

ConnExT: Connectivity Explorer Toolbox

Manual

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Introduction

ConnExT is a toolbox for SPM8 (<http://www.fil.ion.ucl.ac.uk/spm/>). It provides an easy way to visually explore the signal time series and the functional connectivity map of fMRI data. There are various processing options that can be applied to the time series, and the effect can be quickly seen. Another very interesting capability is the option to choose the seed region without difficulty for functional connectivity analysis. The correlation coefficients map is instantaneously displayed.

Therefore, ConnExT can be very useful to test different processing alternatives and seed regions. The results can be saved using the GUI or the command line. For multiple analyses, batch processing can be done.

ConnExT has been tested with MATLAB R2010, using Windows and Linux operational systems.

If you have any suggestion, contribution or bug report about ConnExT or this manual, do not hesitate to contact the author. Feedback from the users is very important.

Installation

To install ConnExT, unzip the contents of *connext.zip* and save them in any folder of your computer. Then add this directory to the MATLAB search path:

- a) MATLAB, File, Set Path..., Add with Subfolders..., select the ConnExT directory, Save, Close

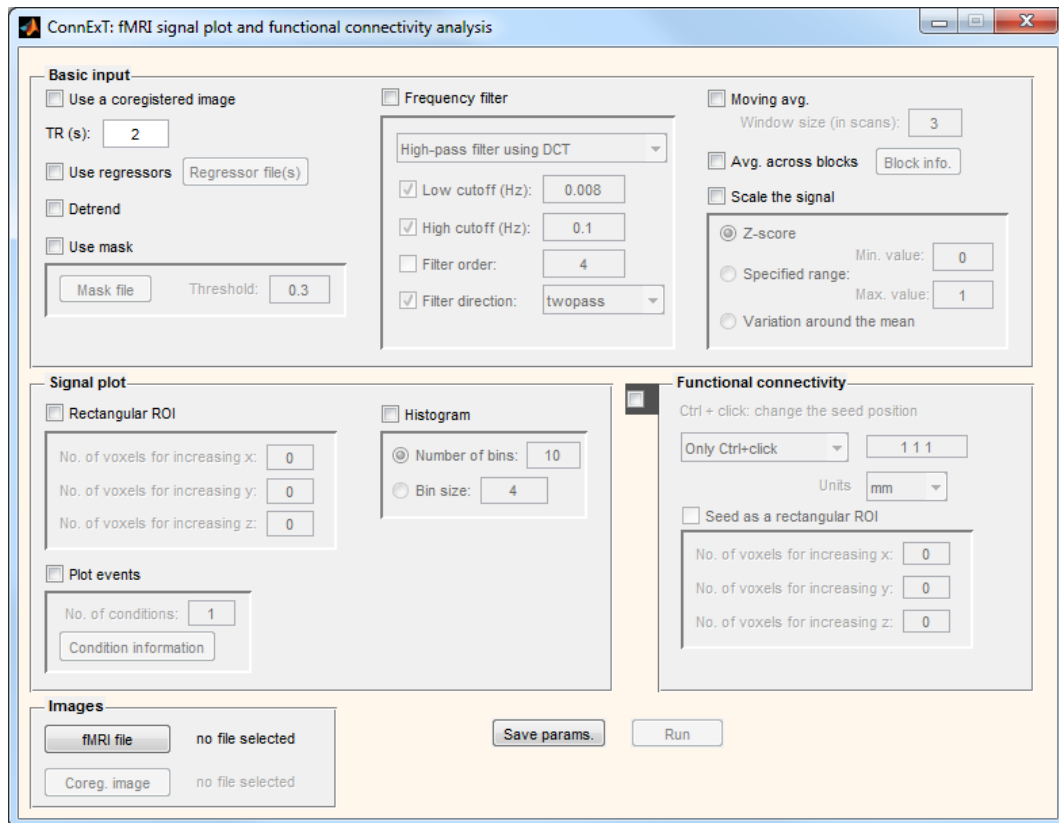
or

- b) `>> addpath(genpath('full_path_to_ConnExT_directory')); savepath;`

Using ConnExT via a graphical user interface

ConnExT can be used through a GUI to plot the fMRI signal and to perform the functional connectivity exploration.

1. Open MATLAB.
2. Type “connext” in the Command Window. The following window will appear (the colors may differ depending on your operating system):



Basic input

Select the processing options to apply to the functional image.

3. To use as underlay an image that is coregistered with the functional scan, check the corresponding box.
4. To remove regressors from the signal using a multiple linear regression, check the corresponding box. Choose the text file(s) containing the time series of the regressors.
5. To apply detrending to the signal, check the corresponding box.
6. To use a mask file, check the corresponding box. Choose the mask file and the threshold value to binarize the mask.
7. To use a frequency filter, check the corresponding box. Choose the type of filter (for some options, the Signal Processing Toolbox is required), the frequency cutoffs, filter order and direction.
8. To apply a moving average, check the corresponding box. Choose the window size.
9. To average across blocks, check the corresponding box. Choose the beginning and duration in units of seconds (if TR is not zero) or scans (if TR is zero).
10. To scale the signal, check the corresponding box. Choose the type of scaling.
11. The processed image can be saved with a button on the SPM Display Window that appears after running ConnExT. If the functional connectivity is calculated, the correlation coefficients will be saved instead. The output file format is NIfTI (nii or img/hdr).

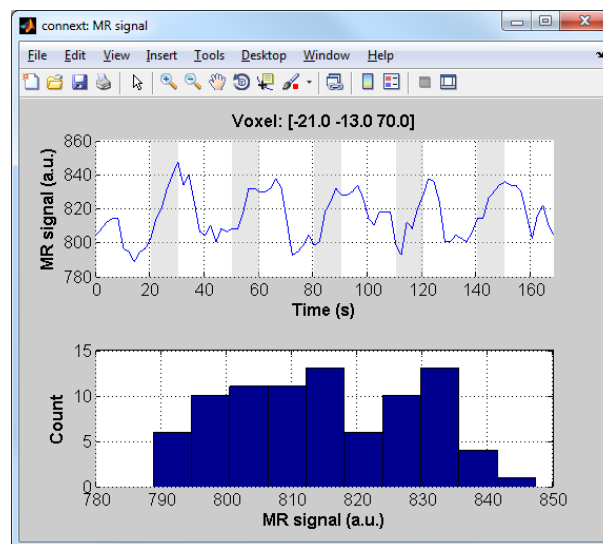
ConnExT will perform the signal processing in this order: masking, removing regressors and detrending (they are performed simultaneously), filtering, moving average, average across events, data scaling.

Signal plot

Choose the way the fMRI signal will be shown. All the positions are shown in millimeters.

12. To plot the signal from a rectangular ROI, check the corresponding box. Choose the number of voxels in each direction.
13. To plot colored rectangular shapes representing the events, check the corresponding box. Choose the number of conditions, condition name, onsets and durations in units of seconds (if TR is not zero) or scans (if TR is zero).
14. To plot the signal histogram, check the corresponding box. Choose the number of bins or bin size. This option is only available when the functional connectivity is not performed.

One example is show below:



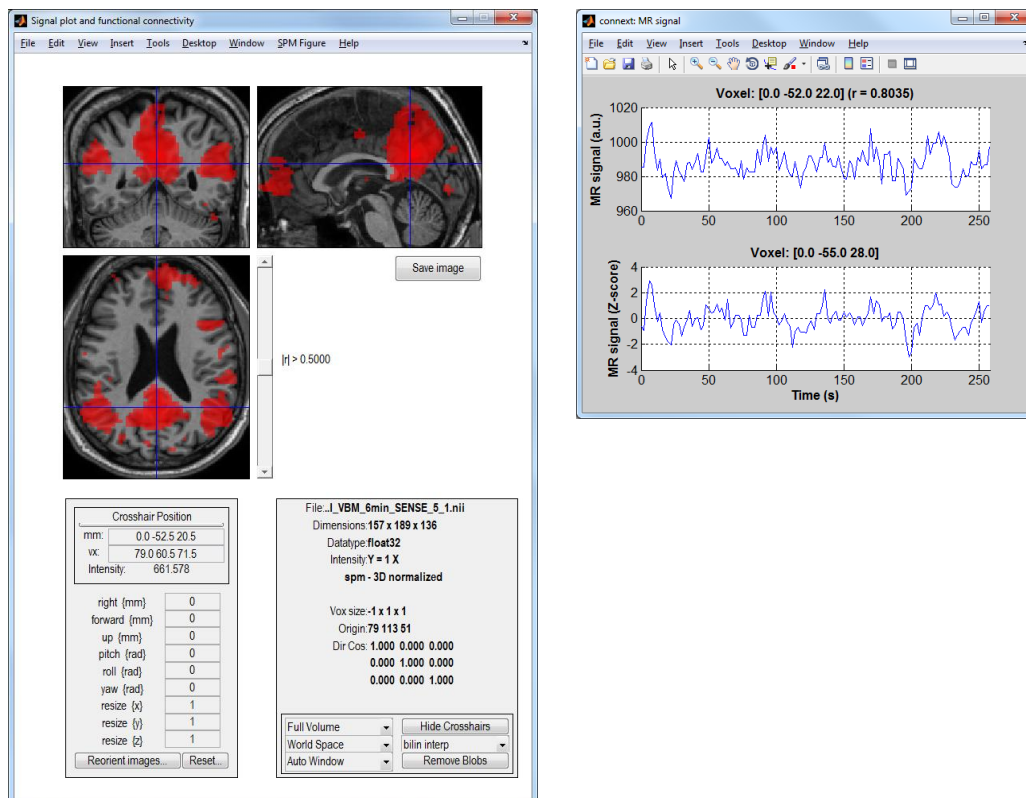
Functional connectivity

Create a map of the correlation coefficients overlaid on the functional or a coregistered image.

15. To perform the functional connectivity, check the corresponding box. The options will be enabled.
16. Choose the type of seed:
 - a. Only Ctrl + click: use Ctrl with mouse click on the image display to choose the seed position.
 - b. Initial seed position: choose the seed position in mm or in voxel coordinates of the functional file.
 - c. Time series: choose a TXT file with the seed time series.

17. To use a rectangular ROI as seed, check the corresponding box. Choose the number of voxels in each direction.

The output is SPM's display window with the brain shown in three orthogonal planes and the correlation coefficients as overlay image (positive values in red, and negative values in blue). A separate figure will be created with the time series of the seed region and the current voxel (voxel positions in mm and the corresponding correlation coefficients between parentheses).



Images

Select the fMRI file. You may also need to select an image that is coregistered with the functional image.

Save and run

All chosen parameters can be saved and later edited through the command line. To run the analysis, click on the Run button. When using the GUI, ConnExT will always show the brain in three orthogonal planes (the tag property of the figure is "Graphics") and the time series of the current voxel (the tag property of the figure is "SPM_MR_signal").

Using ConnExT via command line

In addition to the GUI, analyses with ConnExT can be done using the command line. There are two easy ways:

- a) Choose some or all parameters in the GUI, save them, load the created file, edit the variable and run the analysis with the script *connext.m*.
- b) Edit and run the file *connext_INPUT.m*, based on *connext_INPUT_template.m* (it contains some dummy values). The available options in the scripts and in the GUI are practically the same.

The script *connext.m* (the GUI also calls this function) does most of the job, but other functions are also called. To learn more about what each script does, check the related help text.

Be careful that the GUI always shows the image and the signal. If you don't want to do this using the command line, remember to disable this option (field "*plot*" of the input parameter).

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