Structural Connectome Processing Software

User Manual

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# Installation

Currently the software is only tested on MAC-OSX computers but should run on any platform with Python 3.0 and Docker software support. Note, the installation application is written only for MAC-OSX but the software essentially runs via Bash shell scripts and/or Python scripts so porting to Windows 10 and/or Linux should be trivial.

## MAC-OSX

### Pre-Requisites

* Install Conda or MiniConda Python 3.X: [https://docs.conda.io/projects/conda/en/latest/user-guide/install/index.htmlhttps://docs.conda.io/projects/conda/en/latest/user-guide/install/index.html](https://docs.conda.io/projects/conda/en/latest/user-guide/install/index.htmlhttps:/docs.conda.io/projects/conda/en/latest/user-guide/install/index.html)
  + After installation, open Terminal window and type `python`. The version should be 3.X as installed in previous step.
* Install Docker Desktop, create and account, login and test Docker installation: <https://docs.docker.com/desktop/mac/install/>

### Structural Connectomes Installation

* Download latest package from GitHub: <https://github.com/dbkeator/StructuralConnectomes>
  + Note, you will need to request access to this private repository
* Once downloaded, double-click on “Install.app” which is an AppleScript application that will essentially run the “Install.sh” shell script to do the installation
  + The software is installed in the $HOME/StructuralConnectomes directory where $HOME is your home directory for your user account on the machine.
  + 2 aliases are stored on your Desktop:
    - StructuralConnectomes.app which is the application for doing structural connectome processing
    - Subtract\_FA.app which is the application for subtracting 2 FA maps for estimates of blood-brain-barrier permeability given some manipulation between FA map 1 and 2.
      * Note, in order to run Subtract\_FA.app you must have access to the ANTS Docker container ("dbkeator/roiextract:latest") which is still private. Email [dbkeator@brainimage.net](mailto:dbkeator@brainimage.net) to download this if you are not Dr. Shankle

### Optional Installations

* If you are interested in visualizing specific tractographies you’ll need to install DSI Studio natively on your computer. Instructions can be found here: <http://dsi-studio.labsolver.org/>

# Structural Connectome Processing

This software will produce structural connectomes from diffusion (DTI) magnetic resonance imaging (MRI) acquisitions. It requires a DTI scan with at least 32 directions and a structural MRI.

The software will process any patient scans it finds in the directory passed to the “StructuralConnectomes.app” on the Desktop as shown below.

Graphical user interface, text, chat or text message

Description automatically generated

This will open a Terminal window on your MAC and processing will start. The first time you process a scan many Python libraries and the correct Docker containers will be installed/downloaded. This will take longer to process than subsequent scans where all the required dependencies are local.

Once processing has completed you will find a “Structural\_Connectomes” folder containing “report.html” plus additional files depending on whether the tool was able to find a DICOM-formatted DTI with at least 32 directions and a structural MRI scan.

Graphical user interface, text, application

Description automatically generated

The file “report.html” is a simple way of reviewing the results. If there was a problem this file will briefly describe the problem. If not, it will contain information about the processing.

Graphical user interface

Description automatically generated

Additional files included in the top-level directory include the file “key.txt” will have a written description of all files in the directory, providing a key to what they are. Next there are 3 versions of the structural connectomes “strength” of structural connections: (1) connectome\_matrix\_binary.csv: contains a 0/1 entry as to whether the two anatomical regions are structurally connected; (2) connectome\_matrix\_weighted.csv: contains the number of streamlines connecting the two regions; (3) connectome\_matrix\_normalized\_weighted.csv: contains the number of streamlines connecting the two regions but normalized by the anatomical region pair with the most number of streamlines connecting them. Next the file “Graph\_Theoretic\_Measures.csv” contains the graph theoretic measures computed on the structural connectome. Finally, the FA.nii.gz, MD.nii.gz, and T1.nii.gz are the NifTI-formatted images of the fractional anisotropy (FA.nii.gz), mean diffusivity (MD.nii.gz), and the structural image (T1.nii.gz).

In the output directory containing the structural connectomes, the “Files” directory contains a number of intermediate files that may be useful in the future. Again the “key.txt” file will have information about what all the various files are and can be used as a reference.

One of the potentially useful files is the log file. The file named “connectomes\_batch\*\_log.txt” in the “Files” directory contains a log of all the commands run to produce the structural connectome files. Using the entries in the log file that start with “INFO command:” one could theoretically re-run each step of the processing from a terminal window instead of using the drag-n-drop method.

# Tractography Visualizations

If you are interested in visualizing specific region-to-region tractographies, you can use the files in the “Files/Tracts” folder in the structural connectomes output. In this directory are tract files saved for each pair of regions. To support this you need to install DSI Studio software natively on your computer. You can do that by following the installation instructions.

1. Open DSI Studio from the icon A picture containing logo

   Description automatically generated. Select “Step T3: Fiber tracking” and select the file containing the \*fib.gz extension from the “Files” folder inside of the patient’s folder.

Graphical user interface

Description automatically generated

1. You have now opened the Guided User Interface. To open tractography of the whole brain or specific tracts of interest select “Tracts” on the top panel and “Open Tracts…”.
   1. The whole brain tractography file is called count\_connect.trk.gz and is located in the “Files” folder.
   2. Individual streamline files contain the extension \*.tt.gz located in the “Files/tracts” folder. There is one file for each entry in the connectivity matrix.

A screenshot of a video game

Description automatically generated

Graphical user interface, application

Description automatically generated

1. The tracts or ‘streamlines’ will appear in the GUI. They can be selected or deselected by clicking the check mark next to the file name on the bottom right hand side of the window.

A screenshot of a computer

Description automatically generated with medium confidence

*(An example of whole brain connectivity calculated from a group average of 1021 Human Connectome Project subjects)*

A screenshot of a computer

Description automatically generated with low confidence

*(An example of node-to-node the “Cingulate\_Ant\_R\_Cingulate\_Mid\_R.tt.gz” file)*

1. To visualize the ‘end’ regions for the example streamline above. Select the “Atlas…” tab on the top left-hand side of the window. It is highlighted in the images above in red. Then, select the respective ‘end’ regions you would like to visualize. In this case select “Cingulate\_Ant\_R” and “Cingulate\_Mid\_R”

A screenshot of a computer

Description automatically generated with medium confidence

1. The region files selected will appear in the left hand window. You can select and deselect them by either checking or unchecking the region name.

A screenshot of a computer screen

Description automatically generated with medium confidence

# Subtracting FA Maps

Subtracting FA maps acquired before and after some functional manipulation has been posited as a way to interrogate the integrity of the blood-brain-barrier. To support such comparisons we have included a tool (subtract\_images.py and associated Subtract\_FA.app link on the Desktop) which does the following:

* Registers FA map 2 to FA map 1 using ANTS diffeomorphic registration
* Subtract the registered FA map 2 from FA map 1 and saves the difference as a NifTI image which can be visualized using a variety of free visualization tools.

To perform an FA map subtraction you have a couple of different options. The easiest is to use the Desktop “Subtract\_FA.app” link using the following procedure:

* Copy FA map 2 into the directory where FA map 1 is. Renaming FA map 2 to something different from FA map 1.
* Select FA map 1 and then FA map 2 holding down the “cmd” key on your MAC keyboard.
  + Drag-n-drop the two FA maps onto the Desktop icon “Subtract\_FA.app”

Graphical user interface, text, application

Description automatically generated

* The difference image (i.e. FA\_map1\_minus\_FA\_map2.nii.gz) is then saved in the directory with the original files. It can be viewed with any NifTI viewer. Since the program registered FA map 2 to FA map 1, the difference image is in the space of FA map 1 and can be overlayed on the T1.nii.gz image from the structural connectomes processing of the patient represented by FA map 1.

Table

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