

### aBEAT Tutorial

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# About aBEAT

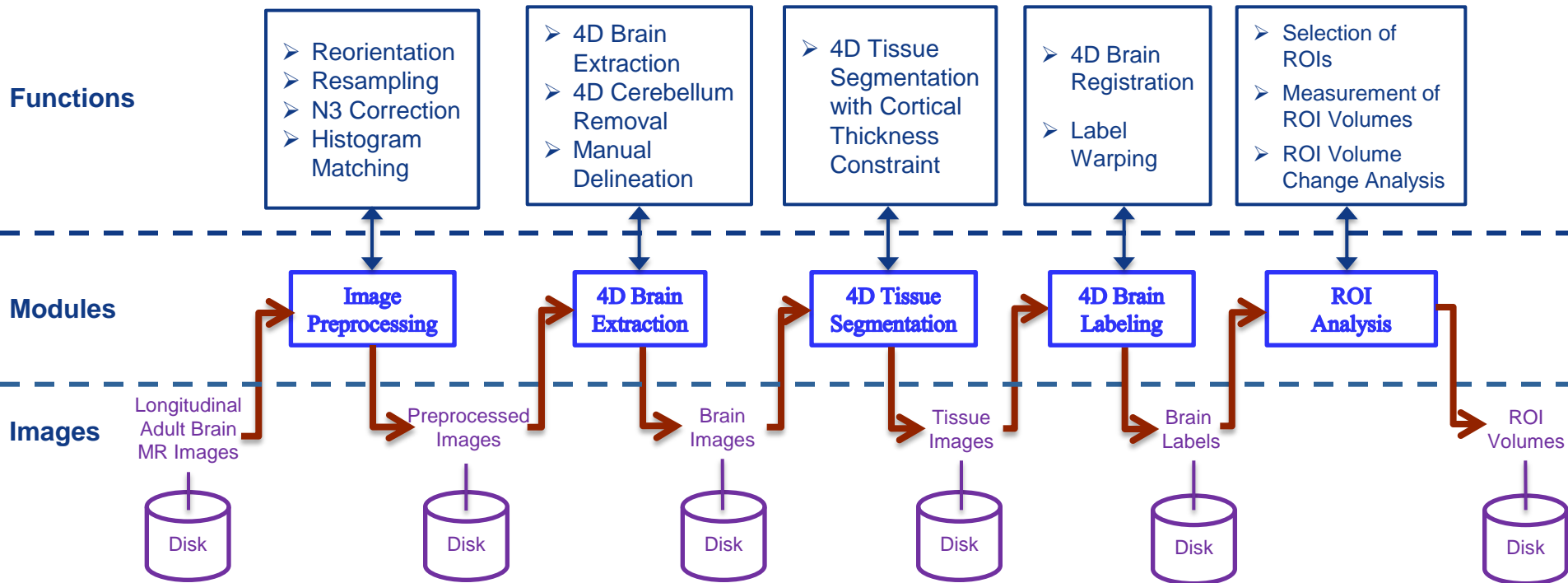
**aBEAT** is a 4D **A**dult **B**rain **E**xtraction and **A**nalysis **T**oolbox with graphical user interfaces to segment, label and analyze longitudinal adult brain MR images.

The **aBEAT** is developed by the IDEA group at the University of North Carolina at Chapel Hill, directed by Dr. Dinggang Shen ([dinggang\\_shen@med.unc.edu](mailto:dinggang_shen@med.unc.edu)).



# About aBEAT

## The architecture of the aBEAT toolbox



## Overview of the Processing Modules

*The longitudinal adult brain MR images of each subject are processed as follows:*

### **1. Image Preprocessing:**

- (a) Reorient original T1 images to the same orientation as the template image (Colin27, eyes right).
- (b) Resample the images to the standard size and resolution (256x256x256 and 1x1x1 mm<sup>3</sup>, as the template image).
- (c) Perform N3 correction on the images.
- (d) Match the histograms of the other time point images to the histogram of the baseline image (1st time point).

### **2. 4D Brain Extraction:**

- (a) Perform 4D brain extraction to extract the brains from the preprocessed images.
- (b) Perform 4D cerebellum removal.
- (c) The automatically extracted brain images can be edited manually to obtain more accurate brain images (optional).

### **3. 4D Tissue Segmentation:**

- Segment the gray matter, white matter and CSF tissues from the extracted brain images longitudinally.

### **4. 4D Brain Labeling:**

- Longitudinal brain images are simultaneously registered to an implicit common template image, which will be registered with the Colin27 template image. The pre-labeled image of the Colin27 template will then be warped to the spaces of the original individual brain images to label the individual brain images.

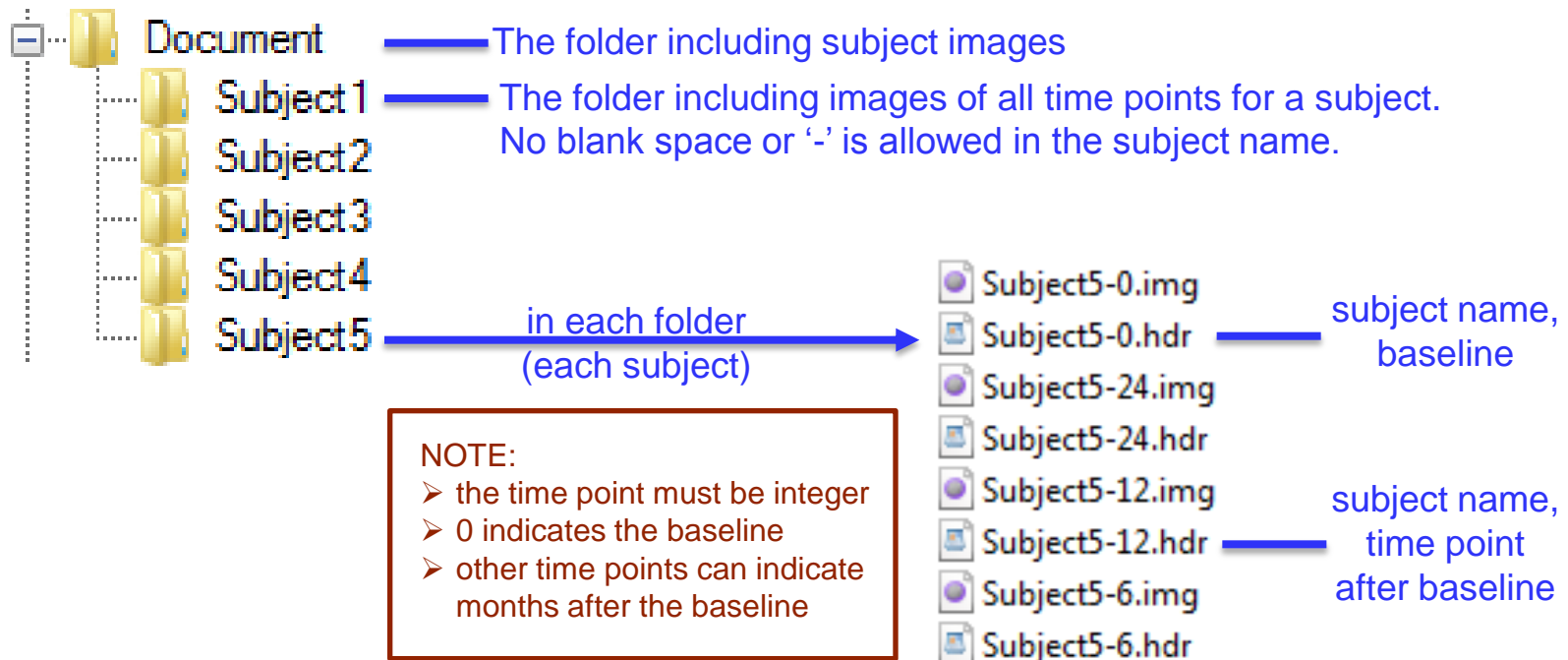
### **5. ROI Analysis:**

- ROIs are selected from the brain labels (45 labels in each hemisphere) or the brain tissues (GM, WM, CSF), and the volumes of the selected ROIs of the longitudinal brain images are measured. The ROI volume change with time can be analyzed.



## Arrangement of Subject Images for aBEAT

- Image modality – T1
- File format – analyze (.hdr with .img)
- Subject image files should be arranged as follows:



# aBEAT Installation

- Operating system: Linux (64 bit)
- Recommended computer: memory  $\geq$  8G, disk  $\geq$  30G
- Installation steps:
  - Download the aBEAT package and unzip the aBEAT.zip (e.g., the package is unzipped in /home/programs/aBEAT).
  - Setup environment for the aBEAT as follows:
    - ❖ Edit the shell resource file in the home directory of the user (**cd ~**):
      - for **csh/tcsh** user, add the following two lines in the .cshrc file:  
*setenv ABEAT\_HOME /home/programs/aBEAT*  
*source \$ABEAT\_HOME/aBEAT.csh*
      - for **bash** user, add the following two lines in the .bashrc file:  
*export ABEAT\_HOME=/home/programs/aBEAT*  
*source \$ABEAT\_HOME/aBEAT.bash*
    - ❖ Restart the shell to update the environment.
  - Use command aBEAT or abeat to start the software.



When you run aBEAT on a computer without enough memory size, or when you want to process a large number of subjects automatically, the aBEAT may run out of the memory. Following are the solutions:

- option 1: increase virtual memory in your Linux system.
- option 2: use command **aBEAT -s** or **abeat -s** to start the software, which will process data sequentially and take less memory, but will take more time.





- Questions ?

There are Frequently Asked Questions (FAQ) listed in the **FAQ.txt** file in the package. The FAQ will answer the questions you may have during the installation and use of the software.

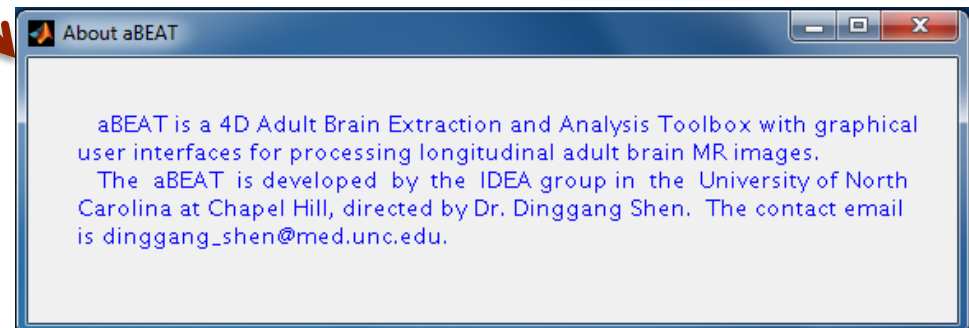
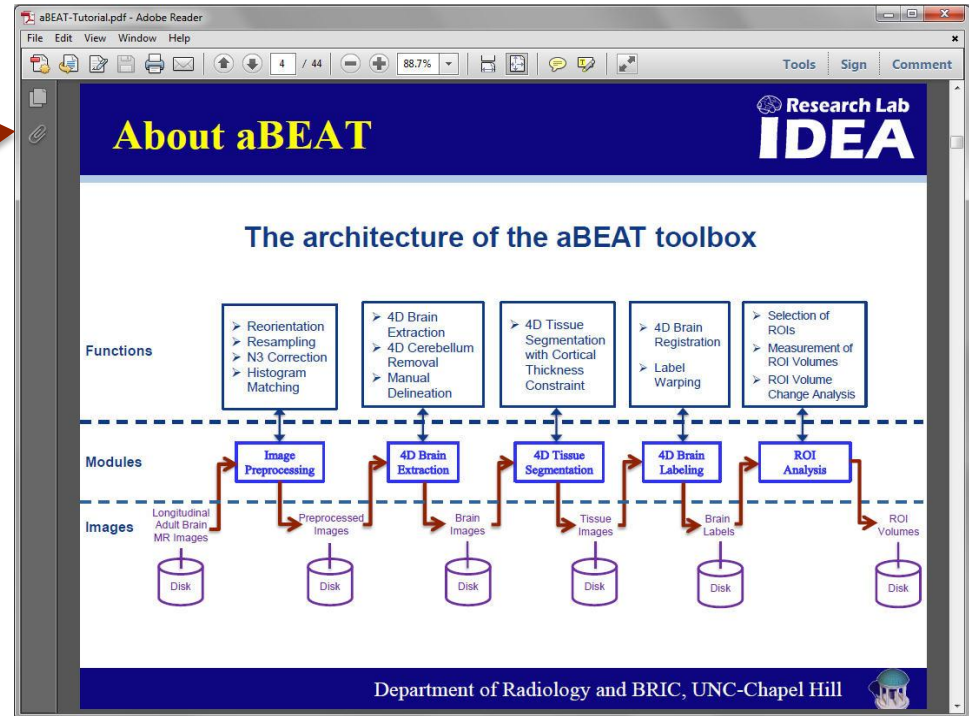
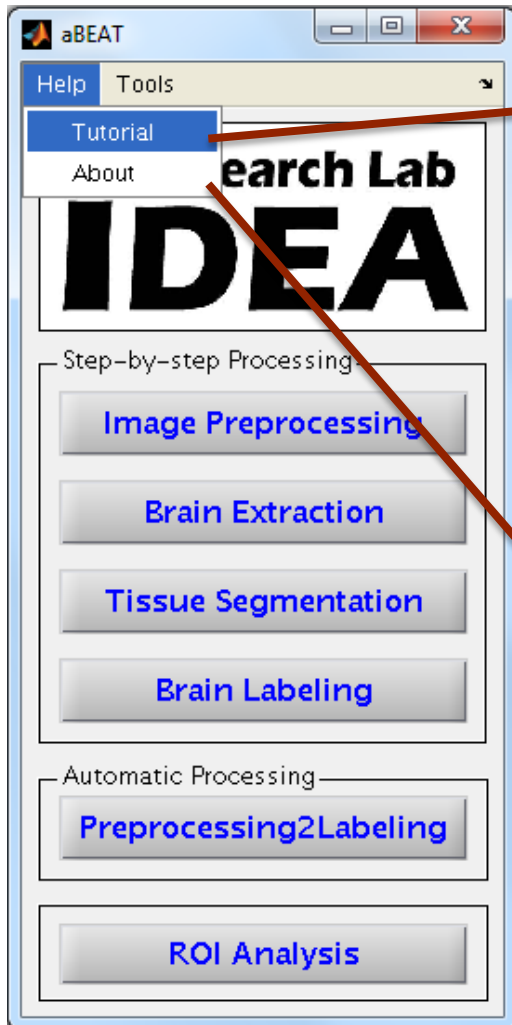
- Start to use

Please go through the FAQ and the following pages of this quick tutorial to learn how to use the software.

You could refer to the respective sections of this tutorial to use the corresponding modules.



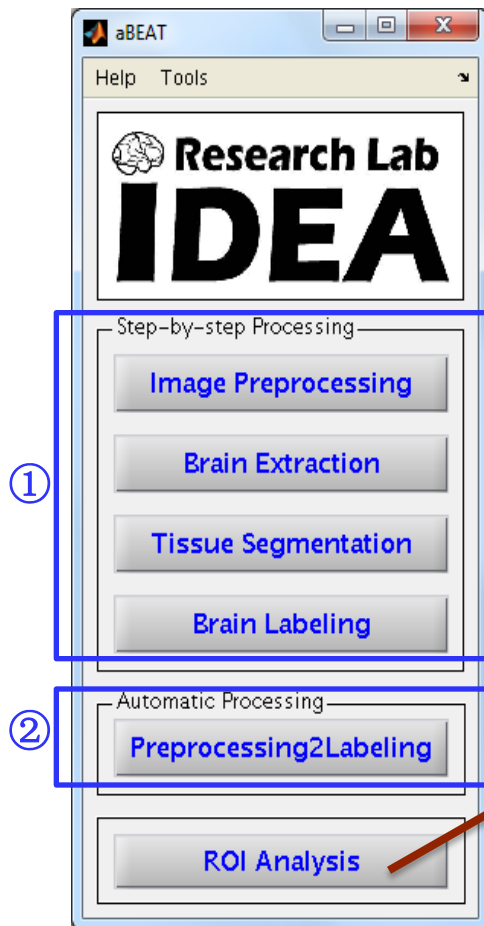
# Main Window



# Main Window

## Possible Processing Options:

(1) process subjects step by step (by ①); (2) process subjects automatically (by ②); (3) process one of your subjects step by step (by ①) to customize parameter values and evaluate results, then process the other subjects automatically from image preprocessing to brain labeling (by ②) using customized parameter values.



❖ Perform image preprocessing, brain extraction, tissue segmentation, and brain labeling on subject images step by step.

❖ Process subject images automatically from image preprocessing to brain labeling.

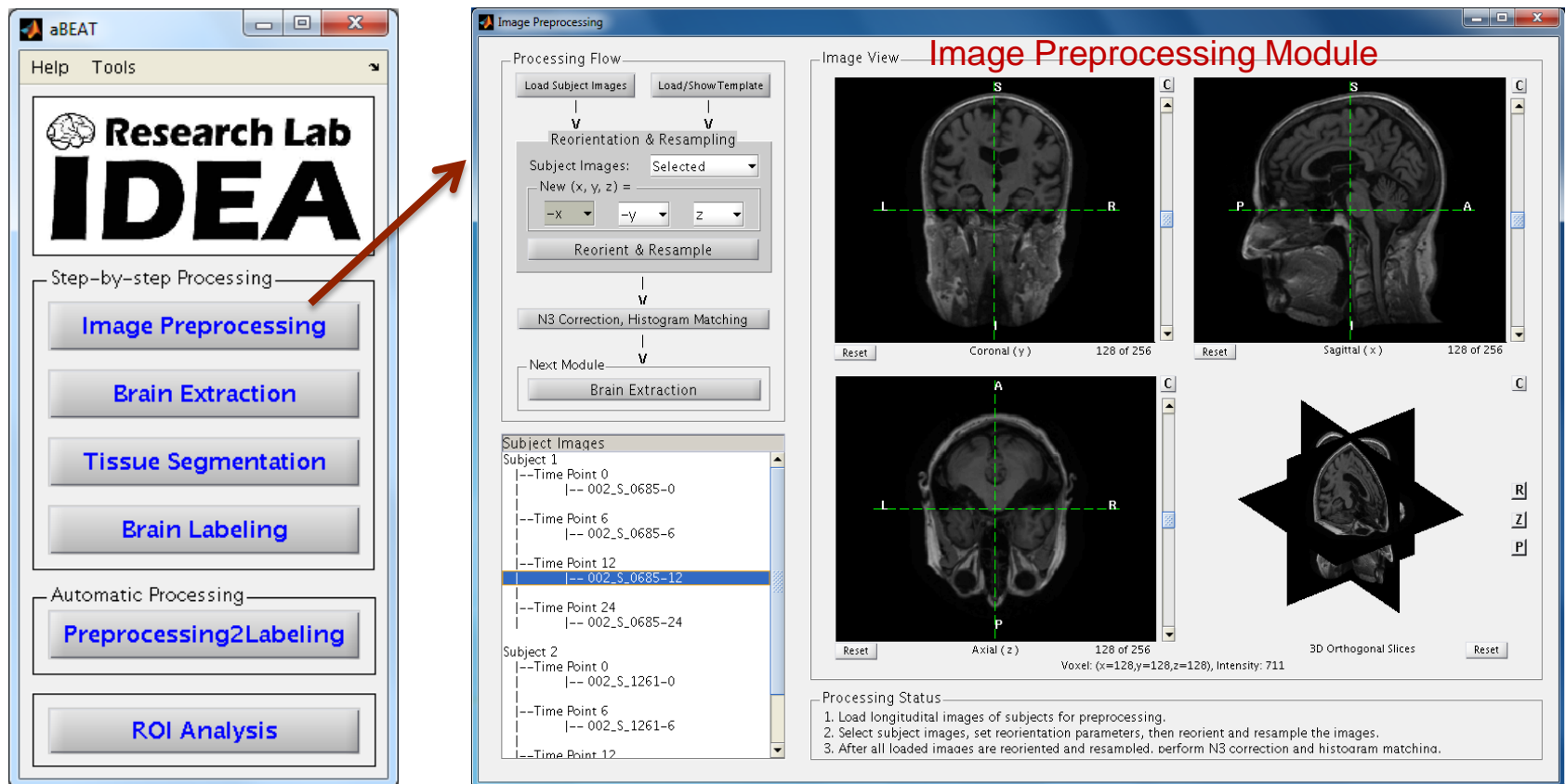
❖ After all subjects are processed, you can analyze ROIs from brain-labeled images or tissue-segmented images of the subjects.



# Image Preprocessing

## Functionality of the Image Preprocessing Module:

- Reorient and resample original images to the same orientation and size as the template image. N3 correction is then performed on the images. For each subject, match the histogram of each image to the histogram of the baseline image.

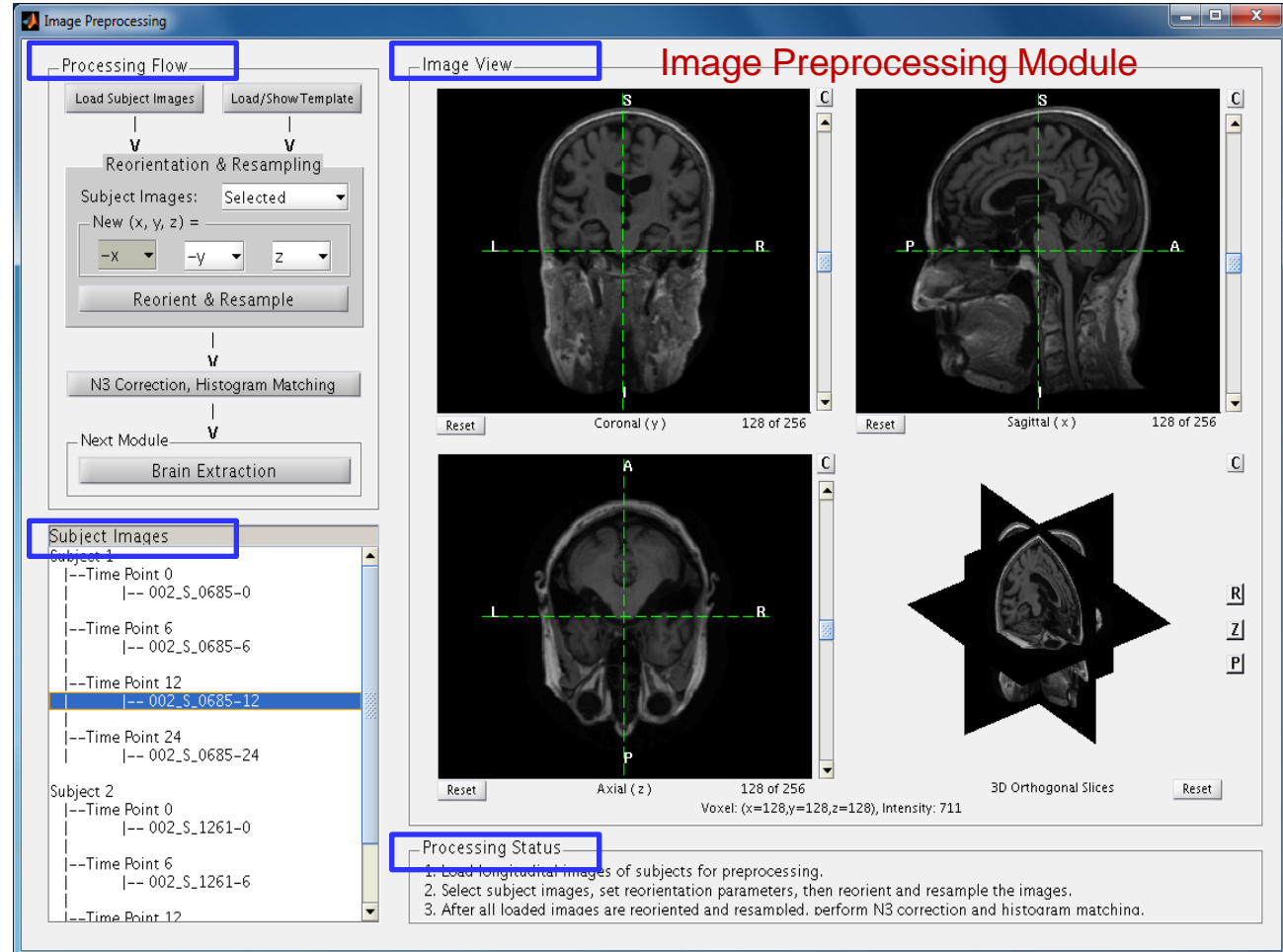


# Image Preprocessing

## Functionality of the Image Preprocessing Module:

It consists of four parts:

- **Processing Flow:**  
the pipeline integrating step-by-step functions for image preprocessing.
- **Subject Images:**  
lists all loaded images and the processed images
- **Image View:**  
windows for interactive inspection of the images.
- **Processing Status:**  
show image preprocessing steps and data processing status.



# Image Preprocessing

## Step 1: Image Loading

**Image Preprocessing**

Processing Flow

1. Load Subject Images

2. Reorientation & Resampling

3. N3 Correction, Histogram Matching

4. Next Module

5. Brain Extraction

Image View

Reset

Processing Status

1. Load longitudinal
2. Select subject in
3. After all loaded

**Load Subject Images**

Image Loading Module

Subject: Automatic Time Point: Automatic

3. Add Images

Finish

Subject 1

- Time Point 0 |-- 002\_S\_0685-0
- Time Point 6 |-- 002\_S\_0685-6
- Time Point 12 |-- 002\_S\_0685-12
- Time Point 24 |-- 002\_S\_0685-24

Subject 2

- Time Point 0 |-- 002\_S\_1261-0
- Time Point 6 |-- 002\_S\_1261-6
- Time Point 12 |-- 002\_S\_1261-12
- Time Point 24 |-- 002\_S\_1261-24

subject images will be loaded automatically.

**Select Directory to Open**

Look In: sample

4. select the folder including subject images

File Name: /home/programs/abeat/sample

Files of Type: All Files

5. OK Cancel

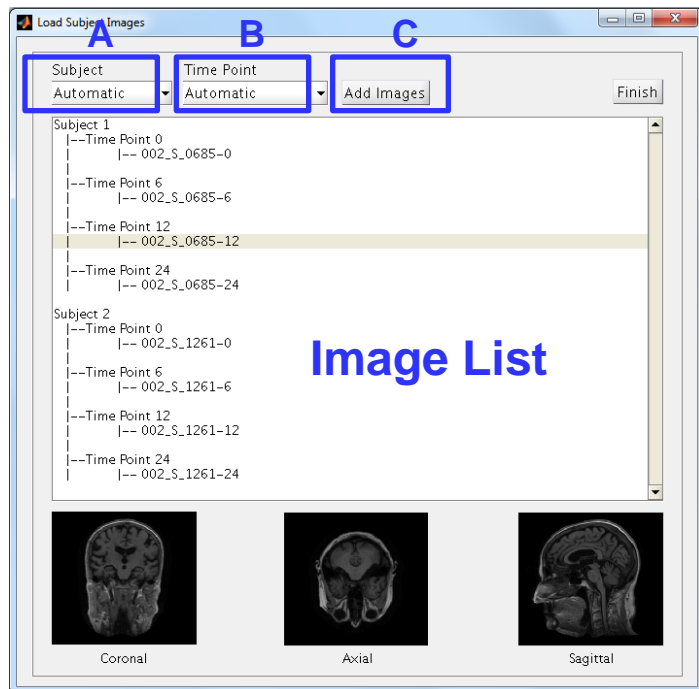
Coronal Axial Sagittal



# Image Preprocessing

## Functions in the Image Loading Module:

1. Load images of all subjects: select 'Automatic' in **A** → **C** → select the folder including all the subjects.
2. Add all images of a subject: select 'Subject j' in **A** and 'Automatic' in **B** → **C** → select the j-th subject folder.
3. Add an image at a time point for a subject: select 'Subject i' in **A**, 'Time Point j' in **B** → **C** → select the i-th time point image.



4. Preview an image: left mouse click the image name to display three orthogonal slices of the image.

**NOTE:** the displayed slices may not be consistent with the 'Axial', 'Coronal' and 'Sagittal' statement before reorientation.

5. Delete a selected (left mouse click to select) image: right mouse click in the image list window and press the 'Delete Images' popup menu.
6. Delete images at a time point: left mouse click a time point (e.g., Time Point 12) → right mouse click and press the 'Delete Images' popup menu.
7. Delete all images of a subject: left mouse click a subject (e.g., Subject 1) → right mouse click and press the 'Delete Images' popup menu.
8. Delete selected images: use 'Shift' or 'Ctrl' key and left mouse button to select images → right mouse click and press the 'Delete Images' popup menu.

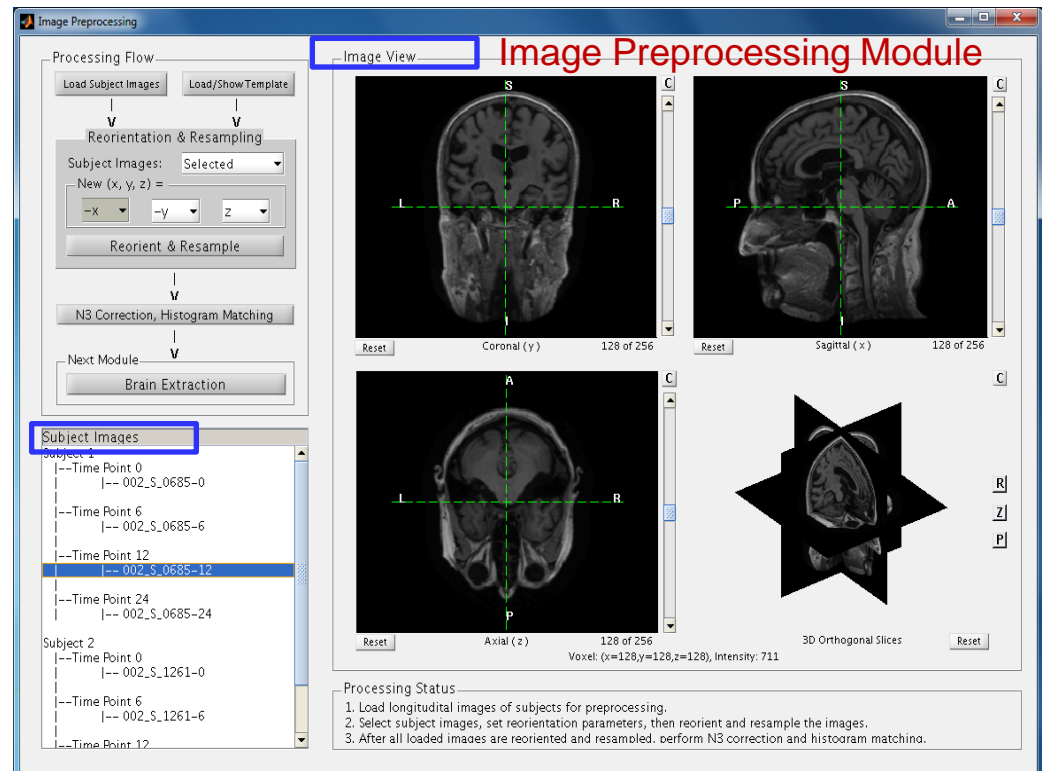
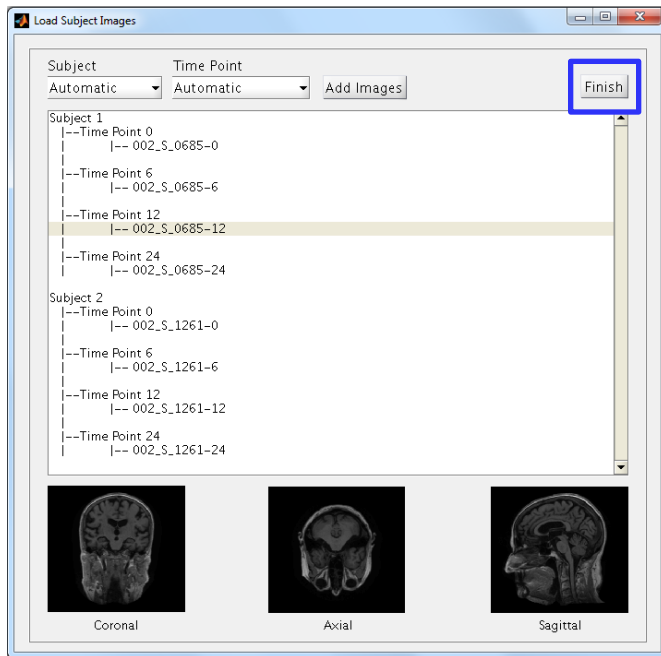




# Image Preprocessing

## Step 2: Interactive Image Inspection

- After all subject images are loaded, press **'Finish'** to return to the Image Preprocessing Module. The loaded images will be in the **'Subject Images'** list.
- Left mouse click an image in the **'Subject Images'** list to display three orthogonal 2D slices and 3D slices of the image.
- Right mouse click in the **'Subject Images'** list to view the property of the selected image, or delete the image.
- **Review slices:** mouse wheel over the 2D slices (in the **'Axial'**, **'Coronal'** and **'Sagittal'** windows), or use the slider.
- **Zoom in/out 2D slices:** right mouse button down (over the 2D slices) and move up/down.
- **Pan 2D slices:** left mouse button down (over the 2D slices) and drag.
- **Cross:** left mouse button down (over the 2D slices)



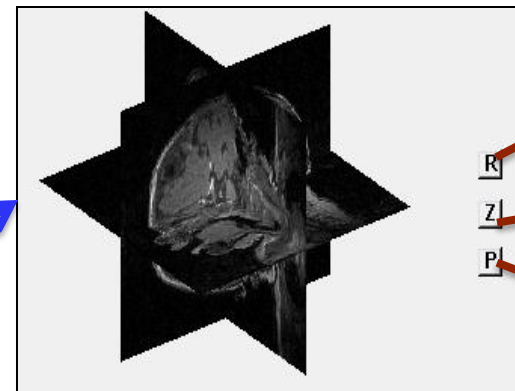
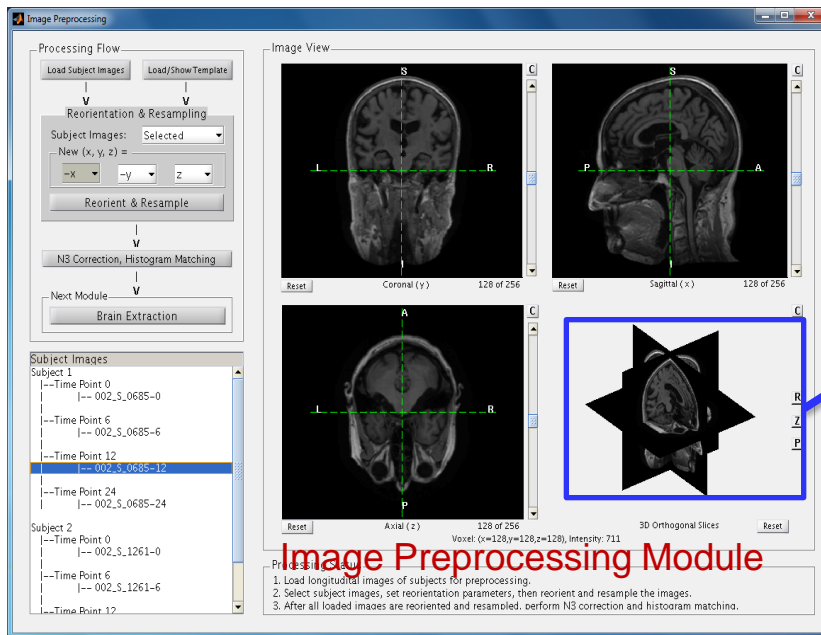


# Image Preprocessing

## Step 2: Interactive Image Inspection (3D slices)

- **Rotate 3D slices:** press the toggled button 'R', then left mouse button down upon the 3D slices and move the mouse
- **Zoom 3D slices:** press the toggled button 'Z', then left mouse button down upon the 3D slices and move up/down
- **Pan 3D slices:** press the toggled button 'P', then left mouse button down upon the 3D slices and move the mouse

**NOTE:** Click the toggled button 'R', 'Z' and 'P' to enable or disable the related manipulation functions.



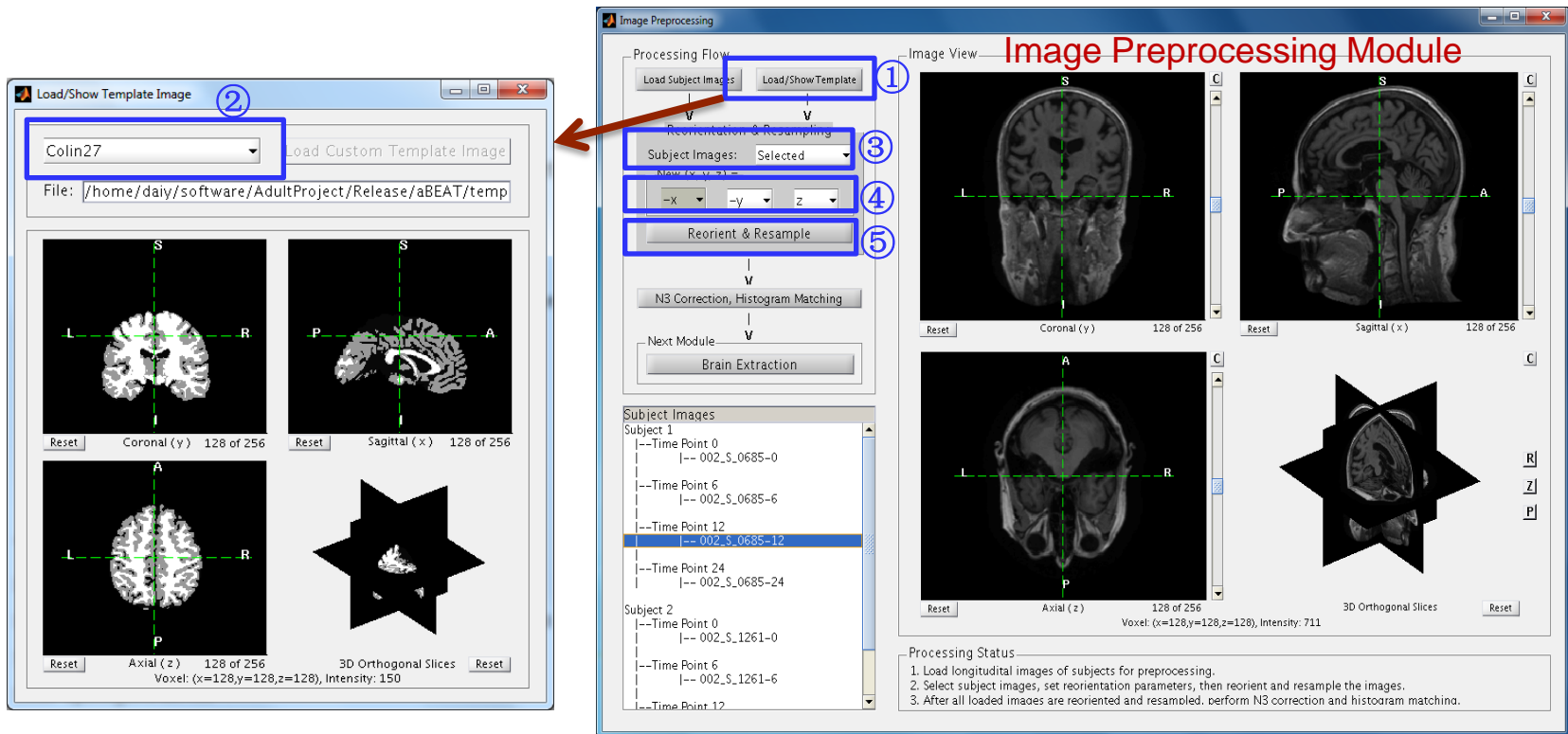
**R** → Rotate  
**Z** → Zoom  
**P** → Pan



# Image Preprocessing

## Step 3: Image Reorientation and Resampling

- The loaded images must be reoriented and resampled to the same orientation and size as the template. The template is used in the preprocessing and brain labeling steps. **The standard orientation used in aBEAT is shown in the left image and the template has volume size (256x256x256) and voxel size (1x1x1 mm<sup>3</sup>).**
- Reorient and resample the loaded images by: ③ (determine the loaded images to be reoriented and resampled) -> ④ (set reorientation parameters) -> ⑤ (reorient and resample the related loaded images)
- **The processed images will be saved as analyze format and stored with the original image files.**



# Image Preprocessing

## Step 3: Image Reorientation and Resampling

- Preview reorientation and resampling result of a selected image: choose 'Selected' option in ① -> select a loaded image in ② (subject images list) -> set reorientation parameters in ③ -> ④.
- Reorient and resample multiple loaded images: choose 'Selected' option in ① -> select multiple loaded images (use Ctrl/Shift and mouse) in ② -> set reorientation parameters in ③ -> ④.
- Reorient and resample All loaded images: choose 'All' option in ① -> set reorientation parameters in ③ -> ④

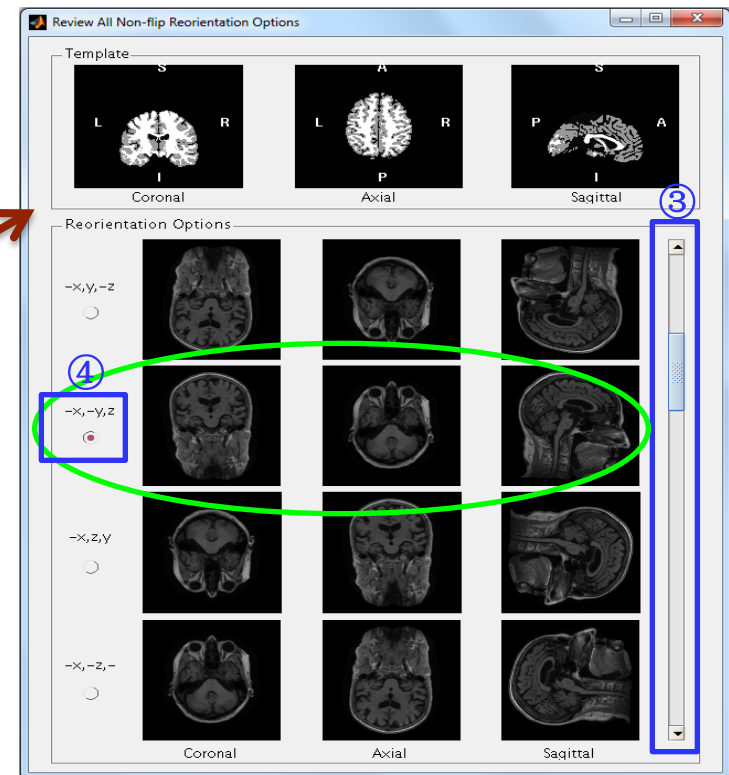
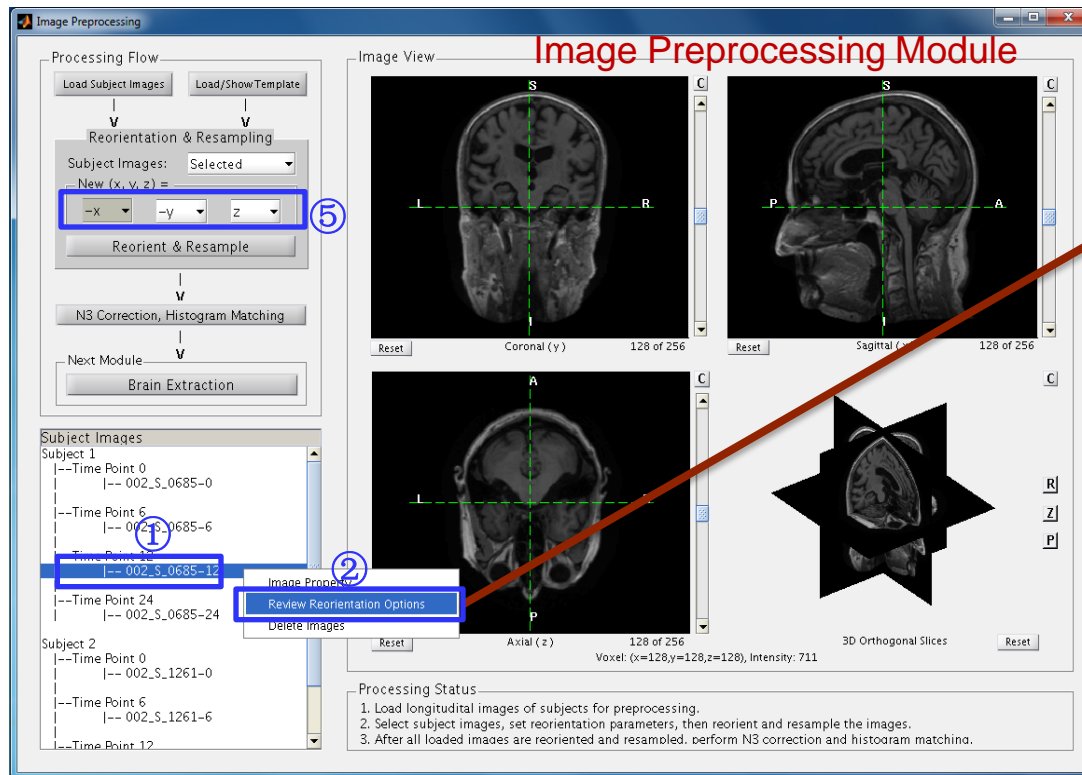
The screenshot shows the 'Image Preprocessing' window. On the left, a dropdown menu is open, showing 'Selected' (highlighted with a blue box and an arrow pointing to it), 'Selected', and 'All'. In the main window, the 'Processing Flow' section has 'Reorientation & Resampling' selected, with 'Subject Images: Selected' and 'Reorient & Resample' buttons highlighted with blue boxes and numbered ③ and ④ respectively. The 'Subject Images' list shows 'Subject 1' with time points 0, 6, 12, and 24, and 'Subject 2' with time points 0, 6, and 12. The 'Image View' section shows three orthogonal slices: Coronal (y), Sagittal (x), and Axial (z), each with a 'Reset' button. A '3D Orthogonal Slices' view is also shown. The 'Processing Status' section at the bottom lists three steps: 1. Load longitudinal images of subjects for preprocessing. 2. Select subject images, set reorientation parameters, then reorient and resample the images. 3. After all loaded images are reoriented and resampled, perform N3 correction and histogram matching.



# Image Preprocessing

## How to set the reorientation parameters ?

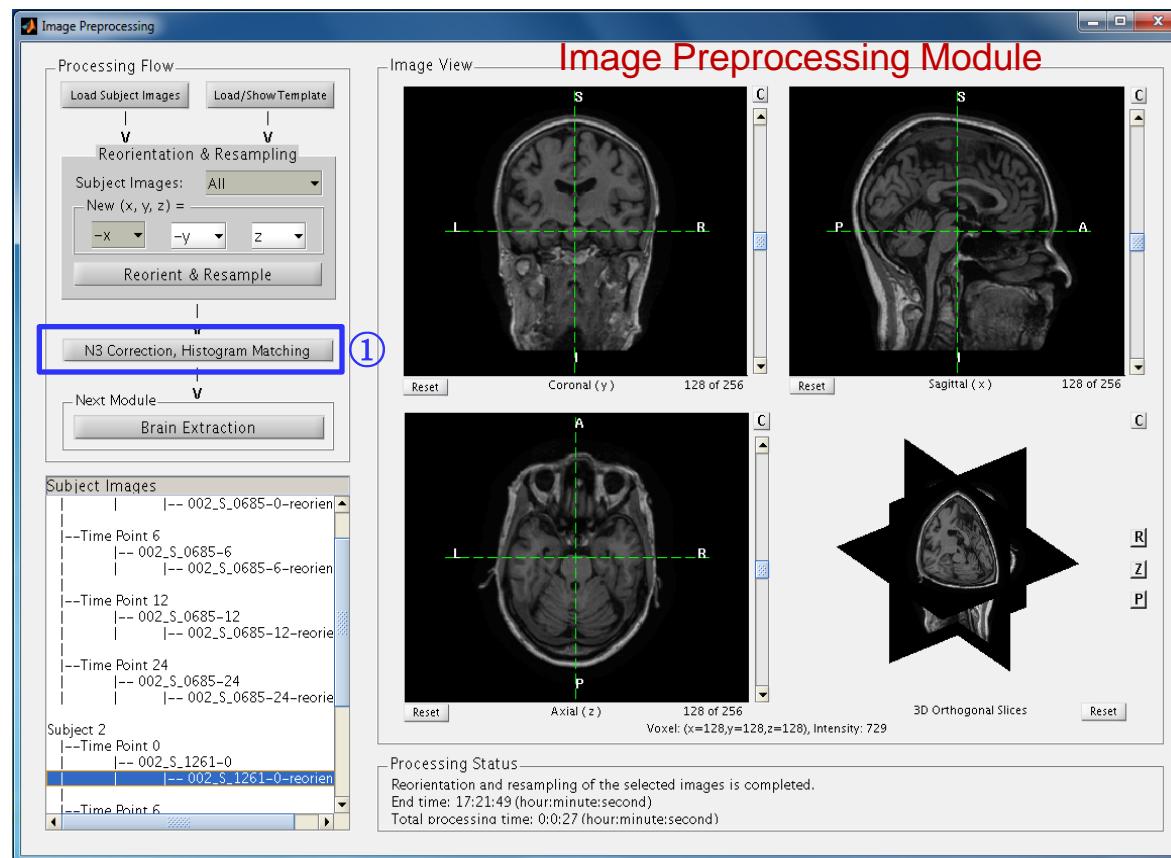
- Step 1: review all non-flip reorientation options by: ① (select a loaded image) -> ② (right click and choose 'Review Reorientation Options'). The selected image will be reoriented with all non-flip reorientation parameters, and the tentatively reoriented images with the parameters will be displayed.
- Step 2: review (use ③) and determine the correct reorientation parameters by comparing the reoriented images with the template image visually.
- Step 3: select the correct reorientation parameters (see ④), the parameters at ⑤ will be updated automatically.



# Image Preprocessing

## Step 4: N3 Correction and Histogram Matching

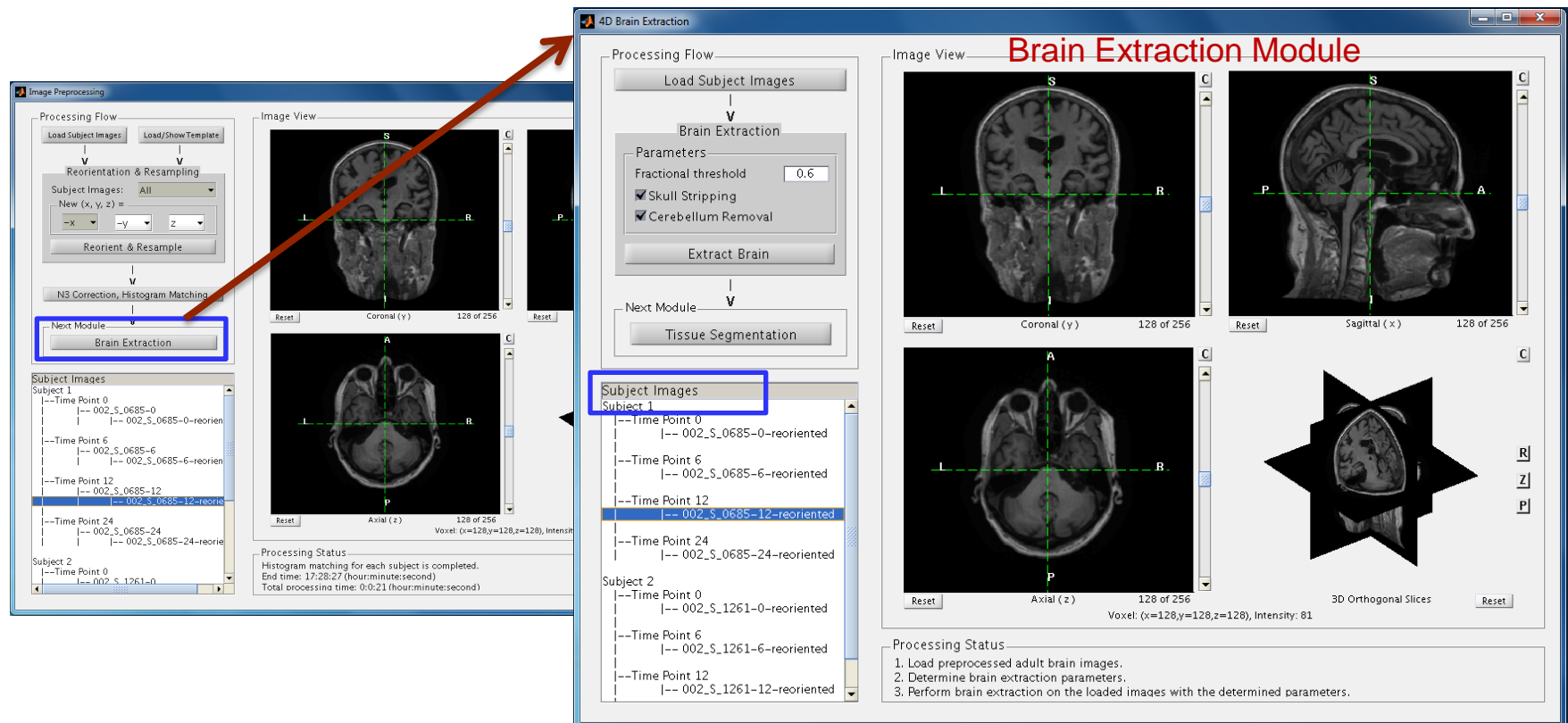
- After all loaded images are reoriented and resampled to the same orientation and size as the template, N3 correction and histogram matching can be performed on the processed images by ①.
- **NOTE: a processed image (e.g., subject-0-reoriented) is named by appending '-reoriented' to the name of the original un-processed image (subject-0).**



# Image Preprocessing

## Step 5: Start the Brain Extraction Module

- After all loaded images are preprocessed (reorientation, resampling, N3-correction, histogram matching) in the Image Preprocessing Module, press '**Brain Extraction**' to start the Brain Extraction Module.
- All the preprocessed images will be transferred into the '**Subject Images**' list of the Brain Extraction Module automatically, and the Image Preprocessing Module will be closed automatically.

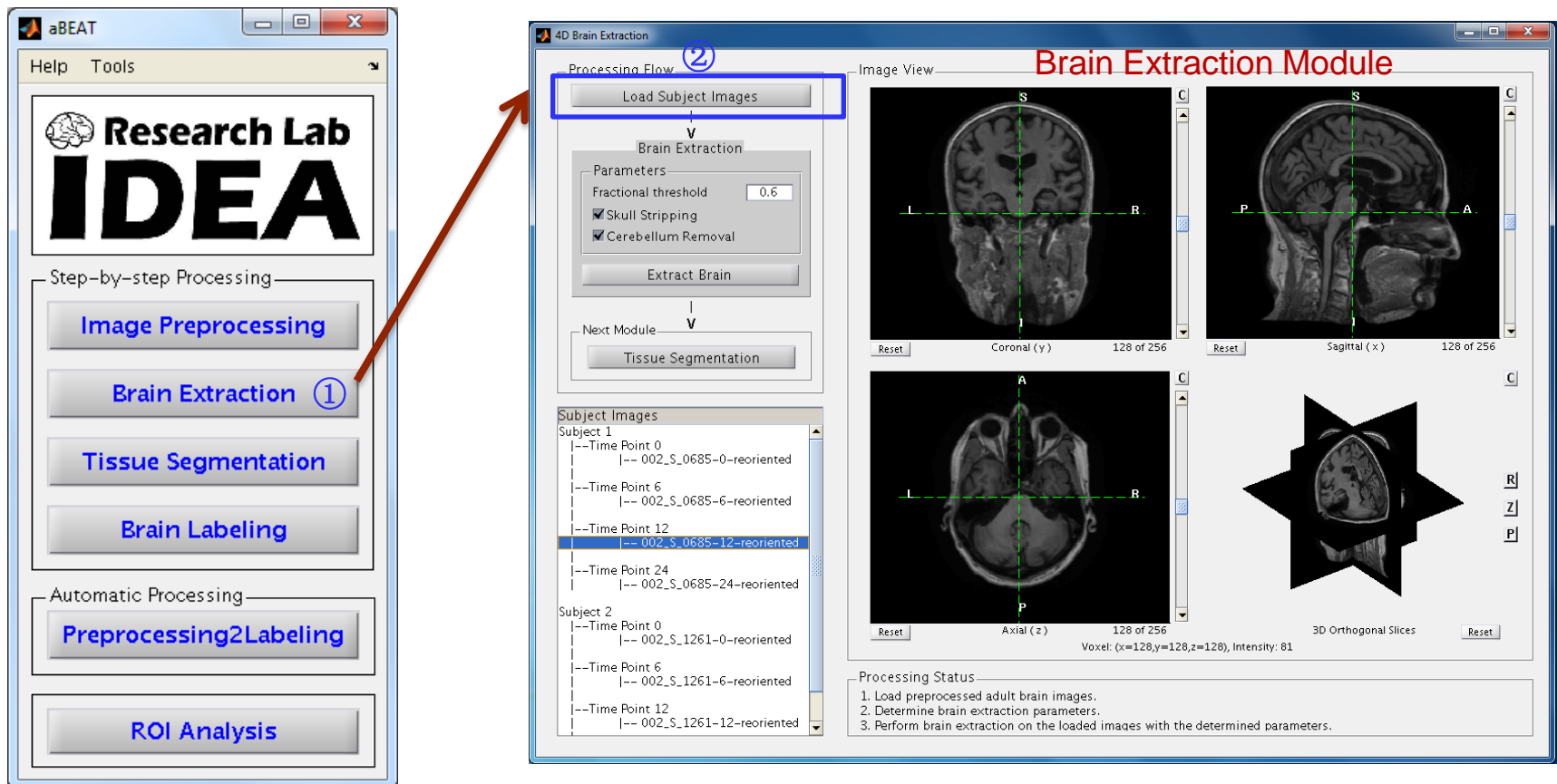




# Brain Extraction

## Step 1: Start the Brain Extraction Module

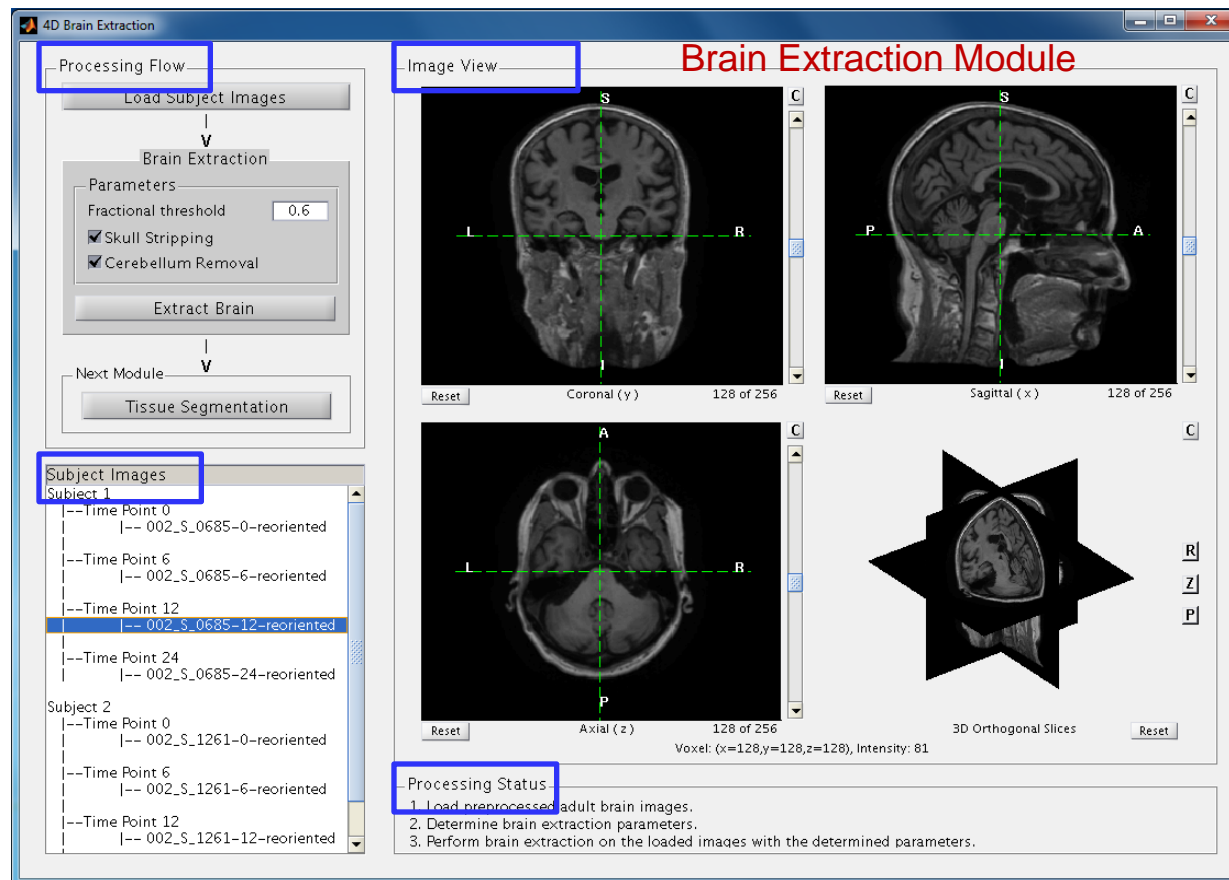
- Suppose preprocessed images are obtained by the Image Preprocessing Module, then **the Brain Extraction Module can also be started from the main window.**
- The preprocessed images (whose file names are ended with '**-reoriented**', can be found where the original un-reoriented images are) can be loaded by ② (the Image Loading Module will be started).



# Brain Extraction

## Functionality of the Brain Extraction Module:

- To perform **4D skull stripping** and **4D cerebellum removal** on the preprocessed images of each subject automatically. In addition, to **edit the automatically brain-extracted images manually** to obtain more accurate brain images (optional).
- The module structure is similar to the structure of the Image Preprocessing Module. Please refer to the image preprocessing for functions such as interactive image inspection.

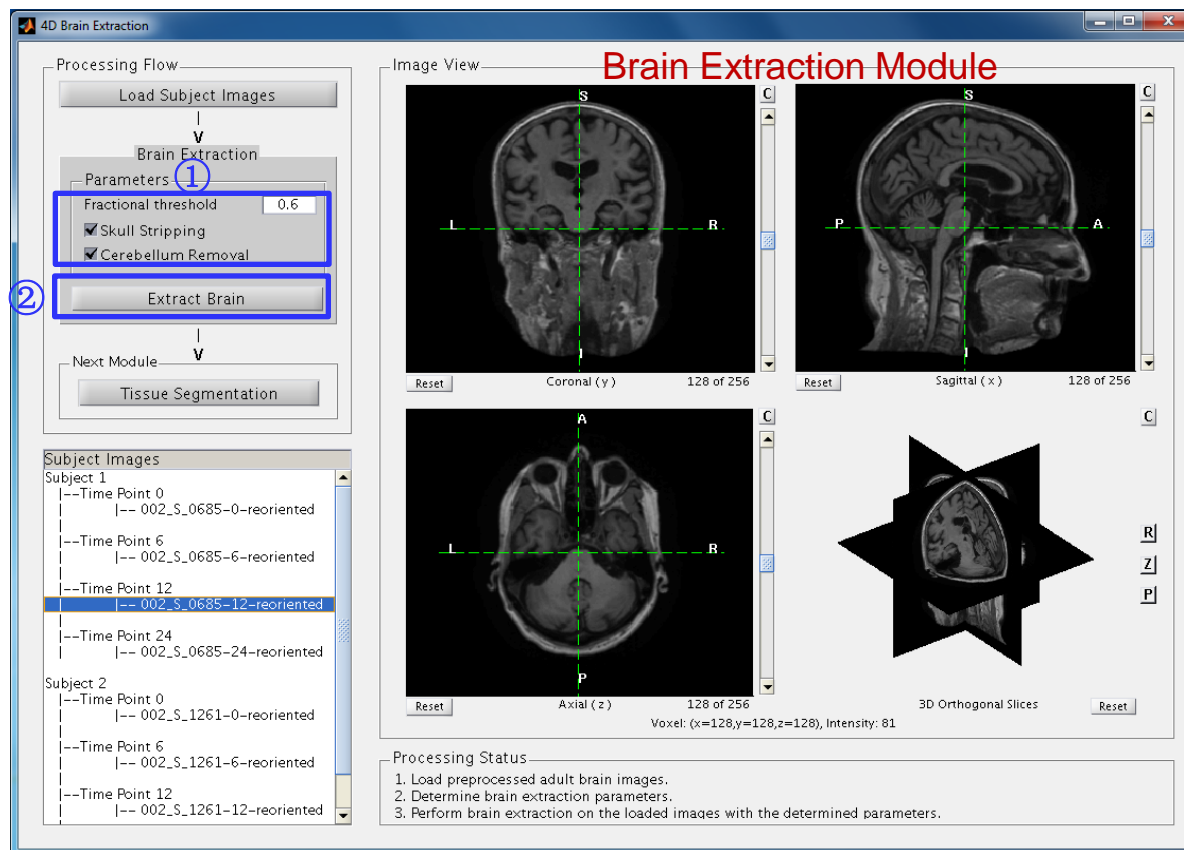




# Brain Extraction

## Step 2: Extract Brain Images

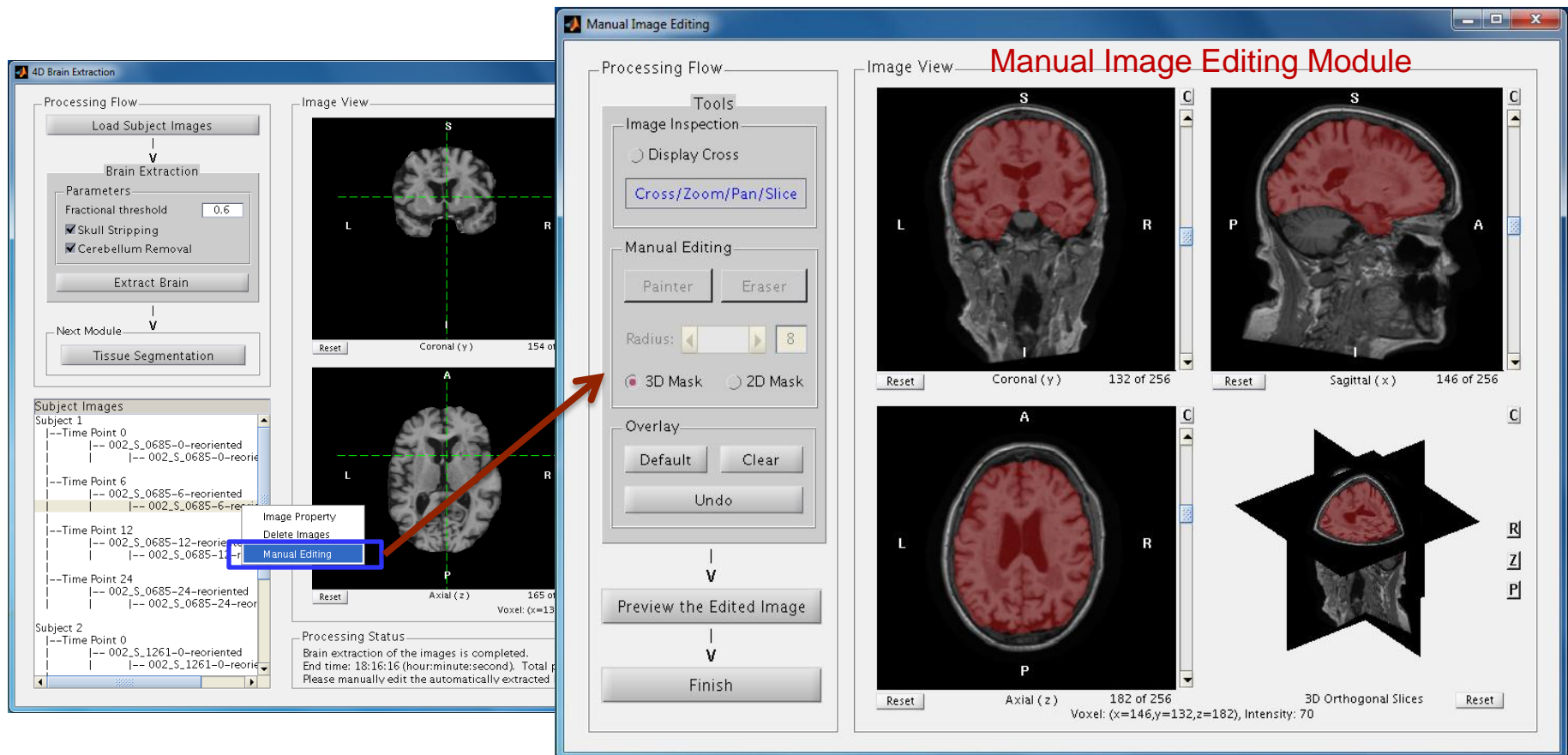
- Firstly set parameters for brain extraction by ①, then perform 4D brain extraction on the loaded images (preprocessed) by ②. Generally, the default parameters can be used. Larger fractional threshold will remove more brain tissues. **The extracted brain images will be saved as analyze format and stored with the original image files as well.**
- If the loaded images are skull-stripped, please check the 'Cerebellum Removal' only to remove the cerebellums without skull stripping.



# Brain Extraction

## Step 3: Manually Edit the Extracted Brain Images

- Select the automatically extracted brain image → right mouse click and select the 'Manual Editing' item on the popup menu.
- An overlay (red mask) from the automatically extracted brain image will be displayed with the un-extracted image (preprocessed image) in the Manual Image Editing Module.



# Brain Extraction

## Step 3: Manually Edit the Extracted Brain Images

1. Click **A** (the '**Cross/Zoom/Pan/Slice**' toggled button) and then interactive inspect the image:

- **Review slices:** mouse wheel over the 2D slices (in the '**Axial**', '**Coronal**' and '**Sagittal**' windows), or use the slider.
- **Zoom in/out 2D slices:** right mouse button down (over the 2D slices) and move up/down.
- **Pan 2D slices:** left mouse button down (over the 2D slices) and drag.
- **Cross:** left mouse button down (over the 2D slices).

2. Click **B/C** (the '**Painter**'/'**Eraser**' toggled button) and then **paint/erase** regions of interest **to/from** the overlay interactively.

- **Painter/Eraser size:** use the radius slider or just input the value (the radius size will be indicated in the slice windows, see the red circle under the cursor).
- **3D/2D Mask:** select 3D/2D Mask to make the painting or erasing operation effective in 3D volume/2D slice space.

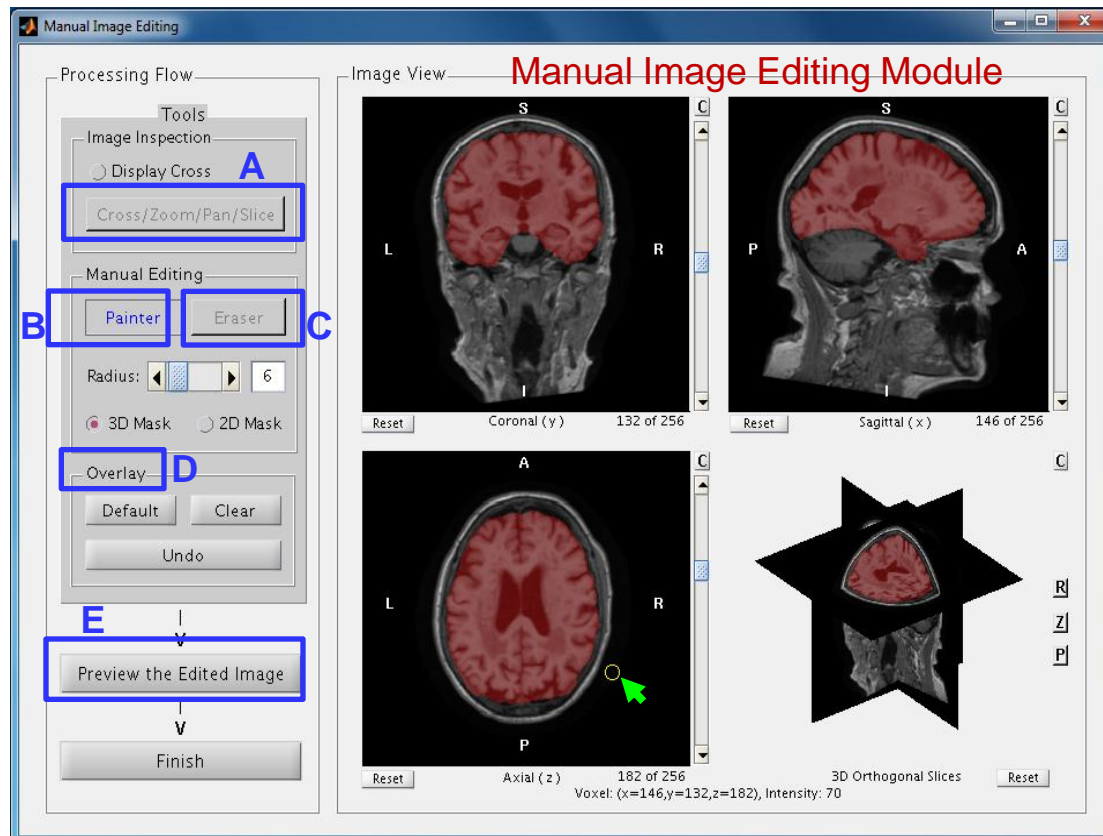
3. Overlay:

- Click '**Default**', '**Clear**' and '**Undo**' in **D** to load default overlay, clear the current overlay and undo the last painting (or erasing) operation, respectively.

4. Preview:

- Click **E** to preview the manually edited brain image obtained with the current overlay.

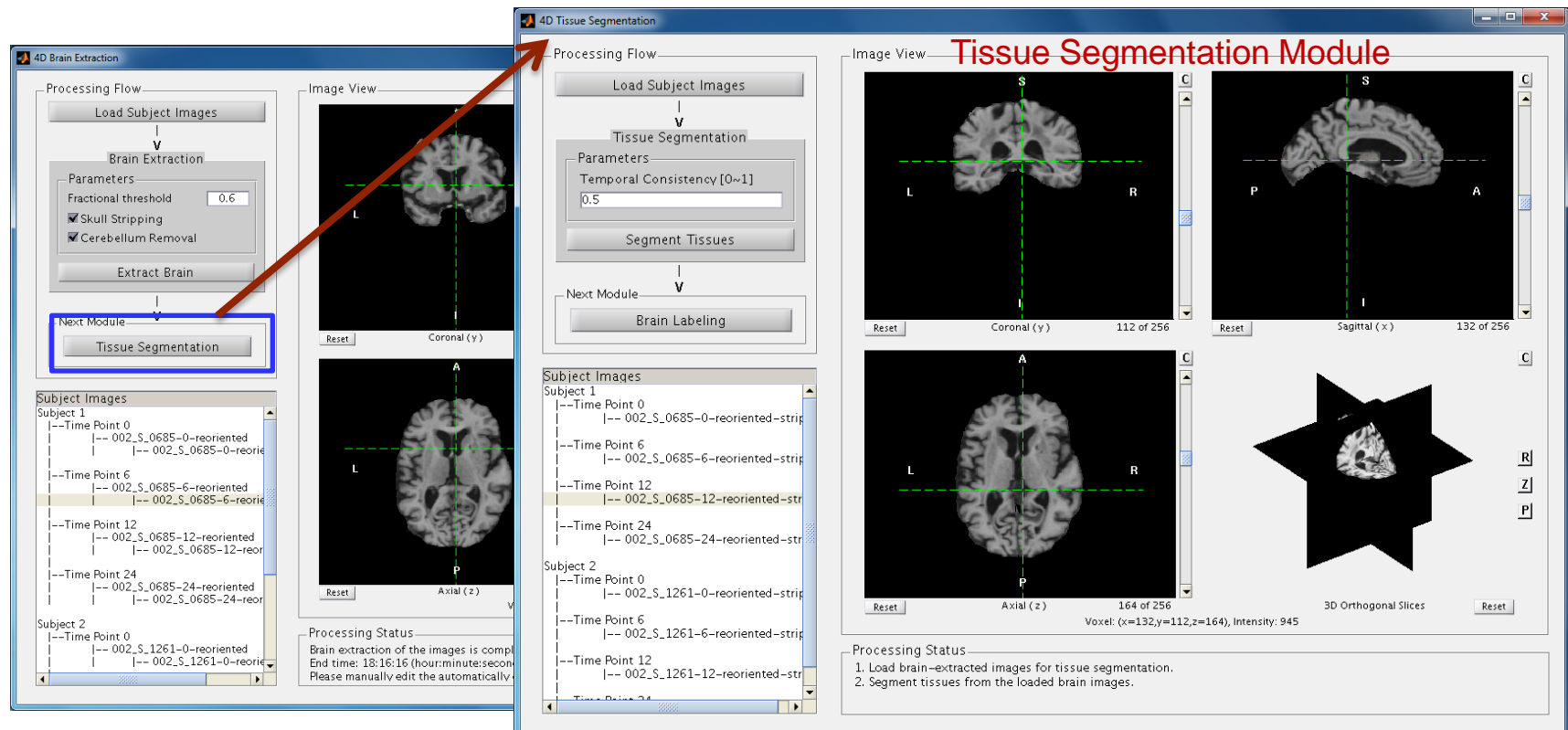
Click '**Finish**' when the manually edited brain image is satisfactory.



# Brain Extraction

## Step 4: Start the Tissue Segmentation Module

- After all brain images are extracted (cerebellum removal and manual image editing may be applied) from the loaded images (preprocessed) in the Brain Extraction Module, press '**Tissue Segmentation**' to start the Tissue Segmentation Module.
- All the extracted brain images will be transferred into the '**Subject Images**' list of the Tissue Segmentation Module automatically, and the Brain Extraction Module will be closed automatically. **NOTE: an extracted brain image (subject-0-reoriented-strip) is named by appending '-strip' to the name of the preprocessed image (subject-0-reoriented).**



# Tissue Segmentation

## Step 1: Start the Tissue Segmentation Module

➤ Suppose extracted brain images are obtained by the Brain Extraction Module, then **the Tissue Segmentation Module can also be started from the main window.**

➤ The extracted brain images (whose file names are ended with **'-strip'**, can be found where the original un-preprocessed and preprocessed images are) can be loaded by ② (the Image Loading Module will be started).

The screenshot displays the aBEAT software interface, which is divided into several sections:

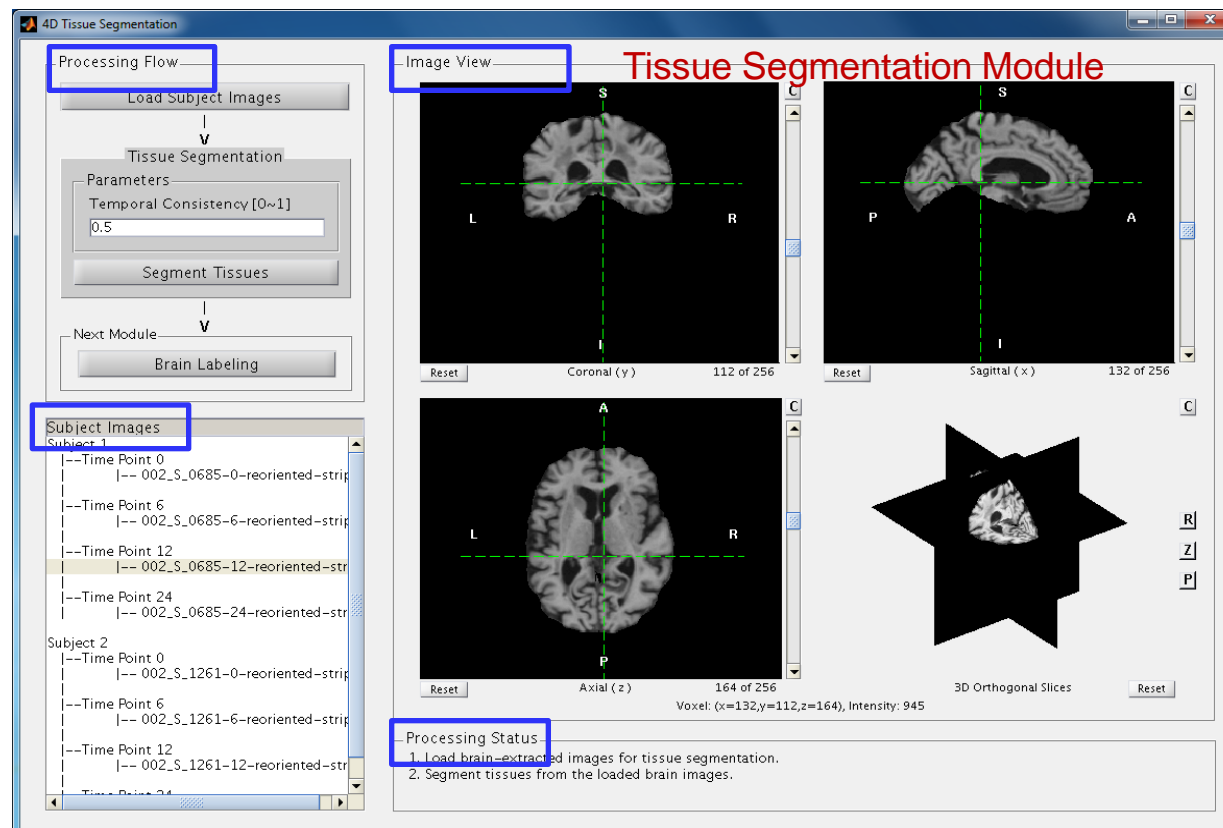
- Main Window (Left):** Features the Research Lab IDEA logo and a "Step-by-step Processing" sidebar. The sidebar includes buttons for "Image Preprocessing", "Brain Extraction", "Tissue Segmentation" (highlighted with a red circle and labeled ①), and "Brain Labeling". Below this is an "Automatic Processing" section with buttons for "Preprocessing2Labeling" and "ROI Analysis".
- 4D Tissue Segmentation Module (Center):** A sub-window showing the processing flow. It includes a "Load Subject Images" button (highlighted with a red box and labeled ②), a "Tissue Segmentation" section with a "Parameters" field for "Temporal Consistency [0~1]" set to 0.5, and a "Segment Tissues" button. Below this is a "Next Module" section with a "Brain Labeling" button. A "Subject Images" list shows two subjects with multiple time points, each ending in "-strip".
- Image View (Right):** Displays three orthogonal slices of a brain image: "Coronal (y)", "Sagittal (x)", and "Axial (z)". Each slice has a "Reset" button. Below the slices is a "3D Orthogonal Slices" view showing a 3D reconstruction of the brain. The "Processing Status" section at the bottom right lists the steps: "1. Load brain-extracted images for tissue segmentation." and "2. Segment tissues from the loaded brain images."



# Tissue Segmentation

## Functionality of the Tissue Segmentation Module:

- To perform **4D tissue segmentation** on the extracted brain images of each subject automatically. The module structure is similar to the structure of the Image Reorientation Module. Please refer to the image preprocessing for functions such as interactive image inspection.



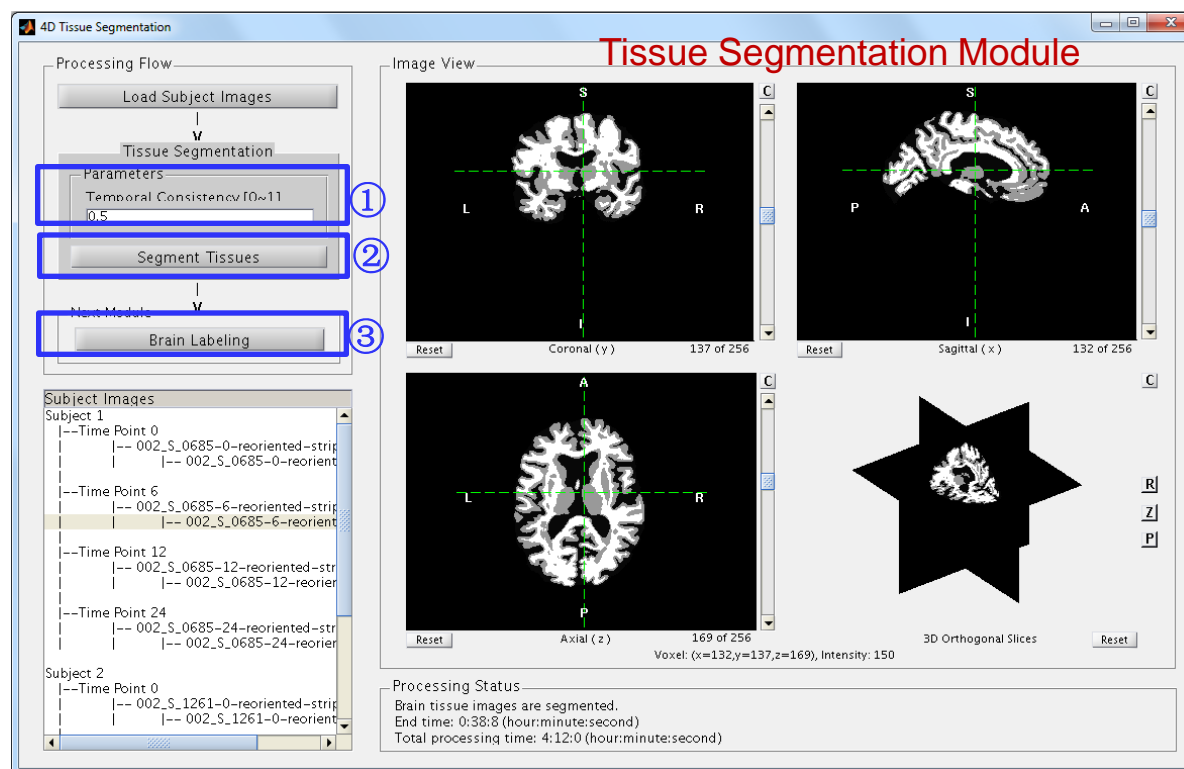


# Tissue Segmentation

## Step 2: Segment Tissues and Start the Brain Labeling Module

➤ 4D tissue segmentation on the loaded images (extracted brain images) can be performed by ① -> ②. **The longitudinally segmented tissue images will be saved as analyze format and stored with the original image files as well. A segmented tissue image is named as, e.g., subject-0-reoriented-strip-seg, which has a '-seg' postfix.**

➤ After 4D tissue segmentation, press ③ ( 'Brain Labeling' ) to start the Brain Labeling Module. All the segmented tissue images will be transferred into the Brain Labeling Module.



# Brain Labeling

## Step 1: Start the Brain Labeling Module

➤ Suppose segmented tissue images are obtained by the Tissue Segmentation Module, then **the Brain Labeling Module can also be started from the main window.**

➤ The segmented tissue images (whose file names are ended with '-seg', can be found where the original un-preprocessed, preprocessed and extracted brain images are) can be loaded by ② (the Image Loading Module will be started).

The screenshot displays the aBEAT software interface, which is divided into several panels. On the left is the 'Main Window' with the 'Research Lab IDEA' logo and a 'Step-by-step Processing' section. This section contains five buttons: 'Image Preprocessing', 'Brain Extraction', 'Tissue Segmentation', 'Brain Labeling' (marked with a circled 1), and 'ROI Analysis'. Below this is an 'Automatic Processing' section with a 'Preprocessing2Labeling' button. An orange arrow points from the 'Brain Labeling' button to the '4D Brain Labeling' window. The '4D Brain Labeling' window is the active module, showing a 'Processing Flow' diagram with steps: 'Load Subject Images' (marked with a circled 2), 'Load/Show Template', 'Brain Labeling', 'Label Brain', 'Next Module', and 'ROI Analysis'. Below the flow is a list of 'Subject Images' for 'Subject 1' and 'Subject 2', each with time points 0, 6, 12, and 24. The right side of the window is the 'Image View' section, titled 'Brain Labeling Module'. It contains three image displays: 'Coronal (y)' (137 of 256), 'Sagittal (x)' (132 of 256), and 'Axial (z)' (169 of 256). Each display shows a brain slice with green dashed lines indicating the axes. Below these is a '3D Orthogonal Slices' view showing a 3D brain model. At the bottom right, a 'Processing Status' section lists two steps: '1. Load tissue-segmented images for brain labeling.' and '2. Register and label the subject images with the template image.'



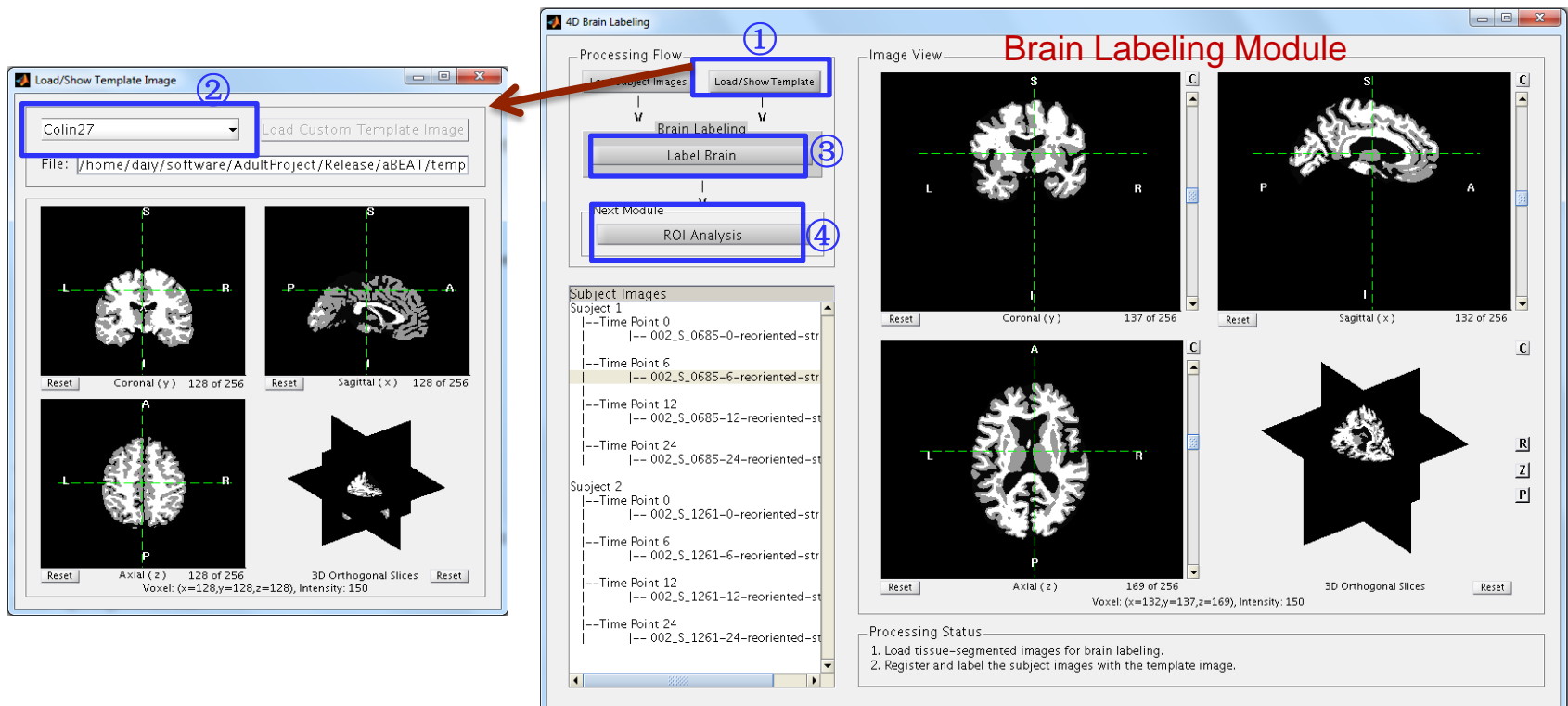


# Brain Labeling

## Step 2: Label Brain Images

➤ A template can be selected for 4D brain labeling. **NOTE: the standard template used in aBEAT is in the template folder of the package. Please make the orientation, image size and file format of a custom template the same as the ones of the standard template, and name the custom template similarly (refer to the template files).**

➤ 4D brain labeling on the subject images can be performed by ③. **The brain labels will be saved as analyze format and stored with the original image files as well (ended with '-aal').** **NOTE: the 4D brain labeling will use both the segmented tissue images and extracted brain images, please make sure they are available before 4D brain labeling.**



# Brain Labeling

## Brain Labels

- There are totally 90 labels (45 in each hemisphere) in each labeled brain image ('aal' image). The anatomical descriptions of the labels are detailed in the following table. The parcellation was defined by "N. Tzourio-Mazoyer et al, Neuroimage, 15: 273-289, 2002"

Index	Region	Index	Region
1	Precentral gyrus left	46	Cuneus right
2	Precentral gyrus right	47	Lingual gyrus left
3	Superior frontal gyrus (dorsal) left	48	Lingual gyrus right
4	Superior frontal gyrus (dorsal) right	49	Superior occipital gyrus left
5	Orbitofrontal cortex (superior) left	50	Superior occipital gyrus right
6	Orbitofrontal cortex (superior) right	51	Middle occipital gyrus left
7	Middle frontal gyrus left	52	Middle occipital gyrus right
8	Middle frontal gyrus right	53	Inferior occipital gyrus left
9	Orbitofrontal cortex (middle) left	54	Inferior occipital gyrus right
10	Orbitofrontal cortex (middle) right	55	Fusiform gyrus left
11	Inferior frontal gyrus (opercular) left	56	Fusiform gyrus right
12	Inferior frontal gyrus (opercular) right	57	Postcentral gyrus left
13	Inferior frontal gyrus (triangular) left	58	Postcentral gyrus right
14	Inferior frontal gyrus (triangular) right	59	Superior parietal gyrus left
15	Orbitofrontal cortex (inferior) left	60	Superior parietal gyrus right
16	Orbitofrontal cortex (inferior) right	61	Inferior parietal lobule left
17	Rolandic operculum left	62	Inferior parietal lobule right
18	Rolandic operculum right	63	Supramarginal gyrus left
19	Supplementary motor area left	64	Supramarginal gyrus right
20	Supplementary motor area right	65	Angular gyrus left
21	Olfactory left	66	Angular gyrus right
22	Olfactory right	67	Precuneus left

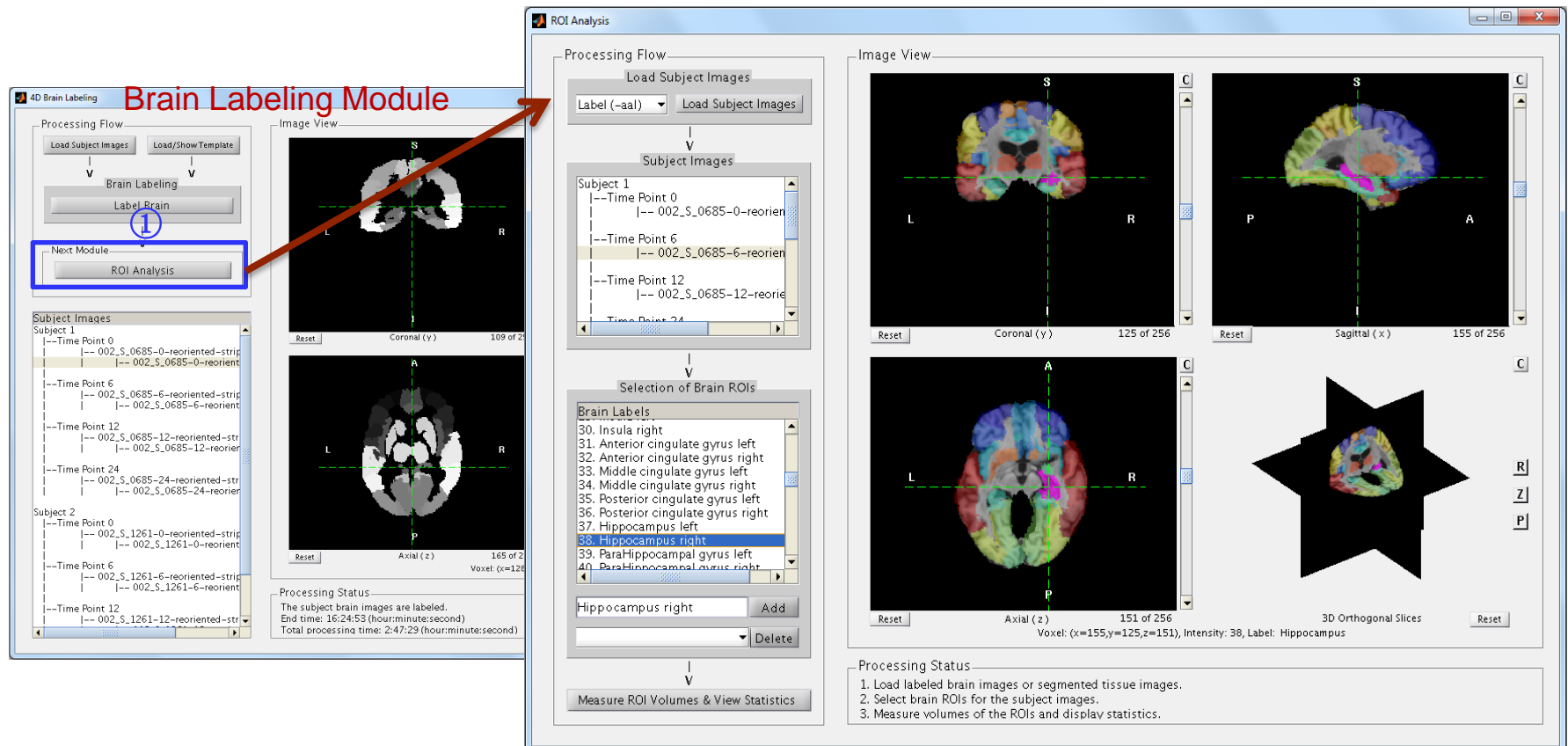
23	Superior frontal gyrus (medial) left	68	Precuneus right
24	Superior frontal gyrus (medial) right	69	Paracentral lobule left
25	Orbitofrontal cortex (medial) left	70	Paracentral lobule right
26	Orbitofrontal cortex (medial) right	71	Caudate left
27	Rectus gyrus left	72	Caudate right
28	Rectus gyrus right	73	Putamen left
29	Insula left	74	Putamen right
30	Insula right	75	Pallidum left
31	Anterior cingulate gyrus left	76	Pallidum right
32	Anterior cingulate gyrus right	77	Thalamus left
33	Middle cingulate gyrus left	78	Thalamus right
34	Middle cingulate gyrus right	79	Heschl gyrus left
35	Posterior cingulate gyrus left	80	Heschl gyrus right
36	Posterior cingulate gyrus right	81	Superior temporal gyrus left
37	Hippocampus left	82	Superior temporal gyrus right
38	Hippocampus right	83	Temporal pole (superior) left
39	ParaHippocampal gyrus left	84	Temporal pole (superior) right
40	ParaHippocampal gyrus right	85	Middle temporal gyrus left
41	Amygdala left	86	Middle temporal gyrus right
42	Amygdala right	87	Temporal pole (middle) left
43	Calcarine cortex left	88	Temporal pole (middle) right
44	Calcarine cortex right	89	Inferior temporal gyrus left
45	Cuneus left	90	Inferior temporal gyrus right



# Brain Labeling

## Step 3: Start the ROI Analysis Module

- After all brain images are labeled in the Brain Labeling Module, press '**ROI Analysis**' to start the ROI Analysis Module.
- All the labeled brain images will be transferred into the '**Subject Images**' list of the ROI Analysis Module automatically, and the Brain Labeling Module will be closed automatically.



# Automatic Processing

In addition to the step-by-step processing, you can process all input images from image preprocessing to brain labeling automatically.

- Load subject images (by ②) -> set parameters for image preprocessing, brain extraction, tissue segmentation, and brain labeling (by ③) -> run automatic processing (by ④) -> start '**ROI Analysis Module**' after automatic processing is done (by ⑤).
- If subject images cannot be reoriented using the same parameters, you can first preprocess them in the '**Image Preprocessing Module**', and then use this '**Automatic Processing Module**' (disable the preprocessing) to perform other processing automatically.

The screenshot displays the aBEAT software interface, which is divided into several panels. On the left, a sidebar contains a 'Step-by-step Processing' section with buttons for 'Image Preprocessing', 'Brain Extraction', 'Tissue Segmentation', and 'Brain Labeling'. Below this is an 'Automatic Processing' section with a button labeled 'Preprocessing2Labeling' (marked with a circled 1) and a 'ROI Analysis' button. The main window is titled 'Automatic Processing (from image preprocessing to brain labeling)'. It features a 'Parameters for Automatic Processing' panel on the left, which includes 'Image Preprocessing' (with 'Reorientation: new (x, y, z) =' and dropdowns for x, y, and z), 'Brain Extraction' (with 'Fractional threshold [0~1]: 0.6' and checkboxes for 'Skull Stripping' and 'Cerebellum Removal'), 'Tissue Segmentation' (with 'Temporal Consistency [0~1]: 0.5'), and 'Brain Labeling' (with 'No Parameter'). Below these parameters are buttons for 'Run Automatically' (marked with a circled 4) and 'ROI Analysis' (marked with a circled 5). A 'Subject Images' list on the left shows 'Subject 1' with four time points: 'Time Point 0' (011\_S\_0005-0), 'Time Point 6' (011\_S\_0005-6), 'Time Point 12' (011\_S\_0005-12), and 'Time Point 36' (011\_S\_0005-36). The right panel, titled 'Image View', shows four brain slices: 'Coronal (y)', 'Sagittal (x)', 'Axial (z)', and '3D Orthogonal Slices'. Each slice has a 'Reset' button. The '3D Orthogonal Slices' view shows a 3D reconstruction of the brain. The 'Processing Status' section at the bottom right lists the steps: 1. Load longitudinal images of subjects. 2. Set options for automatic processing. 3. Run automatically from image preprocessing to brain labeling. An orange arrow points from the 'Preprocessing2Labeling' button in the sidebar to the 'Automatic Processing' window.

**Automatic Processing**

Processing Status

1. Load longitudinal images of subjects.
2. Set options for automatic processing.
3. Run automatically from image preprocessing to brain labeling.



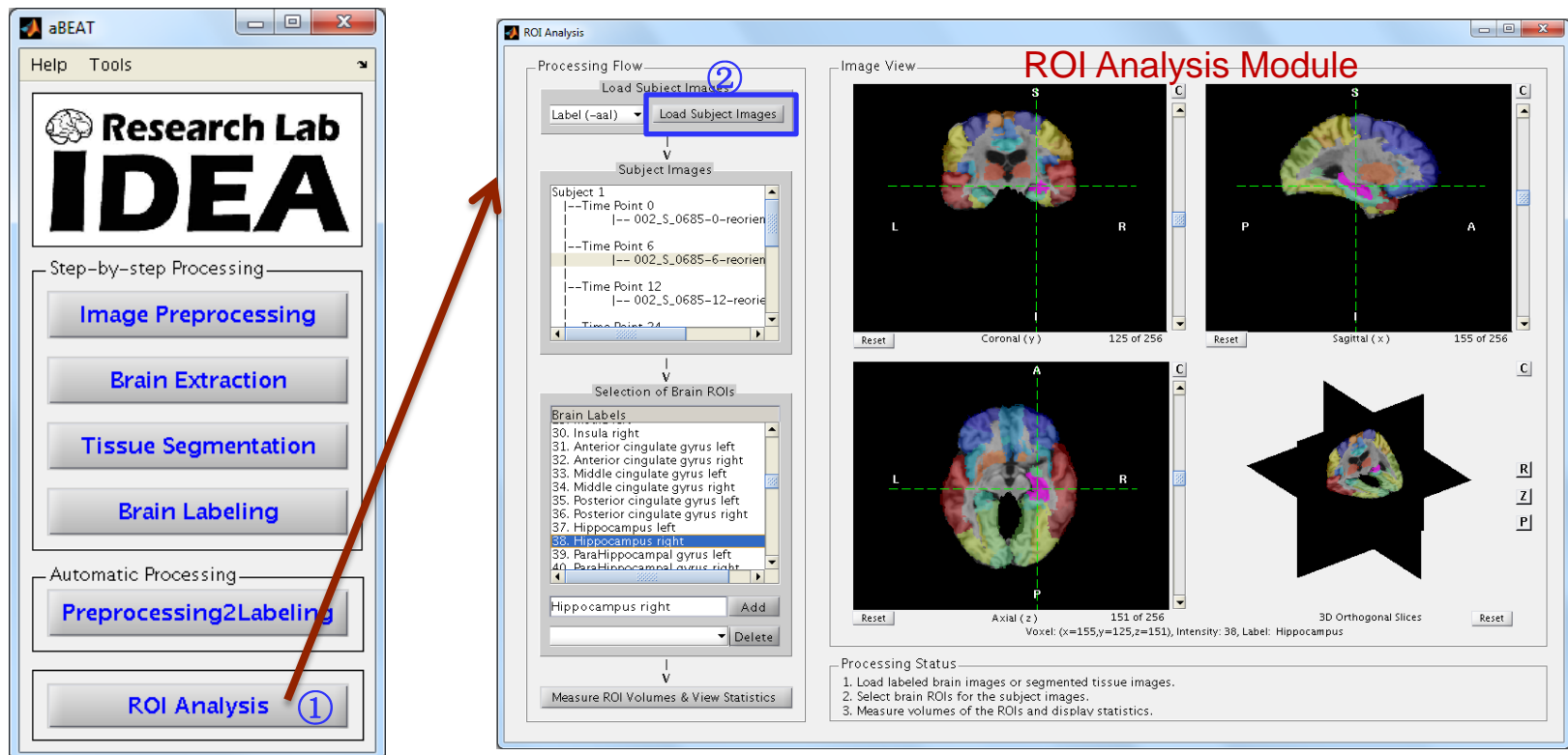
# ROI Analysis

## Step 1: Start the ROI Analysis Module

➤ Suppose labeled brain images are obtained by the Brain Labeling Module, then **the ROI Analysis Module can also be started from the main window.**

➤ The labeled brain images (whose file names are ended with '-aal') can be loaded by ② (the Image Loading Module will be started).

**NOTE: if the brain-extracted image (end with '-strip') is available as well, it will be displayed automatically as the background image and the brain labels will be overlaid on the brain-extracted image.**



# ROI Analysis

## Functionality of the ROI Analysis Module:

- Select ROIs from the brain labels (45 labels in each hemisphere), and measure the volumes of selected ROIs for each subject brain image. Selected brain ROIs of subjects can be analyzed based on the measured ROI volumes.
- **NOTE: the ROI analysis module can also be used to load segmented brain tissue images, and further, select ROIs from the brain tissues (GM,WM,CSF) and analyze selected ROIs of subjects based on measured ROI volumes.**

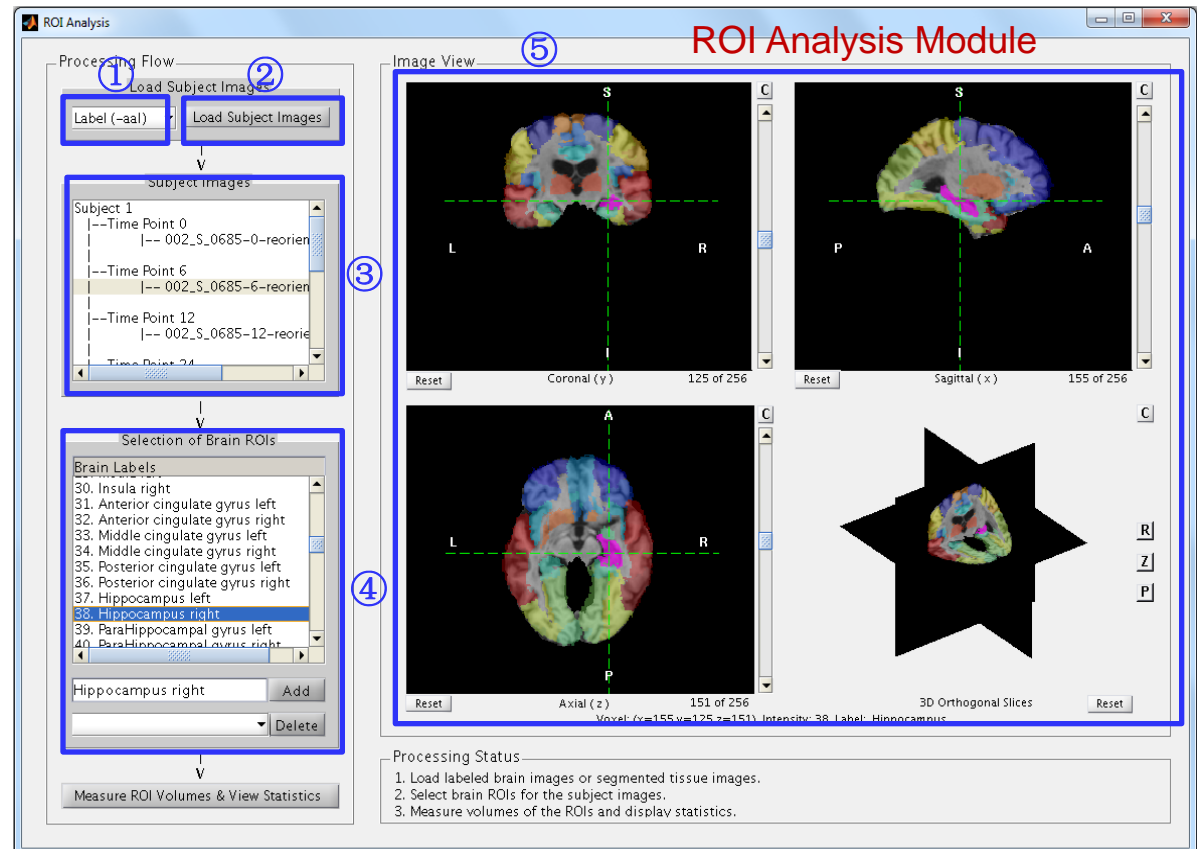
①: select a mode (use brain labels or tissue images for ROI analysis). The default is to use brain labels.

②: load subject images in accordance with ①.

③: loaded subject images.

④: select ROIs from brain labels (or tissues)

⑤: windows for the inspection of a selected image with a tentative ROI.



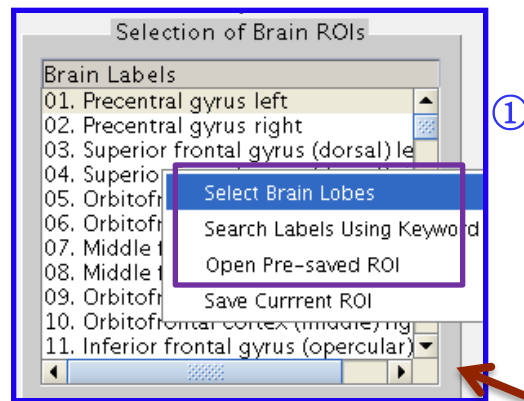


# ROI Analysis

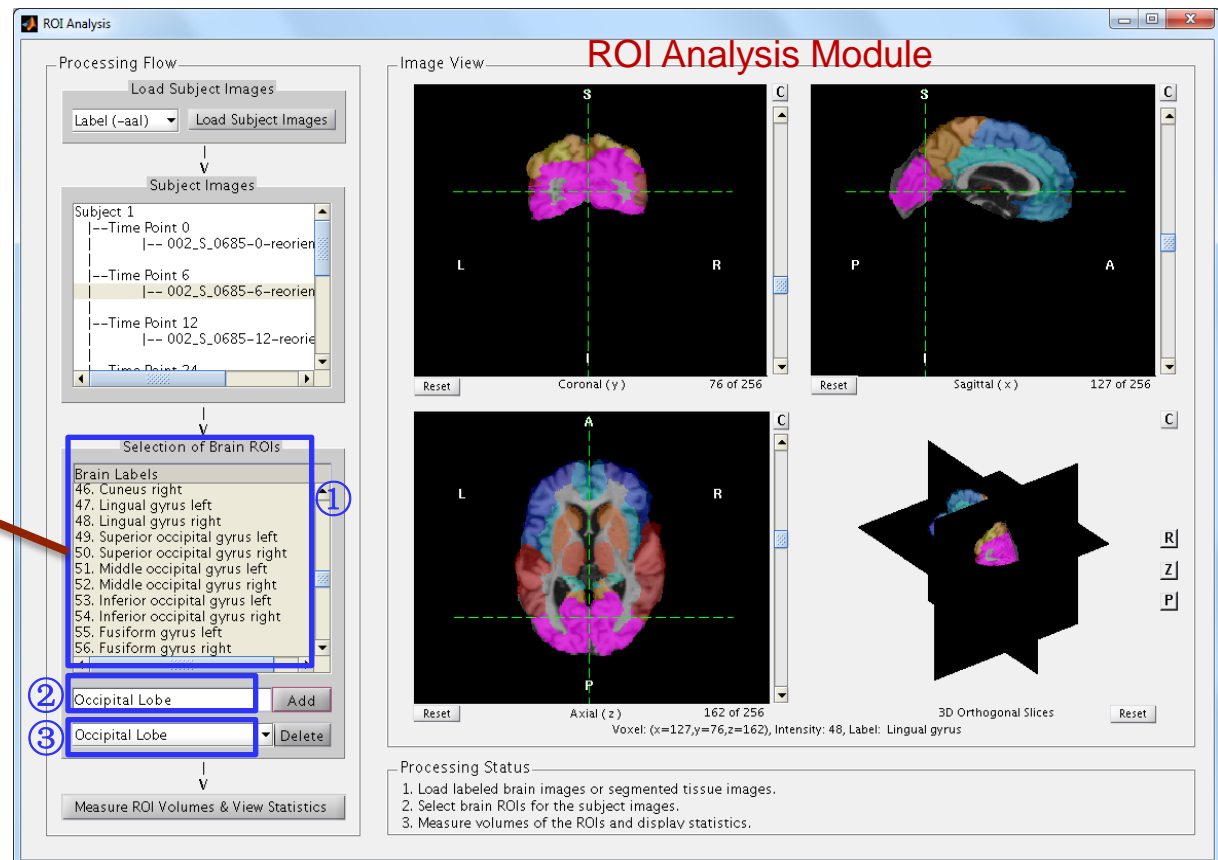
## Step 2: Selection of ROIs

- First, select brain labels of interest in ① (**list of the brain labels**). Selected labels will be highlighted (in pink)
- Second, create ROI name for the selected labels in ② and “Add” the ROI into ③ (**ROI list**).
- Repeat the first and second steps to get all ROIs that will be analyzed.

**NOTE:** a ROI in ③ can be selected and deleted (by “Delete”)



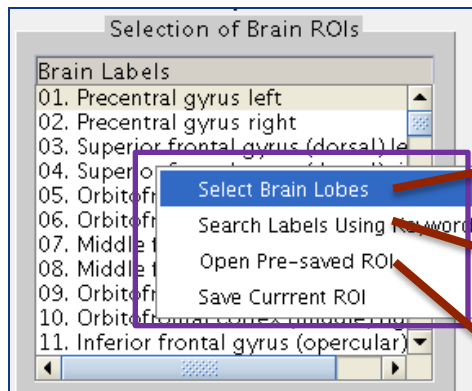
Right mouse click in ① to see the popup menu for the selection of labels of interest



# ROI Analysis

## Four ways for the selection of brain labels of interest

Right mouse click in the list to see the popup menus

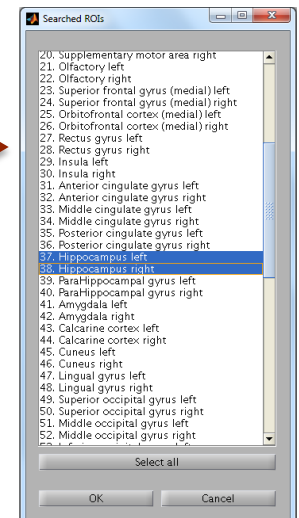
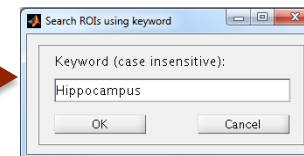
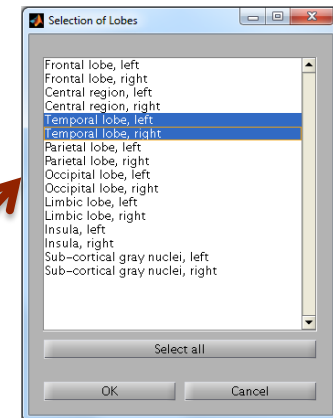


1. Use **Shift/Ctrl** and **mouse left click** to select labels for the ROI.

2. Select labels in a brain lobe from the list of **Brain Lobes**.

3. Search labels in the list of brain labels using a **keyword**.

4. Load labels in a **pre-saved** ROI.

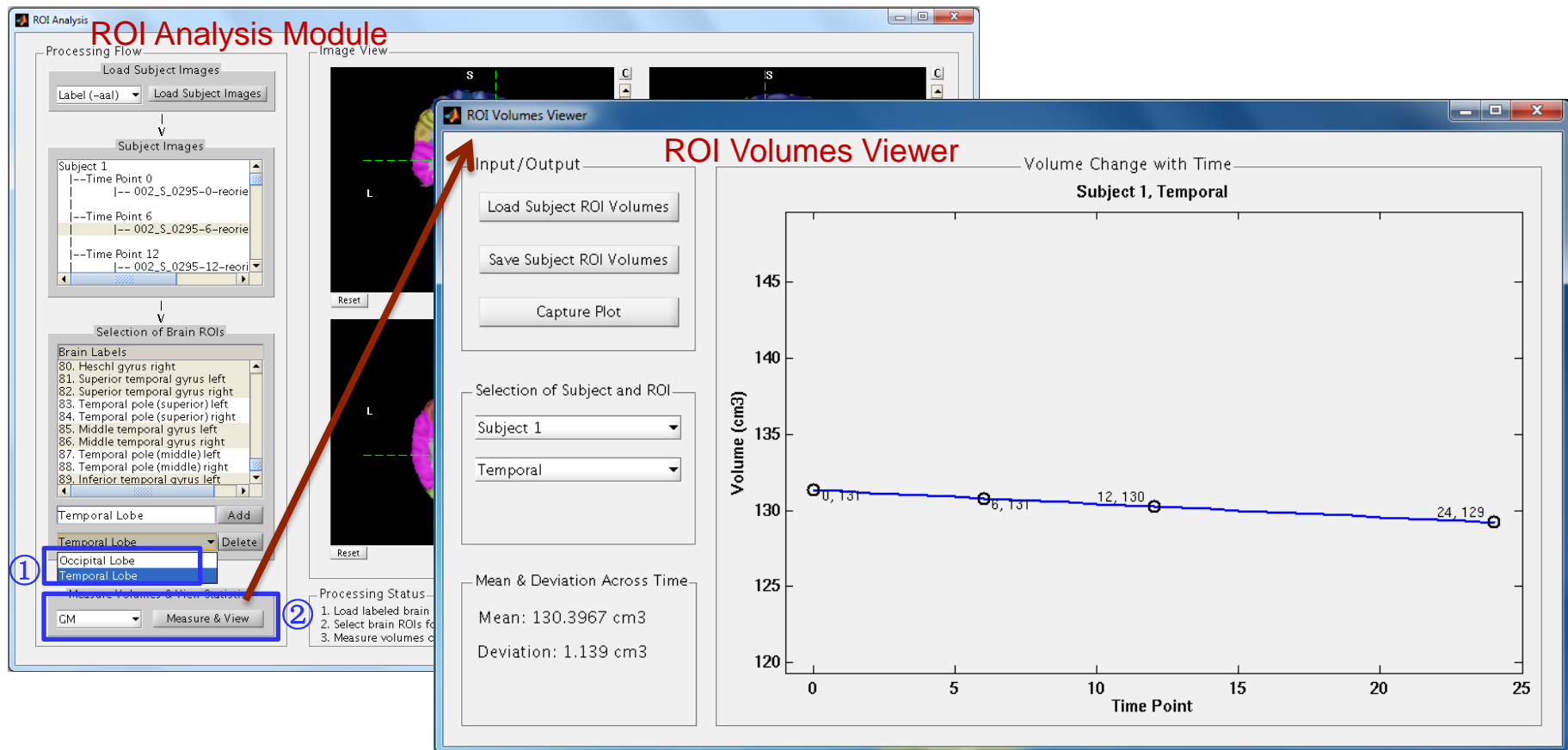




# ROI Analysis

## Step 3: Measure ROI Volumes and View Statistics

- After ROIs are selected and added in ① (ROI list), select a tissue and measure its volumes in selected ROIs for each subject brain image (by ②).
- The tissue volumes in the ROIs of subject images can then be viewed statistically in the ROI Volumes Viewer sub-module.

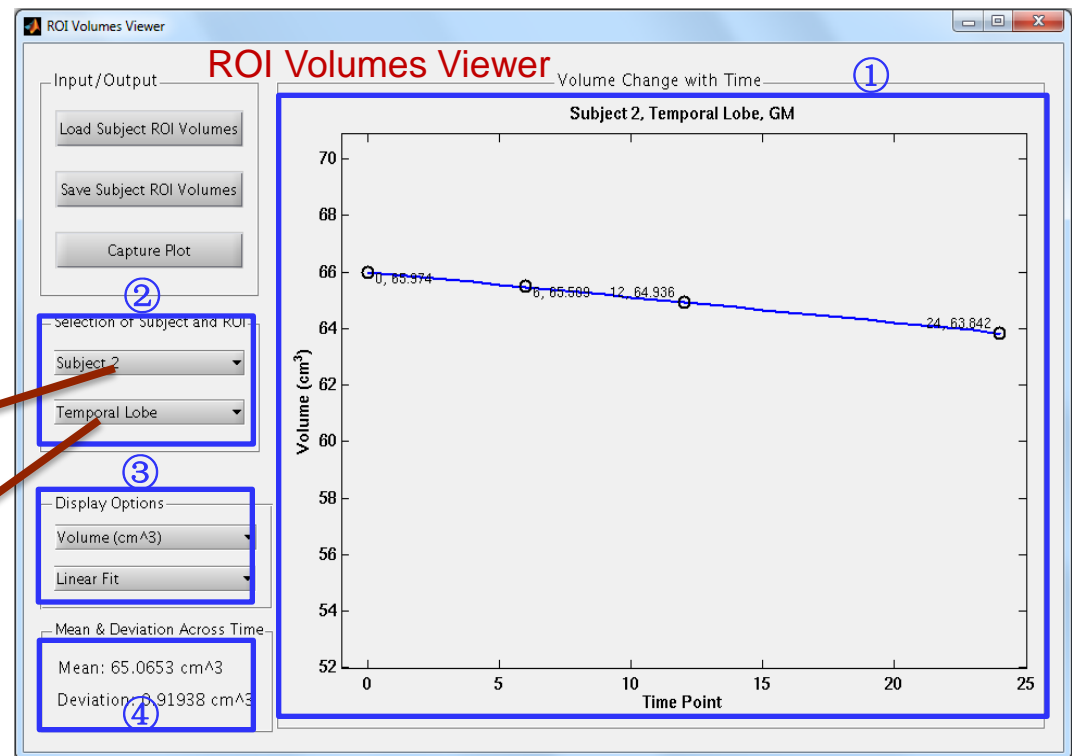
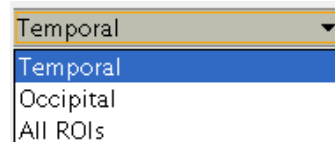
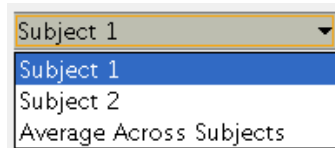


# ROI Analysis

## Step 4: Analyze ROI Volume Changes

- The measured ROI tissue volumes of subject images are buffered in the ROI Volumes Viewer sub-module. The ROI volumes can be exported and saved as **‘.mat’ file of MATLAB**. Pre-saved ROI volumes can be loaded for review.
- The plot in ① displays the change of ROI tissue volumes with time, corresponding to ② (**Selection of Subject and ROI**). The curve display options can be changed by ③. ④ displays the mean and deviation of the serial ROI tissue volumes, corresponding to ①. **The meanings of the plot corresponding to particular selections in ② are as follows:**

- **Subject i, ROI j:**  
volume change of ROI j of Subject i.
- **Subject i, All ROIs:**  
volume change of all ROIs of Subject i.
- **Average Across Subjects, ROI j:**  
average volume change of ROI j across all subjects.
- **Average Across Subjects, All ROIs:**  
average volume change of all ROIs across all subjects.



➤ Image file name regulation of the aBEAT software:  
subject-timepoint -> subject-timepoint-reoriented ->  
subject-timepoint-reoriented-strip -> subject-timepoint-reoriented-strip-seg ->  
subject-timepoint-reoriented-strip-seg-aal

➤ The tool for the display of an image:

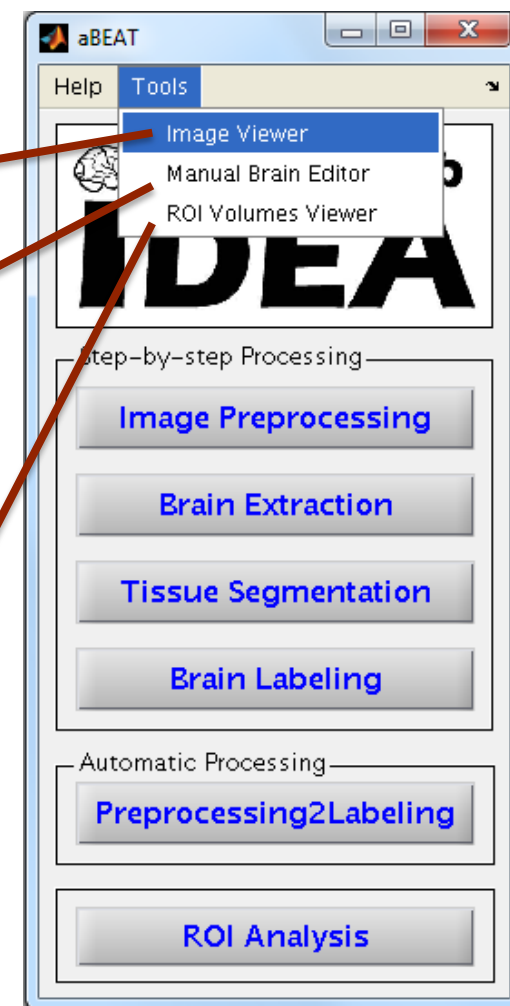
- To select and view an image of analyze format.

➤ The tool for interactive editing of the brain image:

- To select an image file and edit the brain interactively.
- If the automatically extracted brain image is available in the same folder, it will be detected and used as the default brain overlay.
- If the automatically extracted brain image is not available, brain extraction can be performed firstly.
- The interactively edited brain image will be saved with the loaded image and named with a postfix '**-strip**'.

➤ The tool for reviewing ROI volumes of subject images:

- To select and review a pre-saved file (MATLAB '.mat' format) of ROI volumes of subject images.



## aBEAT can also process single time point images of subjects

*If each subject has only single time point image, the subject images are processed as follows:*

### **1. Image Preprocessing:**

- (a) Reorient original T1 images to the same orientation as the template image (Colin27, eyes right).
- (b) Resample the images to the standard size and resolution (256x256x256 and 1x1x1 mm<sup>3</sup>, as the template image).
- (c) Perform N3 correction on the images.

### **2. 3D Brain Extraction:**

- (a) Perform 3D brain extraction to extract the brains from the preprocessed images.
- (b) Perform 3D cerebellum removal on the images.
- (c) The automatically extracted brain images can be edited manually to obtain more accurate brain images (optional).

### **3. 3D Tissue Segmentation:**

- Segment gray matter, white matter and CSF from each extracted brain image using coupled level-sets segmentation.

### **4. 3D Brain Labeling:**

- Each subject brain image is registered with the Colin27 template image, the pre-labeled image of the Colin27 template will then be warped to label the subject brain image.

### **5. ROI Analysis:**

- ROIs are selected from the brain labels (45 labels in each hemisphere) or the brain tissues (GM, WM, CSF), and the volumes of the selected ROIs of the subject brain images are measured. The ROI volumes of the subjects can be analyzed.



## ➤ Programming languages:

- The graphical user interfaces and overall framework of the aBEAT software were implemented in MATLAB. The image processing functions were implemented with the combination of C/C++, MATLAB, Perl and Shell languages.

## ➤ Parallel processing:

- Eight parallel threads are used for image processing. In the image reorientation, resampling and N3 correction steps, all the images are processed by separate threads in parallel. In the histogram matching, 4D brain extraction, 4D tissue segmentation, and 4D brain labeling steps, all subjects are processed by separate threads in parallel, and multiple threads are used as much as possible for the processing of longitudinal images of each subject. The parallel strategy accelerates the image processing largely.

**Computational performance on a computer with 4 CPUs, each CPU (Intel Xeon, 2 GHz) has 10 processor cores:**  
**(1) one subject with four time point images; (2) four subjects, each subject has a single time point image.**

	Preprocessing	Brain Extraction with Cerebellum Removal	Tissue Segmentation	Brain Labeling
(1) Longitudinal Data	2.2 Minutes	16.2 Minutes	4 Hours	2.65 Hours
(2) Cross-sectional Data	2 Minutes	13.4 Minutes	1 Hour	0.95 Hour



# Acknowledgement

- aBEAT is developed by the IDEA group at the University of North Carolina at Chapel Hill. **Dinggang Shen** initiated the project idea and direct the development of the software. **Yakang Dai, Yaping Wang, Li Wang, Guorong Wu, and Feng Shi**, implemented functions and wrote the codes.
- The development of the software is partially supported by **NIH grants EB006733, EB008374, MH088520 and EB008760 to Dinggang Shen**.
- The brain extraction module integrated the method proposed by **Wang et al** [1].
- The tissue segmentation module integrated the method proposed by **Wang et al** [2].
- The brain labeling module integrated the methods proposed by **Wu et al** [3,4].
- Portions of functions of the aBEAT software were implemented based on: the FSL library developed by the **Analysis Group, FMRIB, Oxford, UK**; the MINC package and ANLM tool developed by the **McConnell Brain Imaging Centre of the Montreal Neurological Institute, McGill University**; the ITK toolkit from the **Kitware Inc**.
- [1] Yaping Wang, Jingxin Nie, Pew-Thian Yap, Feng Shi, Lei Guo, and Dinggang Shen. Robust deformable-surface-based skull-stripping for large-scale studies. Proceedings of MICCAI 2011;14(Pt 3):635-642.
- [2] Li Wang, Feng Shi, Gang Li, Dinggang Shen. 4D Segmentation of Longitudinal Brain MR Images with Consistent Cortical Thickness Measurement. STIA 2012, Nice, France, Oct. 1, 2012.
- [3] Guorong Wu, Qian Wang, Dinggang Shen. Registration of Longitudinal Brain Image Sequences with Implicit Template and Spatial-Temporal Heuristics. Neuroimage, 59(1):404-421, Jan. 2012.
- [4] Guorong Wu, Minjeong Kim, Qian Wang, and Dinggang Shen. Hierarchical Attribute-Guided Symmetric Diffeomorphic Registration for MR Brain Images. MICCAI 2012, Nice, France, Oct. 1-5, 2012.



# Acknowledgement

## For the Alzheimer's Disease Neuroimaging Initiative

Data used in preparation of this tutorial were obtained from the Controls in Alzheimer's Disease Neuroimaging Initiative (ADNI) database ([www.loni.ucla.edu/ADNI](http://www.loni.ucla.edu/ADNI)). As such, the investigators within the ADNI contributed to the design and implementation of ADNI and/or provided data but did not participate in analysis or writing of this tutorial. A complete listing of ADNI investigators can be found at: [http://adni.loni.ucla.edu/wp-content/uploads/how\\_to\\_apply/ADNI\\_Acknowledgement\\_List.pdf](http://adni.loni.ucla.edu/wp-content/uploads/how_to_apply/ADNI_Acknowledgement_List.pdf)

Data used in the preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database ([adni.loni.ucla.edu](http://adni.loni.ucla.edu)). The ADNI was launched in 2003 by the National Institute on Aging (NIA), the National Institute of Biomedical Imaging and Bioengineering (NIBIB), the Food and Drug Administration (FDA), private pharmaceutical companies and non-profit organizations, as a \$60 million, 5-year public private partnership. The primary goal of ADNI has been to test whether serial magnetic resonance imaging (MRI), positron emission tomography (PET), other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of mild cognitive impairment (MCI) and early Alzheimer's disease (AD). Determination of sensitive and specific markers of very early AD progression is intended to aid researchers and clinicians to develop new treatments and monitor their effectiveness, as well as lessen the time and cost of clinical trials.

The Principal Investigator of this initiative is Michael W. Weiner, MD, VA Medical Center and University of California – San Francisco. ADNI is the result of efforts of many coinvestigators from a broad range of academic institutions and private corporations, and subjects have been recruited from over 50 sites across the U.S. and Canada. The initial goal of ADNI was to recruit 800 adults, ages 55 to 90, to participate in the research, approximately 200 cognitively normal older individuals to be followed for 3 years, 400 people with MCI to be followed for 3 years and 200 people with early AD to be followed for 2 years.” For up-to-date information, see [www.adni-info.org](http://www.adni-info.org).

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