TOAD tutorial

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Before you start using TOAD, we recommand to read the following articles to better know what analyses are conducted within TOAD :

— Jones, D. K., & Cercignani, M. (2010). Twenty-five pitfalls in the analysis of diffusion MRI data. NMR in Biomedicine, 23(7), 803–820.
— Smith, R. E., Tournier, J. D., Calamante, F., & Connelly, A. (2012). Anatomically-constrained tractography: Improved diffusion MRI streamlines tractography through effective use of anatomical information. NeuroImage, 62(3), 1924–1938.
— Tournier, J.-D., Mori, S., & Leemans, A. (2011). Diffusion tensor imaging and beyond. Magnetic Resonance in Medicine, 65(6), 1532–1556. [PDF]

1 Before you start

1.1 Account on the UNF server

In order to use TOAD at CRIUGM, you need to create an account on the UNF's server. This account could either be an individual or a team account.
To obtain an account, or for all account-related inquiries, please contact the system administrator at the UNF Mathieu Desrosiers.

1.2 Command line

TOAD toolbox is command-line-based that requires entries on a terminal. The introduction to the use of command line and terminal is beyond the purpose of this tutorial. However, there are plenty of resources available for those who need to become familiar with this requirement. For instance :

— A generic tutorial
— Life hacker tutorial

1.3 SSH communication

The use of TOAD requires a remote connection between your computer and the UNF servers (even if you are working from the CRIUGM's analysis room). To do so, it is strongly recommended to use the SSH protocol, which has been installed by default on all Apple and GNU/Linux based computers. For Windows system, please refer to the various external documentations listed below :

— Tutorial on Gamexe.net
— Youtube video demo

1.4 Add TOAD to your session

1.4.1 Verify if TOAD is available

In order to use TOAD, you need to source the TOAD script when you open a session. To do so, open a terminal and establish a session by connecting to one of the UNF's servers (via SSH)

```
# Replace 'username' by your UNF user ID
ssh -Y username@stark.criugm.qc.ca
```

To check the availability of TOAD, type the following command :

```
which toad
```

If the command returns a path such as `/usr/local/toad/...`, you are all set. If the command does not return anything, it means TOAD is not available for your session and you will need to add it.

1.4.2 Add TOAD

If you are using TOAD on an occasional basis, you can source TOAD *each time* you connect to the server, by typing the following command line :

```
source  /usr/local/toad/etc/unf-toad-config.sh
```

Alternatively, you can add this line to your session's profile if you want TOAD to be automatically sourced upon each connection :

1. Open/create the file .bash_profile' using a text editor :

```
vi ~/.bash_profile
```

2. Switch to `edit` mode by pressing the `i` key to add text
3. Copy and paste this line to the end of the document (without the quotation marks) : 'source /usr/local/toad/etc/unf-toad-config.sh'
4. Save and quit the editor by first pressing the ESC' key and then type `:wq` (do not forget to type the colon !)
5. To allow this change to take place, refresh the computer's memory :

```
source ~/.bash_profile
```

2 Data retrieval and preparation

2.1 From the UNF web interface

The easiest and most practical way to retrieve data acquired at the Unité de Neuroimagerie Fonctionnelle (UNF) is to use the platform available at the UNF website. This platform takes care of all that is necessary to prepare and reconstruct the images from the scanner into Dicom format to be ready for download. To access the site : either from **the website of the** [Neuroimaging unit](#) (Menu `Services` then `MRI Data Download`), or directly from **[the download platform of the unit](#)**

2.1.1 Data preparation

1. Before you can download the data, you need to reconstruct them into Dicom format. To do so, go to the UNF data download website https://unf-montreal.ca
2. Enter your user ID and password at the UNF
3. Select the data you want to download and click on `Build images` (keep the default option `tar.gz` for image compression type. TOAD will only work with this type)
4. Give a name to the dataset to be downloaded (in our example, `unf-data`), and click on `submit`

Data will be ready for download after a few moments. **Do not close** your browser window ; we will come back to it later.
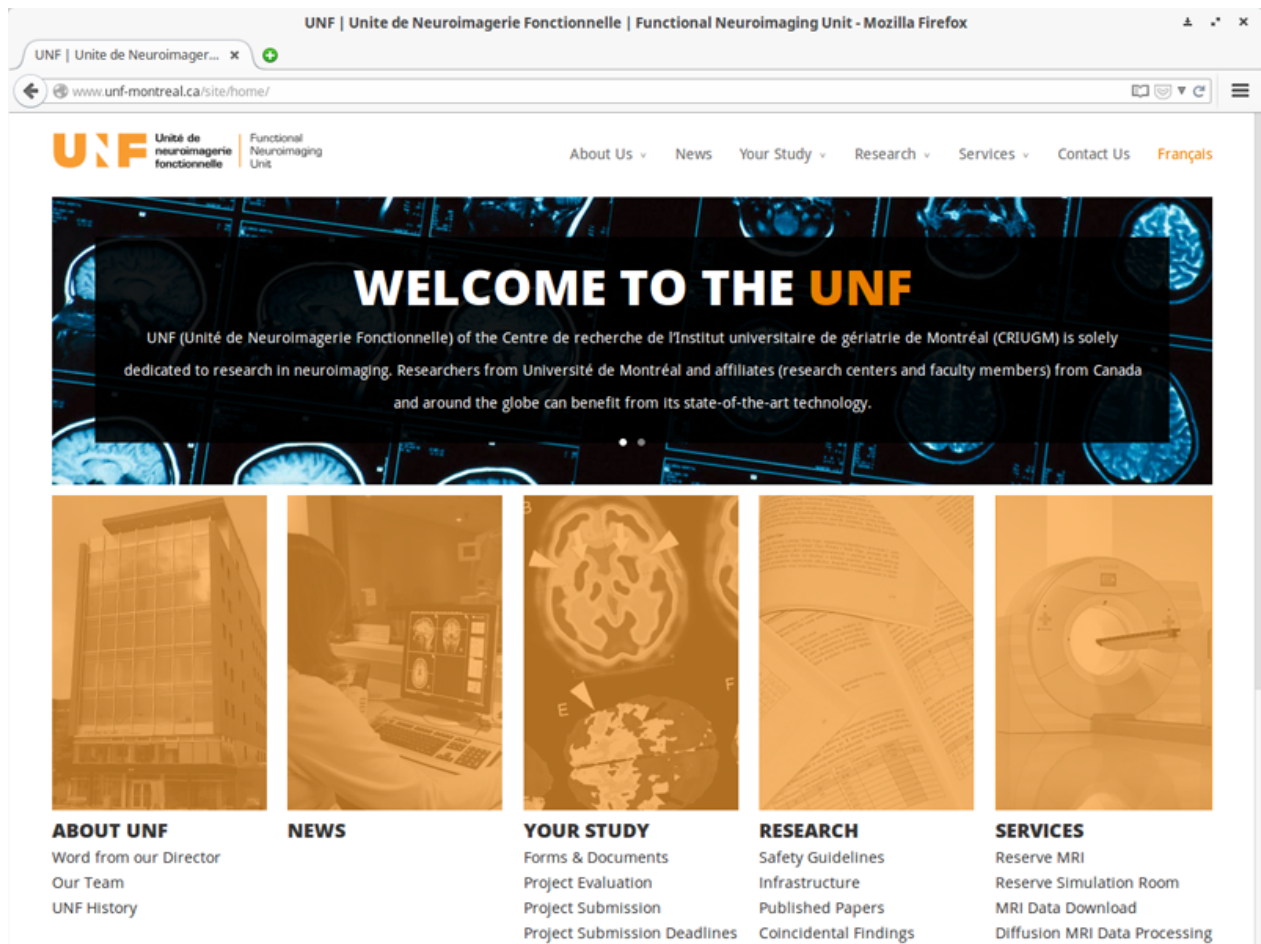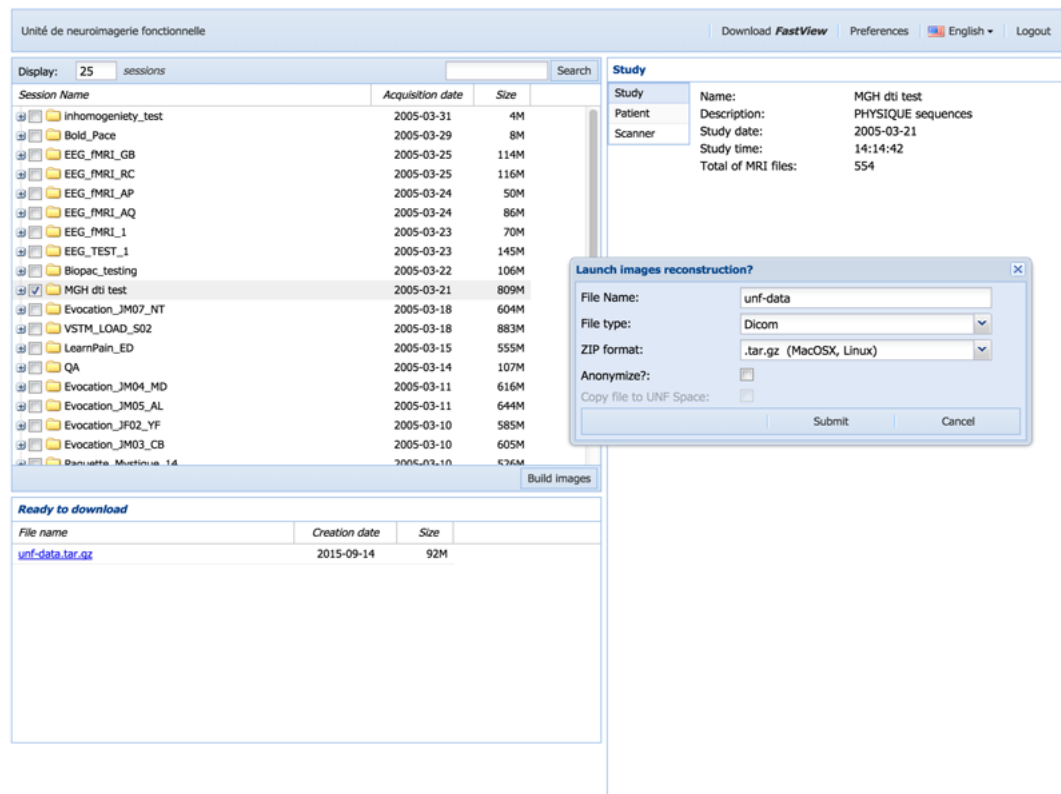
Figure 1 – UNF homepage

Figure 2 – Interface to download imaging sessions

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2.1.2 Data download

In the meantime, open a terminal window and connect to one of the UNF servers (Magma or Stark) via ssh.

```
# Replace 'username' by your user ID at the UNF
ssh -Y username@stark.criugm.qc.ca
```

The server will ask for your login information

FIGURE 3 – Connexion SSH to Stark

Once connected, navigate to your data directory :

```
# Replace 'labname' by the name of the lab/group you belong to
# Replace 'username' by your user ID at the UNF
cd /data/labname/username/
```

If necessary, create a new folder for your project and go to this directory :

```
# Replace 'project_name' by the name of the folder your are naming
mkdir project_name
```

```
# To go to the new folder
cd project_name
```

Download the data prepared by the UNF platform :

1. Go back to the browser window where you are downloading your data.
2. If your data is ready for download (after clicking the `build images` button), you will see a link (in blue) with the name you had specified earlier (`unf-data.tar.gz` in our example) under the section `Ready to download`, located on the left corner of the window. The link will be available for 7 days. Copy the link address by right-clicking on the link-> `Copy link location`, in our example, it would be http://downloads.criugm.qc.ca/user
3. Go back to the previous terminal with the ssh session, and type the command `wget`, followed by pasting the link address :

```
# Type wget, followed by space, then right-click, choose 'Paste', or control-shift-v
wget http://downloads.criugm.qc.ca/username/unf-data.tar.gz
```

Your data are now being downloaded and will be ready to be converted by TOAD into its required format. (see section '3 Data Conversion').
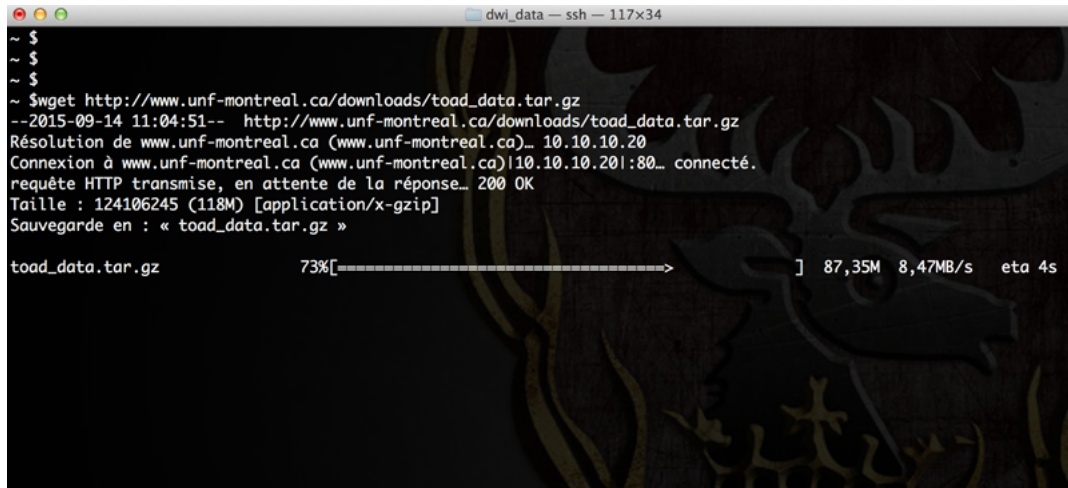
FIGURE 4 – Dowload data with WGET

2.1.3 Data conversion

ATTENTION TOAD uses its own file conversion tool `dcm2toad` to convert DICOM images into NIfTI. It is **strongly recommended** to use this tool for file conversion, because not only can it convert your data, it also generates a configuration file for TOAD. This file contains all existing information that is unique in the raw data which is lost upon conversion when using other softwares.

`dcm2toad` automatically unzips and converts your data. Different options are available (see help by typing `unf2tad -h`). By default, `dcm2toad` creates a new directory called `toad_data` where it stores all the converted files from each subject/session.

```
# Replace 'unf-data.tar.gz' by the name of your data
#   (downloaded from the UNF site)
dcm2toad unf-data.tar.gz


# To specify a target directory into which the converted files are written
#   for example 'DWI'
dcm2toad -d DWI unf-data.tar.gz
```

The software will ask you a series of questions to specify which file corresponds to which type of image (anatomical, diffusion, etc.), and to indicate the study/project ID.

One of the strong features of `dcm2toad` is its ability to manage multiple sessions/subjects simultaneously. It will first show you a list of sessions/subjects found within the downloaded data set. Subject ID followed by an asterisk * indicates the data from that subject have been converted.

When multiple sessions/subjects share the exact same data structure, `dcm2toad` offers the option of applying the setting options chosen for the first subject to the subsequent sessions/subjects.

2.2 From another source of acquisition

2.2.1 Data type

The analysis of diffusion data requires at least 3 types of images from each subject :

1. **anatomical images** (T1, type MPRAGE) : anatomical mask creation, coregistration
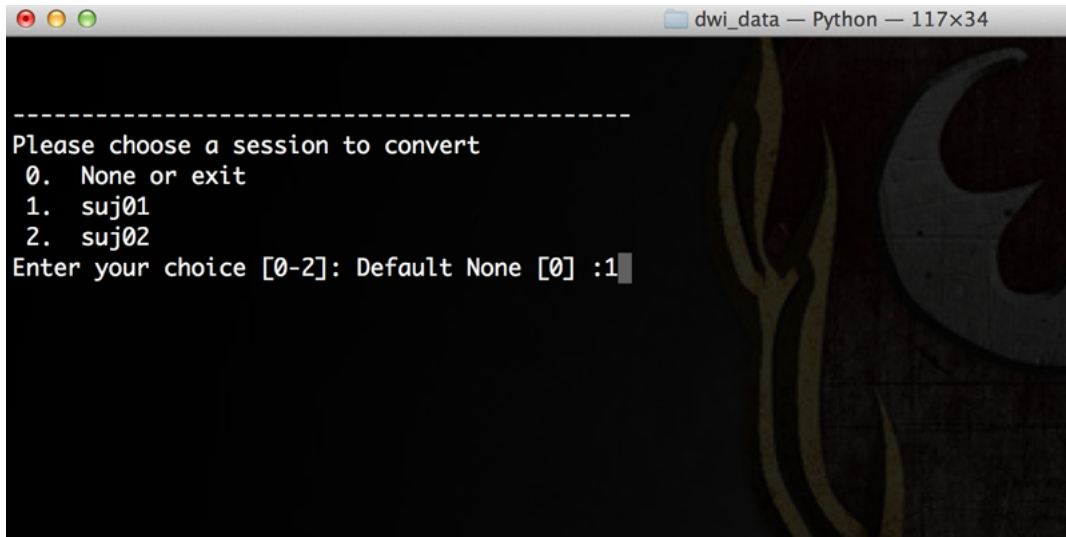2. **diffusion images** (DWI) : white matter tracts (fibre extraction)

FIGURE 5 – dcm2toad in action

3. **acquisition specifications for the diffusion images (the `b-files`) :** specifications for the acquisition of diffusion data (intensity and directions) regrouped in one *(.b) or 2 (.*bval and *.bvec) files.

Other kinds of data that can also be used by in TOAD :
— **geometric distortion/field inhomogeneity corrections** :
— diffusion image acquired in the reverse direction of the main DWI files,
— fieldmap image.
— **output folder from Freesurfer processing**

2.2.2 File format

For simplicity's sake, TOAD only accepts the following file formats :
— neuroimaging : **NIfTI** (.nii)
— encoding : regrouped format **MRTRIX (.b)** or separated **FSL (.bval and .bvec)**.

2.2.3 Data organization

If you have data that are already converted into NIfTI as well as the encoding files, you can directly bypass the TOAD data conversion step. We recommend regrouping your data in the following manner :
— a parent folder containing all the files from your subjects
— individual subject folder containing all the imaging files (*.nii, *.b)

Attention : *in this case, it is your responsibility to ensure that all your files have been correctly converted, and that the encoding file complies with the usual standards (strides . . .). If these data come from a 3T Tim Trio Siemens MRI scanner (as at the UNF), and if you still have the raw data, we strongly recommend to convert the data with the software `dcm2toad` see section Data conversion

2.2.4 File naming

TOAD needs to identify which files correspond to which image. To do so, TOAD uses the prefix that is common to the file name of each type of files. Similarly, all the anatomical images should start by the same prefix ; by default TOAD looks for files that start with `anat`. For diffusion images, TOAD looks for files that start with `dwi` and for the encoding files files starting with `dwi` and with `.b` or `.bval` and `.bvec` as file extension. When the

anterior-posterior or posterior-anterior files are available, TOAD looks for the prefix `b0_ap` and `b0_pa`.

You are free to use any current naming system, as long as it is specified in your configuration file `config.cfg`. It must be consistent across all subjects, unless you specify a new configuration file in the folder.

2.3 Sample data set and demonstration

We suggest you download a sample dataset to discover how the pipeline works by following these steps :

```
# Connect to the UNF server
# Replace 'username' by your user ID at the UNF
ssh -Y username@stark.criugm.qc.ca


# Navigate to your data directory
# Replace 'labname' by the name of the lab/group you belong to
# Replace 'username' by your user ID at the UNF
cd /data/labname/username/


# Create a folder for your project
# Replace 'project_name' by the name of the project
mkdir project_name


# Go into the new folder
cd project_name


# Download the sample data set
wget http://unf-montreal.ca/downloads/toad_dicom.tar.gz
```

3 TOAD

3.1 Running TOAD

Once the imaging data are converted, you simply have to run the command 'toad' from the folder that contains the converted files :

```
# Go to the data-containing folder
cd toad_data


# Run TOAD
toad *
```

Data preprocessing for one subject takes about 2 days to complete. Parallel processing on multiple subjects or large dataset is also possible on the UNF servers, depending on their work load at the given time.

3.2 Verification

One can know the progress of the preprocessing (e.g. how many subjects have been preprocessed) on the UNF servers by simply typing the command 'qstat -f'.

Once the work is finished, you will find a new set of folders under each subject's directory. These folders contain the dataset, masks, and images generated by TOAD's preprocessing pipeline. The results can be quickly verified thanks to QA. . .

Section à développer

In case of any problem, check the log files under the folder 'log', which can be found in each subject that has been preprocessed by TOAD :

```
# Replace 'toad_data' below by the name of the folder used during data conversion.
cd toad_data/subject_name/99-logs

# List all available logs
ls

# To consult a log file, for example 'results.log'
vi results.log
```

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