REST - Time Shift Analysis
Manual

Center for Cognition and Brain Disorder,

Hangzhou Normal University

Zhejiang Key Laboratory for Research in

Assessment of Cognitive Impairments

Catalogue

1. Set Up

1.1 Running environment

Hardware environment:

CPU: Intel 2.0 GHz or above

Memory: 2G or above

Hard Disk: 10G or above

Software environment:

Support of Windows system

Support of Matlab version before 2014a

1.2 Support software

The software listed below needed to be set path in Matlab:

SPM12

RESTplus_V1.1

1.3 Install

Download and unzip software package:

Download the software from http:// www.restfmri.net.
Unzip TSA.zip and add path in Matlab (**Figure 1.1-1.2**).
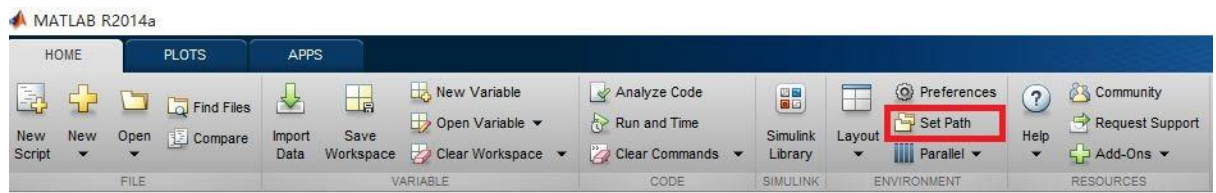
Figure 1.1
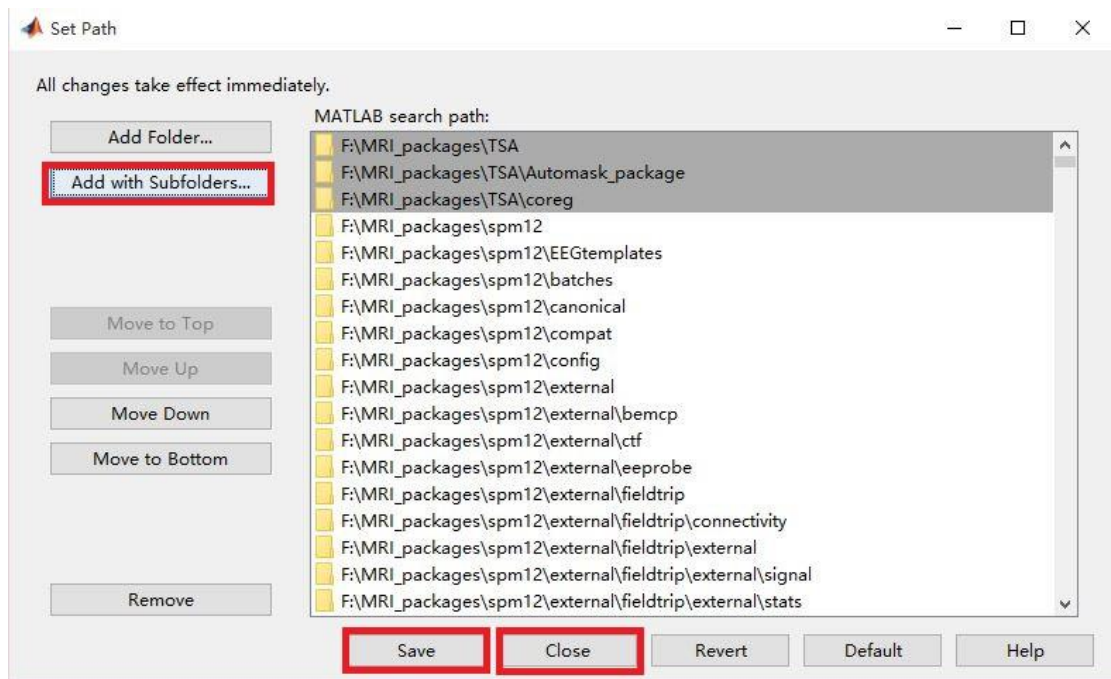
Figure 1.2

Matlab: 'Set Path' -> 'Add with subfolders' -> select the folder 'TSA'
-> 'save' -> 'close'

Then the REST-Time Shift Analysis toolbox has been set up.

The same installing procedure for RESTplus and SPM.

Open the REST-Time Shift Analysis toolbox:

Open the Matlab;

Type 'TSA' in command window and press Enter (**Figure 1.3**);

Then the Main window of the toolbox appears (**Figure 1.4**);

Figure 1.3

Introduction for the Main window of the toolbox (Figure 1.4):

Figure 1.4

1. Main working directory;
2. Preprocessing checkbox;
3. Preprocessing Module, including the format transform of the dicom files to nifty images, remove first n time points, slice timing, realign, smooth, detrend, regress out covariates (6 head motion parameters), filter and automask;
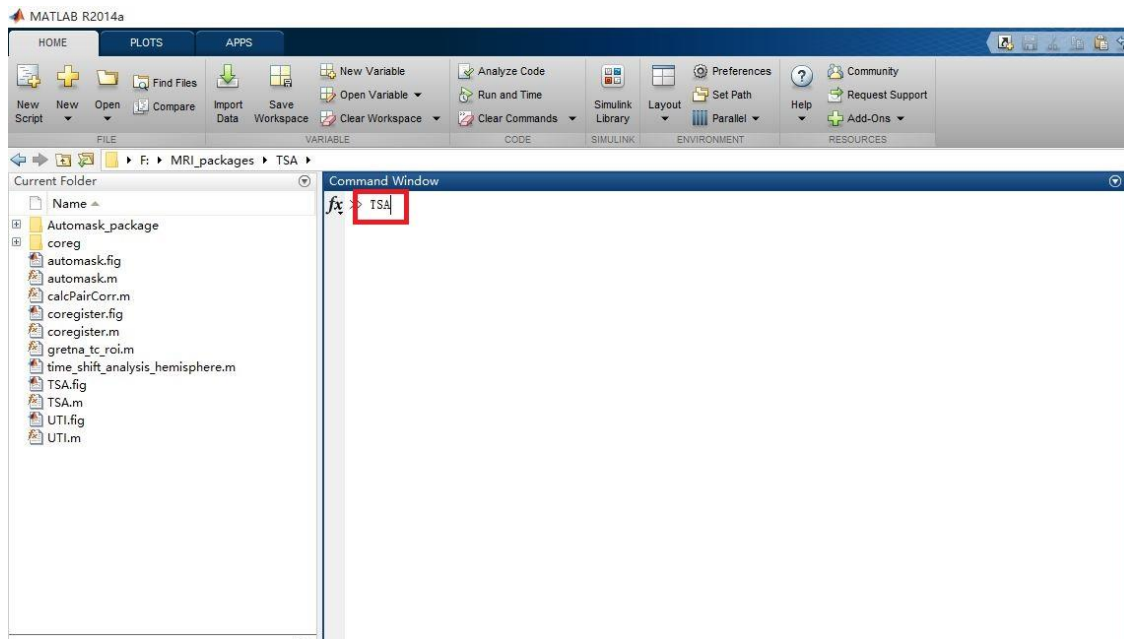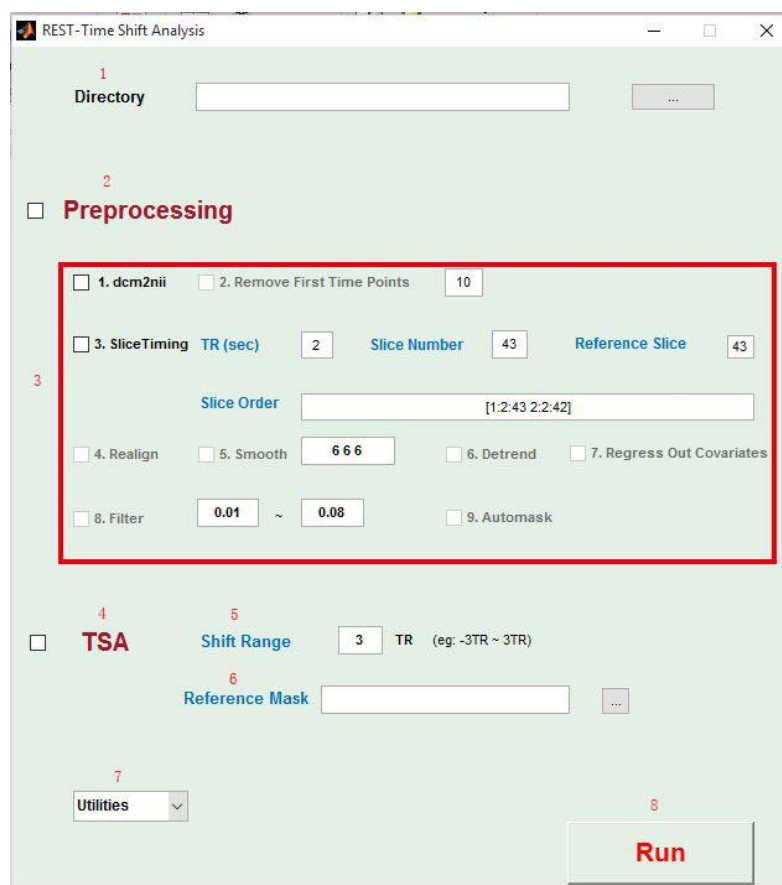4. Time Shift Analysis checkbox;
5. Time shift range of the whole brain voxels;
6. Select the reference mask which will be used to calculate the reference time course;
7. Utilities, including Automask and Coregister;
8. Run the program after finishing setting up the parameters.

2. Software Manual

2.1 Preprocessing Module

Before performing the time shift analysis, you must make sure that the rs-fMRI (resting state functional Magnetic Resonance Imaging) data have been pre-processed.

Click the checkbox before the '**Preprocessing**', then all checkboxes belong to the preprocessing module change to the state being chosen (**Figure 2.1**).

Figure 2.1

(1) dcm2nii

Many scanners produce data in DICOM format. The purpose of this step is to convert DICOM files to NIfTI (Neuroimaging Informatics Technology Initiative) file format.

(2) Remove First Time Points

The first few volumes of the functional images are often discarded for signal equilibrium and to allow the participants' adaptation to the scanning noise. So this step will remove the first several time points. The number you type in the edit-box is the number of time points you want to remove.

(3) Slice Timing

This step can correct the differences in image acquisition time between slices, so the number of slices, slice order and reference slice need to be specified. You must type in the parameters to the edit-boxes.

(4) Realign

This step is used to perform the head motion correction so that the brain is in the same position in every image.

(5) Smooth

The goal of this step is to suppress noise and effects due to residual differences in functional and gyral anatomy during inter-subject averaging. The program will smooth the data with the specified width at half of the maximum value. So you should type appropriate FWHM (full-width-half-maximum) values into the edit-box.

(6) Detrend

This step is used to remove linear trend which could affect further analysis.

(7) Regress out covariates

This step is used to regress out 6 head motion parameters.

(8) Filter

The data is usually bandpass (e.g., 0.01-0.08 Hz) filtered to reduce the effect of very low frequency and high frequency physiological noise. You should type in the frequency band you need to the edit-box.

(9) Automask

This step will make a brain mask in native space using mean functional image from 'Realign'.

After the preprocessing, you will get folders like **Figure 2.2**.
(e.g. 'FunHTA' means the data in this folder have been preprocessed through dcm2nii, remove first time points and slice timing corrected.)
Abbreviation:
 -H dcm2nii
 -T remove first n time points
 -A slice timing
 -R realign
 -S smooth
 -D detrend
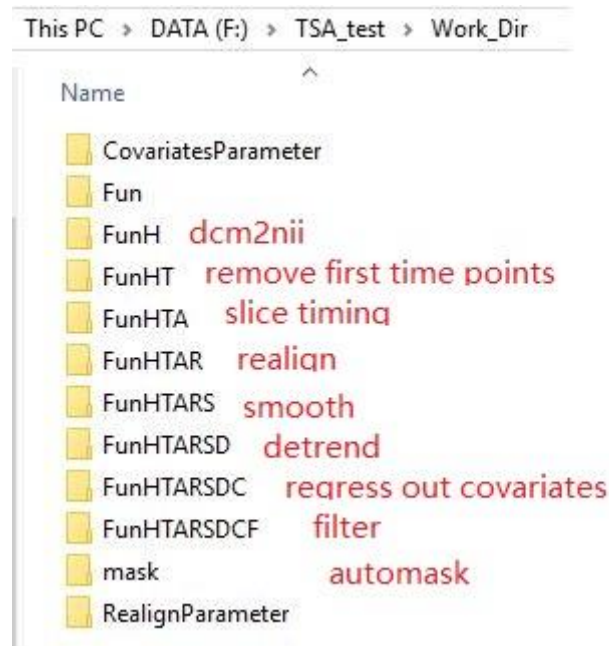 -C regress out covariates
 -F filter

Figure 2.2

2.2 Time Shift Analysis

Time Shift Analysis run with preprocessed rs-fMRI data (**Figure 2.3**).

Firstly, click the checkbox before '**TSA**', then type time shift range in the edit-box.
If you want use your own mask to calculate the reference time course during time shift analysis, you need to choose the mask file by clicking the button after 'Reference Mask'.
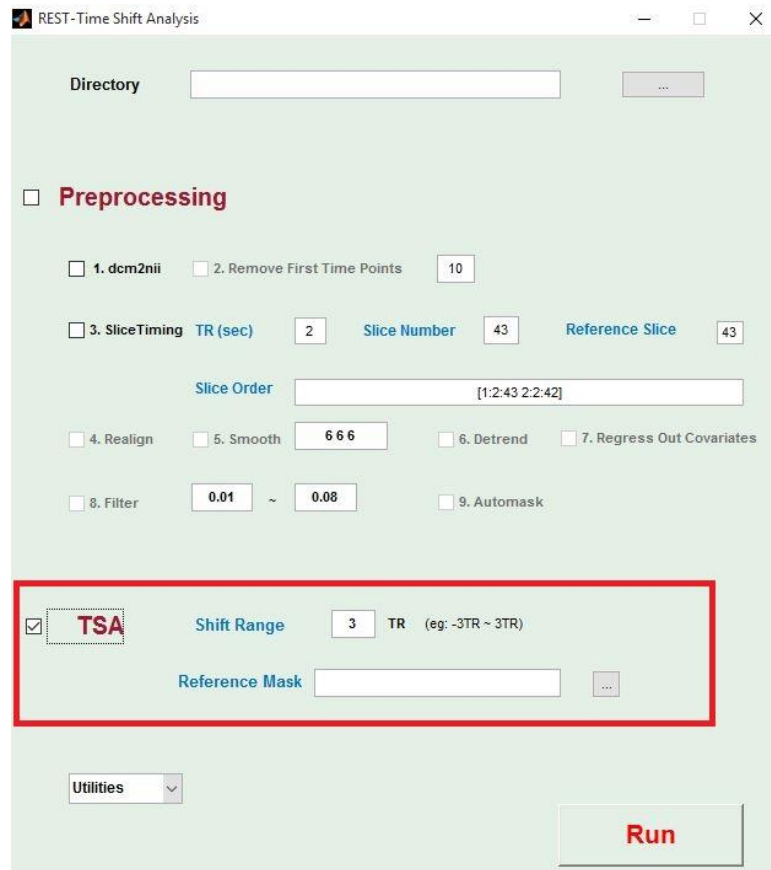
Figure 2.3

2.3 Utilities

There are two utilities in this module: AutoMask and Coregister (**Figure 2.4**).

AutoMask is used to create a brain mask for your own data which will be used in the time shift analysis.
Coregister is used to register clinical image (e.g. DWI, PWI, ASL_CBF) to functional data (mean functional image from 'Realign'). Then the TSA results could overlay on the clinical image.
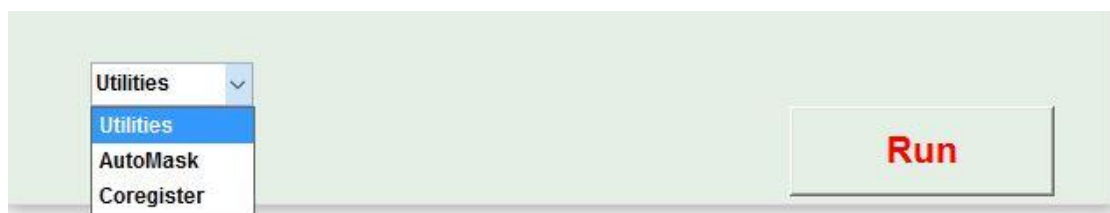

Figure 2.4

3. Examples use of TSA toolbox

3.1 Data Organization

Organize your data as follows (**Figure 3.1**):
1. create a new folder 'Work_Dir'.
2. create a subfolder 'Fun' for storing the functional raw data of subjects.
3. create subfolders for subjects which must be named with the prefix 'sub'.

Finally, copy the data of subjects to the 'sub00*' folders.

Figure 3.1

3.2 Preprocessing + Time Shift Analysis

To select the folder 'Fun' by click the button marked (**Figure 3.2 - 3.3**).
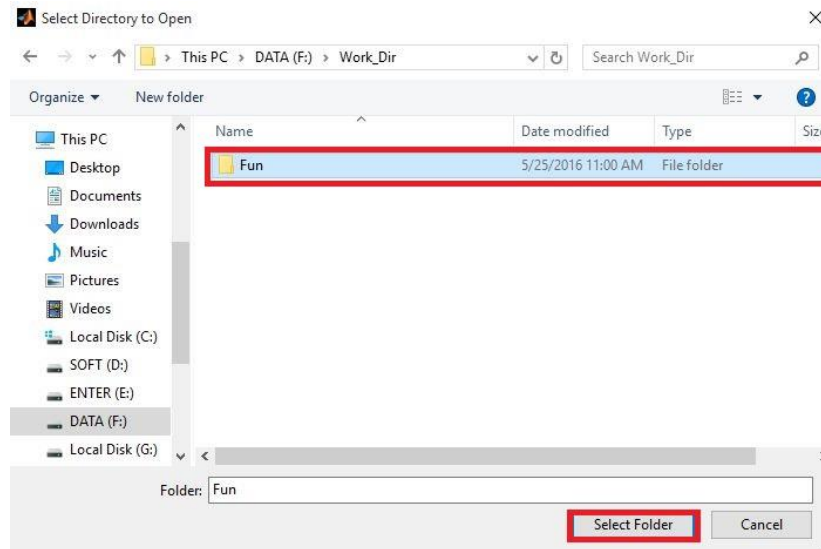

Figure 3.2

Figure 3.3

Then to click the checkbox '**Preprocessing**' (**Figure 3.4**).

Figure 3.4

You could skip **1. dcm2nii** (if your data have been transformed to Nifty format) and **3. slice timing** by remove the check before them. But the steps in gray are essential so that you cannot skip them.

To click the checkbox before '**TSA**', and type in the time shift range to the edit-box (**Figure 3.5**).

Figure 3.5

Finally, click the '**Run**' button.

Note that, if you want to use your own mask to calculate the reference time course during the time shift analysis, select the mask file by yourself (shown in **3.3**).

3.3 Time Shift Analysis only

If the data were already preprocessed, you just want to perform the time shift analysis.

You don't need to click the checkbox of '**Preprocessing**', but to type in the 'TR' to edit-box which belong to the slice timing part and click the checkbox of 'TSA' (Figure 3.6).
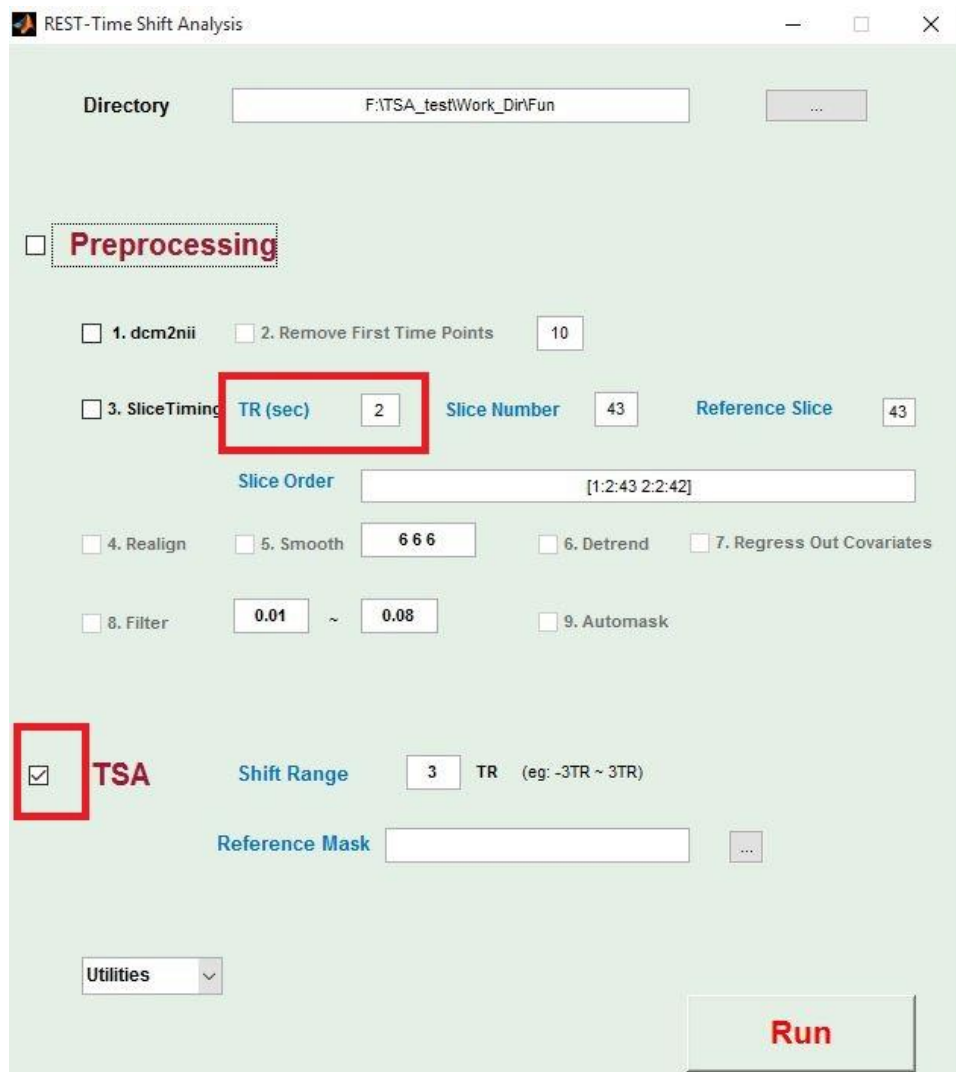
Figure 3.6

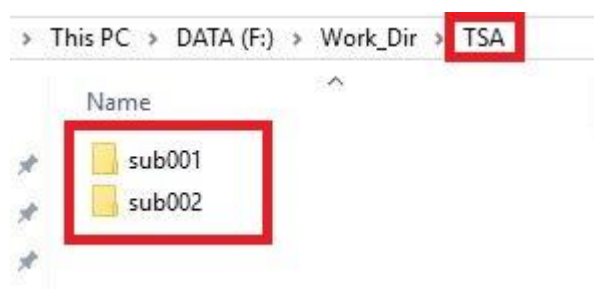To organize the preprocessed data as **3.1**, with folder name 'TSA' (**Figure 3.7**).

Figure 3.7

You should make the mask for your data (e.g. using the 'Automask' in 'Utilities') and put it in the folder 'mask', and subfolders must have the same names as subfolders in 'TSA' (**Figure 3.8**).
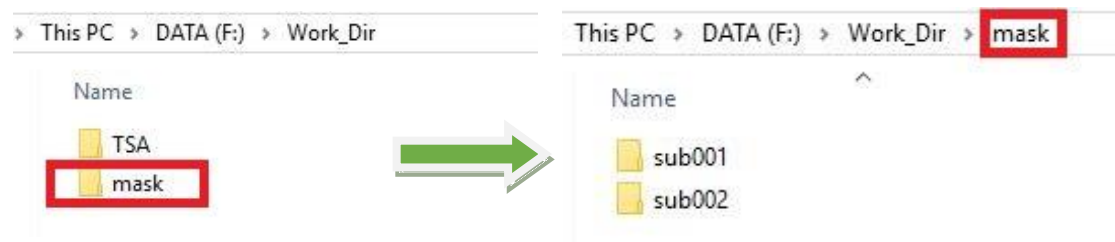
Figure 3.8

To make sure the mask files in these subfolders must be named 'fun_mask.nii' (**Figure 3.9**).

Figure 3.9

To click the directory selecting button (**Figure 3.2**).
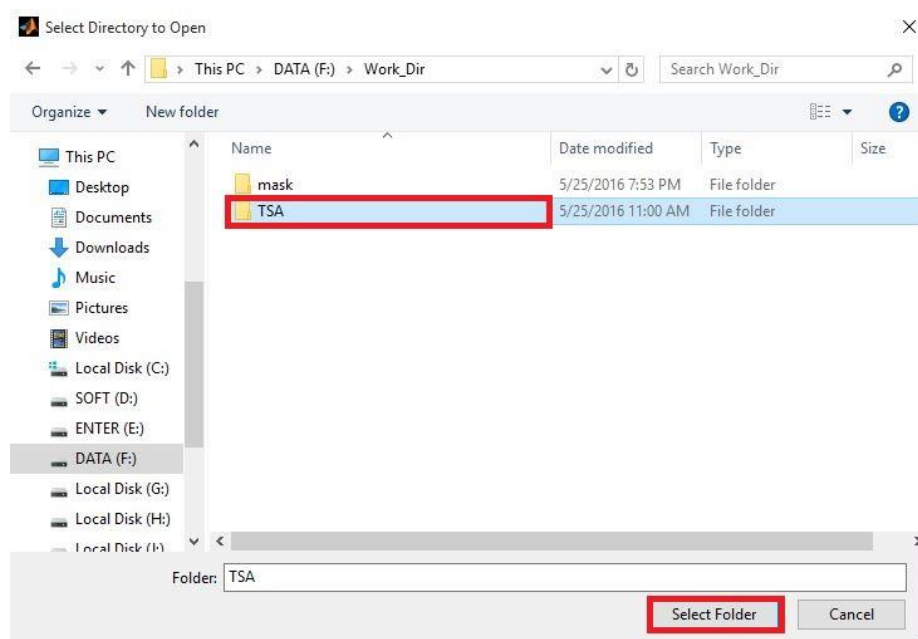To select the folder 'TSA' (**Figure 3.10**).

Figure 3.10

Then to type time shift range in the edit-box, and to click 'Run' button, time shift analysis starts (**Figure 3.11**).

Figure 3.11

Note that, if you want to use your own brain mask to calculate the reference time course during time shift analysis, please select the mask file. And if your own brain mask is specific to one subject, the time shift analysis on group level is unavailable.

To click the button marked (**Figure 3.12**).

Figure 3.12

Firstly, select the folder storing the brain mask, to click 'Select Folder' (**Figure 3.13**), then the mask file will be shown in a file selector, select it and click 'Open' (**Figure 3.14**).
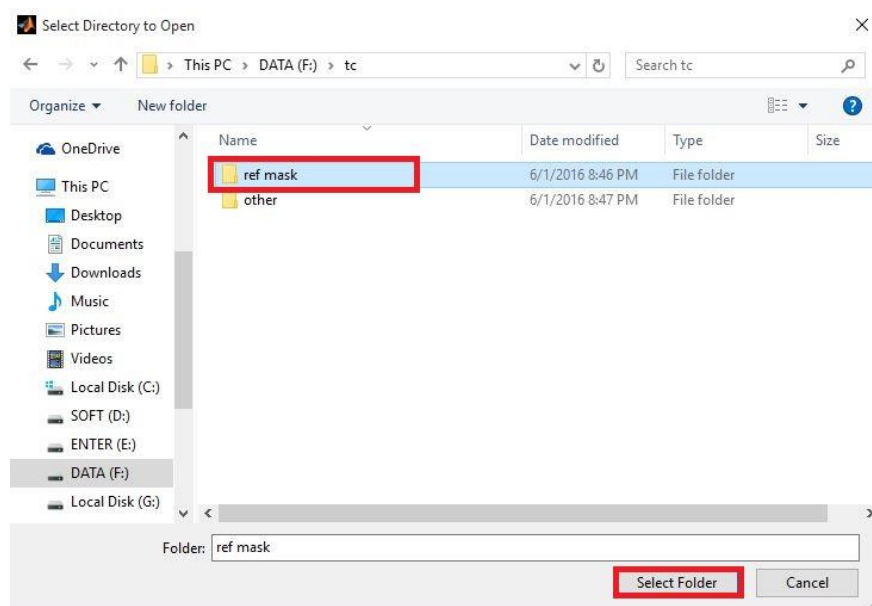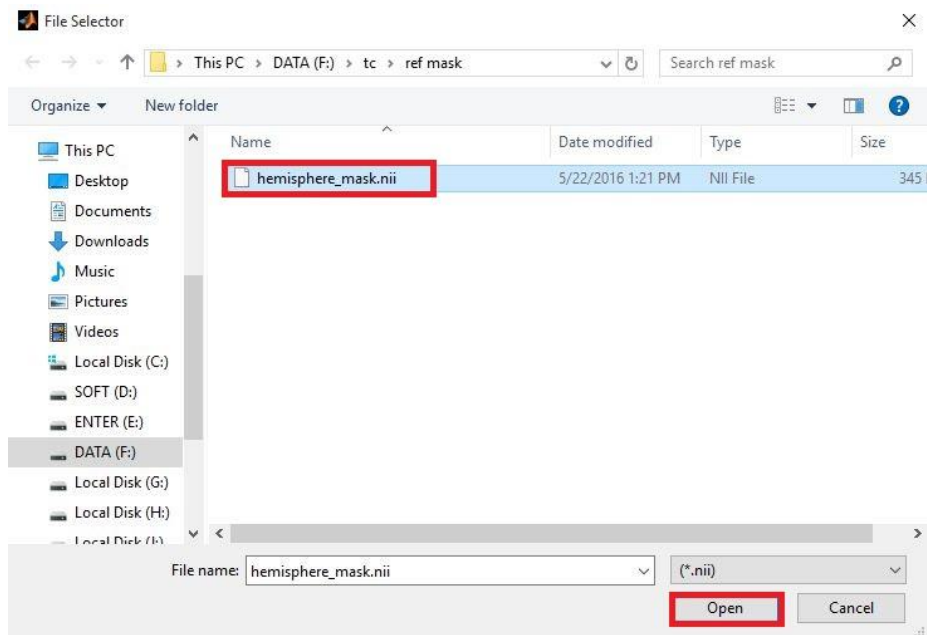
Figure 3.13

Figure 3.14

The final step is to click the '**Run**' button.

3.4 Utilities

To click the pop-up menu labeling 'Utilities', then you can choose to perform 'AutoMask' or 'Coregister' (**Figure 3.15**).

Figure 3.15

(1) AutoMask

Firstly, to click the button marked (**Figure 3.16**), selecting the parent folder of the file that need to be automasked, to click 'Select Folder' (**Figure 3.17**), then the file will be shown in a file selector, select it and
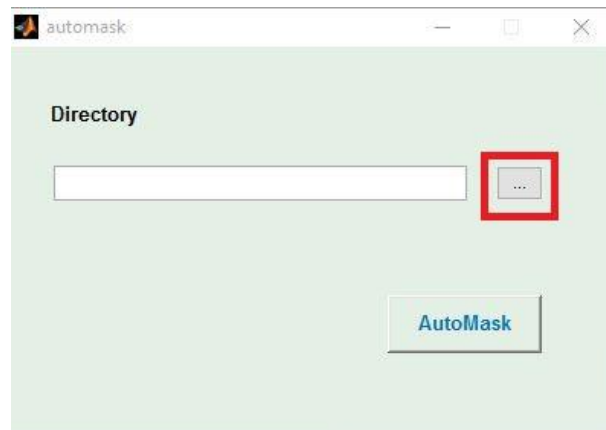
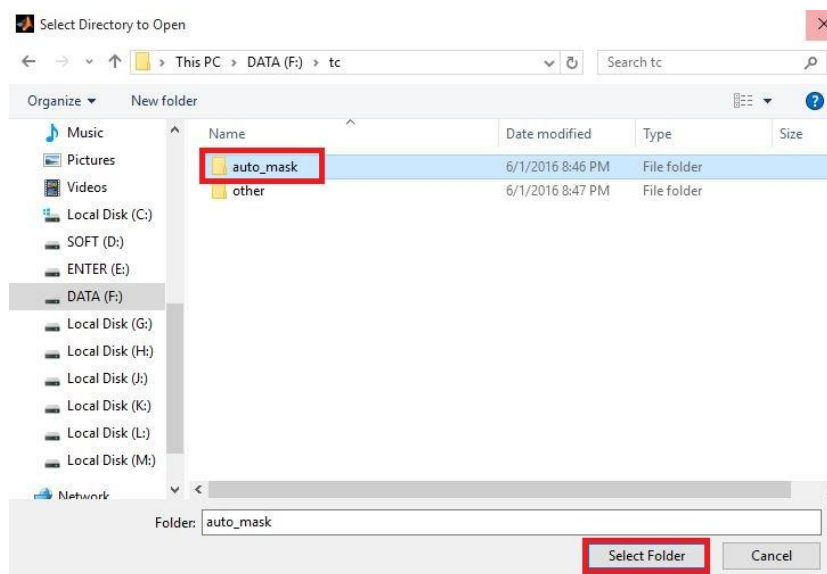click 'Open' (**Figure 3.18**).
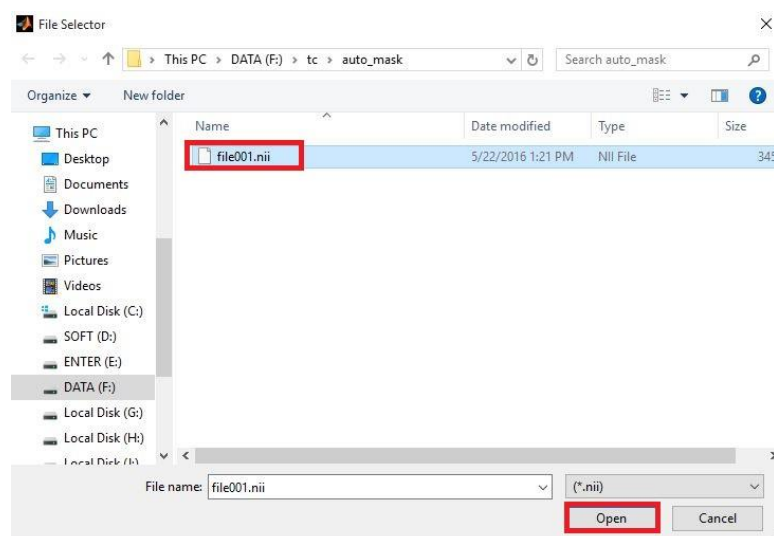

Figure 3.16

Figure 3.17

Figure 3.18

Finally, to click the '**AutoMask**' button.

(2) Coregister

Firstly, you have to create a new folder as work directory.
Then copying all the images that need to do coregister to this folder.
Then to click the buttons marked (**Figure 3.19**), selecting the work directory and corresponding image.
After that, to press the '**Coregister**' button (**Figure 3.20**).
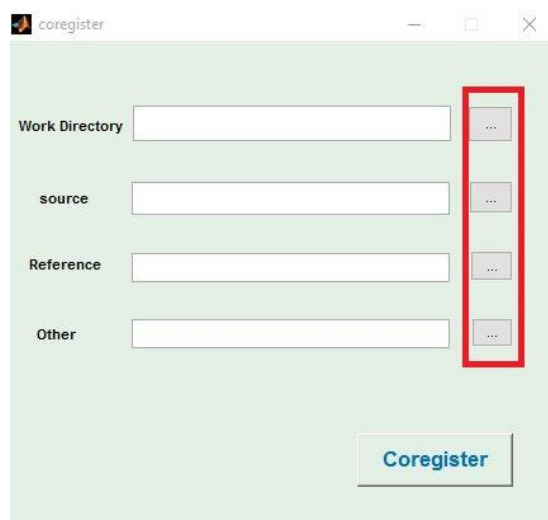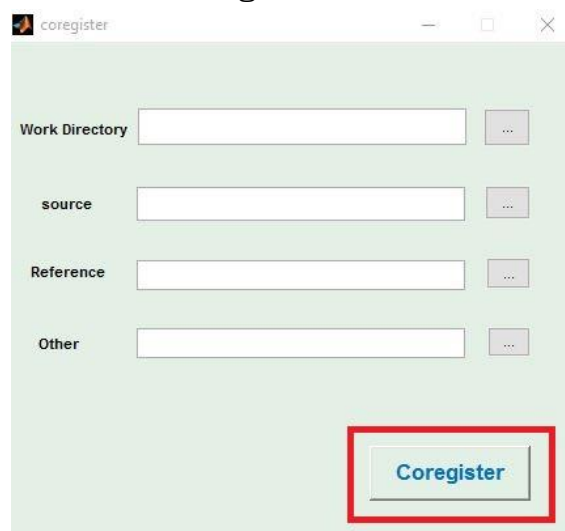

Figure 3.19

Figure 3.20

3.5 Results

If you perform the preprocessing and time shift analysis together by using

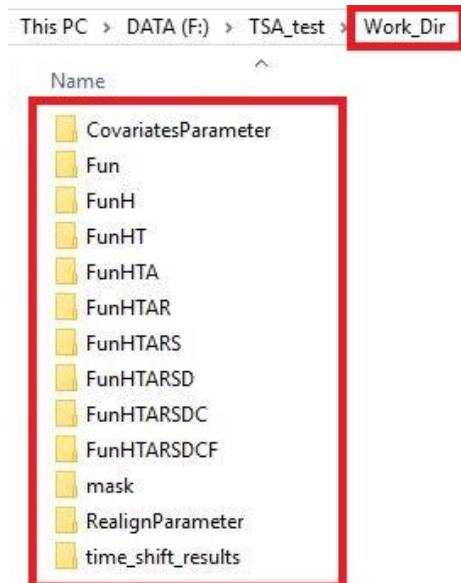this software, then all the files and folders generated are shown in **Figure 3.21** after all the steps.

Figure 3.21

But if you just finish the preprocessing part, the folder named 'time_shift_results' won't appear in folders shown in **Figure 3.21**.

If you performed the time shift analysis only, all the files and folders generated are shown in **Figure 3.22**.
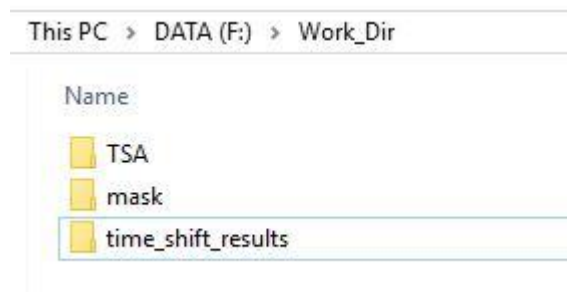

Figure 3.22

And there will be 3 files in the subfolders of 'time_shift_analysis', the file named with a postfix 'oppo' is the final result of time shift analysis (**Figure 3.23**). Note that, the positive values in this image mean delay values (e.g. if TR=2s and the voxel value equals 4, it has 2TR time delay to the reference time course).
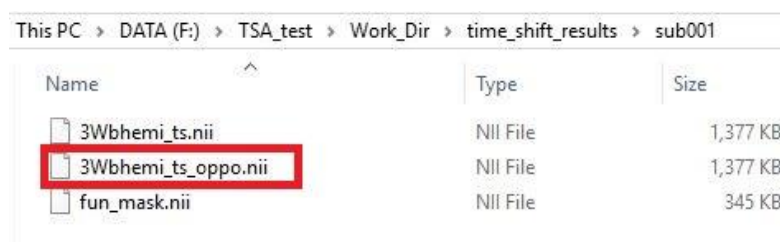
Figure 3.23

4. Appendix

4.1 Coder

Wei Wei (weilisten@163.com)
Lv Yating (lvyating198247@foxmail.com)

4.2 References

[1] Lv Y, Margulies DS, Cameron Craddock R, et al. Identifying the perfusion deficit in acute stroke with resting-state functional magnetic resonance imaging. Ann Neurol 2013;73(1):136–140.

[2] Amemiya S, Kunimatsu A, et al. Cerebral Hemodynamic impairment: assessment with resting-state functional MR imaging. Radiology 2014; 270(2): 548-555.

4.3 Supportive software

SPM12 (http://www.fil.ion.ucl.ac.uk/spm)
RESTplus (http://www.restfmri.net)