

Stable and Consistent Group ICA Toolbox (“MICA” Toolbox)

Manual

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Chapter 1 Introduction

Independent component analysis (ICA) was originally proposed as a blind source separation algorithm in signal processing and has proven a powerful, efficient and reliable tool for exploratory analyses in functional magnetic resonance imaging (fMRI) studies (McKeown et al., 1998; Kiviniemi et al., 2003).

Early applications of ICA focus on single subject fMRI data (i.e. individual-level) (McKeown et al., 1998). To address the challenge of matching single-subject ICA components between subjects in group-level analyses, group ICA (GICA) was developed (see Calhoun et al., 2009 for a review). Temporally concatenation GICA (TC-GICA) has emerged as one of the leading GICA approaches (Calhoun et al., 2001; Beckmann et al., 2005). It concatenates all individual data along the temporal dimension before ICA decomposition. To reduce the huge dimensionality of the concatenated data, a hierarchically multi-stage principal component analysis (MS-PCA) was often adopted and implemented in GIFT (Calhoun et al., 2001) and MELODIC (Smith et al., 2004). Currently, TC-GICA with three-stage MS-PCA reduction (TC-GICA3) is widely used, and several interesting findings have been reported (Calhoun et al., 2008; Jafri et al., 2008; Stevens et al., 2009).

Recently, Zhang et al. (2010) found that, in TC-GICA3, different subject concatenation orders (SCOs) produces variation to the grouping manner in the second-stage PCA reduction, which further leads to variable MS-PCA results and thus instable GICA result. More seriously, such SCO-induced variability will propagate to group-difference analysis and get more serious (Fig. 1). Moreover, we speculated that such variability might, in all likelihood, be present in following analyses of TC-GICA3 outputs, such as correlation analysis between TC-GICA3 results and behavior or clinical measures (Damoiseaux et al., 2008), reliability analysis (Chen et al., 2008), and “functional network connectivity” analysis (Jafri et al., 2008).

Therefore, MICA beta1.2 was designed to solve this problem (i.e., SCO-induced GICA instability).

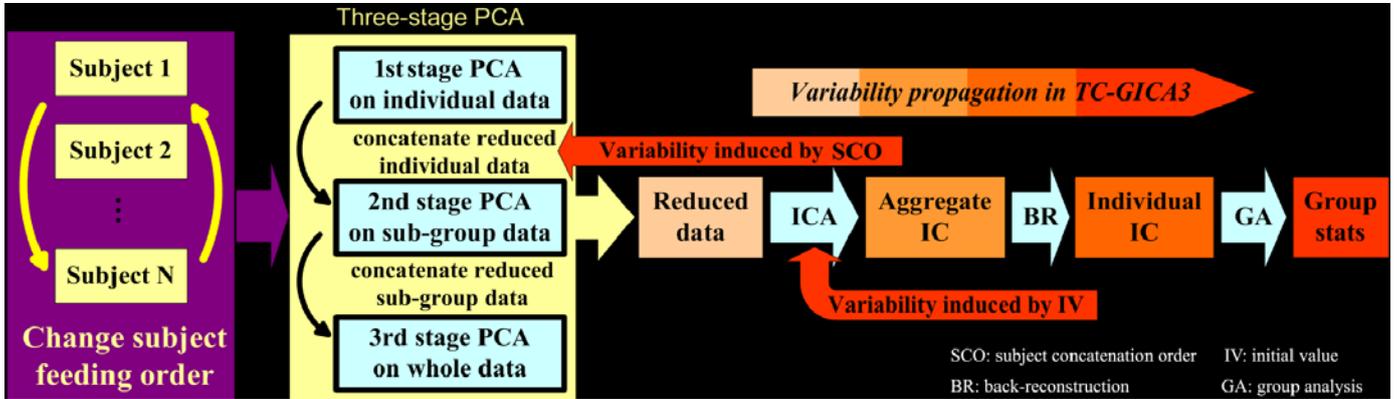


Fig. 1 Instability and its propagation due to SCO and random initial value (IV).

Based on the improved algorithm, Subject Order-Independent Group ICA (SOI-GICA) (Zhang et al., 2010), MICA launches *multiple* GICA (therefore named as “MICA”), each time with randomized initial value and different subject order. Then the multiple results are integrated to form the final output of MICA. It was found that MICA’s result demonstrated higher robustness and accuracy compared to those of the traditional TC-GICA (see Zhang et al., 2010 for detailed proof).

Chapter 2 Technical Summary

Features:

1. GUI-based, easy to use.
2. Fewer parameters need to set.
3. Allow batch processing.
4. Produce log file.
5. Rank components by their stability.
6. Easy to extract the component of interest.

Development language:

MATLAB version 7.1

Compatibility

1. MATLAB version 7.1 or later.
2. No need SPM toolbox or other toolbox.
3. System: Windows or Linux.
4. File format: NIFTI (single-file NIFTI, i.e., *.nii or two-file NIFTI, i.e., *.hdr/img).

Chapter 3 Toolbox Design

MICA toolbox mainly includes GUI module, core computing module and result viewing module. The core computing functions include 1) parameter initialization, 2) MS-PCA reductions, 3) ICA estimation, 4) reconstruction of individual-level components, 5) clustering and aggregate multiple results, 6) calibration and 7) statistical analysis (see Fig. 2 for a flow chart of MICA).

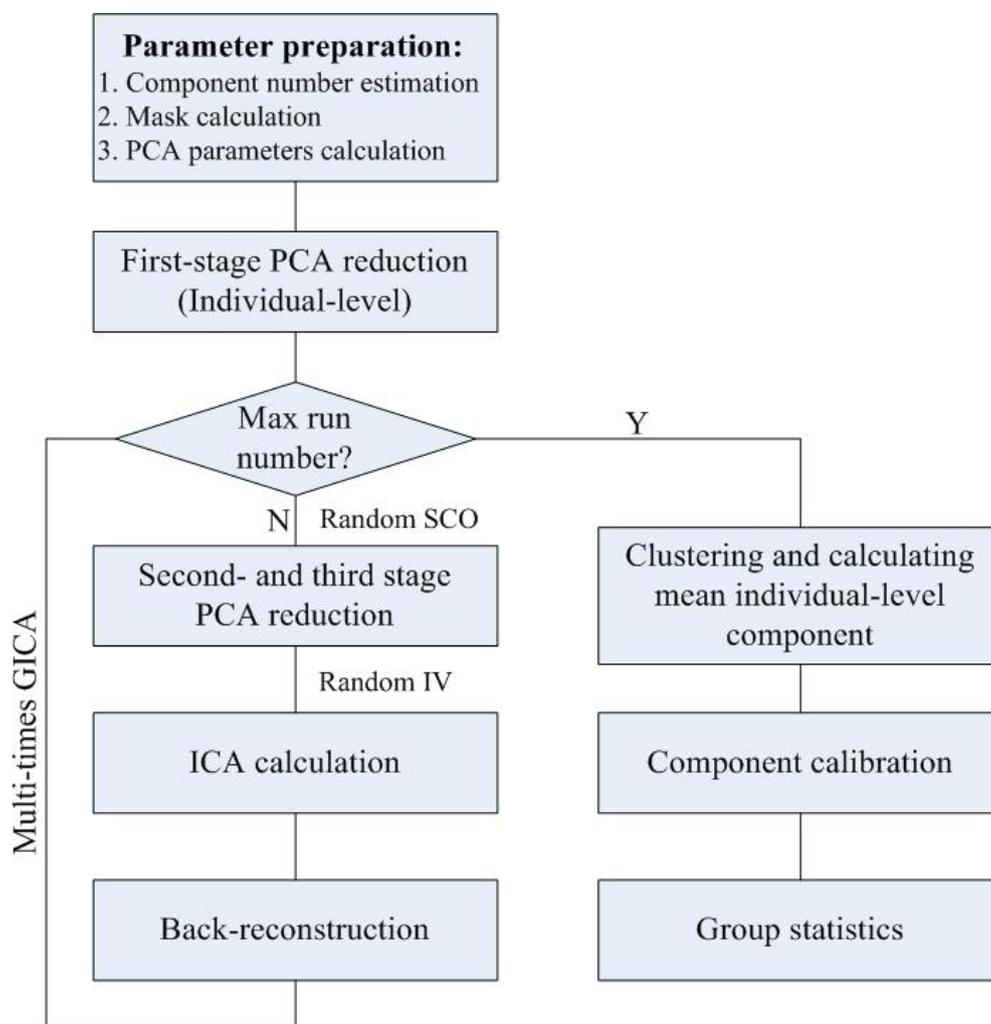


Fig. 2 Flow chart of MICA

The result viewing module includes functions of viewing the resulted component from different angles; utilizing multidimensional scaling (MDS) to assess the stability of each component; and sorting components according to their stability.

Chapter 4 Quick Demo

MICA is used to process functional MRI data, both for task-state and resting-state ones. To provide MICA the preprocessed data, you need to firstly convert DICOM data into NIFTI format (as that used in SPM5/8). Then, use SPM5/8 to preprocess the raw data in conventional way (e.g., slice timing, realignment, normalization and smooth). After that, let MICA do the rest of the works. This quick demo will let you learn MICA in 10 minute.

Using “Add Path”, add the directory of MICA into MATLAB, and type “mica” in MATLAB’s command window. Then, it will open the main GUI of MICA (Fig. 3).

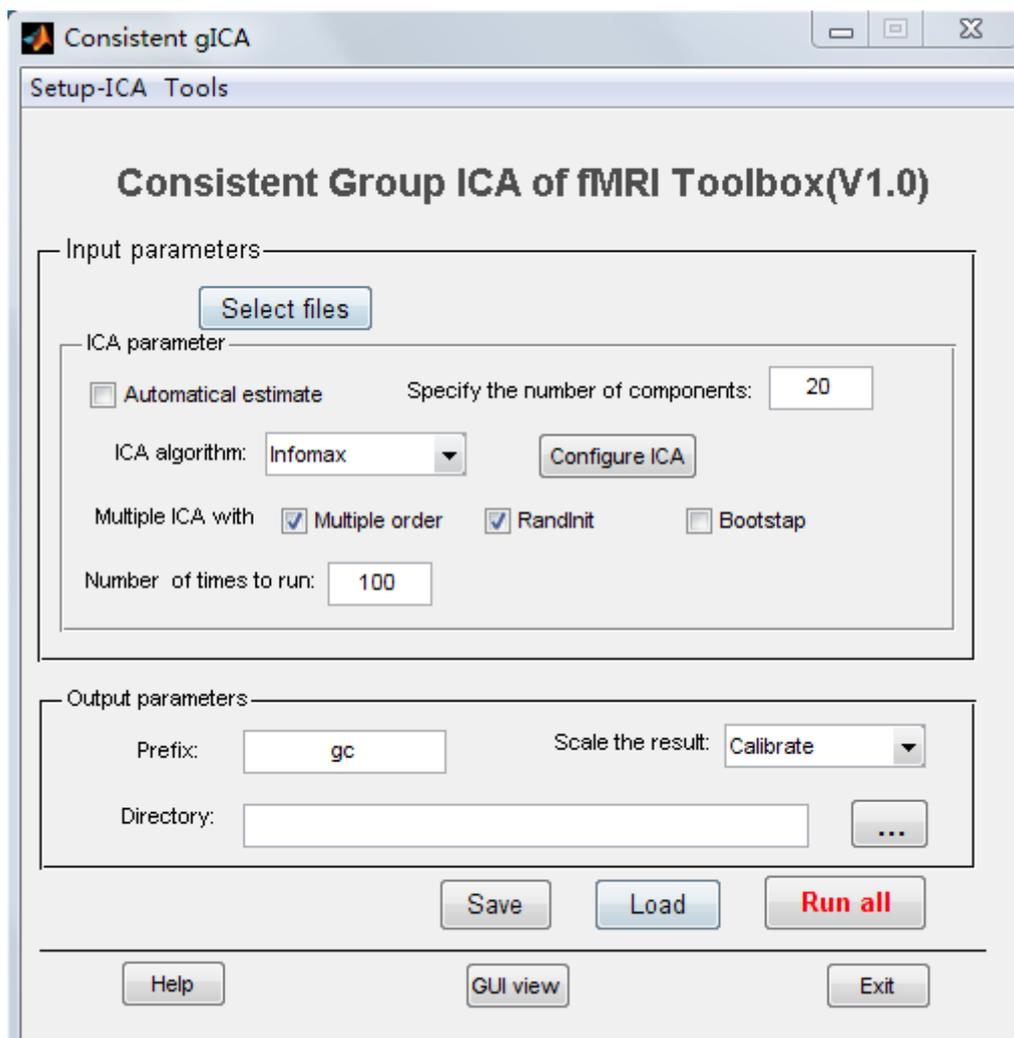


Fig. 3

Click “Select files”, choose one or two groups of subjects. Right click the blank area and select the directory containing all subjects’ data sets. Then MICA will automatically add all sub-directories, each for one subject (see Fig. 4). Click OK.

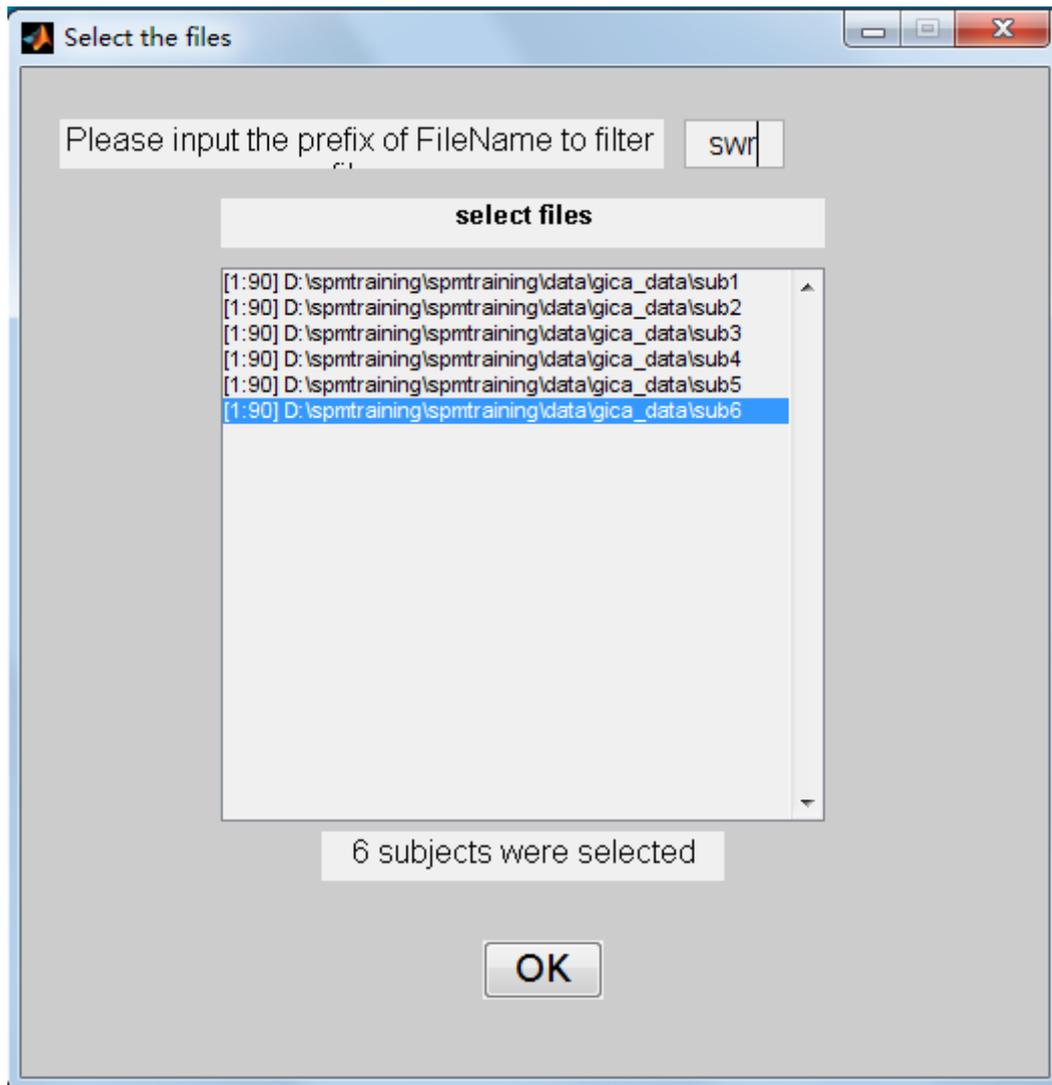


Fig. 4

After data inputting, set input and output parameters in the main GUI. An example of the parameter setting is shown in Fig. 5.

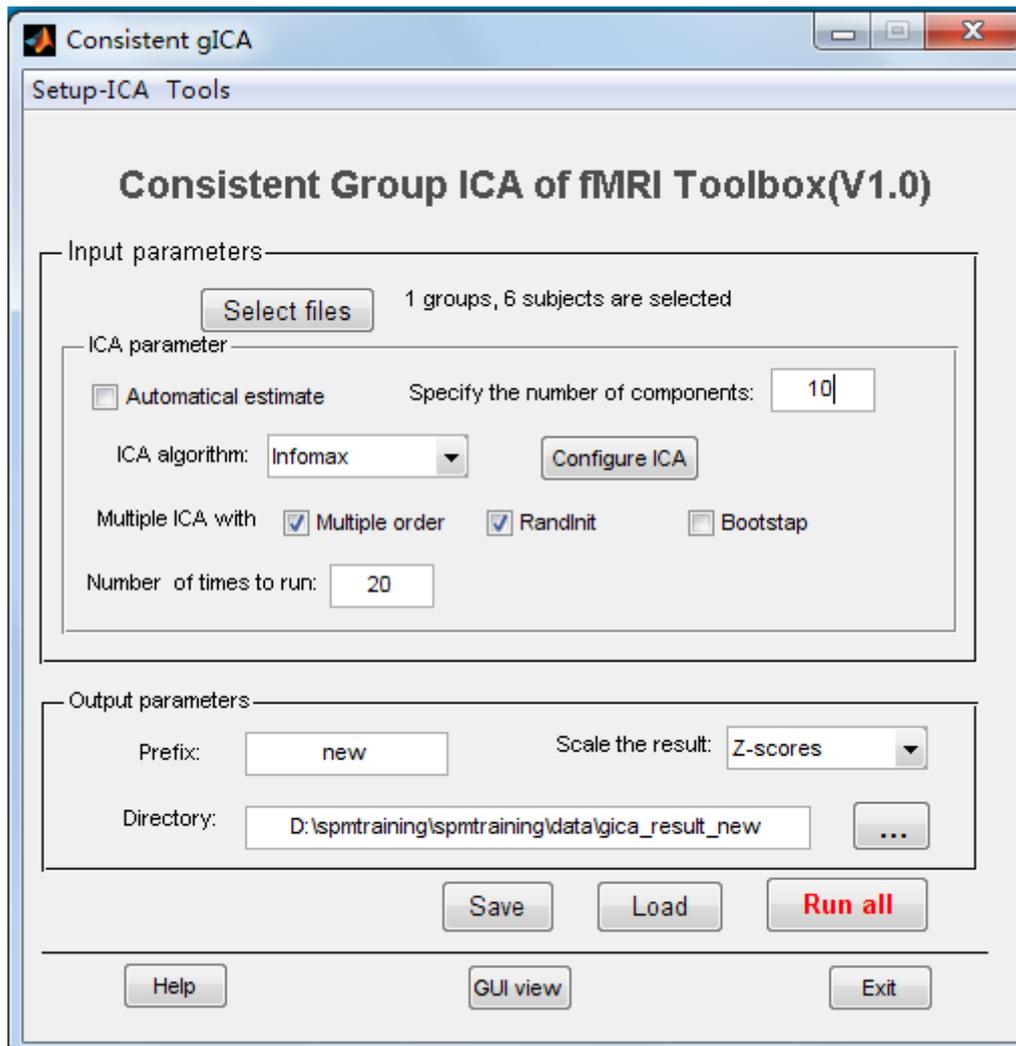


Fig. 5

Then, click “Setup-ICA” menu in the top-left. The detailed GICA parameter setting GUI will pop up (see Fig. 6 for an exemplar setting).

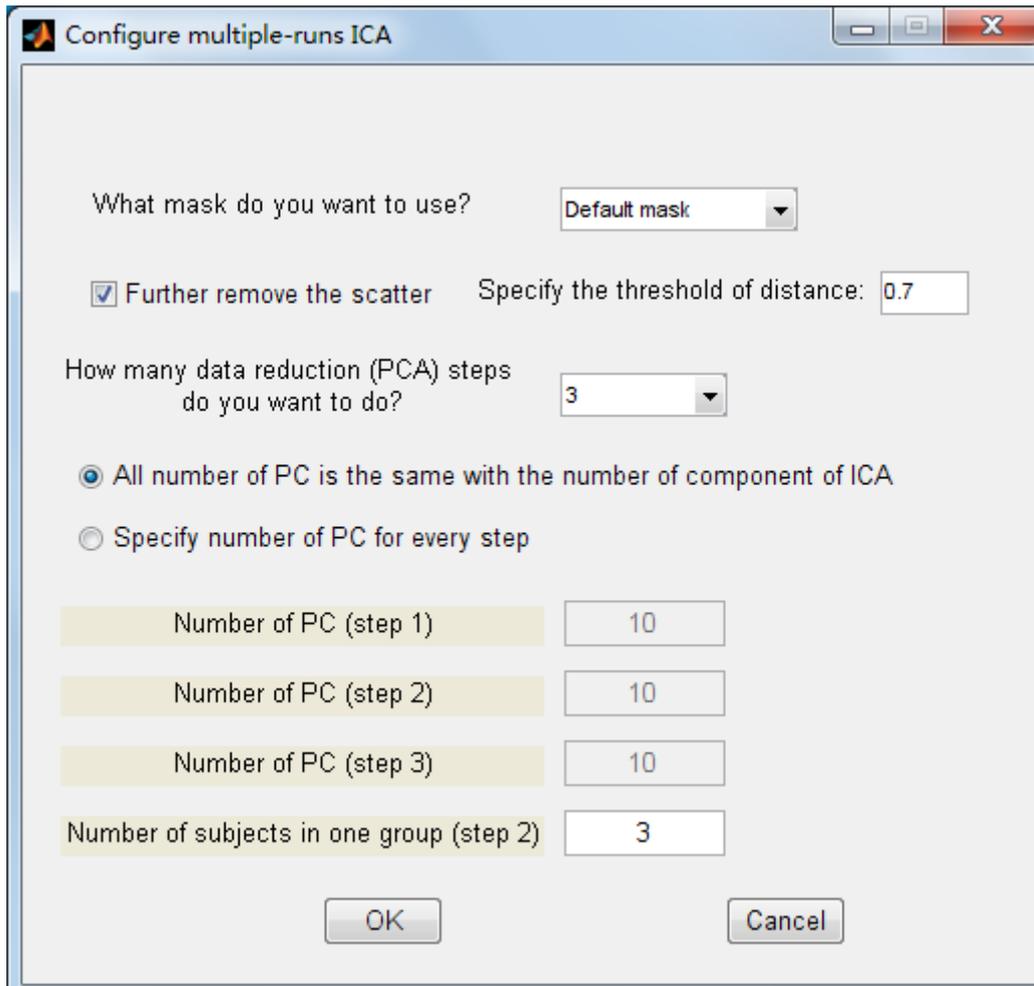


Fig. 6

Then return to the main GUI (Fig. 5). Click “Save” at the bottom and save your parameter settings into a MATLAB “*.mat” files (next time you can click “Load” button to load this mat file and all your parameter settings). Finally, click “Run all” and MICA will get to work (meantime two progress bars show up). After MICA finishes, it will produce some output files (see Fig. 7). In directory “output” saved many zip-files, each for a subject’s all individual-level components (including spatial maps in two-filed NIFTI format and the corresponding time courses in MAT format). Other zip-files shown in Fig. 7 represent group statistics results (mean, STD and T map).

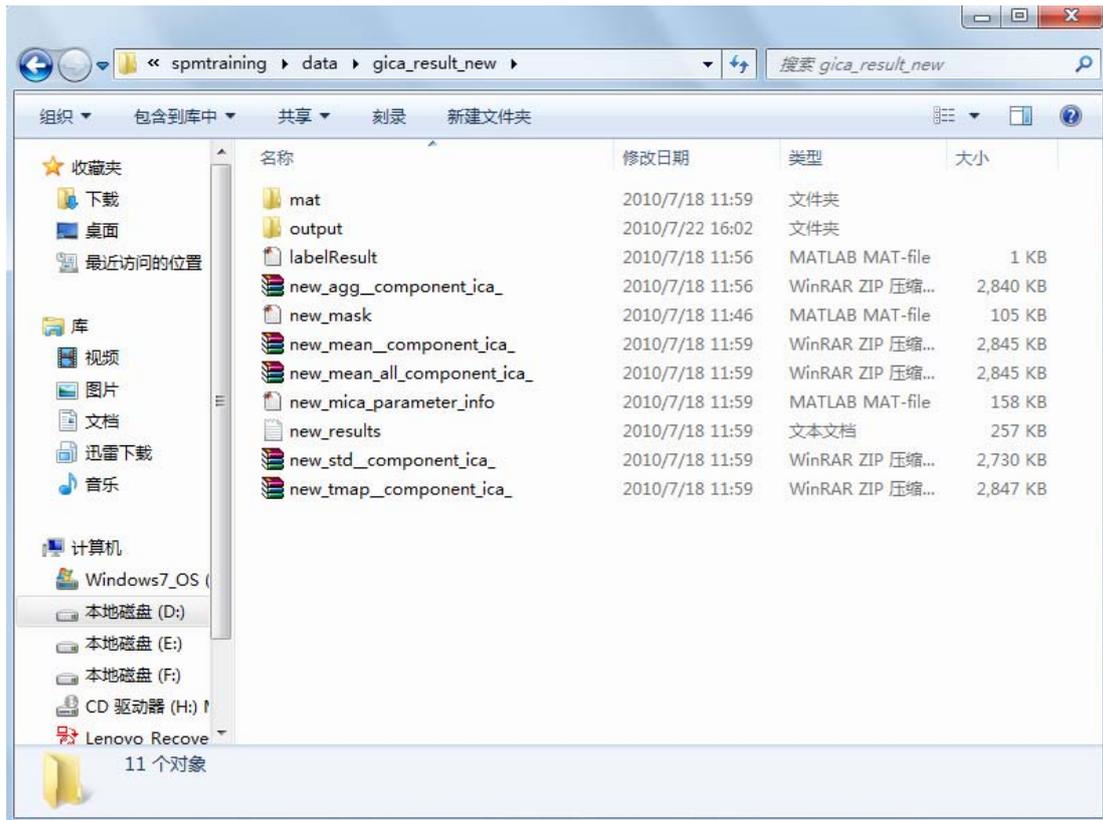


Fig. 7

To view the resulted components, click “GUI view” at the bottom of Fig. 5, the GUI for result view will pop up (Fig. 8). In “View Type” menu, when choosing the first item “MDS”, two MDS plots will show up, using which you can check the stability (both for spatial map and for time course) of one of a subject’s components. When choosing the second item “Ranking component”, a line chart will show up to let you evaluate each component’s stability from high to low (component sorting). The third item “Component” will let you check the resulted components in an orthogonal way.

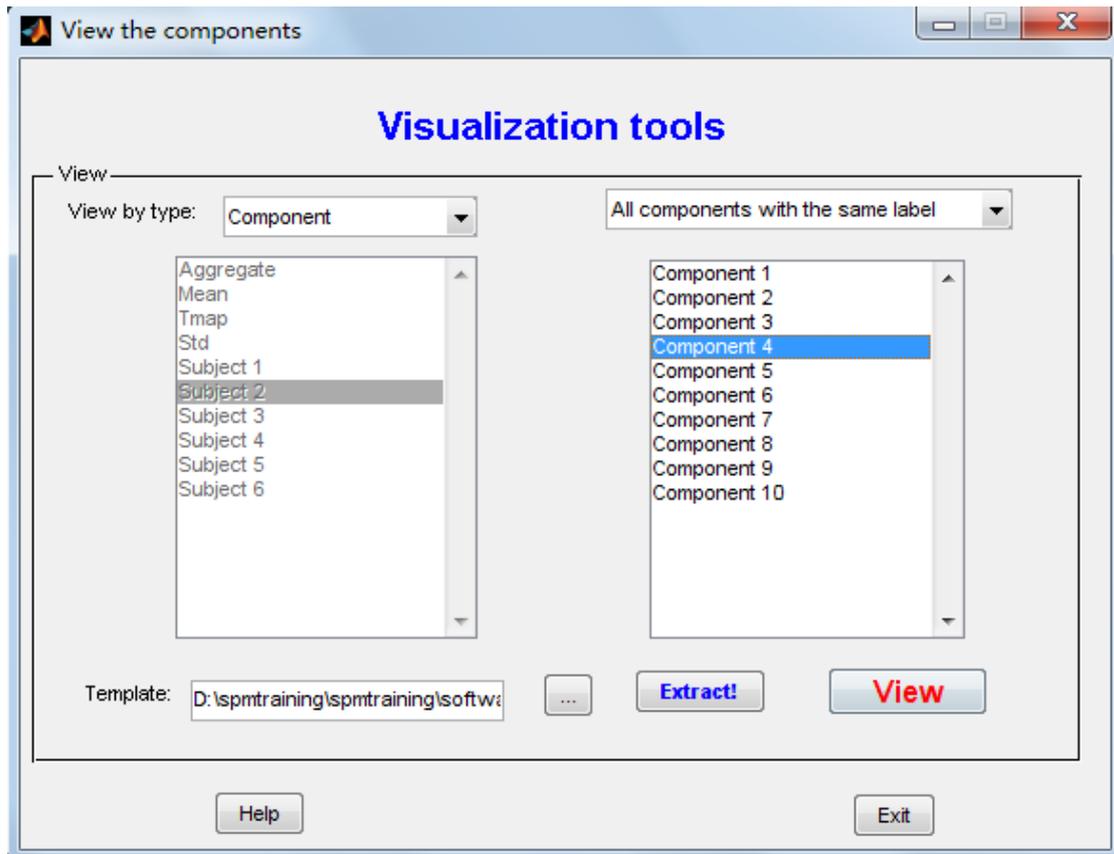


Fig. 8

Chapter 5 Detailed Manual

1. Install MICA

1) Running environment

- Basic hardware requirement: memory > 1 GB, hard disk free space > 20 GB.
- Recommended hardware requirement: memory > 2 GB, hard disk free space > 30 GB (when more subjects are involved), CPU better than Intel Core Duo 2.0 GHz.
- Support of MATLAB (version 7.1 and later, both Linux and Windows version are allowed). No guarantee if using previous version before MATLAB 7.0.
- No need of SPM toolkits or others.
- Screen resolution at least 1024×768.

2) Get the newly updated version of MICA at www.nitrc.org/projects/cogicat/.

3) Unzip MICA.

4) Add the directory and all sub-directories of MICA into MATLAB using “Set Path” → “Add with Subfolders” → “Save” → “Close” (see Fig. 9). If previous version already exists, firstly uninstall it using the method described below.

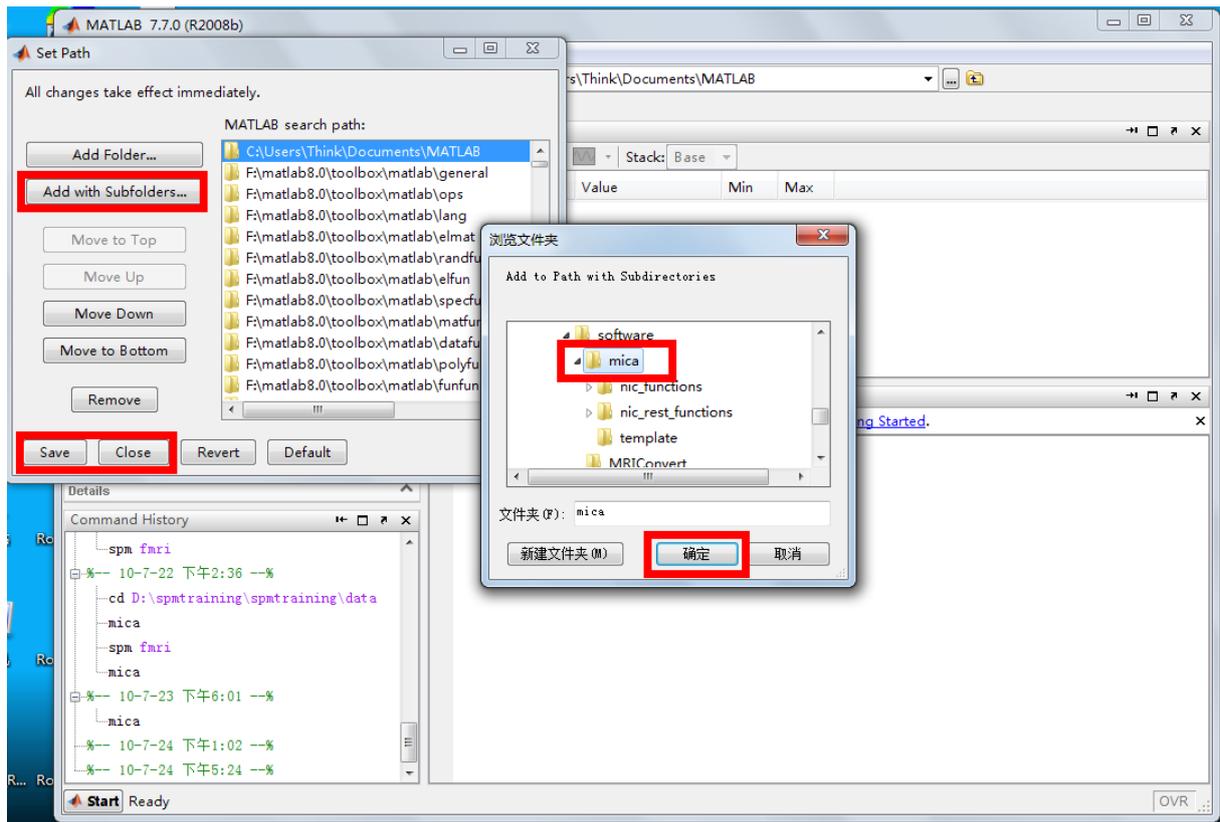


Fig. 9

2. Uninstall MICA

Delete directories related to MICA from MATLAB: Select “File” menu at the top-left of MATLAB → Choose all directories you want to delete → Click “Remove” → Save → Close.

3. Start MICA

- 1) Start MATLAB firstly.
- 2) Type “mica” in MATLAB’s command window (Fig. 10). Then the main GUI will show up (Fig. 3).

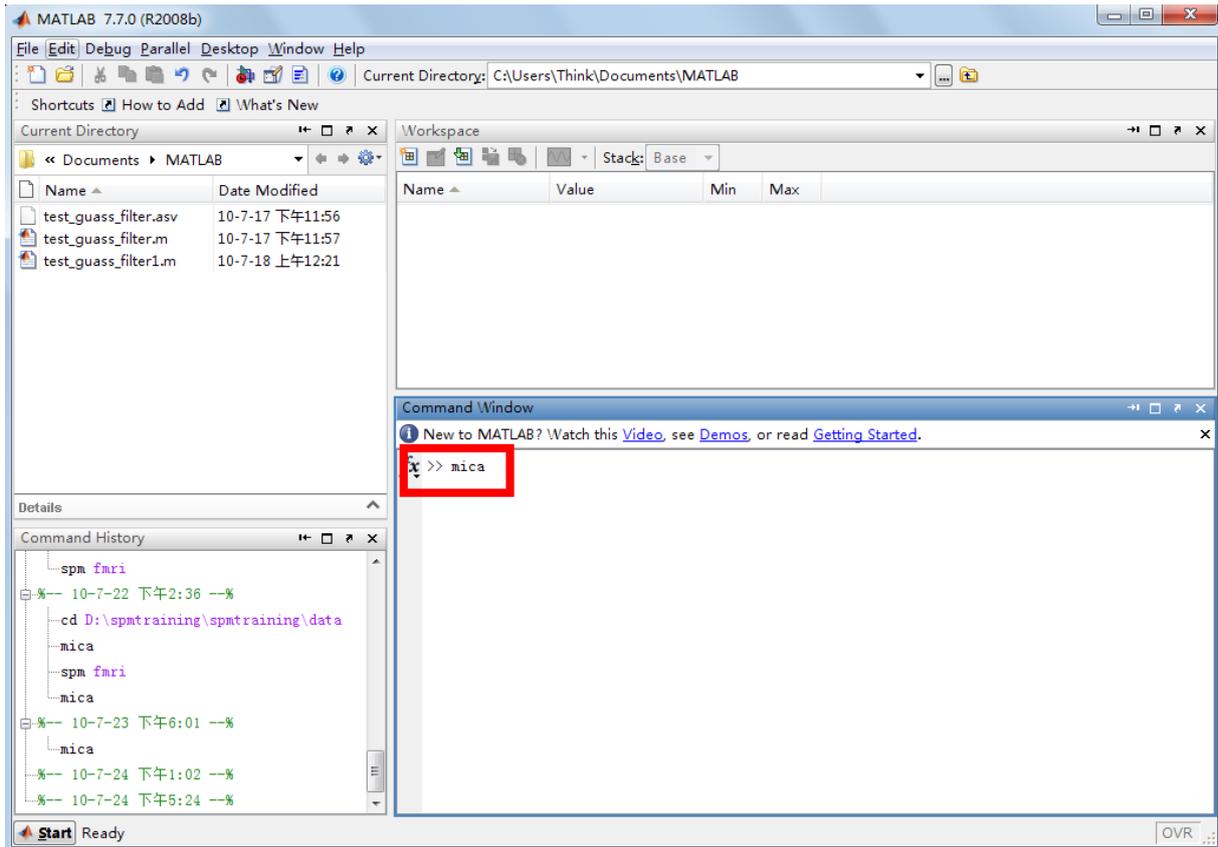


Fig. 10

4. Parameter Setting

1) Specify inputting data

- Click “Select files” button in the main GUI (Fig. 11). A new dialog box (Fig. 12) will pop up to allow you specify inputting data.

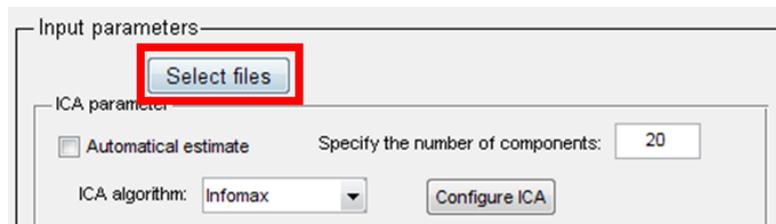


Fig. 11

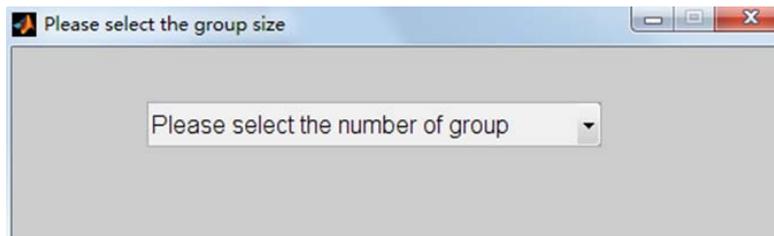


Fig. 12

- In this new dialog box, select the number of group involved (Fig. 13). If you have two groups, select “There are two groups”. If only one, select “There is one group” (here we use one group as an example). If you choose two groups, MICA will create two output directories storing each group’s result separately. Otherwise, MICA only creates one output directory. Please note that MICA actually takes all subjects from all groups into calculation regardless of the group number. So if you have more than two groups, you can simply choose “There is one group” and specify all subjects’ data sets. All you need to do is manually picking up each group’s outputs.

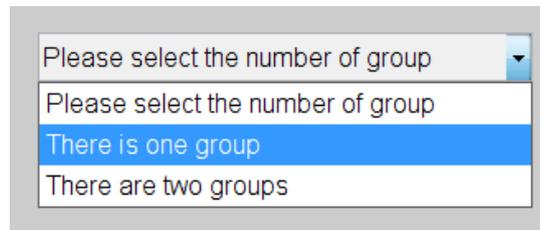


Fig. 13

- If choosing one group, another window will show up (see Fig. 14)

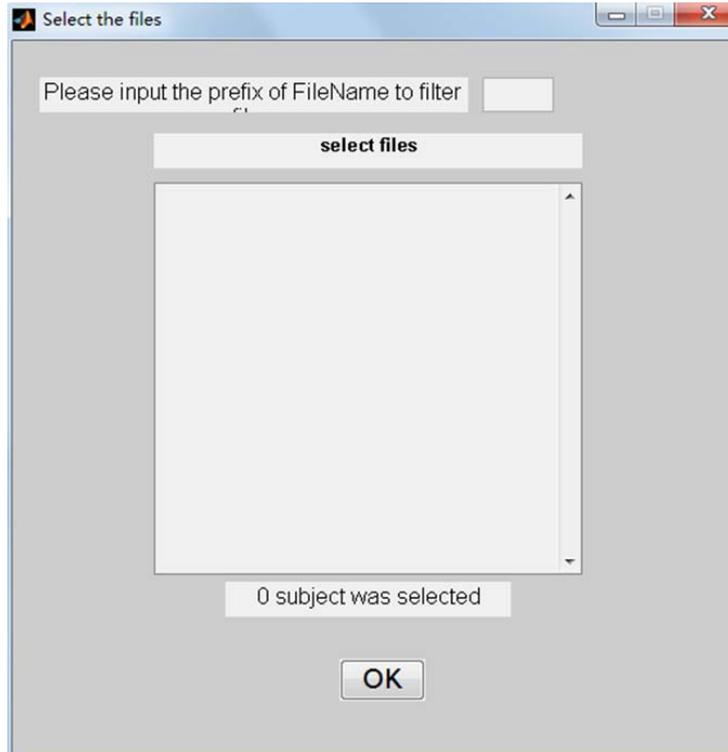


Fig. 14 File selection window

- *Please input the prefix of FileName to filter files:* input the prefix to filter inputting files of interest. Note: if leaves empty, all files will be selected.
- Right click the large empty area in file selection window, a file selection menu will show up (Fig. 15). Choosing “Add a directory” allows you add a directory once a time; “Add recursively all sub-folders of a directory” allows you add all subjects’ data located in the sub-folders under a parent directory (we recommend that each subject’s dataset be saved in a sub-folder. Thus selecting the parent directory using a recursive way will choose all sub-folders, see Fig. 16). If you want to delete some folders that have been selected, select it and choose “Remove selected directory”. If you want to delete all selected folders, choose “Clear all data directories”.

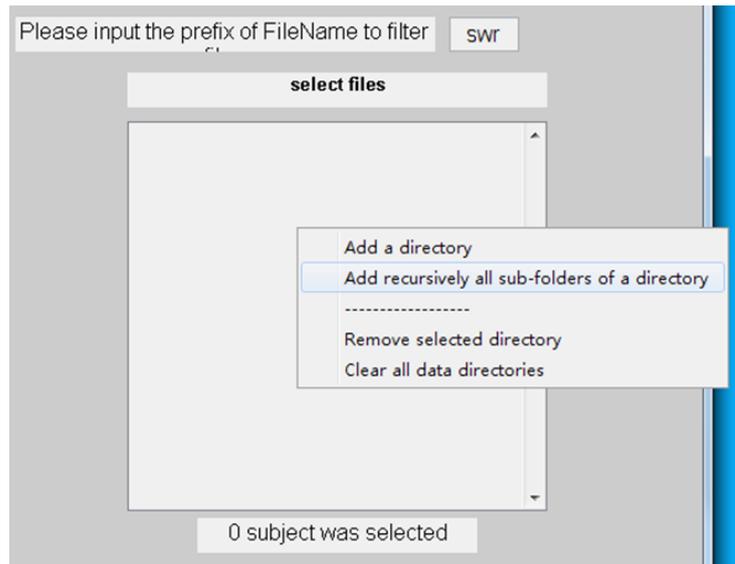


Fig. 15



Fig. 16

- When you finish selecting files, the selected directories will listed automatically and the number of subjects will display at the bottom (Fig. 17).

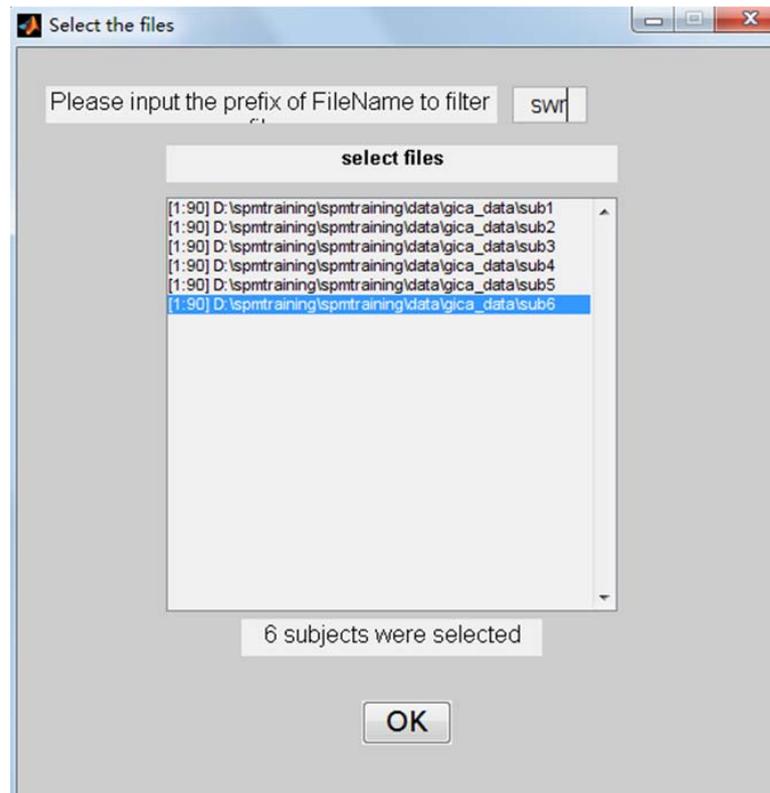


Fig. 17

- Please check if correctly selected all data sets. Then click “OK” to finish specifying files.
- If you choose two groups, then a file-selection window like Fig. 18 will show up. Just specify files for each group separately.

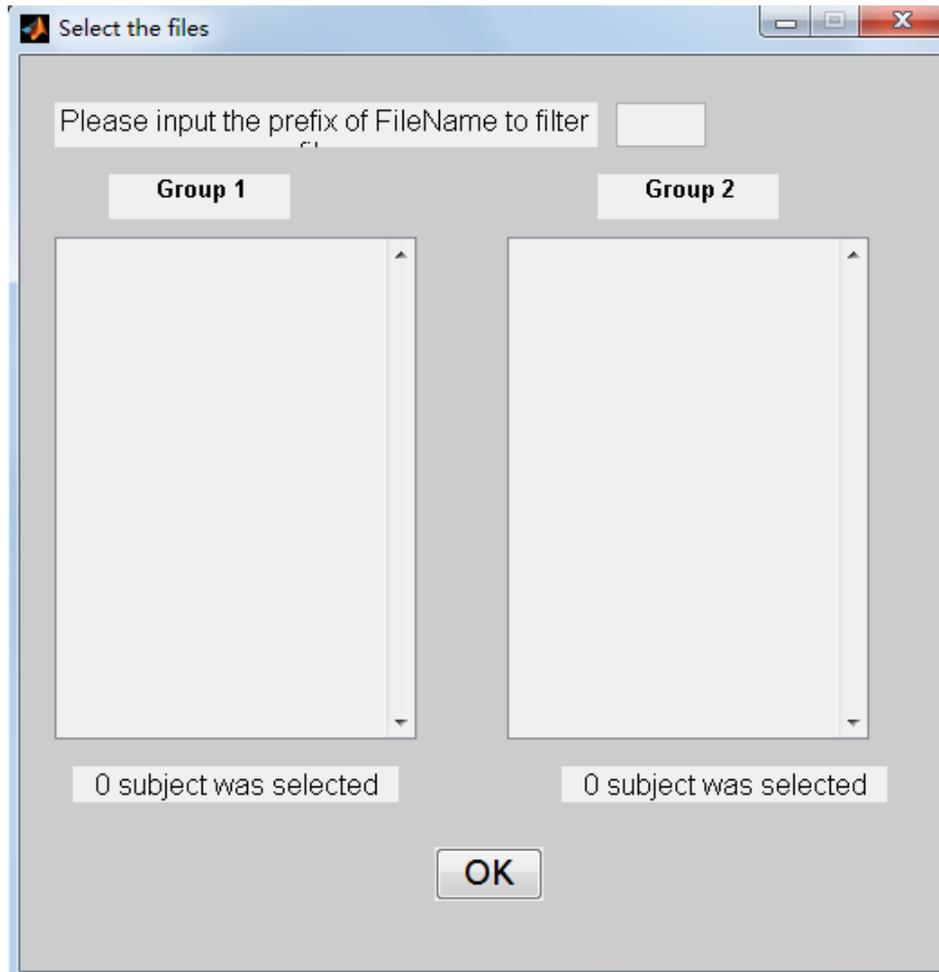


Fig. 18

2) Set up main input/output parameters

- Set up ICA parameters (Fig. 21).
 - *Specify the number of components*: set up component number for ICA calculation. If “Automatical estimate” is checked, MICA will automatically estimate component number. If leaves unchecked, you should enter a integer indicating component number (we strongly recommend to specify it to be 20~30).
 - *ICA algorithm*: choose algorithm of ICA estimation (FastICA or Infomax, we recommend choosing Infomax, see Fig. 19). Click “Configure ICA” in the right to further specify detailed ICA parameters for specific ICA algorithm (see Fig. 20, as they were automatically optimized, we recommend not changing them).

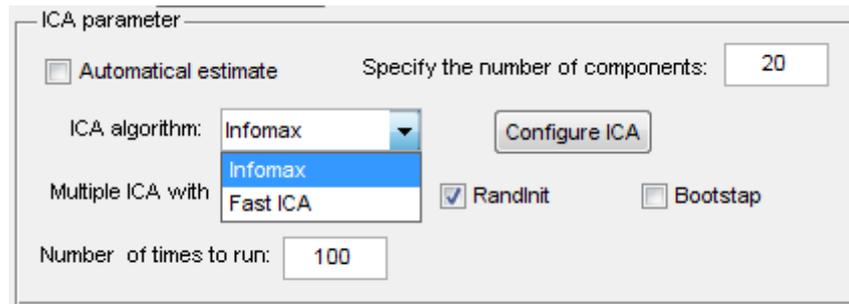


Fig. 19

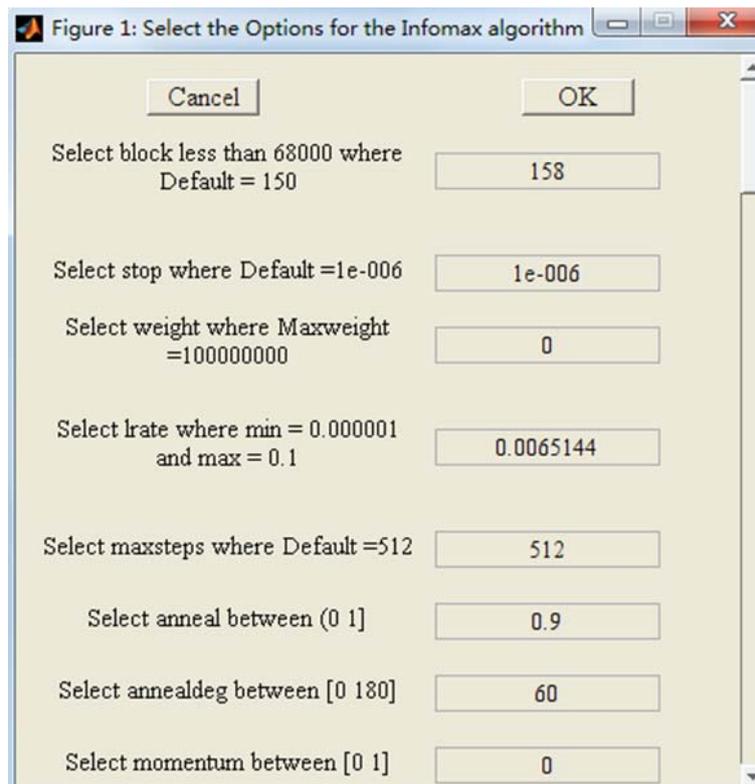


Fig. 20

- *Multiple ICA with*: Set up in which way multiple group ICA runs. **Multiple-order**: using different subject orders (randomized) for multiple group ICA analyses when checked (only works when three-stage PCA reduction is selected, see *User-defined parameter setting* below). **RandInit**: randomized initial value for each time of ICA estimation when checked. **Bootstap**: in current version of MICA this function does not go into effect (so please omit it). Note that we recommend checking the first two options (see Fig. 21).
- *Number of times to run*: set up total run number of group ICA (recommended running time is 50-100, for detailed please refer to Zhang

et al., 2010).

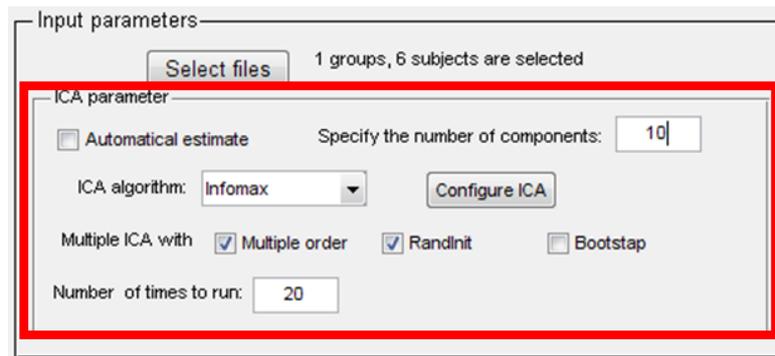


Fig. 21

- Set up output parameters (Fig. 22)
 - *Prefix*: specify the prefix of the outputting files.
 - *Scale the result*: specify using which way to calibrate the resulted component (Fig. 23). Choosing “Calibrate”, the resulted components will be calibrated according to the raw data intensity. Choosing “Z-scores”, the resulted components will be transformed to z -scores (recommended).

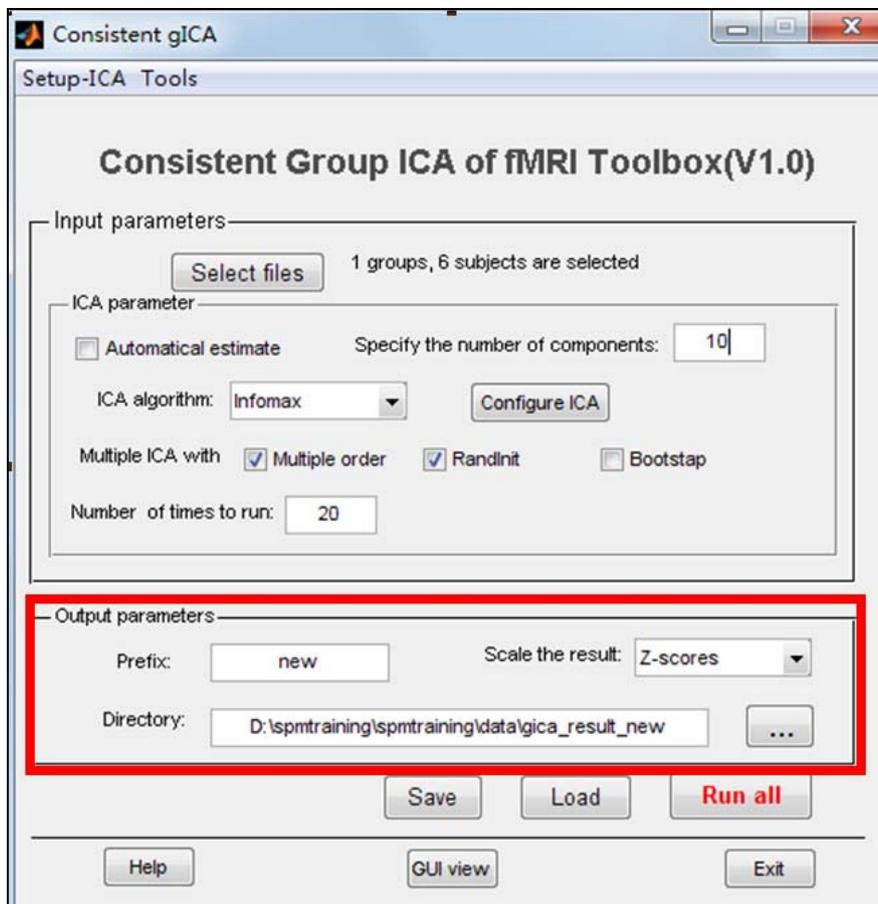


Fig. 22

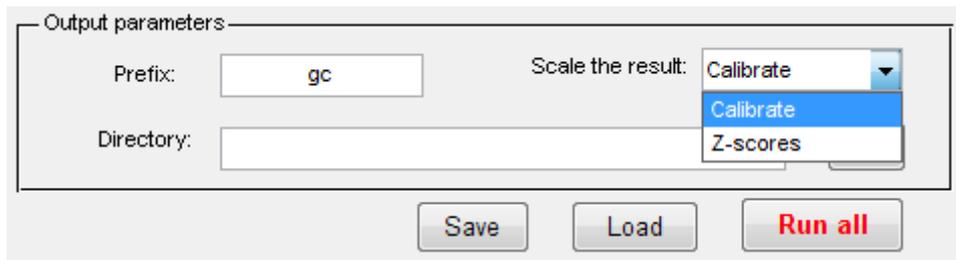


Fig. 23

- *Directory*: Select output directory. Click “...” button in the right, and choose a directory for storing output files (see Fig. 22).

3) User-defined parameters setting

- Click “Setup-ICA” menu in the left-top of the main GUI (Fig. 24).



Fig. 24

- Set up user-defined parameters in the pop-up window (Fig. 25).

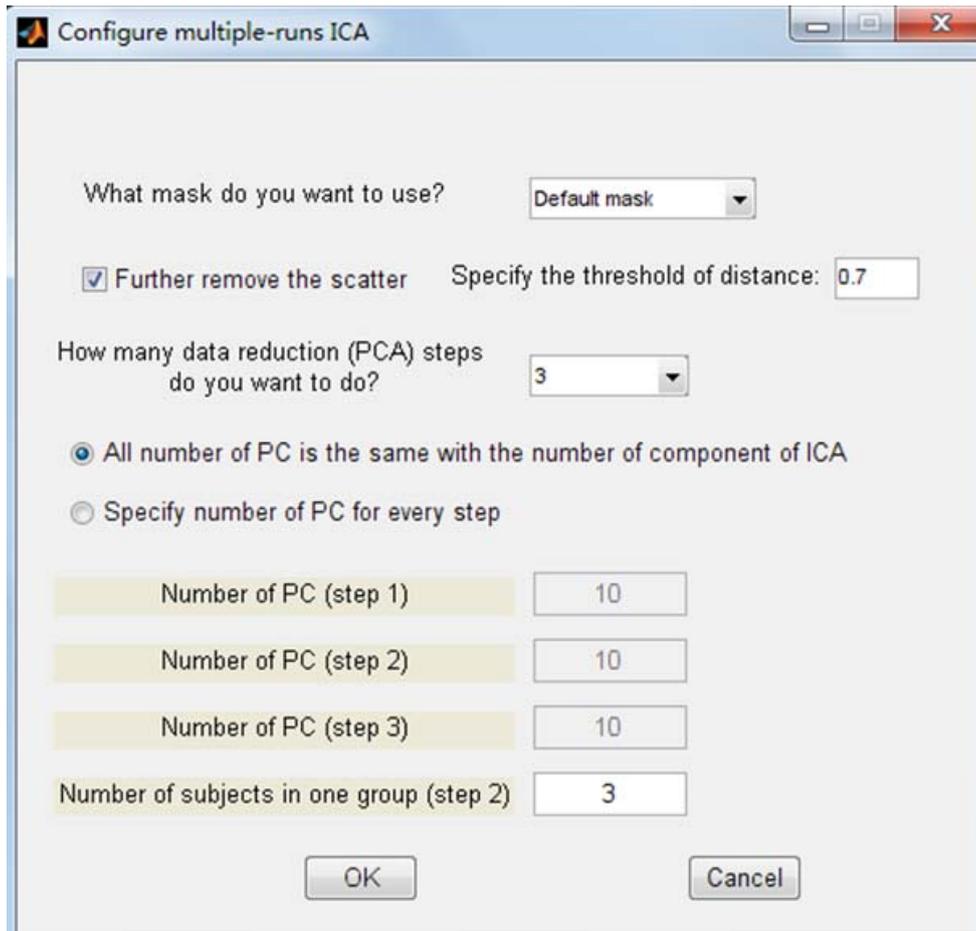


Fig. 25

- *What mask do you want to use?* Select mask file (in NIFTI format) in which GICA was performed. If choosing “Default mask” (recommended), MICA will use the first volume of each subject to generate masks, and then use the overlap across subjects to generate the final brain-tissue mask. If choosing “Select mask” (Fig. 26), a user-specific mask selection window will let you select a mask of interest (with 0s outside of the ROI and 1s inside of it) (Fig. 27). If the resolution of the user-specific mask is different with that of the input data, MICA will automatically resample the mask file to ensure the same resolution as the input data.

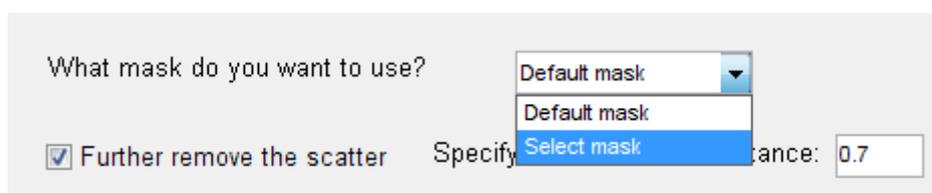


Fig. 26

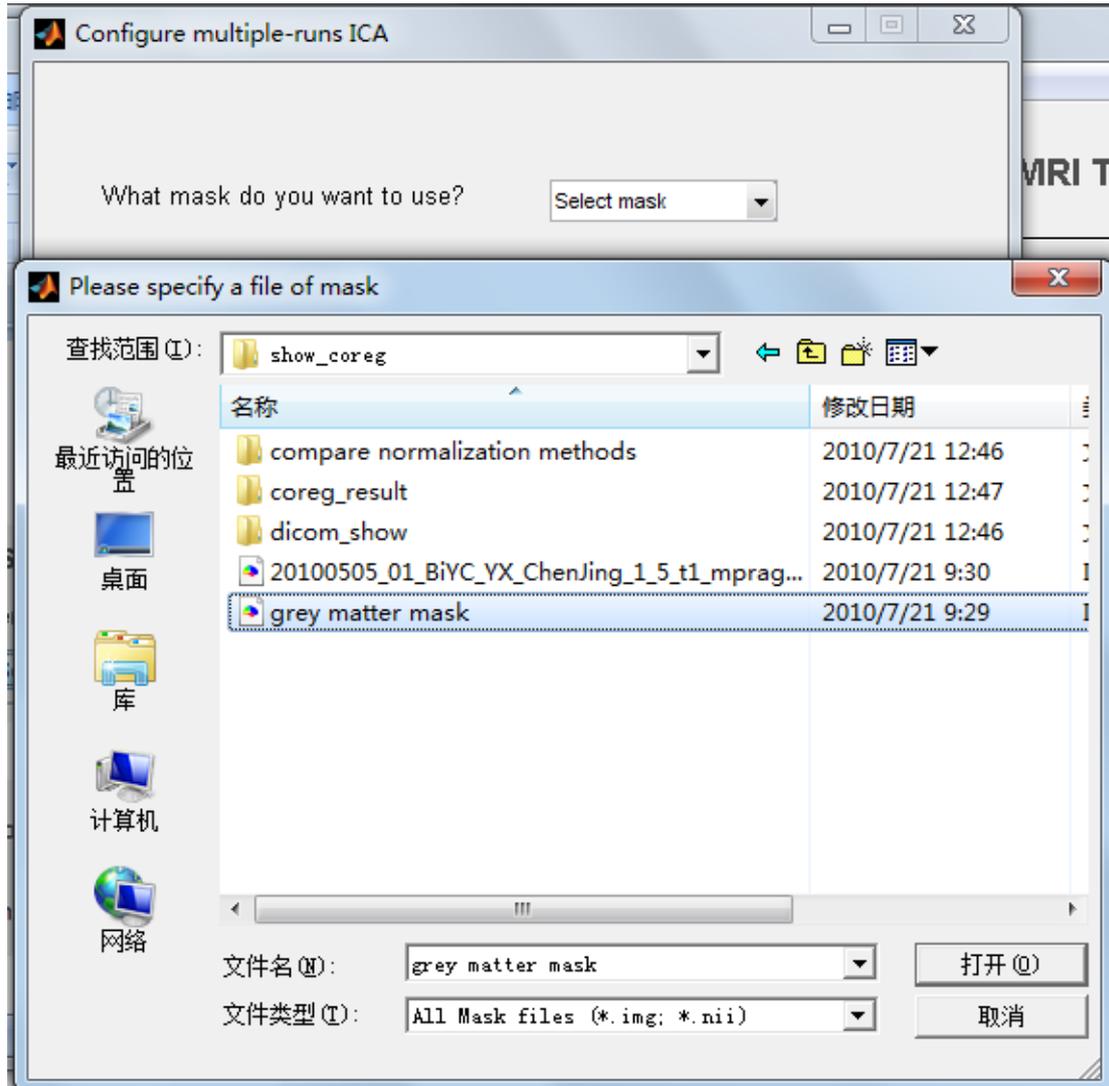


Fig. 27

- *Further remove the scatter:* Decide whether or not to discard outlier component(s) when clustering and result integration. Because of instability of ICA result, some times group ICA will produce the results that are quite different with the results from most of runs. Deleting those outliers will increase accuracy of the final result. So we recommend checking it.
- *Specify the threshold of distance:* Define the criterion of the outlier component. Please input a value from 0 to 1. The bigger this value is, the looser the outlier definition is (i.e., harder to find outliers). The recommend setting is 0.5 – 0.7.

- *How many data reduction (PCA) steps do you want to do?* Specify the number of PCA reduction stages (input integer 1 – 3) (Fig. 28). If subject number is 1, this number is forced to be 1; if subject number is > 1, this number should be 2 or 3; if subject number is > 8, this number is forced to be 3. Please keep as default.

How many data reduction (PCA) steps do you want to do?

All number of PC is the same with the number of component of ICA

Specify number of PC for every step

Fig. 28

- *All number of PC is the same with the number of components of ICA:* the retained data dimensionalities for all of the PCA stages are kept to be the same. If checked, MICA will automatically fill the blanks of “Number of PC (step 1 – 3)” below and keep them the same as the component number you set in *ICA parameters setting* in Fig. 19 (see Fig. 29). We recommend checking it.

All number of PC is the same with the number of component of ICA

Specify number of PC for every step

Number of PC (step 1)	20
Number of PC (step 2)	20
Number of PC (step 3)	20
Number of subjects in one group (step 2)	4

Fig. 29

- *Specify the number of PC for every step.* If you want to manually set up the number of retained PC for each stage, check this option instead. If checked, you can specify number of retained PC for each PCA stage (Fig. 30). Please note that the PC number for the last stage should be equal to or larger than the component number you set in *ICA parameters setting*

in Fig. 19.

<input type="radio"/> All number of PC is the same with the number of component of ICA	
<input checked="" type="radio"/> Specify number of PC for every step	
Number of PC (step 1)	15
Number of PC (step 2)	15
Number of PC (step 3)	15
Number of subjects in one group (step 2)	4

Fig. 30

- *Number of subjects in one group*: When choosing 3 stages of PCA reductions, you need to specify grouping manner in the second stage of PCA reductions, that is, how many subjects in one sub-group before the second stage of PCA reduction. Please keep as default (4 subjects). However, if choosing 2 (or 1) stage of PCA reduction, this option is invisible (e.g., when choosing 2, the GUI changes to be like Fig. 31).

How many data reduction (PCA) steps do you want to do? 2

<input checked="" type="radio"/> All number of PC is the same with the number of component of ICA	
<input type="radio"/> Specify number of PC for every step	
Number of PC (step 1)	20
Number of PC (step 2)	20

OK Cancel

Fig. 31

- After setting up all user-defined parameters, click “OK” and shut down this user-defined parameters setting window.

4) Running MICA

- Before running MICA, it's better to firstly estimate required memory and free

disk space. Click “Tool” menu and select “Estimate Memory” (Fig. 32). A dialog like Fig. 33 will show up to predict the approximate needed memory and disk space. If the requirement is not fulfilled, please consider to change to another high performance workspace or other PC. Note that the amount of the required computing source depends on subject number, component number, GICA running number and some of your user-defined parameters (especially the number of PCA reduction stages).



Fig. 32



Fig. 33

- If your computing source meets the requirement, click the red button “Run all” (Fig. 34) to start MICA. Two progress bars will show up to indicate the progress of computation (Fig. 35). The overall time depends on subject number, component number, GICA running number and the performance of your PC or workstation.



Fig. 34

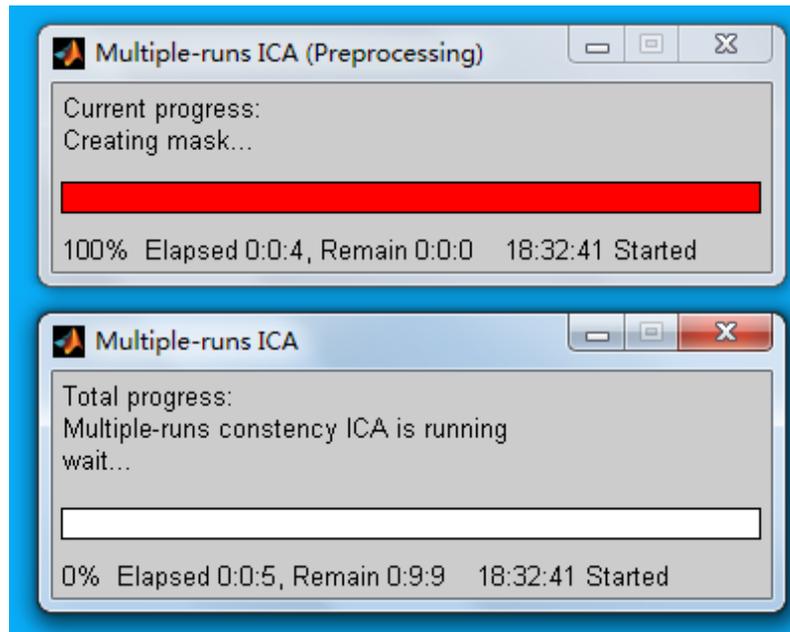


Fig. 35

- It's recommended that save all parameter setting in a MATLAB "*.mat" file before running MICA. Click "Save" button in Fig. 34 and save all parameters. You can use "Load" function to reload all your parameters (and then you can directly click "Start" to run MICA).

5. Output files

When finish running, MICA will generate several new folders and files (Fig. 36). One of them is a log file named "prefix_results.log", saving all information matlab generated (Fig. 37) for error checking.

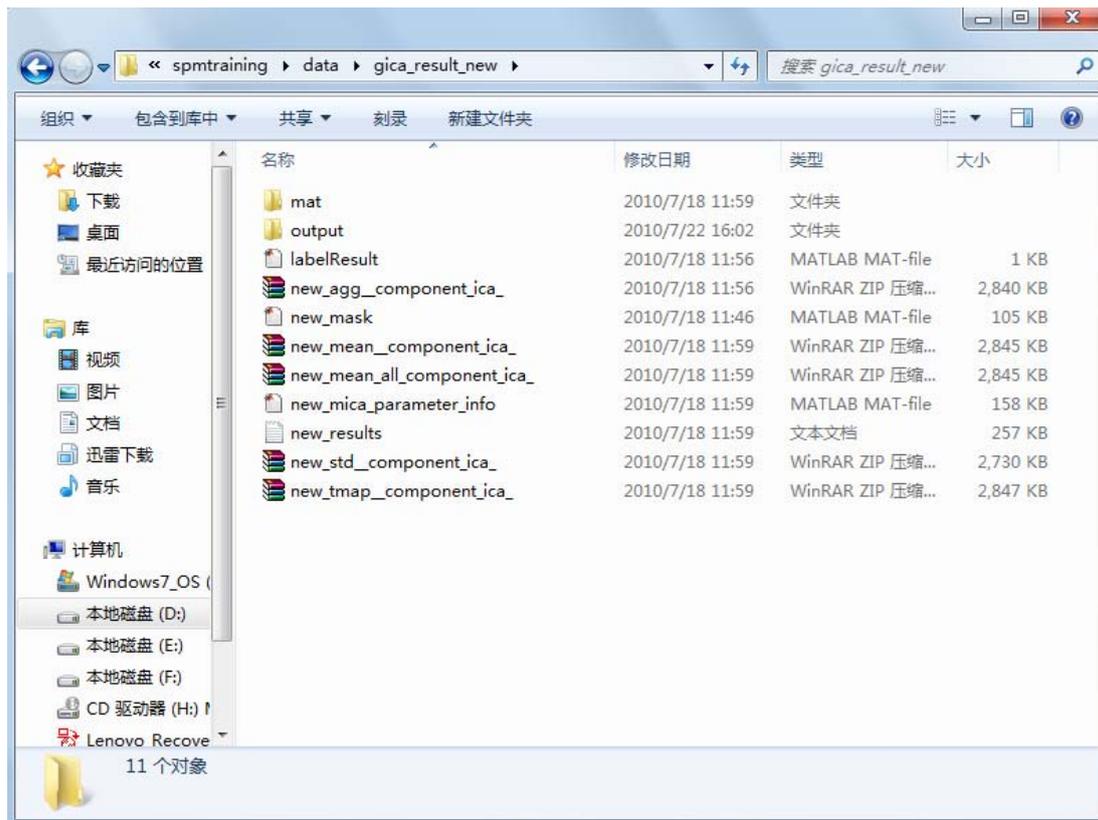


Fig. 36

```

*****Start to run analysis at 2010-07-18 11:45:57*****
[Warning: Calling MEX-file
'D:\spmtraining\spmtraining\software\mica\nic_functions\nic_spm5_files
\nic_spm_slice_vol.dll'.
MEX-files with .dll extensions will not execute in a future
version of MATLAB.]

-----

Generating the default mask using the first file of every subject
Creating Mask
Using first file of each subject to create default mask ...
Done Creating Mask
*****Start to do data reduction and ICA at 2010-07-18 11:46:04*****

-----

```

Fig. 37

The resulted individual-level components for all subjects are stored in *output* folder (Fig. 36), in which all components for a subject are compressed into a ZIP file (Fig. 38).

名称	修改日期	类型	大小
 new_sub001_component_ica_s1_	2010/7/18 11:59	WinRAR ZIP 压缩...	2,852
 new_sub002_component_ica_s1_	2010/7/18 11:59	WinRAR ZIP 压缩...	2,850
 new_sub003_component_ica_s1_	2010/7/18 11:59	WinRAR ZIP 压缩...	2,850
 new_sub004_component_ica_s1_	2010/7/18 11:59	WinRAR ZIP 压缩...	2,851
 new_sub005_component_ica_s1_	2010/7/18 11:59	WinRAR ZIP 压缩...	2,852
 new_sub006_component_ica_s1_	2010/7/18 11:59	WinRAR ZIP 压缩...	2,851

Fig. 38

The aggregated, mean, STD and T-statistics components are compressed into ZIP files, respectively (see Fig. 36). The folder “MAT” contains information for consistency evaluation. All parameters and important informations generated by computing are saved as a MATLAB “*.mat” file, named “prefix_mica_parameter_info.mat”. This file is different from the file you saved in previous step when you finished parameter setting, because the “prefix_mica_parameter_info.mat” also contains many other informations MICA generated. It can be regarded as the updated version of your previously save one. **Please note that if you want view the result, you must firstly use “Load” button to load this mat file (Fig. 39).**

IMPORTANT – if you shut down the MICA toolbox or MATLAB (probably because of some error caused or electrical power down), next time you should reload this mat file (prefix_mica_parameter_info.mat) at first (Fig. 39) and then click “Run all”. Such a procedure allows you resume the processing (restart from where you stop just before) and thus you don’t need to spend lots of time reprocessing from the very beginning.

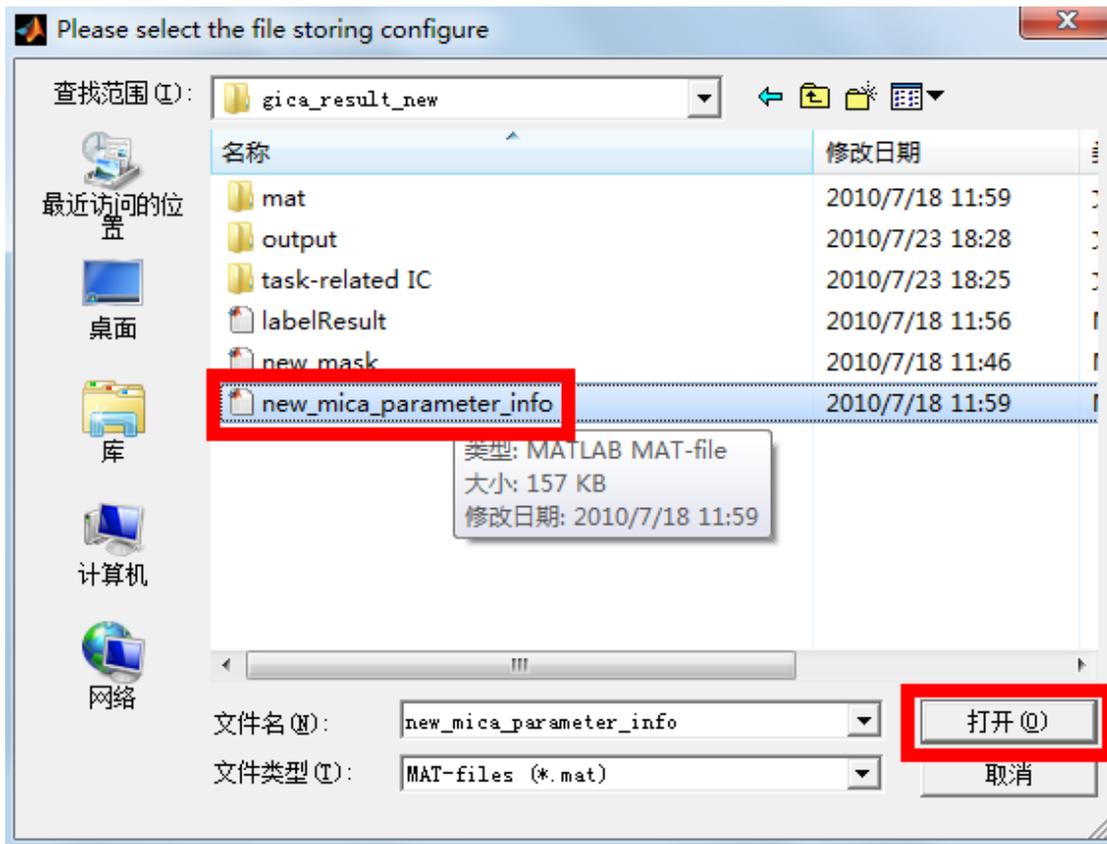


Fig. 39

6. Result View

When MICA finishes running, you can directly click “GUI view” button in the bottom of the main GUI (Fig. 40). Then an orthogonal view GUI window (script courtesy of GIFT group (Calhoun et al., 2001)) will pop up (see Fig. 41).

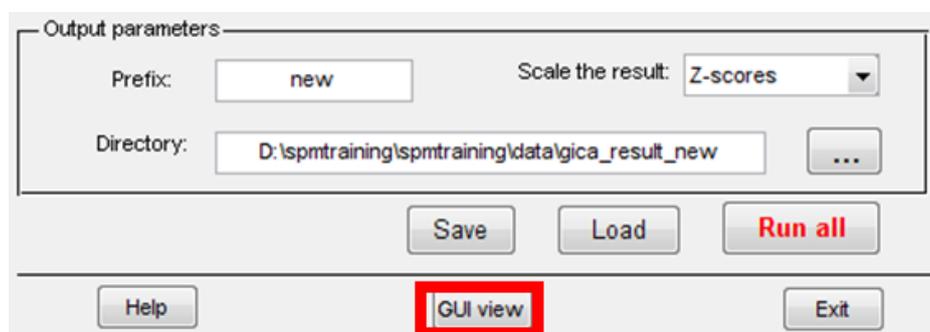


Fig. 40

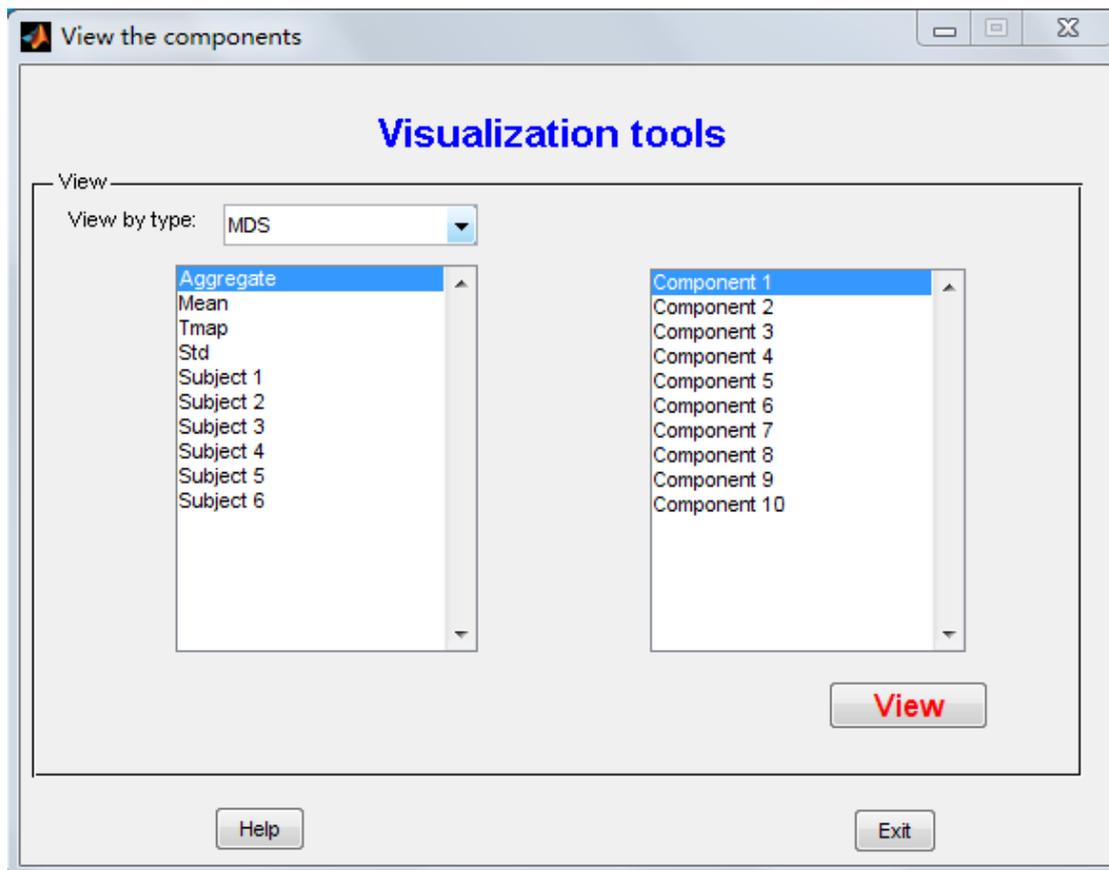


Fig. 41

There are three choices when move to “View by type” menu: MDS, *Ranking component* and *Component* (Fig. 42). Their functions will be introduced one by one:

- MDS – Show distribution of multiple GICA results in 2-D plane. The scatter degree indicates the consistency of a component.
- Ranking component – Show the ranking curve that ranks all components according to their consistency.
- Component – Show spatial map and/or the associated time course of the component(s) of interest.

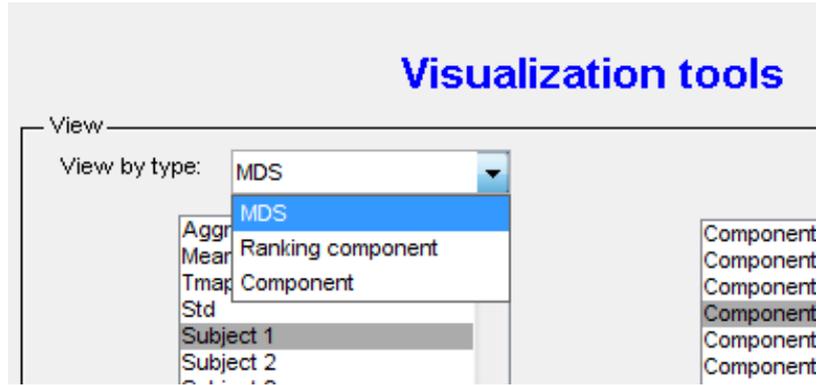


Fig. 42

There are two panels in orthogonal view GUI window (Fig. 43). The left one lists all statistics (aggregate, Mean, Tmap and Std) and all subjects. The right one lists all components.

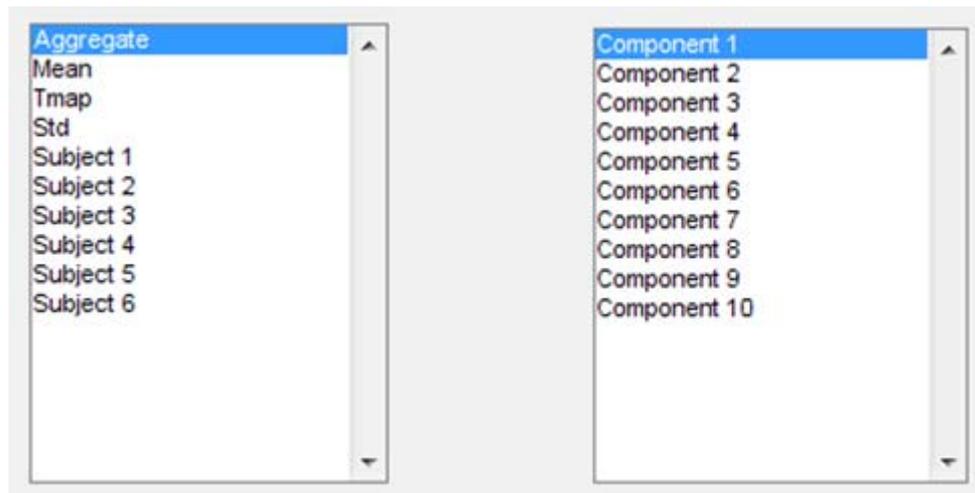


Fig. 43

1) MDS show

- Choose “MDS” in menu and select “Aggregate” or “Subject ID” in the left panel and select the component you want to see in the right lists (Fig. 44).
- Click “View”.
- Two MDS maps will show up, one for consistency evaluation of spatial maps (Fig. 45) and the other for consistency evaluation of time course (Fig. 46).

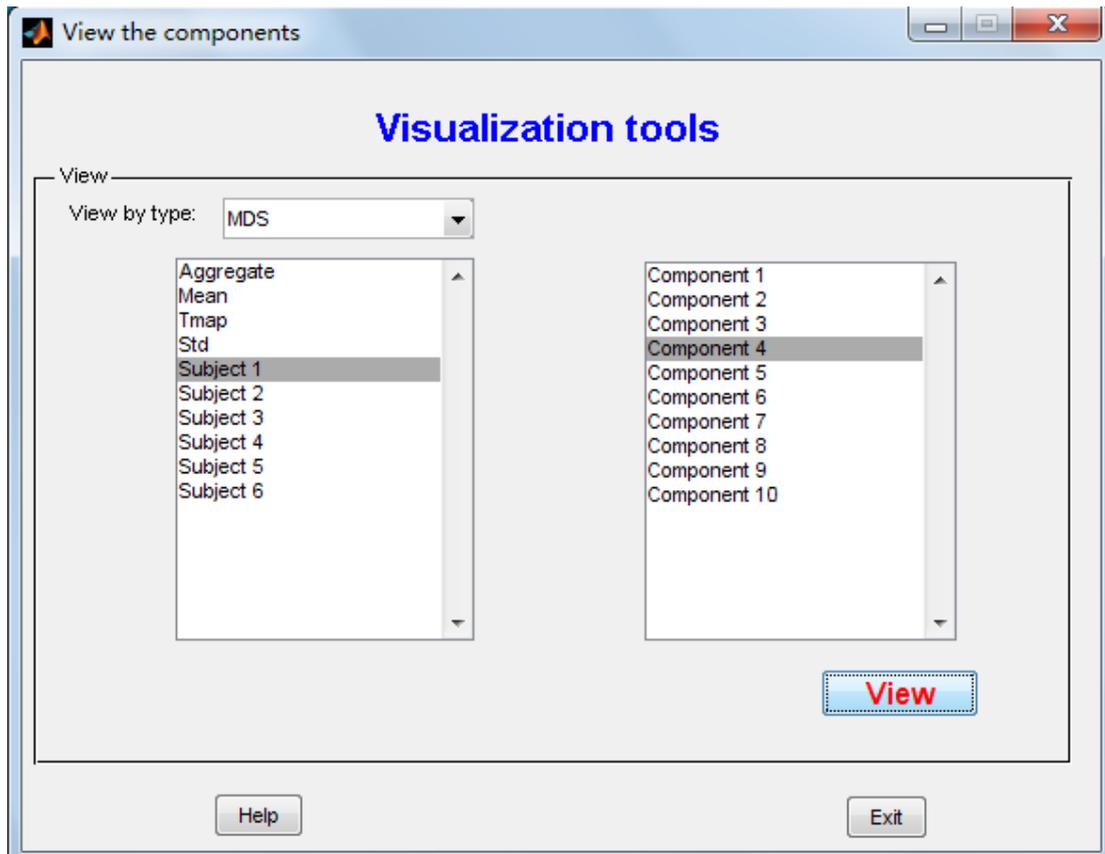


Fig. 44

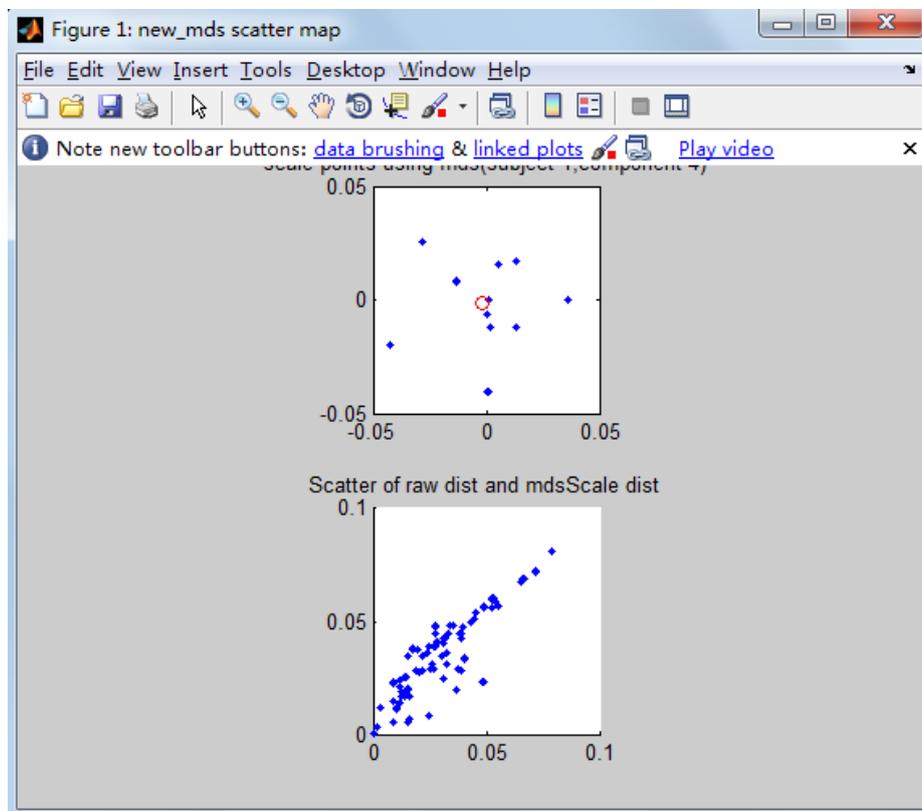


Fig. 45

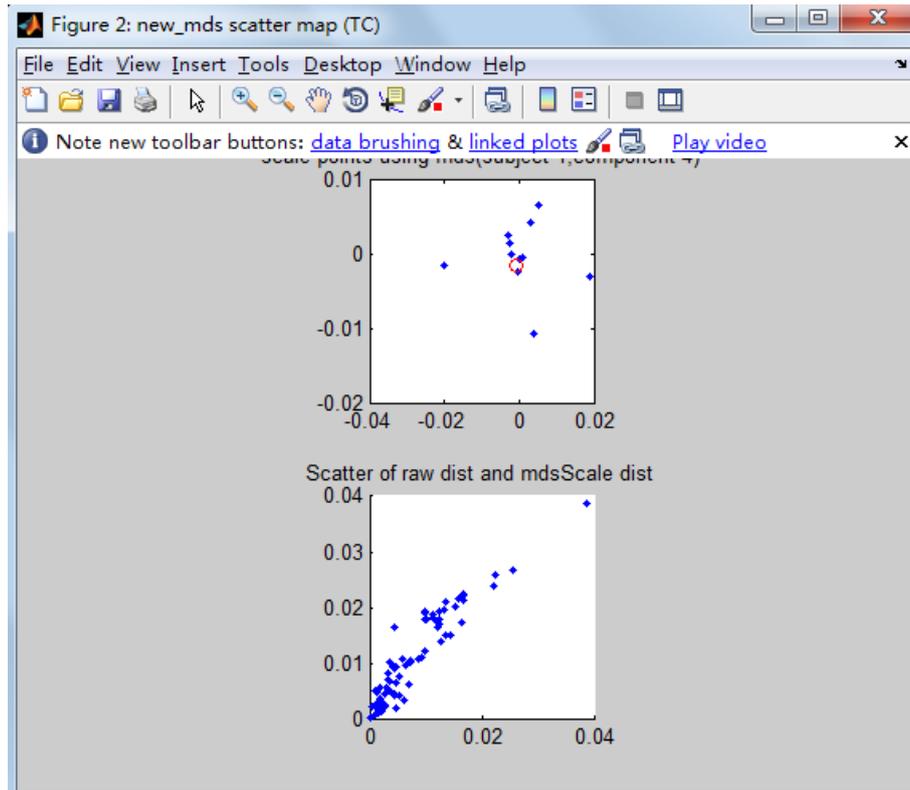


Fig. 46

If you select “Aggregate”, the consistency of the aggregate component is evaluated, giving you an overall assessment of each component’s consistency. If you select a specific subject, the consistency of the individual-level component for a specific subject is evaluated.

In Figs. 45 – 46, the figure in the top shows the relationship between results from multiple GICA runs in a two dimensional space, where the blue dots indicate multiple conventional GICA results and the red circle indicates the MICA result. The range of two axes indicates the degree of consistency. The figure in the bottom shows the goodness of the multidimensional scaling transformation: the more it like a $y = x$ line, the better the transformation is.

2) Ranking component

Choose “Ranking component” (Fig. 47), click View. The component ranking curves will show up (Fig. 48).

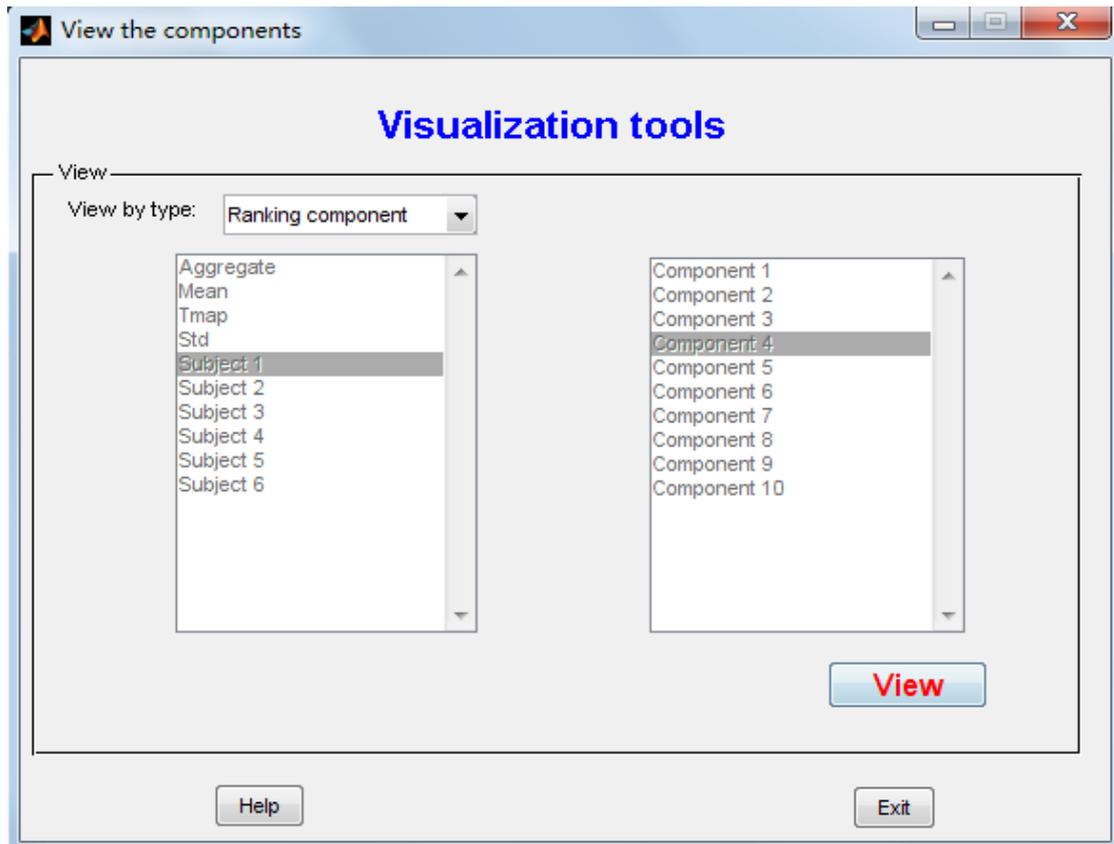


Fig. 47

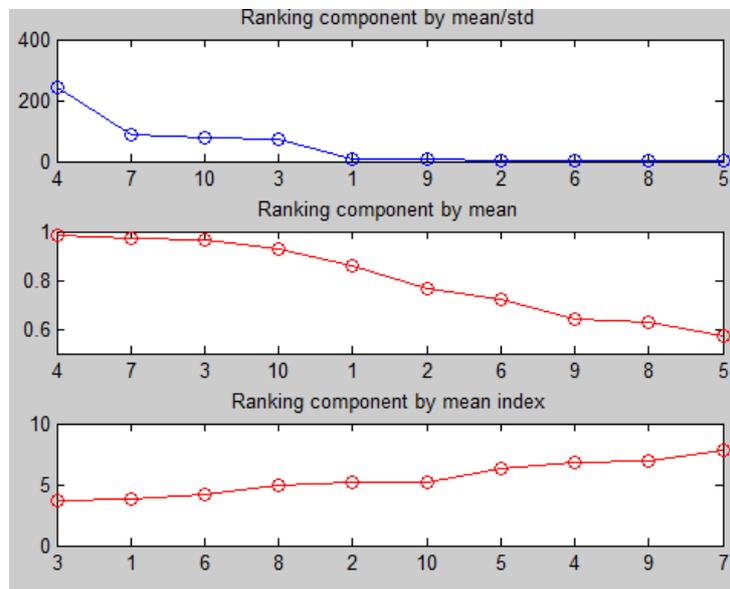


Fig. 48

Component ranking is based on consistency across multiple runs. Here three indices are used (so there are three curves in Fig. 48). Let the number of multiple GICA runs be N , subject number M , component number T , for each individual-level

component $c_{ijk} (i = 1, \dots, N, j = 1, \dots, T, k = 1, \dots, M)$, the mean component across

multiple runs is $m_{jk} = \frac{\sum_{i=1}^N c_{ijk}}{N} (j = 1, \dots, T, k = 1, \dots, M)$. The distance between m_{jk} and

all c_{ijk} can be defined to be $d_{jk} = \frac{1}{N} \sum_{i=1}^N |c_{ijk} - m_{jk}| (j = 1, \dots, T, k = 1, \dots, M)$.

The three consistency measurements are:

■ $t_j = \frac{\text{mean}(d_j)}{\text{std}(d_j)} (d_j = \{d_{j1}, \dots, d_{jM}\})$, sorted by $t_j (j = 1, \dots, T)$, the larger it is, the

more consistent this component is.

■ $m_j = \text{mean}(d_j) (d_j = \{d_{j1}, \dots, d_{jM}\})$, sorted by $m_j (j = 1, \dots, T)$, the larger it is, the more consistent this component is.

■ For each subject $k (k = 1, \dots, M)$, firstly sorted his/her individual-level component by $d_{jk} (j = 1, \dots, T)$. Then each component gets its own order number $l_{jk} (j = 1, \dots, T, k = 1, \dots, M)$. Next, calculate $m'_j = \text{mean}(l_j) (l_j = \{l_{j1}, \dots, l_{jM}\})$, and finally, sorted by $m'_j (j = 1, \dots, T)$. The smaller it is, the more consistent this component is.

3) Component view

Choose “Component” from “View by type” menu. In the other menu in the top right are three items (Fig. 49): (a) *All components of a subejct* (display all components from a certain subject/statistics), (b) *All components with the same label* (display a certain component including all subjects’ individual-level components and the statistics compoennts) and (c) *A component of a subject* (display a certain component for a certain subject or statistics).

■ Display all components of a subejct

- Choose “All components of a subejct” (Fig. 49).
- Select a subject or a statistics in the left panel.

- Select a user-specific (need to be in MNI space) or use the default underlay template image in the bottom left.
- Click “View”, a new display parameter setting dialog shows up (Fig. 50).

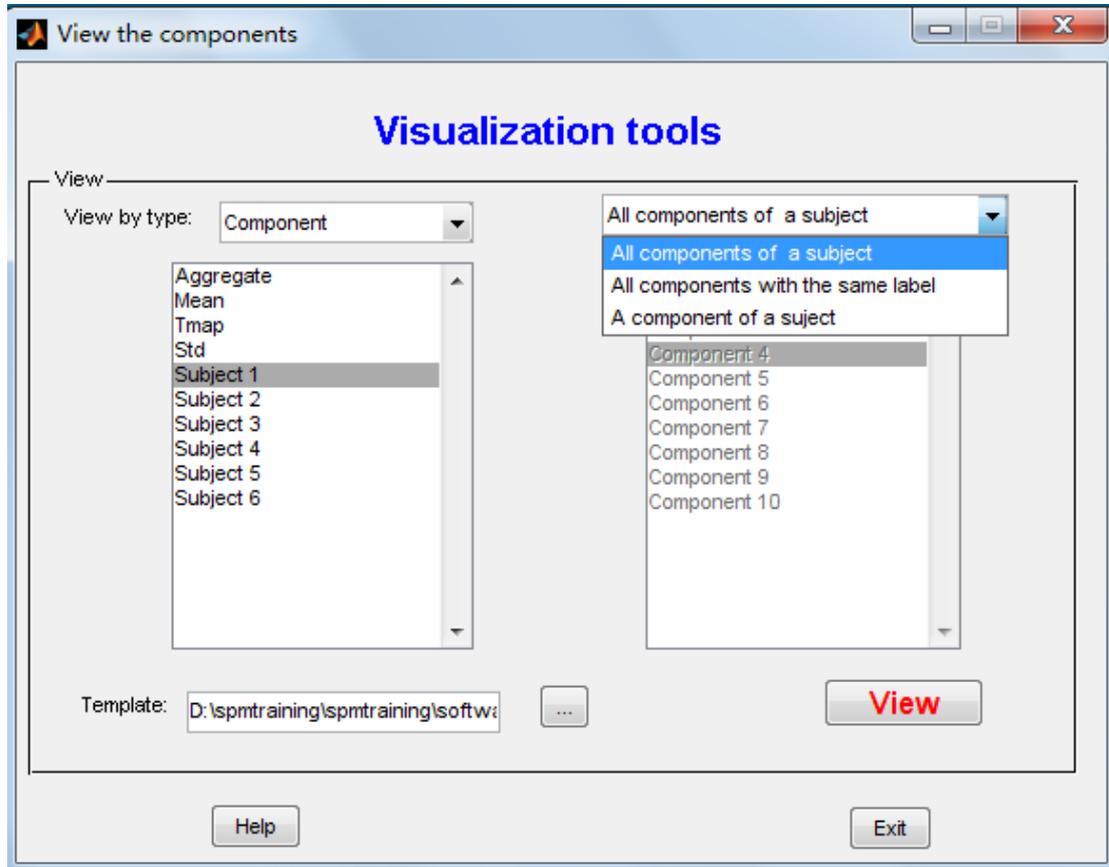


Fig. 49

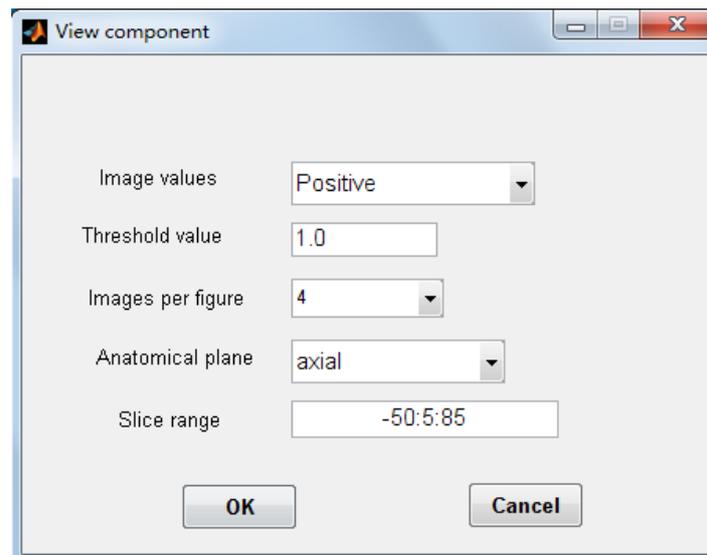


Fig. 50

- Image values: determine only display positive value or only negative value or

both of them or the absolute value.

- Threshold value: default is 1.0
- Images per figure: default is 4
- Anatomical plane: axial, sagittal or coronal.
- Slice range: determine which slice you want to display, recommended to keep as default.
- When setting up all parameters, click “OK”. Then the component view window shows up (Fig. 51). Above the spatial maps is the associated time courses. Please note that, the components is in order of consistency index t_j (with the value in parentheses).

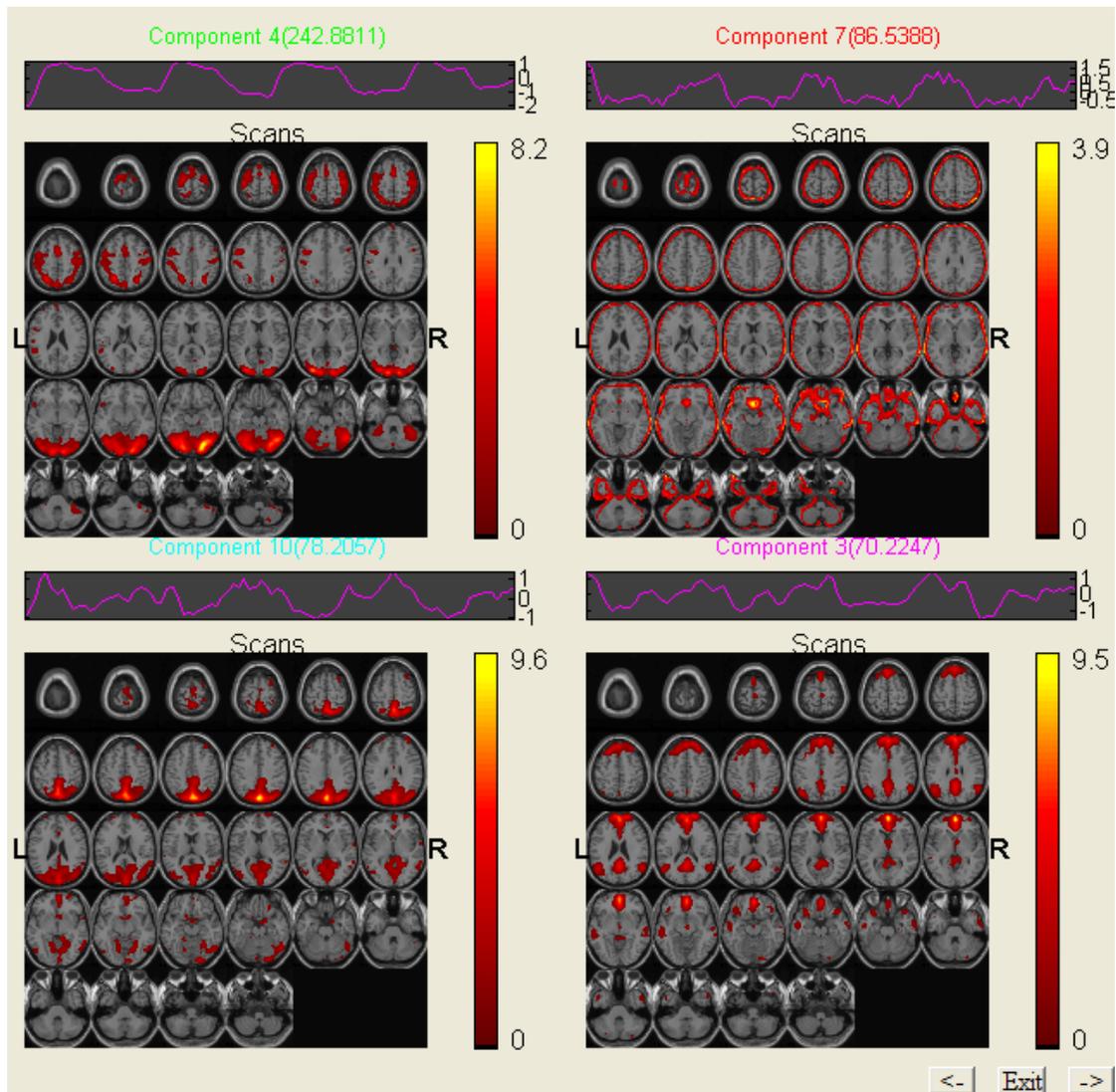


Fig. 51

- Display all components with the same label
 - Choose “All components with the same label”.
 - Select the component you want to view in the right panel.
 - Click “View”.
 - Set up display parameters as described before.

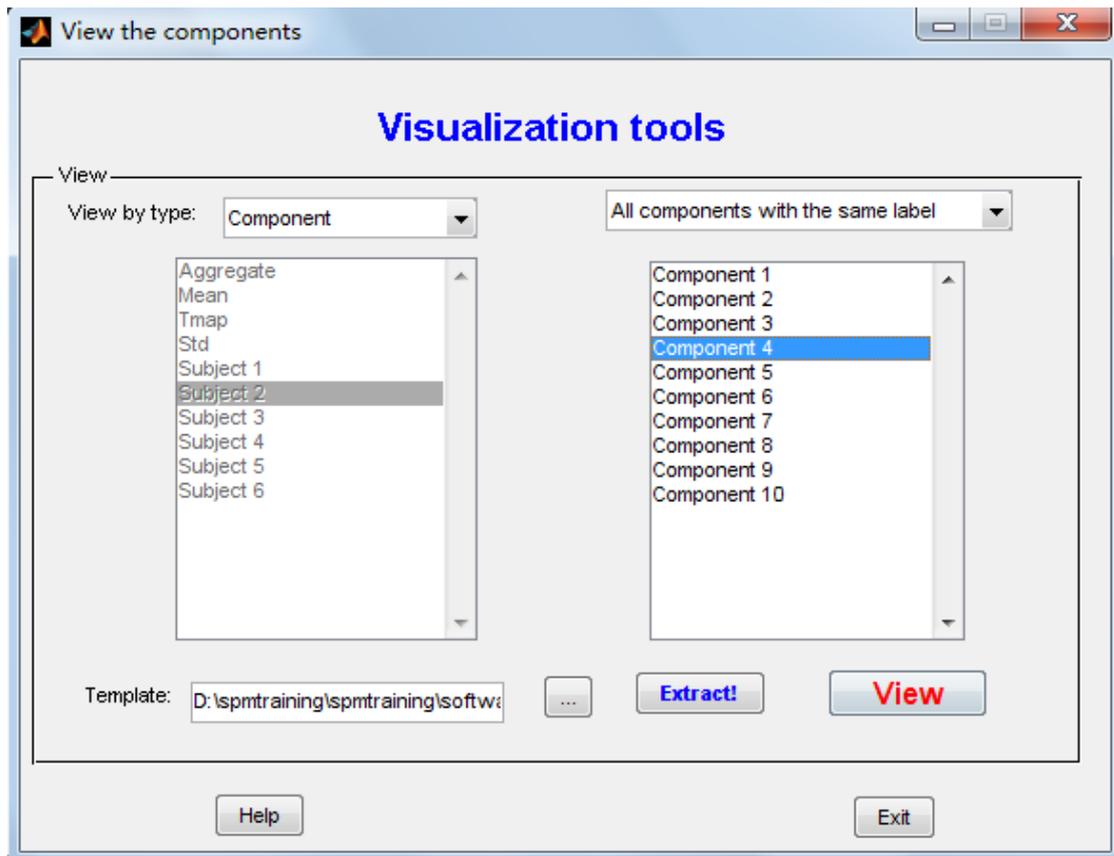


Fig. 52

- Then all subjects' component and the statistics maps for that component will be displayed in new windows like Figs. 53-54. The first three are mean, T-statistics and STD maps and the later are each subject's component.

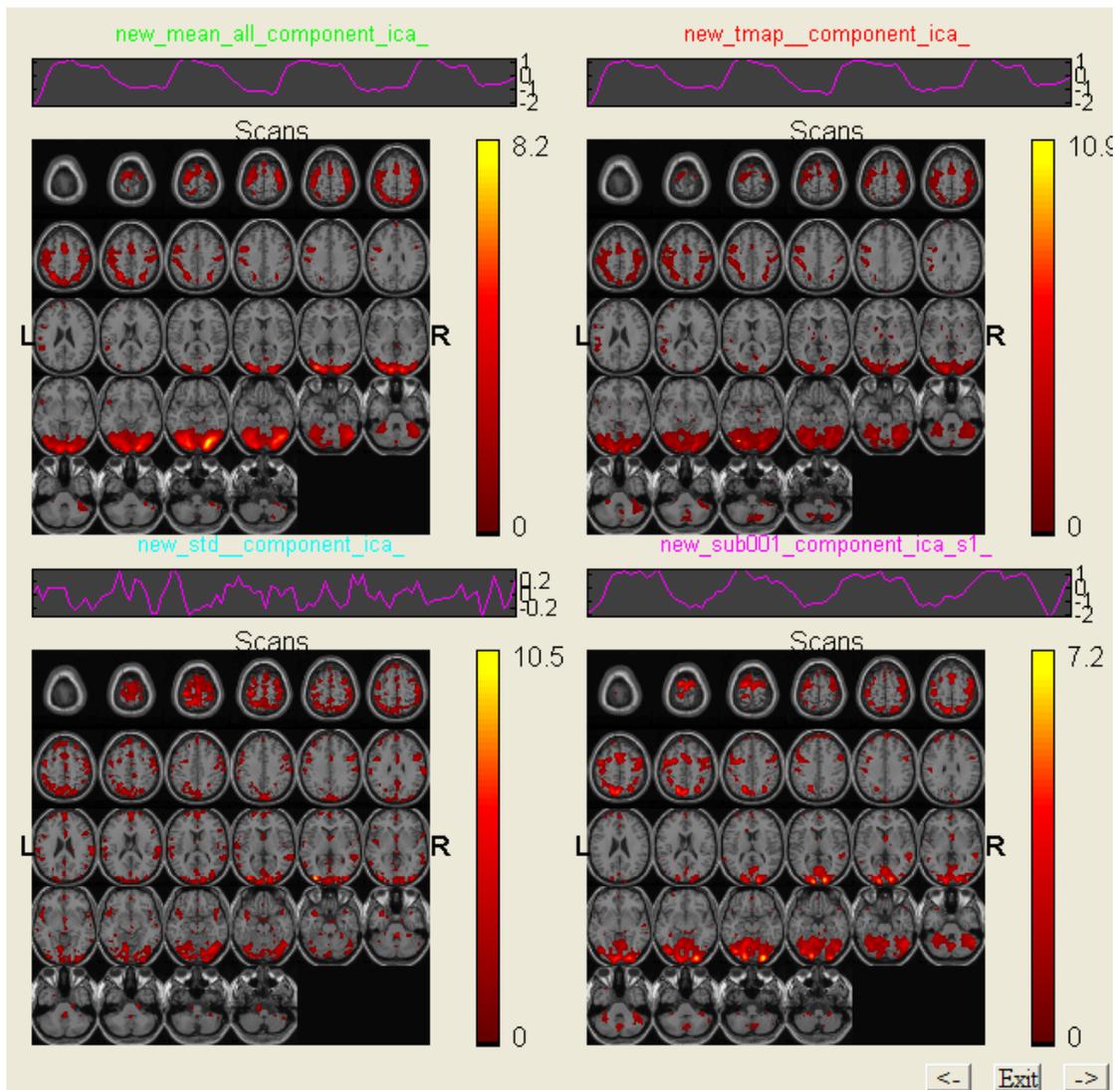


Fig. 53

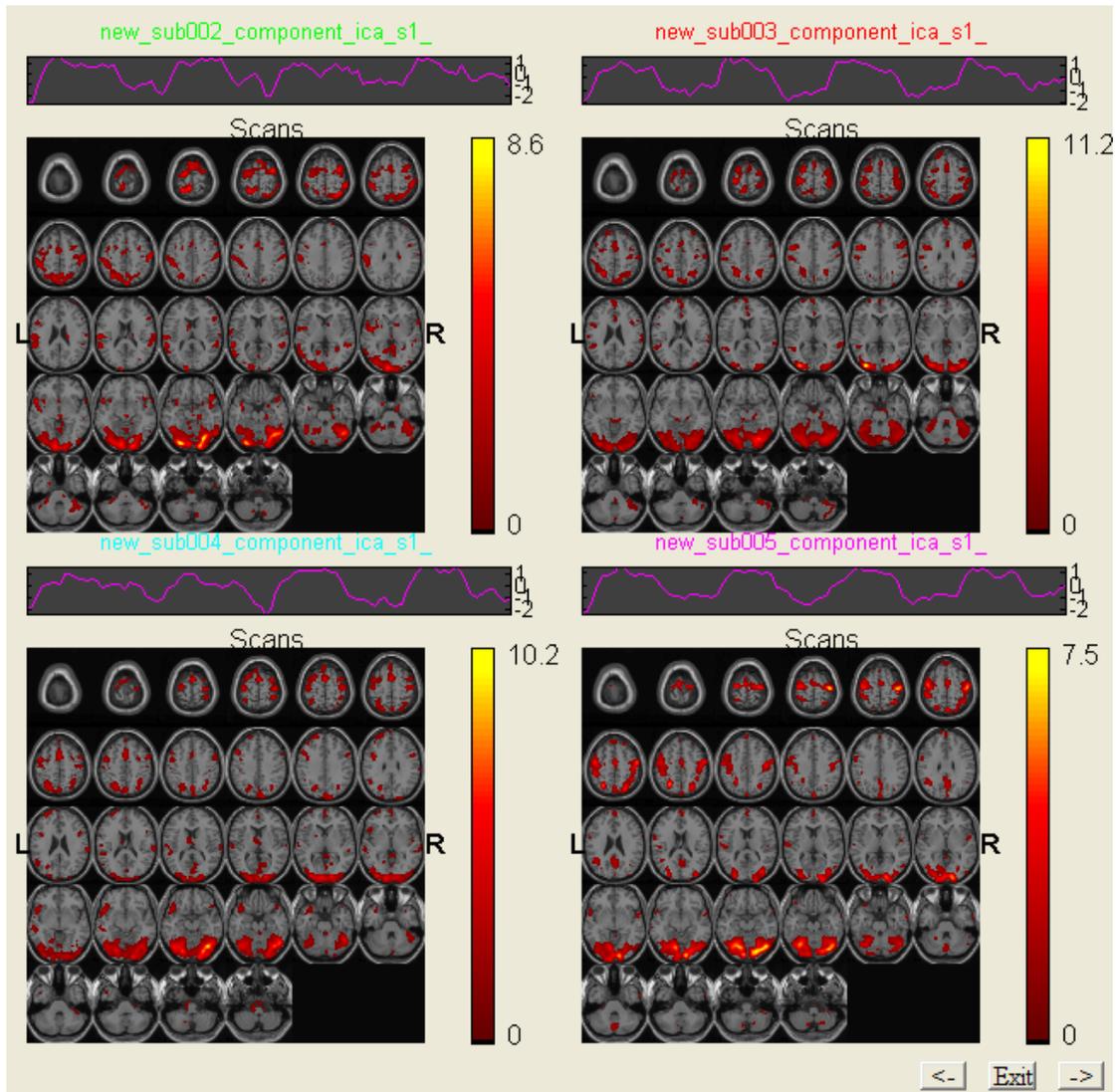


Fig. 54

- If you want to use this component for further analysis, such as group comparison, you should extract this component using “Extract” function.
- Click “Extract!” (Fig. 55).
- Select an output directory to store all the extracted components (Fig. 56) and click OK (Fig. 57).



Fig. 55

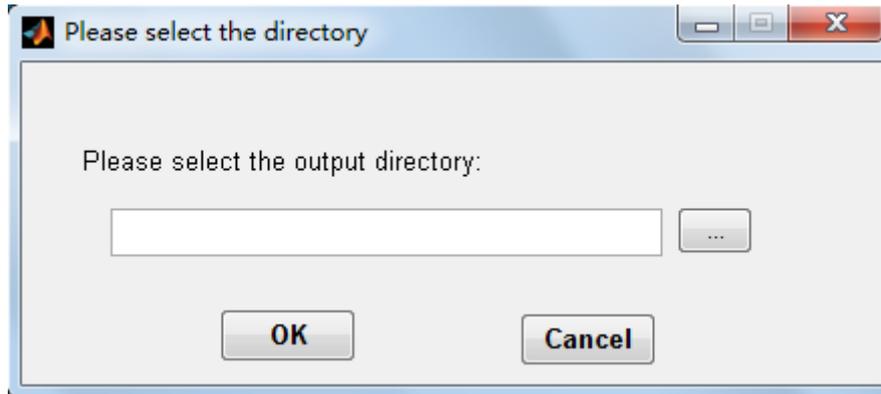


Fig. 56

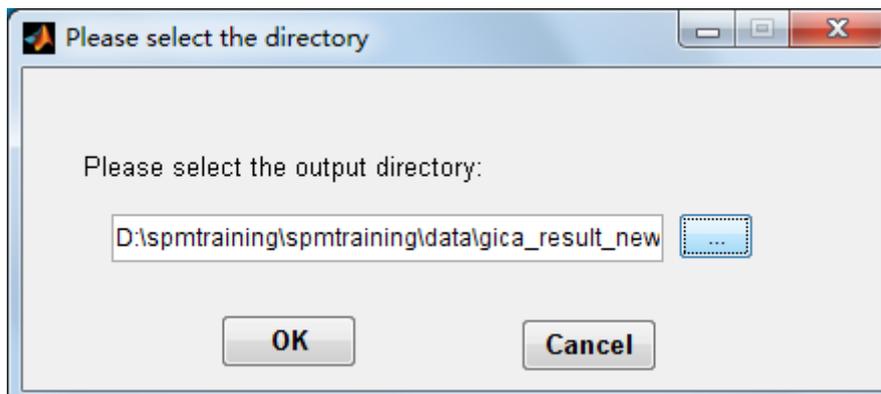


Fig. 57

- Then the component for all subjects will be extracted into this directory. For example, if your interested component is component No.4, then choose this component and extract it. The files “prefix_sub00?_component_ica_s1_004” are the spatial maps in NIFTI format. The file “prefix” is all of the associated time courses in MATLAB’s mat format (can be opened using MATLAB’s “load” function).

名称	修改日期	类型	大小
new	2010/7/23 18:25	MATLAB MAT-file	3 KB
new_sub001_component_ica_s1_004	2010/7/18 11:59	HDR 文件	1 KB
new_sub001_component_ica_s1_004	2010/7/18 11:59	IMG 文件	1,062 KB
new_sub002_component_ica_s1_004	2010/7/18 11:59	HDR 文件	1 KB
new_sub002_component_ica_s1_004	2010/7/18 11:59	IMG 文件	1,062 KB
new_sub003_component_ica_s1_004	2010/7/18 11:59	HDR 文件	1 KB
new_sub003_component_ica_s1_004	2010/7/18 11:59	IMG 文件	1,062 KB
new_sub004_component_ica_s1_004	2010/7/18 11:59	HDR 文件	1 KB
new_sub004_component_ica_s1_004	2010/7/18 11:59	IMG 文件	1,062 KB
new_sub005_component_ica_s1_004	2010/7/18 11:59	HDR 文件	1 KB
new_sub005_component_ica_s1_004	2010/7/18 11:59	IMG 文件	1,062 KB
new_sub006_component_ica_s1_004	2010/7/18 11:59	HDR 文件	1 KB
new_sub006_component_ica_s1_004	2010/7/18 11:59	IMG 文件	1,062 KB

Fig. 58

- Display a component of a subject
 - Select “A component of a subject”.
 - Choose a statistics or a subject in the left panel.
 - Choose a component in the right panel.
 - Click “View” (Fig. 59).

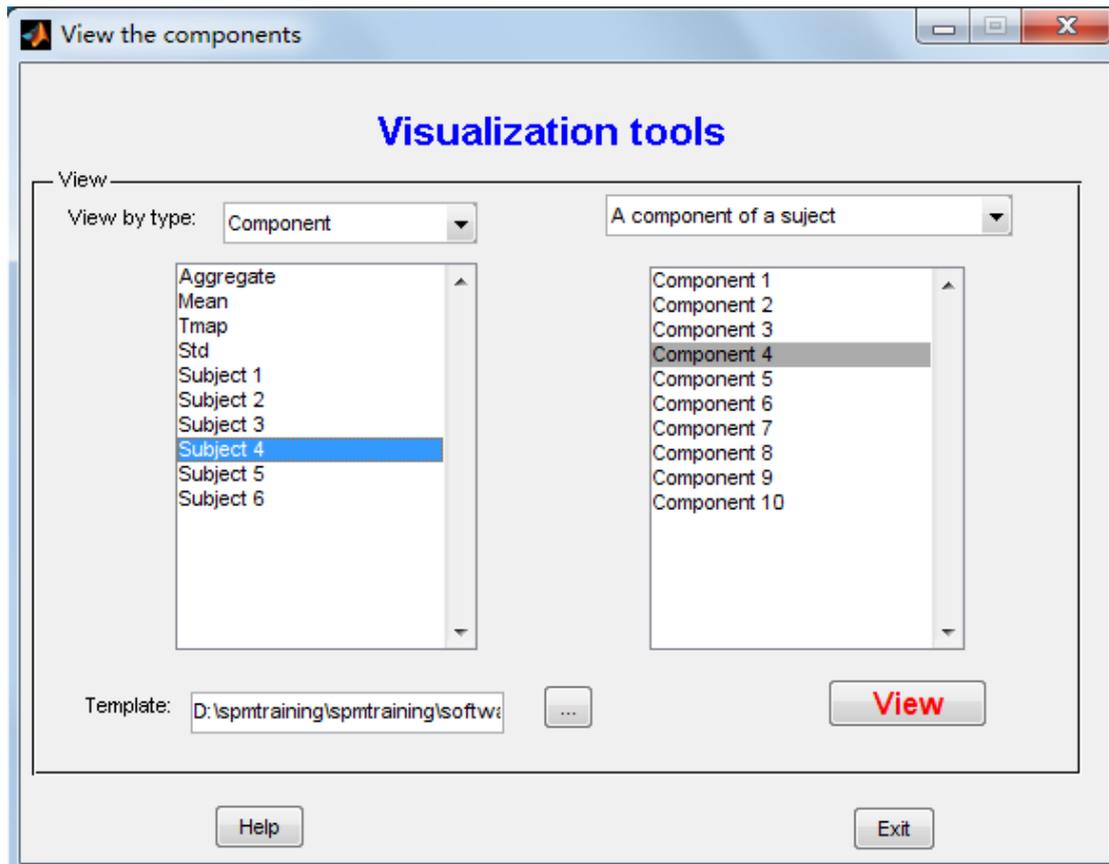


Fig. 59

- Set up display parameters in the pop-up dialog (Fig. 60) and click “OK”.

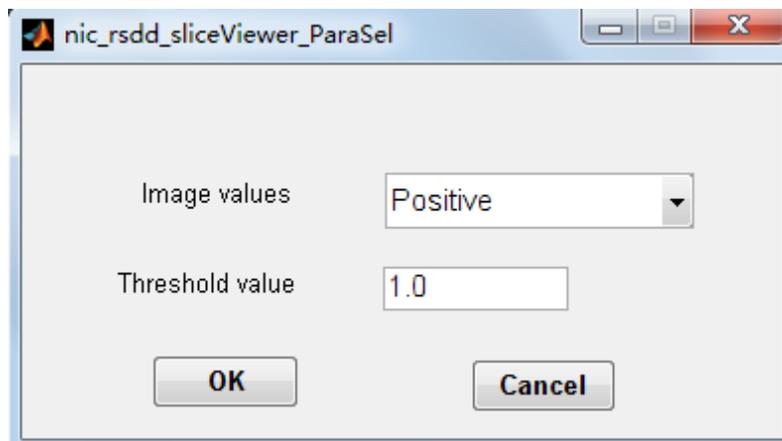


Fig. 60

- A three-view drawing will show up (Fig. 61).

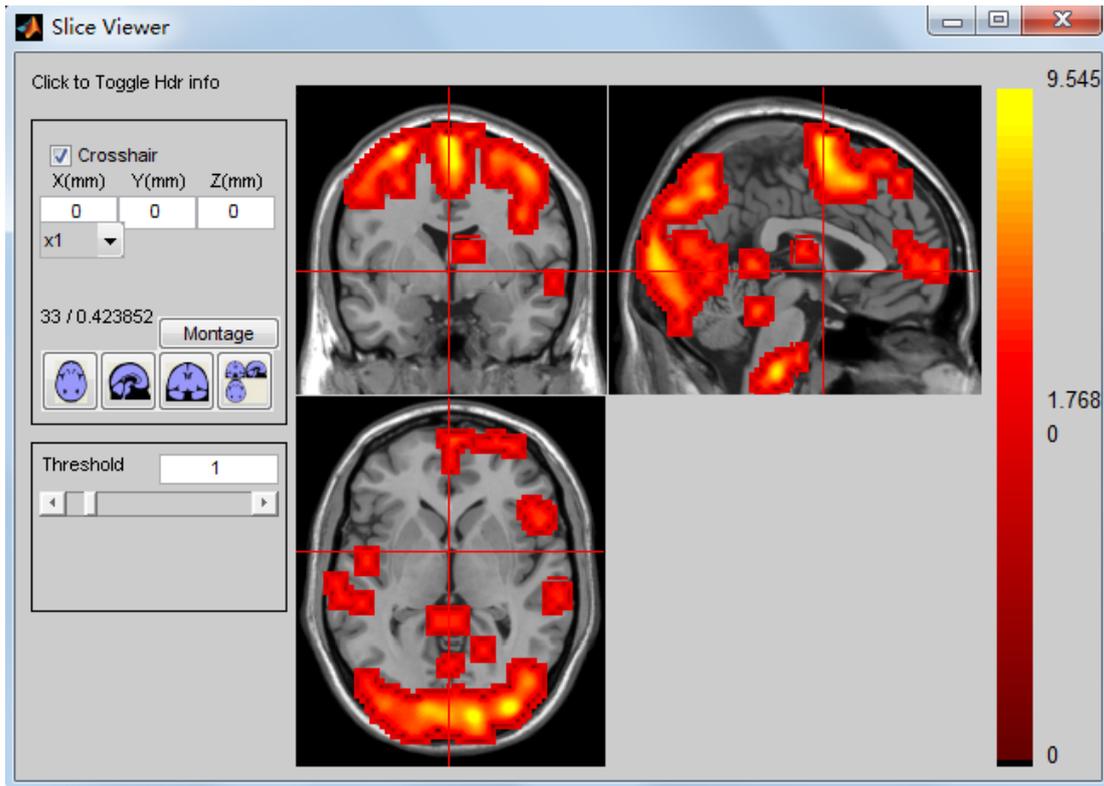


Fig. 61

- If you want to a multi-slice view, firstly click the button of axial or sagittal or coronal view (see Fig. 62). Then click “Montage”.

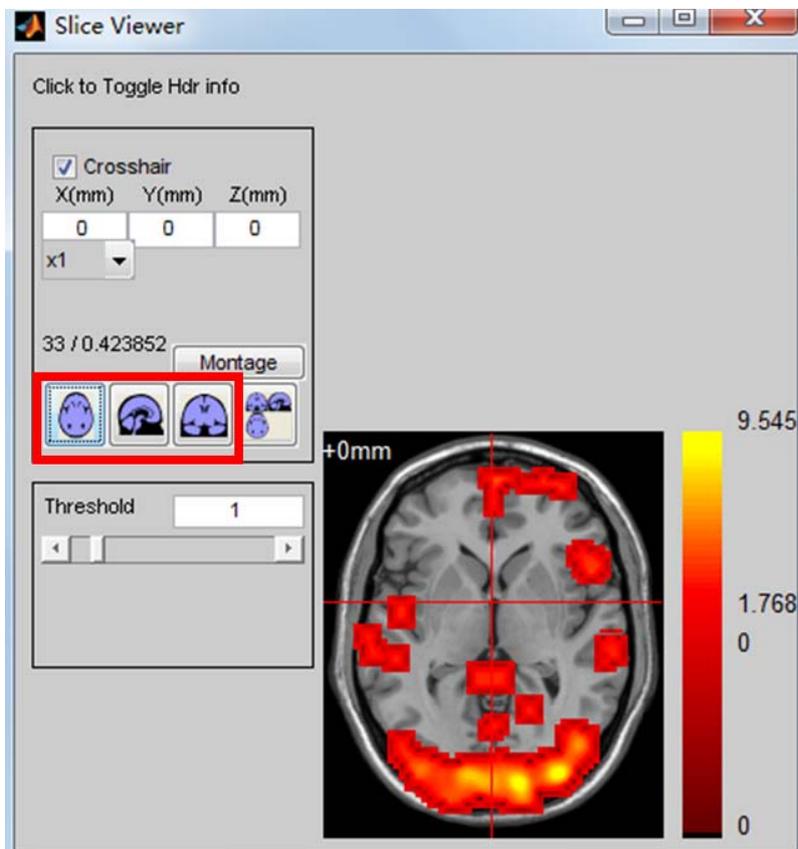


Fig. 62

- A montage setting up dialog will be opened up (Fig. 63). Set up the number of columns and rows, as well as the space between slices. Determine whether to show coordinate's label (1 means yes and 0 means no). Then click “OK”.

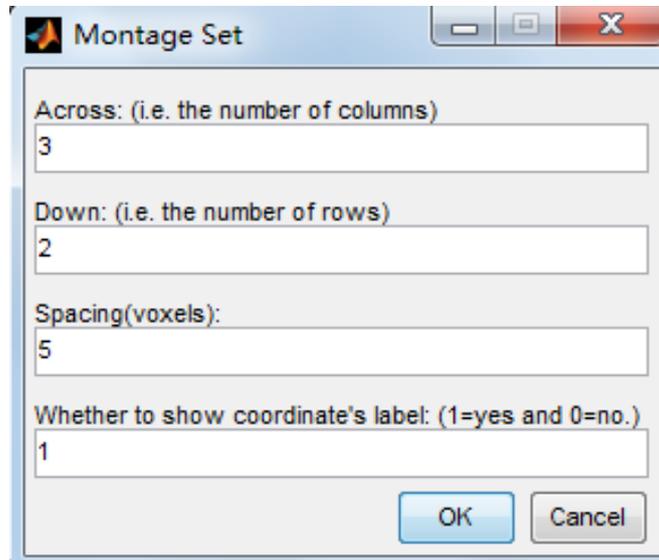


Fig. 63

- Then the multi-slice figure will show up (see Fig. 64 for a axial view and Fig. 65 for a sagittal view).

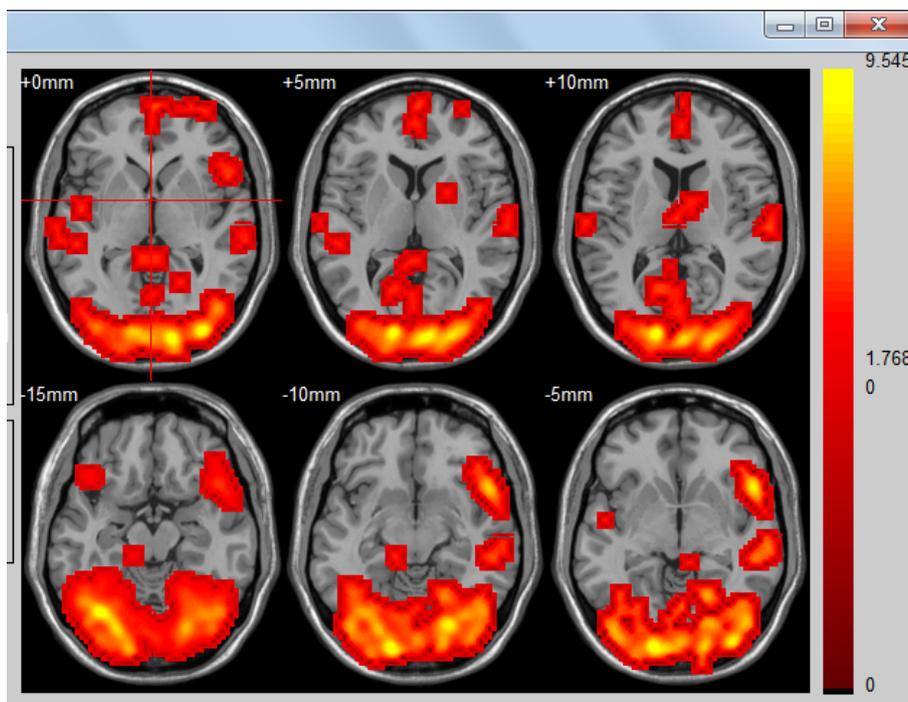


Fig. 64

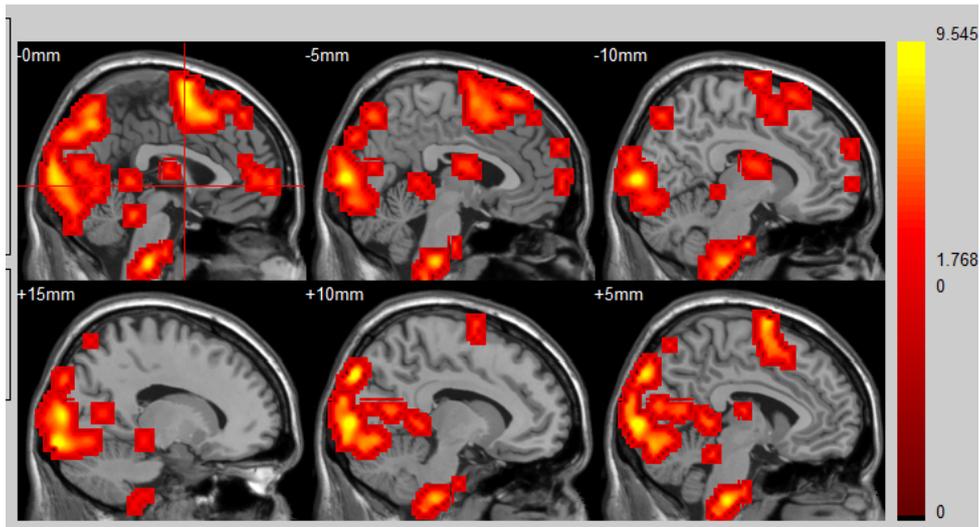


Fig. 65

Appendix

1. MICA download website:

http://www.nitrc.org/frs/?group_id=290&release_id=1076

Current version is [MICA_beta1.2_20100718](#).

You can go to NITRC's main page (<http://www.nitrc.org/>), type "MICA" in the search field and "GO". Then you can find the MICA download link (see Fig. 66).

Fig. 66

2. MICA main webpage (project page @ NITRC):

<http://www.nitrc.org/projects/cogicat/>

Please note that this projects (the website of MICA) is funded by the National Institutes of Health Blueprint for Neuroscience Research, the Neuroimaging Informatics Tools and Resources Clearinghouse (NITRC) facilitates finding and comparing neuroimaging resources for functional and structural neuroimaging analyses—including popular tools as well as those that once might have been hidden in another researcher's laboratory or some obscure corner of cyberspace. NITRC collects and points to standardized information about tools, making the task of finding and comparing them easier than before.

3. MICA forum (including bug report, help posting, updated information, etc.)

http://www.nitrc.org/forum/forum.php?forum_id=1210

4. Homepage of the MICA developing group (NIC group)

<http://psychbrain.bnu.edu.cn/home/chaozhezhu/>

5. Contact us via Email (for some technical supports)

napoleon1982@gmail.com (Mr. Han ZHANG)

6. The original paper describe the detailed algorithm utilized in MICA

Zhang, H., Zuo, X.-N., Ma, S.-Y., Zang, Y.-F., Milham, M.P., Zhu, C.-Z., 2010. Subject order-independent group ICA (SOI-GICA) for functional MRI data analysis. *Neuroimage*. 51(4), 1414-1424.

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