ConnTool

Connectivity**Tool**box
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

Connectivity**Tool**box
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.

Connectivity**Tool**box
How-To (a sketch)

The basic idea is that you have time-course data and you wish to know the voxel-to-voxel correlations. We interpret consistent correlations as bring a signal of a "connection". Connections can have either positive or negative polarity. These correlations can either be saved as brain-wise correlation images or correlation maps. To use the tool you need to have time-series data for each subject along with some masking images (if you wish to implement physiological correction using COMPCOR like methodology).

Prior to the calculation of the correlations the data are preprocessed.

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How-To (a sketch)

There are four main sections of the template script

- Input data specification
- Preprocessing specification
- Region of Interest (ROI) specification
- Output specification

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How-To (a sketch)

Input needed:

- Time-series data
- Optional confound time-series (same as above but prior to smoothing)
- Optional grey, white, and CSF masks
- Optional brain mask
- Optional files to identify bad temporal frames
- Optional realignment (motion) files

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Preprocessing options:

- **D**etrending
- **S**mooth replacement of spikes (read the literature)
- **M**otion regression
- **[G]**lobal signal regression (read the literature)
- **W**hite matter regression (via COMPCOR)
- **C**SF regression (via COMPCOR)
- **[E]**dit spikes by removal (read the literature and see S above)
- **B**and-pass filter data

Bolded *letter is the preprocessing option to be specified.* ***[ ]*** *indicate not recommended.*

You may specify any order of preprocessing. However the recommended order is: ***DSM[G]CW[E]B***

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Region of interest:

Regions of interest can be specified in multiple ways, including images and specific coordinates.

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Output:

You may specify output as either "images" or "maps". Images are NIFTI 3D images of r-correlation and z's. Maps are saved to a '.mat' file for further calculations.

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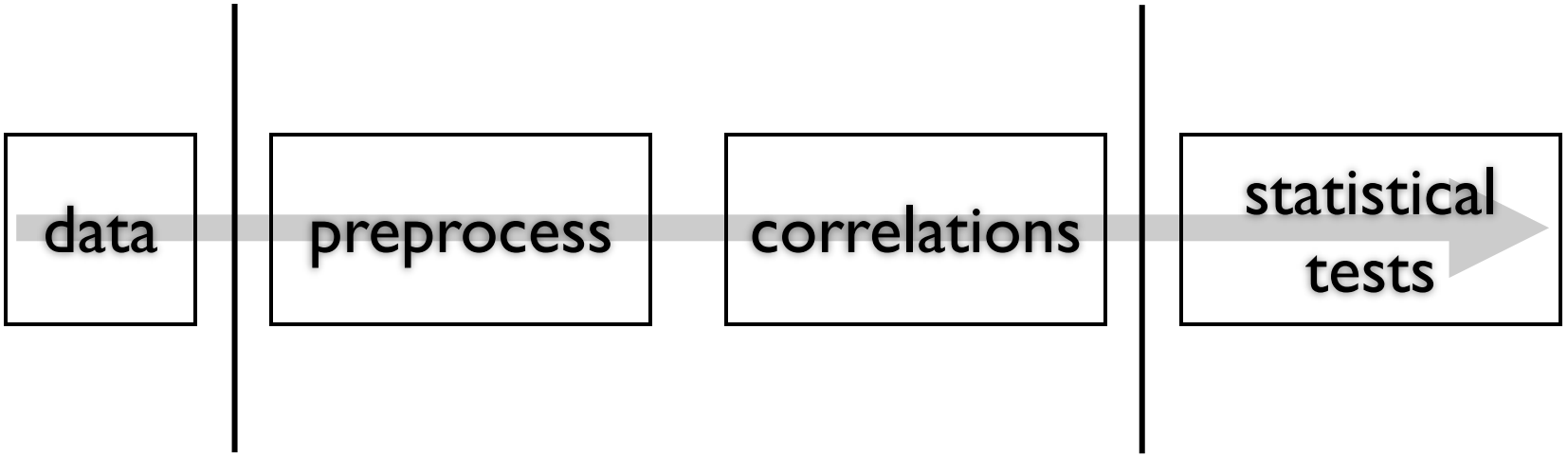
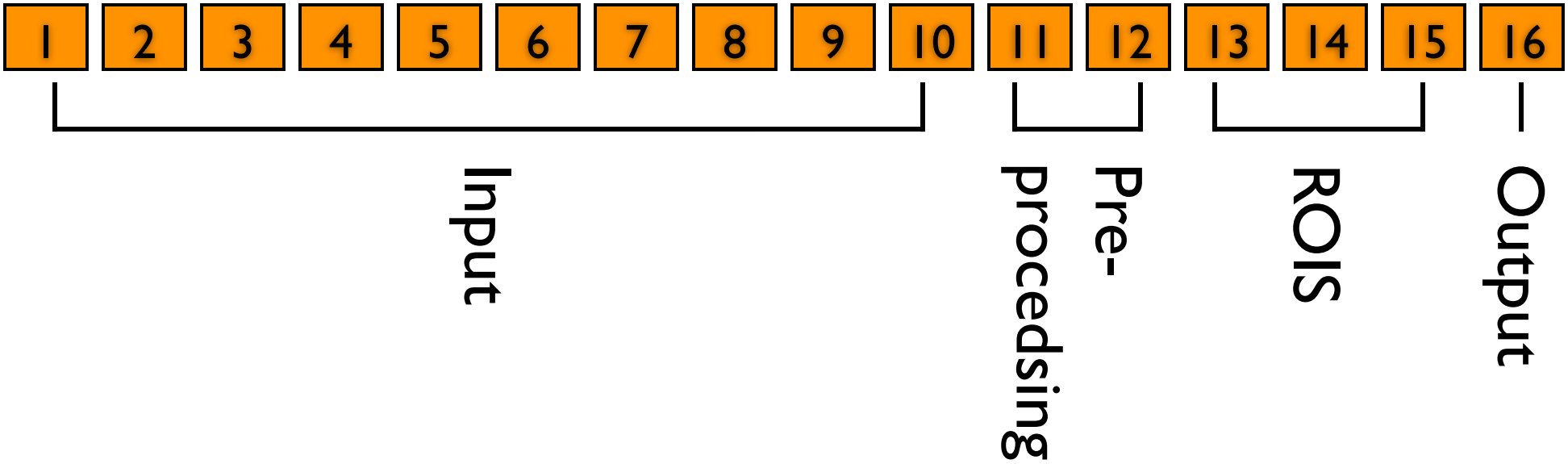
How-To (a sketch)

Domain Responsibility

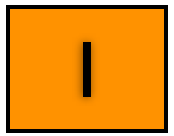


Connectivity**Tool**box
How-To (a sketch)

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 Subjects folders
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
Exp = '/Volumes/ALS/ALS2008/';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% The list of subjects to process
%%% The format is 'subjectfolder',[runs to include]
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
SubjDir = {
    '111129eb',[1];
    '111109ma',[1];
    };

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Specify a subject of the above by indicating which rows
%%% of subjects to include in the current job.
%%% One number per subject you want. If you leave this empty all
%%% subjects will be processed.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
SubjectDirBatch = [1 2];

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%  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';
    };
```



Specify the top-level directory of your experiment.

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

Option subset to process.

Generic path to your time-series data.

List of runs for processing.

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% 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.
%%%
%%% The code implements COMPCOR based on the paper of:
%%%
%%% Behzadi Y, Restom K, Liau J, Liu TT. A Component Based Noise
%%% Correction Method (CompCor) for BOLD and Perfusion Based fMRI.
%%% NeuroImage 2007;37:90?101.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
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'
%%%
%%% Where possible please use "nii" files types.
%%%
%%% NOTE: Eventually img/hdr support will be depricated.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
imagetype = 'nii';
```

2

Name of time-series for confound. It should be your unsmoothed data.

Name of time-series

Image type used

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

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Number of Functional scans to use per run
%%% (if you have more than 1 run, there should be more than 1 value here)
%%%
%%% e.g. if you have three runs it should be:
%%%
%%%     NumScan = [240 240 240];
%%%
%%% If you have subjects with varying number of time points you can pick
%%% the smallest, that will trim them down so they all have the
%%% same effective statistical power.
%%%
%%%
%%% If you are unsure you may enter a super big number and all points
%%% will be taken.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
NumScan = [9999 9999];
```

3

Sample period of your time-series data.

How many time-points to use for each run.

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

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Mode to run ConnTool_batch_mc_central in
%%%    'test'       = test script but do not save parameters or run any
%%%                      ConnTool code
%%%    'parameters' = run script and save parameters for each subject
%%%                       but do not run any ConnTool code
%%%    'presave'    = run ConnTool code on previously saved parameters
%%%    'full'       = generate parameters and immediately run ConnTool code
%%%
%%%    NOTE: If you choose mode 'presave' 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';
```

Mode to run in, if you're unsure just specify '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
%%%                   Typically this starts with "WM_ero"
%%%
%%%     CSFFile   --- name of the CSV image produced by VBM8
%%%                   Typically this starts with "CSF_ero"
%%%
%%% NOTE : Wildcard "*" can be used in the definition of the file names.
%%%
%%% The white matter and CSF masks are use for COMPCOR
%%%
%%% If the grey is specified then a new mask is created which is the AND
%%% of the EPI and the grey. This new mask is used to constrain the
%%% calculations. If you do use this option then you will have a subject
%%% specific mask. This may make doing group analysis troublesome if you
%%% are using 'maps' as the output.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
AnatomyMaskPath = '[Exp]/Subjects/[Subject]/connect/func/coRegRARUN/VBM8/';

GreyFile  = 'w3mm_vbm8_p1ht1spgr.nii';
WhiteFile = 'WM_ero*.nii';
CSFFile   = 'CSF_ero*.nii';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Path and name of explicit mask to use at subject level.
%%% Leaving this blank ('') will use a subject-specific mask
%%%
%%% The EPI mask is used to calculate only in brain.
%%%
%%% NOTE: Subject-specific masks are NOT recommended at all.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
EPIBrainMaskTemplate = ...
    '[mcRoot]/ConnTool/Templates/symmetric_3mm_EPI_MASK_NOEYES.nii';
```

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

Path and name of your brain mask. If you are using 3mm voxels the default should work for you.

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Value threshold to use for each mask.  If left as [] use default 0.75
%%%
%%% If you specify a grey matter mask I suggest you place a low threshold
%%% You may wish to look at the image inside a NII viewer to get a
%%% sense of a sufficient threshold.
%%%
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
GreyThreshold  = [0.05];
WhiteThreshold = [];
CSFThreshold   = [];
EPIThreshold   = [];

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

You can safely leave these alone.

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

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Path Template for pre-filter replacement of spikes.
%%%
%%% This file does NOT have to be present for each subject. If the file
%%% is missing then it's assumed that the correction is not to be done.
%%%
%%% This file should either be a simple text file containing a column-wise
%%% vector of 1s and 0s, or a saved MATLAB .mat file with a
%%% cv variable containing a column of 1s and 0s
%%%
%%%     'moving#'    - local timecourse mean
%%%                    where # is a real number indicating the window
%%%                    e.g.
%%%                        DespikeReplacementOption='moving7';
%%%     'loess#'     - robust loess regression smoothing interpolation
%%%                    where # is a real number indicating the window
%%%                    e.g.
%%%                        DespikeReplacementOption='loess0.15';
%%%     'rloess#'    - robust loess regression smoothing interpolation
%%%                    where # is a real number indicating the window
%%%                    e.g.
%%%                        DespikeReplacementOption='rloess0.15';
%%%     'sgolay#'    - robust loess regression smoothing interpolation
%%%                    where # is a real number indicating the window
%%%                    e.g.
%%%                        DespikeReplacementOption='sgolay7';
%%%     'lowess#'    - robust loess regression smoothing interpolation
%%%                    where # is a real number indicating the window
%%%                    e.g.
%%%                        DespikeReplacementOption='lowess.15';
%%%     'rlowess#'   - robust loess regression smoothing interpolation
%%%                    where # is a real number indicating the window
%%%                    e.g.
%%%                        DespikeReplacementOption='rlowess0.15';
%%%
%%%
```

```
%%% After the data are smoothed, the missing point is then calculated with
%%% an interpolation(interp1) using pchip (cubic).
%%%
%%% This is following:
%%%
%%%     Satterthwaite TD, Elliott MA, Gerraty RT, Ruparel K, Loughead J,
%%%     Calkins ME, Eickhoff SB, Hakonarson H, Gur RC, Gur RE, Wolf DH.
%%%     An Improved Framework for Confound Regression and Filtering for
%%%     Control of Motion Artifact in the Preprocessing of Resting-State
%%%     Functional Connectivity Data.
%%%     NeuroImage 2013;64:240?256.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
DespikeParametersTemplate = ...
    '[Exp]/Subjects/[Subject]/connect/func/[Run]/prefilter_despike.dat';
DespikeReplacementOption  = 'sgolay7';
DespikeReplacementInterp  = 'pchip';
```

Despiking information. It is recommended that you despike **prior** to doing band-pass filtering.

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```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Path Template for post-filter censoring of spikes.
%%%
%%% This file does NOT have to be present for each subject. If the file
%%% is missing then it's assumed that the correction is not to be done.
%%%
%%% 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
%%%
%%%     This ConnTool Toolbox users an FFT filter with a little
%%%     bit of smoothing. If you want to censor your data your should
%%%     see the following papers.
%%%
%%%     See the following 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
%%%
%%%     Carp J. Optimizing the Order of Operations for Movement Scrubbing:
%%%     Comment on Power Et Al. NeuroImage 2012
%%%
%%%     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.
%%%
%%%     Satterthwaite TD, Elliott MA, Gerraty RT, Ruparel K, Loughead J,
%%%     Calkins ME, Eickhoff SB, Hakonarson H, Gur RC, Gur RE, Wolf DH.
%%%     An Improved Framework for Confound Regression and Filtering for
%%%     Control of Motion Artifact in the Preprocessing of Resting-State
%%%     Functional Connectivity Data.
%%%     NeuroImage 2013
%%%
%%%     Fair, D. et al. Distinct Neural Signatures Detected for ADHD
%%%     Subtypes After Controlling for Micro-Movements in Resting State
%%%     Functional Connectivity MRI Data. Front in Sys Neuro 2013
```

```
%%%
%%% More recently this paper came out that shows how to do a correction
%%%
%%%     Ziad S. Saad, Richard C. Reynolds, Hang Joon Jo, Stephen J. Gotts,
%%%     Gang Chen, Alex Martin, Robert W. Cox
%%%     Correcting Brain-Wide Correlation Differences in Resting-State FMRI
%%%     Brain Connectivity. August 2013, 3(4): 339-352.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
CensorParametersTemplate = ...
    '[Exp]/Subjects/[Subject]/connect/func/[Run]/postfilter_censor.dat';
```

Scrubbing information. If you choose to scrub post filtering you should understand the mathematical concept of Gibbs ringing.

Also see the document:
Spike-Filtering-Interaction.pdf
in the Documentation folder.

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```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% DETREND Polynomial order
%%%
%%%    A number, 0-mean
%%%              1-linear
%%%              2-quadratic, starting to get the idea?
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
DetrendOrder  = 2;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% The code users COMPCOR.
%%% Use this many principle components for regression
%%% for the CSF and WM
%%%
%%% PCA COMPCOR Parameter
%%%        Fraction - fraction of variance for principle components
%%%
%%% 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;
Fraction            = 1;

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% 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
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
LowFrequency   = 0.01;
HighFrequency  = 0.1;
Gentle         = 1;
Padding        = 10;
BandpassFilter = 1;
```

Detrending polynomial order

How many components to use from the PCA and what fraction of the data (based on variance ranking) to use.

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

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%
% Bands 1 and 2 for ALFF (Band 1 needed) and fALFF (Band 1 and Band 2 needed)
%
% For fALFF then band 2 should contain band 1
% also the high frequency cutoff should no great than about, and maybe even
% smaller:
%
%   (1-2/nTimePoints)*1/(2*TR)-0.001
%
% Below the 0.0022 is a guess for 240 times points taken at 2 sec TR
%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
LowFreqBand1   = 0.01;
HighFreqBand1  = 0.10;
LowFreqBand2   = 0.00;
HighFreqBand2  = 1/(2*TR)-.0022;
```

II a

Frequencies to use for fALFF and ALFF

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```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% the order to perform the regressions etc
%%%         D = detrend      - Nth order detrend
%%%         S = despike      - by replacement
%%%         M = motion       - by regression, includes dM/dt
%%%         G = global       - Controversial, you should know the lit.
%%%         W = white matter - by PCA
%%%         C = csf          - by PCA
%%%         B = bandpass     - by method selected.
%%%         E = edit         - by removal
%%%
%%%         Suggested order is "DSM[G]CWB"
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
RegressOrder = 'DMCWEB';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% You can save the time course of a single voxel at each step of the
%%% processing to get a sense of what happens.
%%% Leave empty if you don't want it.
%%%
%%% If you do choose to save a voxel time series it will be in the
%%% 'parameters' structure under 'parameters.data.run.sampleTC
%%% each row of the sampleTC is a time-course of the data. The raw time
%%% course will be the 1st row. If detrending is the first RegressOrder
%%% option then the 2nd row will be the data after it's been detrended and
%%% so forth.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
voxelIDX       = 1;
```

The order of doing the preprocessing

Sample voxel to save for plotting

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Type of input
%%%         coordinates - provide the center of each seed and a radius
%%%
%%%                       at the moment if you are wanting alff or falff
%%%                       then put in coordinates and put in something like
%%%                       [0 0 0] to pass muster
%%%
%%%         coordload   - load corridnate 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 = 'coordinates';
```

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 (in voxels, can be fracional
%%% 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.
%%%
%%% You can load a file into the array ROICenters.
%%%
%%% If a ".csv" file you would do:
%%%
%%%    ROICenters = load('myROIs.csv');
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ROICenters = [0 -48 26];
ROISize    = {19};

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% 'coordload' method
%%%
%%% If a '.mat" file you need make sure it contains a single array
%%% with each row being an ROI and columns are x,y,z, in MNI mm.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
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' methods
%%%
%%% 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' methods
%%%
%%% 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';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%
%%% '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;
    ];
```

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.

Extra ROIS to add to the list if you wish.

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Where to output the data and what to call it.
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
OutputTemplate  = '[Exp]/FirstLevel/[Subject]/[OutputName]/';
OutputName      = 'ConnToolTest5';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% Type of output
%%%       images - output R and Z images of correlation with each seed
%%%       maps   - output R,P, and Z matrices of correlations between seeds
%%%       falff  - output the falff maps only.
%%%       alff   - output the alff maps only.
%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

OutputType     = 'images';

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% 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;
```

Name of output

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.

Connectivity**Tool**box
How-To (a sketch)

Once you have the code edited appropriately you can execute from the matlab command line. I suggest that once 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.

Connectivity**Tool**box
How-To (a sketch)

Supplementary Information

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Input **Conn**ectivity**Tool**box Output

How-To (a sketch)

Subject data

time-series data

realign.dat

WM_ero

CSF_ero

Configuration

ROIS

ConnTool_mc_batch_template

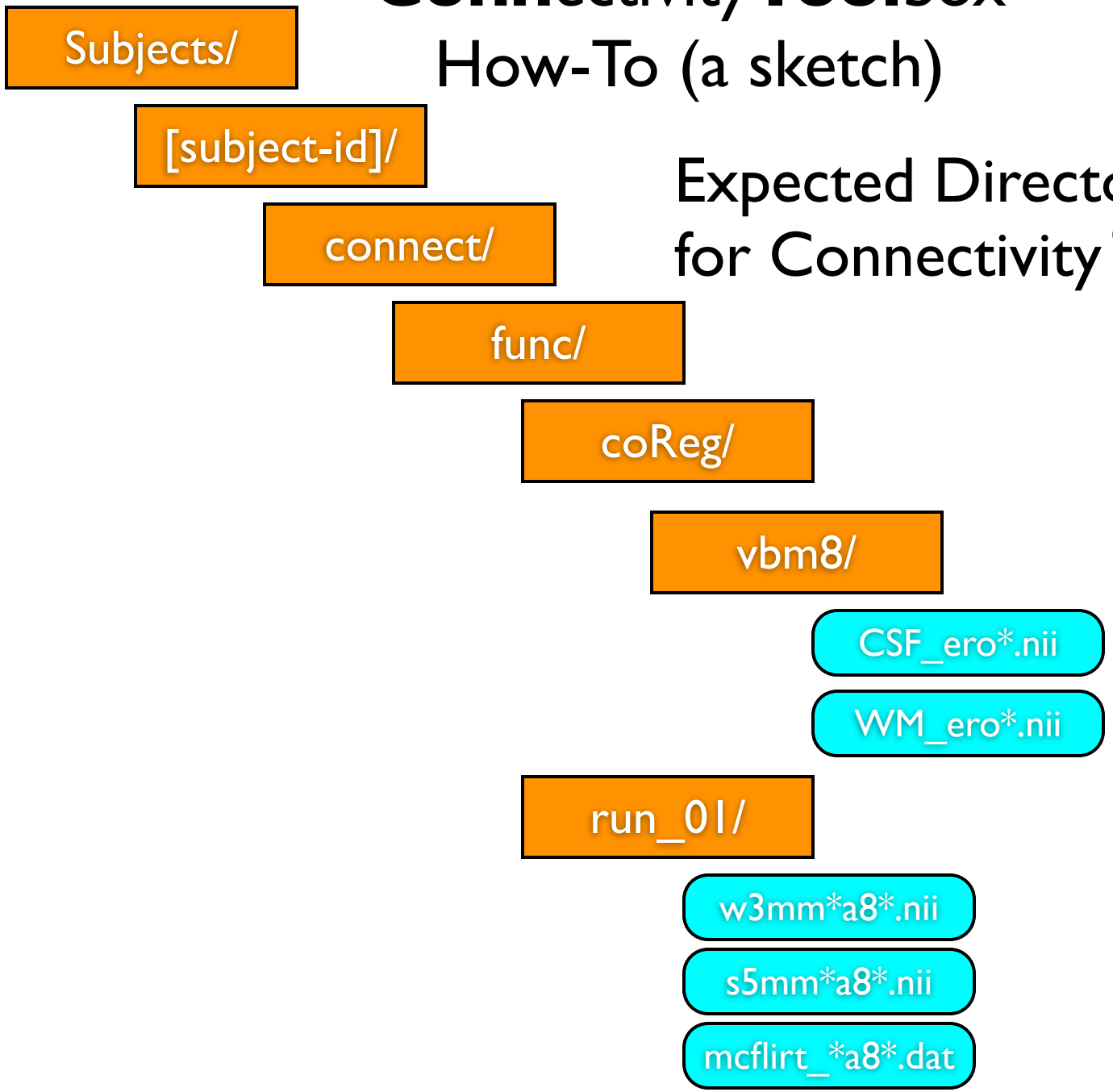
```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% GENERAL OPTIONS
%%% These options are shared among many of our scripts
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%% 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 = {
    'll1129eb',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.

Connectivity**Tool**box
How-To (a sketch)



Expected Directory Structure for Connectivity Toolbox

Connectivity**Tool**box

Output

[OutputName]_parameters.mat

parameters

'maps'

[OutputName]_corr.mat

rMatrix zMatrix pMatrix

Or

[OutputName]_parameters.mat

parameters

'images'

[OutputName]_rmap_xxxx.nii

[OutputName]_zmap_xxxx.nii

[OutputName]_ pmap_xxxx.nii

Connectivity**Tool**box
How-To (a sketch)

If you like you may concatenate runs into a single connectivity run. The concatenation takes place after the preprocessing.

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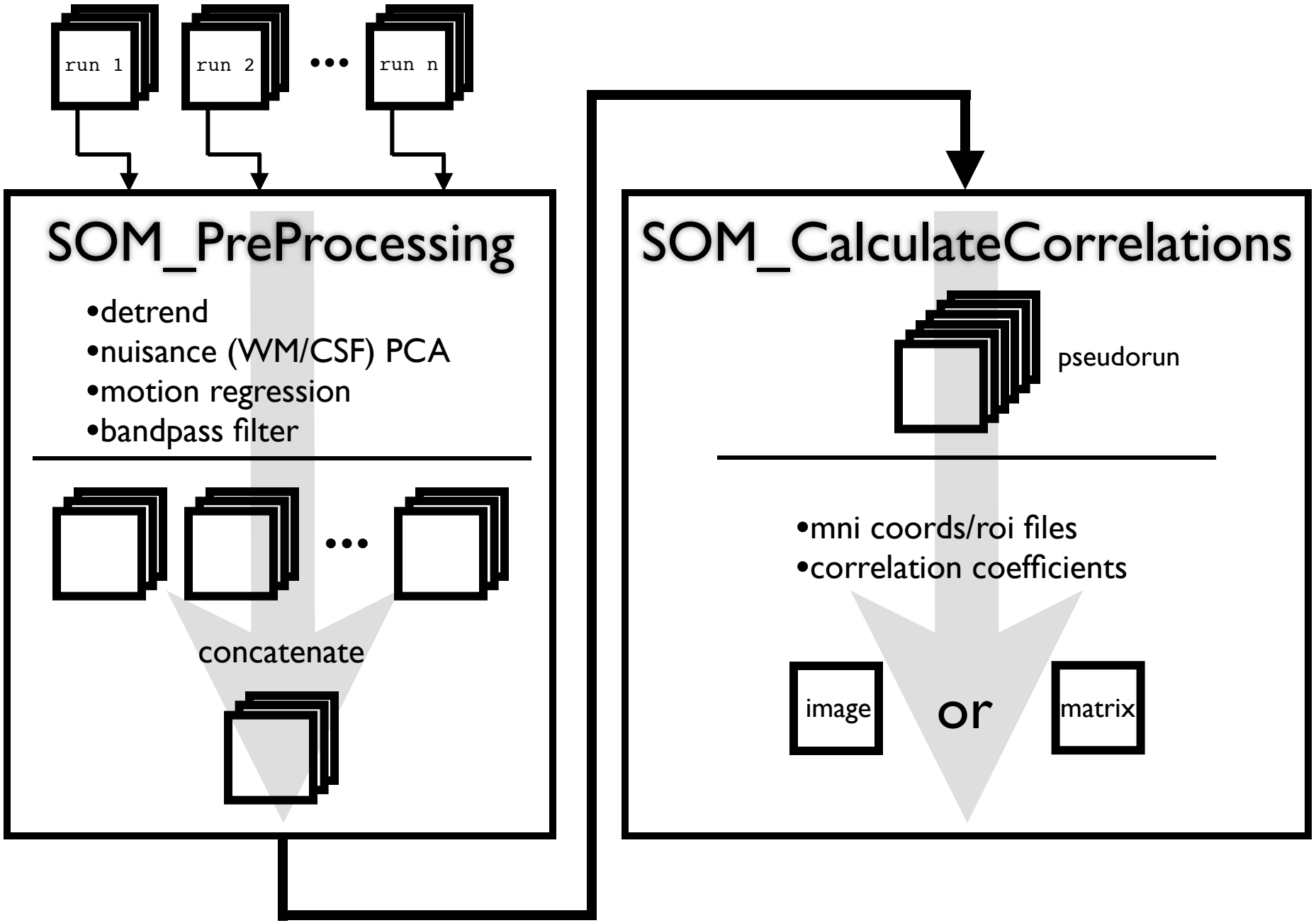
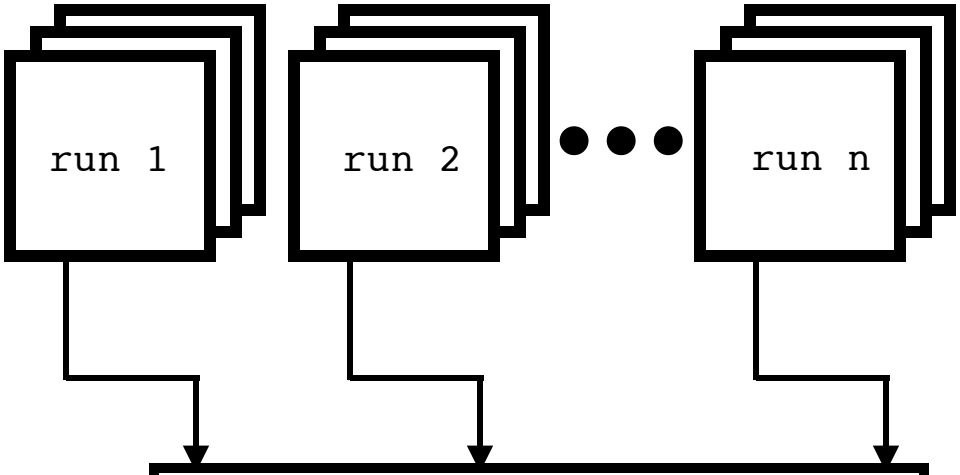
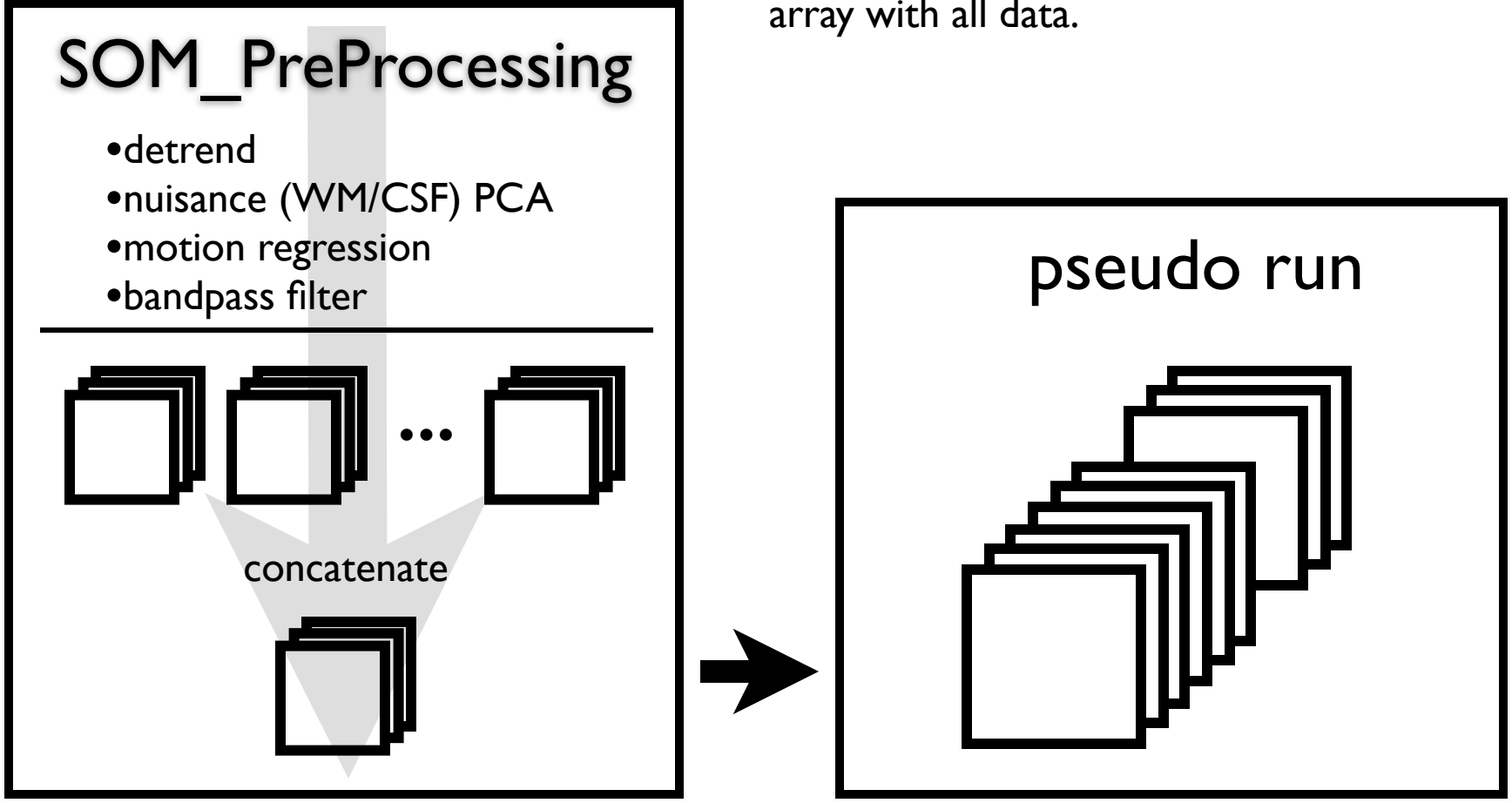

run 1
run 2
run n
SOM_PreProcessing
•detrend
•nuisance (WM/CSF) PCA
•motion regression
•bandpass filter
concatenate
SOM_CalculateCorrelations
pseudorun
•mni coords/roi files
•correlation coefficients
image
or
matrix



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

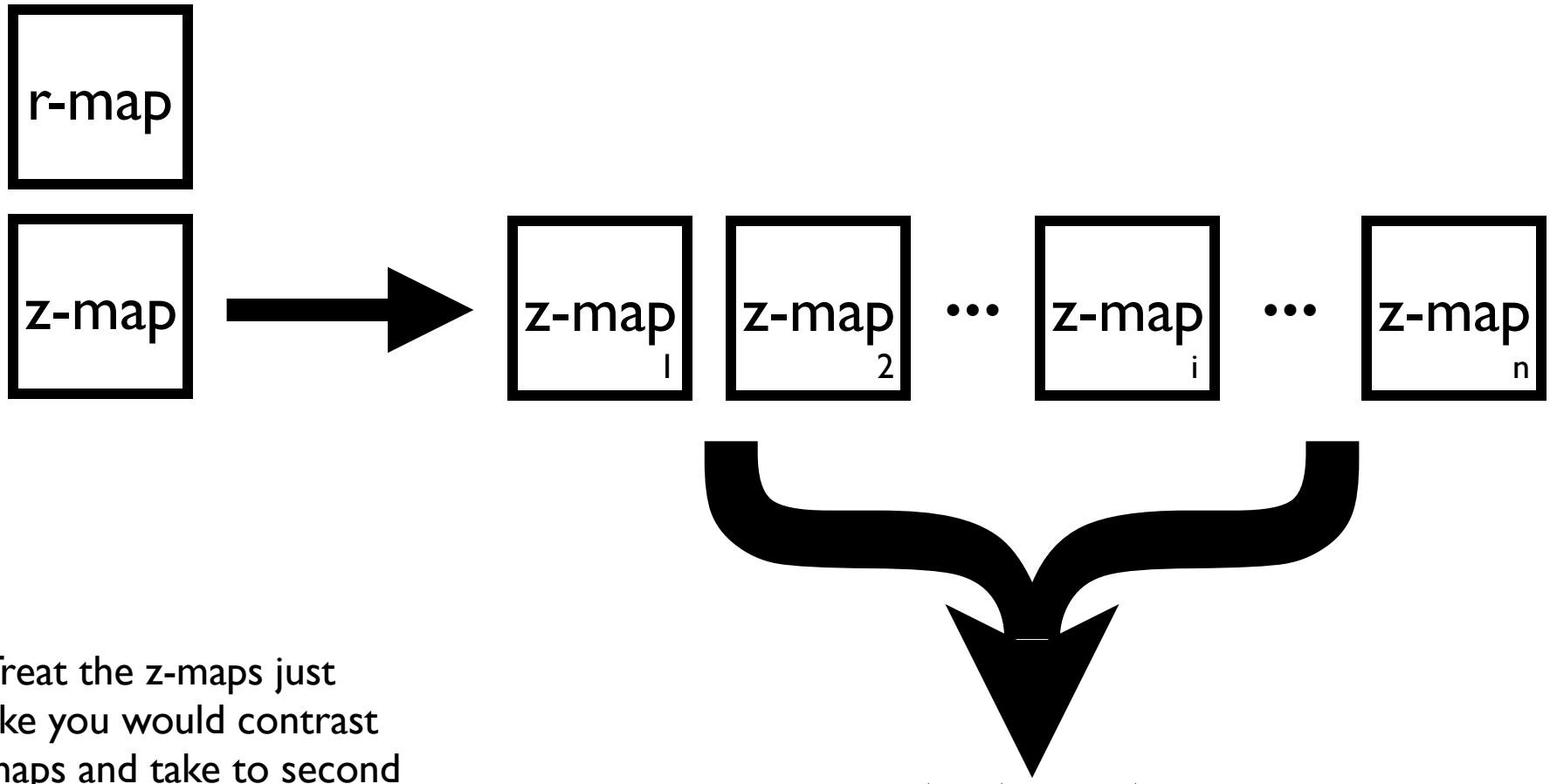


Connectivity**Tool**box
How-To (a sketch)

Output can be either the 'maps' or 'images'. Images can be used in SPM just as you would a contrast images. Maps are written to a MATLAB .mat file in the output directory. To use those you will need to be familiar with matlab matrices.

Now what?

Image based

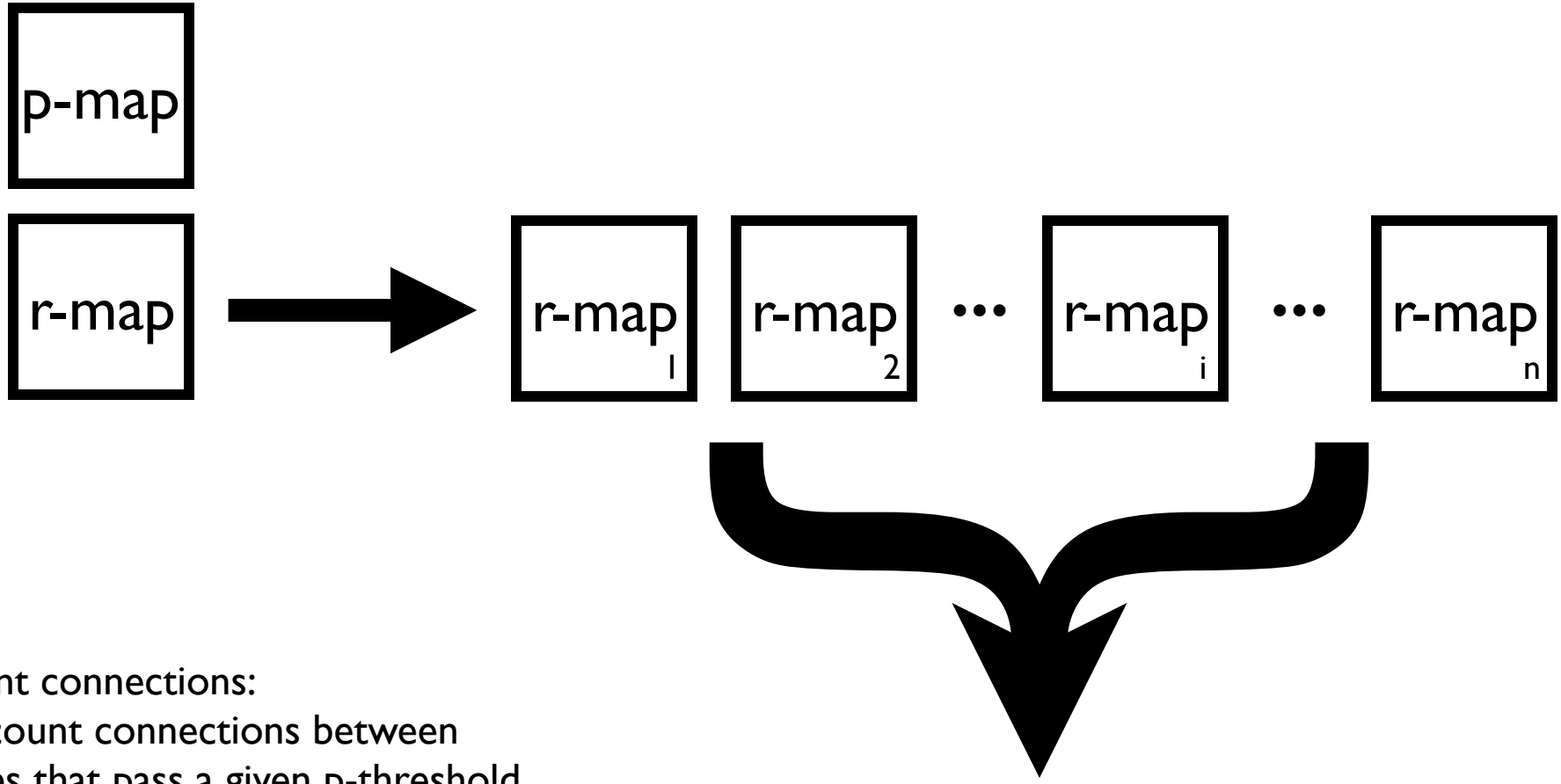


Treat the z-maps just like you would contrast maps and take to second level.

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 fits your fancy. do on r-maps or on p-maps.

Extra information on ROIs

Defining ROIs

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

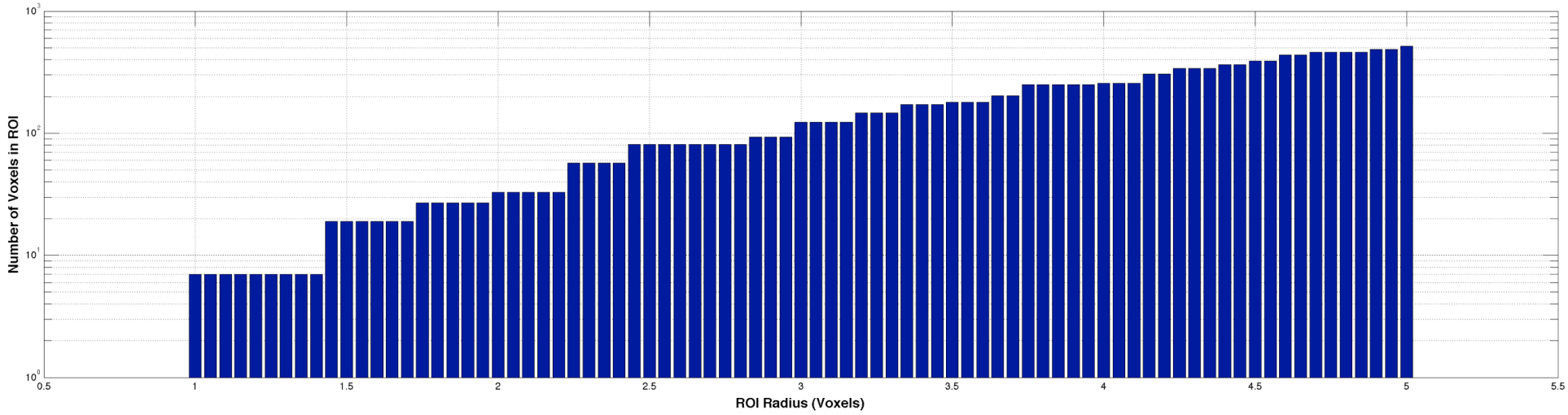
```
parameters.mni.
   coodinates      = [x0 y0 z0;
                      x1 y1 z1;
                      ...
                      xn yn zn];
   size            = #;
                Or
   size.XROI       = [-1  0 -1];
       .YROI       = [ 0  0  0];
       .ZROI       = [ 0  0  0];
```

So specify you own use:

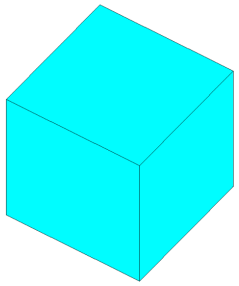
Or, have the code build the arrays

```
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,:);
```

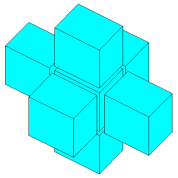
Obviously, some range of radii will give same ROI definition.



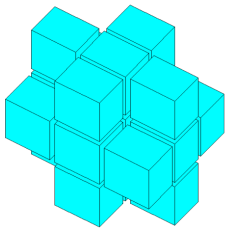
n Voxels : 1, Radius = 0.000000



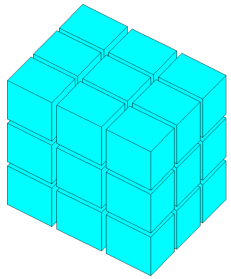
n Voxels : 7, Radius = 1.000000



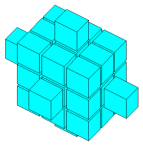
n Voxels : 19, Radius = 1.450000



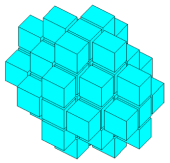
n Voxels : 27, Radius = 1.750000



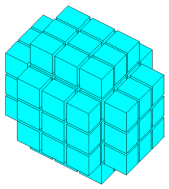
n Voxels : 33, Radius = 2.000000



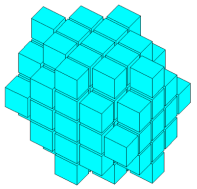
n Voxels : 57, Radius = 2.250000



n Voxels : 81, Radius = 2.450000



n Voxels : 93, Radius = 2.850000



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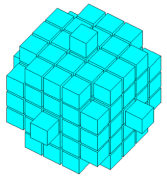
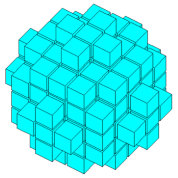
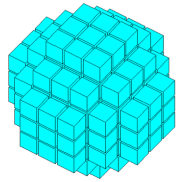
n Voxels : 123, Radius = 3.000000



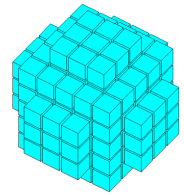
n Voxels : 147, Radius = 3.200000



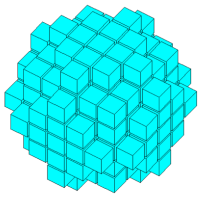
n Voxels : 171, Radius = 3.350000



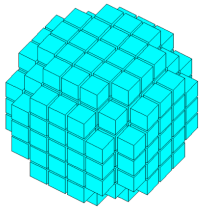
n Voxels : 179, Radius = 3.500000



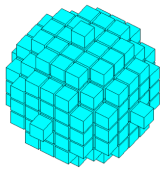
n Voxels : 203, Radius = 3.650000



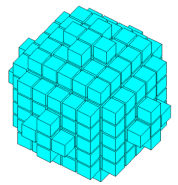
n Voxels : 251, Radius = 3.750000



n Voxels : 257, Radius = 4.000000



n Voxels : 305, Radius = 4.150000



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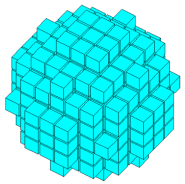
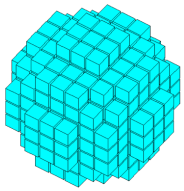
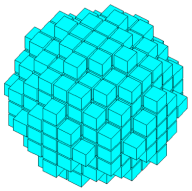
n Voxels : 341, Radius = 4.250000



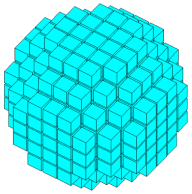
n Voxels : 365, Radius = 4.400000



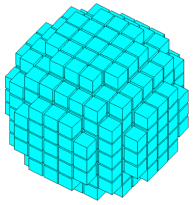
n Voxels : 389, Radius = 4.500000



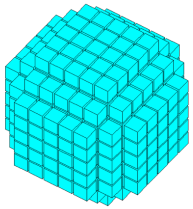
n Voxels : 437, Radius = 4.600000



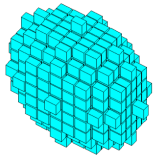
n Voxels : 461, Radius = 4.700000



n Voxels : 485, Radius = 4.900000

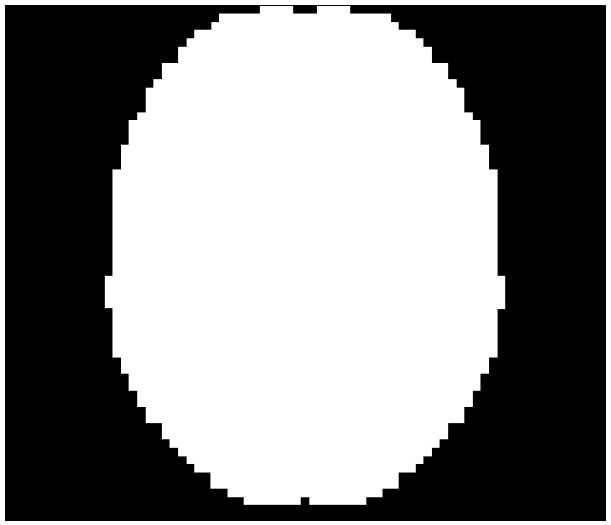


n Voxels : 515, Radius = 5.000000



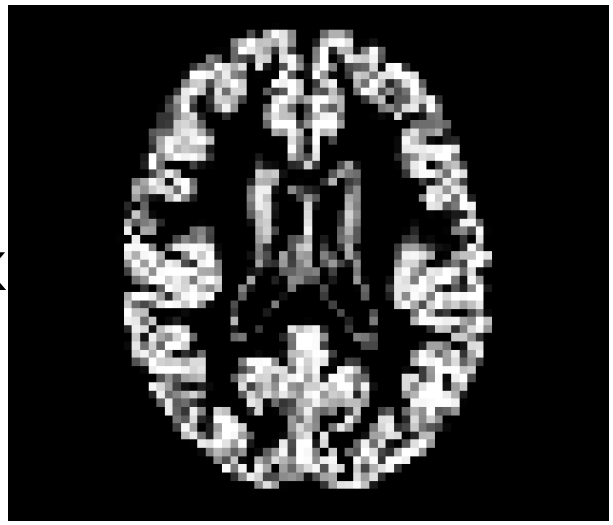
Result of using a EPI and grey mask

EPI



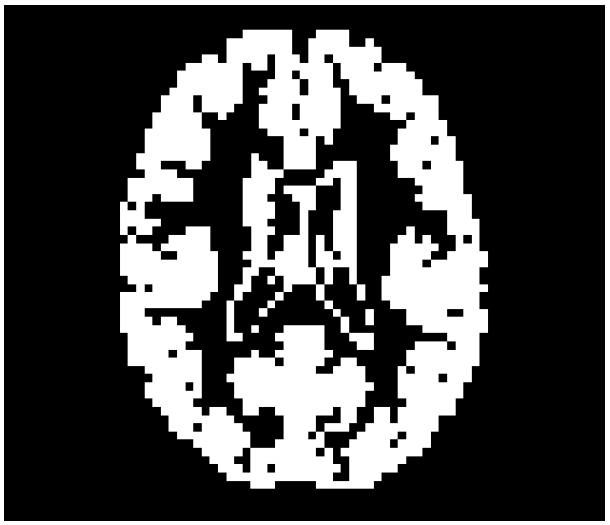
x

Grey Segment



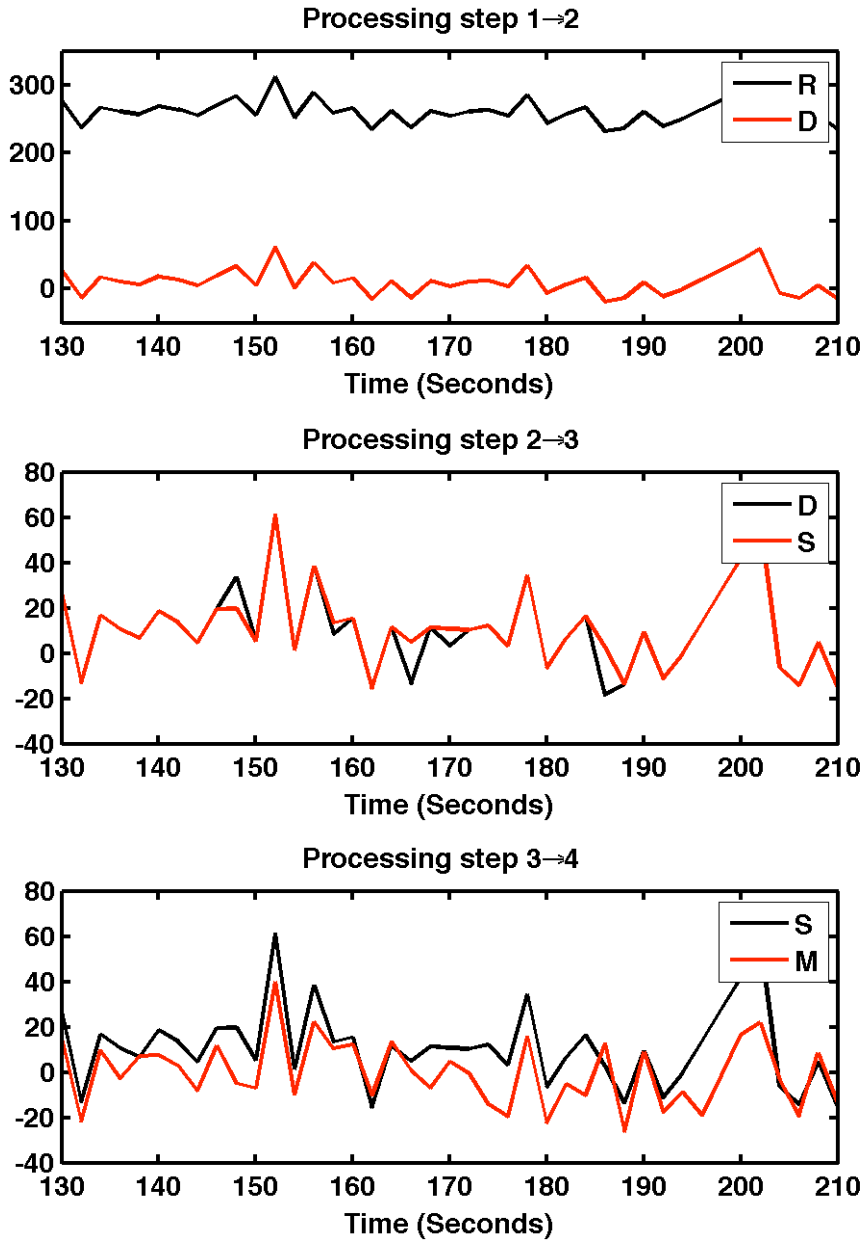
=

Final Mask

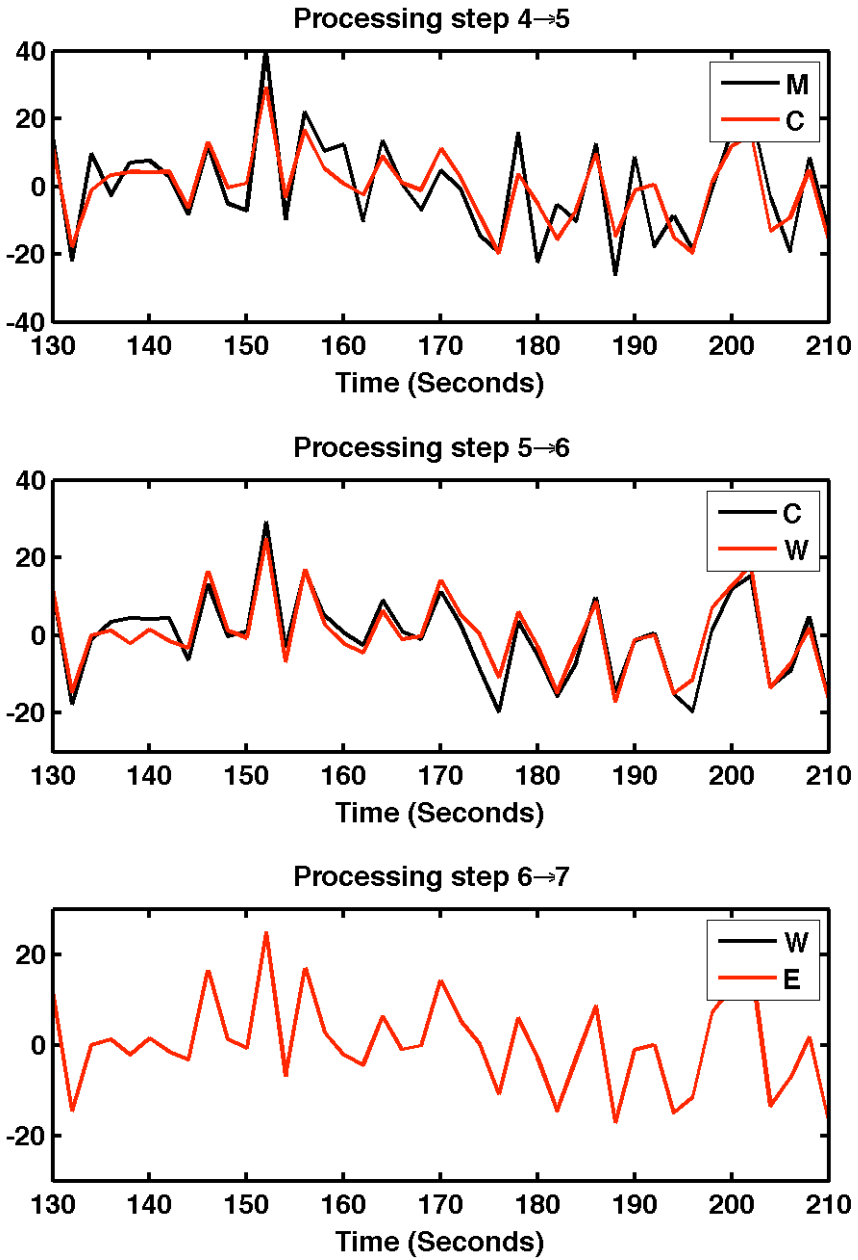


Sample Preprocessing Effects on Time-series

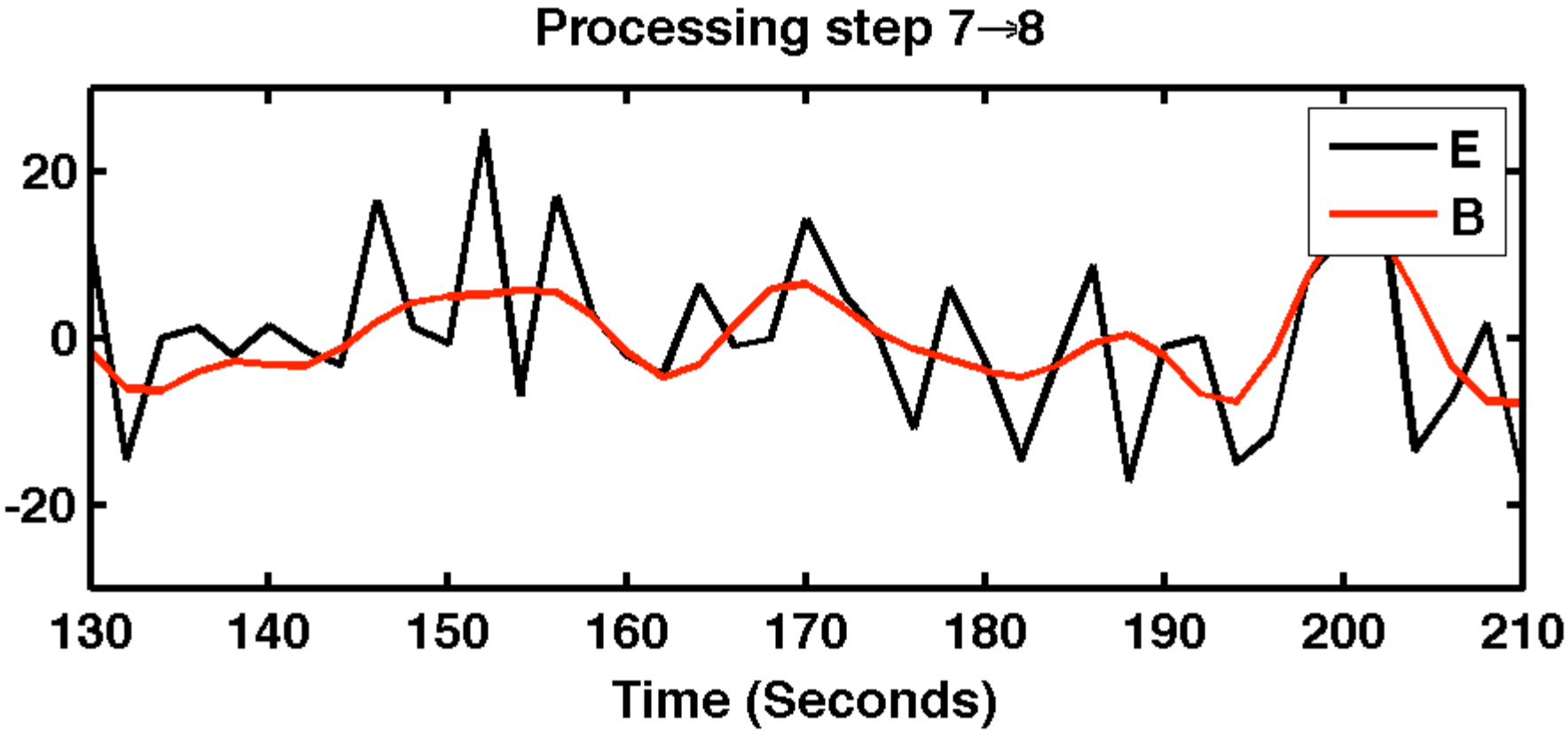
For each stage the input is in black and the result is in red



Sample Preprocessing Effects on Time-series



Sample Preprocessing Effects on Time-series



The final (red) time course is what is used for correlation calculations

Enjoy!