

HFR_ai: a toolbox for finding Homologous Functional Regions Across Individuals

Part0: Download HFR_ai.tar.gz and add it in MATLAB

Part1: Individual parcellation

Part2: HFR_ai

Part3: Create FC matrix

If you will use this toolbox, please make sure you have installed FREESURFER and add the directory of “matlab” , which is in the FREESURFER software, into your Matlab
(<https://surfer.nmr.mgh.harvard.edu/fswiki/>)

Organized by Meiling Li, 2017/05/31

Part0: Download HFR_ai.tar.gz and add it in MATLAB

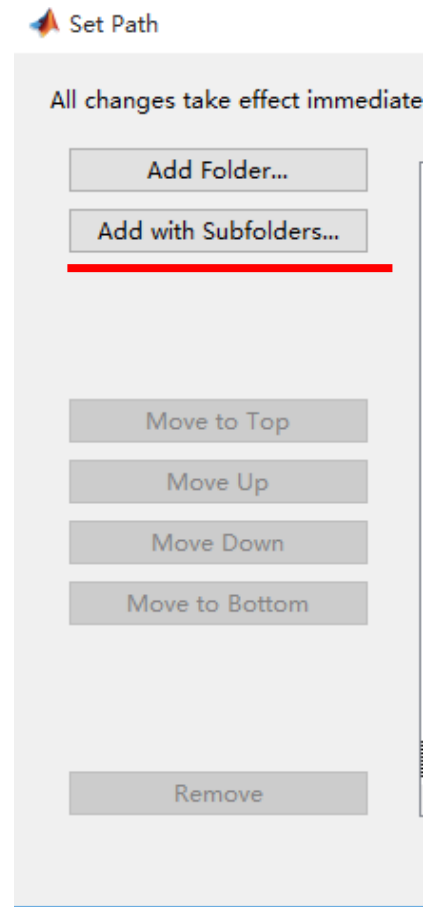
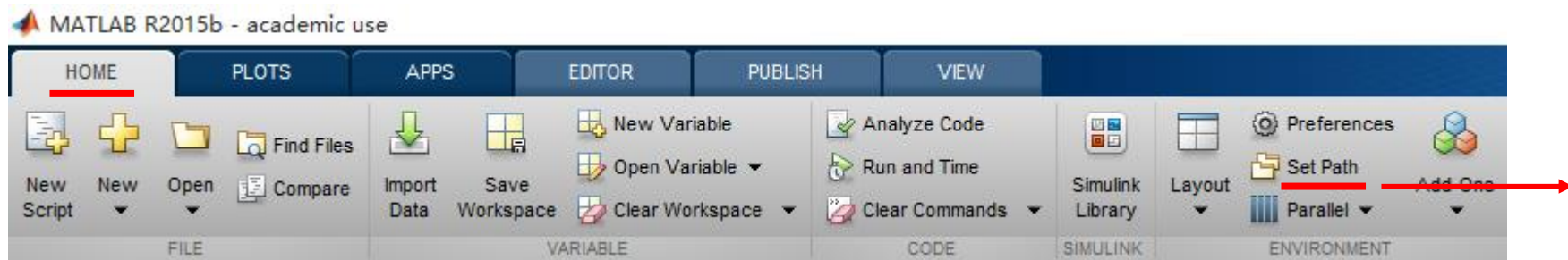
a. Download this toolbox here: <http://nmr.mgh.harvard.edu/bid/DownLoad.html>

b. Unpack the HFR_ai.tar.gz in your directory like
tar -zxvf HFR_ai.tar.gz you will get a directory named HFR_ai

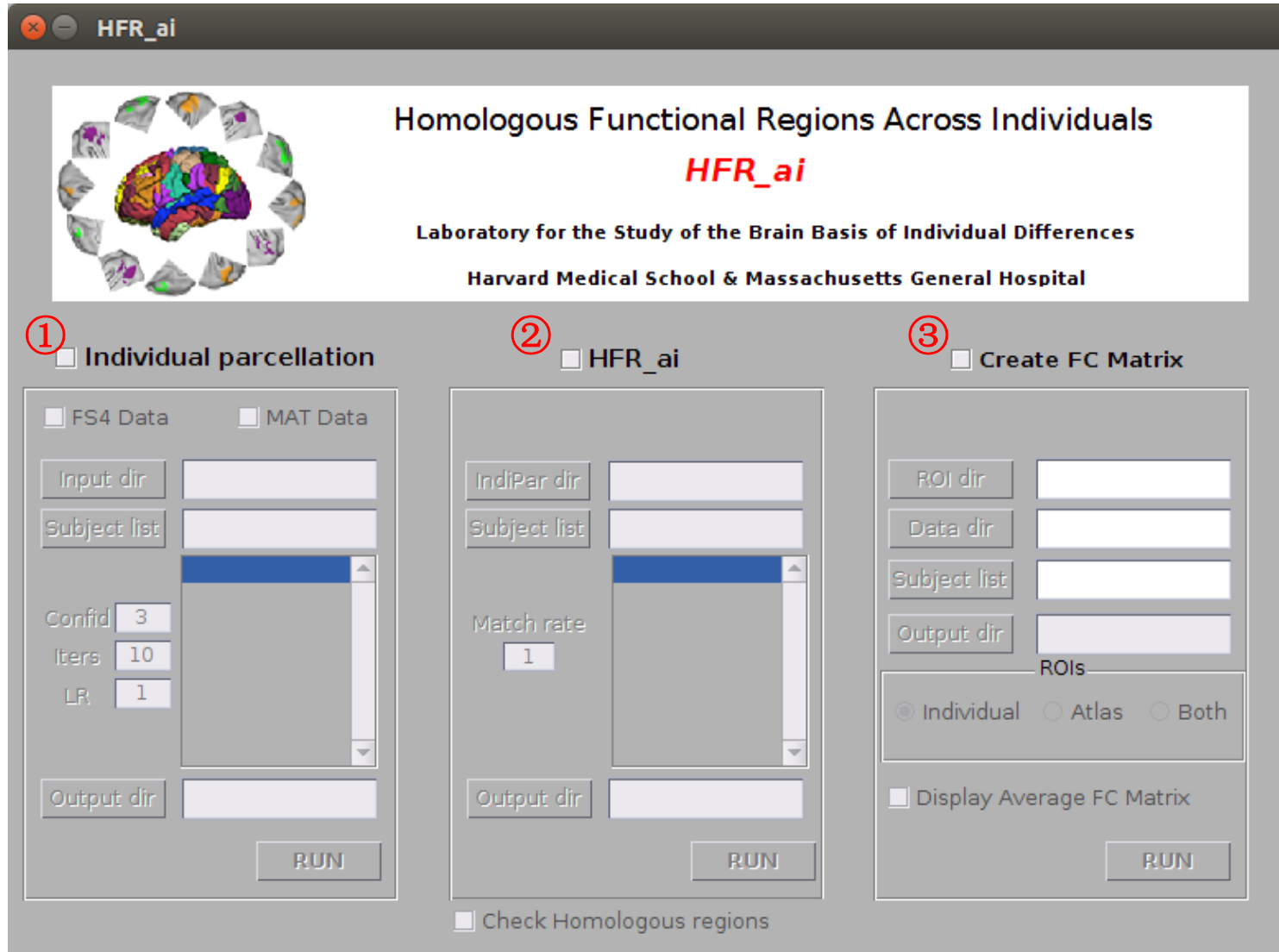
c. Open MATLAB in your terminal, and add this toolbox(HFR_ai) in the toolstrip like:

HOME->Set Path -> Add with Subfolders -> Save -> Close

or use the MATLAB command “addpath(genpath('/Path/HFR_ai'))” if you use only once.



d. Type “**HFR_ai**” and Return in the command window, then you should see the following interface, if you have added this toolbox successfully.



HFR_ai Pipeline summary:

1. **Individual parcellation.** Parcellating individualized functional networks proposed in Wang et al. 2015, NN.
2. **HFR_ai.** Finding the homologous functional regions across individuals.
3. **Create FC Matrix.** Calculating the ROI-ROI functional connectivity based on ROIs from HFR_ai and the corresponding ROIs from atlas.

Part1: Individual parcellation

Input dir:

the preprocessed data projected on fsaverage4.

The supported data type is “.nii.gz”(FS4 Data), and “.mat” (MAT Data). The preprocessed data is suggested to name and place like the following structure (next page).

Subject list:

a TXT file recorded all the subject ID you would like to do parcellation.

```
SubList.txt x
sub_001
sub_002
sub_003
sub_004
sub_005
```

Confid:

Confidence, the default value is 3, if the input value is extremely large, it will select the vertices with maximum confidence as the seed in the iteration.

Iters:

the terminating iteration number in the parcellation. The default value is 10.

LR:

whether to combine the same network of left hemisphere and right hemisphere, “1” means “Yes”, “0” means “No”. The default value is 1.

The screenshot shows the HFR_ai software interface. At the top, there is a logo of a brain with colored regions and the title "Homologous Functional Regions Across Individuals" with "HFR_ai" in red. Below the title is the affiliation: "Laboratory for the Study of the Brain Basis of Individual Differences" and "Harvard Medical School & Massachusetts General Hospital".

The interface is divided into three main sections:

- Individual parcellation:** This section is highlighted with a red box and a red circle with the number 1. It contains:
 - Checkboxes for "FS4 Data" (checked) and "MAT Data" (unchecked).
 - Input fields for "Input dir" and "Subject list", both set to "/mnt/sp5/HFR_ai/E".
 - A list box containing subject IDs: sub_001, sub_002, sub_003, sub_004, sub_005, sub_006, sub_007, sub_008. "sub_001" is selected.
 - Input fields for "Confid" (3), "Iters" (10), and "LR" (1).
 - An "Output dir" field set to "/mnt/sp5/HFR_ai/E".
 - A "RUN" button.
- HFR_ai:** This section contains:
 - Input fields for "IndiPar dir" and "Subject list".
 - A "Match rate" input field set to 1.
 - An "Output dir" field.
 - A "RUN" button.
 - A checkbox for "Check Homologous regions" at the bottom.
- Create FC Matrix:** This section contains:
 - Input fields for "ROI dir", "Data dir", "Subject list", and "Output dir".
 - Radio buttons for "ROIs": "Individual" (selected), "Atlas", and "Both".
 - A checkbox for "Display Average FC Matrix".
 - A "RUN" button.

Data Directory Structure

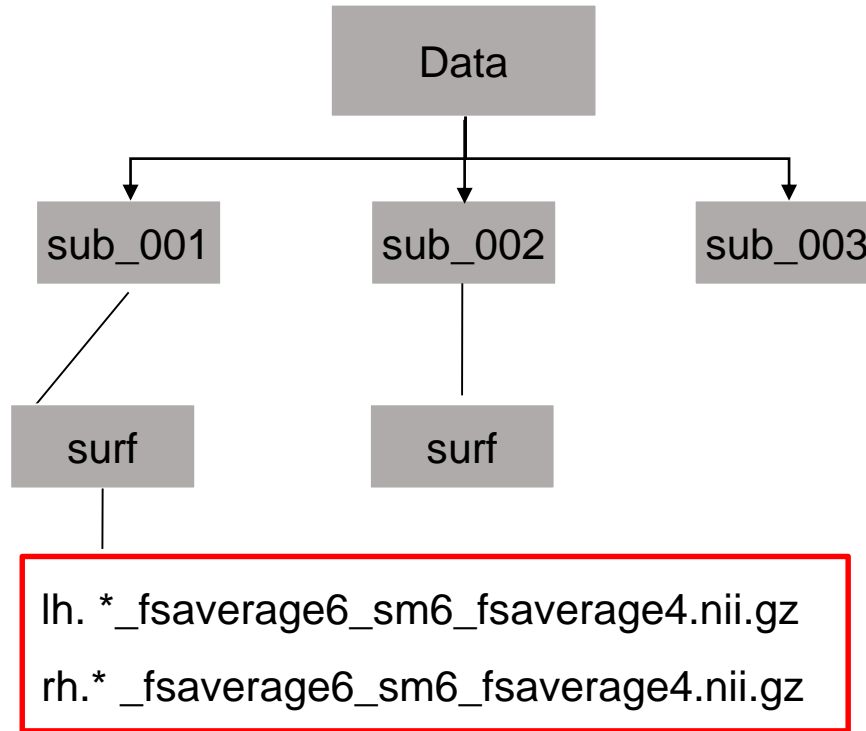
FS4 Data

1. Project Name

2. Subject Names

3. surf

4. Data on fsaverage4



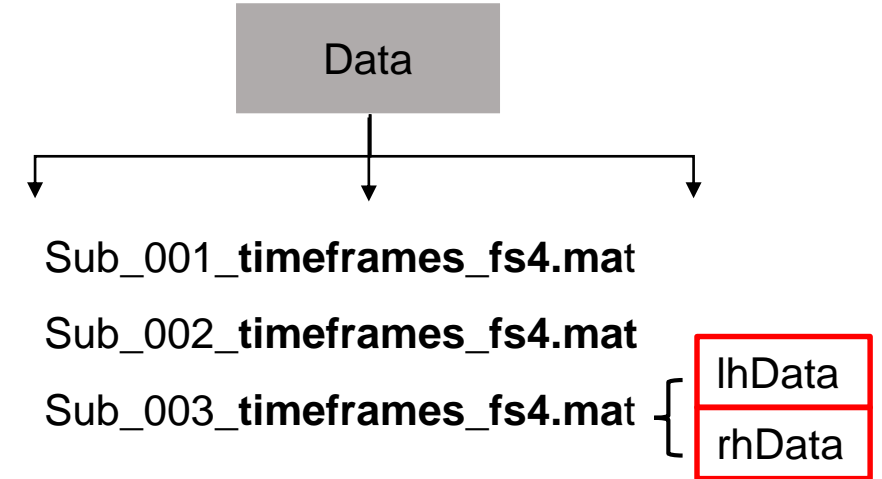
Note: The last dimension of the data is the number of time frames

FS4 Data example:

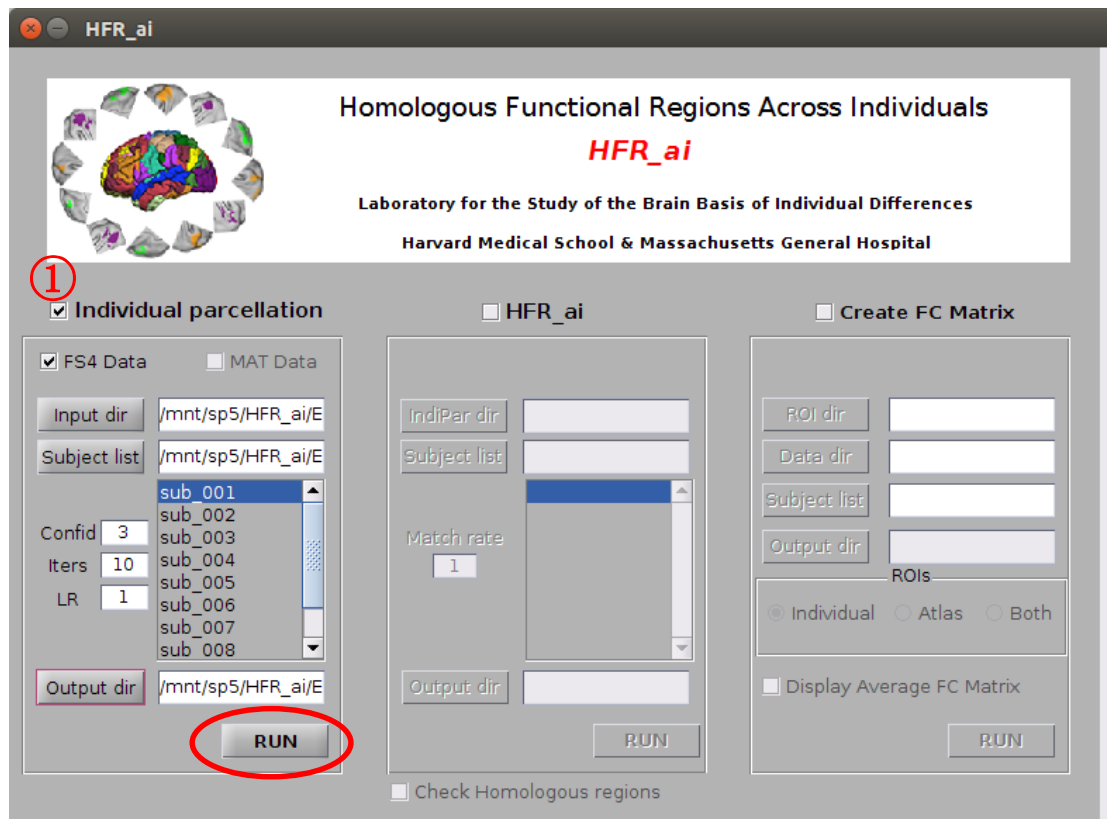
lh.sub_001_bld013_rest_reorient_skip_faln_mc_g1000000000_bpss_resid_fsaverage6_sm6_fsaverage4.nii.gz

rh.sub_001_bld013_rest_reorient_skip_faln_mc_g1000000000_bpss_resid_fsaverage6_sm6_fsaverage4.nii.gz

MAT Data



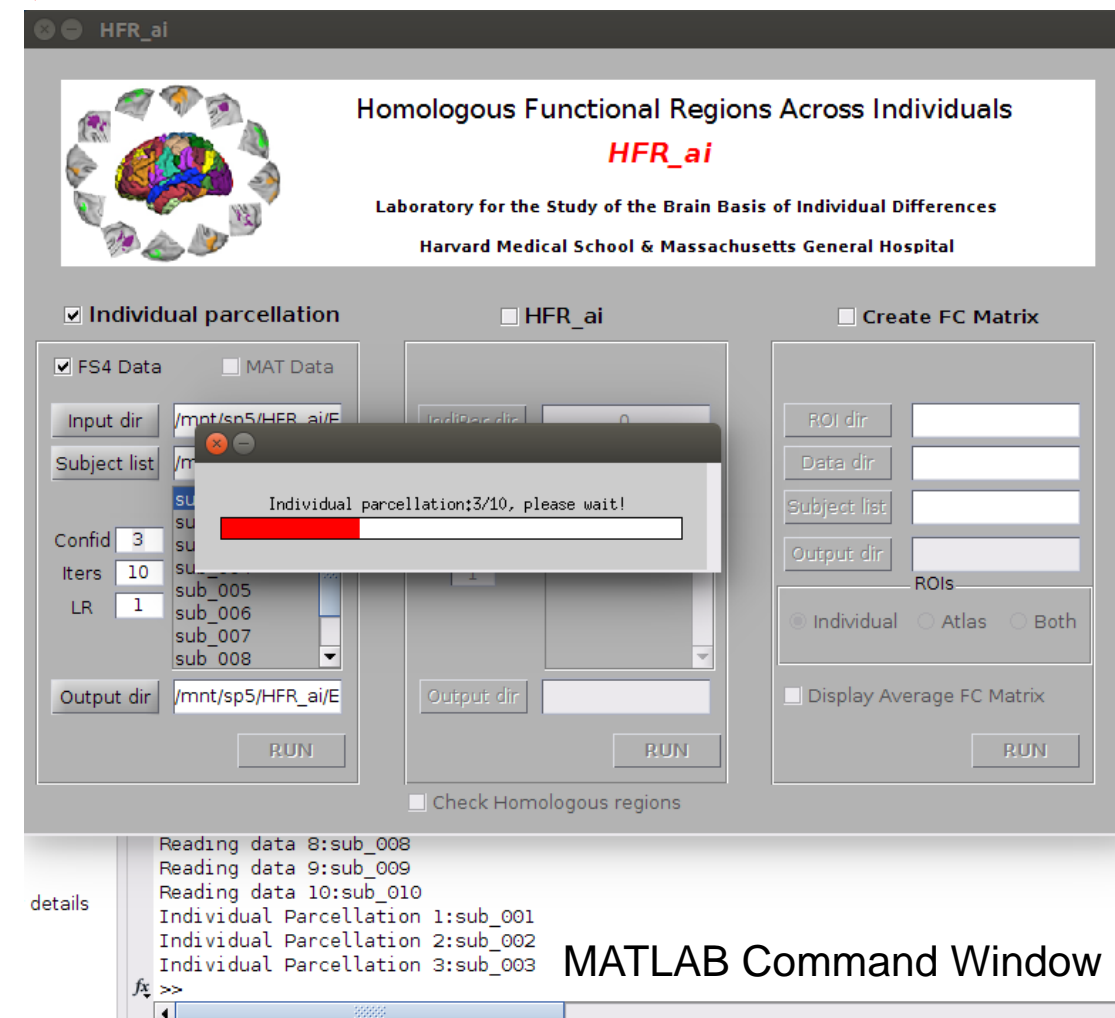
If you have organized your preprocessed data, please name the time frames on the left hemisphere as variable “lhData”, and the time frames on the right hemisphere as “rhData”. The dimension of ?hData is 2562*time frames number. Save them as “SubName_timeframes_fs4.mat” and place all the mat files in one file.



Click the RUN after all be set, then you will see the individual parcellation starts running! 🌹

Do not close the wait bar! Just wait!

This Part will generate two files:
/Output dir/Organized Data
/Output dir/IndiPar



Part2: HFR_ai

Indipar dir:

Individual parcellation results obtained from Part1.

eg: /Output dir/IndiPar

Subject list:

a TXT file recorded all the subject names you would like to find Homologous functional regions across these subjects.

SubList.txt x

```
sub_001  
sub_002  
sub_003  
sub_004  
sub_005
```

Iter:

Iter time (parcellation result) you would like to be further used, to get the homologous functional regions.

Match Rate:

The Match rate (0~1) means the minimum ratio that subjects have a given ROI when matching the ROIs across subjects.

Eg: “1” means all subjects have matched that ROI, the kept ROI is homologous in function across all individuals.

“0.8” means that at least 80% subjects have matched ROI(i.e. we can find this ROI in at least 80% subjects.)

HFR_ai

Homologous Functional Regions Across Individuals

HFR_ai

Laboratory for the Study of the Brain Basis of Individual Differences

Harvard Medical School & Massachusetts General Hospital

☐ Individual parcellation

☒ HFR_ai

☐ Create FC Matrix

☒ FS4 Data ☐ MAT Data

Input dir: /mnt/sp5/HFR_ai/E

Subject list: /mnt/sp5/HFR_ai/E

sub_001
sub_002
sub_003
sub_004
sub_005
sub_006
sub_007
sub_008

Confid: 3

Iters: 10

LR: 1

Output dir: /mnt/sp5/HFR_ai/E

RUN

IndiPar dir: /mnt/sp5/HFR_ai/E

Subject list: /mnt/sp5/HFR_ai/E

sub_001
sub_002
sub_003
sub_004
sub_005
sub_006
sub_007
sub_008

Iters: 10

Match rate: 1

Output dir: /mnt/sp5/HFR_ai/E

RUN

☐ Check Homologous regions

ROI dir:

Data dir:

Subject list:

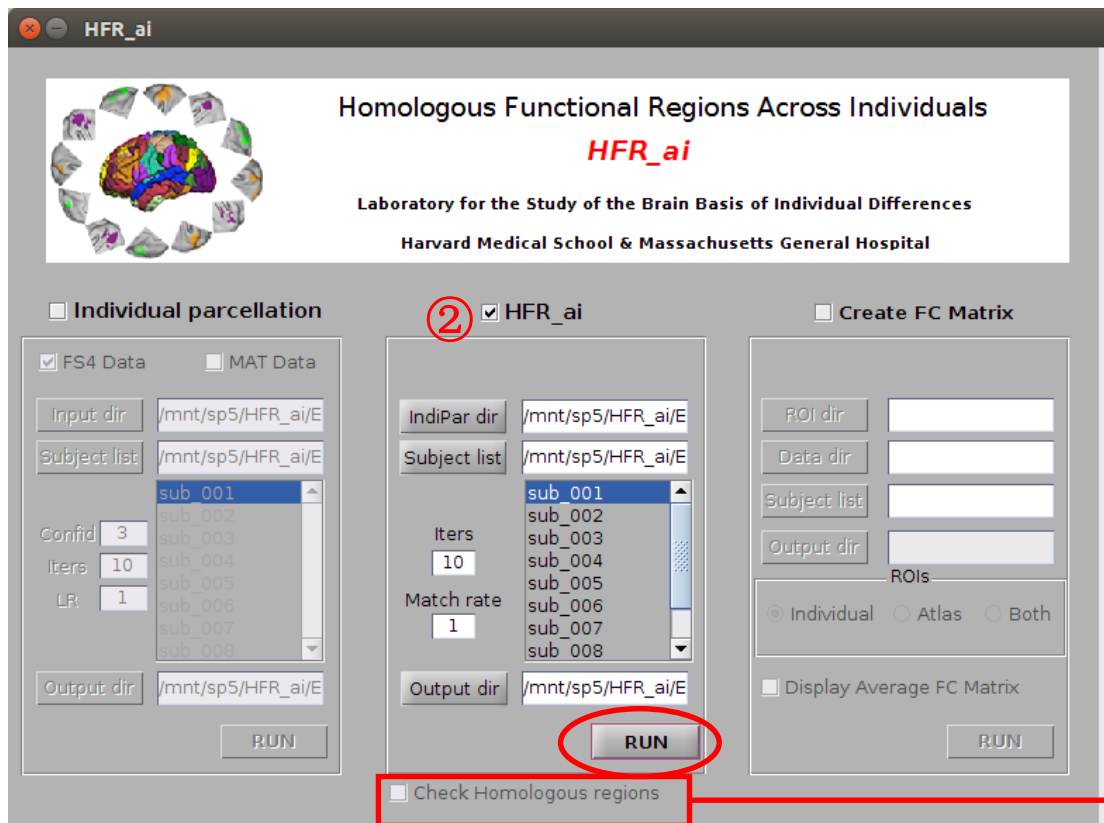
Output dir:

ROIs

☒ Individual ☐ Atlas ☐ Both

☐ Display Average FC Matrix

RUN



Click the RUN after all be set, then you will see the HFR_ai starts running! 🌹

It may take some time to match the ROIs according to the subjects number. After generated the homologous regions, please check them.



It will display the homologous ROIs on the surface (shown on fsaverage5 using the corresponding ROIs from Atlas). If the number of homologous regions across individuals is extremely small and the homologous ROIs even can not cover the most of the surface, it is not suggested to do further analysis using the individualized ROIs.

Homologous functional regions can be found here:

/Output dir/MatchRate1/

Which also includes the corresponding ROIs on atlas.

Part3: Create FC Matrix

ROI dir:

Homologous regions obtained from Part2.

eg: /Output dir/MatchRate1/

Do NOT select the “Indi_Matched_ROIs” or “GrpTemplate_Matched_ROIs”.

Data dir:

The preprocessed resting state fMRI data(organized data)

Eg: /Output dir/OrganizedData

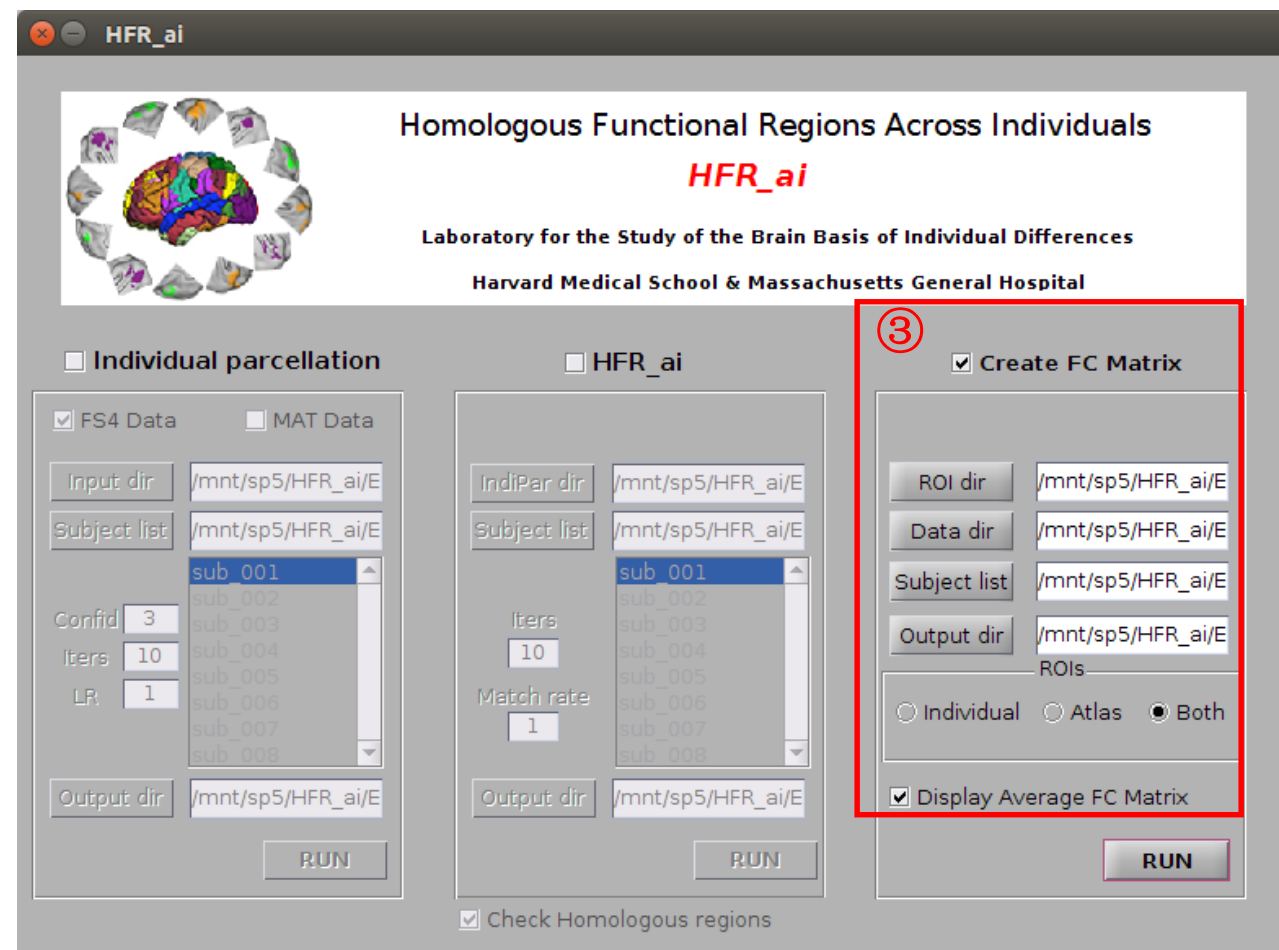
Subject list:

a TXT file recorded all the subject names you would like to calculate the ROI-ROI FC and check the mean FC across these subjects.

```
SubList.txt x
sub_001
sub_002
sub_003
sub_004
sub_005
```

ROIs:

ROIs used to calculate the ROI-ROI functional connectivity.



The screenshot shows the HFR_ai software window titled "Homologous Functional Regions Across Individuals". The interface is divided into three main sections. The left section is for "Individual parcellation" and the middle section is for "HFR_ai". Both sections have identical input fields: "Input dir" and "Subject list" (both set to "/mnt/sp5/HFR_ai/E"), a list of subjects (sub_001 to sub_008), "Confid" (3), "Iters" (10), "LR" (1), and "Output dir" (set to "/mnt/sp5/HFR_ai/E"). The right section, highlighted with a red box and a circled '3', contains the "Create FC Matrix" options. It includes fields for "ROI dir", "Data dir", "Subject list", and "Output dir", all set to "/mnt/sp5/HFR_ai/E". Below these fields are radio buttons for "Individual", "Atlas", and "Both" (selected). At the bottom of the right section is a checkbox for "Display Average FC Matrix" (checked) and a "RUN" button. The bottom of the window has a checkbox for "Check Homologous regions" (checked).

HFR_ai

Homologous Functional Regions Across Individuals

HFR_ai

Laboratory for the Study of the Brain Basis of Individual Differences

Harvard Medical School & Massachusetts General Hospital

☐ Individual parcellation ☐ HFR_ai

☒ FS4 Data ☐ MAT Data

Input dir: /mnt/sp5/HFR_ai/E

Subject list: /mnt/sp5/HFR_ai/E

sub_001
sub_002
sub_003
sub_004
sub_005
sub_006
sub_007
sub_008

Confid: 3

Iters: 10

LR: 1

Output dir: /mnt/sp5/HFR_ai/E

☒ Create FC Matrix

ROI dir: /mnt/sp5/HFR_ai/E

Data dir: /mnt/sp5/HFR_ai/E

Subject list: /mnt/sp5/HFR_ai/E

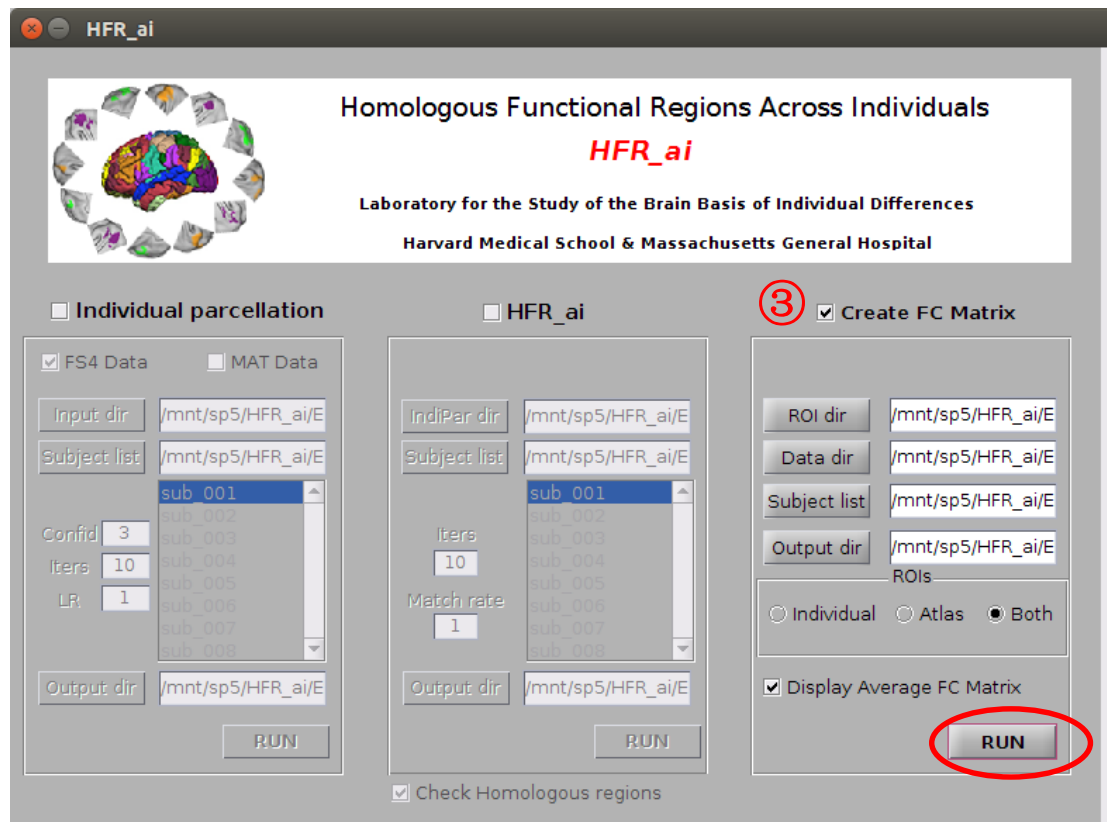
Output dir: /mnt/sp5/HFR_ai/E

Individual Atlas Both

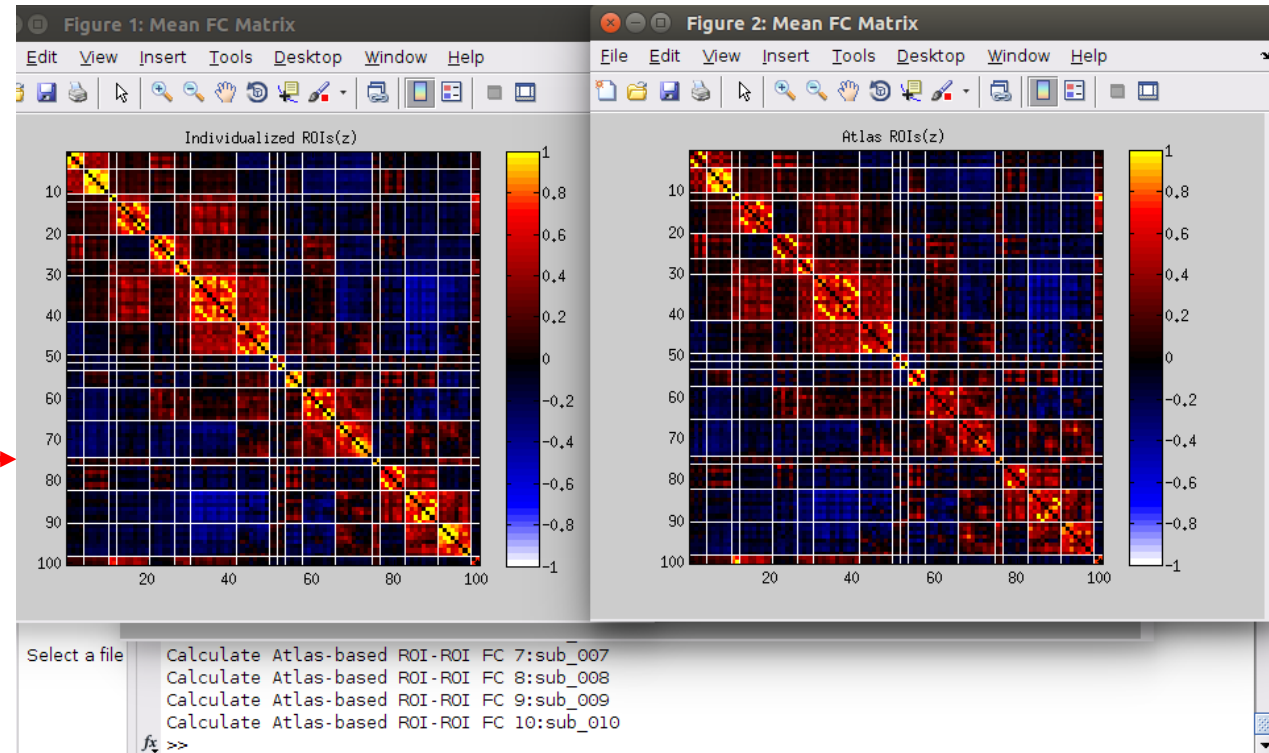
☒ Display Average FC Matrix

☒ Check Homologous regions

RUN RUN RUN



Click the RUN after all be set, then you will see the average FC matrix. 🌹



Check the FC Matrix here:

/Output dir/MatchRate1/ROI2ROIFC_Indi

/Output dir/MatchRate1/ROI2ROIFC_Atlas