Practical 1: MRI Data Management

This practical will guide you through key concepts for preparing and viewing raw data.

Part 1: You will learn how to convert you scan files.

Part 2: You will learn how to organize your dataset.

Exploring the Human Brain: tfMRI Hackathon
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Before you start

An Ubuntu 16.04LTS container is available with all the practical required softwares installed. Please follow the **Setup: User Guide** tutorial to activate this container.

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Part1: Converting your scan files

Why

1. You've collected some data using your scanner.
2. You would like to perform minimal preprocessing.
3. Your data comes off the scanner as a set of DICOM format files.
4. Most softwares do not work with DICOM format files; they work with NIFTI format files.

The DICOM files

1. The DICOM format files from one scan are typically in one folder/directory on your file system.
2. Each DICOM format file (.dcm) can contain a single slice (a single 2D image).
3. Multiple slices from essentially one time point make up one volume
4. Alternatively, each DICOM format file can contain a single volume (a 3D image representing one time point).
5. Multiple volumes from different time points make up one 'scan' .
6. The NIFTI file format contains one scan (1 volume per time point, each volume consisting of multiple slices).
7. The DICOM files listed below are the slices from a Structural T1w scan:

```
$ ls -l $HOME/dicom/sub-04_T1w
     -rwxrwxrwx 1 ag239446 ag239446 124664 Jul 18 07:24 0.dcm
     -rwxrwxrwx 1 ag239446 ag239446 124664 Jul 18 07:24 1.dcm
     -rwxrwxrwx 1 ag239446 ag239446 124664 Jul 18 07:24 10.dcm
     -rwxrwxrwx 1 ag239446 ag239446 124662 Jul 18 07:24 100.dcm
     -rwxrwxrwx 1 ag239446 ag239446 124660 Jul 18 07:24 101.dcm
     …
```

8. In this case, each DICOM file contains a single slice (2D image).
9. This structural scan is a single volume (one time point) made up of 160 slices.
10. The tool we will use to convert these to a NIFTI format file does not use the file names to determine how to combine the DICOM files into a single NIFTI format file for the scan. Instead it uses information stored in the DICOM headers for each DICOM file.

Examining the DICOM files

1. It is not necessary to view the DICOM format files to convert them to NIFTI. But it may provide some insight into what images and headers are in the files.
2. The **DicomBrowser** (http://nrg.wustl.edu/software/dicom-browser) tool has been installed on the container for you to examine DICOM files. You can start the DicomBrowser to examine the DICOM files for the Structural T1w scan using a command like the following:

```
$ DicomBrowser
```

3. This should open a separate window titled 'DicomBrowser'.
4. Choose *File → Open...* to select a directory of DICOM files to browse.
5. In the File Name: text box in the file selection dialog, enter **`/home/mydata/dicom/sub-04_T1w`** and then select the *Open* button.
6. After an opening progress dialog is displayed and finishes, you should see a folder icon labeled **Patient anon** in the left panel of the DicomBrowser window. See Figure 1.
7. To the left of the folder icon expanded there is a graphic that indicates that the folder is currently not.
8. Continue expanding sub-folders until you see a listing of images corresponding to the files in your DICOM directory. See Figure 2.
9. By selecting an individual image file, you can then see the DICOM header information for that file in the right hand panel of the DicomBrowser window.

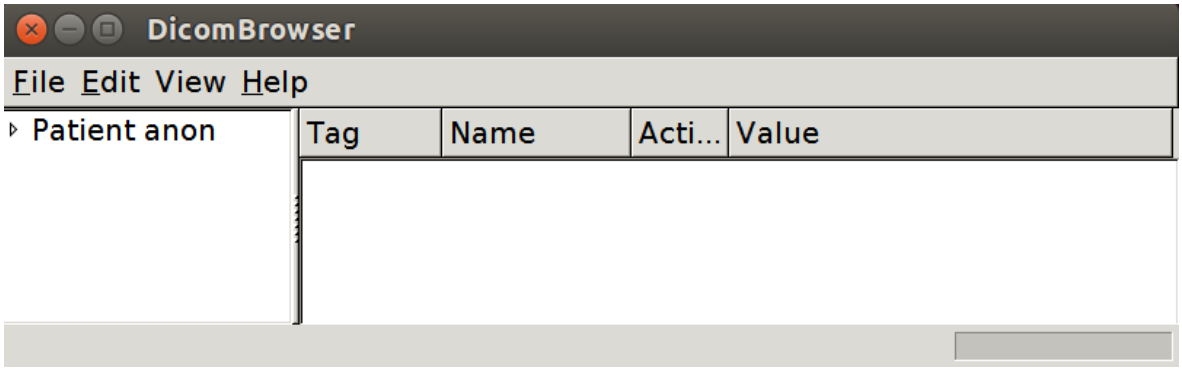

Figure 1: DicomBrowser after a folder has been selected

Figure 2: DicomBrowser expanded to individual image files

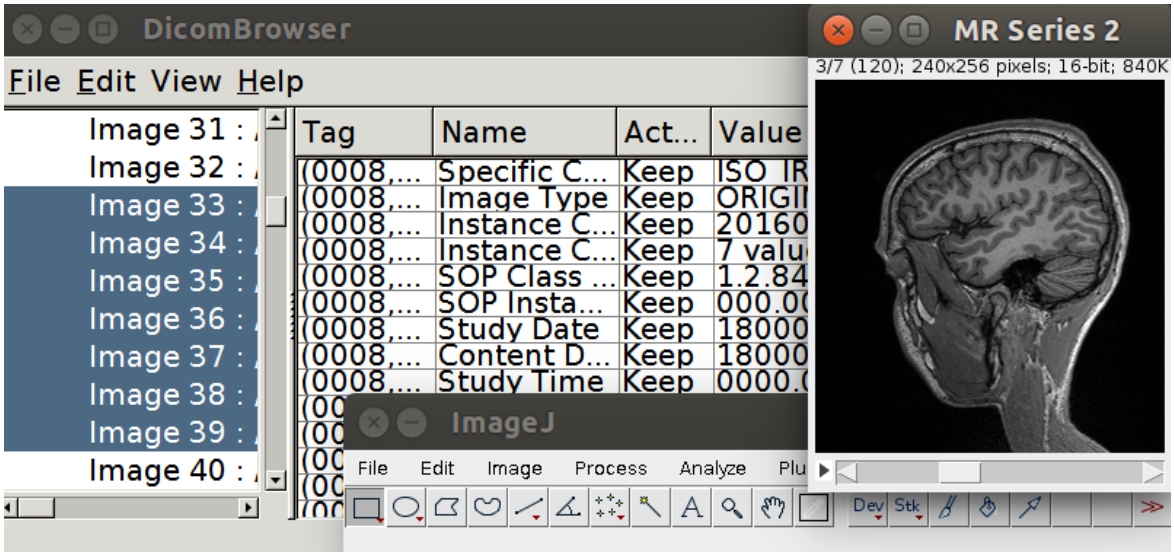

Figure 3: DicomBrowser multi-slices viewer

10. By selecting *View → View selected images* with at least one of the image files selected, you can view the selected images in a separately launched image viewer window.
11. Each image represents a slice from a single volume. You can also select a sequential range of images by clicking on one image and then shift-clicking on another image. If you then select *View → View selected images*, an image viewer will be presented which allows you to scroll through all the selected slices. See Figure 3.
12. Close the image window (containing the actual images) and the window titled ImageJ (by selecting the x in the window frame) before closing the DicomBrowser window.

Converting files from DICOM format to NIFTI format

1. We will use the **dcm2niix** (https://github.com/rordenlab/dcm2niix) tool for converting from DICOM to NIFTI format.
2. The dcm2niix tool has already been installed for you and your PATH environment variable has been set so that you can invoke this command line tool by just issuing a dcm2niix command.
3. A simple form of the dcm2niix command looks like:

```
$ dcm2niix –z y –o <output-directory> <input-directory>
```

4. The –z y part of the command tells dcm2niix to compress the resulting NIFTI file.
5. The –o <output-directory> part of the command tells dcm2niix where to place the resulting NIFTI file.
6. The <input-directory> part of the command tells dcm2niix where to find the DICOM files to use to produce the NIFTI file.
7. To convert the DICOM files to a single NIFTI file, issue a command like the following:

```
$ mkdir $HOME/nifti
$ dcm2niix -z y -f '%f_%p' -o $HOME/nifti $HOME/dicom/sub-04_T1w
     Chris Rorden's dcm2niiX version v1.0.20180622 GCC6.3.0 (64-bit Linux)
     Found 160 DICOM file(s)
     Warning: Empty protocol name(s) (0018,1030)
     Warning: Unable to append protocol name (0018,1030) to filename (it is
empty).
     Convert 160 DICOM as /home/mydata/nifti/sub-04_T1w (240x256x160x1)
     Conversion required 6.756005 seconds (4.355330 for core code).
```

9. Over in the $HOME/nifti directory, you should find the results of this conversion. Notice the name of the NIFTI format file provided in the output of the dcm2niix command above. It is named following the BIDS formatting rules. You also have a Json file with the same name containing the sequence parameters.
10. You can use **fslview** (https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslView) to examine the NIFTI file. To use fslview, enter commands like the following:

```
$ cd $HOME/nifti
$ fslview *.nii.gz
```

11. You should see a single 3D volume of the T1-weighted structural scan. See Figure 4.
12. You can dump the NIFTI header using the **fslhd** (https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Fslutils) command:

```
$ fslhd *.nii.gz
```

Notes about NIFTI file conversion

1. In both conversions above, the dcm2niix program selected the name of the resulting NIFTI file. As we'll see below, you might want to rename these files to follow a different naming convention.
2. There are other tools that can be used to perform DICOM to NIFTI conversion. One of the most popular of these tools is dcm2nii (note the lack of an x on the end). This is the 'classic' version of the dcm2nii converter. The primary difference between dcm2nii and dcm2niix can be summarized as follows:

> *While dcm2nii is generally robust and useful, active development has moved to dcm2niix. In general, dcm2niix is typically better suited for modern DICOM images. On the other hand, dcm2nii is useful for archival studies with legacy proprietary format that predated DICOM.*

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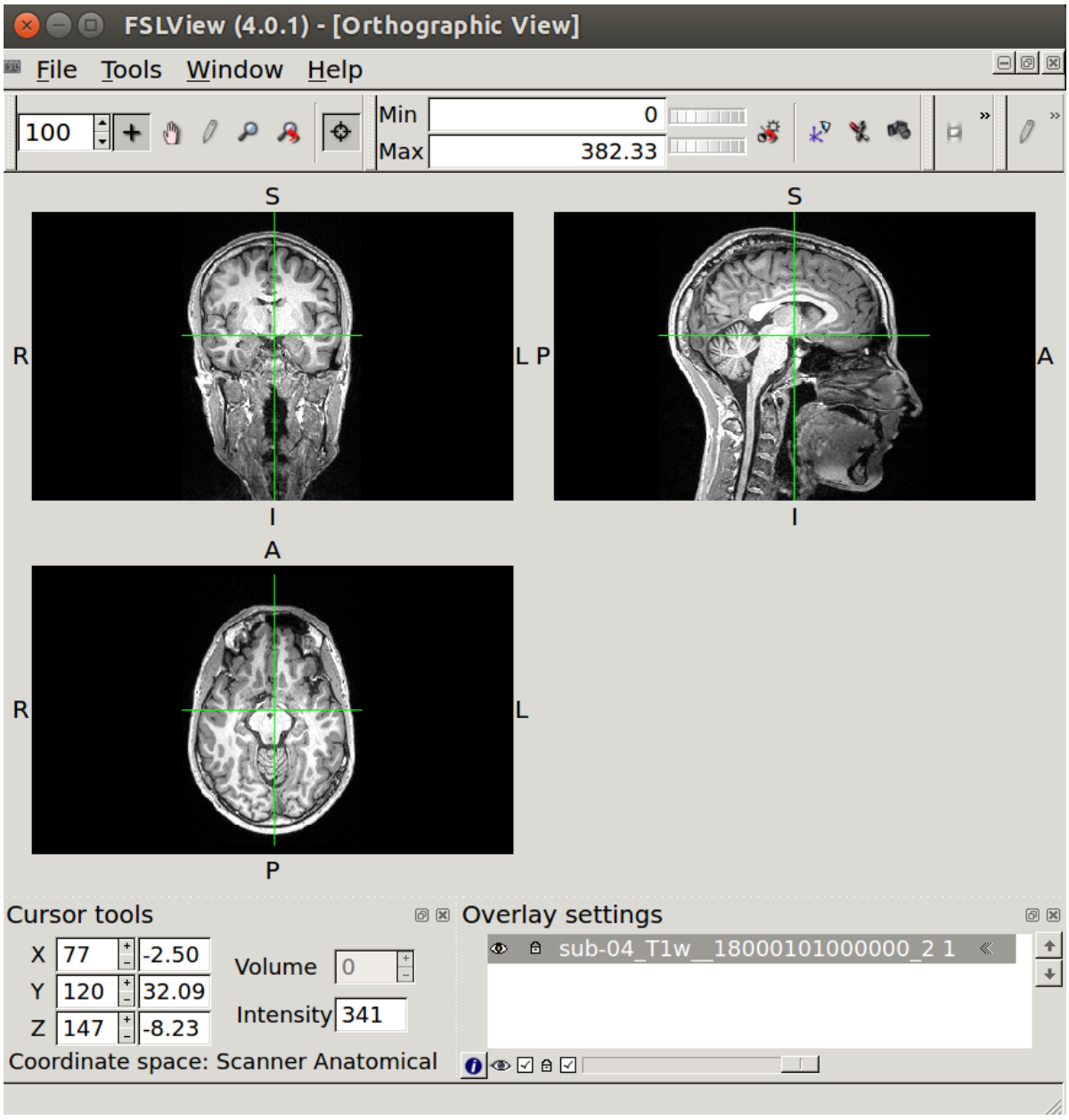

Figure 4: rendering a NIFTI image with FSLView

3. You will need to perform this DICOM to NIFTI conversion for all the scans you want to process with the processing scripts (Structural T1w, and functional BOLD resting state and/or task scans, etc.)

Part2: Organizing your unprocessed scan files

For this tutorial we used the **BIDS** (http://bids.neuroimaging.io/) file placement and file naming conventions. You are not required to follow these placement and naming conventions but we encourage you to use it.

Why

1. It's an international standard.
2. It's a simple and intuitive way to organize and describe your neuroimaging and behavioral data.

   Neuroimaging experiments result in complicated data that can be arranged in many different ways. So far there is no consensus how to organize and share data obtained in neuroimaging experiments. Even two researchers working in the same lab can opt to arrange their data in a different way. Lack of consensus (or a standard) leads to misunderstandings and time wasted on rearranging data or rewriting scripts expecting certain structure. Here we describe a simple and easy to adopt way of organizing neuroimaging and behavioral data.

3. *It is then easy to share your data.*

Inspect a BIDS dataset

You can explore the dataset provided for this practical:

```
 $ tree $HOME/localizer/sourcedata
/home/mydata/localizer/sourcedata
|-- dataset_description.json
|-- participants.tsv
|-- sub-S01
|   `-- ses-V1
|       |-- anat
|       |   `-- sub-S01_ses-V1_acq-maskface_T1w.nii.gz
|       `-- func
|           |-- sub-S01_ses-V1_task-localizer_bold.json
|           `-- sub-S01_ses-V1_task-localizer_bold.nii.gz
|-- sub-S02
|   `-- ses-V1
|       |-- anat
|       |   `-- sub-S02_ses-V1_acq-maskface_T1w.nii.gz
|       `-- func
|           |-- sub-S02_ses-V1_task-localizer_bold.json
|           `-- sub-S02_ses-V1_task-localizer_bold.nii.gz
|-- sub-S03
|   `-- ses-V1
|       |--


$ ls $HOME/localizer/derivatives
```

Note that the **sourcedata** folder contains all the row data, and that the associated TSV files contain the metadata. The rules used to organize this folder are really strict. All the processed data are organized in the

derivatives folder. Only recommendation are available in the BIDS documentation on how to organize this folder.

Validation tools (also available online) enables us to check the dataset integrity and let you easily spot missing values:

```
$ bids-validator ${HOME}/localizer/sourcedata
       Summary:                Available Tasks:        Available Modalities:
       62 Files, 1.34GB        Localizer               T1w
       20 - Subjects                                   bold
       1 - Session
```