analyseMRI *T1-weighted+FLAIR* User Manual

1   ANALYSEMRI

The analyseMRI software is meant for specific analysis of the Hippocampus, Amygdala and Cerebral Cortex in terms of their volume (relative to the cerebral white matter volume), based on T1-weighted MRI scans, and MRI voxel intensity (relative mode, variance and standard deviation), based on FLAIR MRI scans. This software was developed based on MRI scans performed on a Philips Achieva 3T scanner, but can be used on any T1-weighted scan with isotropic voxel resolution and any FLAIR scan resolution.

2   REQUIREMENTS

An up-to-date installation of FreeSurfer [1] is required to perform the segmentation of the brain T1-weighted MRI scan into its subregions. FreeSurfer is free and open-source, but requires Linux or MacOS. An installation of the analyseMRI program is required (only supported on Windows). If the installation sequence detects that no MATLAB runtime (keep in mind, this is free and free of license requirements) is installed, the installation sequence will install a MATLAB runtime as well (analyseMRI including the runtime is around 1.5GB).

3   PREPROCESSING

3.1   DATA FORMAT

The T1-weighted MRI scan file should be present in either the Neuroimaging Informatics Technology Initiative 'NIfTI' (.nii) data format or in the Digital Imaging and Communications in Medicine 'DICOM' (.dcm) data format. The FLAIR MRI scan file should be present in the Neuroimaging Informatics Technology Initiative 'NIfTI' (.nii) data format.

3.2   SEGMENTATION

From the folder where the T1-weighted scan file is located, right-click on an empty space in this folder and select 'Open in Terminal'. Start FreeSurfer, and run the following command:

```
recon-all –s <patient-name> –i <scan-file-name>.nii –all
```

Keep in mind that the patient name should be composed as follows:
YY + C/D + XXX
Here **YY** represents a two-letter research abbreviation (to be chosen by the user), **C** represents a healthy

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[1] https://surfer.nmr.mgh.harvard.edu/

control, **D** represents a suspected diagnosable or diagnosed patient, **XXX** represent a three-digit patient number. For example: *AMD001*

Keep in mind that this operation may take anywhere from 8 to 12 hours to finish. Do not close the terminal in this time period. If the process is finished with a 'Finished without errors' message, you can proceed closing this terminal window.

3.3 OUTPUT

In the 'subjects' folder of your FreeSurfer edition directory, open the generated patient folder (the folder name is the patient-name as specified in the segmentation command above), navigate to the 'mri' folder and open this folder. Right-click on an empty space in this folder and select 'Open in Terminal'. Start FreeSurfer, and run the two following commands:

```
mri_convert --in_type mgz --out_type nii brain.mgz brain.nii
```

```
mri_convert --in_type mgz --out_type nii aseg.mgz aseg.nii
```

These commands ensure that the two required data files, the T1-weighted image (brain.nii) and the so-called atlas file (aseg.nii) are saved in the 'NIfTI' file format, in this same patient folder.

3.4 FILE FOLDER

Anywhere in your file directory (this directory will later be called the 'source directory') create a folder, named as the patient name. Keep in mind that the patient name should be composed as follows:
YY + C/D + XXX
Here **YY** represents a two-letter research abbreviation (to be chosen by the user), **C** represents a healthy control, **D** represents a suspected diagnosable or diagnosed patient, **XXX** represent a three-digit patient number. For example: *AMD001*

Copy the generated brain.nii and aseg.nii files into this folder.

Also, rename the FLAIR scan .nii file into FLAIR.nii and copy this file into the aforementioned created folder.

Check the following before commencing the analysis steps:

- You have created a folder, named according to the patient name convention
- In this folder, three files are located: brain.nii, aseg.nii and FLAIR.nii

4 ANALYSIS

4.1 USING ANALYSEMRI

The analyseMRI program is designed to be used, as easily as possible, without any prior technical knowledge. It provides both objective quick immediate results and objective elaborate detailed and numerical results in several auto-saved files. During use, the user will be asked a total of four questions in a terminal window. Detailed guidance on how to answer these questions is presented along the way. Keep in mind: close and restart the program for each new scan analysis.

Open analyseMRI and wait until the first question appears:

```
Enter patient number YY+C/D+XXX
```

Now type/enter the patient number (the same patient number as the name of the folder created in section 3.4 above). For example: *AMD001*

PRESS ENTER

The second question appears:

```
Enter source directory in double quotations with backward slash, end
with backward slash
```

Now type/enter the source directory where the folder (created in section 3.4 above) is located, exactly as is stated in the question. For example: *"C:\sourcefolder\"*

PRESS ENTER

The third question appears:

```
Enter target directory in double quotations with backward slash, end
with backward slash
```

Now type/enter the target directory where you want the resulting output files to be located, exactly as is stated in the question. For example: *"C:\targetfolder\"*

PRESS ENTER

The fourth and last question appears:

```
Enter the isotropic voxel dimension of the T1-weighted scan in
millimeter
```

Now type/enter the isotropic voxel dimension of the T1-weighted scan as an integer number (scale of millimeters). For example: "*1*"

PRESS ENTER

The program will run for at most a minute, displaying data and several figures along the way. These are the figures you will find later in the target folder, as will be explained in the next section. The program can be aborted by pressing enter at any of the four posed questions.

4.2 RESULTS

The program is finished once for each of the analyzed structures (left hippocampus, right hippocampus, left amygdala, right amygdala, left cerebral cortex, right cerebral cortex) a quick-view result appears. Here is stated whether the structure relative volume is larger or smaller that a healthy control average, whether the structure relative intensity mode (most frequent voxel relative intensity value) is higher or lower than a healthy control average, whether the structure voxel intensity variance is higher or lower than a healthy control average and whether the structure voxel intensity standard deviation is higher or lower than a healthy control average.

Next follows a list of the absolute structure volumes in cubic millimeter.

Finally, the program searches for definite one-sided hyperintensity in the hippocampus and amygdala. If e.g. the left hippocampus has a higher intensity mode *and* lower variance than the right hippocampus, the program detects a left-sided hippocampus hyperintensity and displays this in the quick-view results.

'Relative' means that the value has been related to (i.e. divided by) its corresponding value of the Cerebral White Matter of the corresponding hemisphere. This creates objective, patient-to-patient comparable, numerical information.

Navigate to the target directory and you will find a newly generated folder named as the patient name. Opening this folder you will find two spreadsheets, one containing the numerical results behind the quick-view results (analytics_<patient-name>.xlsx) and one containing the column names of the other spreadsheet, i.e. the parameter names (analytics_colnames.xlsx).

In this spreadsheet, 'rel' means relative, 'LH' means Left Hippocampus, 'RH' means Right Hippocampus, 'LA' means Left Amygdala, 'RA' means Right Amygdala, 'LCX' means Left Cerebral Cortex and 'RCX' means Right Cerebral Cortex.

Aside from these spreadsheets you will find two subfolders, named 'Box' and 'Histo'.
In the 'Box' subfolder all the generated intensity-related boxplots are saved in both .eps and .png data formats. In the 'Histo' subfolder all the generated intensity-related histograms are saved in both .eps and .png data formats.

5 SUPPORT

For any related questions, feedback or ideas for improvement, please contact the developer via the following email address: analysemri@gmail.com