Image conversion with MRICRON.

Introduction

These instructions pertain to running on a Macintosh computer, chances are there will be variations on a Linux or Windows platform.

Terms
Programs and software packages are capitalized , eg MATLAB, MRICRON, SPM12, TERMINAL

Data storage.
In our work, a complete set of anatomical and fMRI scans for an individual animal comprise about 400-500MB of data. Processing times in SPM12 are hindered by slow access, eg. to network storage., although network storage makes for good backup. If many scans are to be produced or analyzed we recommend a dedicated computer with 64bit architecture, a fast processor and fast storage (SSD type). RAM should be at least 16GB.

c&p is used in this document for copy and paste

Step 1 Convert images with MRIcron

Having recommended a dedicated workstation above, these instructions pertain to running from a networked central drive in a folder called “Micturition fMRI”.

Images from a Bruker magnet come in DICOM format and must be converted to NIfTI format for processing using SPM (SPM12). NIfTI format was designed for analysis of brain images and is also used by other image processing software packages.

Conversion can be done within SPM12 or with MRICRON, with the latter preferred as our attempts to convert within SPM12 have generated errors and hangs.

MRICRON is available from
(http://www.cabiatl.com/mricro/mricron/dcm2nii.html)

Use TERMINAL (Macintosh Unix command line application) to run MRICRON,

Type or c&p `cd /Volumes/Micturition\ fMRI/mricron`

This should take you to the MRICRON folder within the Micturition fMRI folder and start MRICRON

Identify your source folder and make a new folder to save the converted images

In TERMINAL use command: `./dcm2nii -4 N -g N -o Drag-and-Drop-outfolder Drag-and-drop-input-directory`

"Drag-and-drop- xxx-folder" as it implies means if you click on the folder's icon and drag it into the TERMINAL window so that the pathway to that folder will be laid out for you saving immense typing efforts and much frustration when you type it wrong. Do this for both source and receiving folders. **Note** the receiving (output) folder comes before the input (source) folder

example:

```
ALD6B014:mricron MBP2$ ./dcm2nii -4 N -g N -o
/Volumes/Micturition\ fMRI/MLZ\ DICOM\ Image\ /MLZ_2016_11_04/9_GEFC_2_
MLZ_2016_11_04_C57_BL6_Male_7_m__E12_P1_2.16.756.5.5.100.587859362.3176
8.1478286326.5/niftii
/Volumes/Micturition\ fMRI/MLZ\ DICOM\ Image\ /MLZ_2016_11_04/9_GEFC_2_
MLZ_2016_11_04_C57_BL6_Male_7_m__E12_P1_2.16.756.5.5.100.587859362.3176
8.1478286326.5
```

This command converted images on R:Micturition fMRI in an MLZ DICOM Image subfolder in a MLZ_2016_11_04/9_GEFC_2_MLZ_2016_11_04_C57_BL6_Male_7_m__E12_P1_2.16.756.5.5.100.587859362.31768.1478286326.5 subfolder to the nifti folder within.

An experiment will be given a folder name usually with date, genotype and mouse gender. Subfolders will contain specific anatomical and functional scans. The anatomical scans are usually titled Tripilot, T2, T2 axial, GEFC. Functional scans can be identified by the EPI title or by the very large number of images within the folder, typically 30000 for a 40 minute scan.

The 30000 Dicom images are converted to 1200 NIfTI images. Each NIfTI image represents the entire 2s scan of the brain, thus it is the whole brain area scanned (25 slices Dicom x 1200 scans = 30000 Dicom images).

We also recommend converting the anatomical scans as these can be viewed in the SPM12 view window and can help with reorientation.