

SRQL

Semi-automated Robust Quantification of Lesions

Welcome! Here, we've created a toolbox that aims to make lesion quantification more robust. This toolbox includes the following three important features: (1) semi-automated white matter intensity correction, (2) a report of descriptive statistics on lesions, and (3) an option to perform analyses in native or standard space.

These scripts were developed by Kaori Ito.

Any troubleshooting issues with these scripts can be directed to both Kaori Ito (kaoriito@usc.edu) and the Neural Plasticity and Neurorehabilitation Laboratory (nprl@usc.edu).

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GETTING STARTED

Before you start running the scripts, please make sure that the following steps are completed to organize your data.

1. Project Directory Setup

We suggest building your project directory as follows:

SRQL_parent_directory/

-> inputs/

-> dataset_01

-> subj01 (within this folder should be subj01_Anatomical.nii, etc.)

-> subj02 (within this folder should be subj02_Anatomical.nii, etc.)

-> dataset_02

-> subj01 (within this folder should be subj01_Anatomical.nii, etc.)

-> subj02 (within this folder should be subj02_Anatomical.nii, etc.)

...

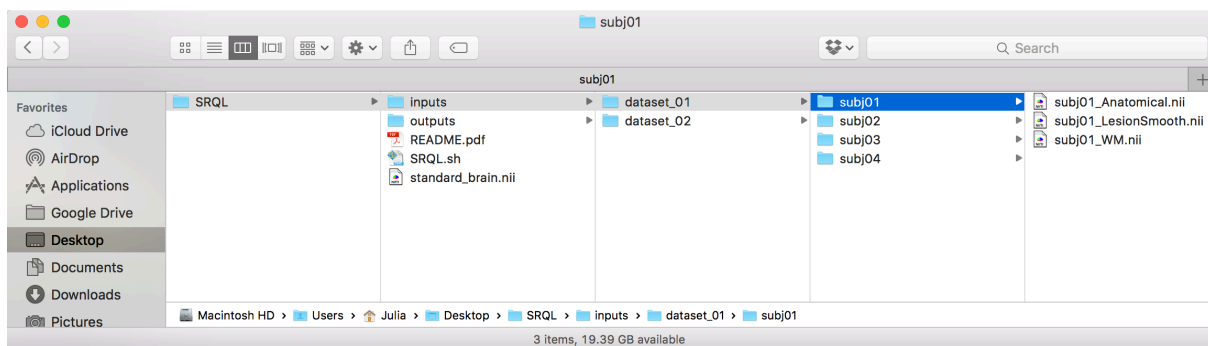
-> outputs/

-> SRQL.sh

...

NOTE: There should be no duplicate file names with different extensions in folders (e.g. subj01_Anatomical.nii and subj01_Anatomical.nii.gz – one of these should be moved or deleted); only nifti files should be in each subject folder.

Here is an example of how the directories should appear:



2. Installing Software

FSL must be installed on your computer. You also need a bash terminal.

The executable of FSL need to be in the user's PATH environment (most times this is already setup if the programs are already installed on the machine). For Mac/Linux users, to see if this is set up, type:

```
nano ~/.bash_profile
```

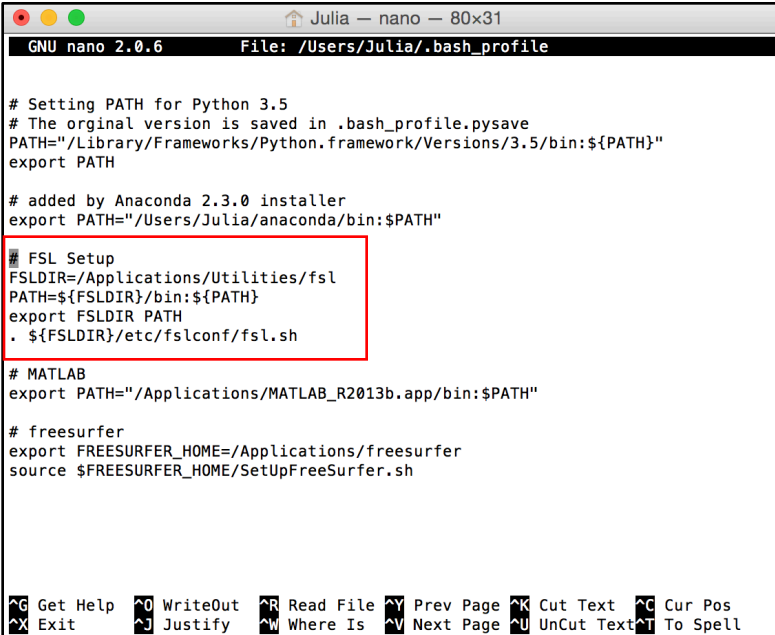
(or .bash_rc or other equivalent profile) in the terminal (this file may be a different name/path). If this is not set up for a given program, you will need to manually type the following in:

```
export PATH="<directory>/<program>/bin:$PATH"
```

(but replace <directory>/<program> with your specific path to the program - for instance, you might use the following line:

```
export PATH="/Applications/Utilities/fsl/bin:$PATH"
```

You should have this PATH environments, similarly structured, in your bash profile:



```
GNU nano 2.0.6 File: /Users/Julia/.bash_profile

# Setting PATH for Python 3.5
# The original version is saved in .bash_profile.pysave
PATH="/Library/Frameworks/Python.framework/Versions/3.5/bin:${PATH}"
export PATH

# added by Anaconda 2.3.0 installer
export PATH="/Users/Julia/anaconda/bin:${PATH}"

# FSL Setup
FSLDIR=/Applications/Utilities/fsl
PATH=${FSLDIR}/bin:${PATH}
export FSLDIR PATH
. ${FSLDIR}/etc/fslconf/fsl.sh

# MATLAB
export PATH="/Applications/MATLAB_R2013b.app/bin:${PATH}"

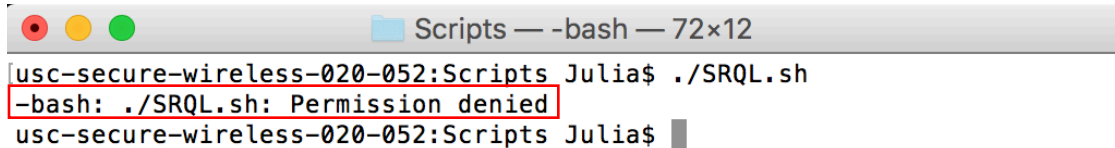
# freesurfer
export FREESURFER_HOME=/Applications/freesurfer
source $FREESURFER_HOME/SetUpFreeSurfer.sh

^G Get Help ^O WriteOut ^R Read File ^Y Prev Page ^K Cut Text ^C Cur Pos
^X Exit ^J Justify ^W Where Is ^V Next Page ^U UnCut Text ^T To Spell
```

3. Make Script Executable

The SRQL scripts must be executable.

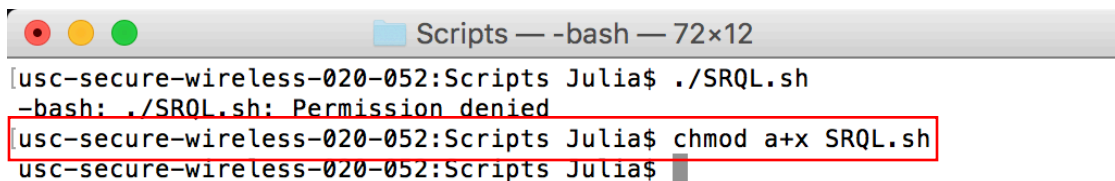
If when running scripts, you receive an error that looks like this:

A terminal window titled "Scripts — -bash — 72x12" with a macOS-style title bar (red, yellow, green buttons). The prompt is "[usc-secure-wireless-020-052:Scripts Julia\$". The user enters "./SRQL.sh". The output is "-bash: ./SRQL.sh: Permission denied", which is highlighted with a red box. The prompt returns to "[usc-secure-wireless-020-052:Scripts Julia\$".

```
[usc-secure-wireless-020-052:Scripts Julia$ ./SRQL.sh  
-bash: ./SRQL.sh: Permission denied  
usc-secure-wireless-020-052:Scripts Julia$
```

It usually means that your script is not executable.

To make the scripts executable, use the chmod command, with a+x arguments. For instance:

A terminal window titled "Scripts — -bash — 72x12" with a macOS-style title bar. The prompt is "[usc-secure-wireless-020-052:Scripts Julia\$". The user enters "./SRQL.sh", which results in "-bash: ./SRQL.sh: Permission denied". The user then enters "chmod a+x SRQL.sh", which is highlighted with a red box. The prompt returns to "[usc-secure-wireless-020-052:Scripts Julia\$".

```
[usc-secure-wireless-020-052:Scripts Julia$ ./SRQL.sh  
-bash: ./SRQL.sh: Permission denied  
[usc-secure-wireless-020-052:Scripts Julia$ chmod a+x SRQL.sh  
usc-secure-wireless-020-052:Scripts Julia$
```

RUNNING THE SCRIPT

When GETTING STARTED steps are complete, you can run the SRQL script and give responses to the prompts.

4. Run SRQL

To run SRQL, type the following into the terminal: `./SRQL.sh`

```
usc-secure-wireless-020-052:Scripts Julia$ ./SRQL.sh
```

Once the script is running, you will be presented with the following prompts:

1. Enter the path of your input directory.

If you are wanting to run one dataset (one folder with one or more subjects), enter the path where this one dataset is

```
Please specify the location of your input directory. (e.g., /Users/Lily/ProjectX/Input_Data)
/Users/Julia/Desktop/SRQL/inputs
```

If you are wanting to run multiple datasets (multiple folders with one or more subjects in each folder), enter in the path where all the datasets are located

```
Please specify the location of your input directory. (e.g., /Users/Lily/ProjectX/Input_Data)
/Users/Julia/Desktop/SRQL/inputs/Dataset_01
```

2. Enter the path of the directory where the outputs should go.

```
Please specify the location you would like your outputs to be stored. (e.g., /Users/Lily/ProjectX/Outputs)
/Users/Julia/Desktop/SRQL/outputs
```

3. When running one dataset – enter ‘n’; multiple datasets - enter ‘y’

```
Are you running more than one group? ('y'/'n')
y
```

4. Enter the lesion mask identifier

```
Please specify your lesion mask identifier/wildcard (e.g., lesion_mask if subj01_lesion_mask or F013_lesion_mask is your identifier)
LesionSmooth
```

5. Enter the white matter identifier

```
Please specify your white matter mask identifier/wildcard (e.g., WM if subj01_WM or F013_WM is your identifier)
WM
```

6. Enter 'y' if you want the the lesion standardized; 'n' if you do not want the lesion standardized

```
Output lesion data in standard space? ('y'/'n')
```

```
y
```

7. Enter 'y' if you have already performed the skull stripping; 'n' if you have not

```
Have you performed skull stripping on your anatomical images? ('y'/'n')
```

```
y
```

8. If you entered 'y' for performing the skull stripping, you will be prompted to provide the identifier

```
Please specify skull stripped brain identifier (e.g., brain)
```

```
Brain
```

9. If you entered 'y' for outputting lesion data in standard space, you will be asked if you have already normalized your anatomical data to standard space

```
Have you normalized your anatomical data to standard space? ('y'/'n')
```

```
y
```

10. If you entered 'y' for already normalizing your anatomical data, you will be asked to provide the identifier

```
Please specify the identifier for the normalized brain (e.g., 'brain_reg')
```

```
Brain_Reg
```

Tips

Tip (1): To change directories, use the command “cd” followed by the directory you want to move to

```
usc-secure-wireless-020-052:~ Julia$ cd /Users/Julia/Desktop/SRQL
```

Tip (2): To locate the directory path of a given file from the Finder on a Mac, right click on the file and click “Get Info”. The portion in the red box is the path. You may highlight this and copy and paste it into the terminal. Make sure folders are separated by ‘/’ – e.g., Users/Julia/Desktop/SRQL

