      'test'      = test script but do not save parameters or run any
%%                    SOM code
%%      'parameters' = run script and save parameters for each subject
%%                    but do not run any SOM code
%%      'som'        = run SOM code on previously saved parameters
%%      'full'       = generate parameters and immediately run SOM code
%%
%%      NOTE: If you choose mode 'som' then most variables except
%%      SubjDir and OutputTemplate/OutputName will be ignored as they
%%      will be loaded from the already existing parameter file for each
%%      subject.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
Mode = 'full';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Pointers to for anatomic images.
%%
%%      AnatomyMaskPath --- this should point to the VBM8 processed data
%%
%%      GreyFile  --- name of a grey matter image from VBM8 -- Just leave
%%                    blank, in general don't use this option.
%%
%%      WhiteFile --- name of the WM image produced by VBM8
%%
%%      CSFFile   --- name of the CSV image produced by VBM8
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
AnatomyMaskPath = '[Exp]/Subjects/[Subject]/connect/func/coRegRARUN/VBM8/';

GreyFile  = [];
WhiteFile = 'WM_ero*.nii';
CSFFile   = 'CSF_ero*.nii';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Where to output the data
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
OutputTemplate = '[Exp]/FirstLevel/[Subject]/[OutputName]';
OutputName     = 'censortest';

```

Mode to run in, if you're unsure just specify 'full';

Information on where to find the output of the vbm8HiRes command.

Path for output directory and name of output file.

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Path and name of explicit mask to use at subject level.
%% Leaving this blank (') will use a subject-specific mask
%%
%% NOTE: Subject-specific masks are NOT recommended at all.
%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
BrainMaskTemplate = ...
    '[mcRoot]/ConnTool/Templates/symmetric_r3mm_EPI_MASK_NOEYES.nii';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Path Template for realignment parameters file
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
RealignmentParametersTemplate = ...
    '[Exp]/Subjects/[Subject]/connect/func/[Run]/mcflirt*a8*.dat';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Path Template for file containing timepoints to censor from the data
%% This file should either be a simple text file containing a column of
%% 1s and 0s, or a saved MATLAB .mat file with a cv variable containing a
%% column of 1s and 0s
%%
%% Robert DOES NOT RECOMMEND CENSORING YOUR DATA.
%%
%% This ConnTool Toolbox users an FFT filter with a little
%% but of smoothing. If you want to censor you take the risk of
%% created artifactual correlations across the whole brain
%%
%% See the following three papers:
%%
%% Power JD, Barnes KA, Snyder AZ, Schlaggar BL, Petersen SE.
%% Spurious but Systematic Correlations in Functional Connectivity
%% MRI Networks Arise From Subject Motion. NeuroImage 2012;59:214-2154.
%%
%% Carp J. Optimizing the Order of Operations for Movement Scrubbing:
%% Comment on Power Et Al. NeuroImage 2012:1-3.
%%
%% Power JD, Barnes KA, Snyder AZ, Schlaggar BL, Petersen SE.
%% Steps Toward Optimizing Motion Artifact Removal in Functional
%% Connectivity MRI; a Reply to Carp. NeuroImage 2012:1-3.
%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
CensorTemplate = [];

```

Masking image to spatially constrain the correlations. Make sure it matches the size of your images.

Where to find the realignment files (output from *realignfMRI*)

Prior to using censor please make sure to read and fully understand the literature. Also see the document: *Spike-Filtering-Interaction.pdf* in the Documentation folder.

Censor vector for removing time-points from data.



```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Constrain results to only regions in GreyMatterTemplate (1=yes, 0=no)
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```
MaskGrey = 0;
```

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Value threshold to use for each mask. If left as [] use default 0.75
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```

GreyThreshold = [];
WhiteThreshold = [];
CSFThreshold = [];
EPIThreshold = [];

```

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% the order to perform the regressions etc
%%      D = detrend
%%      G = global
%%      W = white matter
%%      C = csf
%%      M = motion
%%      B = bandpass
%%
%%      Suggested order is "DM[G]CWB"
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```
RegressOrder = 'DMCWB';
```

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% The code users COMPCOR.
%% Use this many principle components for regression
%% for the CSF and WM
%%
%% Behzadi Y, Restom K, Liau J, Liu TT.
%% A Component Based Noise Correction Method (CompCor) for BOLD and
%% Perfusion Based fMRI. NeuroImage 2007;37:90â€“101.
%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```
PrincipalComponents = 5;
```

Whether or not to mask the data for grey only. Best to leave “0”

You can safely leave these alone.

The order of doing the preprocessing

How many components to use from the PCA

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Bandpass Filter Settings
%%      LowFrequency - low frequency cutoff
%%      HighFrequency - high frequency cutoff
%%      Gentle - 0 = no rolling, 1 = rolling, 2 = extra rolling
%%      Padding - number of timepoints to pad on beginning/end
%%      BandpassFilter - 0 = Matlab filter, 1 = SOM_Filter_FFT
%%      Fraction - fraction of variance for principle components
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
LowFrequency    = 0.01;
HighFrequency   = 0.1;
Gentle          = 1;
Padding         = 10;
BandpassFilter  = 1;
Fraction        = 1;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% Type of input
%%      coordinates - provide the center of each seed and a radius
%%
%%      coordload   - load coordinate from the specified file
%%
%%      files       - provide a list of ROI files
%%
%%      directory   - provide a directory containing ROI files and the
%%                    script will load all images in that directory to
%%                    use as ROIs
%%
%%      grid        - make a grid based on provided spacing and masked
%%                    by provided mask
%%
%%      gridplus    - make a grid based on provided spacing and masked
%%                    by provided mask, as above. Additionally, add
%%                    the extra ROI points specified in ROIGridCenters
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ROIInput = 'coordload';

```

Band-pass filtering information and “Fraction” is for the PCA analysis. In general you can use these defaults.

What method to specify coordinates for seeds.

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% coordinates method
%%%
%%% If specifying ROI coordinates you need to provide a list of centers in
%%% MNI coordinates (mm) and a radius in voxels.
%%% NOTE: ROISize will be used as the radius of a sphere at each point. If
%%% you'd prefer to use the predefined 1,7,19, or 27 voxel sizes you will
%%% need to specify the size as a cell (i.e. {19})
%%%
%%% See the MethodsCore/ConnTool/Documentation for more help on ROI size.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```

ROICenters = [0 -5 10];
ROISize    = {19};

```

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% coordload method
%%%
%%% You can load a file into the array ROICenters.
%%%
%%% If a ".csv" file you would do:
%%%
%%%     ROICenters = load('myROIs.csv');
%%%
%%% If a ".mat" file you need to load the file and then assign the variable.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```

ROIFile = '[mcRoot]/ConnTool/Templates/V_MNI_12mmgrid.mat'
ROISize = {19};

```

Explicitly list your ROIs in the array, one per row. And specify how many voxels in each ROI. See the ROI information at the end of this document.

The code can read in a CSV files of coordinates (one row per x-y-z, or it can read a matfile and assuming a single array will use that array to assign the ROIs.

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% files and directory method
%%%
%%% If specifying ROI images you need to provide an ROI folder as well as a
%%% cell array list of ROI images. If specifying an ROI directory, you only
%%% need to specify an ROITemplate. The script will then load all images
%%% in that directory to use as the ROIImages cell array.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ROITemplate = '[Exp]/ROIS';
ROIImages = {
    'image1.nii';
    'image2.nii';
};

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% grid and gridplus method
%%%
%%% If specifying ROI grid you need to provide a spacing and ROI size as
%%% well as an optional mask for grid point inclusion (a mask is strongly
%%% encouraged as not using one will return coordinates from across the entire
%%% bounding box).
%%% NOTE: ROIGridSize will be used as the radius of a sphere at each grid
%%% point. If you'd prefer to use the predefined 1,7,19, or 27 voxel sizes
%%% you will need to specify the size as a cell (i.e. {19})
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ROIGridSpacing      = 12;
ROIGridSize         = {19};
ROIGridMaskTemplate = ...
    '[mcRoot]/ConnTool/Templates/symmetric_3mm_EPI_MASK_NOEYES.nii';

```

Specify a directory to read all images from ('directory') or to read the list of files ('files') from.

The code can place a grid of ROIs on the brain. You specify the spacing in mm and how big to make each ROI. You also need to specify a brain mask.

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% gridplus extra
%%%
%%% ROIGridCenters is used in 'gridplus' mode to specify additional ROIs
%%% that you would like to include in addition to the regular grid. They
%%% will be added to the end of the list of ROIs and will use ROIGridSize
%%% for sizing.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```

ROIGridCenters = [
    10 10 10;
   -10 10 10;
   -22 0 -22;
    22 0 -22;
];

```

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Type of output
%%%
%%%     images - output R and Z images of correlation with each seed
%%%     maps    - output R and P matrix of correlations between seeds
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```

OutputType      = 'maps';

```

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Options for 'maps'
%%%
%%%     correlation type can be 'full' or 'partial'
%%%
%%%     You can also save the power spectrum of the ROIs when running
%%%     in 'maps' mode. This will only save the power spectrum of
%%%     single run.
%%%     1 - save power spectrum
%%%     0 - do not save power spectrum
%%%
%%%     save ROI time courses
%%%     1 - save ROI time courses to same location as R and P matrices
%%%     0 - do not save ROI time courses
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

```

```

OutputCorrType = 'full';
OutputPower    = 0;
saveroiTC      = 0;

```

Extra ROIs to add to the list if you wish.

Do you want correlation matrices or images.

If running “maps” and your number of ROIs << timePoints then you can run ‘partial’ correlation instead of ‘full’ You can also save the power-spectrum of ROIs and the time-courses as well.

# ConnectivityToolbox

## How-To (a sketch)

Once you have the code edited appropriately you can execute from the matlab command line. I suggest that one you run the command to then archive as a record for later use.

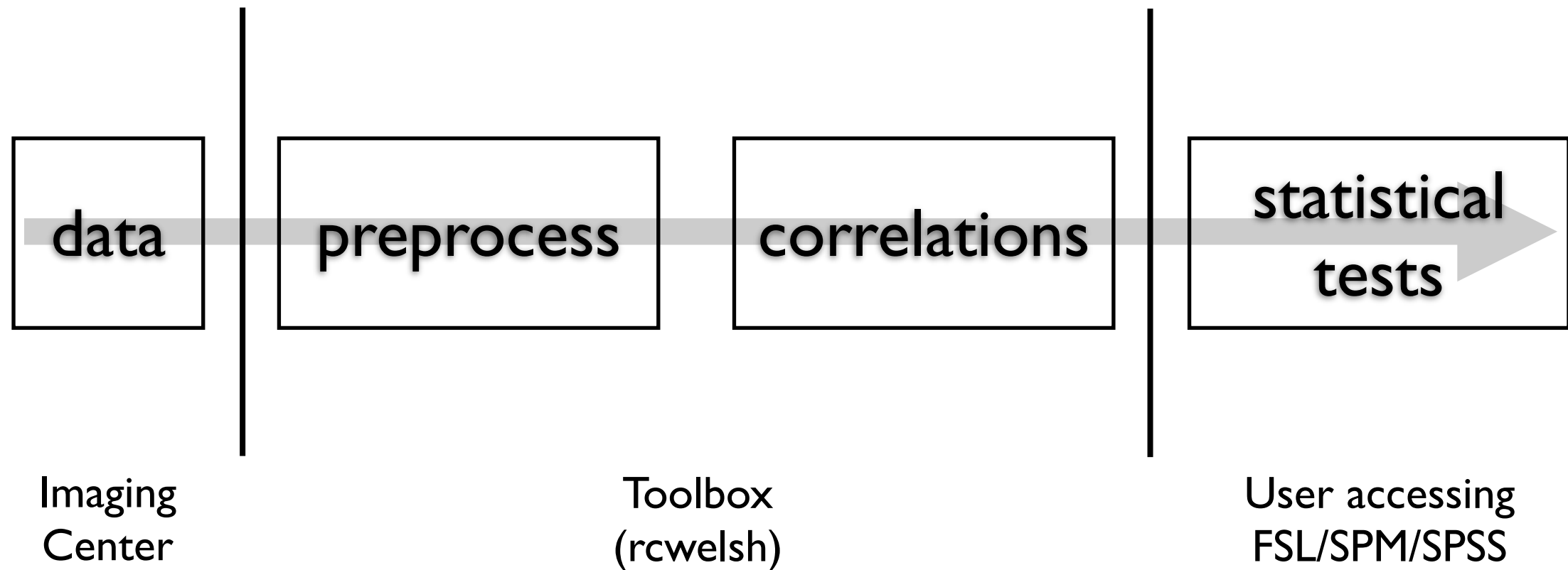
For each subject a log file, a parameters file, and the results file are created. These will be in the FirstLevel directory tree you specified. If your option was for image output you can treat those as “contrast” images and enter them into a second-level analysis. You should take the ***zmap*** images.

# Supplementary Information

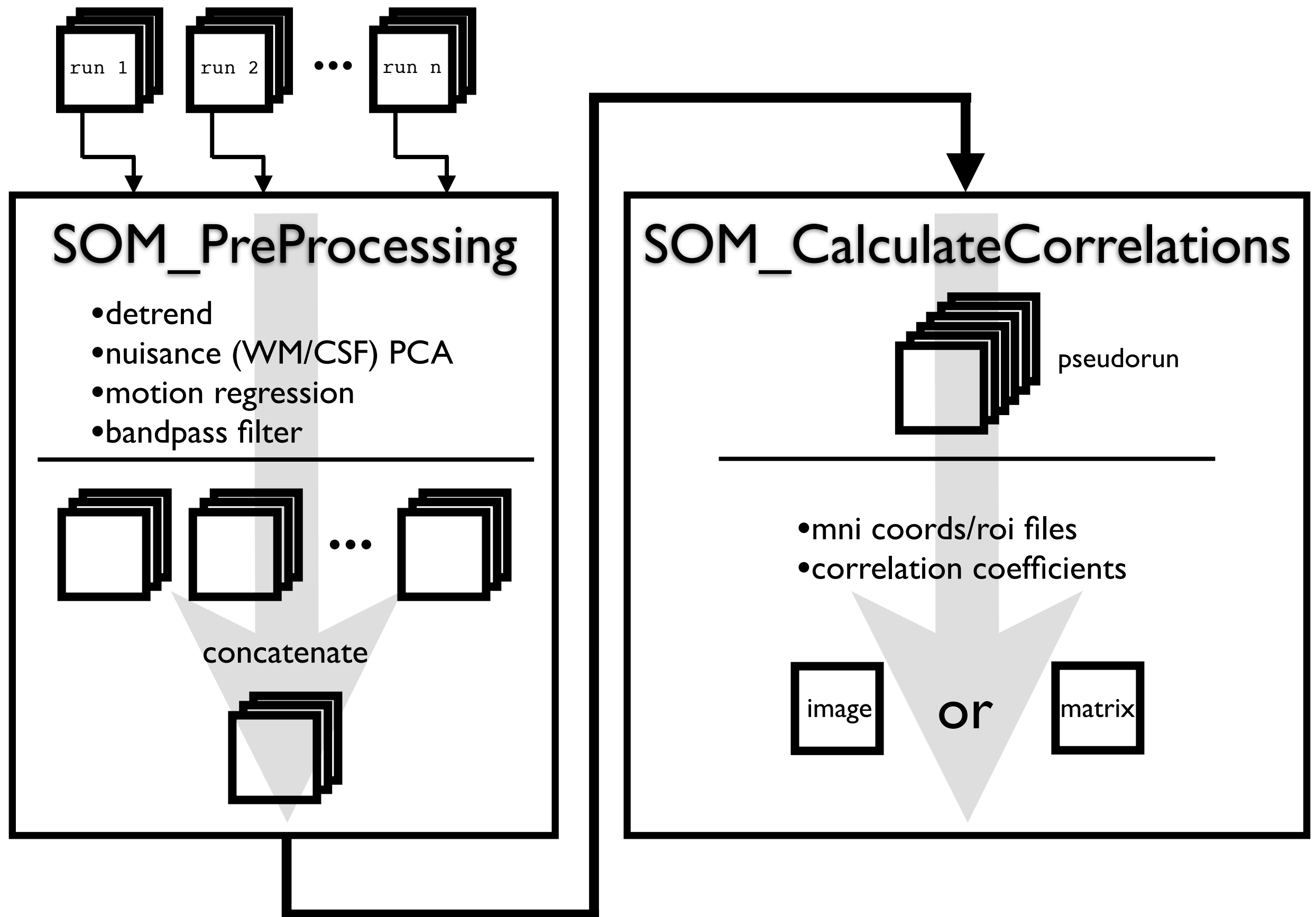
# ConnectivityToolbox

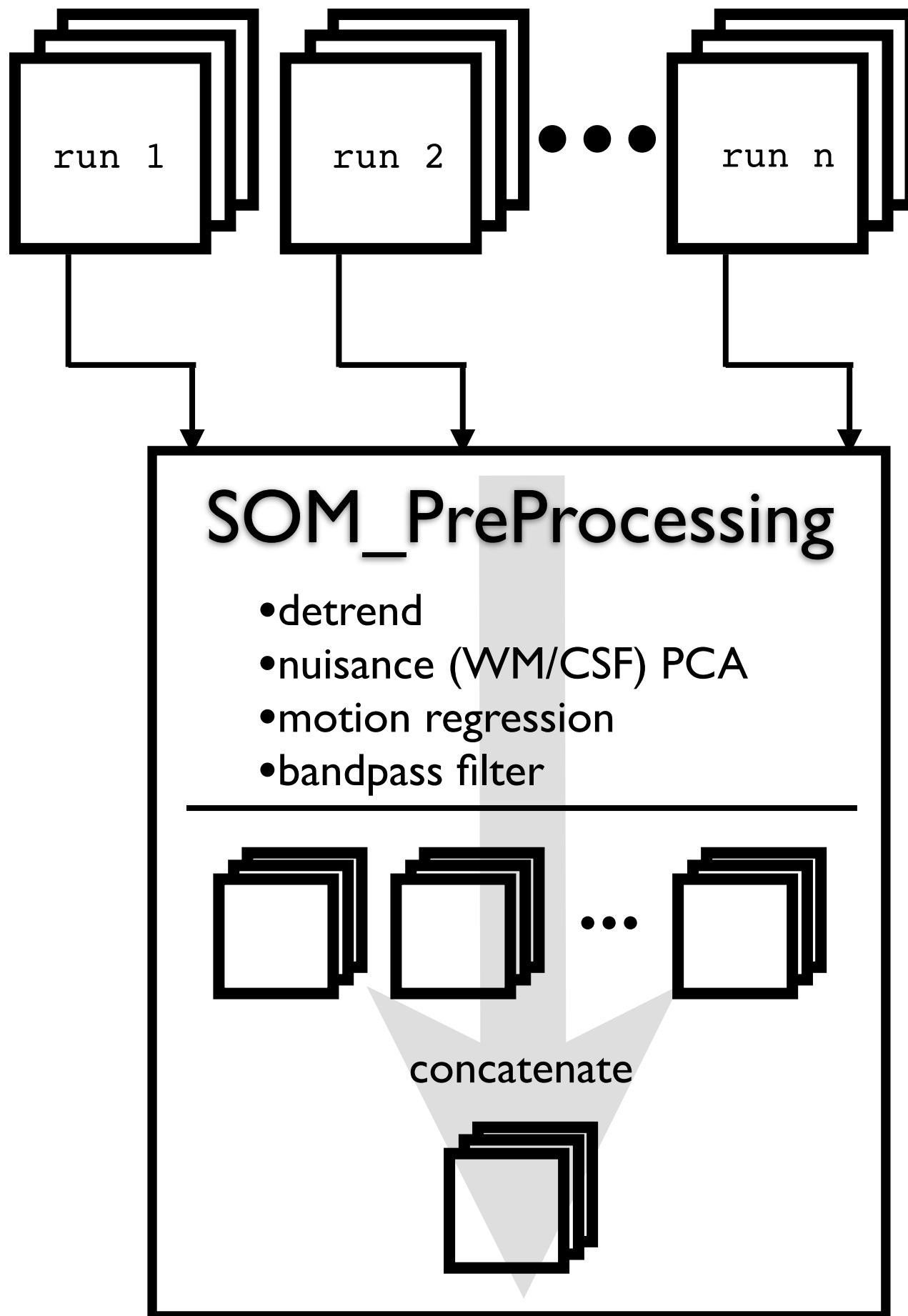
## How-To (a sketch)

### Domain Responsibility

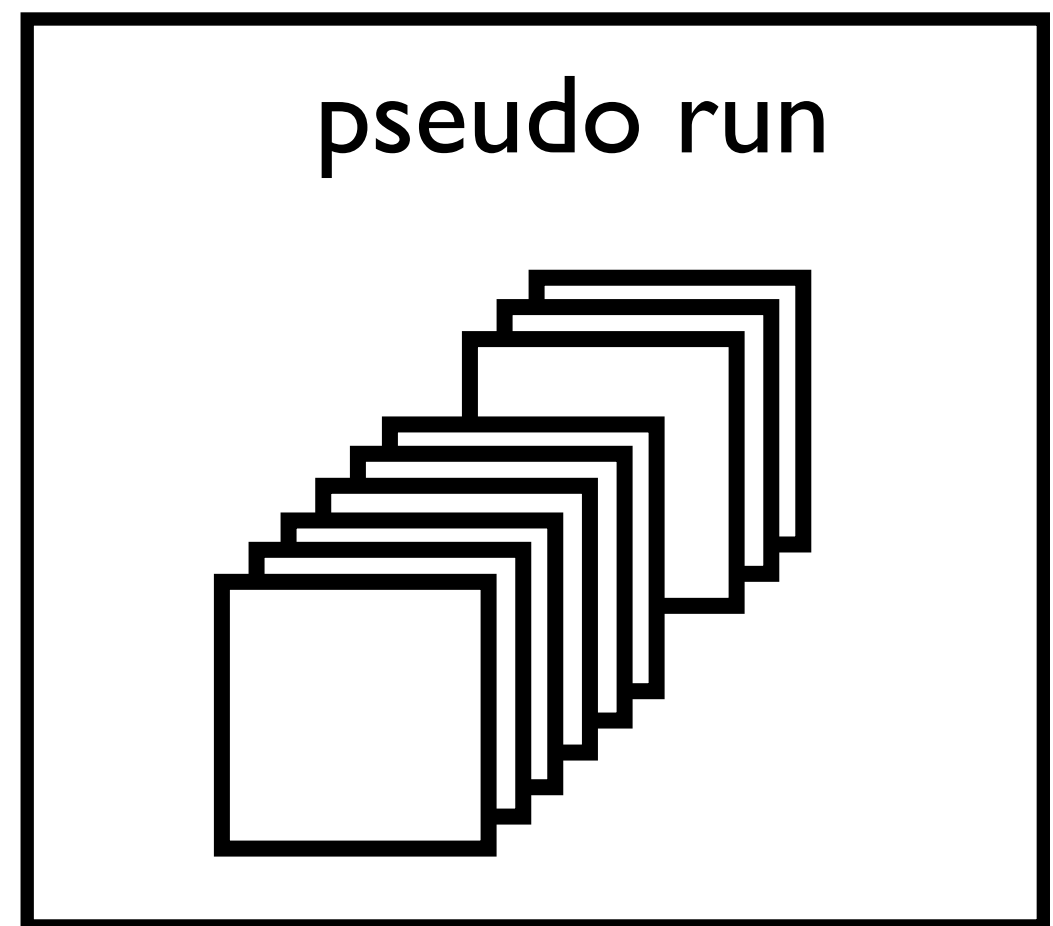






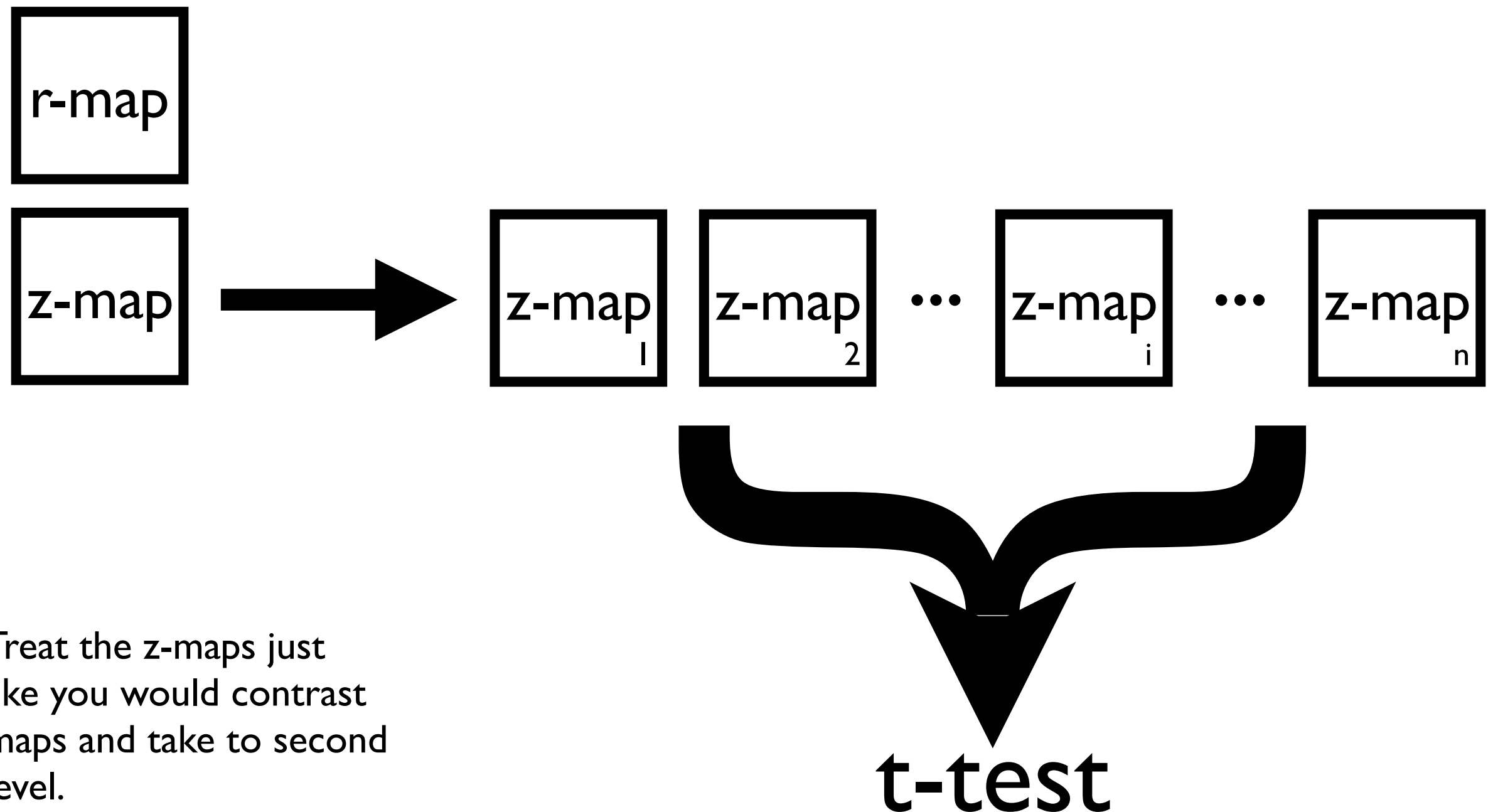


To create pseudo run,  
specify multiple runs to  
SOM\_PreProcess and it will return a single  
array with all data.



# Now what?

Image based

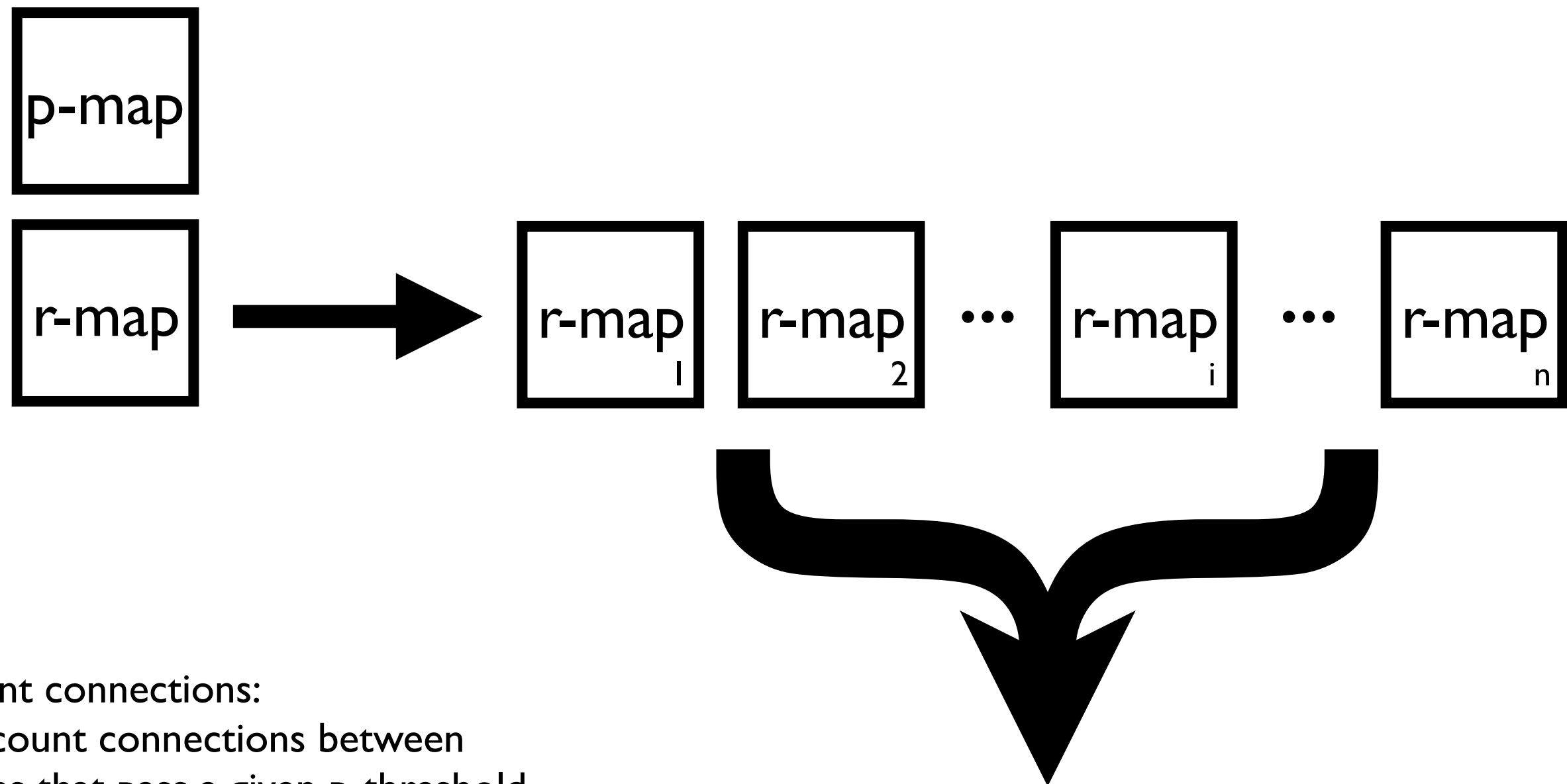


Treat the z-maps just like you would contrast maps and take to second level.

1 or 2-sample etc.

# Now what?

mat based



Count connections:  
e.g. count connections between  
nodes that pass a given p-threshold.  
this can be done on the single  
subject level etc.

perform whatever statistic  
fit your fancy. do on r-maps or  
on p-maps.

# Defining ROIs

You can use the built-in ROI standard objects, or you can specify your own. Recognized sizes are 1, 7, 19, 27.

```
parameters.mni.  
coordinates      = [ x0 y0 z0;  
                    x1 y1 z1;  
                    ...  
                    xn yn zn ] ;  
size             = # ;
```

Or

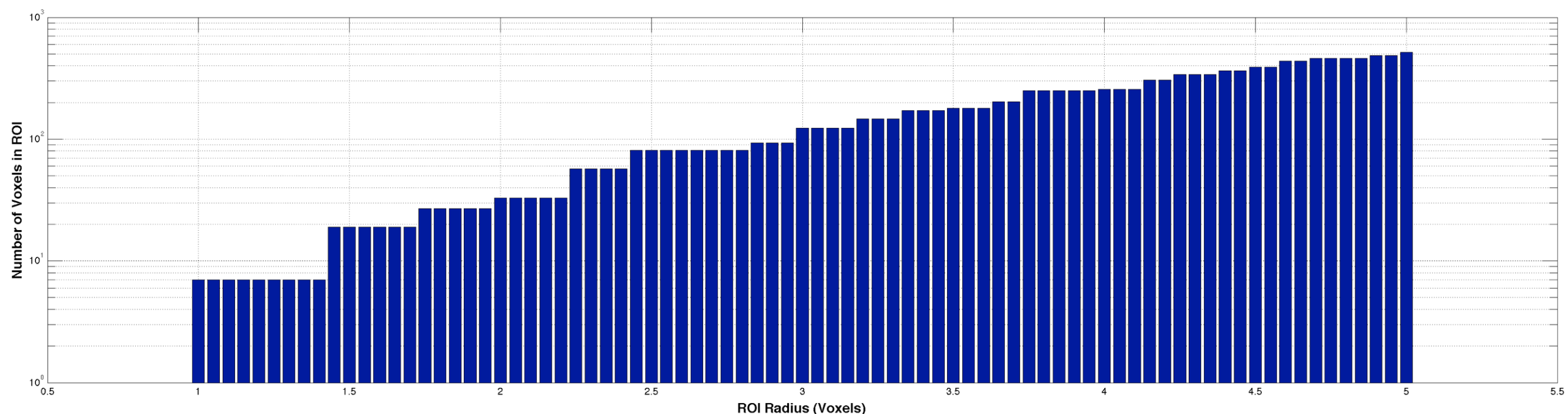
```
size.XROI        = [ -1    0   -1 ] ;  
                  .YROI    = [  0    0    0 ] ;  
                  .ZROI    = [  0    0    0 ] ;
```

So specify you own use:

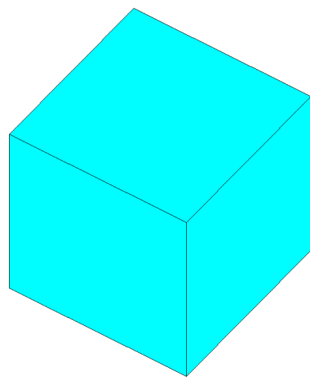
Or, have the code build the arrays

```
XYZ = SOM_MakeSphereROI(radius);  
parameters.rois.mni.size.XROI=XYZ(1,:);  
parameters.rois.mni.size.YROI=XYZ(2,:);  
parameters.rois.mni.size.ZROI=XYZ(3,:);
```

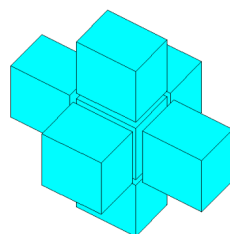
Obviously, some range of radii will give same ROI definition.



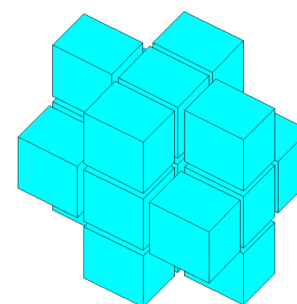
n Voxels : 1, Radius = 0.000000



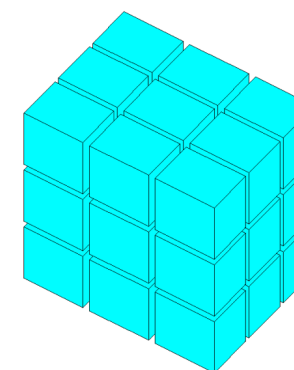
n Voxels : 7, Radius = 1.000000



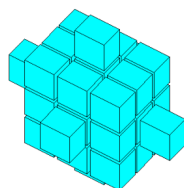
n Voxels : 19, Radius = 1.450000



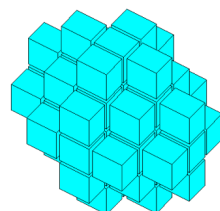
n Voxels : 27, Radius = 1.750000



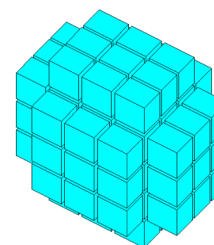
n Voxels : 33, Radius = 2.000000



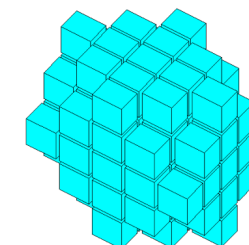
n Voxels : 57, Radius = 2.250000



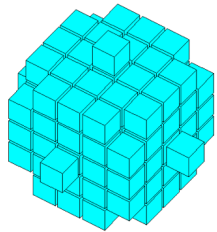
n Voxels : 81, Radius = 2.450000



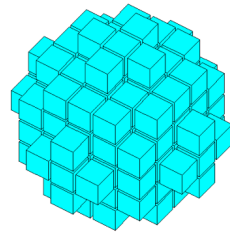
n Voxels : 93, Radius = 2.850000



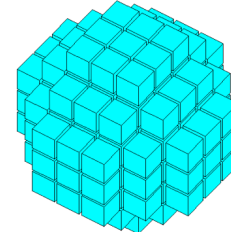
n Voxels : 123, Radius = 3.000000



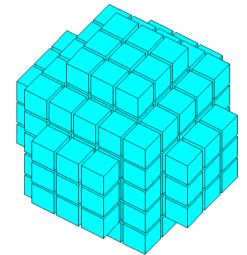
n Voxels : 147, Radius = 3.200000



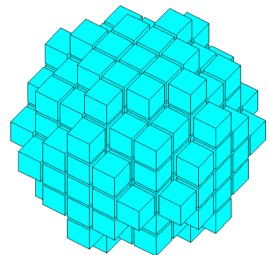
n Voxels : 171, Radius = 3.350000



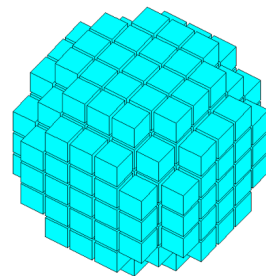
n Voxels : 179, Radius = 3.500000



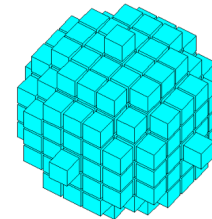
n Voxels : 203, Radius = 3.650000



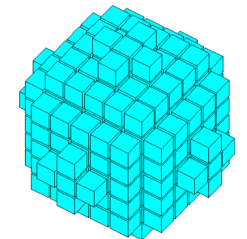
n Voxels : 251, Radius = 3.750000



n Voxels : 257, Radius = 4.000000

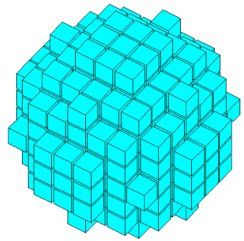


n Voxels : 305, Radius = 4.150000

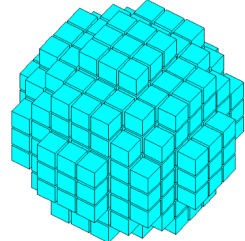




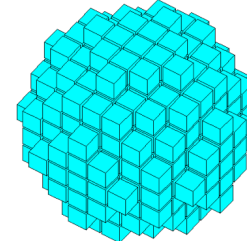
n Voxels : 341, Radius = 4.250000



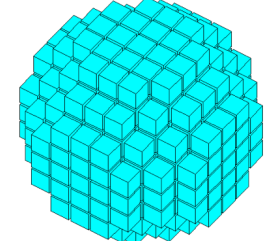
n Voxels : 365, Radius = 4.400000



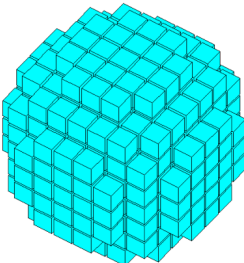
n Voxels : 389, Radius = 4.500000



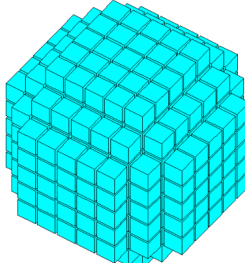
n Voxels : 437, Radius = 4.600000



n Voxels : 461, Radius = 4.700000



n Voxels : 485, Radius = 4.900000



n Voxels : 515, Radius = 5.000000

