

SRQL v2.0

Semi-automated Robust Quantification of Lesions, 2.0

Welcome! Here, we've created a toolbox that aims to make lesion quantification more robust. This toolbox includes the following two important features: (1) semi-automated white matter intensity correction, and (2) a report of descriptive statistics on lesion.

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 (npnl@usc.edu).

TABLE OF CONTENTS

Getting Started Pages 3 – 5

- 1. Project Directory Setup Page 3
- 2. Installing Software Page 4
- 3. Make Scripts Executable Page 5

Running the Script Pages 6 – 9

- 4. Run SRQL Page 6
- 5. Organizing the Final Files Page 8

Additional Tips Page 10

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

→ subj01 (within this folder should be subj01_Lesion.nii.gz, subj01_T1.nii.gz, etc.)

→ subj02 (within this folder should be subj02_Lesion.nii.gz, subj02_T1.nii.gz, etc)

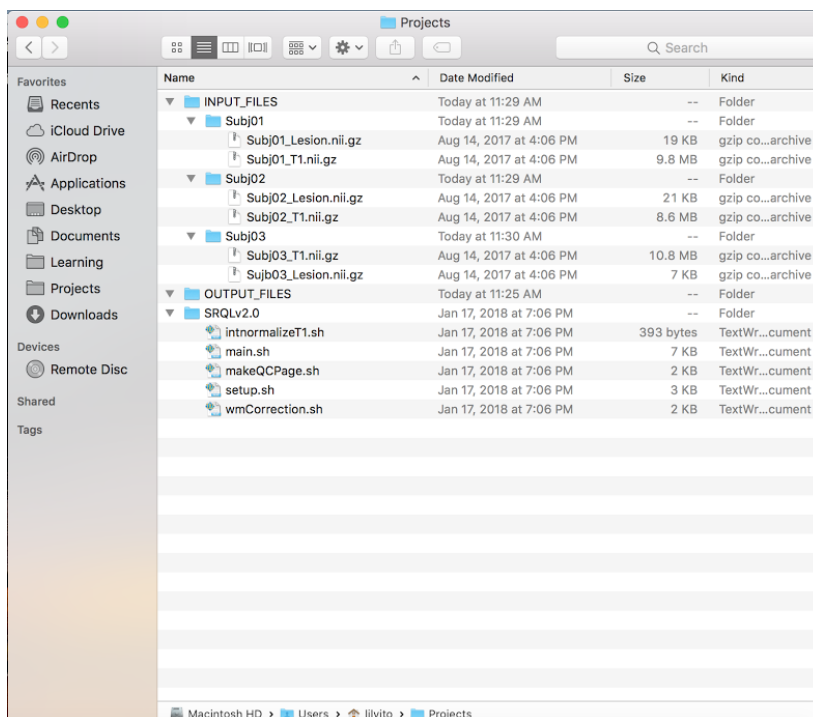
→ outputs/

→ SRQL.sh

Each subject directory should at least include (1) a T1 structural file (or anatomical image), and (2) a lesion mask file. Each subject directory can also include a (1) a white matter mask file, and (2) skull-stripped brain file (optional).

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 and **FSLeYes** (found here:

<https://users.fmrib.ox.ac.uk/~paulmc/FSLeYes/>) 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`

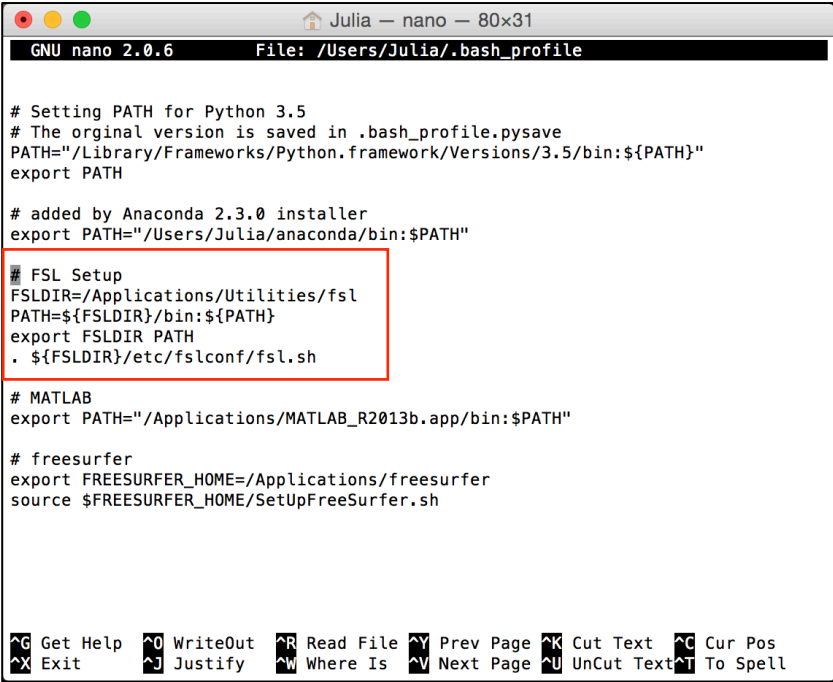
(or `.bash_rc` or other equivalent profile) in the terminal (this file may be a different name/path). If this is not set up for a given program, you will need to manually type the following in:

`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.

When running scripts, if you receive an error that looks like this:

```
[guest-wireless-hsv-nat-207-151-021:SRQLv2.0 lilyito$ ./main.sh  
-bash: ./main.sh: Permission denied
```

It usually means that your script is not executable

Should say main.sh

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

```
[guest-wireless-hsv-nat-207-151-021:SRQLv2.0 lilyito$ ./main.sh  
-bash: ./main.sh: Permission denied  
[guest-wireless-hsv-nat-207-151-021:SRQLv2.0 lilyito$ chmod a+x ./main.sh  
[guest-wireless-hsv-nat-207-151-021:SRQLv2.0 lilyito$ ./main.sh
```

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: `./main.sh`

```
[guest-wireless-hsv-nat-207-151-021:SRQLv2.0 lilyito$ cd /Users/lilyito/Projects/SRQLv2.0  
[guest-wireless-hsv-nat-207-151-021:SRQLv2.0 lilyito$ ./main.sh]
```

```
SRQL (circle) Toolbox 2.0 Copyright (C) 2017 Kaori L Ito & Sook-Lei Liew  
This program comes with ABSOLUTELY NO WARRANTY.  
This is free software, and you are welcome to redistribute it under certain  
conditions;  
please visit <https://www.gnu.org/licenses/gpl.html> for details.
```

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

1. *Enter the path of your input directory to the dataset.*

```
Specify the location of your input directory. (e.g., /Users/Lily/ProjectX/Input_Data)  
/Users/lilyito/Projects/INPUT_FILES
```

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

```
Specify the location of your desired output directory. (e.g., /Users/Lily/ProjectX/Outputs)  
/Users/lilyito/Projects/OUTPUT_FILES
```

3. *Enter the anatomical mask identifier*

```
Specify your anatomical image identifier/wildcard. (e.g., T1 if Subj01_T1 or F013_T1 is  
your anatomical image.)  
T1
```

4. *Enter the lesion mask identifier*

```
Specify your lesion mask identifier/wildcard (e.g., lesion_mask if subj01_lesion_mask or  
F013_lesion_mask is your identifier)  
Lesion
```

From this point on, the steps differ based on whether or not you have already performed 1) skull stripping and 2) white matter identification and have those files housed within the subject directory...

5. Indicate whether skull stripping has already been performed ('y' or 'n')

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

Yes (y) → SRQL will request the file identifier

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

```
Brain
```

No (n) → SRQL will perform skull stripping and create an output file (may take additional time to run)

6. Indicate whether white matter segmentation has already been performed ('y' or 'n')

```
Have you performed white matter segmentation on your subjects? ('y'/'n')
```

Yes (y) → SRQL will request the file identifier

```
Please specify identifier for white matter mask (e.g., c1)
```

```
seg_2
```

No (n) → SRQL will perform white matter segmentation and create an output file (may take additional time to run)

7. Indicate the percent of intensity values you want to have removed from the mask (5% is standard)

```
Indicate the percentage of intensity values you would like to have removed from your mask.  
Note: 0% indicates no white matter correction will be made (default: 5%)
```

```
5
```

8. Indicate whether you would like to create a quality control page ('y' or 'n')

**NOTE: This requires pre-installation of FSLeves*

```
Create a quality control page? ('y'/'n')  
Note: This requires pre-installation of fsleves
```

Yes (y) → SRQL will create an HTML file of all of the lesion masks in the output folder

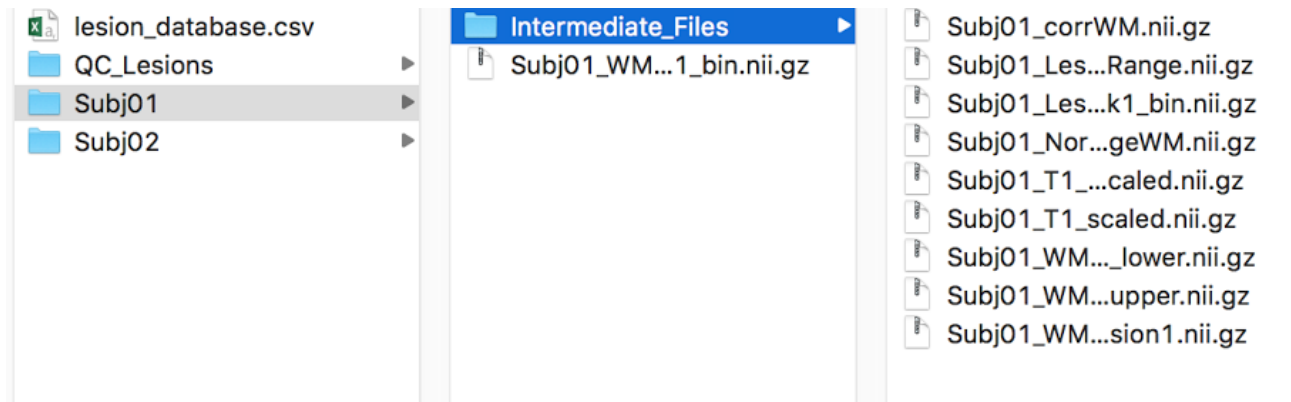
No (n) → SRQL will not produce a quality control page

OUTPUT DATA

5. SRQL Output Files

Each subject will have its own directory housed under the “output files” directory specified in Step 2, with...

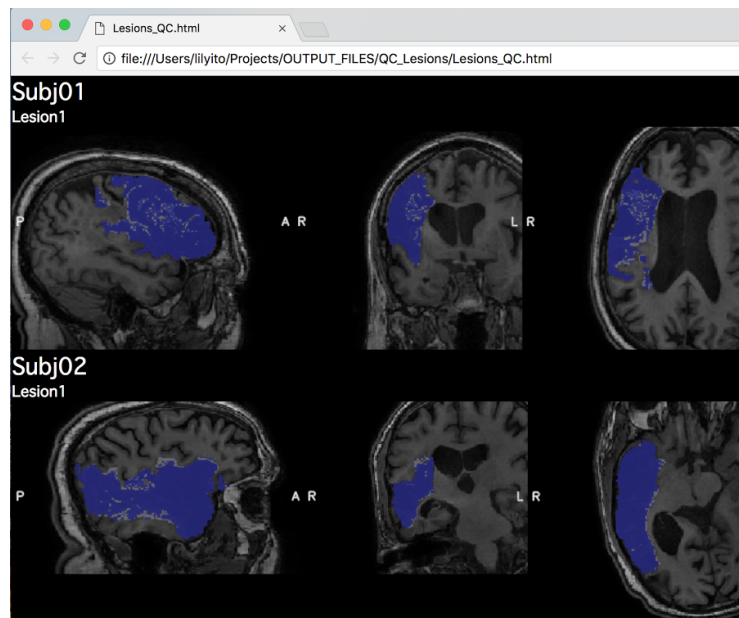
- 1) A corrected lesion mask file (SubjectID_WMAdj_Lesion_bin.nii.gz)
- 2) A directory with Intermediate files (all of the steps SRQL took to create the final lesion mask)



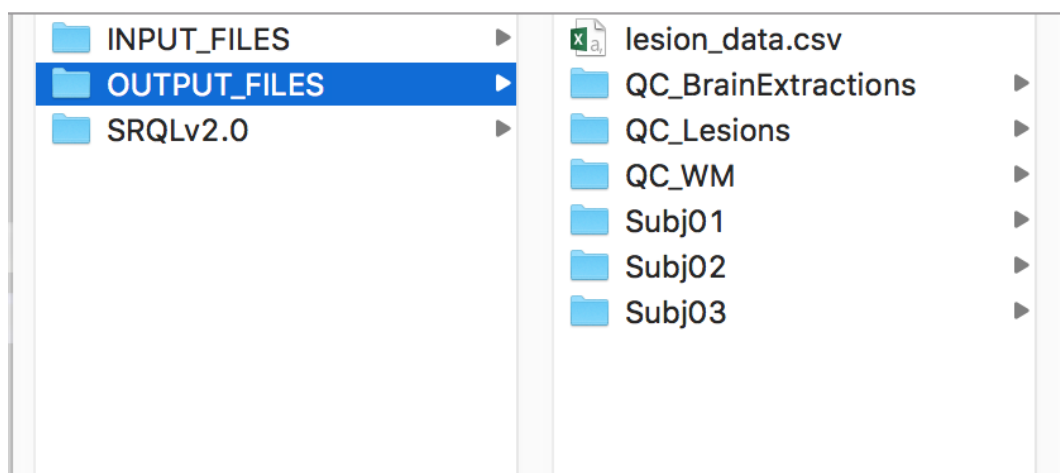
You will also find a lesion_database.csv file, which will contain meta-data information on each subject’s corrected lesion mask.

	A	B	C	D	E	F
1	Subject	Total_Native_Brain_Volume	Mean_White_Matter_Intensity	Lesion1_Hemisphere	Lesion1_Original_Lesion_Volume	Lesion1_Corrected_Lesion_Vol
2	Subj01	1421269	56.837467 R		89029	
3	Subj02	1385472	52.26324 R		104524	

If the user specified for a quality control page, SRQL will create a /QC_Lesions directory, in which HTML link can be found to view screenshots of all the adjusted lesions.



If you said “yes” to skull stripping and white matter segmentation you will also see a /QC_BrainExtractions (skull stripping) and /QC_WM (white matter segmentation) directory in your output directory for you to visualize the quality of the preprocessing steps.



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

