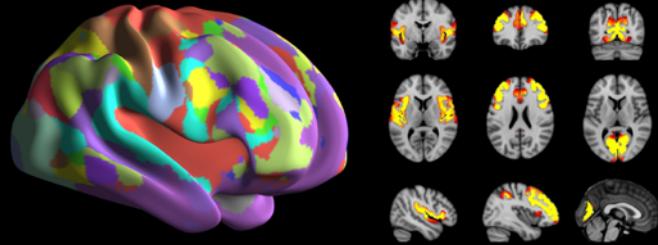


pNet

(Personalized Functional Network Modeling)



Manual

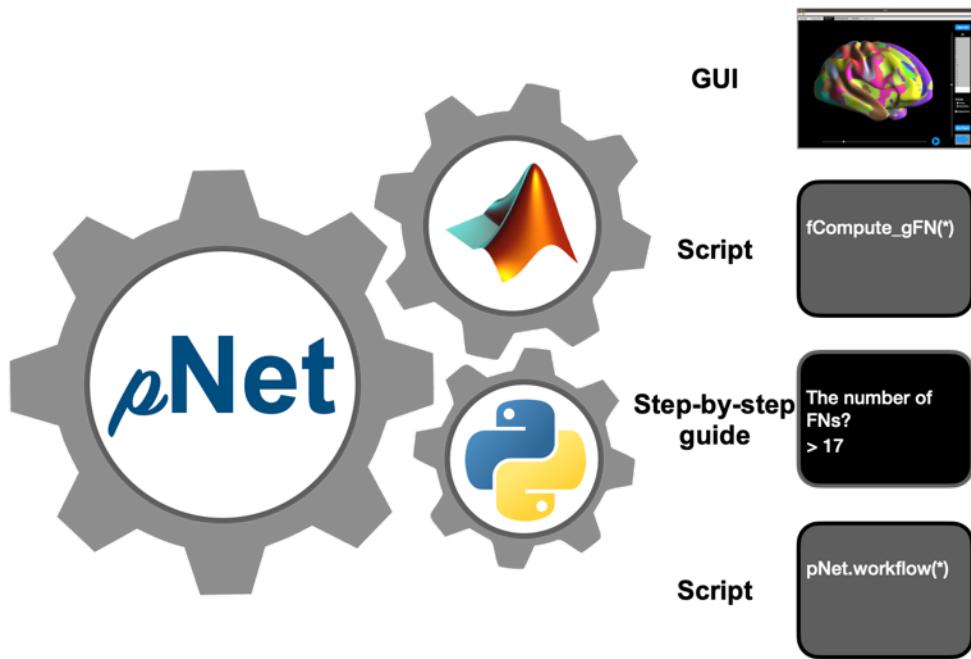
A guideline for pNet

Yuncong Ma

Toolbox Overview

pNet is designed to provide a user-friendly interface to perform personalized functional network (pFN) computation and visualization. It is open-source, cross-platform, and expandable. The toolbox is built with support for MATLAB and Python users. The MATLAB version offers GUI and code scripts. The Python version uses NumPy for simple code development, and PyTorch for high computation performance. And it provides a step-by-step guide in terminal command. pNet provides streamlined workflow to carry out computation and visualization of pFNs. It also integrates several statistical methods to investigate the relationship between pFNs and behavior data. In addition, quality control is available to check the quality of pFN modeling results.

This toolbox can be downloaded from <https://github.com/YuncongMa/pNet> and <https://github.com/MLDataAnalytics/pNet>.

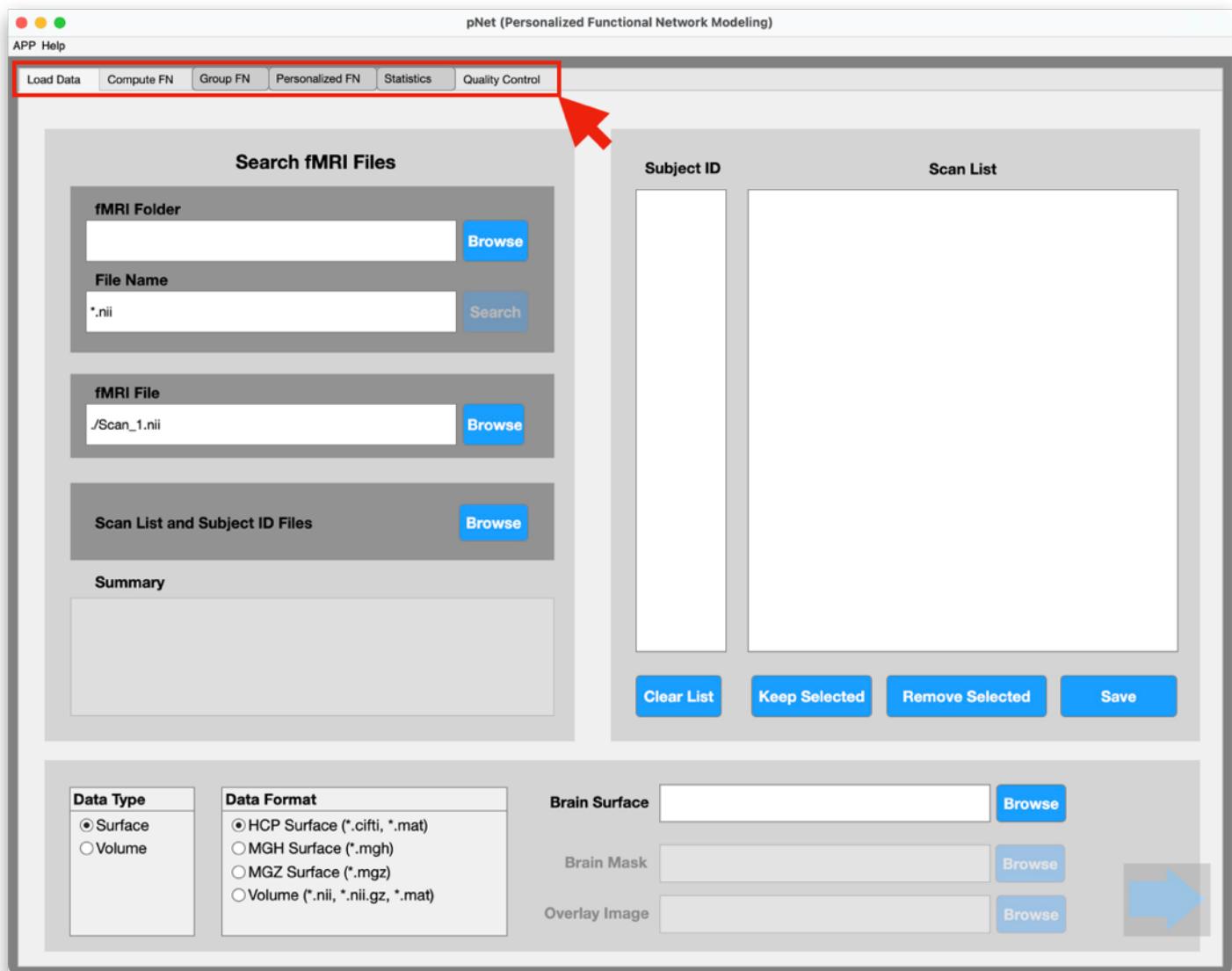




pNet GUI snapshots

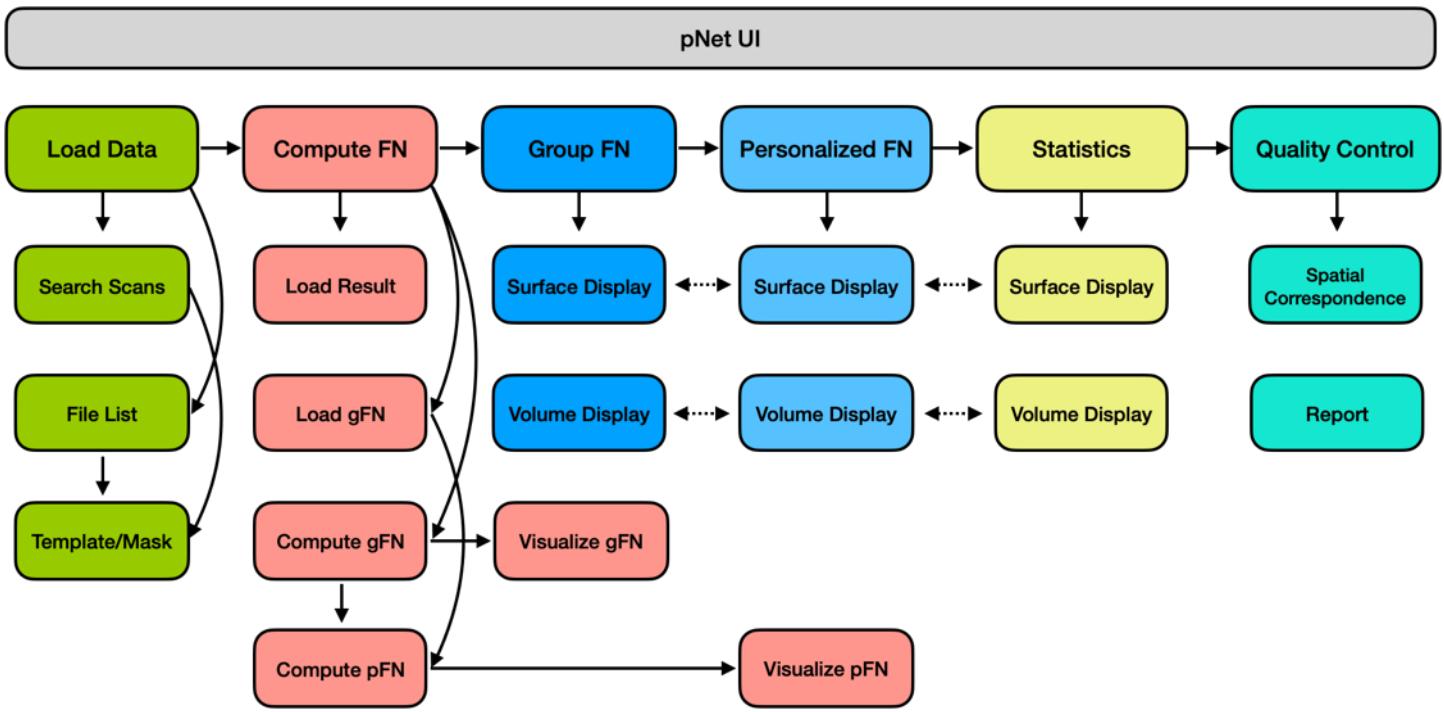
- (A) The data input module for loading fMRI scans and brain template files.
- (B) The FN computation module to setup computation parameters for both the group-level and individualized FNs.
- (C) Surface-based visualization of both group and personalized FNs ($k=17$) using HCP S1200 dataset, with left panel showing a binarized atlas generated from the group FNs and the right panel showing five views of three personalized FNs. All the color bars of intensity maps were set from the maximum value of the map to its half value.
- (D) Volume-based visualization of both group and personalized FNs ($k=17$) from Zhen's multi-cohort iSTAGING study, with left panel showing a binarized functional atlas generated from the group FNs and the right panel showing a three-slice view of three personalized FNs.
- (E) Surface-based visualization of a personalized FN.

- (F) Surface-based visualization of the maximum t value (two sample t-test, FDR correction, p-value=0.001) of sex differences of individualized FNs (k=50) of the HCP S1200 dataset.
(G) A module for quality control, showing one scan with two FNs mismatched to their group-level counterparts.



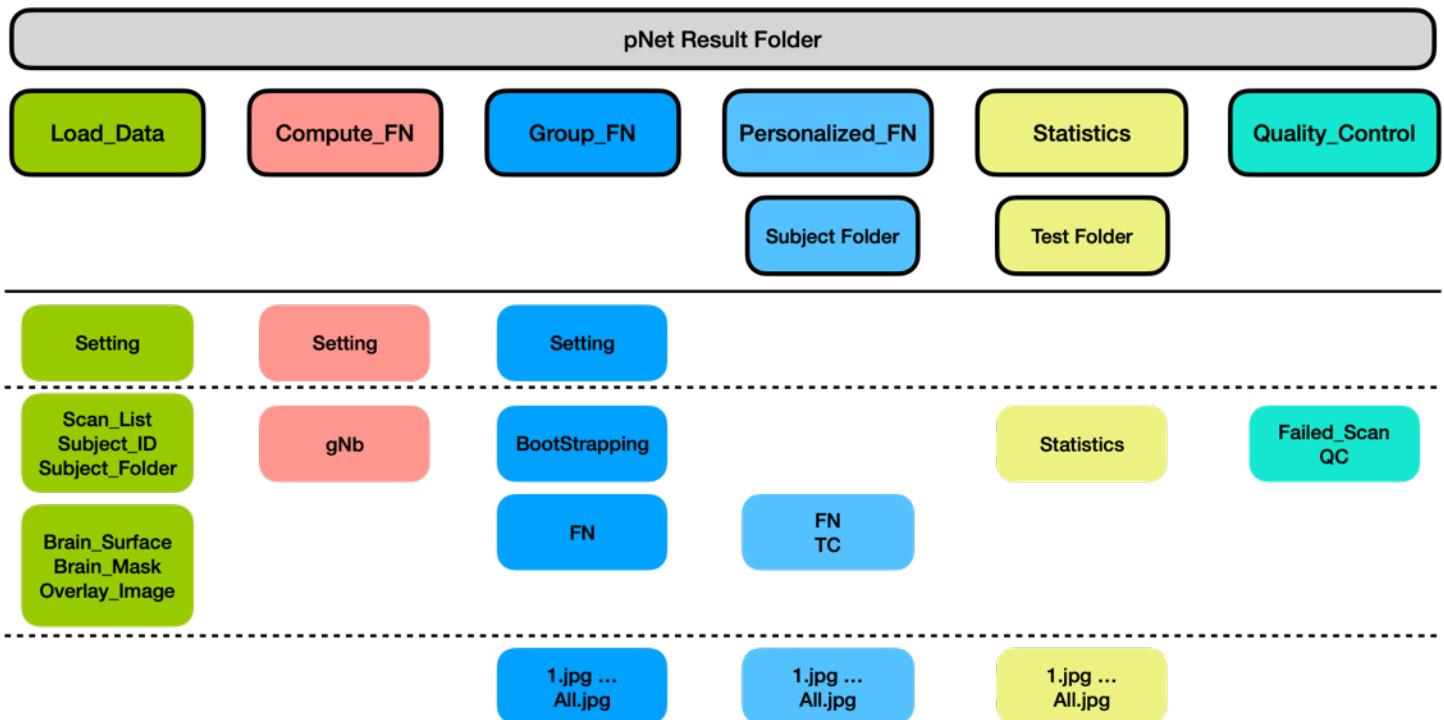
Tabs (highlighted in the red box) for different modules to search data, setup FN computation, check results of group-level and personalized FN, conduct statistics, and quality control.

pNet provides a unified and intuitive design of UI and data structure. It consists of six modules



The workflow of pNet UI.

It consists of six major modules, including data loading, FN computation, group-level FN display, personalized FN display, statistics, and quality control. The six modules correspond to six major UI panels in pNet, and six subfolders in the pNet result folder. The pNet UI is designed to follow the left-to-right workflow direction to setup each step. Curved arrows show alternative workflows. The FN computation module (colored in light red) can use precomputed group-level FNs to derive personalized FNs as one option. Precomputed visualization of group-level and personalized FNs will be used in the two display modules (group FN and personalized FN). pNet features synchronized display to facilitate the comparisons between group-level and personalized FNs, as well as statistical results. The dashed double-sided arrows denote this display synchronization between three modules.



Data structure in the pNet result folder.

Folders are noted in boxes with black borders above the black horizontal line, and files are in boxes without black border, separated into three categories (setting, data, and figure files) by the dashed lines. Boxes are color coded for different modules. In the first three modules, the setting files are present. In the personalized FN folder, subfolders are named by subject information. In statistics folder, subfolders are named by their method information.

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App Installation

This chapter provides guidelines about ways to run this toolbox. The MATLAB version only runs successfully on MATLAB no older than 2021a. The Python version requires Python version 3.8.

For MATLAB version

Users can use the toolbox in several ways as shown below:

1. Run from the MATLAB command window.
2. Install pNet as a MATLAB app.

For Python version

1. Install anaconda with Python=3.8
2. Create a conda environment for pNet

```
$ conda env create --name pnet -f environment.yml
```

3. Or install other required packages in an existing conda environment

```
$ pip install numpy scipy scikit-learn pandas h5py  
$ conda install -c conda-forge nibabel  
$ conda install pytorch  
$ conda config --add channels conda-forge  
$ conda install mesalib vtk  
$ pip install matplotlib surfplot  
$ python -m pip install -U scikit-image
```

4. Activate conda environment

```
$ conda activate pnet
```

5. Download the whole pNet toolbox and import it to your Python environment

```
$ git clone https://github.com/YuncongMa/pNet <User's directory>
```

System and hardware requirement

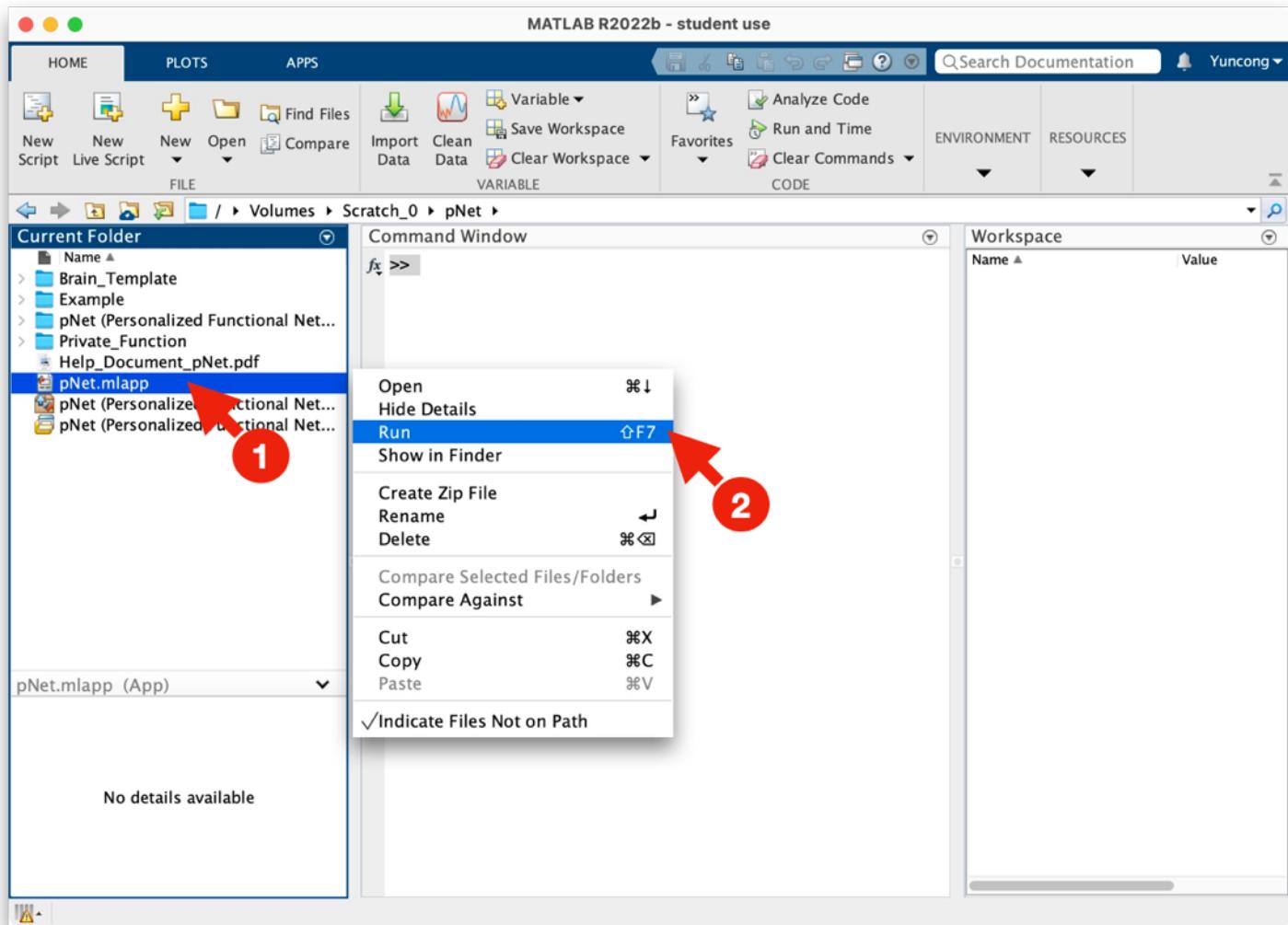
It is recommended to have at least 4 CPU cores, 16GB memory (RAM), and 10GB free disk space. Please be aware that more CPU, memory and disk space will be needed to process bigger data or use parallel computation. MATLAB older than 2021a does not have some essential APP UI functions to give correct UI layout. As pNet is mostly tested on 2022b, it is recommended to use this version or later.

MATLAB	macOS (Intel CPU)	macOS (Apple Silicon)	Linux	Windows 10
2020b				✗
2021a	✓	✓	✓	✓
2021b	✓			✓
2022a	✓			✓
2022b	✓			✓
2023a	✓			✓



Run in MATLAB

This method requires to download all the functions and app icons to run pNet in MATLAB. Make sure that the subfolder `Private_Function` and the help document are available in the app folder.

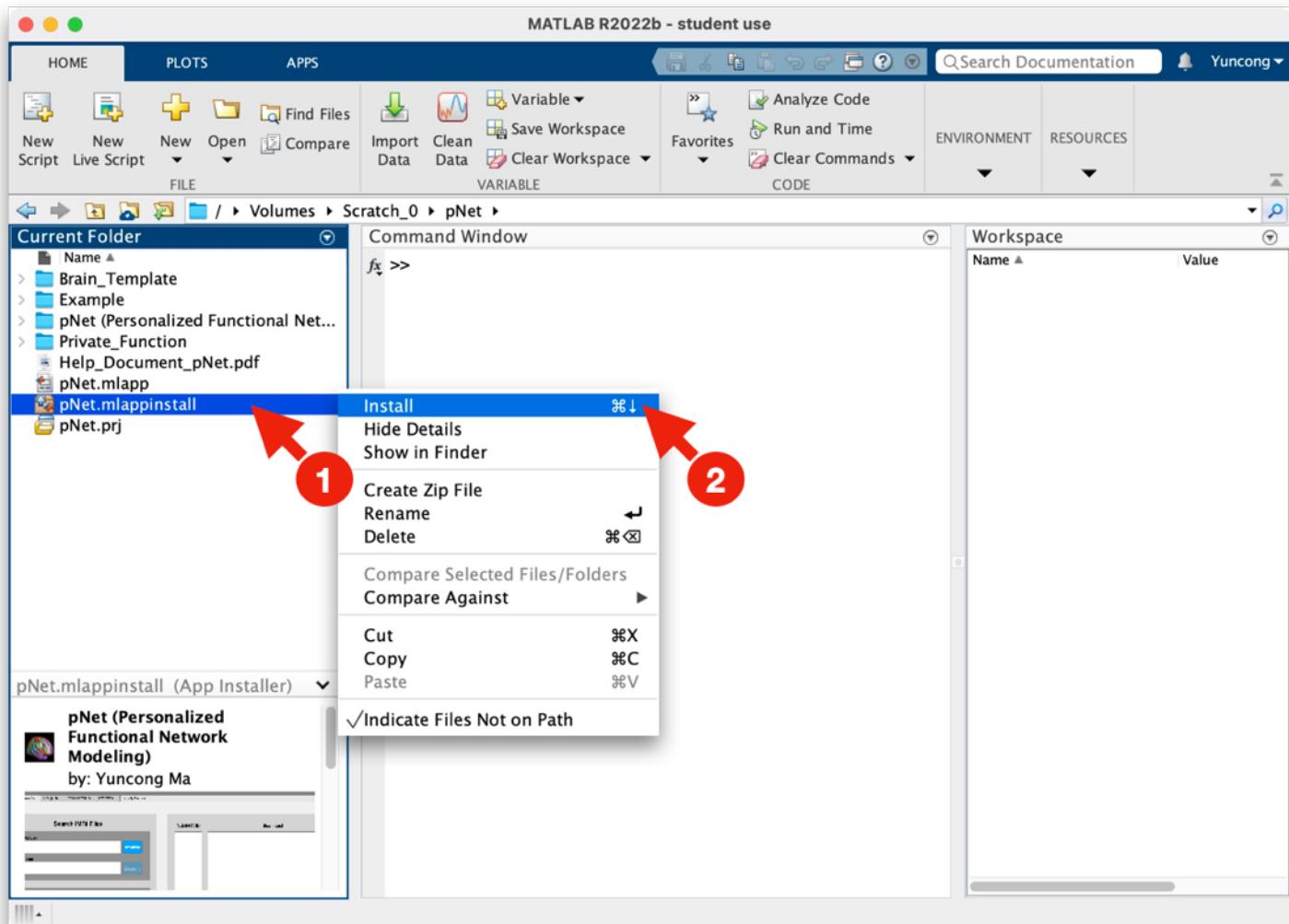


Run the pNet app.

(1-2) Open the pNet folder, and right click the pNet.mlapp, and click the run option.

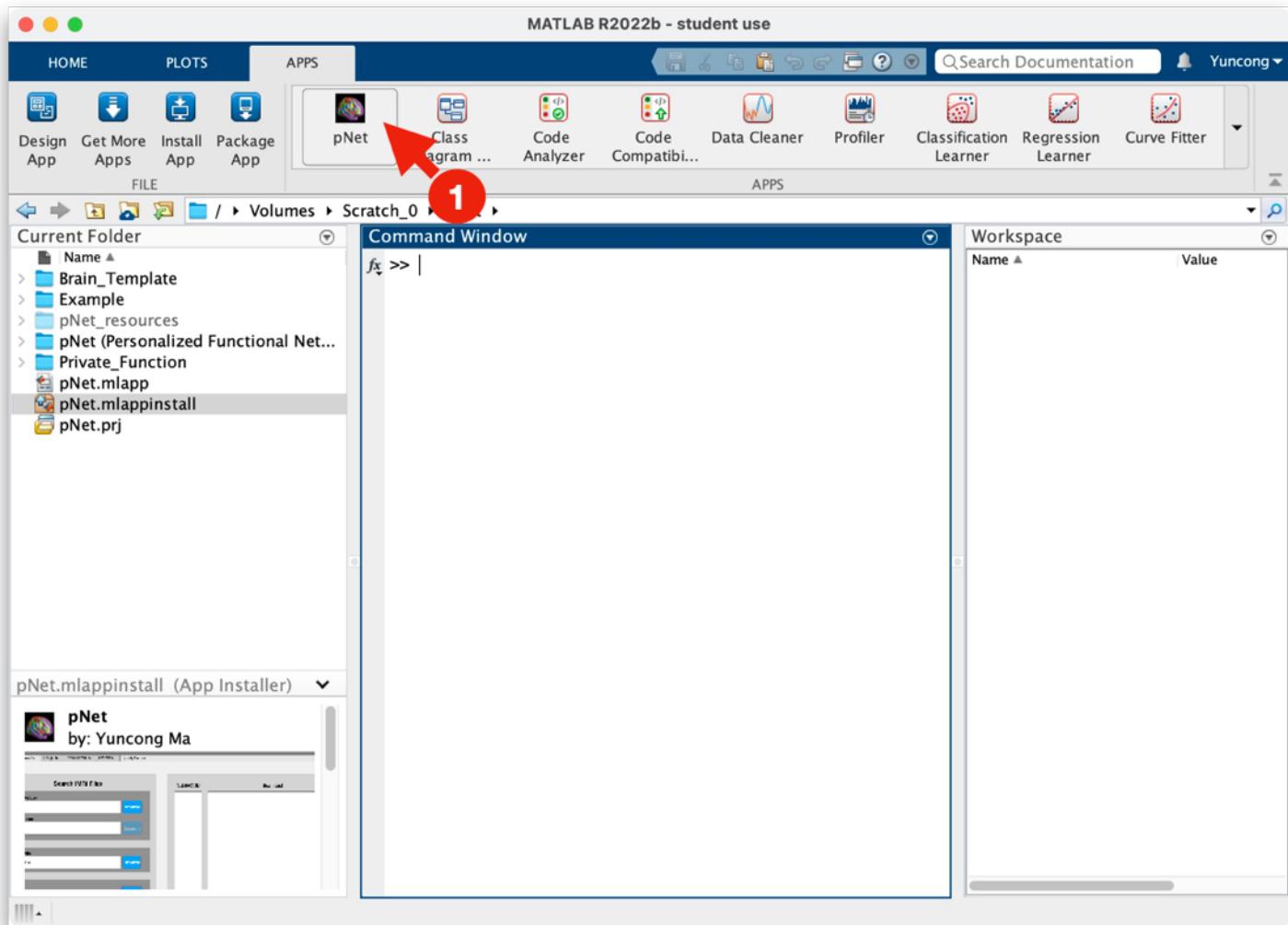
Install pNet as a MATLAB app.

This way will allow users to use the app without navigating to the app folder, or adding the app folder to the path.



Install the pNet app UI.

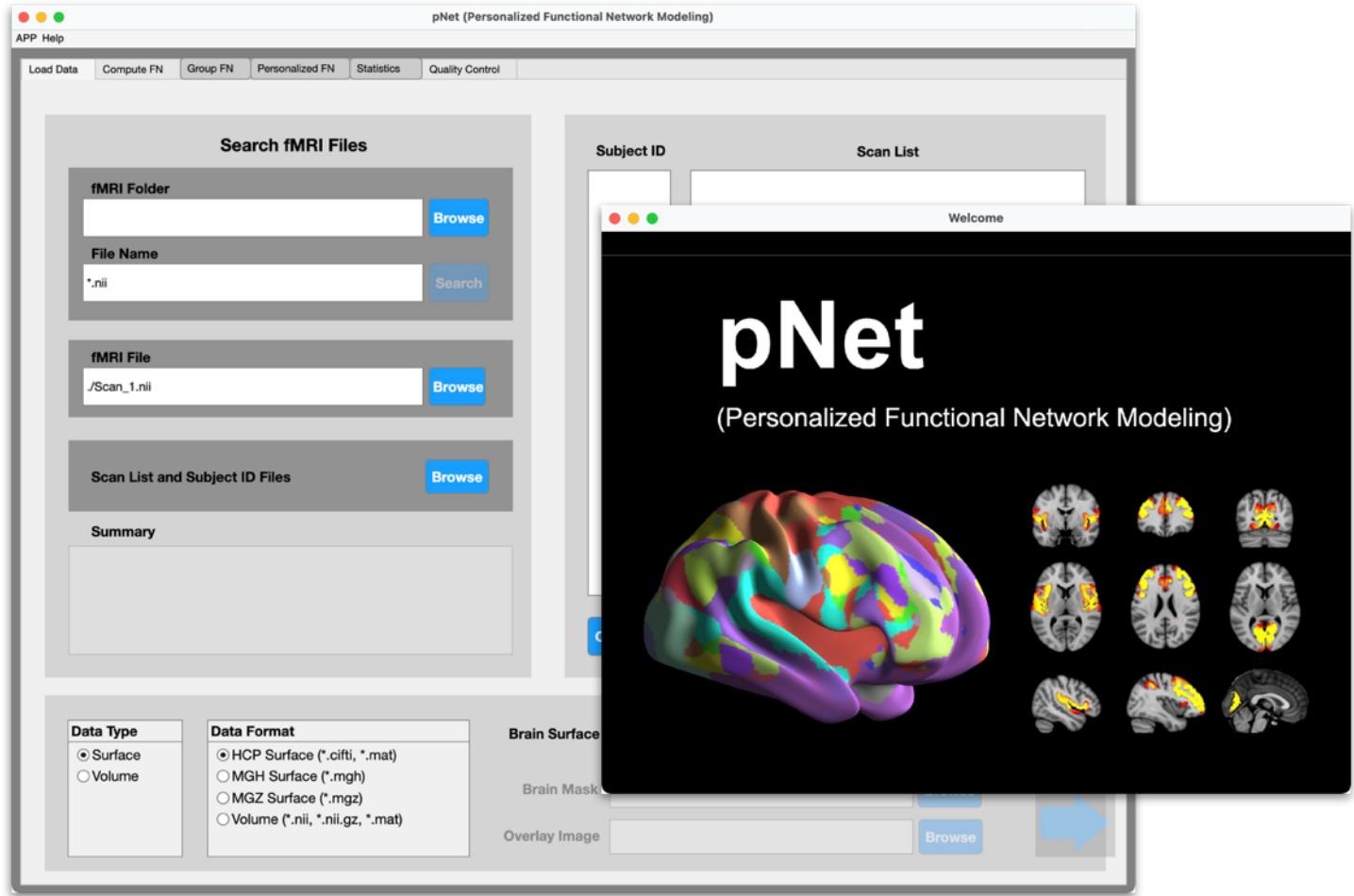
(1-2) Double click or right click on the file “pNet.mlappinstall” to install the software on MATLAB.



Run the pNet app from the APPS menu.

- (1) Open the APPS menu tab, and click on the pNet app.

Users will see a welcome page, and a main user interface (UI). The main UI contains multiple tabs on the top for different modules to setup the computation and visualization. Users could simply use the order from left to right to follow the workflow of this toolbox.



The app welcome page (right window with black background) and the main UI.

Run compiled pNet with MATLAB Runtime

There are two options to get a standalone software with or without the free MATLAB runtime software (<https://www.mathworks.com/products/compiler/matlab-runtime.html>). Several pre-compiled pNet versions are provided in the subfolder “Compiled_Runtime”. Download the version compatible to your computer’s operation system, and download and install the MATLAB runtime software. Double click the compiled pNet file (pNet.exe in Windows) to run the app. Details can be found in the README.txt in each subfolder containing the compiled pNet software.

Compile pNet as a standalone software

MATLAB (academic or commercial license) allows users to compile the source code with their modifications or preference of different MATLAB Runtime versions. Details can be found on MATLAB website: <https://www.mathworks.com/help/compiler/create-standalone-app-using-application-compiler-app.html>. When a MATLAB APP is deployed, some functions cannot be used, such as “addpath”. Also, the code will be operation-system dependent, if terminal command or other non-

MATLAB functions were used. This requires sufficient software development experience to ensure the compatibility. Some examples can also be found in the source code of pNet. Please check the startup function in the file pNet.mlapp.

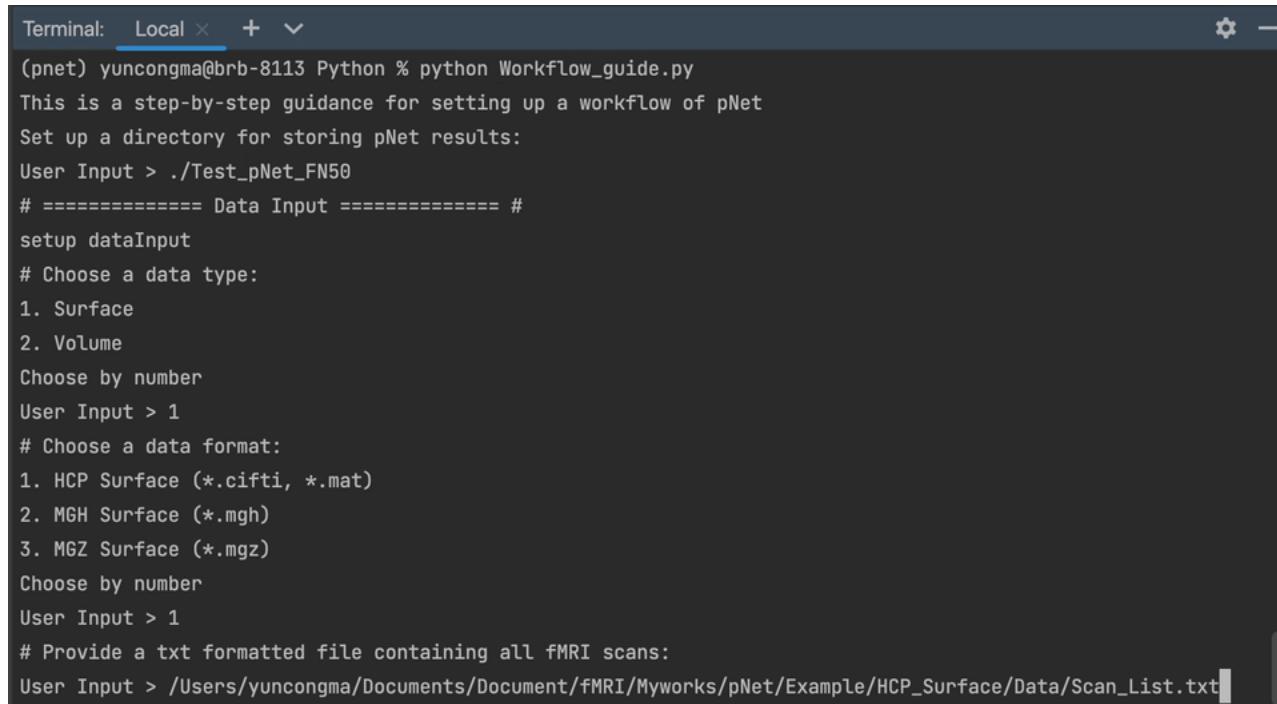
Run the Python version

The Python version can be executed on a local computer using PyCharm, VSCode or similar apps. It also has a server mode to interact with desired server environment for processing large datasets with multi-job execution capability.

pNet offers to a step-by-step guide to setup a workflow for running the Python version on a local computer. To do that, simply run the following terminal command in the conda environment.

```
$ python Workflow_guide.py
```

Users will be guided to type in the directory of the result folder, choose data type and so on.



The screenshot shows a terminal window titled "Terminal: Local". The window displays a step-by-step guide for setting up a workflow in pNet. The user is prompted to set up a directory for storing results, choose a data type (Surface or Volume), and a data format (HCP Surface, MGH Surface, or MGZ Surface). Finally, the user is asked to provide a txt formatted file containing all fMRI scans, with the path specified as "/Users/yuncongma/Documents/Document/fMRI/Myworks/pNet/Example/HCP_Surface/Data/Scan_List.txt".

```
Terminal: Local + ▾
(pnet) yuncongma@brb-8113 Python % python Workflow_guide.py
This is a step-by-step guidance for setting up a workflow of pNet
Set up a directory for storing pNet results:
User Input > ./Test_pNet_FN50
# ===== Data Input ===== #
setup dataInput
# Choose a data type:
1. Surface
2. Volume
Choose by number
User Input > 1
# Choose a data format:
1. HCP Surface (*.cifti, *.mat)
2. MGH Surface (*.mgh)
3. MGZ Surface (*.mgz)
Choose by number
User Input > 1
# Provide a txt formatted file containing all fMRI scans:
User Input > /Users/yuncongma/Documents/Document/fMRI/Myworks/pNet/Example/HCP_Surface/Data/Scan_List.txt
```

Screenshot of the step-by-step guide.

A Python script will be generated after finishing all required settings.

```

# Customized Python script for pNet workflow, built at 2023-10-05 10:29:26
# Generated by running python Workflow_guide()
# To run this python code, use the terminal command line below
# python ./Test_Workflow.py

## Load packages
import pNet
# setup and run a customized workflow
pNet.workflow_simple(
    dir_pnet_result='./Test_pNet_FN50',
    dataType='Surface',
    file_scan='/Users/yuncongma/Documents/Document/fMRI/Myworks/pNet/Example/HCP_Surface/Data/Scan_List.txt',
    dataFormat='HCP Surface (*.cifti, *.mat)',
    file_Brain_Template='/Users/yuncongma/Documents/Document/fMRI/Myworks/pNet/Brain_Template/HCP_Surface/Brain_Template.json',
    K=50,
    Combine_Scan=False
)

```

An example Python script generated by the step-by-step guide.

The Python version has a server mode, which has an example Python script (Example_Workflow_Server.py) for fast deployment.

The main difference of this script comparing to the workflow running on a local computer is the settings for the server environment. It includes the following inputs.

1. ‘dir_pnet’: directory of the pNet toolbox
2. ‘dir_env’: directory of the desired virtual environment, ex. ‘./anaconda3/envs/pnet’
3. ‘dir_python’: directory of the python in the virtual environment, ex. ‘./anaconda3/envs/pnet/bin/python’
4. ‘submit_command’: the command line to submit a bash job. In SGE system, ‘qsub’ is used to submit bash jobs to the server. An example SGE command is ‘qsub -terse -j y’. No space is required at the end of this command string.
5. ‘thread_command’: the command to specify the thread number for a bash job. In SGE system, it is ‘-pe threaded’. The thread number can be set to ‘4’ for a particular job, which will be set like ‘-pe threaded 4’ in the command line.
6. ‘memory_command’: the command to specify the memory request for a bash job. In SGE system, it is ‘-l h_vmem=’. The memory request can be set to ‘50G’ for a particular job, which will be set like ‘-l h_vmem=50G’ in the command line.
7. ‘log_command’: the command to specify the log file for a bash job. In SGE system, it is ‘-o’. The log file command line will be like ‘-o ./server_job_pFN.log’.

```

# Yuncong Ma, 12/5/2023
# A customizable pNet workflow in server mode
#
# ===== Terminal command ===== #
# Activate a conda env with required packages for running pNet
# $ source activate /cbica/home/mayun/.conda/envs/pnet
# Run the customized python script for a pNet workflow in server mode
# $ python /cbica/home/mayun/Projects/NiChart/Script/Workflow_OASIS_server.py

# basic python packages
import os
import sys

# ===== Server mode ===== #
# setup the directory of the pNet toolbox folder
dir_pnet = '/cbica/home/mayun/Projects/NiChart/pNet'
sys.path.append(os.path.join(dir_pnet, 'Python'))
import pNet

# get the directory of the Conda Python environment
dir_env = '~/.conda/envs/pnet'
dir_python = '~/.conda/envs/pnet/bin/python'

# Setup server commands
submit_command = 'qsub -terse -j y'
thread_command = '-pe threaded '
memory_command = '-l h_vmem='
log_command = '-o '

```

Screen shot of the example Python script to run a pNet workflow in server mode.

Data Input

This chapter provides guidelines to search and organize fMRI can files, load brain template files.

Search for fMRI files

Users need to firstly select the data type and data format.

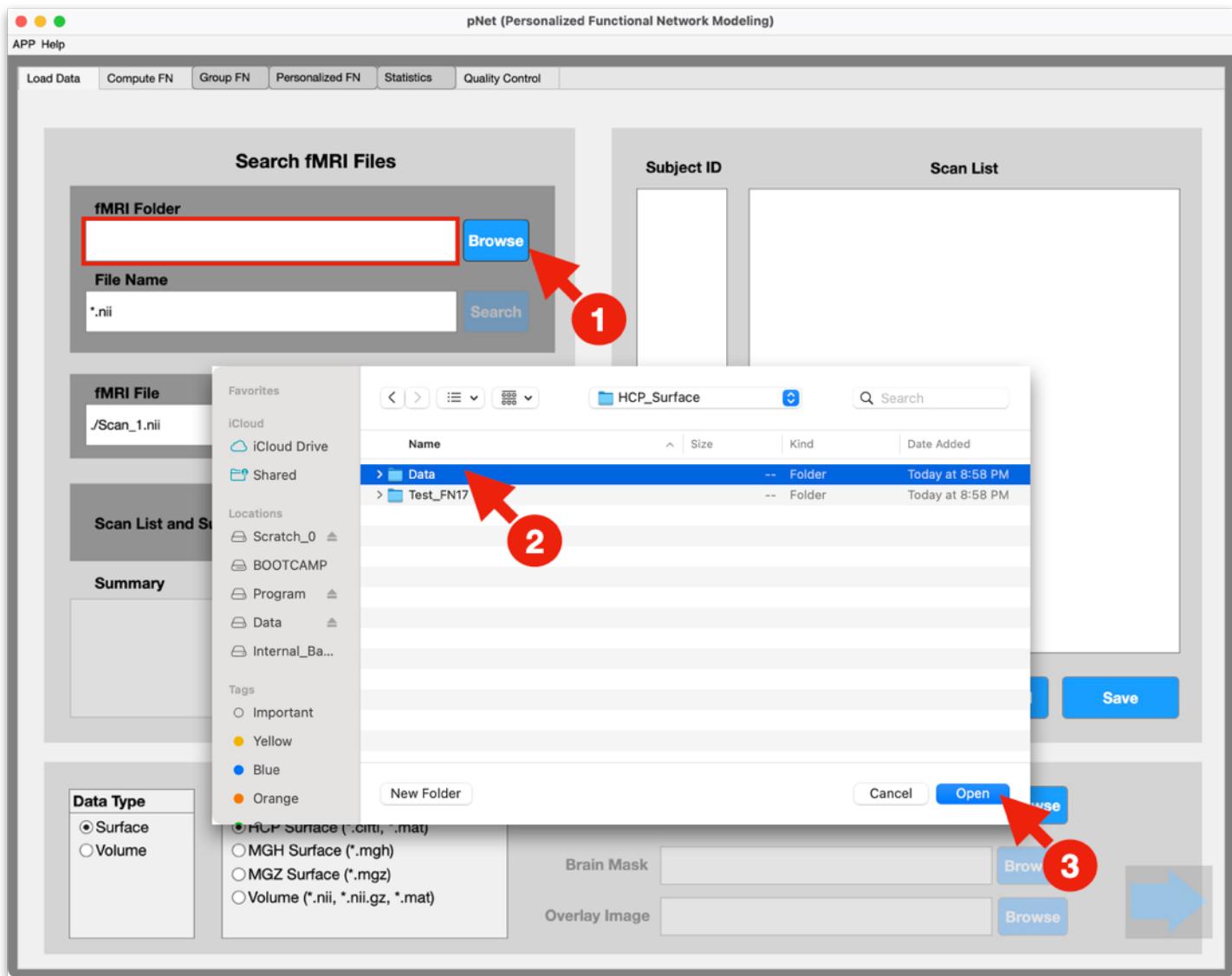
The screenshot shows the 'Search fMRI Files' section of the pNet application. On the left, there are three main input fields: 'fMRI Folder' (with a 'Browse' button), 'File Name' (containing '.nii' with a 'Search' button), and 'fMRI File' (containing '/Scan_1.nii' with a 'Browse' button). Below these is a 'Scan List and Subject ID Files' field with a 'Browse' button. To the right, there are two columns: 'Subject ID' and 'Scan List'. At the bottom are four buttons: 'Clear List', 'Keep Selected', 'Remove Selected', and 'Save'. At the very bottom, there are two dropdown menus: 'Data Type' (with 'Surface' selected) and 'Data Format' (with 'HCP Surface (*.cifti, *.mat)' selected). Red arrows point from the numbers 1 and 2 to the 'Data Type' and 'Data Format' dropdowns respectively. To the right of these dropdowns are three more input fields: 'Brain Surface' (with a 'Browse' button), 'Brain Mask' (with a 'Browse' button), and 'Overlay Image' (with a 'Browse' button). A large blue arrow points to the right at the bottom right of the screen.

Select the data type and format.

- (1) Select the data type.
- (2) Select the data format.

The toolbox offers three ways to find fMRI scan files.

1. Search fMRI files based on their extension in a folder.

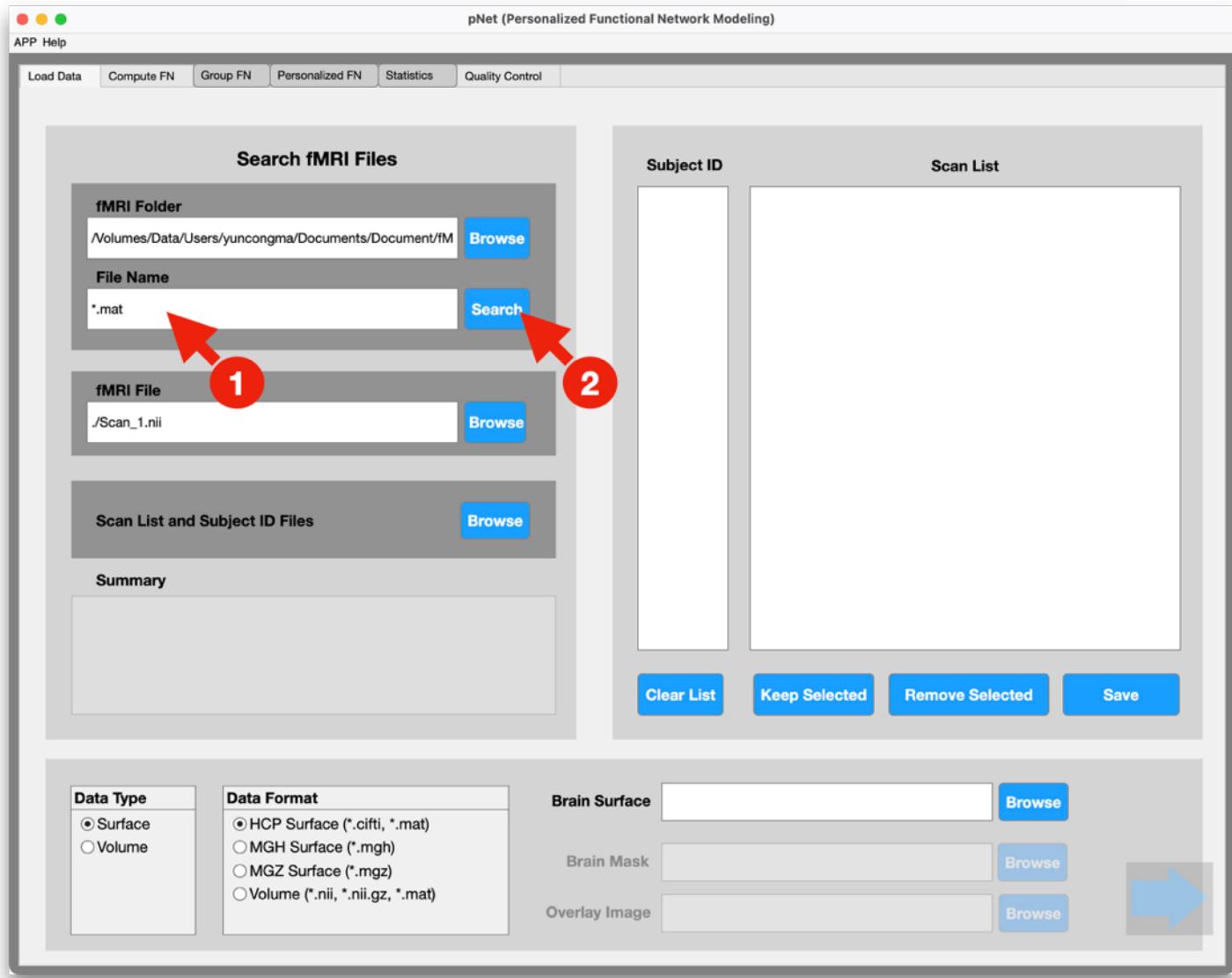


Select the data folder.

(1) Click browse button to open the folder selection window.

(2) Select the folder, and click the open button

(3) to finish the folder selection. The full folder directory information will appear in the white input field (highlighted in the red box). Users can also type in the full folder directory into the white input field (highlighted in the red box).



Setup the file extension information.

- (1) Specify the file extension, such as “*.mat” or “*.nii.gz”.
- (2) Click search button to perform file searching function.

pNet (Personalized Functional Network Modeling)

APP Help

Load Data Compute FN Group FN Personalized FN Statistics Quality Control

Search fMRI Files

fMRI Folder
 Browse

File Name
 Search

fMRI File
 Browse

Scan List and Subject ID Files **Browse**

Summary
 Find 20 fMRI scans
 Find 10 subjects or subject folders
 Subject has 2 - 2 fMRI scans
 Subject has 2 fMRI scans on average

Subject ID	Scan List
100206	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
100206	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
100307	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
100307	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
100408	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
100408	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
100610	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
100610	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101006	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101006	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101107	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101107	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101309	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101309	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101410	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101410	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101915	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
101915	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
102008	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res
102008	/Volumes/Data/Users/uncongma/Documents/Document/fMRI/Myworks/NMF/Res

Clear List **Keep Selected** **Remove Selected** **Save**

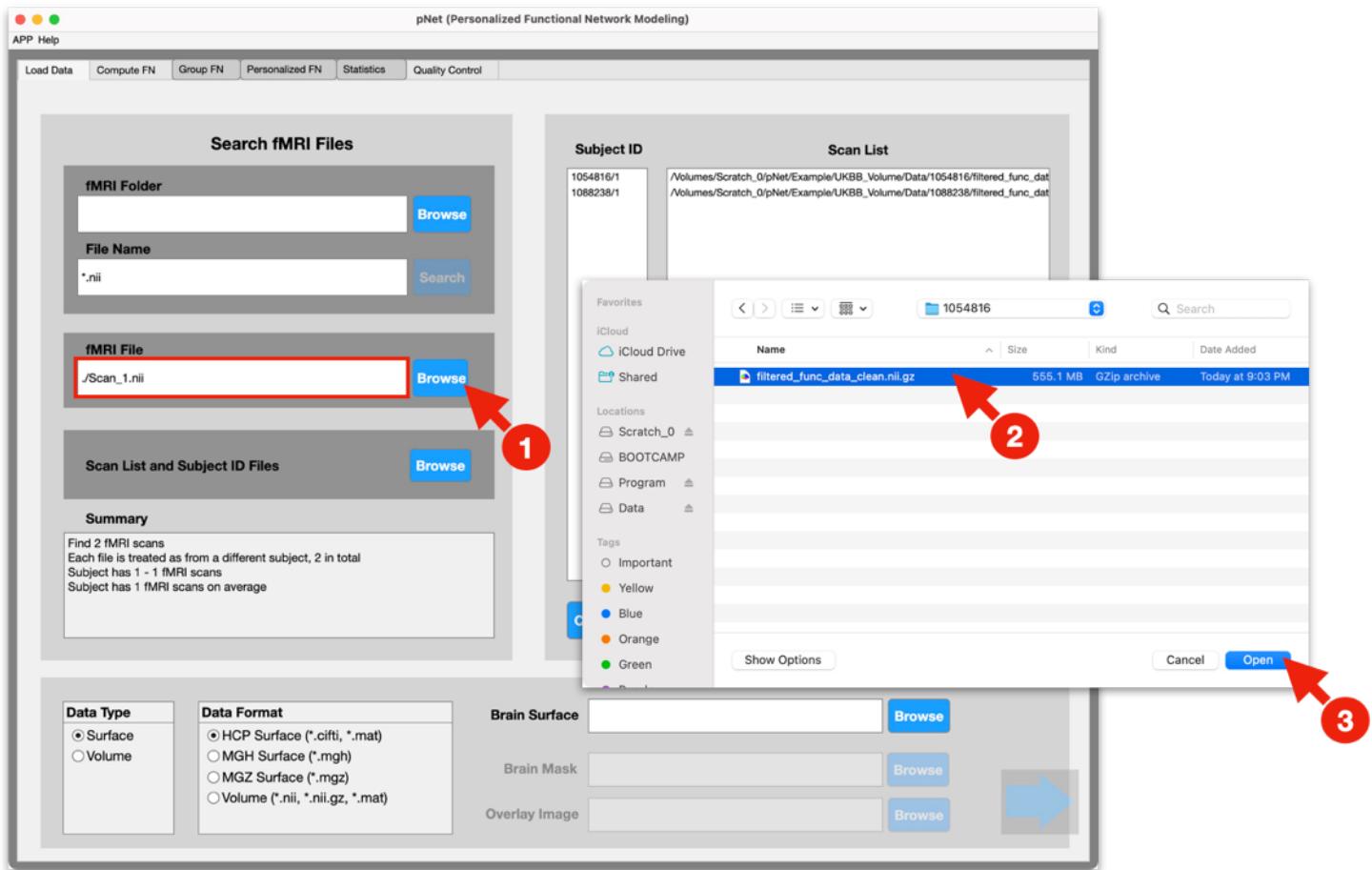
Data Type
 Surface
 Volume

Data Format
 HCP Surface (*.cifti, *.mat)
 MGH Surface (*.mgh)
 MGZ Surface (*.mgz)
 Volume (*.nii, *.nii.gz, *.mat)

Brain Surface **Browse**
Brain Mask **Browse**
Overlay Image **Browse**

Check the summary and navigate through the extracted subject ID and corresponding file directory. Summary module highlighted in the red box shows the total number of files, the range of file number per subject, average file number per subject. Error messages will also be shown if there is any.

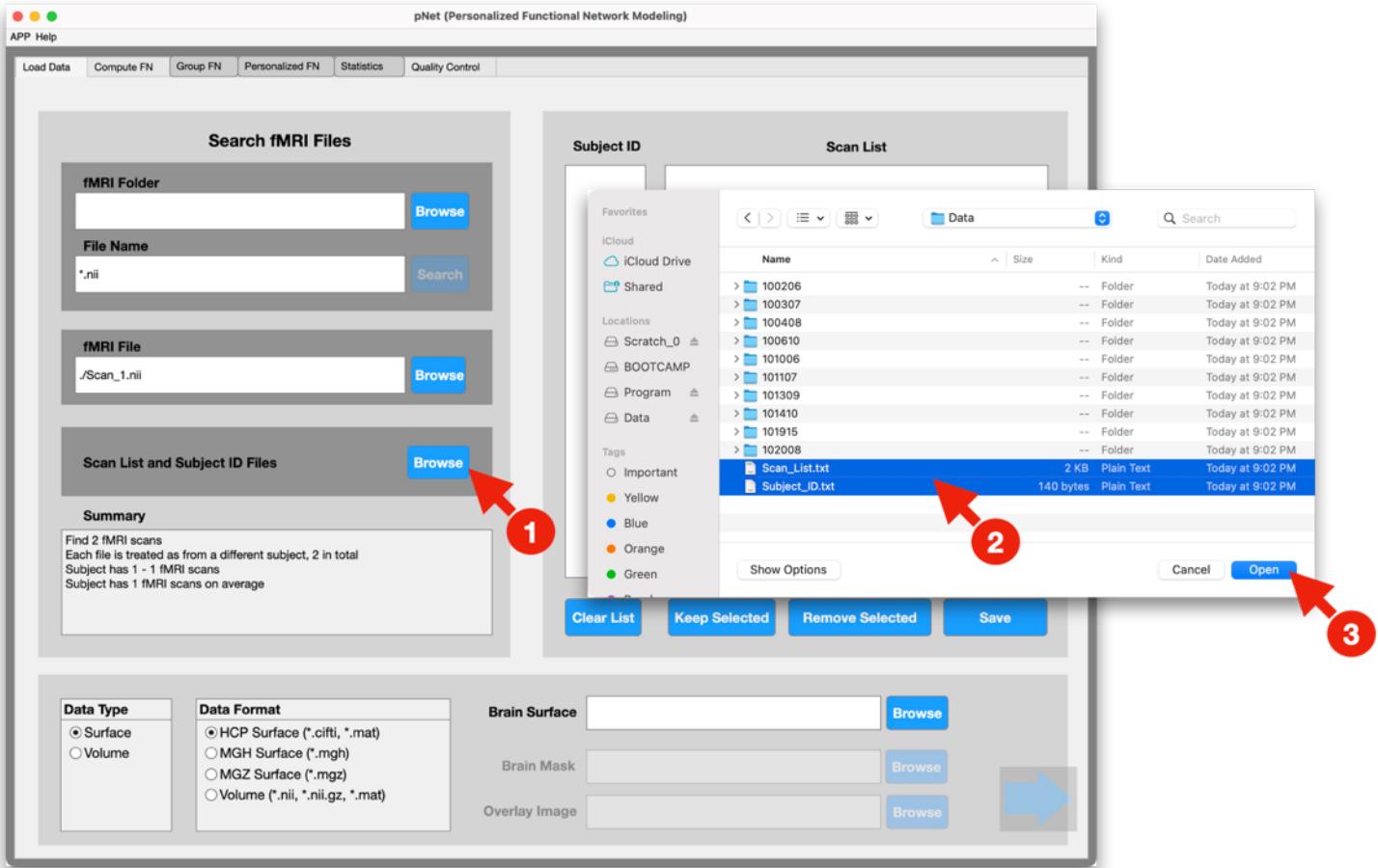
2. Select fMRI files



Select fMRI files.

- (1) Click the browse button.
- (2) Manually select one or multiple fMRI files with supported extensions, and click the open button
- (3) to load the full file directories. Users can also use the input field (highlighted in the red box) to type in the full file directories.

3. Load prepared file list information in txt format.

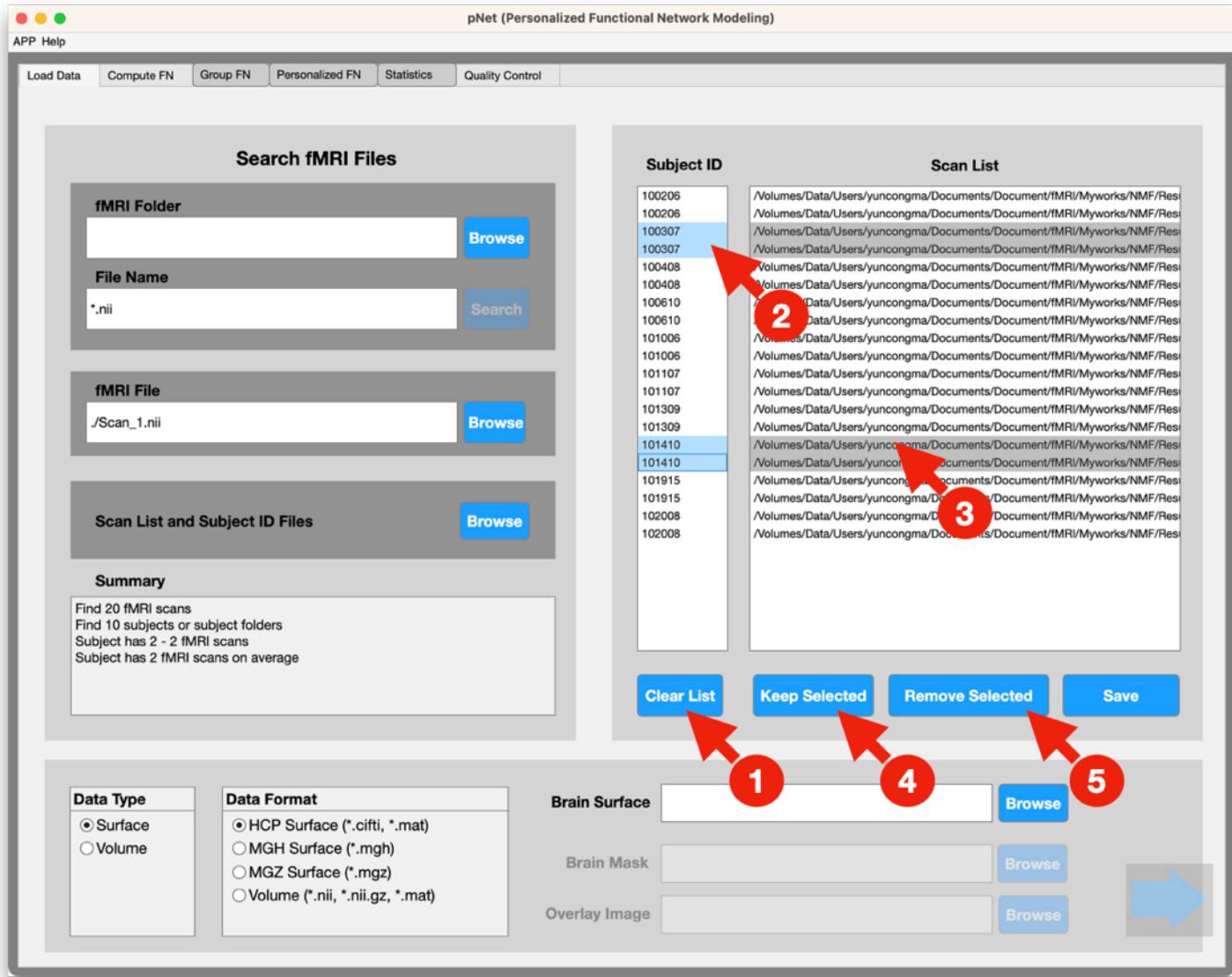


Load fMRI scan list and subject ID files.

- (1) Click the browse button.
- (2) Choose the text file containing full directories of fMRI scan files, and another text file containing subject ID information for each corresponding fMRI scan. The subject ID information file is not necessary. When it is not provided, automatic subject ID information will be extracted.
- (3) Click the open button to read those files.

Organized fMRI scan files

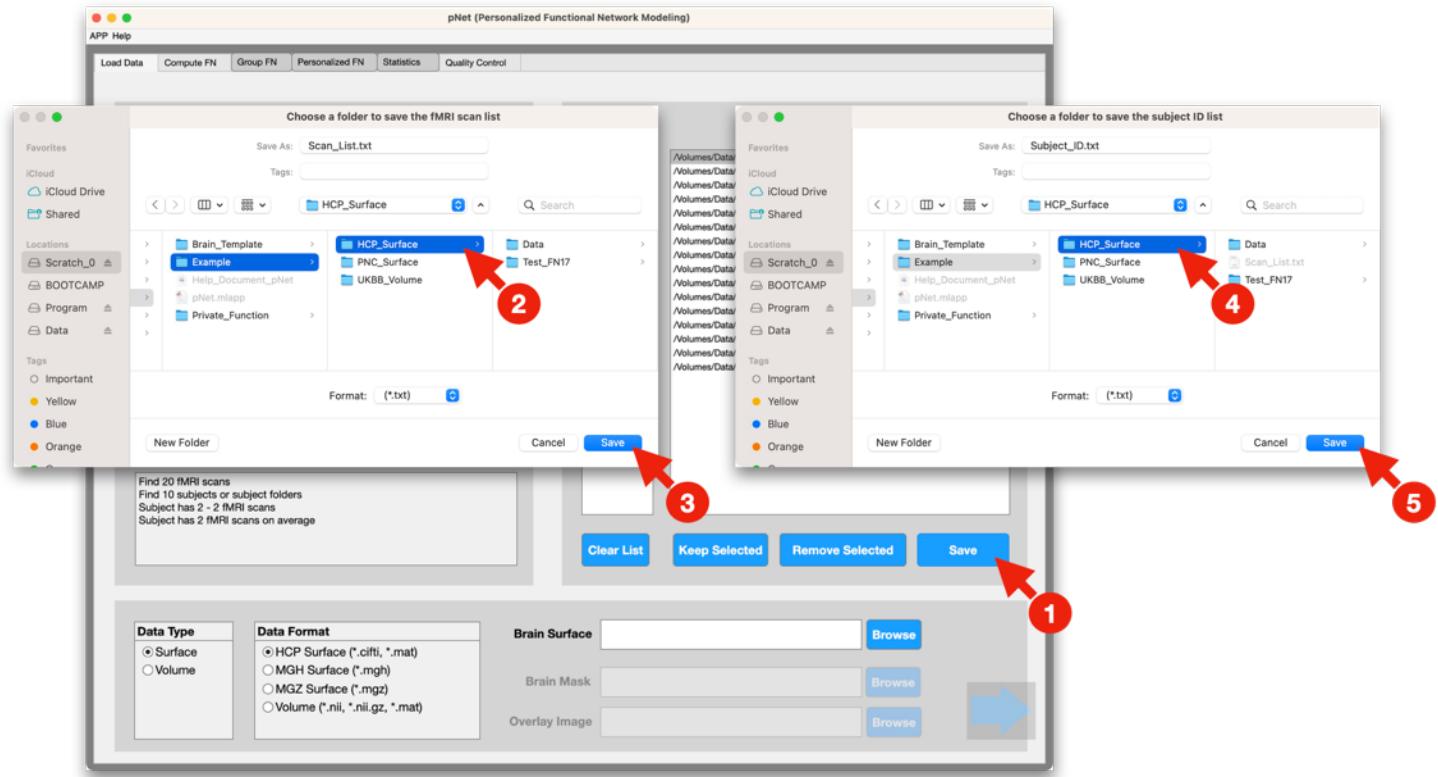
1. Clear, select or remove fMRI scan files



Remove, select or remove fMRI scan files.

- (1) Click the clear list button to empty the subject ID and scan list.
- (2-3) Select one or multiple files (hold command key in macOS, or hold control key in Windows and Linux) based on their subject ID or scan list.
- (4) Keep the selected fMRI scan files.
- (5) Remove selected fMRI scan files.

2. Save the fMRI scan list and subject ID information into text files



Save the subject ID and scan list information into text files.

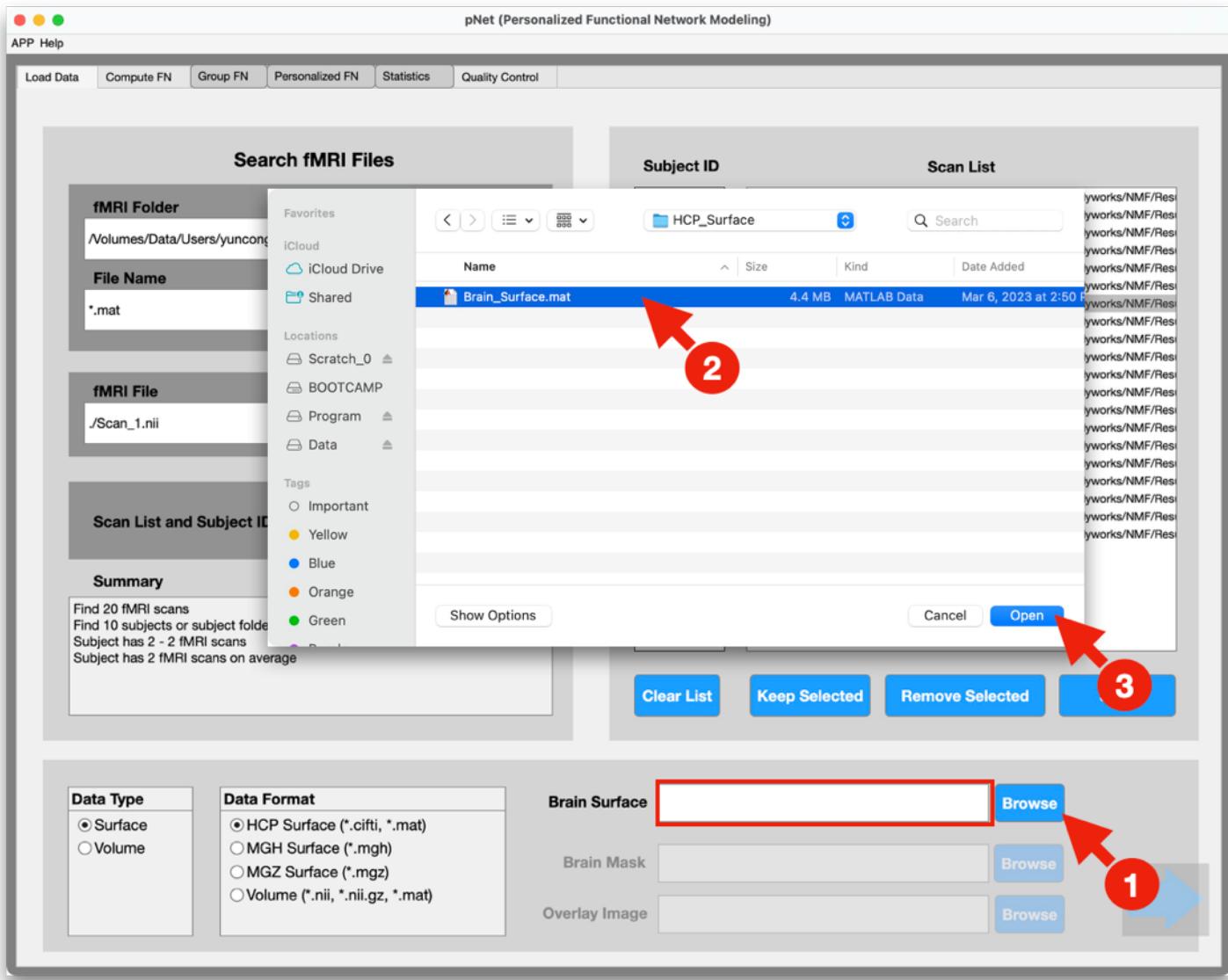
- (1) Click the save button. A new window will be promoted for saving the scan list.
- (2) Select the folder to store the scan list file with the name “Scan_List.txt” in default.
- (3) Click the save button to save the scan list file.
- (4) Select the folder to store the scan list file with the name “Subject_ID.txt” in default.
- (5) Click the save button to save the subject ID file.

Load brain template

Surface and volume data types require different brain template files for both computation and visualization of group-level and personalized FNs.

1. Surface data type.

It requires to load a file called “Brain_Surface.mat”. This file a variable named as “Brain_Surface” with three fields: “Shape”, “Shape_Inflated”, “MW”.

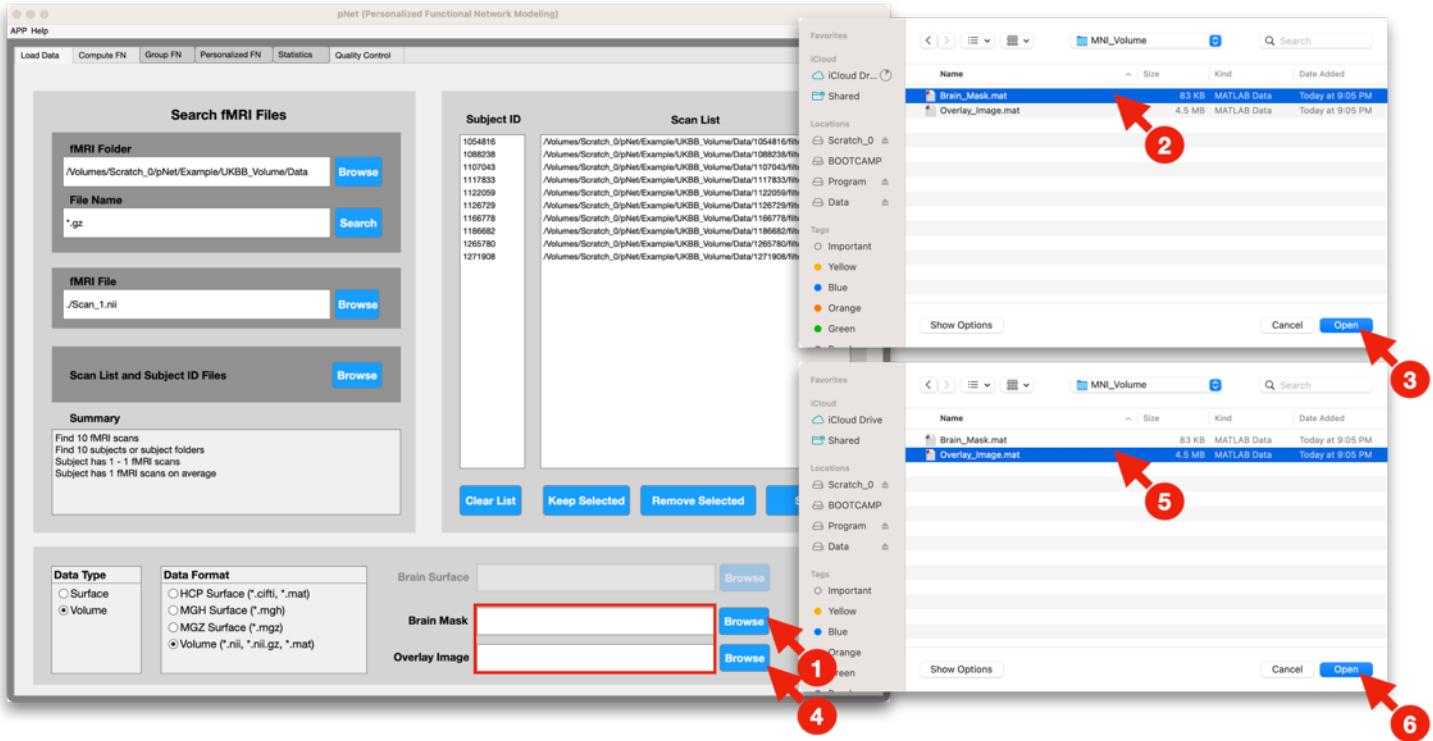


Load the brain surface file for surface data type.

- (1) Click the browse button.
- (2) Select the file “Brain_Surface.mat”.
- (3) Click open or double click the file to load it. Full file directory of the brain surface file will appear in the input field (highlighted in the red box). Users can also type in this information directly into the input field.

2. Volume data type.

It requires to load two files: “Brain_Mask.mat” and “Overlay_Image.mat”. The brain mask file is a binarized 3D mask to specify voxels to contain useful fMRI signals. The overlay image is a 3D image file that will be used as a background for overlaying group-level and personalized FNs.



Load brain templates for the volume data type.

- (1) Click the browse button to load brain mask file, or use the input field (highlighted in the red box) to type in the full directory of the brain mask file. Example files can be found in the toolbox subfolder “/Brain_Template/MNI_Volume/Brain_Mask.mat”.
- (2-3) Select the brain mask file, and click open button to load.
- (4) Click the browse button to load the overlay image file, or use the input field (highlighted in the red box) to type in the full directory of the overlay image file. Example files can be found in the toolbox subfolder “/Brain_Template/MNI_Volume/Overlay_Image.mat”.
- (5-6) Select the overlay image file, and click open button to load.

FN Computation

Personalized FN models

This module is designed to facilitate the setup and carry out the computation of personalized FNs. In particular, pNet computes the personalized FNs with either SR-NMF or GIG-ICA, both of them yielding personalized FNs that are regularized with group-level FNs for establishing spatial correspondence across individuals (Cui et al., 2020; Du and Fan, 2013; Li et al., 2016; Li et al., 2017).

For GIG-ICA, any group ICA methods can be used to compute the group-level FNs for guiding the computation of the personalized FNs, such as GIFT and MELODIC (Beckmann and Smith, 2004; Calhoun et al., 2009), and then the group-level FNs can be used as guidance information for computing the personalized FNs (Du and Fan, 2013).

For SR-NMF, the personalized FNs are computed jointly for a group of subjects regularized by group sparsity (Li et al., 2016; Li et al., 2017). However, such a joint computation of personalized FNs does not scale well to large scale datasets due to its prohibitive computational memory usage (fMRI data of all scans have to be considered simultaneously). To improve its scalability, SR-NMF has been extended with the similar strategy of GIG-ICA to compute the personalized FNs with regularization information provided by group-level FNs, which can be computed using a bootstrapping strategy by sampling the large datasets (Cui et al., 2020). Specifically, we concatenated a subset of fMRI scans (100 in default) from randomly selected subjects along the time dimension and employed the spatial-regularized NMF method to compute its FNs. This process was repeated multiple times to generate a set of FNs from different subsets. We then applied the normalized cut clustering method to fuse these FNs, obtaining robust group-level FNs. Subsequently, these group-level FNs were used as the initial spatial component to compute personalized FNs. The temporal component of each FN was estimated using a weighted average of the fMRI signal based on its spatial component. Personalized FNs were obtained for each subject or scan by optimizing the NMF objective function, with a spatial correspondence constraint ensuring that personalized FNs spatially align with their group-level counterparts. We present the basic concepts of the NMF-based fMRI signal decomposition and the spatial correspondence constraint below.

Given an fMRI dataset containing n subjects (this can also be scans, if multiple scans are not combined for each subject), each subject has a temporally concatenated fMRI scan noted as $X^i \in R^{T \times S}, i = 1, \dots, n$, where T is the number of time points, and S is the number of spatial nodes (voxel for volume data type, and vertex for surface data type). For K FNs, their spatial and temporal components are both nonnegative, and noted as below.

$$V^i = (V_{s,k}^i) \in R^{S \times K} \quad (1)$$

$$U^i = (\mathbf{U}_{s,k}^i) \in R^{T \times K} \quad (2)$$

For each subject, its fMRI data can be decomposed as a multiplication of U and V with a white noise term.

$$\begin{aligned} X^i &\approx U^i(V^i)' + E^i, E^i \sim N(0, \sigma I), \\ s.t. \quad &U^i, V^i \geq 0, \forall 1 \leq i \leq n \end{aligned} \quad (3)$$

The initialization of personalized FNs using group-level FNs speeds up the convergence of personalized FNs, as well as encouraging the spatial similarity between them. However, there are rare cases in which several personalized FNs may have higher spatial similarity to other group-level FNs. Specifically, for the k -th personalized FN of subject i , it is deemed to have the highest spatial correspondence to its group-level counterpart than others. This can be computed as follows.

$$\Delta Sim_{i,k} = Corr(FN_{i,k}^p, FN_k^g) - \max_{j, j \neq k} Corr(FN_{i,k}^p, FN_j^g) \quad (4)$$

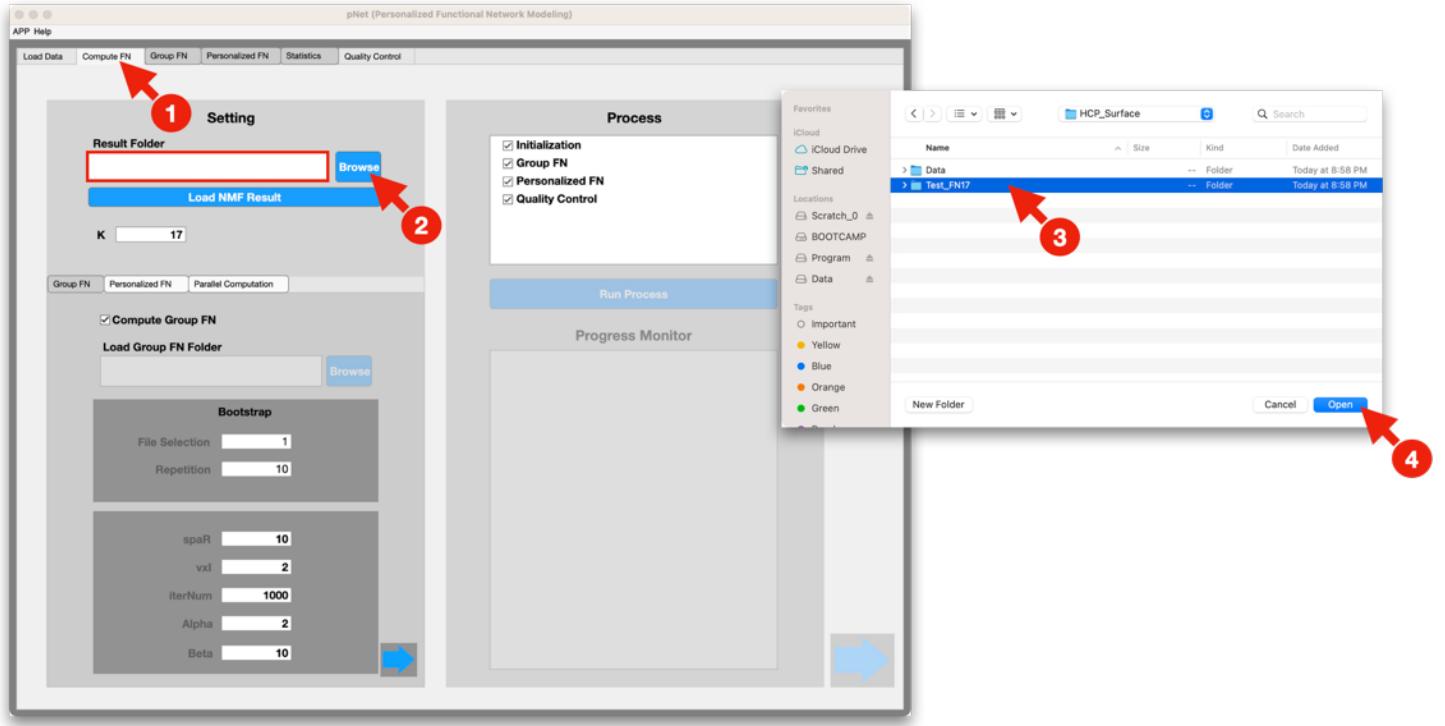
Where $\Delta Sim_{i,k}$ is the difference of spatial similarity between the personalized FN ($FN_{i,k}^p$) and its corresponding group-level counterpart FN_k^g , and the maximum spatial similarity between the personalized FN ($FN_{i,k}^p$) and other group-level FNs FN_j^g . If $\Delta Sim_{i,k} > 0$, this personalized FN has higher spatial similarity to its corresponding counterpart. If this holds true for all personalized FNs, the spatial correspondence is ensured. The formula for quality control for a single subject fMRI data is noted below.

$$QC_i = \min_k \Delta Sim_{i,k} \quad (5)$$

We have embedded quality control within the computation of personalized FNs to assure the spatial correspondence between group-level and personalized counterparts, thus eliminating potential discrepancies between them. This criterion is enforced during the iterative update of U and V. Specifically, at the end of each iteration, the spatial correspondence is assessed. If the criterion is not satisfied, the results from the previous iteration will be utilized as the final results. Otherwise, the iteration continues until either the maximum number of iterations is reached or the changes in the objective function become negligible.

Setup result folder

The toolbox store all the fMRI file information, brain template files, results and figures of group-level and personalized FN, and other files in one result folder. The fMRI files will not be stored in the result folder to save storage space.

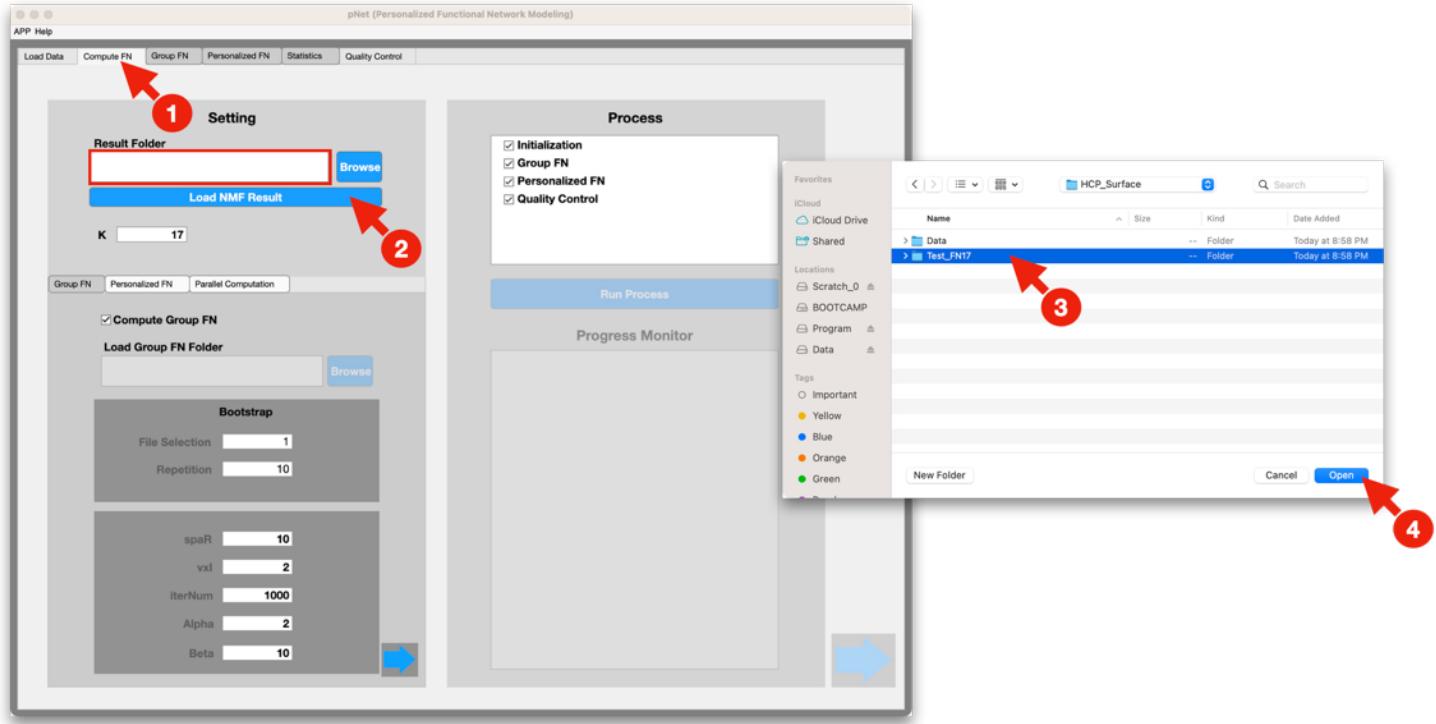


Select the result folder.

- (1) Navigate to the module “Compute FN”.
- (2) Click the browse button to select the result folder, or type in the full directory of the desired result folder.
- (3-4) Select the folder to store result, and click open button.

Load pre-computed results

The toolbox can automatically load pre-computed results for convenience. Users just need to simply select the result folder, all the information including fMRI scan file and subject ID, number of FNs, parameters of personalized FN computation will appear on the user interface.



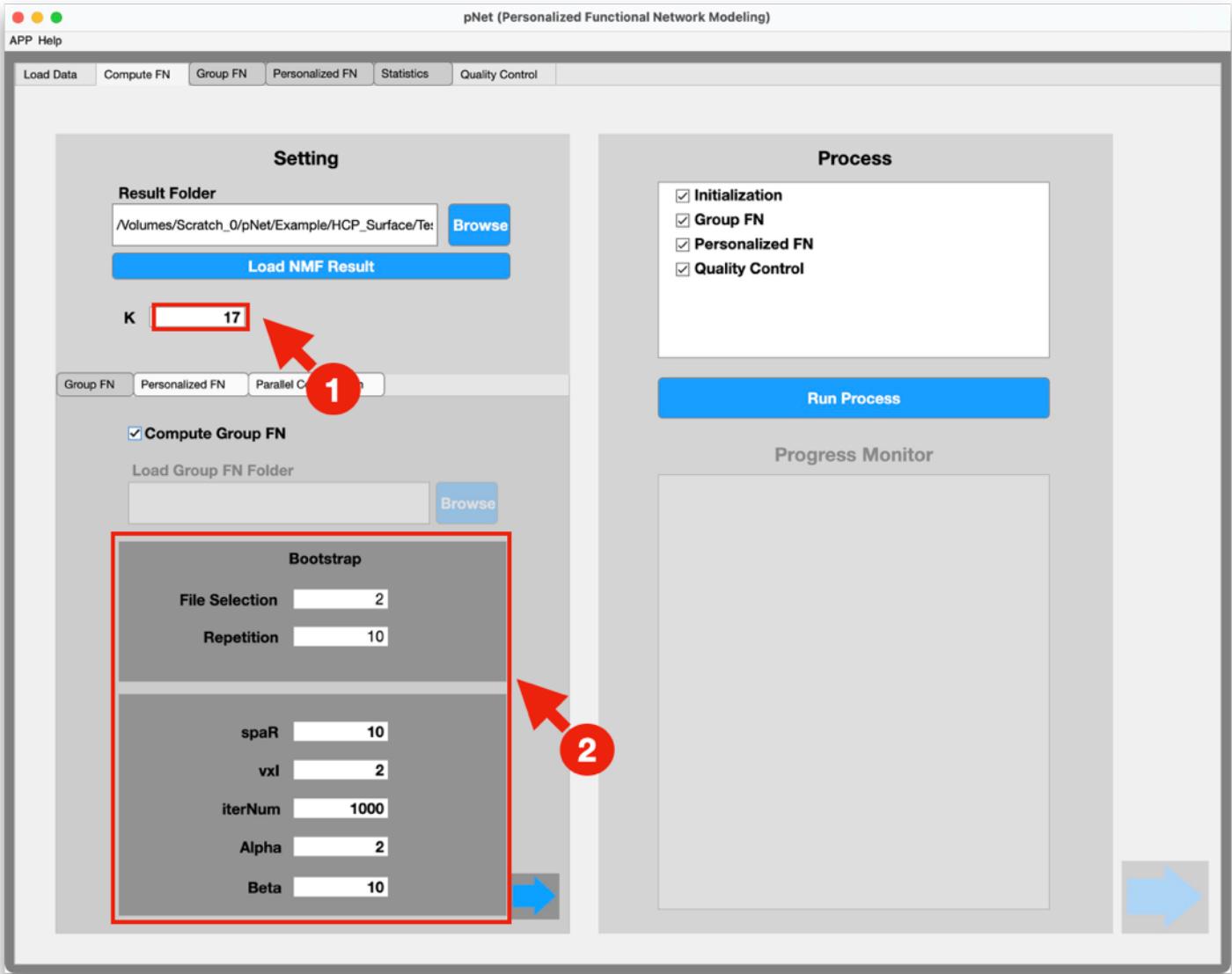
Select the folder containing precomputed results.

- (1) Navigate to the module “Compute FN”.
- (2) Click the browse button to select the result folder, or type in the full directory of the desired result folder (highlighted in the red box).
- (3-4) Select the folder to store result, and click open button. The toolbox will automatically check the integrity of the result folder. Then it will load results and jump to the group FN module to show precomputed group FN figures.

Setup group-level FN

The toolbox allows users to either load a precomputed group-level FN or perform the group-level FN computation using the data available.

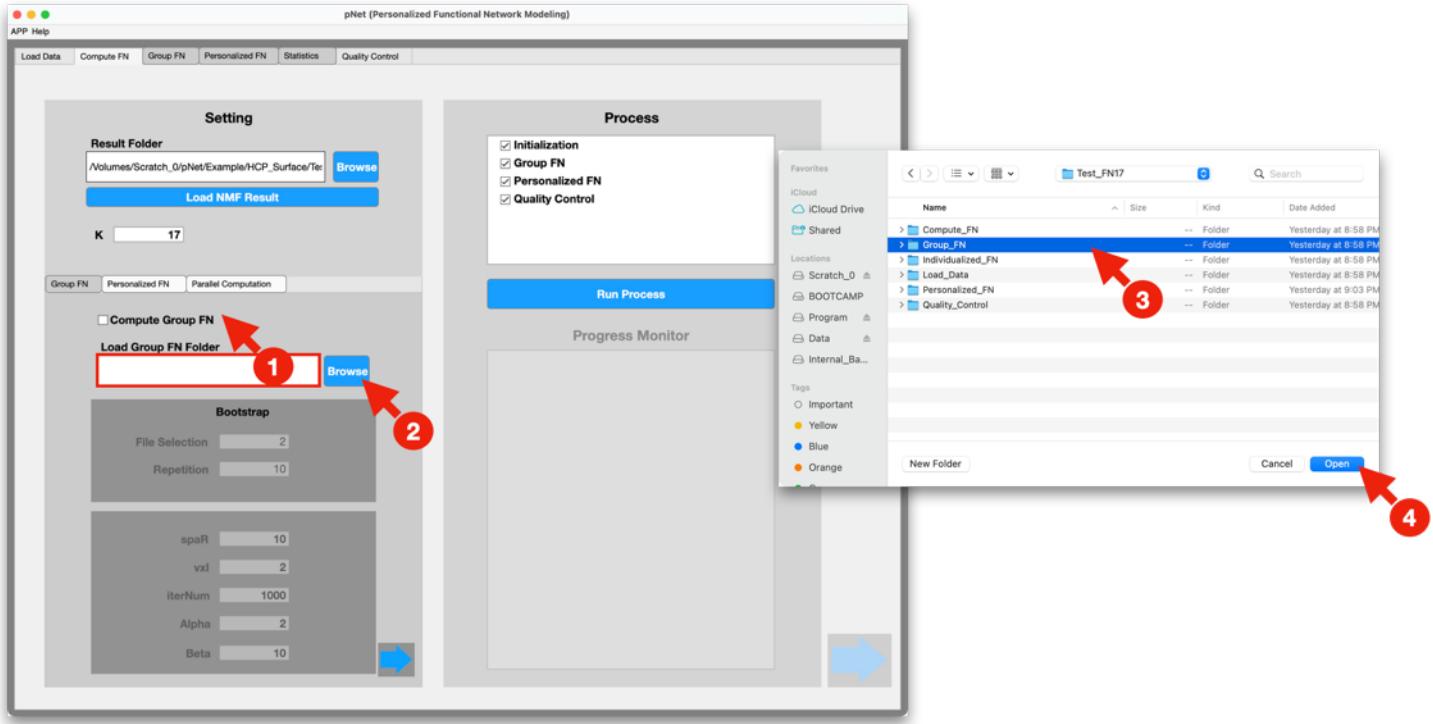
1. Setup the group-level FN computation



Setup the group-level FN computation parameters.

- (1) Set a desired number of FNs. 7 and 17 have been widely used to get large scale FNs.
- (2) Set additional parameters if preferred. The bootstrap section has two parameters that affect how the fMRI scans will be randomly sampled. The parameter "File Selection" is the number of fMRI scans will be selected as a subset to compute group-level FNs. The parameter "Repetition" is the number of runs to randomly sample a small subset and get multiple different versions group-level FN to fuse into a robust estimation of group-level FNs. Other parameters are for advanced users. Their details can be found in the manuscript.

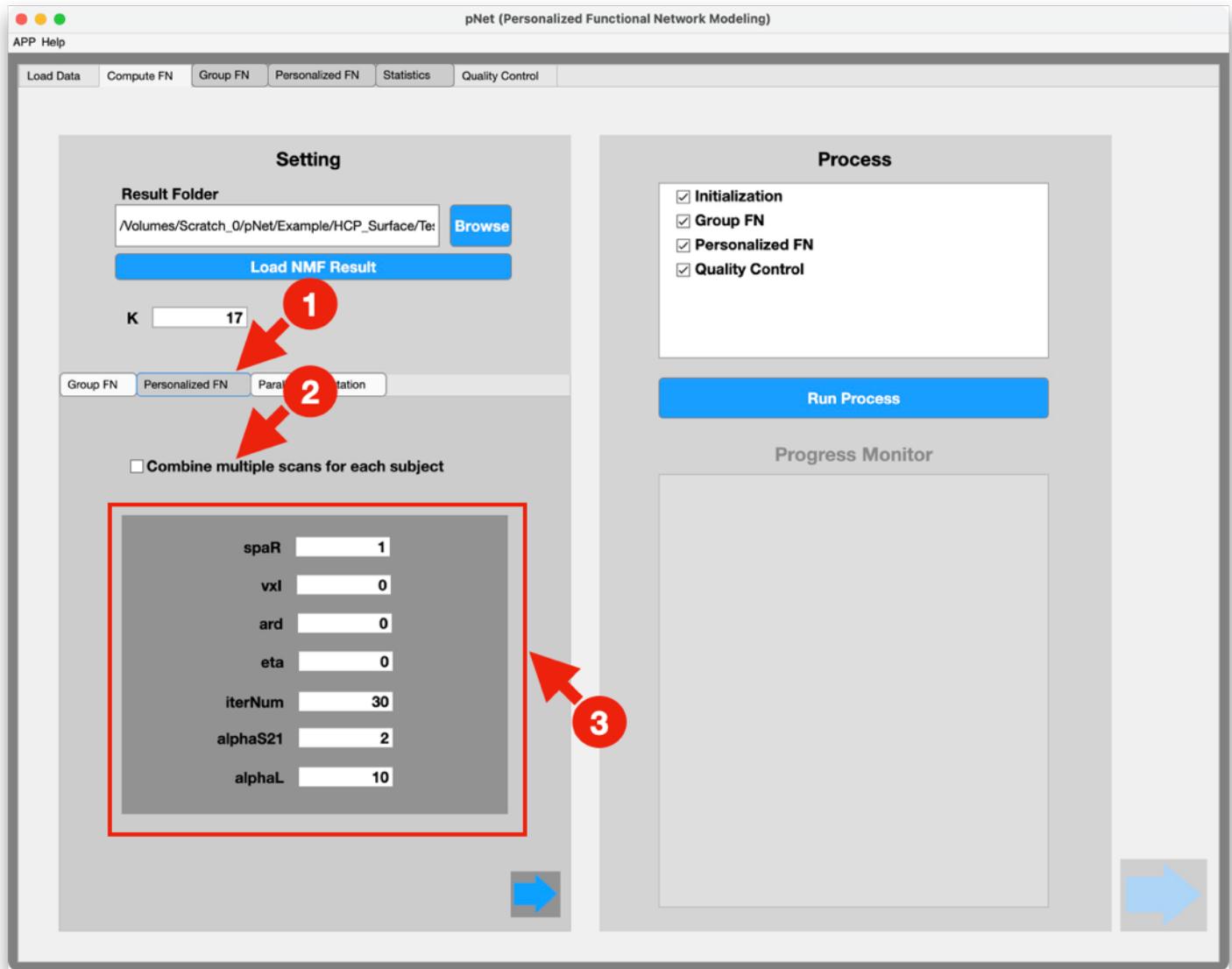
2. Load a precomputed group-level FN file



Load precomputed group-level FN results in a folder.

- (1) Click the check box “Compute Group FN” to disable the group-level FN computation.
- (2) Click the browse button or type in the directory of the folder containing group FN results in the input field (highlighted in the red box).
- (3-4) Select the group-level FN folder, and click open button to load the result.

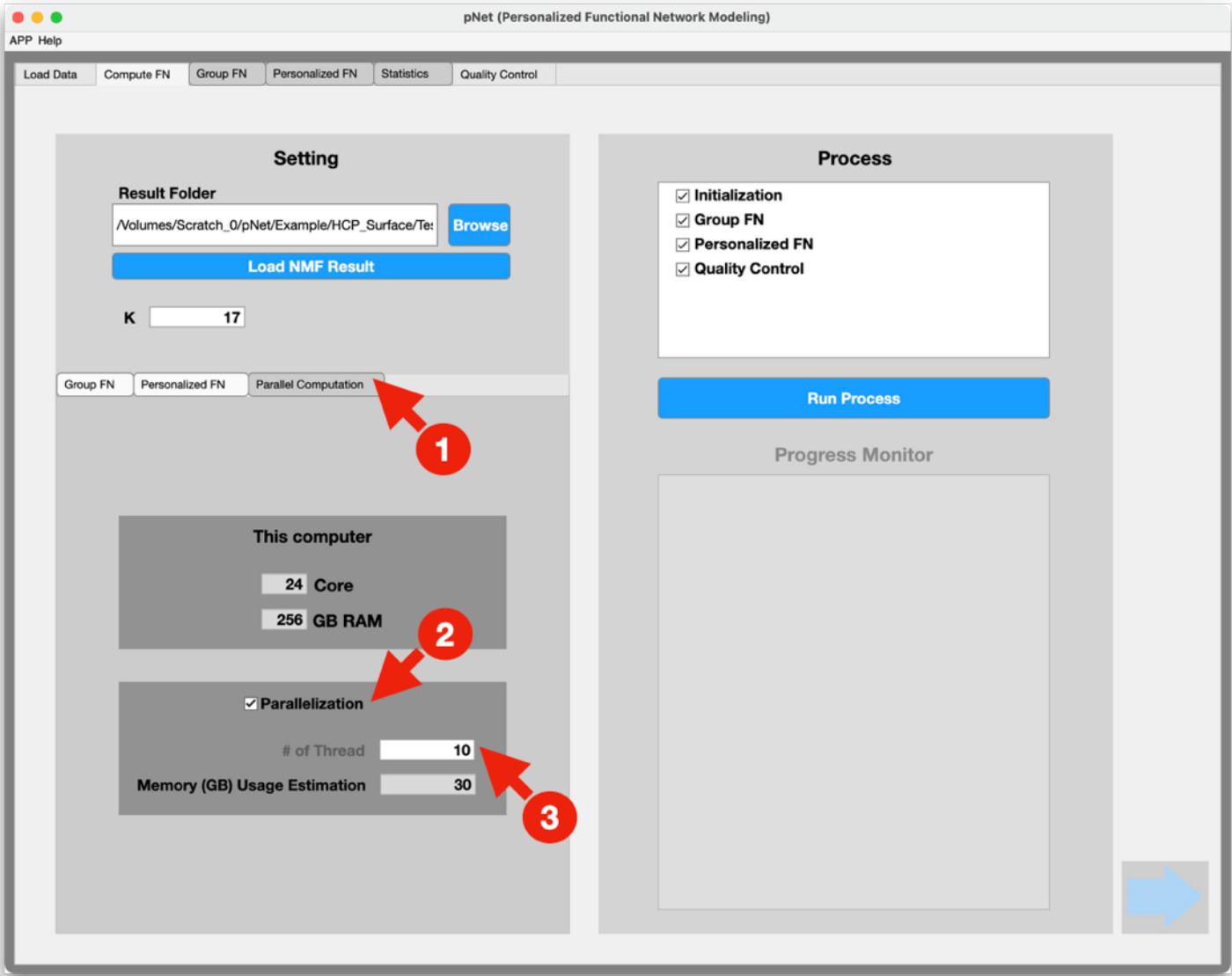
Setup personalized FN computation



Setup parameters for personalized FN computation.

- (1) Navigate to the module “Personalized FN”.
- (2) Click the check box to combine multiple fMRI scans for each subject, if preferred.
- (3) Additional parameters for personalized FN computation, only intended for advanced users.

Setup parallel computation

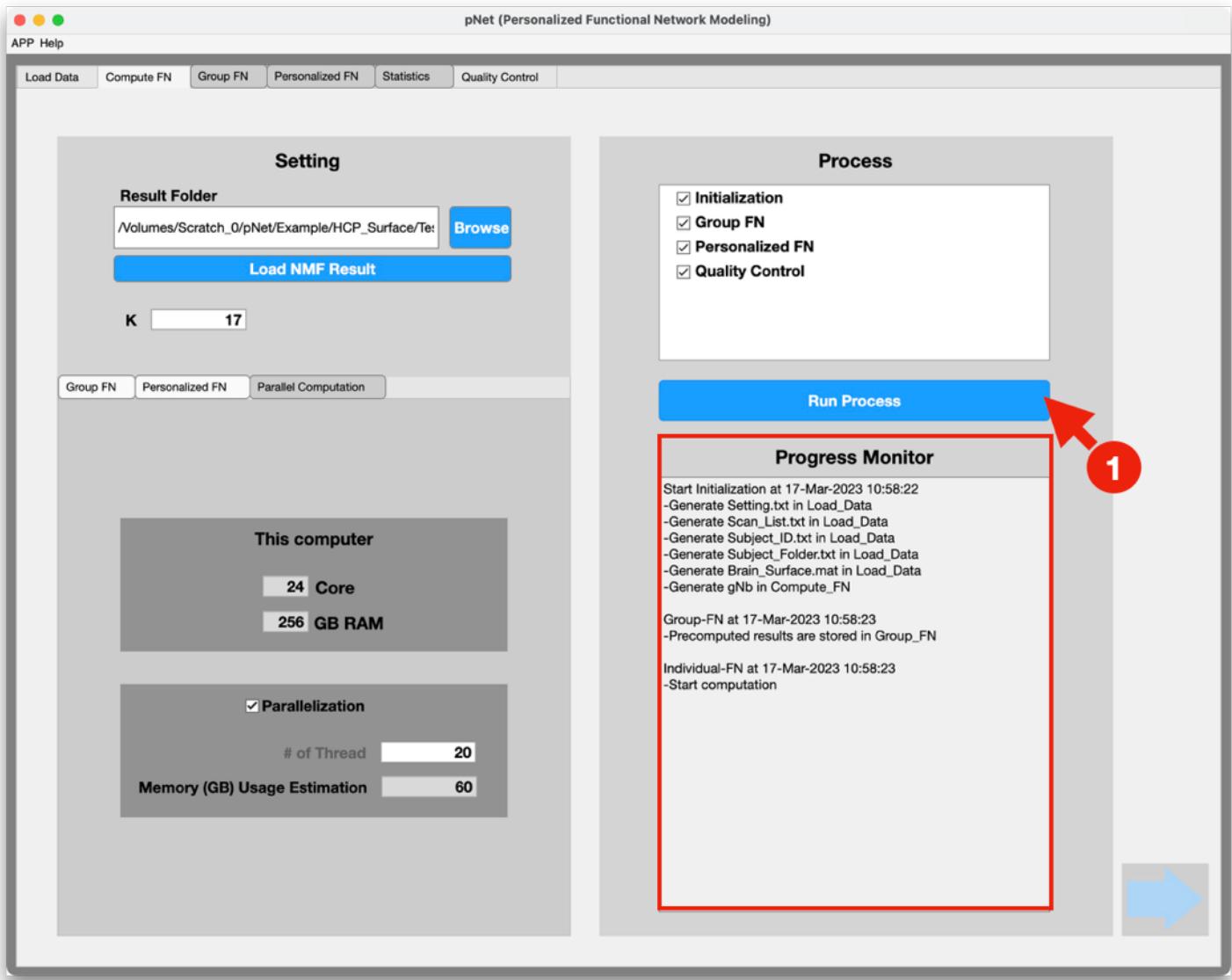


Setup parameters for parallel computation.

- (1) Navigate to the parallel computation module.
- (2) Enable parallelization by clicking the check box.
- (3) Set a desired number of threads for parallel computation. Please make sure that the estimated memory usage is within the hardware limit, which is displayed in the above section "This computer".

Run the FN computation

Once all the required settings are done, the button "Run Process" on the right of the "Compute FN" module will be enabled. Simply click it run all the computation and visualization for personalized FNs.



Run the personalized FN computation.

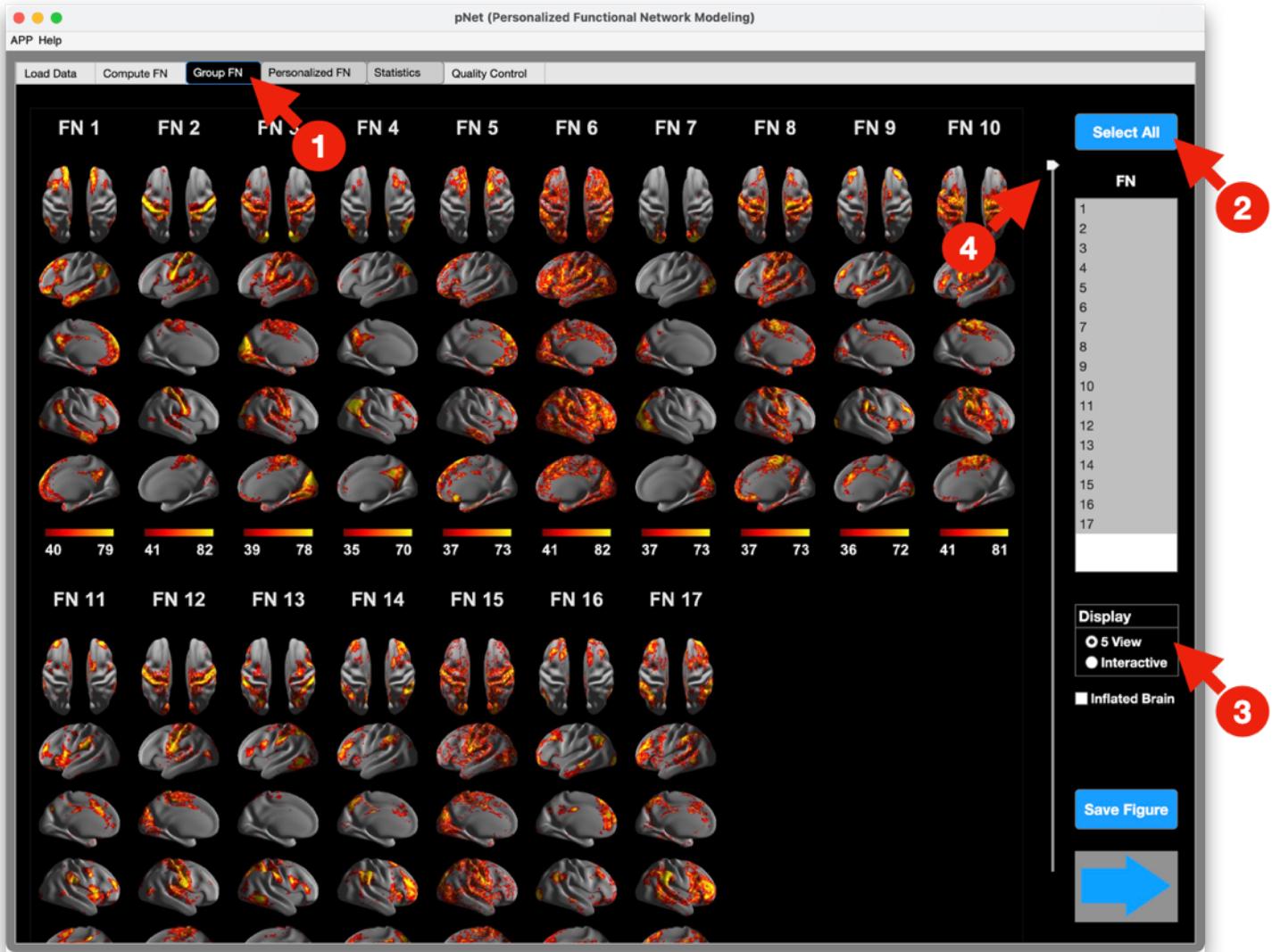
- (1) Click the button “Run Process”.
- (2) Progress monitor (highlighted in the red box) will show the progress of each major steps of initialization, group-level FN computation, personalized FN computation and visualization. The UI will automatically jump to the next module “Group FN” to show group-level FN results.

Group-level FN

This toolbox provides precomputed figures of group-level FNs for fast navigation, and interactive display to check results according to users' preference.

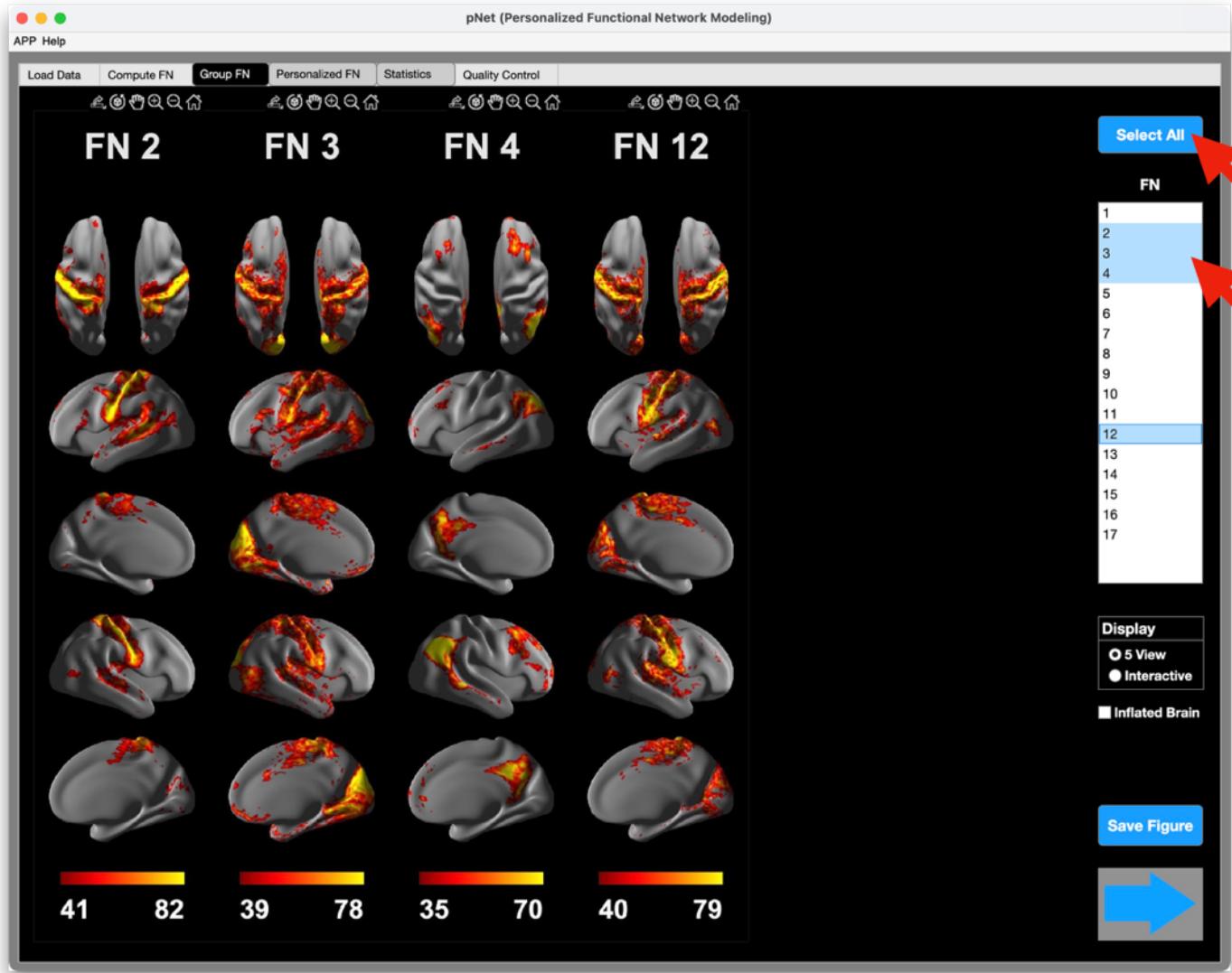
Surface data

1. Precomputed visualization



Check all group-level FNs.

- (1) Navigate to group FN module. In default, all group-level FNs will be displayed in one large figure.
- (2) Click the select all button, if needed.
- (3) Select the 5 view display option, if needed.
- (4) Drag the scroll bar to navigate through the entire figure.

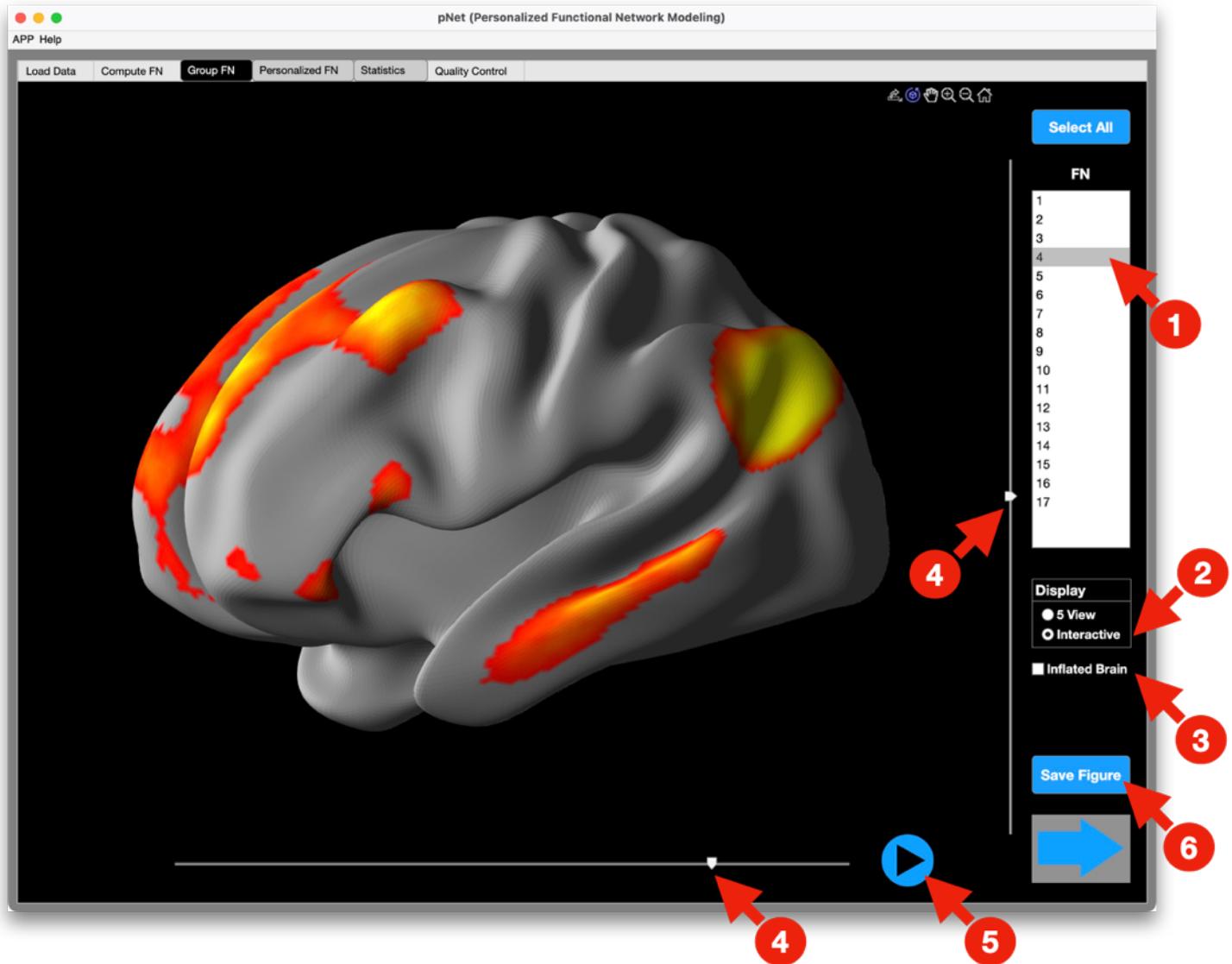


Check selected group-level FNs.

- (1) Select one or multiple group-level FNs. Hold command key in macOS, or hold control key in Windows or Linux to select multiple group-level FNs.
- (2) Click select all button to go back to the default view of all group-level FNs selected.

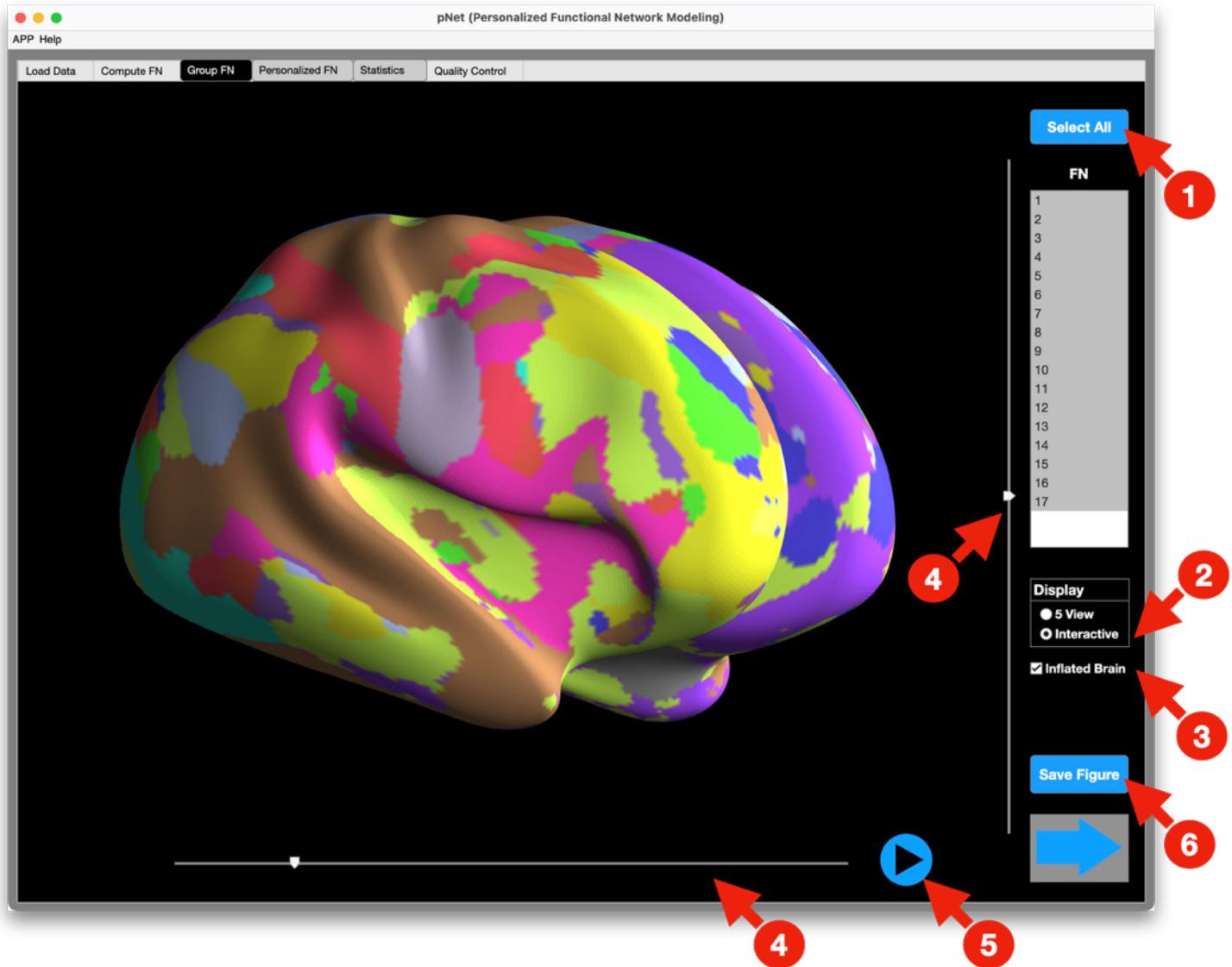
2. Interactive visualization

This interactive visualization allows the user check the group-level FN from different view angles.



Check a single group-level FN on the brain surface.

- (1) Select one group-level FN.
- (2) Select the interactive display option.
- (3) Click the check box to overlay results on an inflated brain surface, if the inflated brain surface is available.
- (4) Drag the vertical or horizontal scroll bar to change the view angle.
- (5) Start automatic change of the horizontal scroll bar to have a constantly rotating view of the brain.
- (6) Save this figure.

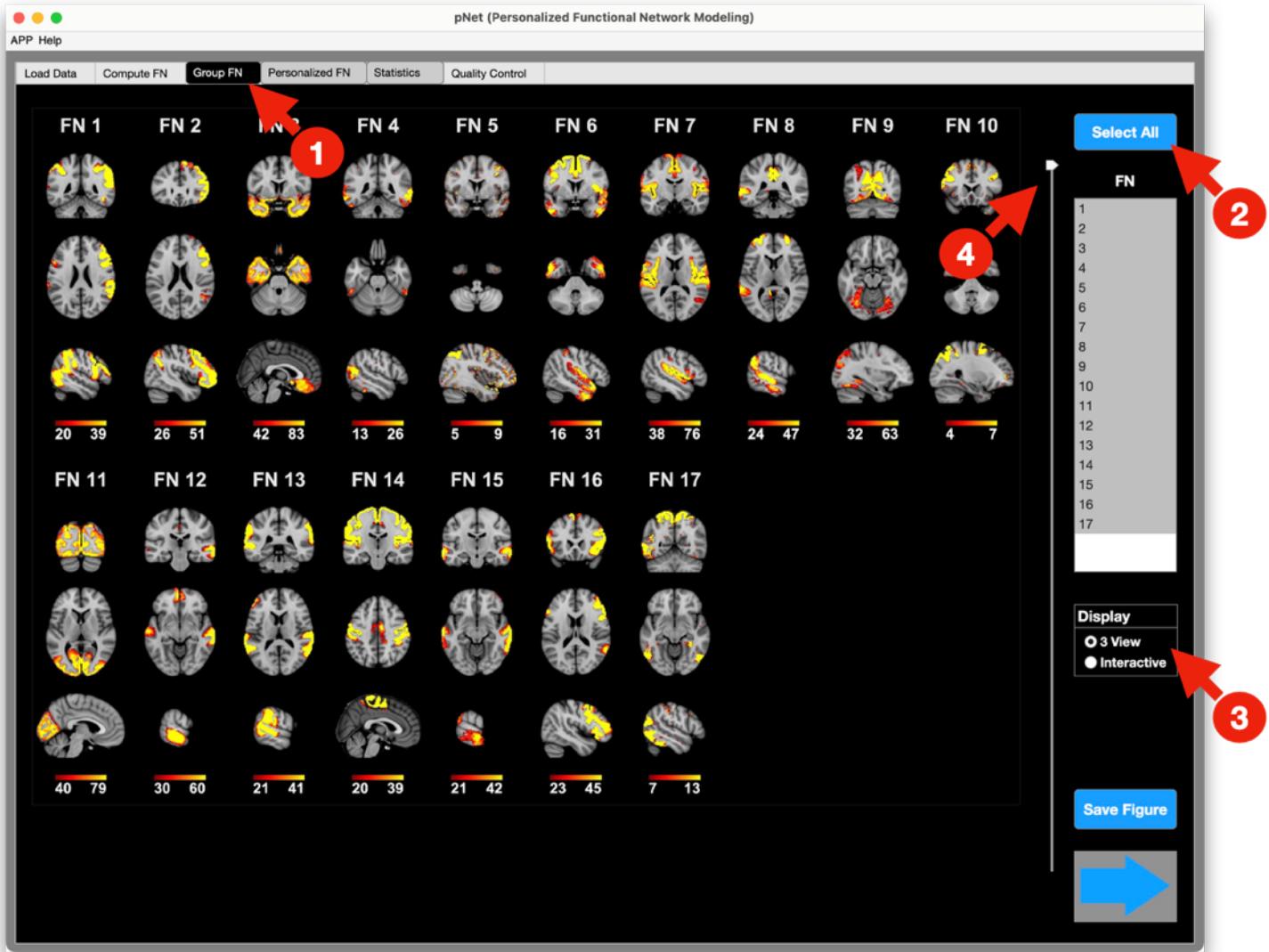


Check the functional atlas for binarized group-level FNs.

- (1) Click the select all button to include all group-level FNs.
- (2) Select the interactive display option.
- (3) Click the check box to overlay results on an inflated brain surface, if the inflated brain surface is available.
- (4) Drag the vertical or horizontal scroll bar to change the view angle.
- (5) Start automatic change of the horizontal scroll bar to have a constantly rotating view of the brain.
- (6) Save this figure.

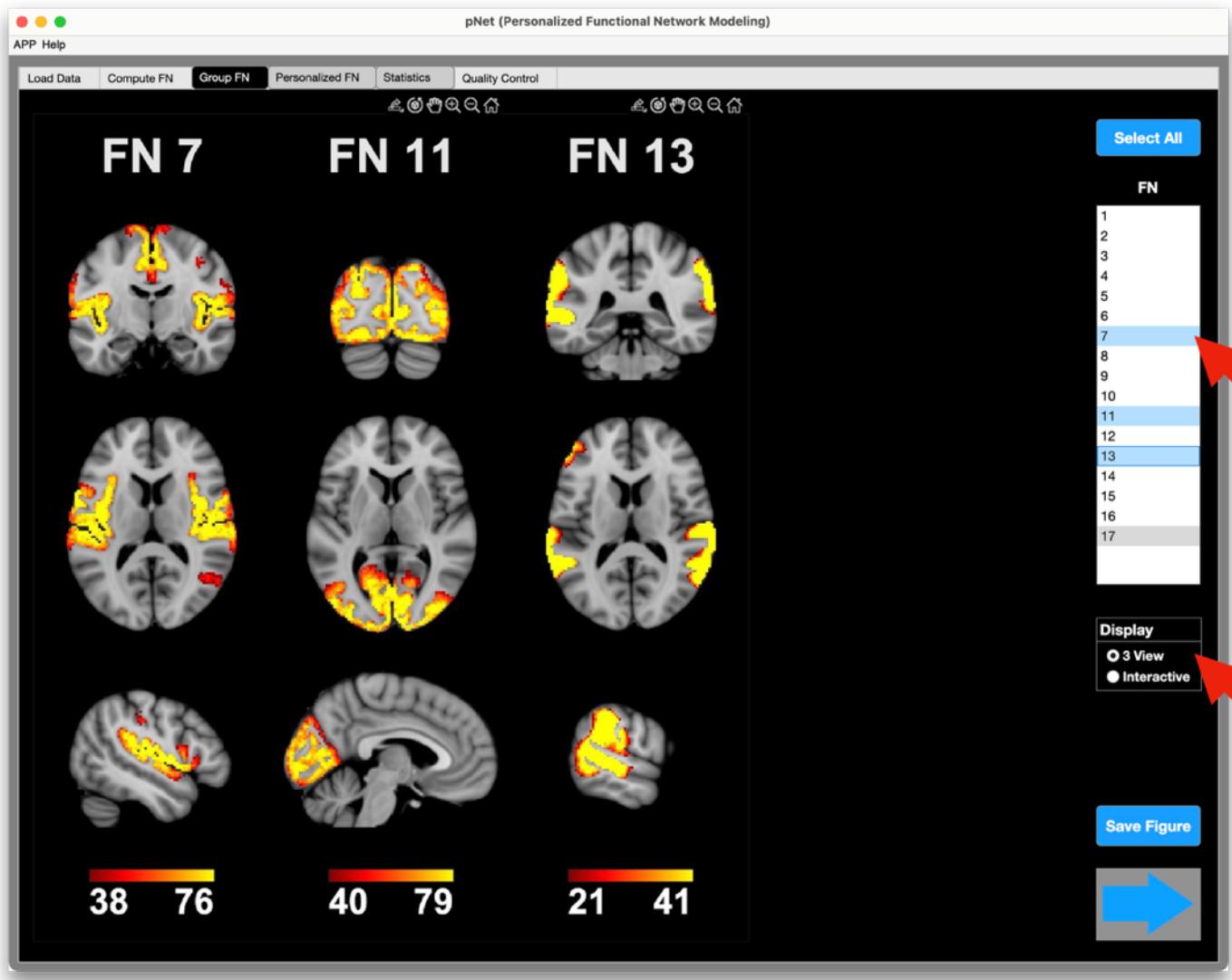
Volume data

1. Precomputed visualization



Check all group-level FNs.

- (1) Navigate to group FN module. In default, all group-level FNs will be displayed in one large figure.
- (2) Click the select all button, if needed.
- (3) Select the 3 view display option, if needed.
- (4) Drag the scroll bar to navigate through the entire figure.



Check selected group-level FNs.

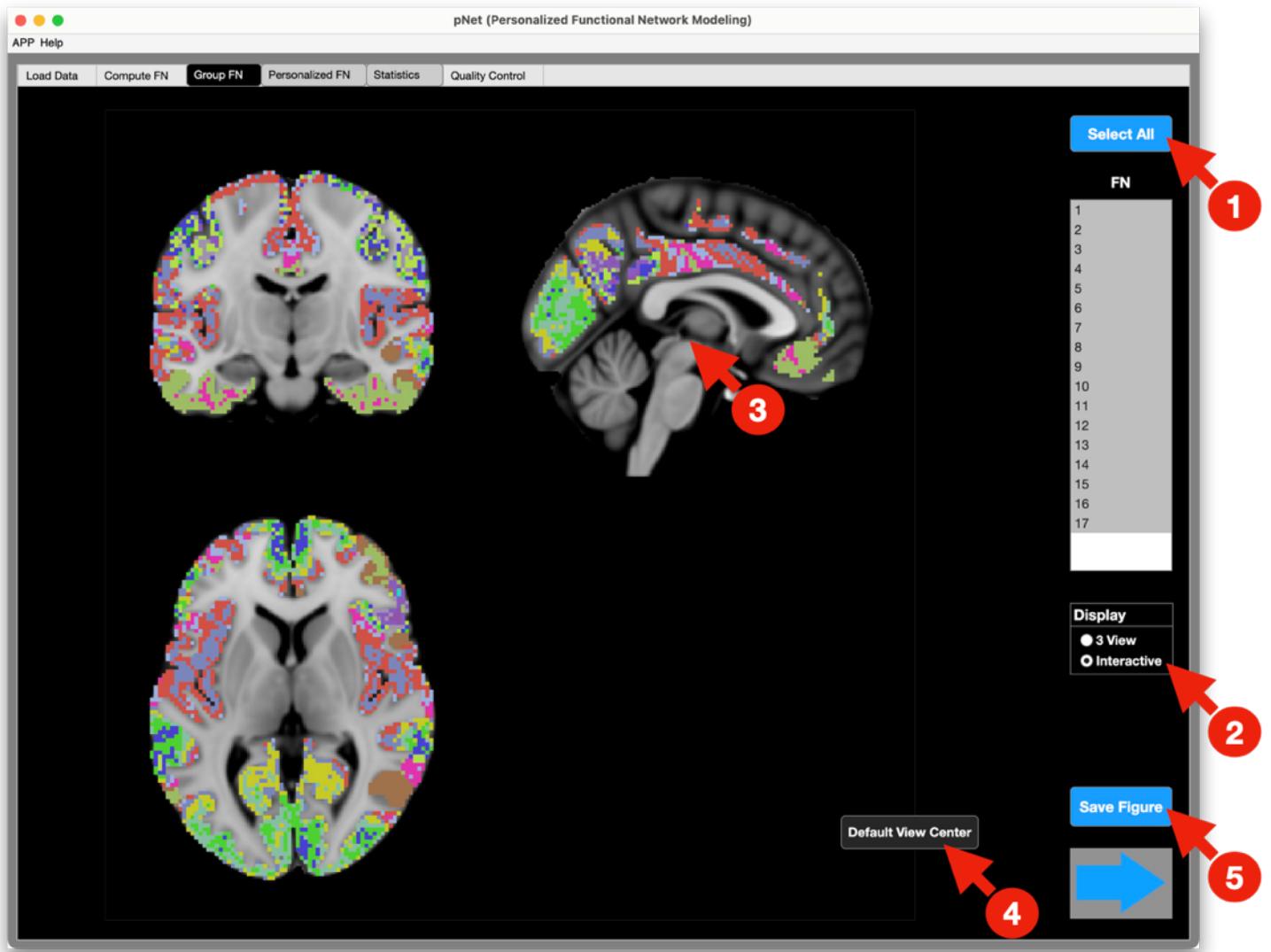
- (1) Select one or multiple group-level FNs. Hold command key in macOS, or hold control key in Windows or Linux to select multiple group-level FNs.
- (2) Click select all button to go back to the default view of all group-level FNs selected.

2. Interactive visualization



Check a single group-level FN

- (1) Select one group-level FN.
- (2) Select the interactive display option.
- (3) Click on the display to change the view center.
- (4) Click the default view center button to go back to the default view center.
- (5) Save this figure.



Check functional atlas using binarized group-level FN results

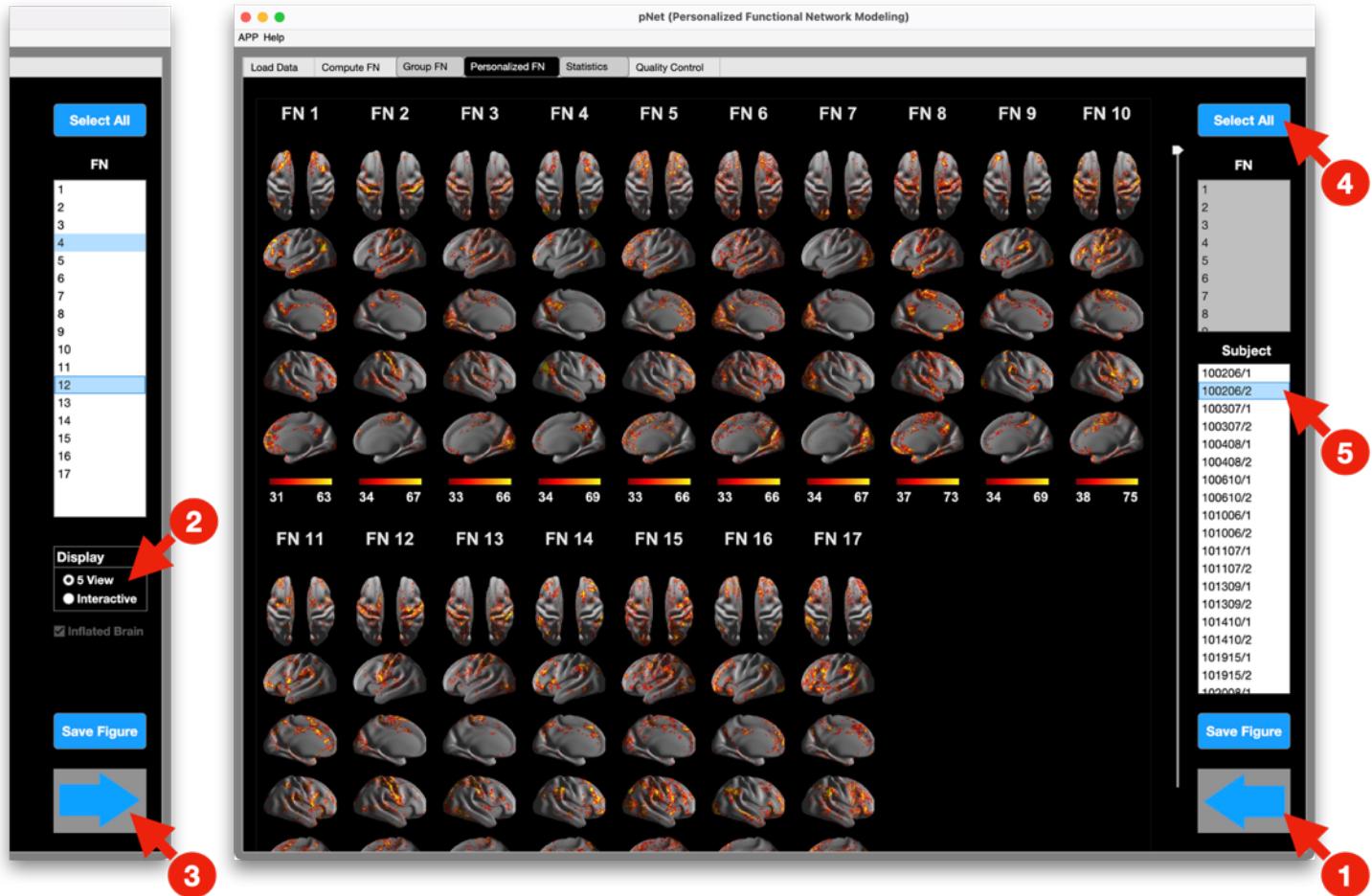
- (1) Click the select all button to include all group-level FNs.
- (2) Select the interactive display option.
- (3) Click on the display to change the view center.
- (4) Click the default view center button to go back to the default view center.
- (5) Save this figure.

Personalized FN

This toolbox provides precomputed figures of personalized FNs for fast navigation, and interactive display to check results according to users' preference.

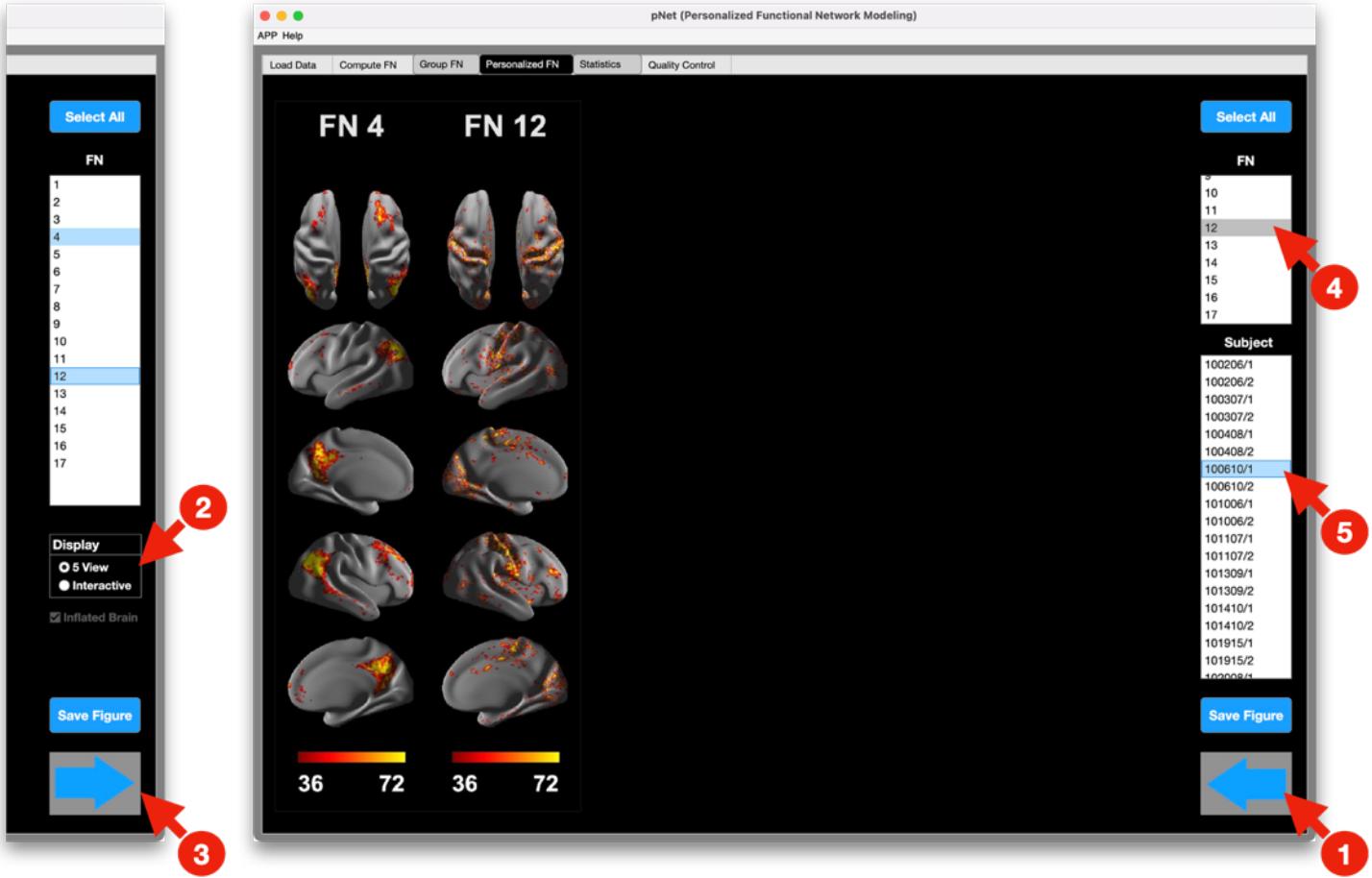
Surface data

1. Precomputed visualization



Check precomputed figures for personalized FNs.

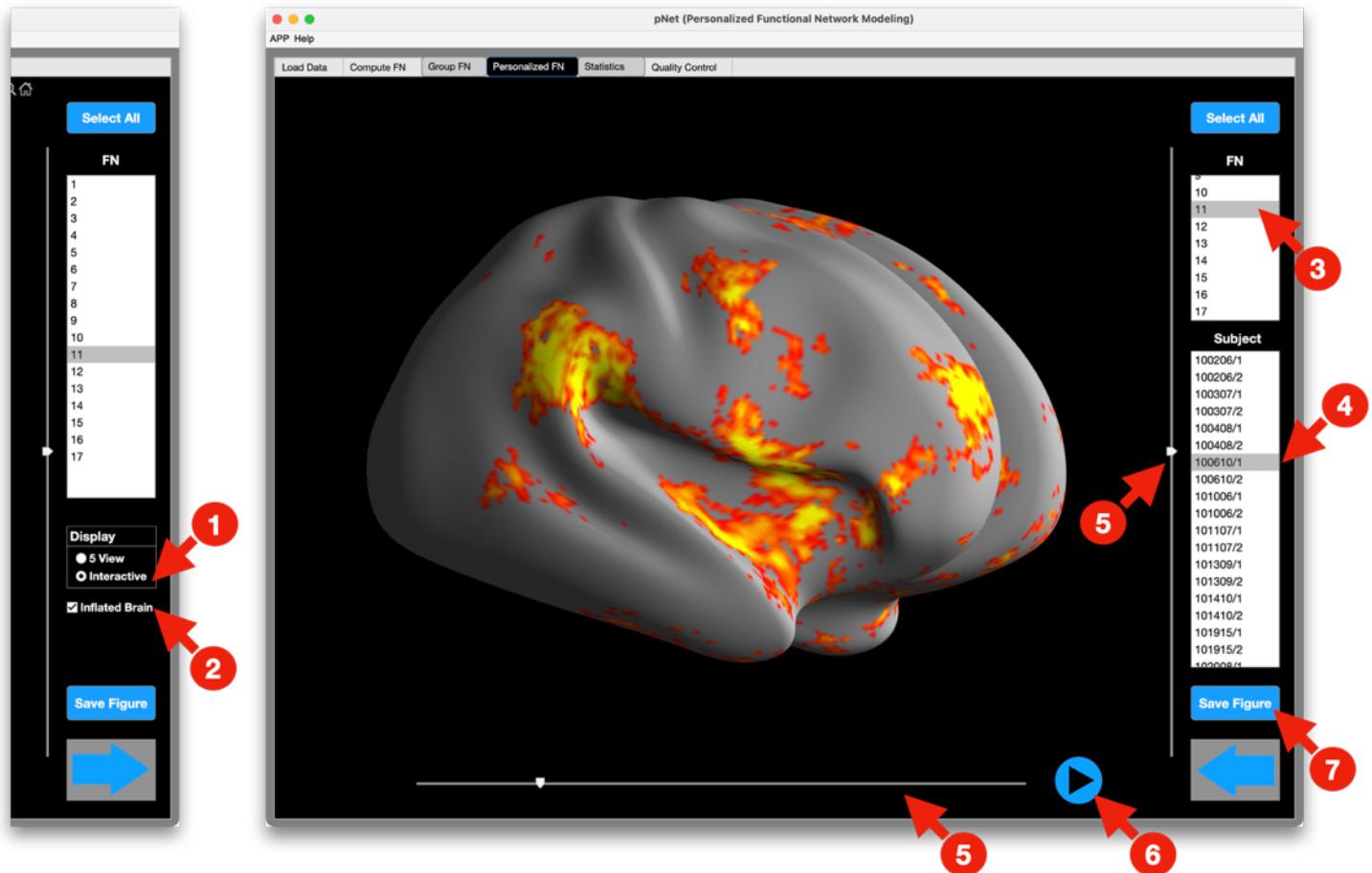
- (1) Navigate to the group FN module.
- (2) Choose the 5 view display mode.
- (3) Navigate to the personalized FN module.
- (4) Click the select all button.
- (5) Select another subject. Users can also use the up or down arrow key to select the subject above or below.



Check selected personalized FNs.

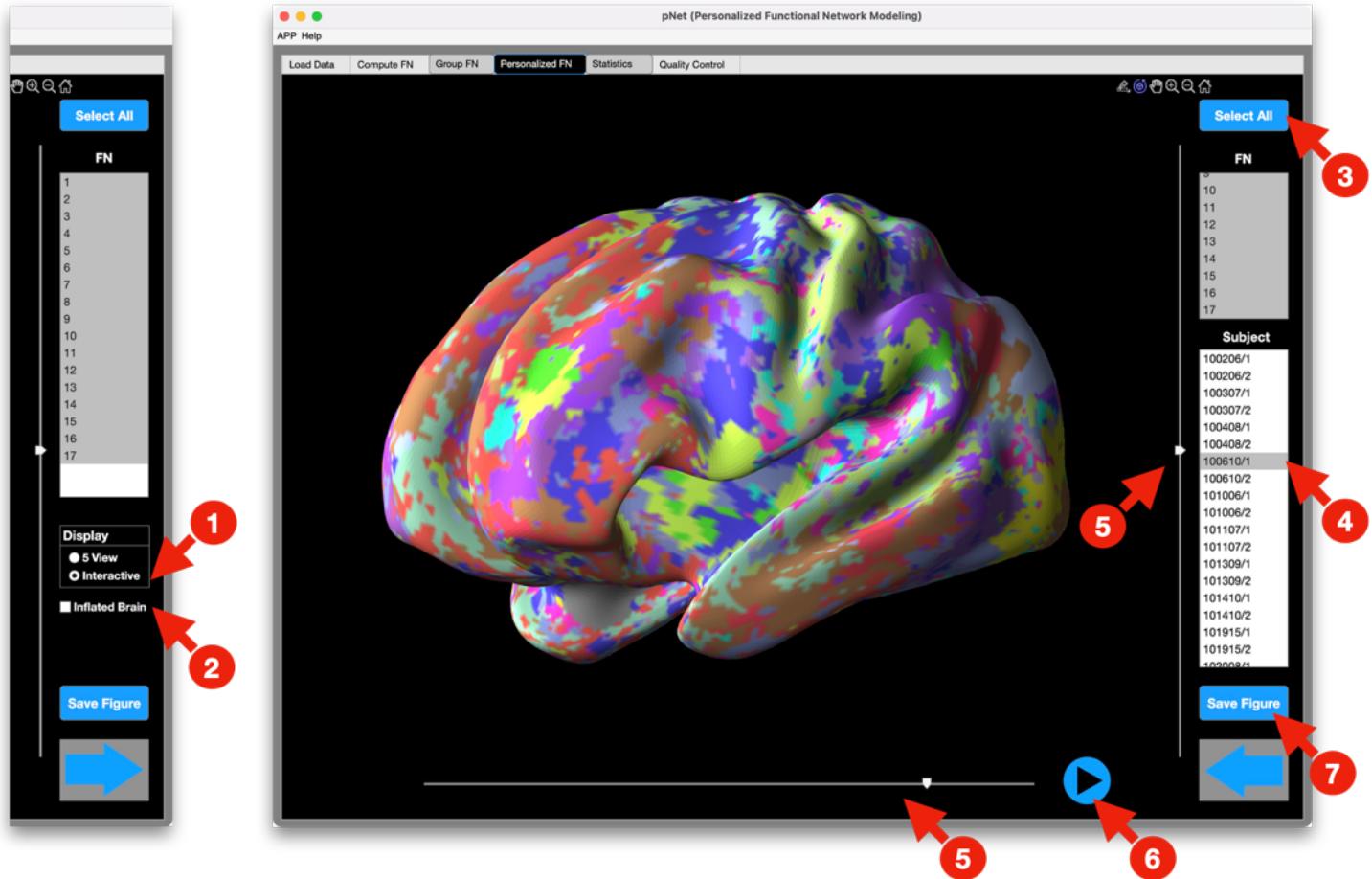
- (1) Navigate to the group FN module
- (2) Select the 5 view display option.
- (3) Navigate to the personalized FN module.
- (4) Select one or multiple personalized FNs. Hold command key in macOS, or hold control key in Windows or Linux to select multiple personalized FNs.
- (5) Select another subject. Users can also use the up or down arrow key to select the subject above or below.

2. Interactive visualization



Check a single personalized FN on the brain surface.

- (1) Navigate to the group FN module, and select the interactive display option.
- (2) Select the inflated brain if desired.
- (3) Navigate to the personalized FN module, select one desired personalized FN for display.
- (4) Select another subject. Users can also use the up or down arrow key to select the subject above or below.
- (5) Drag the vertical or horizontal scroll bar to change the view angle.
- (6) Start automatic change of the horizontal scroll bar to have a constantly rotating view of the brain.
- (7) Save this figure.

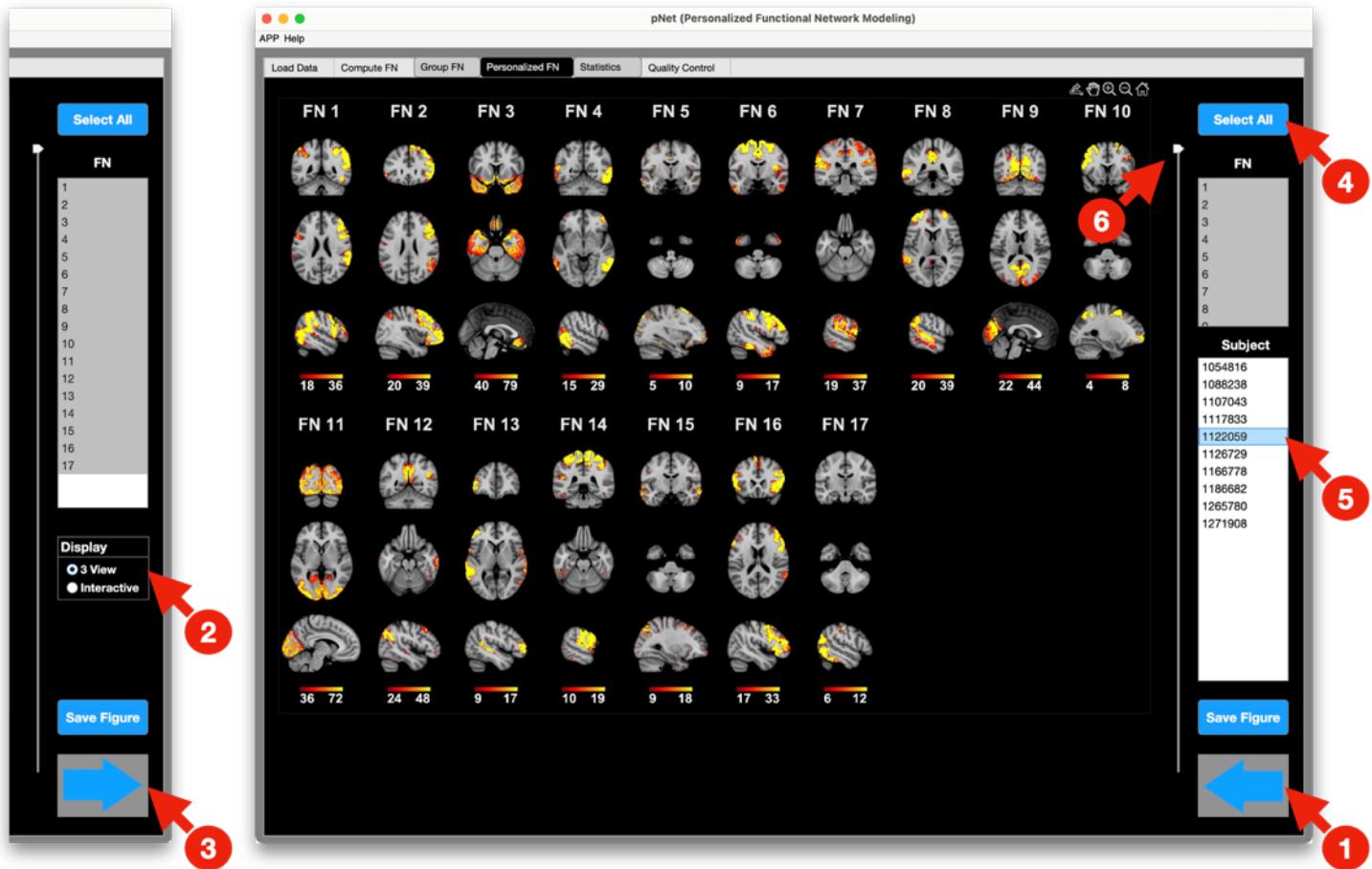


Check the functional atlas of a single subject.

- (1) Navigate to the group FN module, and select the interactive display option.
- (2) Select the inflated brain if desired.
- (3) Navigate to the personalized FN module, click the select all button if needed.
- (4) Select another subject. Users can also use the up or down arrow key to select the subject above or below.
- (5) Drag the vertical or horizontal scroll bar to change the view angle.
- (6) Start automatic change of the horizontal scroll bar to have a constantly rotating view of the brain.
- (7) Save this figure.

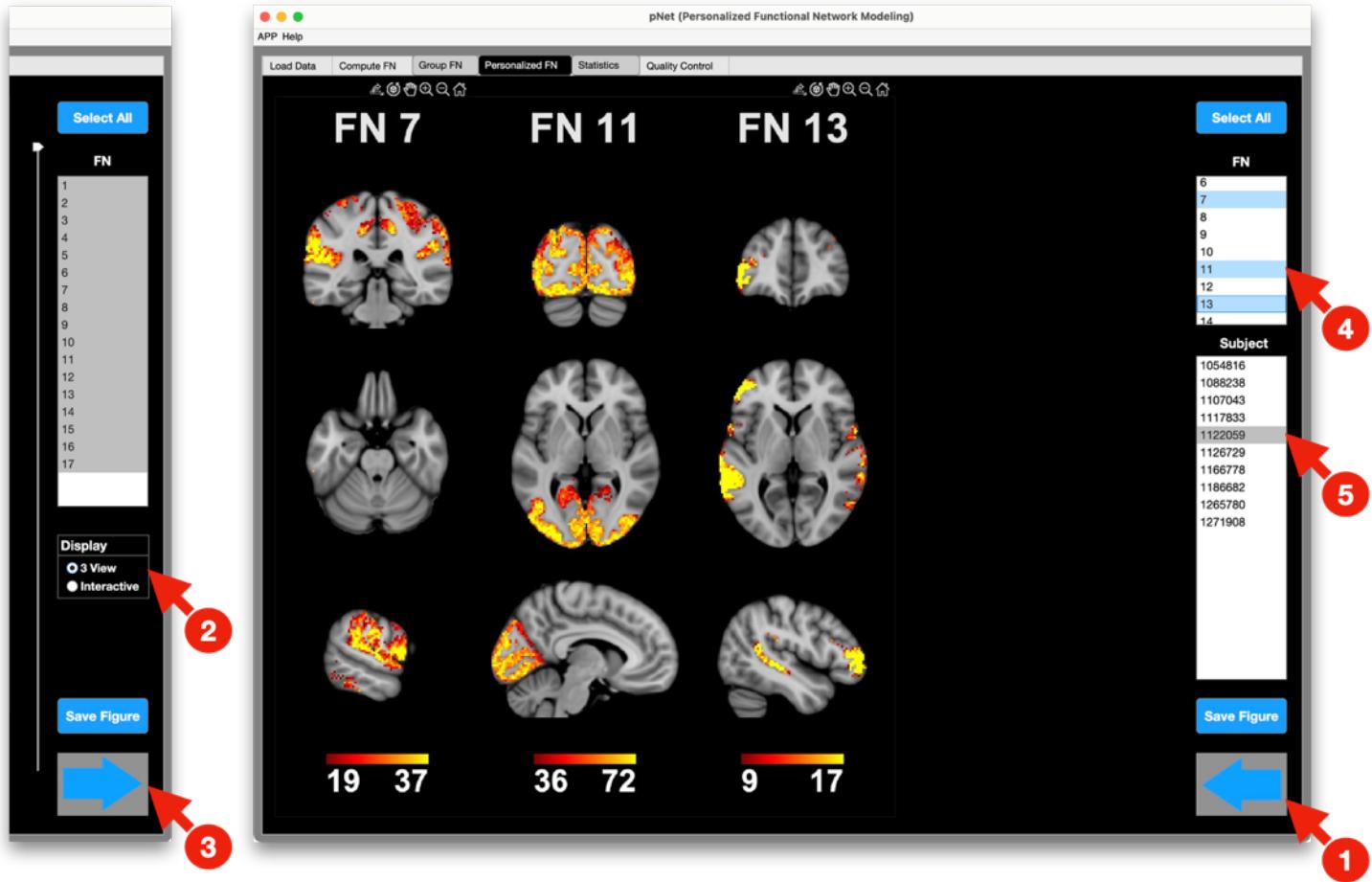
Volume data

1. Precomputed visualization



Check precomputed figures for personalized FNs.

- (1) Navigate to the group FN module.
- (2) Choose the 3 view display mode.
- (3) Navigate to the personalized FN module.
- (3) Click the select all button, if needed.
- (5) Select another subject. Users can also use the up or down arrow key to select the subject above or below.
- (6) Drag the vertical scroll bar, if needed.



Check selected personalized FNs.

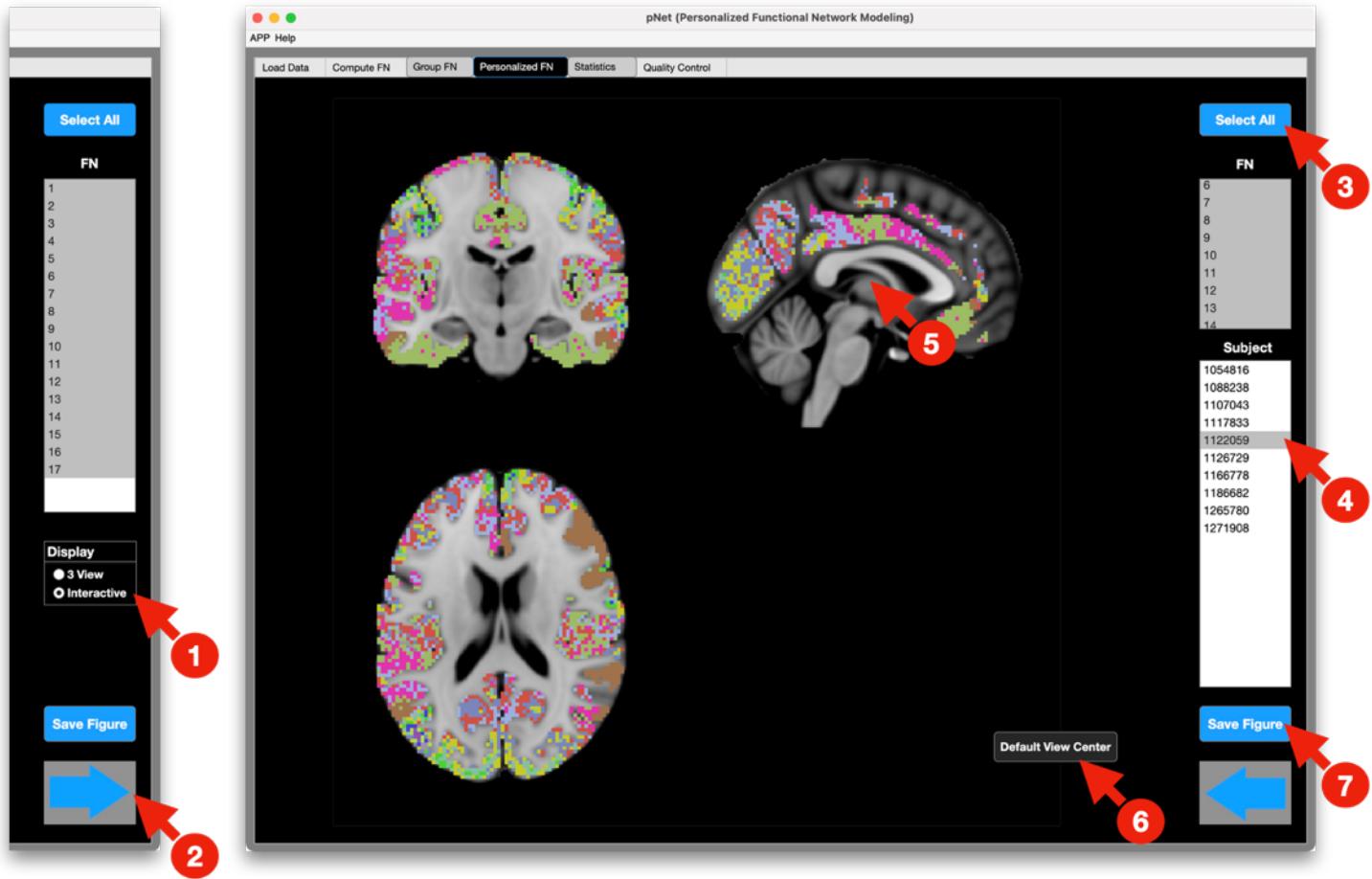
- (1) Navigate to the group FN module.
- (2) Select the 3 view display option.
- (3) Navigate to the personalized FN module.
- (4) Select one or multiple personalized FNs. Hold command key in macOS, or hold control key in Windows or Linux to select multiple personalized FNs.
- (5) Select another subject. Users can also use the up or down arrow key to select the subject above or below.

2. Interactive visualization



Check a single personalized FN.

- (1) Navigate to the group FN module, and select the interactive display option.
- (2) Navigate to the personalized FN module
- (3) Select one desired personalized FN for display.
- (4) Select another subject. Users can also use the up or down arrow key to select the subject above or below.
- (5) Click on the display to change the view center.
- (6) Click the default view center button to go back to the default view center.
- (7) Save this figure.



Check the functional atlas of a single subject.

- (1) Navigate to the group FN module, and select the interactive display option.
- (2) Navigate to the personalized FN module.
- (3) Click select all button, if needed.
- (4) Select another subject. Users can also use the up or down arrow key to select the subject above or below.
- (5) Click on the display to change the view center.
- (6) Click the default view center button to go back to the default view center.
- (7) Save this figure.

Compare group-level and personalized FN

Users can easily compare group-level and personalized FNs using the fast navigation buttons on the right bottom of the group-level and personalized FN modules. The display settings for group-level and personalized FNs are synchronized automatically for convenience.



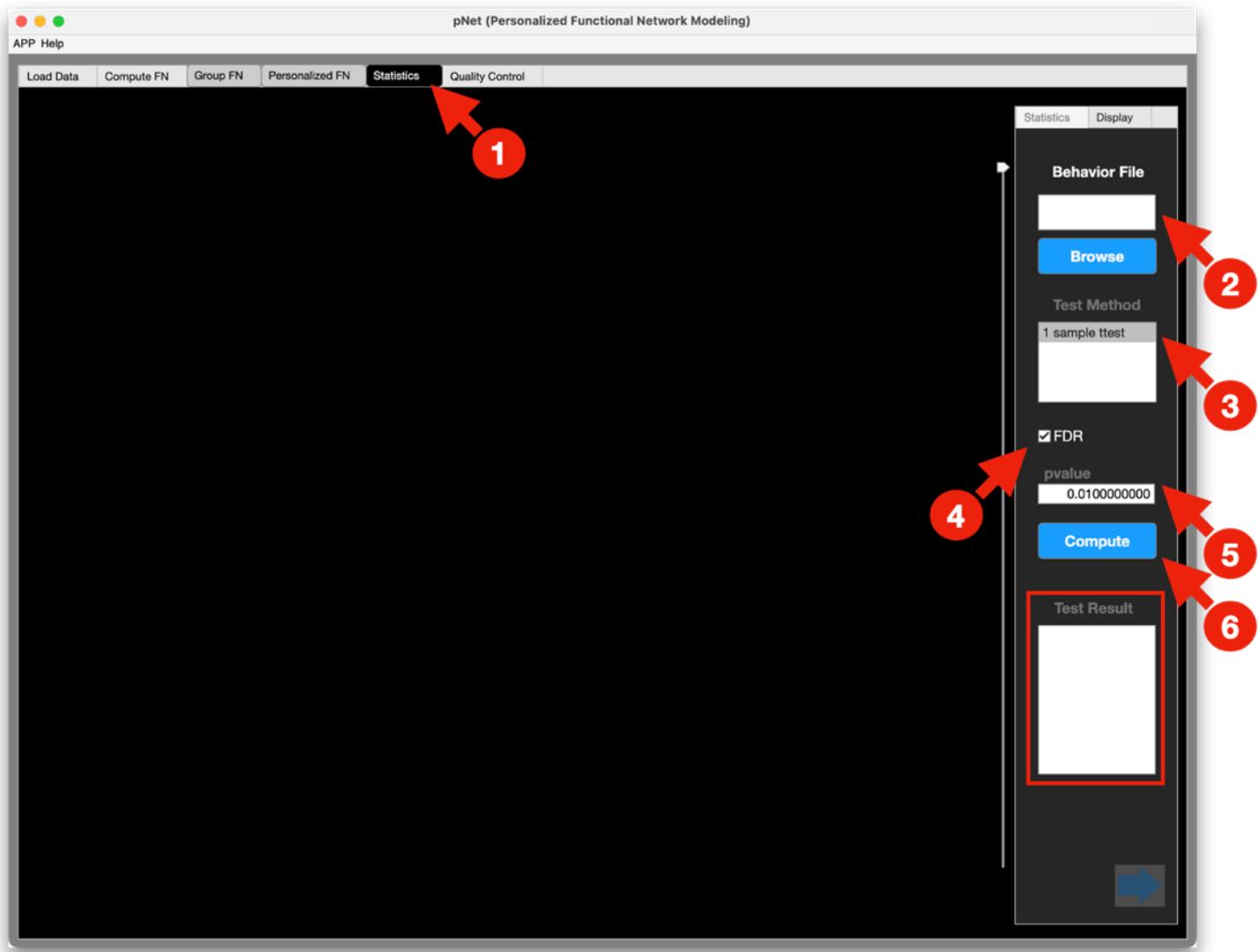
Fast navigation between group-level and personalized FN modules.

- (1) The right arrow button on the group-level FN module navigates to the personalized FN module.
- (2) The left arrow button on the personalized FN module navigates to the group-level FN module.

Statistical Analysis

This toolbox has implemented one-sample t-test to show the significance of each personalized FN, and two-sample t-test to show the significant difference of each personalized FN in two groups. The visualization options are as same as those for group-level and personalized FNs. In addition, the visualization for statistical results are synchronized with that for group-level and personalized FNs. It allows users to navigate to the group-level and personalized FN modules for fast comparisons.

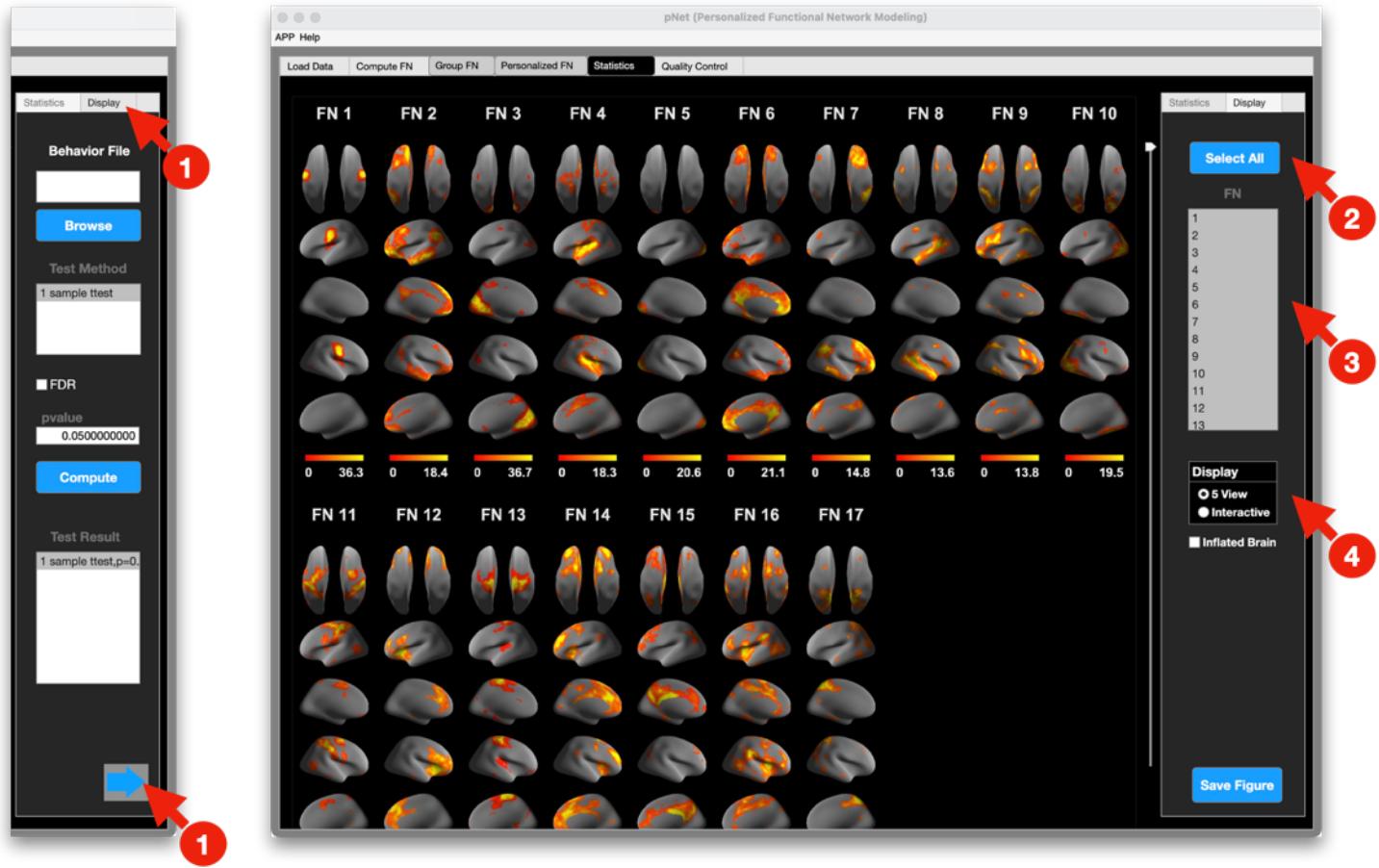
One-sample t-test



Setup one-sample t-test.

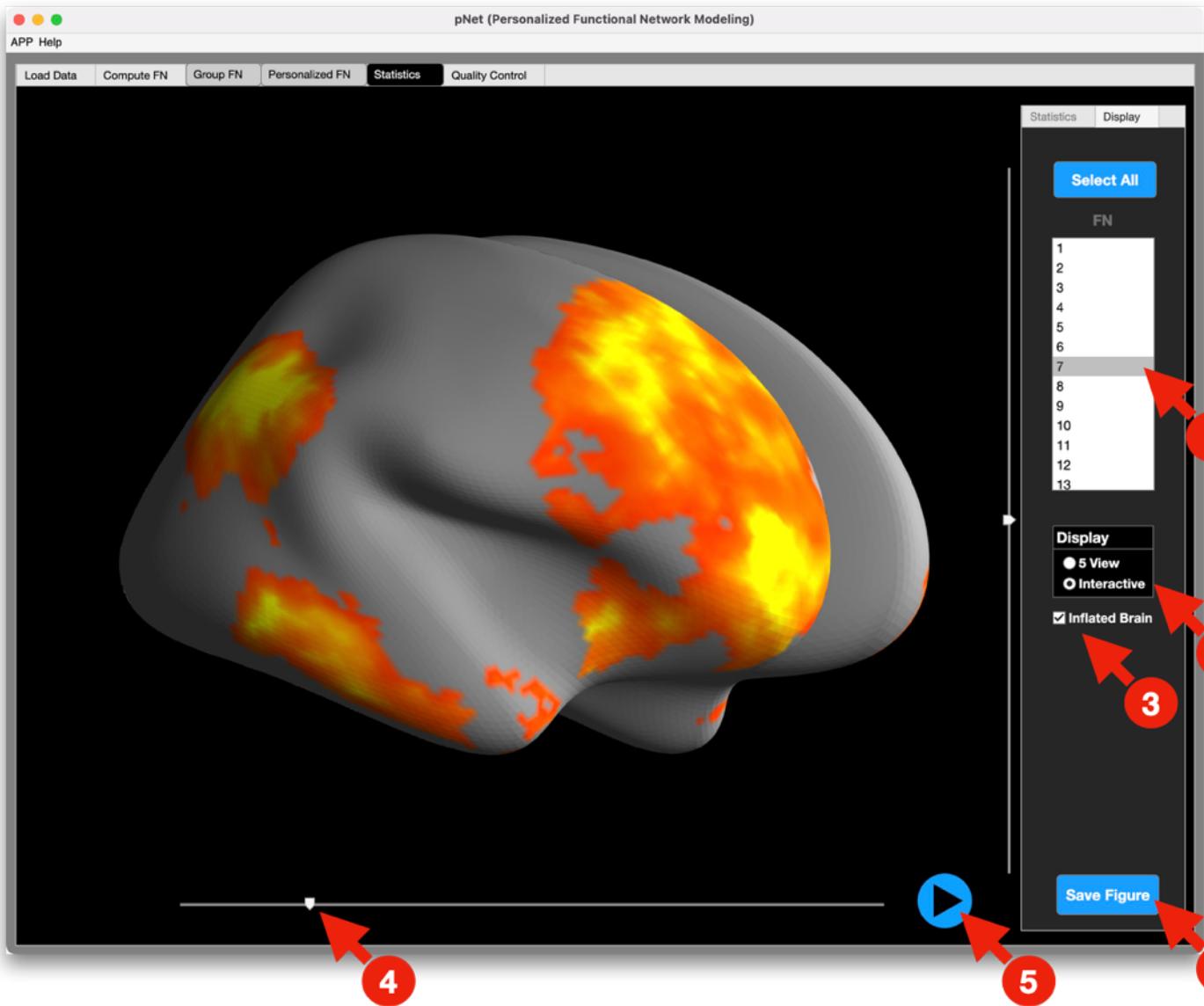
- (1) Navigate to the statistics module.
- (2) Make sure that the behavior file is empty.
- (3) Select the 1 sample t-test method.

- (4) Check FDR correction, if needed.
 - (5) Set the p-value threshold.
 - (6) Click the compute button to run the statistical analysis. A popup window will show the progress of statistical computation, and another window will show the progress of result visualization.
- Once the computation and visualization finish, a new test result will be added into the test result list box.



Check precomputed visualization.

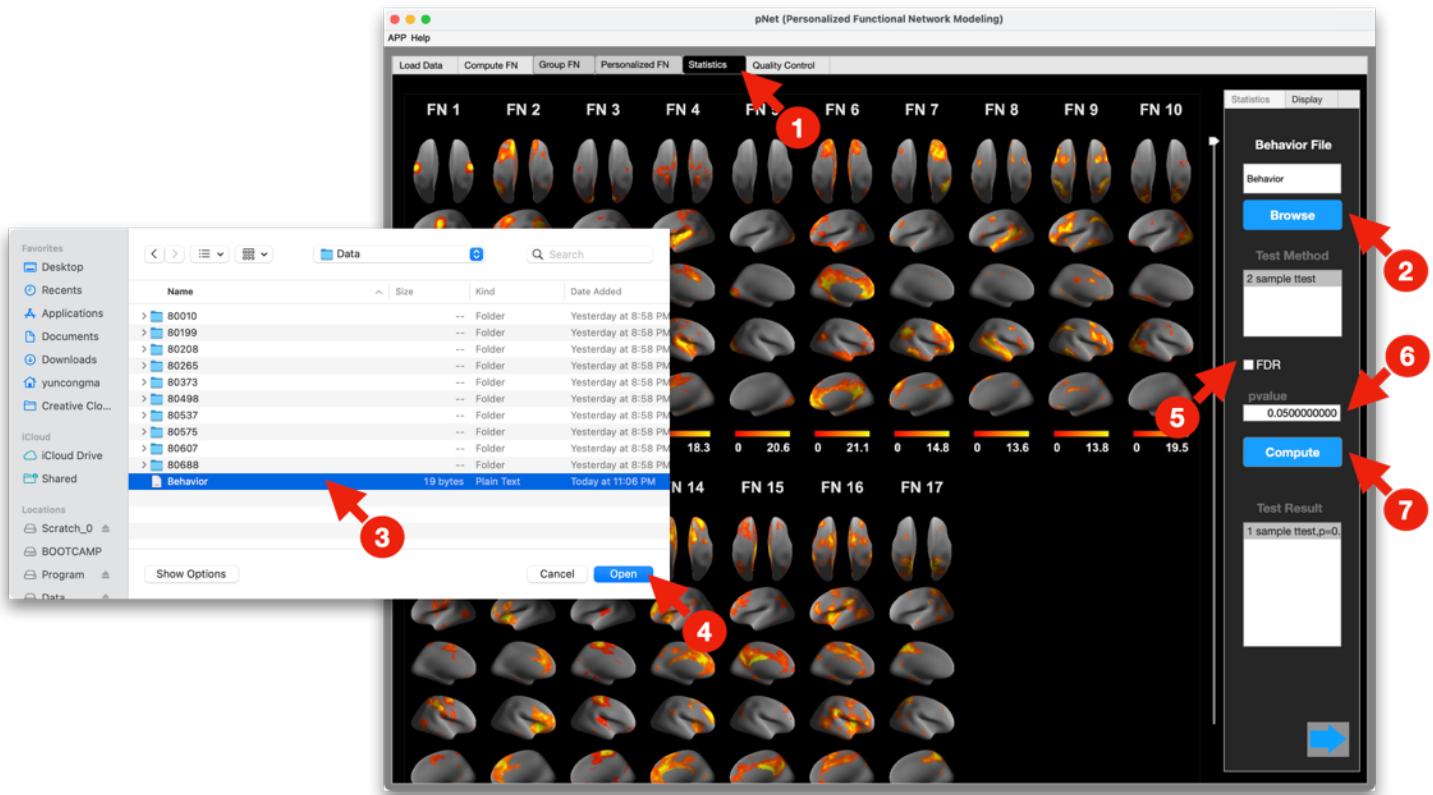
- (1) Navigate to the display module.
- (2) Click the select all button, if needed.
- (3) Select one or multiple FNs.
- (4) Select the 5 view display option, if needed.



Check interactive visualization.

- (1) Select one FN.
- (2) Select the interactive display option.
- (3) Choose the inflated brain, if preferred.
- (4) Drag the scroll bar to change the view angle.
- (5) Click the play button to have a constantly rotating view of the brain.
- (6) Click the save figure button to save this figure.

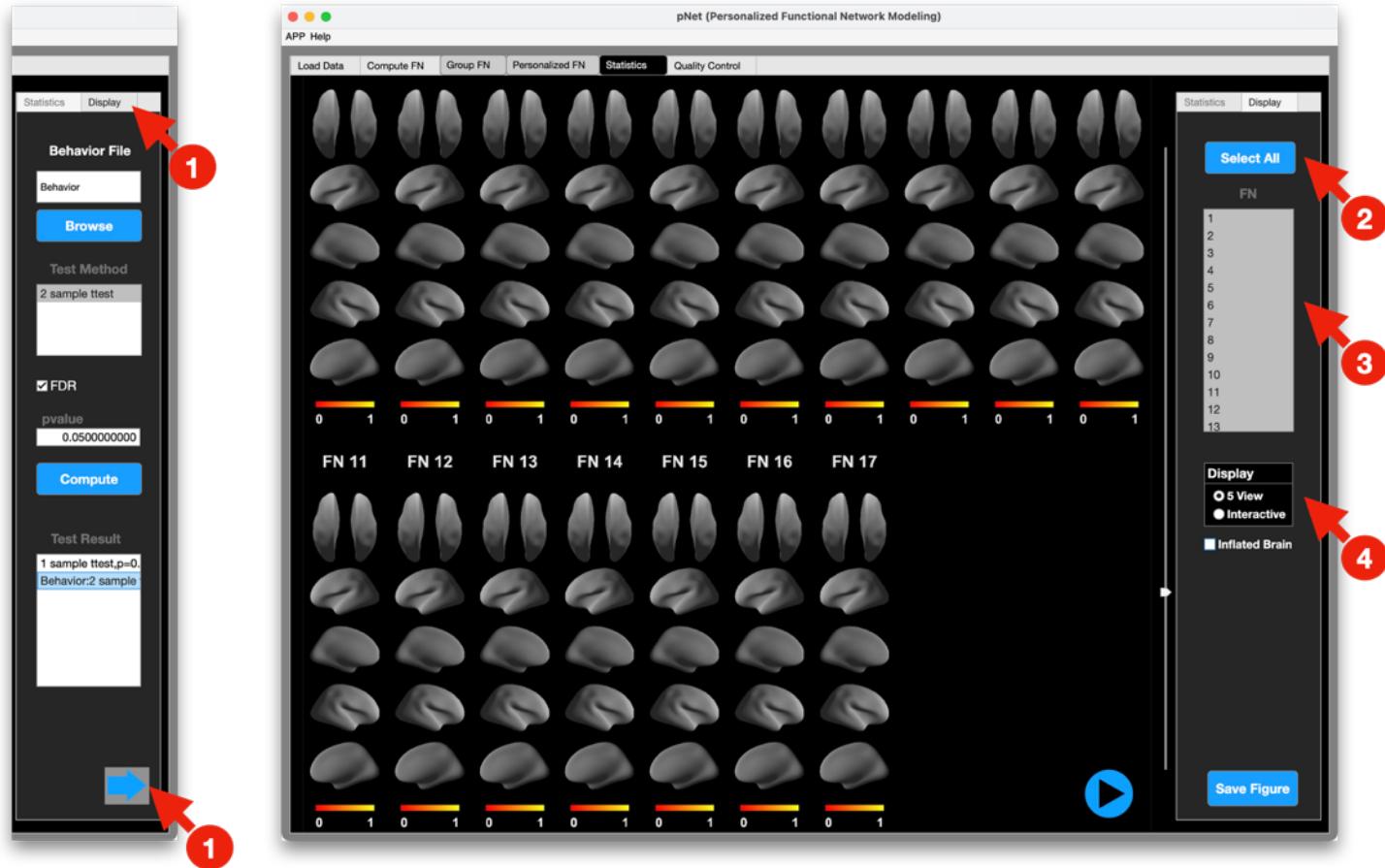
Two-sample t-test



Setup the two-sample t-test

- (1) Navigate to the statistics module.
- (2) Click the browse button to read a behavior file.
- (3) Select the behavior file in txt format, which contains a column of 0-1 to specify the two groups.
- (4) Click open button.
- (5) Select the FDR correction, if preferred.
- (6) Setup the p-value threshold.
- (7) Click the compute button to run the statistical analysis. A popup window will show the progress of statistical computation, and another window will show the progress of result visualization.

Once the computation and visualization finish, a new test result will be added into the test result list box.

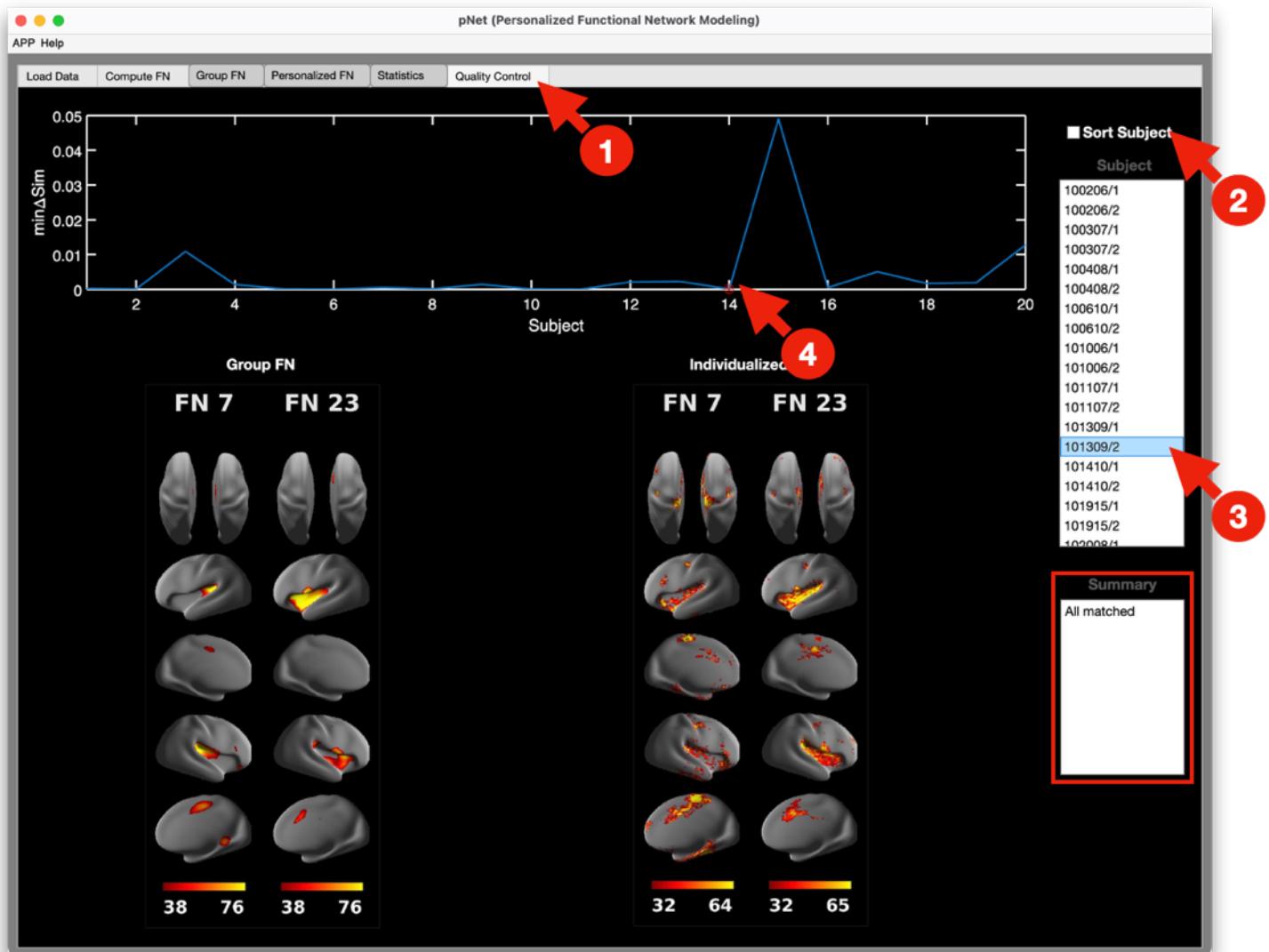


Check the two-sample t-test results

- (1) Navigate to the display module.
- (2) Click the select all button, if needed.
- (3) Select one or multiple FNs, if preferred.
- (4) Choose the display option.

Quality Control

The quality control is to ensure the spatial correspondence between personalized FNs and corresponding group-level FNs, and highlight the benefit of using personalized functional network modeling in terms of functional coherence. Specifically, the personalized FNs needs to have the highest spatial similarity (defined by Pearson correlation) to their corresponding group-level FNs. The minimum spatial similarity value for all personalized FNs is noted as the $\text{min}\Delta\text{Sim}$ for each subject. If $\text{min}\Delta\text{Sim}$ is smaller or equal to 0, it means that there is at least one personalized FN mismatch to the group-level FN or has no higher spatial similarity. Since our personalized FN computation method has quality assurance built in, all results will meet the quality control. Here we show one example with two mismatched FNs which will not be obtained from the toolbox.

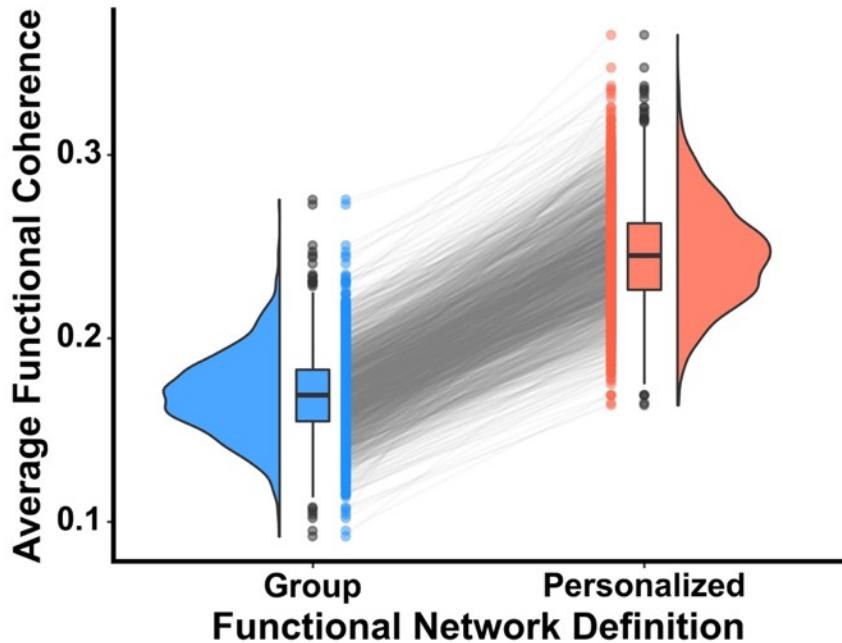


Check quality control.

- (1) Navigate to the quality control module.
- (2) Unselect the “Sort Subject” box, if needed. This allows to show quality control results of all subjects.
- (3) Choose subject to see the quality control result.
- (4) Alternatively, click on the top middle figure, quality control index ($\text{min}\Delta\text{Sim}$), to see navigate to the result of that subject.

Quality control summary of the selected subject is shown in the red box.

Our personalized FN model optimizes the overall data fitting, which naturally enhances functional coherence which reflects the within-network similarity. The functional coherence of a pFN is calculated as the weighted average of correlation between the pFN signal and signals of all voxels/vertices, and further averaged across FNs, obtaining average functional coherence for each scan or subject. As shown below, the average functional coherence is enhanced for each scan, demonstrating the advantage of our pFN modeling method.



Average functional homogeneity.

Blue: average functional homogeneity obtained using the group FN definition for each subject or combined scans. Orange: average functional homogeneity obtained using the personalized FNs for each subject or combined scans.

Web Report

pNet generates a web-based report (HTML format) for fast visual examination without using the MATLAB GUI version. A screenshot of an example web report is shown as below. This report provides description of the dataset, pFN model parameters, and figures for the gFNs, pFNs from a few subjects, quality control, as well as hyperlinks to pFNs of all subjects in the dataset. For faster web browsing experience, low resolution figures (ex. All(Compressed).jpg) are loaded to save memory usage.

pNet Report

This is a brief report summarizing the results obtained using pNet.

pNet is an open-source toolbox ([GitHub link](#)) to obtain personalized functional networks from fMRI data.

pNet is developed by Yong's lab ([lab link](#)).

Report is generated at 2023-12-19 09:38:44

Essential settings for this pNet workflow

The personalized functional network modeling is based on the method named as SR-NMF.

The number of FNs is set to 17.

The fMRI data type is 'Volume' with format as 'Volume (*.nii, *.nii.gz, *.mat).'

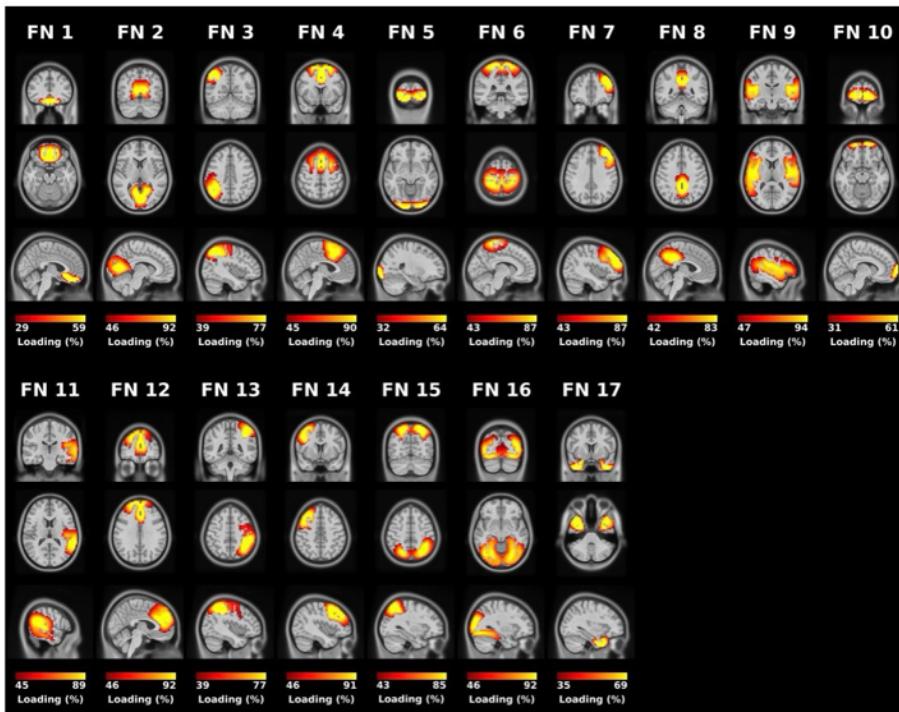
The whole fMRI dataset contains 1754 scans from 521 subjects.

Parameters for the data input are stored in './Data_Input/Setting.json'

Parameters for the personalized FN modeling are stored in './FN_Computation/Setting.json'

Group Functional Networks (gFNs)

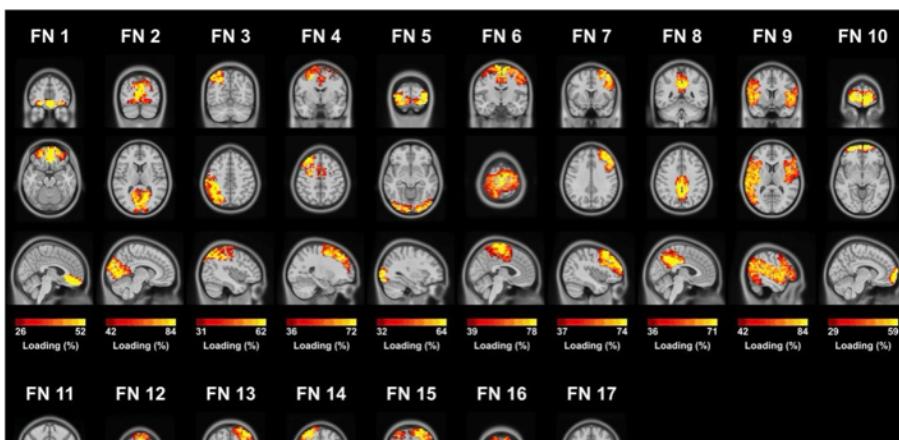
The group FNs are derived using the whole fMRI dataset



Personalized Functional Networks (pFNs)

A few examples of personalized FNs derived from several subjects are shown as below.

[Links to all pFNs are at the end of this web report.](#)

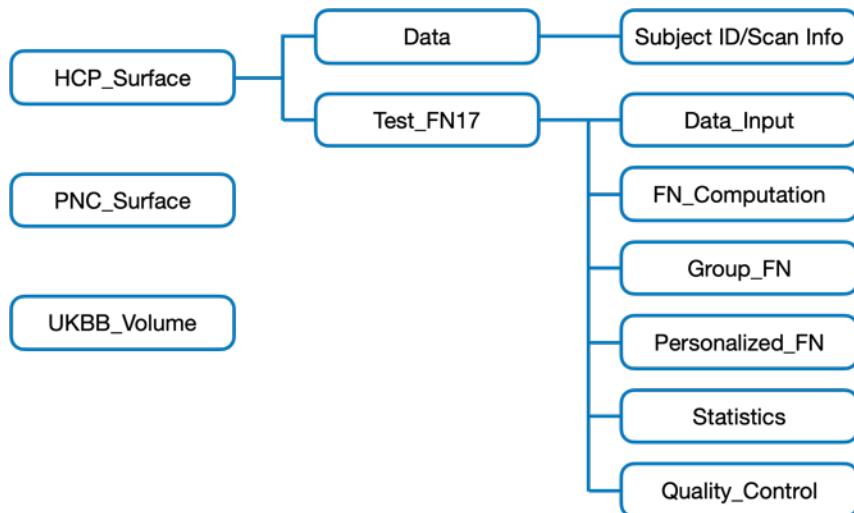


Screenshot of a web-based report

Example

We provided three examples for users to learn how to run the personalized FN computation, and navigate through the precomputed results. For each example, we provide examples of simulated fMRI data, and precomputed results of real fMRI data. Examples can be accessed on Google Drive: https://drive.google.com/drive/folders/1xkCy-0WqYvPA9ooq8txTdc0GsGC-YXMq?usp=share_link.

The data organization is as below.



Data organization of examples

1. HCP surface data. (2 subjects, 2 scans per subject, 400 volumes per scan) in .mat format.
Precomputed results of 10 subject data are stored in subfolder "Test_FN17".
2. PNC surface data (2 subjects, 1 scan per subject, 300 volumes per scan) in .mgh format.
Precomputed results of 10 subject data are stored in subfolder "Test_FN17".
3. UKBB volume data (2 subjects, 1 scan per subject, 200 volumes per scan) in .nii.gz format.
Precomputed results of 10 subject data are stored in subfolder "Test_FN17".

Each data folder contains simulated data organized by their subject ID, noted by a number, and scan information for multiple fMRI sessions or scans. For example,

Each precomputed result folder contains six subfolders. Each subfolder corresponds to one module in the pNet APP. For example, subfolder "Load_Data" contains setting information, fMRI scan list, brain mask file and others, which is required to be set in the data loading module.

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