UCHANGE structural neuroimaging pipeline

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Abstract

Citation: Kirstie Whitaker UCHANGE structural neuroimaging pipeline. **protocols.io**
dx.doi.org/10.17504/protocols.io.eu5bey6
Published: 25 Oct 2017

Before start

Input Files

You must have the appropriate input files in the displayed directory structure:

Multi-parametric mapping (MPM) input files:

- **R1.nii.gz** -- 3D NIFTI image containing longitudinal relaxation rate (R1) values in MPM subject space
- **R2s.nii.gz** -- 3D NIFTI image containing transverse relaxation rate (R2s) values in MPM subject space
- **MT.nii.gz** -- 3D NIFTI image containing magnetisation transfer (MT) values in MPM subject space
- **A.nii.gz** -- 3D NIFTI image containing proton density (A) values in MPM subject space
- **PDw.nii.gz** -- 3D NIFTI image containing proton density weighted (PDw) values in MPM subject space

Diffusion weighted imaging (DWI) imaging input files:

- **dti.nii.gz** -- 4D NIFTI image containing 63 diffusion weighted acquisition and 6 non-weighted acquistions (total N=69) in DTI subject space
- **bvals** -- text file containing one row of 69 values representing the diffusion weightings for the 69 volumes in **dti.nii.gz**
- **bvecs** -- text file containing three rows of 69 values representing the x, y, and z components of the diffusion directions for the 69 volumes in **dti.nii.gz**

Software Installations

You must also have the following software libraries installed:

- **Freesurfer**: https://surfer.nmr.mgh.harvard.edu/fswiki/DownloadAndInstall
- **FSL**: http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation
- **Anaconda**: https://www.continuum.io/downloads

From within **Anaconda** install the following python packages:

- VTK by typing `conda install vtk`
- Mayavi by typing `conda install mayavi`
- Nibabel by typing `pip install nibabel`
- pysurfer by typing `pip install pysurfer`

Protocol

Step 1.

Check or complete software installation

You must have the following software libraries installed:

- **Freesurfer**: https://surfer.nmr.mgh.harvard.edu/fswiki/DownloadAndInstall
- **FSL**: http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation
- **Anaconda**: https://www.continuum.io/downloads

From within **Anaconda** install the following python packages following the command below:

- VTK
- Mayavi
- Nibabel
- pysurfer

cmd COMMAND (Linux)

```
conda install vtk
conda install mayavi
pip install nibabel
pip install pysurfer
```

Install the required python packages after installing Anaconda.

Step 2.

Set up your .bashrc file

NOTE: The image for this file has been removed from the public version of this protocol as it gives away some information about

Open gedit and make sure your .bashrc file contains the following text:

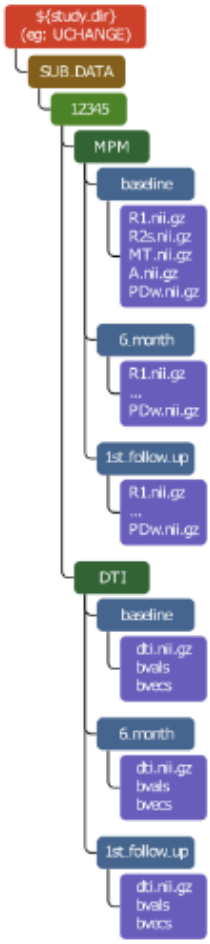
cmd COMMAND

```
# .bashrc

# Source global definitions
if [ -f /etc/bashrc ]; then
    . /etc/bashrc
fi

# User specific aliases and functions

#-------------------------------------
# Define the DRIVERS directory location
drivers_dir=/scratch/bmu-nspn/DRIVERS

#-------------------------------------
# Edited on July 15th
# By Kirstie Whitaker
# kw401@cam.ac.uk

FSLDIR=${drivers_dir}/FSL_5_0_9/fsl/
FSL_DIR=${drivers_dir}/FSL_5_0_9/fsl/
. ${FSLDIR}/etc/fslconf/fsl.sh
PATH=${FSLDIR}/bin:${PATH}
export FSLDIR
export PATH

#---------------------------------------
# Set up Matlab
module load matlab/r2014a

#---------------------------------------
# Set up Freesurfer
data_dir=$HOME
export SUBJECTS_DIR=${data_dir}

export FREESURFER_HOME=${drivers_dir}/FREESURFER_DEV/freesurfer
source $FREESURFER_HOME/SetUpFreeSurfer.sh

#---------------------------------------
# added by Anaconda2 4.0.0 installer
export PATH="/scratch/bmu-nspn/DRIVERS/ANACONDA/bin:$PATH"
```

Step 3.

Set up directory structure

You must have the appropriate input files in the displayed directory structure:



Inside **SUB_DATA** are directories named with the subject IDs.

Inside each subject directory is one for the high resolution structural scans (either **MPM** or **MPRAGE**) and one for the DTI data (**DTI**).

Within each of these folders are folders for the timepoint (occasion) such as (**baseline**, **6_month**, **1st_follow_up**, **T1_AP** etc).

Then within the occasion folder are the input files as described below:

Multi-parametric mapping (MPM) input files:

- **R1.nii.gz** -- 3D NIFTI image containing longitudinal relaxation rate (R1) values in MPM subject space
- **R2s.nii.gz** -- 3D NIFTI image containing transverse relaxation rate (R2s) values in MPM subject

space
- **MT.nii.gz** -- 3D NIFTI image containing magnetisation transfer (MT) values in MPM subject space
- **A.nii.gz** -- 3D NIFTI image containing proton density (A) values in MPM subject space
- **PDw.nii.gz** -- 3D NIFTI image containing proton density weighted (PDw) values in MPM subject space

OR, if you don't have MPM files:

Highres MPRAGE input file:

- **highres.nii.gz** -- 3D NIFTI image containing T1 weighted values in MPRAGE subject space

Diffusion weighted imaging (DWI) imaging input files:

- **dti.nii.gz** -- 4D NIFTI image containing 63 diffusion weighted acquisition and 6 non-weighted acquistions (total N=69) in DTI subject space
- **bvals** -- text file containing one row of 69 values representing the diffusion weightings for the 69 volumes in **dti.nii.gz**
- **bvecs** -- text file containing three rows of 69 values representing the x, y, and z components of the diffusion directions for the 69 volumes in **dti.nii.gz**

Step 4.

Put the fsaverageSubP folder in the SUB_DATA directory

The fsaverageSubP directory contains the 308 parcellation and needs to be in the SUB_DATA directory in order to map the parcellation to individual subject space.

Copy the fsaverageSubP folder from the FS_SUBJECTS directory in the UCHANGE_ProcessingPipeline GitHub repository into the SUB_DATA directory.

Step 5.

Mask background and brain extract MPM images

NOTE: You can skip this step if you only have MPRAGE data (as highres.nii.gz).

The multi-parametric mapping (MPM) images have been calculated from the three acquisitions with different relaxation parameters and two fields maps. The models used to fit the data together make sense in the brain, but create very variable (noisy) values outside of the head. The first step is to brain and head extract the proton density weighted image (**PDw.nii.gz**) and apply these masks to the quantitative MPM images. Note that the <MPM>_brain.nii.gz files that are output have been

eroded by 3 voxels from the original output of FSL's bet command.

The commands are contained in the **NSPN_mpm_bet_mask.sh** script.

Example usage: **NSPN_mpm_bet_mask.sh SUB_DATA/12345/MPM/baseline/PDw.nii.gz**

Specifically it runs:

- **fslreorient2std** to make sure all MPM files are in FSL's standard alignment and saved in .nii.gz format
- **bet** with the **-A** option on the PDw.nii.gz image to create the head and brain masks
- **fslmaths** with the **-ero** option to erode the brain mask by 3mm
- **fslmaths** with the **-bin -mul** options to apply the brain and head masks to the R1, R2s, MT and A mpm images

You can find the code in the UCHANGE_ProcessingPipeline github repository here.

USAGE: NSPN_mpm_bet_mask.sh <pdw_file>

DESCRIPTION: This code conducts a brain and head extraction of the PDw image to which the quantitative multiparametric mapping (MPM) images have been aligned. It then uses the head mask to set all voxels outside of the head to zero for the quantitative MPM images and uses the brain mask to create brain extracted versions of the MPM images (where all voxels outside of the brain have been set to zero).

INPUTS:

- **pdw_file** : Proton density weighted file to which the MPM quantitative maps are aligned.

EXPECTS: The following files should be in the same directory as the input file:

- R1.nii.gz
- MT.nii.gz
- R2s.nii.gz
- A.nii.gz

OUTPUTS: The following output files are in the same directory as the input file. Additionally a sub-directory called **PDw_bet** is created and contains all the files created by FSL's bet command.

- **R1_head.nii.gz**
- **R1_brain.nii.gz**
- **R2s_head.nii.gz**
- **R2s_brain.nii.gz**
- **MT_head.nii.gz**
- **MT_brain.nii.gz**
- **A_head.nii.gz**
- **A_brain.nii.gz**

Step 6.

Run Freesurfer's Recon-all command

Next step is to run Recon-all.

If you have MPM data then you need to do this in a couple of steps because we want to apply our own brain extraction masks. The commands are in **NSPN_Reconall_MPM.sh**.

You can see the commands in the template file: **dev_reconall_MPM_TEMPLATE.sh**.

If you only have an MPRAGE scan then you can just run **NSPN_Reconall_MPRAGE.sh**.

Step 7.

Quality control

DO YOUR QC CHECKS!! Everything else beyond this point is dependent on having accurate surfaces!

This step needs some documentation, but there's some useful notes at https://github.com/KirstieJane/NSPN_MRIProcessing/wiki/Freesurfer-Edits-%28BCNI%29

You need to be on one of the graphics nodes (eg: login-gfx1)

1. Claim your participant (for this scan occasion) in the google doc.

2. Open up the scan information in freeview using the command below. Remember to first set your nspn_id and occ variables.

3. Make any necessary edits to the **wm.mgz** file and add control points to the file **tmp/control.dat**.

4. Add your subject ID to a text file, called, for example, sublist_fsEdits_KW_20160715 and saved in your home directory.

5. Repeat steps 1-4 for any additional participants that you're processing in this batch.

6. Submit all edits using the following command:

/scratch/bmu-nspn/SCRIPTS/LoopCommandOverSubjects.sh ${data_dir} ${sublist} /scratch/bmu-nspn/TEMPLATE_SCRIPTS/dev_reconallEdits_TEMPLATE.sh 2100

7. Update the google doc with this information.

Have a cup of tea and relax. Your edits will be complete in approximately 20 hours time.

AND you need to put vglrun infront of the freeview command!

cmd COMMAND

```
# Set up some variables
data_dir=/scratch/bmu-nspn/UCHANGE # Change this to fit your needs
sublist=/home/kw401/sublist_fsEdits_KW_20160715 # Change this to fit your needs

sub=12345 # Change this for each subject you're checking
occ=baseline # Change this as needed

# Open up the surfaces
# You should be able to just copy and paste this command once you've set the variable above
SUBJECTS_DIR=${data_dir}/SUB_DATA/${sub}/SURFER/${occ}/
vglrun freeview -v ${SUBJECTS_DIR}/mri/T1.mgz \
            ${SUBJECTS_DIR}/mri/brainmask.mgz \
            ${SUBJECTS_DIR}/mri/wm.mgz:colormap=heat:opacity=0.4 \
         -f ${SUBJECTS_DIR}/surf/lh.white:edgecolor=yellow \
            ${SUBJECTS_DIR}/surf/lh.pial:edgecolor=red \
            ${SUBJECTS_DIR}/surf/rh.white:edgecolor=yellow \
            ${SUBJECTS_DIR}/surf/rh.pial:edgecolor=red \
            ${SUBJECTS_DIR}/surf/lh.inflated:visible=0 \
            ${SUBJECTS_DIR}/surf/rh.inflated:visible=0 \
         -c ${SUBJECTS_DIR}/tmp/control.dat
```

You may get an error when loading up the files in freeview if the tmp/control.dat file doesn't exist. If this is true (eg, on your first editing pass) then just say ok and ignore the error, otherwise take a look to see if the file has been named incorrectly!

Step 8.

Run Freesurfer's Trac-all

This has a side effect of processing the DTI data for you so you can extract values later on :)

ANNOTATIONS

Sarah Morgan 20 Oct 2017

Might be worth commenting that this takes quite a long time? (I think it took over a day per subject for me)

Step 9.

Parcellate brain

Run NSPN_Parcellation_PostEdits.sh.

This step is part of the **dev_ParcAndExtract_TEMPLATE.sh** template script.

You can find the code in the UCHANGE_ProcessingPipeline github repository here.

USAGE: **NSPN_Parcellation_PostEdits.sh <study_dir> <sub> <occ>**

DESCRIPTION: This code creates the 308 parcellation for each person in their freesurfer space, and should be applied after recon-all edits have been completed.

INPUTS:

- **study_dir**: The directory containing the SUB_DATA folder which itself contains directories named by sub_id.
- **sub_id**: Subject ID. These folders should be inside SUB_DATA and themselves contain directories called SURFER and MPM.
- **occ**: The scan occasion. One of baseline, 6_month, 1st_follow_up, CBSU, UCL, WBIC, t1 and t2. This directory contains the output of recon-all and is found inside the subject's SURFER directory.

EXPECTS:

- All the output files from recon-all should exist in the relavent occasion directory in the subject's SURFER directory.
- All quality control editing should have been conducted.
- The fsaverageSubP directory containing the standard space parcellation should exist inside the SUB_DATA directory.

OUTPUTS: The following files are created inside the relavent occasion directory in the subject's SURFER directory:

- **parcellation/500.aparc.nii.gz**
- **label/lh.500.aparc.annot**
- **label/rh.500.aparc.annot**

Assign lobes

Step 10.

Run NSPN_AssignLobes.sh

This step is part of the **dev_ParcAndExtract_TEMPLATE.sh** template script.

You can find the code in the UCHANGE_ProcessingPipeline github repository here.

Just a little bit of code to assign regions to lobes.

[DOCUMENTATION INCOMPLETE]

ANNOTATIONS
Sarah Morgan 20 Oct 2017

I didn't do this bit (or the next) so I can't really comment. Might be worth saying when you need to run them though? (and when you don't)

Resample surfaces

Step 11.

Run NSPN_ResampleSurfaces.sh

This step is part of the **dev_ParcAndExtract_TEMPLATE.sh** template script.

You can find the code in the UCHANGE_ProcessingPipeline github repository here.

You need to sample the surfaces at 10% depths from the grey/white matter boundary (0%) to the pial surface (100%). Note that when we present the data we'll use a more intutive cortical depth where the pial surface will be 0% and the grey/white matter boundary will be 100%, but the reason we code it this way around when creating the data is because Freesurfer measures all distances FROM the grey/white matter boundary.

This code will also sample 20 different surfaces projecting at 0.1mm steps into white matter from the grey/white matter boundary.

[DOCUMENTATION INCOMPLETE]

Transform Quantitative Maps to freesurfer space

Step 12.

Run NSPN_TransformQuantitativeMaps.sh

This step is part of the **dev_ParcAndExtract_TEMPLATE.sh** template script.

You can find the code in the UCHANGE_ProcessingPipeline github repository here.

[DOCUMENTATION INCOMPLETE]

ANNOTATIONS

Sarah Morgan 20 Oct 2017
Link is incorrect, should be:
https://github.com/KirstieJane/UCHANGE_ProcessingPipeline/blob/master/NSPN_TransformQuantitativeMaps.sh

USAGE: NSPN_TransformQuantitativeMaps.sh <study_dir> <sub> <occ>

DESCRIPTION: This code takes the freesurfer directories and their fellow MPM directories and transforms the MPM and DTI measures so they are all in the same space.

INPUTS:

- study_dir : The directory containing the SUB_DATA folder which itself contains directories named by sub_id.
- sub_id : Subject ID. These folders should be inside SUB_DATA and themselves contain directories called SURFER and MPM.
- occ : The scan occasion. One of baseline, CBSU, UCL and WBIC. This directory contains the output of recon-all and is found inside the subject's SURFER directory.

EXPECTS:

Recon-all, trac-all and quality control edits must have been completed. NSPN_mpm_bet_mask.sh must also have been completed and the MPM directory should be inside the subject's directory at the same level as the SURFER dir.

OUTPUTS:

At the end the ${sub_id}SURFER/${occ}/mri directory will contain:

A.mgz MT.mgz R1.mgz R2s.mgz
FA.mgz L1.mgz L23.mgz MD.mgz MO.mgz

Extract ROIs

Step 13.

Extract ROIS

Run NSPN_ExtractRois.sh

This step is part of the **dev_ParcAndExtract_TEMPLATE.sh** template script.

You can find the code in the UCHANGE_ProcessingPipeline github repository here.

[DOCUMENTATION INCOMPLETE]

This is an important step as it is the one that pulls out the regional values for the different measures for a bunch of segmentations and parcellations.

Segmentations:

- wmparc
- aseg
- lobesStrict

Parcellations:

- aparc
- 500.aparc
- lobesStrict
- HCP
- Yeo2011_7Networks_N1000

Importantly the parcellations are extracted at multiple different depths: in 10% increments from the grey/white matter surface (0%) to the pial surface (100%) and in 0.1mm steps from the grey/white matter boundary to 2mm in to white matter.

USAGE: **NSPN_ExtractRois.sh** <study_dir> <sub> <occ>

ANNOTATIONS

Sarah Morgan 20 Oct 2017

Link is incorrect, should be:
https://github.com/KirstieJane/UCHANGE_ProcessingPipeline/blob/master/NSPN_ExtractRois.sh

INPUTS:
study_dir : The directory containing the SUB_DATA folder which itself contains directories named by sub_id.
sub_id : Subject ID. These folders should be inside SUB_DATA and themselves contain directories called SURFER and MPM.
occ : The scan occasion. One of baseline, CBSU, UCL and WBIC. This directory contains the output of recon-all and is found inside the subject's SURFER directory.

EXPECTS:
Recon-all, trac-all and quality control edits must have been completed.
NSPN_TransformQuantitativeMaps.sh, NSPN_Parcellation.sh, NSPN_AssignLobes.sh and NSPN_ResampleSurfaces.sh must also have been completed.

OUTPUTS:
Statistics from all segmentations and parcellations for all MPM and DTI measures along with the standard Freesurfer morphological measures, in the directory ${sub_id}/SURFER/${occ}/stats.

(Are there any other outputs Kirstie?)

Combine all subject's extracted data into one directory

Step 14.

This step looks for the output of NSPN_ExtractRois.sh for all scans in each subject's directory and then combines that information together in the FS_ROIS folder within the study directory (<study_dir>).

Run NSPN_Report_ROIstats_Allsubs.sh <study_dir>

Note that <study_dir> expects to find SUB_DATA within it and then the standard NSPN directory structure.