

Documentation of How to Use the Intergroup Registration Toolkit

1. Purpose of this Project:

The purpose of this project is to perform image registration between two groups of populations (e.g., young population and old population, normal control population and AD disease population)

4. How to use the Toolbox:

The proposed algorithm has 2 major steps:

- (1) Perform Groupwise Registration on images within the fixed group and moving Group.
- (2) Estimate the deformable transformation from the moving group to the fixed group based on the registered images in each group by step (1) by extracting the statistical features from their segmentation groundtruths via multi-channel diffeomorphic Demons algorithm.

Please follow the following procedures in order. Except explicit mentioning, the running path is in the root directory.

Running Environment: Currently this software package can only be used under the Linux environment

Suppose the software package is extracted to the folder \$SOFTWARE_HOME.

PreProcessing: Perform the Following Procedure

1(a): If in C-shell:

```
vi ~/.cshrc
```

Inside the ~/.cshrc file, add the following three lines at the end of the file:

```
setenv PATH $SOFTWARE_HOME /Programs/:${PATH}
setenv FSLOUTPUTTYPE ANALYZE
setenv LD_LIBRARY_PATH $SOFTWARE_HOME
```

save the file, then type “source ~/.cshrc”

1(b): If in Bash-shell:

vi ~/.bashrc

Inside the ~/.bashrc file, add the following three lines at the end of the file:

```
export LD_LIBRARY_PATH$SOFTWARE_HOME
```

```
export PATH=$PATH: $SOFTWARE_HOME /Programs
```

```
export FSLOUTPUTTYPE=ANALYZE
```

save the file, then type “source ~/. bashrc”

2. Then, go to the directory:

```
$SOFTWARE_HOME
```

Type in:

```
cd ..
```

```
chmod 777 $SOFTWARE_HOME/ -R
```

(Note: Regions highlighted by yellow denotes the path you need to adjusted for your own machine)

(a) In the root directory, you can see two folders: GroupA and GroupB, which denote the moving group and fixed group directory, respectively. Place images in analyze format (i.e., with .hdr and .img files) and their segmentation groundtruths in analyze format belonging to the moving group and fixed group to folders GroupA and GroupB, respectively. Also, create a label information txt file under the root directory, which contains the label information.

In the demo example, images na01_cbq.img ,...,na10_cbq.img are used as moving group images, with their segmentation groundtruths na01_seg.img,...,na10_seg.img (segmentation of three tissue types: white matter, gray matter, and CSF). Images na11_cbq.img,...,na20_cbq.img are used as fixed group images, with their segmentation groundtruths na11_seg.img,...,na20_seg.img. The label information txt file is "labelinfo.txt" which contains information about tissue label value correspondence in the segmentations

(b) In folders GroupA and GroupB, create the image file list and the corresponding segmentation groundtruth file list in txt format containing the images and their segmentation groundtruths you placed in Step (a).

In the demo example, in folder GroupA, the corresponding lists are "FileList.txt" and "AS.txt". In folder GroupB, the corresponding lists are "FileList.txt" and "BS.txt".

(c) Run Matlab. Set the root directory as the working directory in Matlab, then execute: "InterGroupGUI" in the command window, the software GUI will prompt out

(d) Fill in the number of images in GroupA and GroupB, respectively in the corresponding GUI places under the tag "Groupwise Registration WithinGroups" and the image file list name. You can also see the number of iterations parameters editable field in the GUI to adjust the registration algorithm, the larger the value, the better the accuracy, but also longer running time. Normally, using the default parameter values can give you good results and tradeoff between running time and registration accuracies.

In the Demo example, you should fill in "10" in both the field "Number of Images" in GroupA and GroupB's tag (Since both groups contain 10 images), and the "Image File List Name" field should fill "FileList.txt", matching the step in Step (b)

(e) Click the "Perform Within Group Registration" button, wait until this step is finished

Once this step is finished, a message will prompt out the Matlab command window:

"Within Group Registration Done!"

(f) After Step (e) is finished, fill in the "Segmentation File List Name" file for GroupA and GroupB under the tag "InterGroup Registration with Multi-Channel Demons", as well as the label information file in the Field "Label Information File". Again, you can see fields which you can adjust the iterations of the registration algorithms, generally keeping the default parameters can give you good results in a reasonable time.

In the Demo example, the "Segmentation File List Name" for GroupA and GroupB are "AS.txt" and "BS.txt", respectively (see Step (b)), and the label information file name is "labelinfo.txt" (see Step (a)).

(g) Click the button "Perform Inter Group Registration"

(h) Once Step (g) is done, you can check the results in the root directory. The registered images are named as "WarpedImage j .img", and their corresponding warped segmentation groundtruths are named as "WarpedSeg j .img", and the corresponding deformation field DeformField j .raw (where $j=1,\dots,M$), M is the number of total images in the fixed and moving groups (e.g., 20 in the demo example). Let M_a and M_b denotes the number of images in GroupA and GroupB, images from "WarpedImage1.img" to "WarpedImage M_a .img" are warped images from GroupA, while images from "WarpedImage M_a+1 .img" to "WarpedImage M .img" are warped images from GroupB.

Note that the deformation field is applied on the Affine registered images in GroupA and GroupB named "Affine_Atlas*_M.img", not the originally images you placed.

Once this step is done, a message will prompt out the Matlab command window:

"Inter Group Registration Done!"

5. Reference:

[1] "A Statistical Framework for Inter-Group Image Registration", Neuroinformatics 10(4): 367-378 (2012) [Shu Liao, Guorong Wu, Dinggang Shen]