Instructions for using the shell scripts of the « FW kit »

Summary:

I. Components

Different files are provided in the distributed directory **/scripts_FW_CONSORTIUM/**:

- **MAIN_script_FW.sh**: batch that launches the main shell script,
- **mrn.py**: script that computes the FW map
- **FMRIB58_FA_1mm_thr:** White matter mask (FSL FMRIB58_FA map thresholded at 3000)
- **Example:** directory containing input data and example of script to run the kit

II. Prerequisites

a) Hardware:

- Computer with Linux or Mac OS X.
- For Windows, a Linux virtual machine is needed, e.g. the NeuroDebian Virtual Machine (http://neuro.debian.net/vm.html)

b) Software:

- Mandatory: (1) An installation of the FMRIB Software Library (FSL, https://www.fmrib.ox.ac.uk/fsl). FSL is a free tool. See license details at: https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Licence. (2) An installation of Python and of the following python libraries: "matplotlib" and "dipy".
- Optional: dcm2niix (https://github.com/rordenlab/dcm2niix). This tool is designed to convert neuroimaging data from the DICOM format to the NIfTI format. This software is open source. The bulk of the code is covered by the BSD license. Some units are either public domain or use the MIT license.

III. Usage

a) Input needed

- Full path to the 4D DTI volumes (nii.gz format)
- Full path to the brain mask image (nii.gz format)
- Full path to the bval file
- Full path to the bvec file
- Full path for the output directory

b) Modifications that must be done in both scripts before launching

Open **MAIN_script_FW.sh** file in /scripts_FW_CONSORTIUM/ directory. Three paths at the top of the script should be modified including FWMRN_PATH, BINFSL_PATH and PYTHON_EXEC (see below).

```
# MODIFY FOLLOWING DIRECTORIES
# FSL_PATH IS THE MAIN FSL PATH AND SHOULD CONTAIN BIN/, CONFIG/, LIB/... SUBDIRECTORIES)
# PYTHON_EXEC IS THE PATH FOR THE PYTHON EXECUTABLE
set FWMRN_PATH = /data/home/maillard/scripts_FW_CONSORTIUM/
set BINFSL_PATH = /data/condorWorkspace/fsl/
set PYTHON_EXEC = /usr/bin/python
```

- FWMRN_PATH: must be replaced by the path leading to the **/scripts_FW_CONSORTIUM/** directory
- BINFSL_PATH: must be replaced by the path leading to the FSL main directory
- PYTHON_EXEC: must be replaced by the path of the python executable

c) Before running the script for the first time

Make sure the script is executable by running the following commands:

cd /scripts_FW_CONSORTIUM/

chmod +x MAIN_script_FW.sh

d) How to run the script

Example:

```
MAIN_script_FW.sh /dirsubject1/data.nii.gz /dirsubject1/brain_mask.nii.gz /dirsubject1/file.bval /dirsubject1/file.bvec
/myoutputdir/
```

IV. Pipeline

During the process, the main script will:

1) Create a new directory for the output files. The directory is defined by the user (see section III. a.)
2) Compute the FW map, FW-corrected FA and FW-corrected MD maps, as well as FW-uncorrected FA and FW-uncorrected MD maps (named respectively FW1_1shell_fwfit, FA1_1shell_fwfit, MD1_1shell_fwfit, FA_wls_dti and MD_wls_dti).
3) Compute transformation parameters (named nat2std_warp) from the subject's DTI space into the FSL FA template space
4) Coregister FW and FW-corrected FA maps in the FSL FA template space (named respectively FW1_1shell_fwfit_warp, FA1_1shell_fwfit,_warp and MD1_1shell_fwfit_warp)
5) Compute the mean FW and FW-corrected FA metrics within white matter voxels and store measures in the "summary.txt" file.

V. Comments

The 4D DTI volume as well as the brain mask image must have the nifty format and be compressed using gzip (i.e. **nii.gz** format).

The bval and bvec files must be compatible with FSL format, i.e. with the following dimensions (numbers of rows x numbers of columns):

- bval: 1 x # of DTI volumes
- bvec: 3 x # of DTI volumes

and have, respectively, the ".bval" and ".bvec" extensions.

At the first use, users may encounter error message for the following reasons: first, one or more Python library may be missing. Users should contact their IT to fix this issue. Second, paths for programs' directory, modified by the user in the main script before initial launch, may be incorrect. We don't expect any other issues.