User manual for DMRI data processing

ATR Neural Information Analysis Laboratories(Dec. 1, 2017)

Contents

DMRI data processing program

1. Introduction

This user manual is intended to explain how to obtain the Connectivity Matrix from dMRI (diffusion MRI) data and to describe the procedures to set the environment variables to carry out dMRI data processing. For advanced installation information concerning the software used in this program, please check out "3.Required software" section.

2. Operating System

OS: Linux 64bit

3. Required software

1. MRTrix 0.2.10

    http://jdtournier.github.io/mrtrix-0.2/index.html

    https://www.nitrc.org/projects/mrtrix/

    Perform Fibertrack.

2. FSL 4.1 or later

    This program is used for tasks such as image processing.

    http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/

3. SPM8

    This program is used to bias collection of structural image.

    http://www.fil.ion.ucl.ac.uk/spm/software/spm8/

4. FreeSurfer 4.5 or later

    This program is used to extract the shape of the brain cortex.

    https://surfer.nmr.mgh.harvard.edu/

5. MATLAB

    All the operations of this program have been verified and works under Matlab 2013a.

6. VBMEG2.0

    program directory:$VBMEG

4. PC and software

- **Main PC**

  <<Role>>

  - Prepare for Fiber Tracking.

  - Process Fiber tracking result.

  <<Software>>

  - FSL4.1, FreeSurfer4.5, MATLAB2013a

    (installation is needed.)

  - VBMEG2.0, SPM8

    (add path to your MATLAB.)

- ssh connection

- **Fiber Tracking PC(s)**

  <<Role>>

  - Fiber tracking.

  <<Software>>

  - MRTrix0.2.10

    (installation is needed.)

- **data directory**

  Data should be accessed through same paths across the PCs.
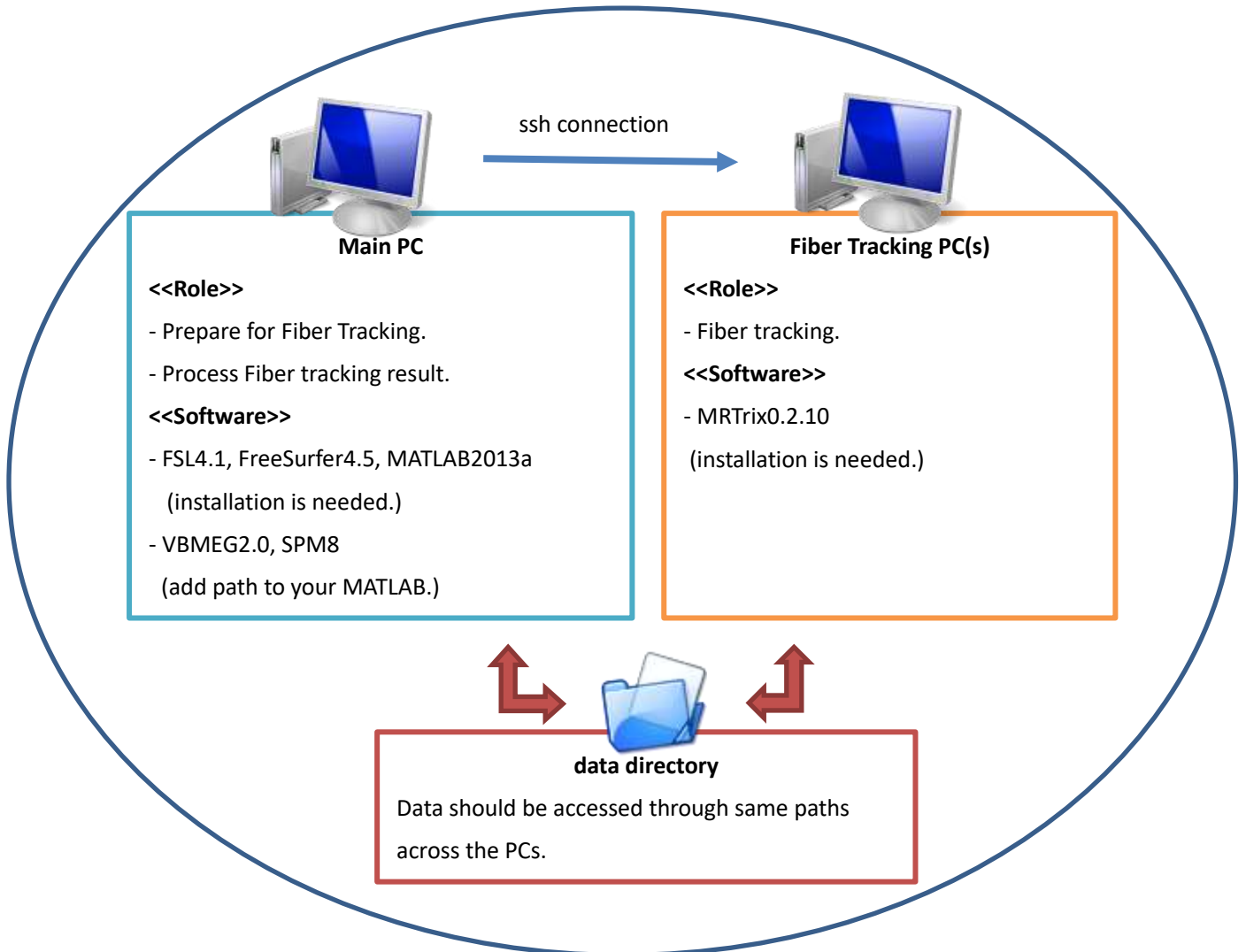
- Main PC: a single computer for preprocessing.
- FiberTracking PC: muliple computers for parallel processing.
- Data should be accessed through same paths between Main PC and Fiber PC.
- SSH connection between MainPC and FiberTrackingPC should be established without password(4.1 How to set up ssh connection without password)

4.1. How to set up ssh connetion without password

Please type as below on Linux terminal.(Example : for rhayashi)

```
$ ssh-keygen -t rsa

 Generating public/private rsa key pair.

 Enter file in which to save the key (/home/cbi/rhayashi/.ssh/id_rsa):

 [ENTER]
 Created directory '/home/cbi/rhayashi/.ssh'.
 Enter passphrase (empty for no passphrase):
 [ENTER]
 Enter same passphrase again:
 [ENTER]
Your identification has been saved in /home/cbi/rhayashi/.ssh/id_rsa.
Your public key has been saved in /home/cbi/rhayashi/.ssh/id_rsa.pub.
 The key fingerprint is:
 b3:5f:2a:7f:cb:42:dd:ae:bb:cf:ab:cd:ef:gh:ij:96

$ cd /home/cbi/rhayashi/.ssh
$ cat id_rsa.pub >> authorized_keys
```

After this settings, connect to **all the fibertracking host** via ssh on Linux terminal to add them to

known hosts. For example, if you use cbi-node20, 21, 22, then run the ssh connection 3 times in

```
_rhayashi@myhost<1> ssh cbi-node20

The authenticity of host 'cbi-node20 (xxx.xxx.xx.xxx)' can't be established.

RSA key fingerprint is e8:f6:5e:94:b5:af:b8:70:85:7f:ab:cd:ef:gh:ij:c0.

Are you sure you want to continue connecting (yes/no)? yes

Warning: Permanently added 'cbi-node20,xxx.xxx.xx.xxx' (RSA) to the list of known
hosts.
```

total.

5. Tutorial data

The following data is located in /home/cbi-data5/DTI/sample.

    /home/cbi-data5/DTI/sample/3D   T1 Structure image (DICOM format)

    /home/cbi-data5/DTI/sample/DTI   DMRI data (DICOM format)

Processing results of the tutorial are output in:

    /home/cbi-data5/DTI/processed

6. Preparation

How to set the external software path .

Edit $VBMEG/vbmegrc

```
# for FreeeSurfer
FREESURFER_HOME=/home/cbi-
data20/common/software/external/freesurfer/freesurferv4.5.0
# for FSL
FSLDIR=/home/cbi-data20/common/software/external/fsl/fsl4.1
# for MRtrix
MRTRIXDIR=/home/cbi-data20/common/software/external/mrtrix/mrtrix0.2
```

How to copy the configuration file of MRTrix in your own Linux Home directory.

$>dmri_setenv

```
Analyse.LeftToRight: false
NumberOfThreads: 8
```

    NumberOfThreads is set in accordance with the number of cores and the usage of the host to perform FiberTracking. The number of threads cannot exceed the number of cores of the host.

Start analysis

1.   Start Matlab

    $>/home/cns/matlab/r2013a/bin/matlab

2.   Go to the VBMEG directory and run the configuration script

    (those operations under Matlab)

    cd ＄VBMEG

    vbmeg;

3.   Add SPM8 path to your MATLAB.

4. Edit $VBMEG/dmri_set_parm_tutorial.m and set T1 directory, DMRI directory and output directory.

```
==============================================================
p.t1_dicom_dir    = '/home/cbi-data5/DTI/sample/3D'  % T1-DICOM
p.dmri_dicom_dir = '/home/cbi-data5/DTI/sample/DTI'; % DMRI-DICOM
p.output_dir      = '/home/cbi-data5/DTI/processed';  % output directory
==============================================================
```

5. load parameter.

   p = dmri_set_parm_tutorial;

6. process data (the next chapter).

   All of the processing steps are described in

   $VBMEG/functions/tool_box/dmri_processor/dmri_tutorial.m.

7. MRI data preprocessing

1. Convert DICOM format file to NIfTI (.nii) format

 dmri_process_T1_dicom_convert(p);

<<Output file>>

$OUTPUT_DIR/struct/Subject.nii

2. Bias correction of NIfTI format structure image by SPM8

dmri_process_T1_bias_correct(p);

<<Output file>>

$OUTPUT_DIR/struct/mSubject.nii

3. Convert NIfTI format structure image to FSL processing format (.nii.gz) to extract brain image and brain mask image

dmri_process_T1_brain_extract(p);

The parameter "p.t1_brain_threshold" has to be set between 0 and 1.0. The smaller the value is, the larger the area for extraction is going to be. To find a good value, you can use fslview to see the result.

<<Output file>>

$OUTPUT_DIR/struct/struct.nii.gz

$OUTPUT_DIR/struct/struct_brain.nii.gz (Brain image)

$OUTPUT_DIR/struct/struct_brain_mask.nii.gz (Brain mask image)

✏️<<Confirmation Step>>

In Matlab, run the command that is those two lines together:

dmri_system('fslview $OUTPUT_DIR/struct/struct_brain.nii.gz $OUTPUT_DIR/struct/struct.nii.gz')

Please make sure that the brain region extraction is a success. To confirm that, focus on the structural image of the brain and use the slider to vary the transparency which is located at the bottom of the screen. (See the image below)
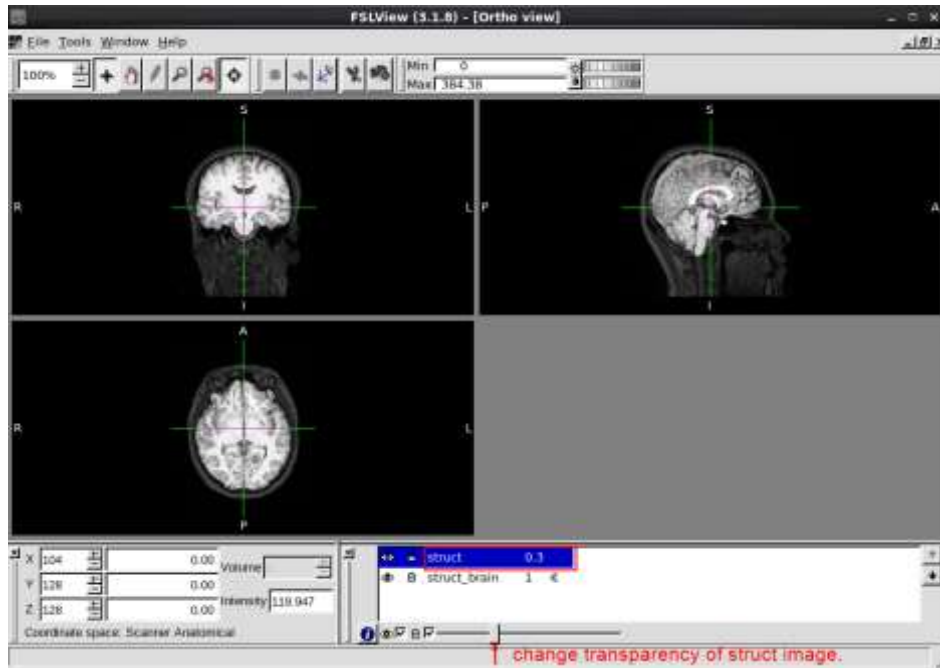
Case of failure
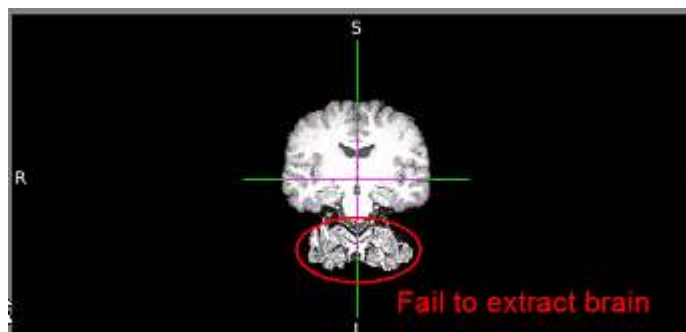
8. dMRI data preprocessing

1. Extract the DWI image from the DICOM image

dmri_process_DWI_import(p);

<<Output file>>

$OUTPUT_DIR/DWI/data_dwi.nii.gz

$OUTPUT_DIR/DWI/data_dwi.bvec

$OUTPUT_DIR/DWI/data_dwi.bval

2. Adjust the DWI with motion correction

dmri_process_DWI_motion_correct(p);

<<Output file>>

$OUTPUT_DIR/DWI/data_dwi_m.nii.gz

$OUTPUT_DIR/DWI/data_dwi_m.bvec
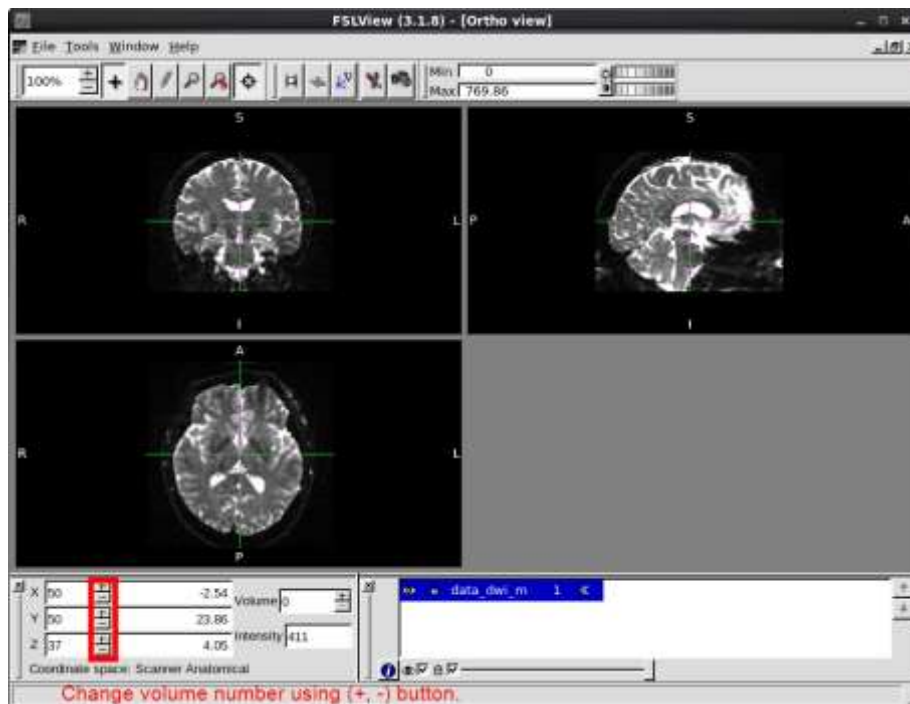
$OUTPUT_DIR/DWI/data_dwi_m.bval

⚠️<<Confirmation Step>>

Command：From Matlab, execute this external command

dmri_system('fslview $OUTPUT_DIR/DWI/data_dwi_m.nii.gz')

The goal of this step is to check if there is any great positional shift between each image.

3. Extraction of brain image and brain mask image from DWI image

dmri_process_DWI_brain_mask_extract(p);

The threshold parameter(p.dmri_brain_threshold) is set between 0 and 1.0 depending on the image. The smaller the value is, the larger the area of extraction is. Find a good value while checking the result with fslview.

<<Output file>>

$OUTPUT_DIR/DWI/data_dwi_m_brain.nii.gz

$OUTPUT_DIR/DWI/data_dwi_m_brain_mask.nii.gz

⚠️<<Confirmation Step>>

From Matlab, execute the external command that is those two lines together:

dmri_system('fslview $OUTPUT_DIR/DWI/data_dwi_m_brain.nii.gz

                $OUTPUT_DIR/DWI/data_dwi_m.nii.gz');

Please make sure that the brain region extraction is a success. To confirm that, focus on the DWI image and use the slider to vary the transparency which is located at the bottom of the screen. (See the image below)
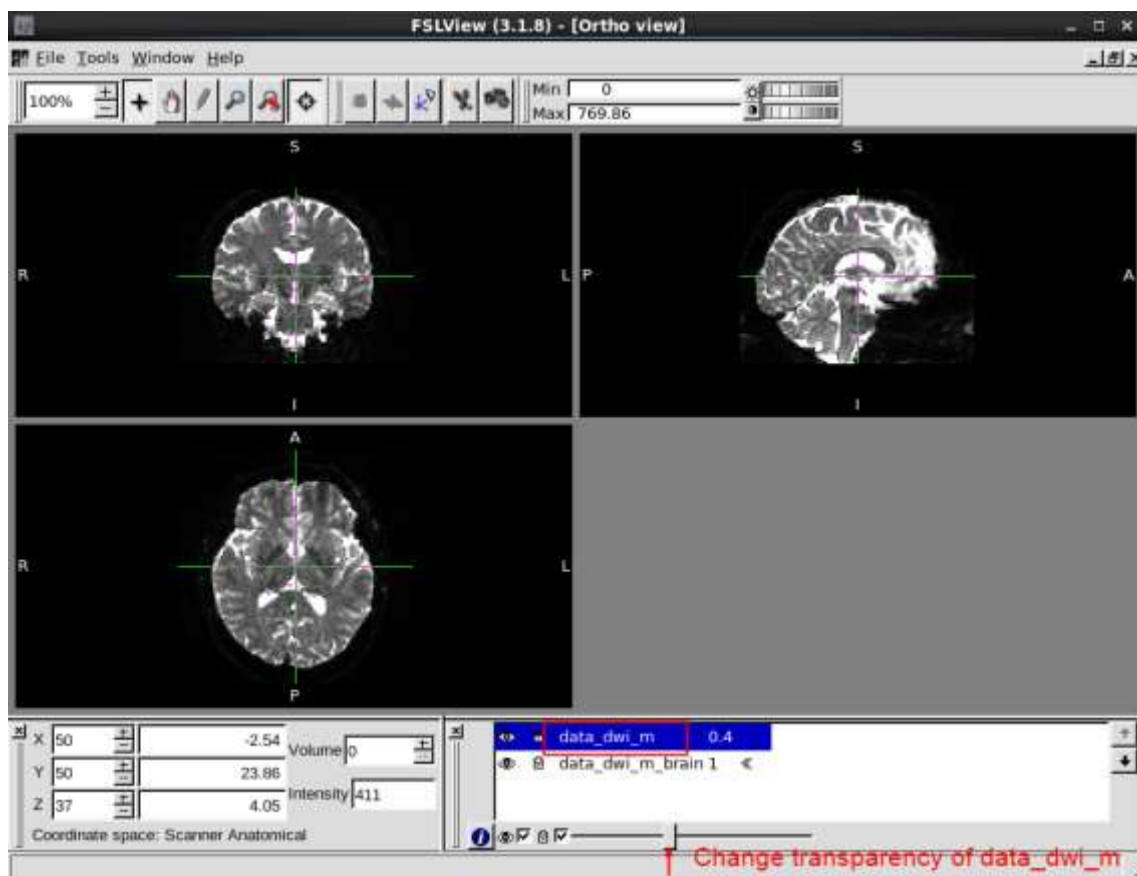
4. Make a FA (Fractional anisotropy) image from DWI image

dmri_process_FA_image_coreg_create(p);

<<Output file>>

$OUTPUT_DIR/DWI/data_FA_coreg.nii.gz

9. Coregistration

1. Use FreeSurfer to extract cortical shape and cortical area information

dmri_process_T1_freesurfer(p);

※It takes about 24 hours.

   If you have already creaeted Freesurfer data, please set it to p.ref_fs_dir.

<<Output file>>

$OUTPUT_DIR/freesurfer/Subject

🏮<<Confirmation Step>>

dmri_freesurfer_surf_view('$OUTPUT_DIR/freesurfer/Subject');

Make sure that there is a cortex and structural image.

2. Image space alignment processing

dmri_process_images_coregister(p);

It does the alignment of FA image space with structural image space and FreeSurfer space.

<<Output file>>

The directory below is created to include spatial transformation information.

$OUTPUT_DIR/transwarp_info/

3. Removal of ambient noise in FA image

dmri_process_FA_image_clean(p);

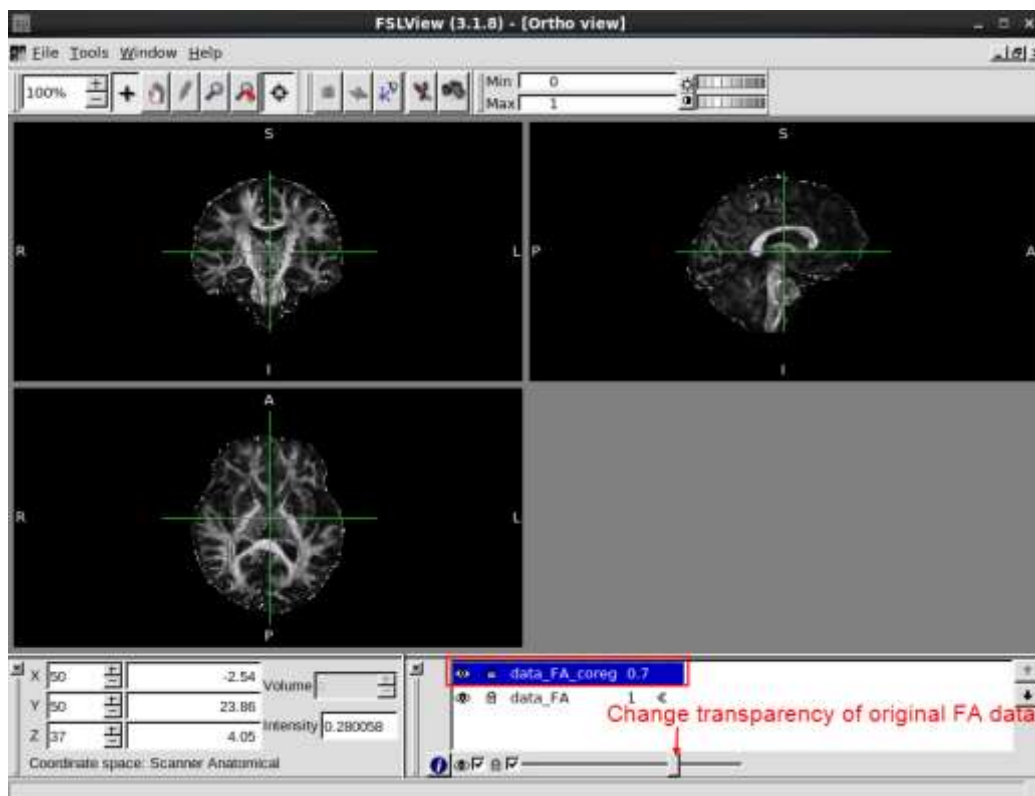Remove the FA image ambient noise by using the T1 structure image mask.

<<Output file>>

$OUTPUT_DIR/DWI/data_FA.nii.gz

<<Confirmation Step 1>>

From Matlab, execute the external command that is those two lines together:

dmri_system('fslview $OUTPUT_DIR/DWI/data_FA.nii.gz

$OUTPUT_DIR/DWI/data_FA_coreg.nii.gz');

Confirm that the white point-like noise around the FA image has been removed. To display changes between the original image and the after noise reduction image, select the original image (data_FA_coreg.nii.gz) and move the transparency slider to confirm the removal of noise. (See image below)
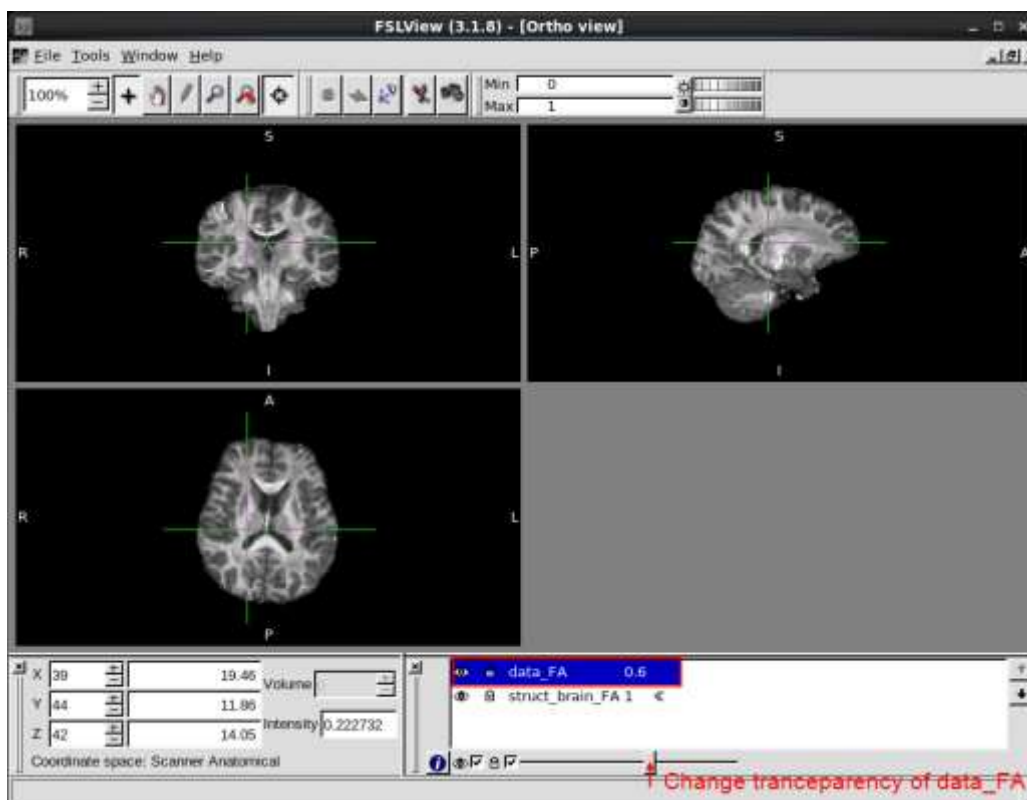
<<Confirmation Step 2>>

From Matlab, execute the external command that is those two lines together:

dmri_system('fslview $OUTPUT_DIR/DWI/struct_brain_FA.nii.gz

$OUTPUT_DIR/DWI/data_FA.nii.gz');

Confirm that the alignment is correct by displaying the structural image and FA image. To do so, select the FA image and move the transparency slider to view the overlapping state of the two images.

<<Troubleshooting>>

If the T1 brain extraction does not work, it may not remove correctly the FA image ambient noise.

In that case, use the following command (which use MRTrix function) to remove FA image ambient noise.

dmri_system('erode data_dwi_m_brain_mask.nii - | erode - - | erode - - | mrmult

data_FA_coreg.nii - data_FA.nii'); (the .nii.gz has to be unzip by gunzip into .nii beforehand)

(When executing the command to create data_FA.nii.gz, the DWI image process will extract from the DWI image the brain image and brain mask image only if the extraction of brain region was successful. In other words, it this step doesn't work, verify the DWI brain regions extraction step.)

10. Parcellation & ROI generation

1. Data capture process of cortex model

Capture the cortical model of FreeSurfer from VBMEG

dmri_process_cortex_import(p);

* If you have already created Freesurfer and VBMEG files,

   Please set them to parameter.

   FreeSurfer subject directory   : p.ref_fs_dir

   VBMEG brain file(.brain.mat)   : p.ref_brain_file

   VBMEG area file(_aal.area.mat) : p.ref_aal_area_file

<<Output file>>

$OUTPUT_DIR/vbmeg/Subject.brain.mat (Only use this file)

$OUTPUT_DIR/vbmeg/Subject.area.mat

$OUTPUT_DIR/vbmeg/Subject.act.mat

$OUTPUT_DIR/vbmeg/Subject_aal.area.mat

$OUTPUT_DIR/vbmeg/Subject_atlas.area.mat

$OUTPUT_DIR/vbmeg/Subject_brodmann.area.mat

2. Cortex partitioning (parcel) processing

dmri_process_cortex_parcel(p);

To partition the cortex from here, the program will singled out each of 2000 vertices. The result will be saved in parcels.mat.

<<Output directory>>

$OUTPUT_DIR/vbmeg/fs_info

<<Output file>>

$OUTPUT_DIR/vbmeg/parcels.mat

3. Creation of a volume file of FA space based on segmentation information

dmri_process_FA_parcel_volume_files_create(p);

<<Output file>>

$OUTPUT_DIR/parcels/

・parcel_all.nii.gz(Volume file that contains all the parcels)

・parcel1-N.nii.gz(Volume file that contains each parcel individually)

・parcel_ex1-N.nii.gz(Volume file with all the parcels except the ParcelIn from each parcel).

・parcel_mm_coord.mat(Save the parcel in mm coordinate system of the FA space)

<<Confirmation Step>>

It is possible to display the parcel as follows using dmri_parcel_view function. Please check if there are any strange places. When you are finished, Close by File->close.
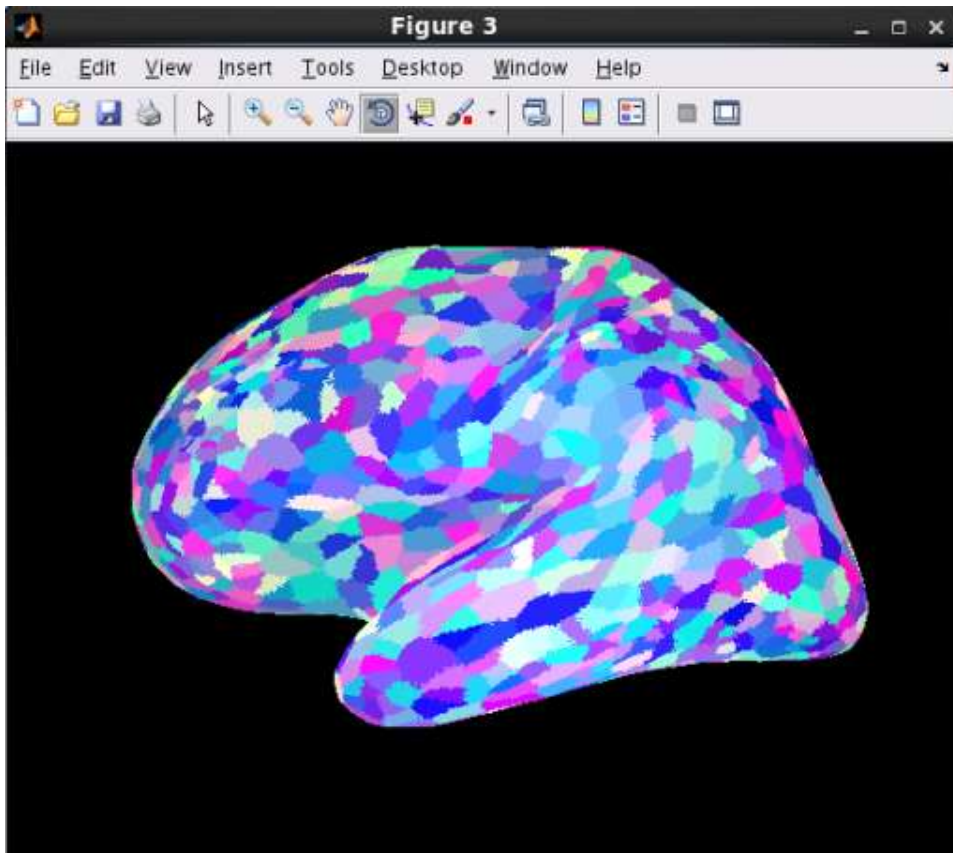
4. Creation of the area mask Volume file that performs FiberTracking

(Included area: area mask = white matter + all of parcels)

dmri_process_fiber_tracking_mask_create(p);

<<Output file>>

$OUTPUT_DIR/fibertrack/wm.nii.gz (White matter)

$OUTPUT_DIR/fibertrack/parcel_wm.nii.gz (area mask)

11. Estimate fiber orientation distribution

dmri_process_fodf_calc(p);

※This process uses MRTrix. It should then be performed on the host where MRTrix is to work.

<<Output file>>

$OUTPUT_DIR/fibertrack/CSD6.mif (Only use this file)
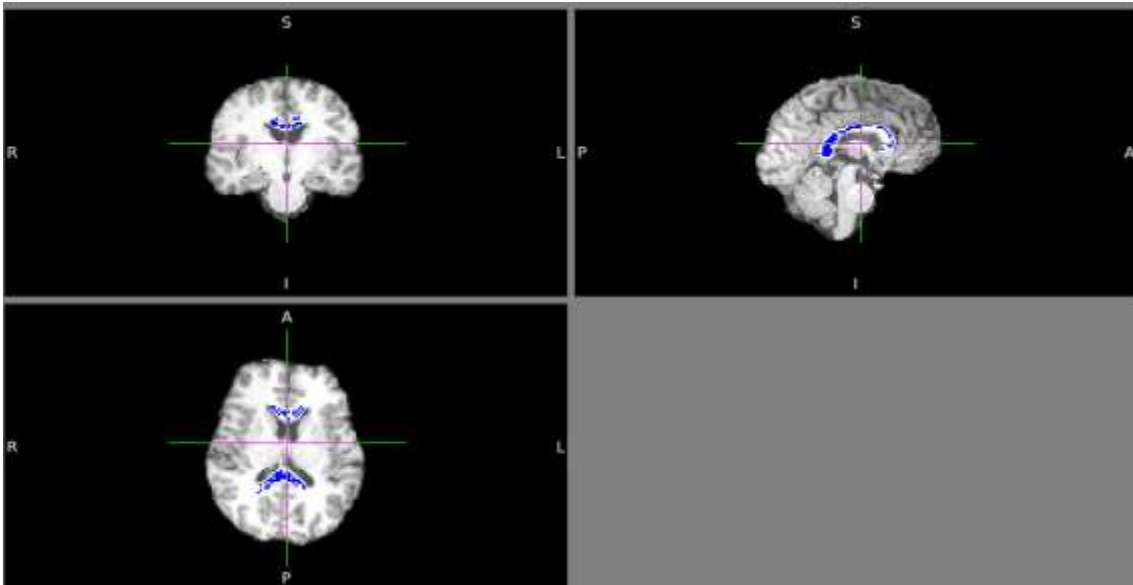
$OUTPUT_DIR/fibertrack/response.txt

$OUTPUT_DIR/fibertrack/max_cluster_val

$OUTPUT_DIR/fibertrack/sf.nii.gz

🟡 <<Confirmation Step 1>>

From Matlab, execute the external command that is those two lines together:

dmri_system('fslview $OUTPUT_DIR/DWI/struct_brain_FA.nii.gz $OUTPUT_DIR/fibertrack/sf.nii.gz

　　　　　　–l Blue');

"l" is a lowercase "L". If the main part of the white matter is displayed in blue, then it is OK. When the brain extraction from T1 failed, some places other than the brain might become blue. In that case, the function "erode", used in section 9.3 troubleshooting, should be execute to remove ambient noise around FA image.

🟡 <<Confirmation Step 2>>

1. Run the Matlab function below (included in this program)
   dmri_mrview($OUTPUT_DIR/DWI/data_FA.nii.gz);
   Tool：http://jdtournier.github.io/mrtrix-0.2/general/mrview.html
2. Once the tool has launched, press F9 to get the dialog box on the right side of the screen. Then, change the button with "Tractography" written on it to "Orientation plot".
3. Select from the browse button $OUTPUT_DIR/fibertrack/CSD6.mif, then check the overlay button. The fiber orientation density function will then be plotted for each voxel.
   ※Since the plotting is slow, it is preferable to enlarge the image by using Crtl + mouse wheel. To check whether the estimation is correct, look around the intersection of the corpus callosum and cortex spine road since there is a plurality of direction possible in that area; like in the

following figure (Tournier, OHBM 2012 educational course slides).
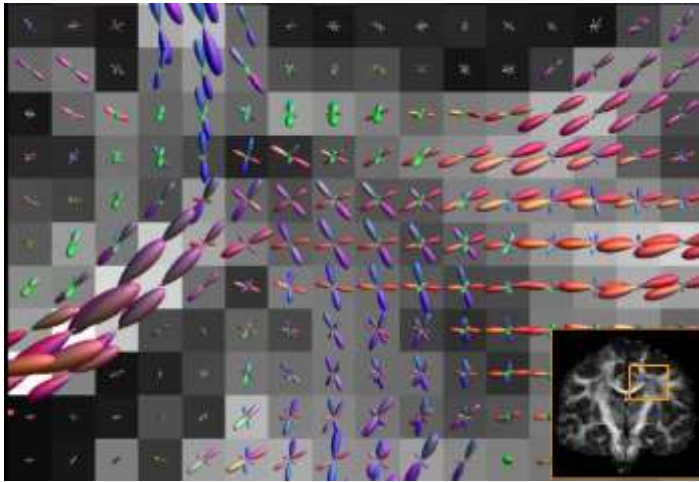
12. Tracking fibers

1. Run the fiber tracking function.

dmri_process_fiber_tracking_execute(p);

When this function is executed, FiberTracking process will run on the host specified by p.host. MRTrix independently runs on each host. Set NumberOfThreads not to exceed the number of CPU cores of specified host. FiberTracking process creates so many TCK-files. In order to convert them into MAT-file, the number of MATLAB processes which is specified by p.Nworker will run in parallel on the host executing this function. Please set this value not to exceed the number of CPU cores of the running host.

 <<Output file>>

$OUTPUT_DIR/fibertrack/anat_matrix.mat

<<If you want to suspend the execution>>

If you stop the process by pressing Crtl + C. In this case, a temporary folder named

"tpf3f1c622_27a1_43d7_b24d_51ef9c223644"

inside $OUTPUT_DIR/fibertrack/ is created. It is possible to remove it. Also, it is possible to terminate a process running on another host. If the folder cannot be removed, it might be because the process is still using it, try again after a short amount of time.

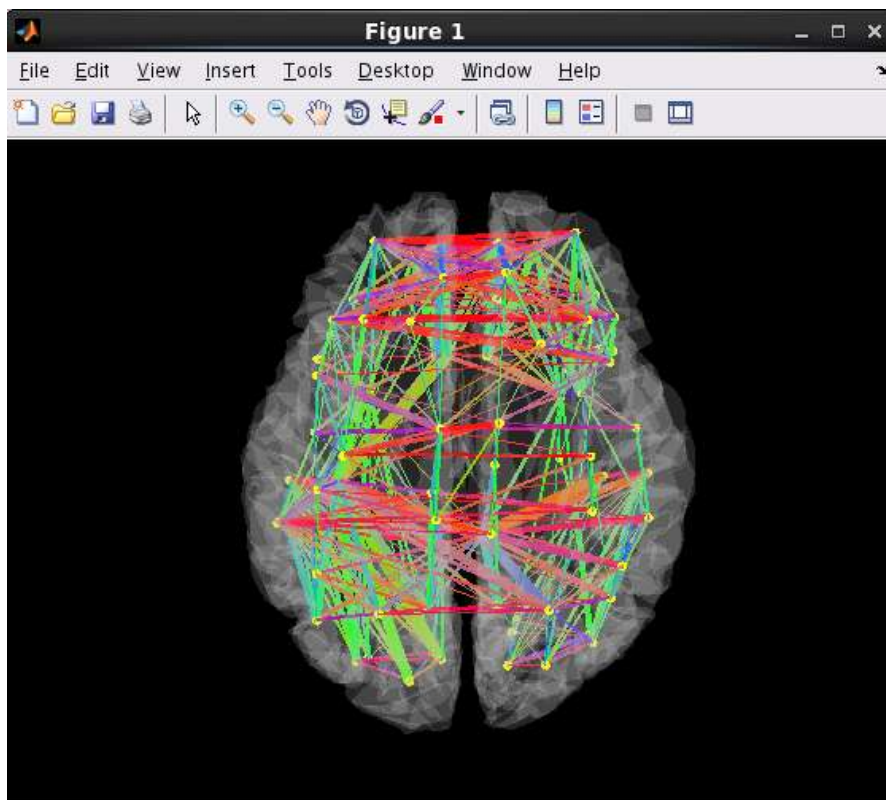2. Make the Diffusion MRI file by calculating the anatomical binding parameters

dmri_process_connection_calc(p);

<<Output file>>

$OUTPUT_DIR/connectivity/connectivity.dmri.mat

<<Confirmation step>>

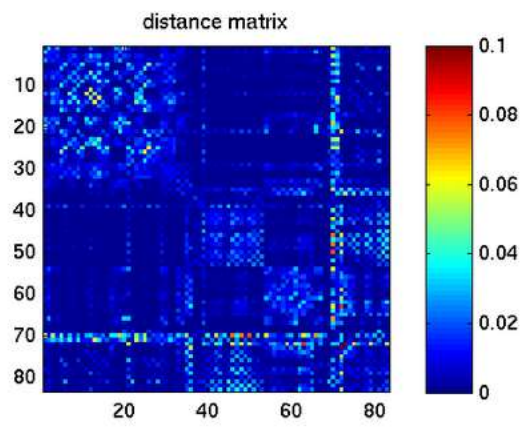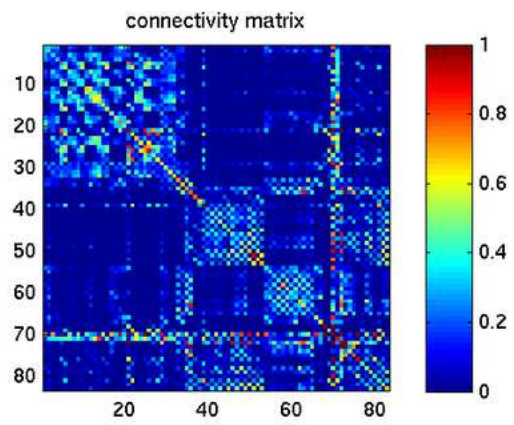Confirm that the connection is not deflected to one side of brain.

figure: connectivity matrix between brain regions. distancee matrix of fiber.

Change log

2015/6/3 Change chapters. The usage of DTI changes to dMRI.

2015/7/17 Changes associated with the function names (from dti_ to dmri_).

2015/8/27 English version

2015/8/28 Added confirmation step of result(tutorial_connection_calc.m)

2015/9/9 Added figure(tutorial_connection_calc.m – connectivity matrix between brain regions)

2016/7/29 Replaced VBMEG_HOME and SPM8_HOME path with official path.

2016/8/31 change erode command description.

        Change structure image format from LAS Analyze to NIfTI.

        Added step : "Create spm normalization file."

        Data capture process of cortex model : (optional)

2016/10/3 external command(!) replaced with dmri_system() function.

        The method to launch this software is changed.

        (Terminal Environment setting is not necessary.)

2016/10/31 Replace tutorial function with dmri_process_* functions.

2016/11/16 Added 4.PC and software

        6.1. How to set up ssh connection withou password

2017/1/11 Added SSH connection to fiber tracking hosts

2017/1/31 Removed SPM normalization file creation.

2017/3/2 Added explanation for NumberOfThreads, p.Nworker

2017/6/30 Added about ref_fs_dir, ref_brain_file, ref_aal_area_file.

2017/7/21 Modified "How to set up ssh connection without password" for an easy-to-understand.