Deconvolution Procedure

Described here is the detailed procedure you may follow in order to deconvolve your **fMRI data**.

Prerequisites: Have the following toolbox loaded into Matlab path-
NIFTI Toolbox
[new deconvolution]HRF_Est_Toolbox
spm8
I suggest you to put all toolboxes inside the 'toolbox' folder in the Matlab main folder, and add those paths permanently to Matlab startup.

Deconvolution steps:

1. Pre-process the data (**do not do filtering***)
   *This is very important

2. Kindly have the folder 'deconvolution' in your computer now. It has many files and folders, and you need to refer to those files/folders in order to understand the instructions given below, so kindly keep it open before continuing reading. The execution files in the folder are as below:

   perform_dec.m :
   Performs deconvolution on all MAT files (one after the other) present in 'run_deconv' folder. Deconvolved data is saved as MAT files in the 'save_deconv' folder.

   exec_deconv.m :
   It is a Function which is called inside perform_dec.m

   mat_extraction.m :
   Extract 4-D mat file (timex91x109x91) from 4-D NIFTI images

3. Put all data, i.e. NIFTI files (hdr/img) for all subjects, in the **nifti_data** folder.

4. Convert NIFTI files (hdr/img) into MAT files (one 4-dimensional MAT file per subject):
   Run **mat_extraction.m**. Deconvolution is performed on MAT files, hence this step is necessary.
   Warning: There should be no other folders than your subjects inside the **nifti_data** folder.
   Warning: Once you start program execution, do not move or delete any subjects in the **nifti_data** folder, including completed subjects.

5. All MAT files generated from previous step will be in a folder called **output_matrix**
   -Since deconvolution of one subject might take around 3 hours (per subject), it is advisable to not run the deconvolution for all subjects at once.

- the deconvolution code (**perform_dec.m**) takes inputs from the **run_deconv** folder. So, move MAT files of those subjects you want to deconvolve into the 'run' folder. Remaining files (to be done later) will stay in the **output_matrix** folder.
  Warning: There should be no other folders than your subjects inside the **run_deconv** folder.
  Warning: Once you start program execution, do not move or delete any subjects in the **run_deconv** folder, including completed subjects.

6. Run the deconvolution code **perform_dec.m**. Deconvolved files are saved into a folder called **save_deconv**. They are MAT files.
   - Do not delete any files. Once execution of a set is complete, and program has stopped running, you can put completed '*run_deconv*' files into the **output_matrix_over** folder. This will be helpful because deconvolution takes lot of time, and it may be wiser to do it in separate batches if you have a large fMRI dataset.

7. Deconvolved data in **save_deconv** folder will have the same filename as the input MAT file.
   - Another set of files starting with "param_" will be created in the **param** folder. They are important parameters obtained during deconvolution (ex: param_sub_302_1_nf).
   - Using Rename Master, rename all the files in **save_deconv** with a suffix '_dc' (meaning deconvolved). This will help you differentiate between conventional data and deconvolved data
   Ex: *sub_314_2_gm_nf* becomes *sub_314_2_gm_nf_dc*
   Ex: *param_sub_302_1_gm_nf* becomes *param_sub_302_1_gm_nf_dc*

8. Deconvolution complete! 190 channel fMRI time series (190x1000 MAT files, for example) can be extracted from the deconvolved MAT files. Please proceed to the folder **timeseriesextract_deconv**

Timeseries Extraction steps:

Here is the detailed procedure you may follow in order to extract timeseries from your deconvolved data. Have the following toolbox loaded into Matlab path- NIFTI Toolbox

9. Kindly open the **timeseriesextract_deconv** folder before proceeding. It has many files and folders, and you need to refer to those files/folders in order to understand the instructions given below. The files in the folder are as below:

   - cc200_91x109x91.nii : cc200 template
   - cc200_91x109x91_125chan (hdr/img) : cc200 template obtained after removing zero-channels, finally only 125 regions out of 190 are covered. This example has been chosen to illustrate how to implement this procedure when the data does not have all 190 channels but a subset of it, which is due to incomplete brain coverage (to get higher sampling rate). As an example 125 channels is chosen. You can view the '.img' file in xjview, which will give you the clear picture. This will be useful during interpretation of the final results.

- cc200_centroids.mat : contains the centroids and names of all the 190 channels in the same order in which the 190 channels are extracted
- channels_190.xlsx : contains all 190 channels with their names. Information taken from cc200_centroids.mat file
- channels_125.xlsx : contains 125 non-zero channels with their names and centroids. Information taken from cc200_centroids_125.mat file
- channels_final_125.mat : contains those 125 channel indices (among 190 channels), which are finally used. Obtained from zero_channels_dir.m
- convert_timeseries_190to125.m : this code takes 190 channel timeseries from the 'data_save' folder (i.e. MAT files of all timeseries extracted subjects), and chooses only 125 channels, thus saving Tx125 MAT files for each subject (T=timepoints) in the 'data_save_125' folder (explanation provided later)
- Extract_timeseries_dec.m : extracts timeseries from all subjects whose data is present in 'data_do' folder. Timeseries data is saved as Tx190 MAT file for each subject (T=timepoints) in the 'data_save' folder
- zero_channels_dir.m : 'zero channel' is defined as a channel which has absolute zero value throughout, i.e. variance is exactly equal to zero, it has no data. This happens because during data acquisition whole brain is not scanned; which actually reduces TR (and thus increasing time resolution and sampling rate). Only a part of the brain is scanned. This code will take inputs from 'data_save' folder.

- zerochannels.mat : contains:
  - channel{i} = all the zero-channels for subject-i (i'th subject in 'data_save' folder)
  - numchans(i) = number of zero-channels for subject-i
- zeroindices.mat : contains:
  - vals = the channel numbers (among 190 channels) which are faulty
  - freq2(i) = number of subjects in 'data_save' folder which have the channel 'vals(i)' as a zero-channel

10. Put data of all subjects (one MAT file per subject) in the **data_do** folder.
    -Warning: There should be no other files than your subjects inside the **data_do** folder.
    -Warning: Once you start program execution, do not move or delete any subjects in the **data_do** folder, including completed subjects.

11. Run the Timeseries extraction code (**Extract_timeseries_dec.m**). Timeseries extracted files are saved in the **data_save** folder. They are MAT files of size Timepoints*190 and will have the same filename as the input data filename

12. Now that you have obtained the 190 channel fMRI time series, not all channels in all subjects have valid data. Some regions are not covered/scanned by the MRI scanner during data acquisition so that a smaller TR is achieved, thus giving better time resolution in fMRI data (higher sampling rate). So not all 190 channels contain data, and thus such channels have to be identified and eliminated.

    If there is full coverage of the brain in the data you have, then:
    - You do not need to worry about the following MAT files in the folder (no need to see or assess): cc200_centroids.mat, channels_final.mat, zerochannels.mat, zeroindices.mat
    - You do not need to worry about the following codes in the folder (no need to see or assess): zero_channels_dir.m
    - You will need to understand and execute only the following codes:
    Extract_timeseries.m, convert_timeseries_190to125.m

13. Here is how you can obtain 125 channel timeseries data of non-zero channels (for example) from the 190 channel timeseries data obtained in step 11.
    - have all 190 channel data in **data_save** folder. You may not have to act on this since the data will be in this folder automatically after step 11 is completed
    - run the code **convert_timeseries_190to125.m**
    - 125 channel data is saved in the folder **data_save_125**. You would need to use only this data in future studies.

14. How to use xjview :
    - You can download xjview for free, and run the setup
    - Enter xjview in Matlab
    - File -> Open Images -> cc200_91x109x91.img (for example)
    - In the x, y and z coordinate boxes below, enter the coordinates of the region, and it will point to it
    - You can overlap multiple images by selecting multiple from OpenImages.

Estimated execution time on a 3.30GHz Intel Xeon computer with 16GB RAM:
NIFTI to MAT conversion - 3.5min per subject
Deconvolution - 2h30m per subject
Timeseries extraction - 40min per subject
Obtaining 125 channel data from 190 - less than a minute for the whole dataset

Estimated file sizes per subject:
NIFTI files = 3.36GB
MAT files prior to deconvolution = approx 1.2GB
MAT files 'deconvolved' = approx 820MB
Timeseries MAT files (1000x190) = approx 790KB
(each subject had 1000 time points, each being 91x109x91 image)