HAMMER-SUITE User Manual

1 Introduction

HAMMER-SUITE provides a friendly environment for medical image processing. It is distributed with a cranial image processing pipeline. The pipeline processes raw brain MRI data through pre-processing (skull removal, bias correction, etc), segmentation, and registration. The pipeline can be automatically executed on either a single image or multiple images. Also, components of the pipeline can be individually applied, e.g., performing only segmentation to the loaded image. Therefore, HAMMER-SUITE is quite a flexible platform for processing and analyzing brain MRI data. This manual is accompanying the HAMMER-SUITE release package, briefing usages of the software.

The core of the HAMMER-SUITE release is featured by the image registration function powered by the HAMMER registration algorithm [1]. HAMMER (Hierarchical Attribute Matching Mechanism for Elastic Registration) has proven to be one of the popular brain image registration methods in the community. It takes advantage of the attribute vectors in characterizing features of driving voxels, in order to establish reliable correspondences between images. By reducing the dissimilarity of attribute vectors in the hierarchical fashion, HAMMER can acquire not only accurate but also robust registration performance.

The software of HAMMER-SUITE is released by the IDEA Lab of the Biomedical Research Imaging Center (BRIC) in the University of North Carolina at Chapel Hill. The IDEA Lab is devoted to the development of novel image analysis methods and tools, as well as applications to various clinical researches and trials. The developed methods include deformable registration, deformable segmentation, and multivariate pattern classification algorithms. These methods have been applied to various studies on brain diseases and development (including MCI, AD, Schizophrenia, and Neonate Development Study), heart, breast cancer, and prostate cancer. For more details, please visit the website of the lab: http://www.med.unc.edu/bric/ideagroup.

2 Installation

Prior to installation, please make sure that several requirements should be met on your computer:

- **TCL/TK**
  HAMMER-SUITE provides GUI powered by KWWIDGETD, which needs the running environment of TCL/TK. Please acquire the free and open-source release of TCL/TK from http://www.tcl.tk/software/tcltk/.

- **Perl**

Some scripts are written in Perl as in HAMMER-SUITE. Usually Linux/Unix system supports Perl naturally. For Windows users, special attention should paid to install Perl running environment. You could get it from www.activestate.com/activeperl. *If you have any uncertainty, please contact your system administrator for more information.*

• ***Microsoft Runtime Redistributable Kit***
This is for Windows users only. You may need to install Microsft Runtime Redistributable Kit. If you have Microsoft Visual Studio available, you can skip this step.

Now please download our latest releases. We now have provided 3 versions for 64bit Linux/Unix, 32 bit Windows, and 64 bit Windows, respectively. Please choose the proper release package to download.

After download, please extract all files. Then, for Linux/Unix users, please add the "tools" subdirectory to $PATH in user profile. Similarly, Windows users must add the "win32" subdirectory to the environment variable $PATH.

After the software has been correctly installed, you are now free to start the executable binary ./HAMMER-GUI/HAMMER-GUI and perform image processing tasks.

3   Quick Start

HAMMER-SUITE provides a variety of functions to process brain MR images. For raw data, the default pipeline performs skull removal and cerebellum removal in pre-processing. Then, tissue segmentation is performed to classify regions of white matter (WM), grey matter (GM), and cerebrospinal fluid (CSF), respectively. HAMMER registration is applied and warps the subject to the space of the template. After registration has finished, the tissue density map (Ravens map [2]) related to the deformation field is calculated for convenience of subsequent analysis.
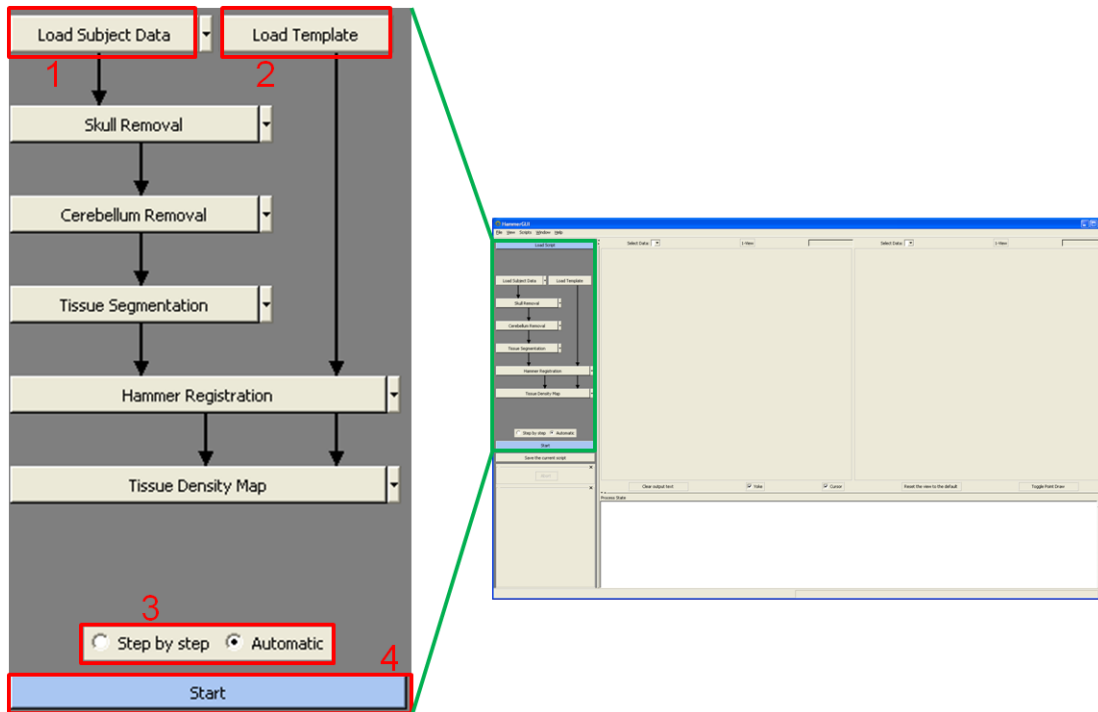
Figure 1. Quick start requires only 4 simple steps: 1) load subject data, 2) load template, 3) select automatic mode, and then 4) click "start".

Only 4 simple steps are needed to start a quick automatic task in HAMMER-SUITE as in Figure 1:

1) Load subject data.
   Navigate to the path of the subject data and select the subject image (or multiple subject images). Note that multiple images can be selected and processed together. The subject image should be of the Analyze format, which is also compatible with ITK.

2) Load template.
   The template should be pre-segmented into WM (labeled with intensity 250), GM (with intensity 150), and CSF (with intensity 10). It also needs to be of the Analyze format. Currently we only support the template with 'unsigned char' (8-bit) data type. The sample of the template can be found as /HAMMER-GUI/data/template.img.

3) Select the "automatic" mode.
   Please select the "automatic" mode, to rule out future interruption and manual interaction.

4) Click "start" and wait for results.
   The whole processing time cost may vary according to different situations. In general, it takes 30 minutes for pre-processing, and 20 minutes for registration.

Final results as well as intermediate files share the same destination directory with the input subject data. After each component in the pipeline has finished, the output will be written to the output directory by appending a suffix to the original file name of the subject data. The suffix

indicates the component which has yielded the output. The component and its corresponding suffix are listed in the following:

Component	Suffix	Note
Skull Removal	_strip	Suffix "_conv" might be applicable and appended due to mandatory data type cast by the pipeline.
Cerebellum Removal	_cere	
Tissue Segmentation	_seg	
HAMMER Registration	_reg	
Tissue Density Map	_RAVENSmap_XX	"XX" can only be "GM/WM/VN", indicating RAVENS maps for GM, WM, and ventricle, respectively.

All outputs are in the Analyze format, which are easy to interpret.

4   Specification

In this chapter, we will elaborate the details of HAMMER-SUITE. If you have more questions, please refer to the following FAQ or contact us directly (hammer.unc@gmail.com).

4.1   Layout

In general, the layout of HAMMER-SUITE is divided into 4 areas as in Figure 2: (1) Area 1 for pipeline control; (2) Area 2 for component control; (3) Area 3 for data rendering; (4) Area 4 for status monitoring.
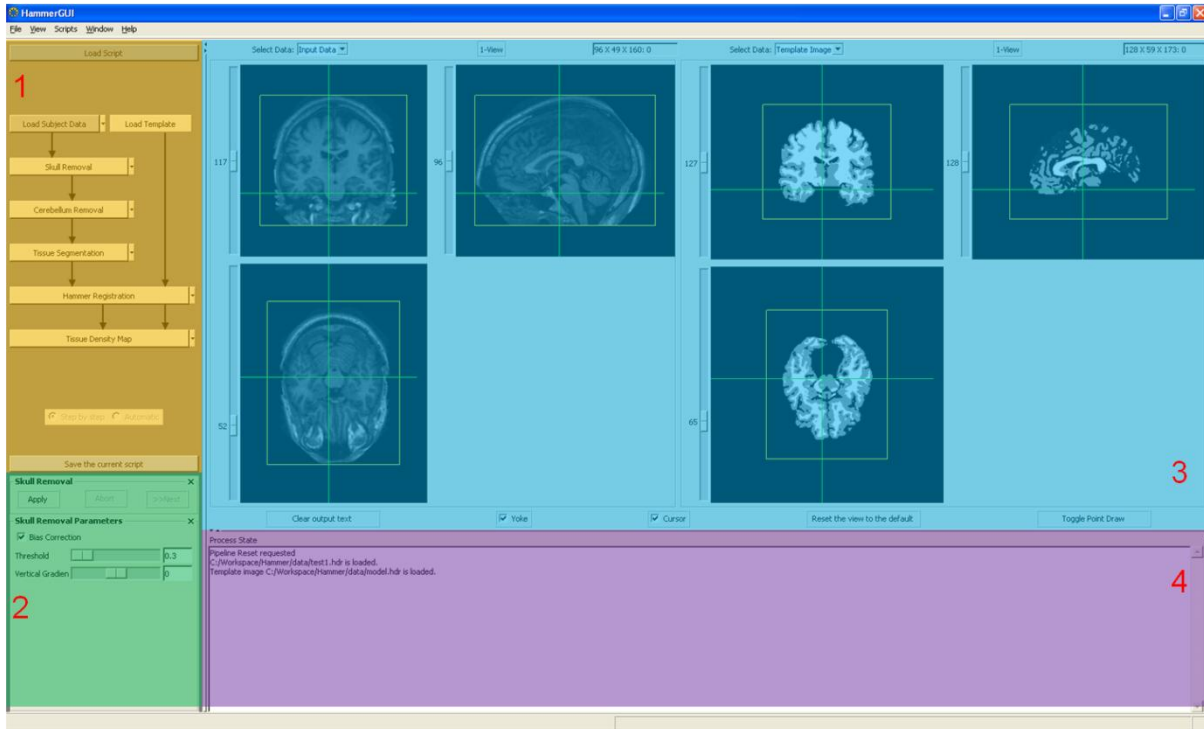
Figure 2. Layout of HAMMER-SUITE contains 4 areas typically.

4.2 Pipeline

All image processing tasks are arranged in a single pipeline by HAMMER-SUITE. Besides loading subject/template data, there are 5 component functions available at HAMMER-SUITE currently. When starting the software, the default pipeline is automatically loaded, providing a complete process procedure for raw brain MR data. The 5 components are for skull removal, cerebellum removal, tissue segmentation, HAMMER based registration [1], and tissue density map calculation [2], respectively. Details related to each component are discussed in Section 4.3.

The default pipeline can be modified to cater for different application scenarios, as each component can be disabled by clicking the arrow right adjacent to the component button. As shown in Figure 3, if the user only wants to obtain tissue segmentation results for given data, the last two components can be disabled. Then, the pipeline will abort after successfully returning from segmentation component.
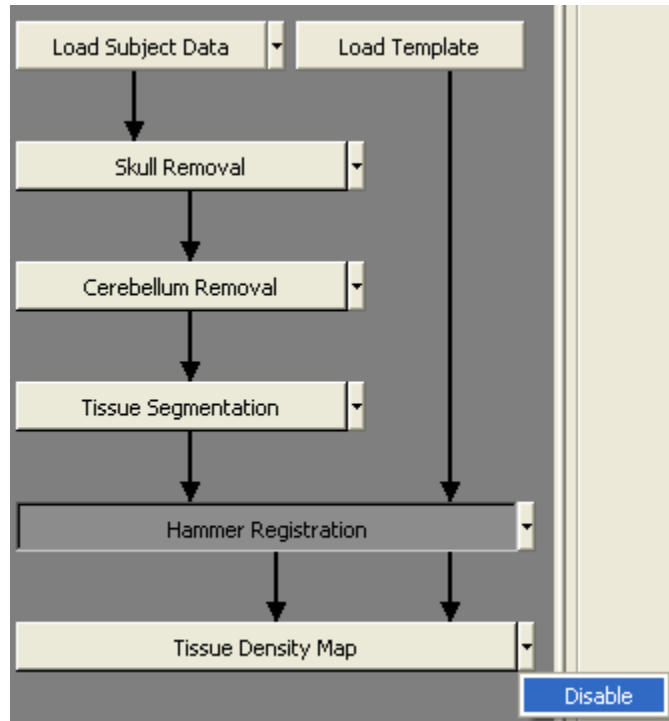
Figure 3. The example to disable particular components in pipeline.

The pipeline supports both "automatic" and "step-by-step" modes now. In the automatic mode, the only thing that the user should do is to click "start" pipeline, if the pipeline has been configured correctly. The software will perform all processing steps and write outputs automatically. In the step-by-step mode, after clicking "start" pipeline, the first component in the pipeline will be activated. The user should then click "apply" right below the "start" pipeline button. This will enable the current component to run until it has finished and returned. Then, the user should click "next" to activate the following component in the pipeline, and "apply" the component once more.

The automatic and the step-by-step modes are used in different scenarios. The user can use the step-by-step mode to determine optimal configurations and parameters for a series of data, since this mode allows human interaction and review of image processing outputs. When all settings are done, the user may switch to the automatic mode and process multiple datasets together. In the automatic mode, no human interaction is required, though the user can use "abort" to force the program to quit.

4.3 Component

The pipeline is constructed by connecting individual components. The order of the connected components determines the way that the input data will be processed. HAMMER-SUITE of

current stage has 5 components: skull removal, cerebellum removal, tissue segmentation, HAMMER based registration, and tissue density map calculation. Users can click the button in the pipeline, and access to configurations of the corresponding component.

- **Skull removal**

Skull removal is usually the very first step for the raw data processing since our image segmentation and registration algorithms are designed for skull-stripped images.

Parameter	Value
Bias Correction	Yes

- **Cerebellum Removal**

Cerebellum removal is the step to remove cerebellum and brainstem related structures from the data, in that image registration is focused on cerebrum nowadays. Note that this step is not mandatory and should be complied with the template used in the pipeline. If the template has no cerebellum incorporated (as the template we provided), cerebellum removal should be deployed to the incoming subjects. Otherwise, this step can be bypassed.

Parameter	Value
N3 Correction	Yes
Eye Orientation	Left/Right
HAMMER Iteration	[1,10]

- **Tissue Segmentation**

This component segments the brain into WM, GM, and CSF. And finally we will label the WM with intensity 250, GM with intensity 150, and CSF with intensity 10.

Parameter	Value
Artifact-Removal Threshold	[0,100] (default: 50)
Artifact-Removal Correction Size	[0,5] (default: 1)
Bias Correction Kernel Width	[0.05, 0.5] (default: 0.15)
Bias Correction Change of CV	[1e-2,1e-4] (default: 1e-3)

Bias Correction Iteration	[1,100] (default: 50)

- **HAMMER Registration**

HAMMER-SUITE provides two different versions of HAMMER registration algorithm now. The first one is TPS-HAMMER, which generates deformation field by TPS interpolation. The second one is a fast version of HAMMER, which has been optimized on Intel CPUs. Users are encouraged to use the fast version of HAMMER for better speed performance, if they are powered with Intel CPUs.

Parameter	Value
Iteration	[1,100] (default: 20 for TPS, 50 for fast Hammer)
Step Ratio	[0,1] (default: .0.05)
Similarity Threshold	[0,1] (default: 0.6)

4.4 Image Rendering

Two image rendering views are provided. In general, the loaded subject data appear in the left, while the right viewer is for the template. However, results output by components in the pipeline can be accessed by both two views. Users can use the drop down boxes on top of the viewers to navigate to the data selected.

By clicking "1-view/3-view", the data can be rendered in different ways. Also, below the viewers, the panel allows user to determine whether two views are synchronized or whether cursors are displayed. The "cursor" check-box controls whether the cross-cursor is displayed upon image renderings. The "yoke" check-box controls whether the two rendering views are synchronized. Users are allowed to adjust the brightness and contrast when pressing down the right button of the mouse and move around.

5 FAQ

Q1. X-win is forced to close when initializing the software.

A: We have encountered this problem sometimes by using X-win32 on Windows 7. However, tests show that X-win32 8.1 plus Windows XP do not have such a problem. As the result, users

are encouraged to run HAMMER-SUITE from the terminal on Windows XP. For Windows 7, it is more stable to use Cygwin instead of the latest version of X-win.

Q2.After installing Tcl/Tk, there is still an error suggesting lacking Tcl/Tk files in initializing HAMMER-SUITE.

A: Please copy the two library files "libtcl8.5.so" and "libtk8.5.so" to the directory of HAMMER-SUITE if encountered with this problem. Users can use other versions of Tcl/Tk installations besides version 8.5.

6   Reference

[1]   D. Shen and C. Davatzikos, "HAMMER: Hierarchical attribute matching mechanism for elastic registration," *Medical Imaging, IEEE Transactions on,* vol. 21, pp. 1421-1439, 2002.

[2]   A. F. Goldszal, C. Davatzikos, D. L. Pham, M. X. H. Yan, R. N. Bryan, and S. M. Resnick, "An Image-Processing System for Qualitative and Quantitative Volumetric Analysis of Brain Images," *Journal of Computer Assisted Tomography,* vol. 22, pp. 827-837, 1998.