1. XNAT and its main features

XNAT is an open-source imaging informatics software platform dedicated to helping you perform imaging-based research.
XNAT's core functions manage importing, archiving, processing and securely distributing imaging and related study data.

- Account Management
All access to any XNAT site is restricted to valid users of the site.
User accounts determine the data and pages which are accessible to visitors of the site.

- Creating and Managing Projects
Data stored within XNAT is organized according to projects.
To manage data within your XNAT you will need to create projects which your data can be assigned to.

- Creating and Managing Subjects
Most experiment data in XNAT is associated directly with a subject. In turn, a subject can have multiple experiments. Subject information can be as brief and simple as an identifier. Or, it can contain in-depth demographic information. Either way, creating a subject is required to add imaging data (as well as subject assessment data).
There are multiple ways to store subjects in XNAT:
"Create Subject" form in the website UI
StoreXML
Upload Spreadsheet
REST

-Defining, creating and managing experiments
"Experiments" is the term used in XNAT to describe data that is gathered or measured from direct interaction with a subject.
These types of data can range from a simple consent form signed by a subject at the beginning of a study to demographic data gathered about the subject, their medication list, blood test results,
behavioral assessments for cognitive psychology measures, to MR or PET sessions taken when the subject is in the scanner.
Each experiment corresponds to a data type in XNAT.

- User roles and permissions
By default, XNAT defines three common project roles: Owners, Members, and Collaborators. As a project owner, you have the ability to add specific users to your project within these roles.
These users will then have the permissions associated with their defined role (which overrules the default accessibility permissions).

-Uploading imaging data
The most common purpose for XNAT usage is to store imaging data. The list of imaging types which XNAT supports is continually expanding. Currently DICOM, Analyze, ECAT, IMA, and NRD are supported in varying degrees. XNAT supports several modalities, including MRI, CT, and PET.
If you have a scanner on site, imaging data can be uploaded directly from the scanner via a DICOM C-Store connection. Otherwise, you will commonly be receiving imaging data via the Upload Applet or zipped archives of scan data, and using the ZIP uploader.
Advanced users may use REST scripts to upload data and files

- Viewing image files
XNAT comes bundled with a Java applet that allows users to view images from an MR Session in the browser window.

- Downloading files
There ar ethree modalities for downloading the files:
- download applet - XNAT includes a download applet for downloading files from multiple imaging sessions
- download with REST API - A common mechanism for downloading data is to use the REST API. Using this tool usually requires some mild scripting, but it gives you the most flexibility for choosing what to download.
- download script - most common script is ArcGet

- Pipelines
Pipelines in XNAT are powerful mini-applications that can be run on your project data, to aid in complex processing or leverage the power of large computing clusters. Some pipeline-enabled workflows are carried out automatically without any human intervention, like auto-QC'ing images as they are added to your project archive.
Others require a person to do manual steps, such as drawing a region of interest.

Pipeline Engine

Pipeline Engine is a Java-based framework that links sequential activities, human and computer, into a defined process flow and manages how data moves from step to step in that flow based on the results of each step. In most laboratories, some processes (or pipelines) are carried out automatically without any human intervention while others require a person to do manual steps, such as drawing a region of interest. Pipeline Engine facilitates both fully automated and semi-automated workflows. Pipelines can be executed up to a step, then notify a user(s) to perform the manual task, and finally restart the pipeline from the next step. The process flow is defined in am XML document called the *pipeline descriptor* and the executables are defined in a separate XML document called *resource descriptors*.

Pipeline engine is a standalone tool. However, when used with XNAT one can:

- set up project-based workflows with project specific and experiment specific parameters,

- track a pipeline and send email notifications
- capture provenance information as the pipeline executes

- Searching and browsing XNAT data
Once you have project data stored in your XNAT installation, users need to be able to find it. XNAT provides a number of ways of accessing and locating stored data.

2. Scan formats

- T1 MRI
One of the most important features of MRI is that it can generate images depicting a number of different contrast characteristics.
T1 is when they programme the machine to only look at the longitudinal movement of protons. T1 images are usually used to look at normal anatomical details.
Anatomical MRI is T1 weighted.
T1 is best for looking at brain structure because fat appears very bright and bone marrow contains a great deal of fat.

- dMRI (diffusion magnetic resonance imaging)
Diffusion MRI (or dMRI) is a magnetic resonance imaging (MRI) method. It allows the mapping of the diffusion process of molecules, mainly water, in biological tissues, in vivo and non-invasively.
Molecular diffusion in tissues is not free, but reflects interactions with many obstacles, such as macromolecules, fibers, and membranes.
Water molecule diffusion patterns can therefore reveal microscopic details about tissue architecture, either normal or in a diseased state.

- DWI (Diffusion weighted imaging) synonym: diffusion weighted MRI
DWI derives its image contrast from differences in the motion of water molecules between tissues. Such imaging can be performed quickly without the need for the administration of exogenous contrast medium.
The technique yields qualitative and quantitative information that reflects changes at a cellular level and provides unique insights about tumor cellularity and the integrity of cell membranes.

- bvals , bvecs
bvals and bvecs, contain the information on the diffusion-sensitising magnetic field gradients (note that some nifti conversion tools will create bvals and bvecs information and some will not).
bvals contains a scalar value for each applied gradient, corresponding to the respective b-value. bvecs contains a 3x1 vector for each gradient, indicating the gradient direction.

The entries in bvals and bvecs are as many as the number of volumes in the dwidata file.So the ith volume in the data corresponds to a measurement obtained after applying a diffusion-sensitising gradient with a b-value given by the ith entry in bvals and a gradient direction given by the ith vector in bvecs.

3. FSL

FSL is a comprehensive library of analysis tools for FMRI, MRI and DTI brain imaging data. It could be used either by FSL main GUI or the commond-lines. The advantage of the GUI lies in its simplicity but the drawback is the less flexibility comparing to the command-lines. FSLView as the display tool could be completely separate use from processing and analysis. Currently FSL only accepts the input files in NIFTI format, and the DICOM files need to be converted to NIFTI after acquisition and before processing. The convertion from DICOM to NIFTI could be fulfilled by several methods, such as dcm2nii from mricron or dcmstack. In the GUI there are nine popular modules defined, and depending on the input file types, they fall into functional-oriented, structural-oriented or diffusion-oriented modules.

The ***structural-oriented*** functions include:

–BET brain extraction

–BET (Brain Extraction Tool) deletes non-brain tissue from an image of the whole head. It can also estimate the inner and outer skull surfaces, and outer scalp surface, if you have good quality T1 and T2 input images.

–FAST segmentation - tissue segmentation

–FAST (FMRIB's Automated Segmentation Tool) segments a 3D image of the brain into different tissue types (Grey Matter, White Matter, CSF, etc.), whilst also correcting for spatial intensity variations (also known as bias field or RF inhomogeneities). The underlying method is based on a hidden Markov random field model and an associated Expectation-Maximization algorithm. The whole process is fully automated and can also produce a bias field-corrected input image and a probabilistic and/or partial volume tissue segmentation. It is robust and reliable, compared to most finite mixture model-based methods, which are sensitive to noise.

–FLIRT linear registration

–FLIRT (FMRIB's Linear Image Registration Tool) is a fully automated robust and accurate tool for linear (affine) intra- and inter-modal brain image registration.

The ***functional-oriented*** functions involve :

–SUSAN noise reduction

–SUSAN noise reduction uses nonlinear filtering to reduce noise in an image (2D or 3D) whilst preserving the underlying structure. It does this by only averaging a voxel with local voxels which have similar intensity.

–FEAT FMRI analysis

–FEAT automates as many of the analysis decisions as possible, and allows easy (though still robust, efficient and valid) analysis of simple experiments whilst giving enough flexibility to also allow sophisticated analysis of the most complex experiments. The data modelling which FEAT uses is based on general linear modelling (GLM), otherwise known as multiple regression. It allows you to describe the experimental design; then a model is created that should fit the data, telling you where the brain has activated in response to the stimuli.

– MELODIC ICA

–MELODIC (Multivariate Exploratory Linear Optimized Decomposition into Independent Components) 3.0 uses Independent Component Analysis to decompose a single or multiple 4D data sets into different spatial and temporal components. For ICA group analysis, MELODIC uses either Tensorial Independent Component Analysis (TICA, where data is decomposed into spatial maps, time courses and subject/session modes) or a simpler temporal concatenation approach. MELODIC can pick out different activation and artefactual components without any explicit time series model being specified .

The ***DTI-oriented*** functions incorporate "FDT diffusion".

FDT (FMRIB's Diffusion Toolbox) is a software tool for analysis of diffusion weighted images. FDT includes tools for data preprocessing, local diffusion modelling and tractography. Each stage in FDT is run separately.

Besides these functional modules, there is a simulator called "POSSIUM MRI simulator", which is a software tool to produce realistic simulated MRI and FMRI images or time series. POSSUM (Physics-Oriented Simulated Scanner for Understanding MRI) includes tools for the pulse sequence generation, signal generation, noise addition and image reconstruction.

4. Mrtrix 3

MRtrix provides a set of tools to perform diffusion-weighted MRI white matter tractography in the presence of crossing fibres, using Constrained Spherical Deconvolution and a probabilisitic streamlines algorithm.

Common tasks:

–Basic DWI processing
–Get from the raw DW image data to performing some steamlines tractography.

–Anatomically Constrained Tractography (ACT)

–SIFT: Spherical-deconvolution informed filtering of tractograms

–SIFT, or 'Spherical-deconvolution Informed Filtering of Tractograms', is a novel approach for improving the quantitative nature of whole-brain streamlines reconstructions. By producing a reconstruction where the streamlines densities are proportional to the fibre densities as estimated by spherical deconvolution throughout the white matter, the number of streamlines connecting two regions becomes a proportional estimate of the cross-sectional area of the fibres connecting those two regions. We therefore hope that this method will attract usage in a range of streamlines tractography applications.

–Structural connectome construction

–Generating a connectome from HCP diffusion & structural data

5.MNE

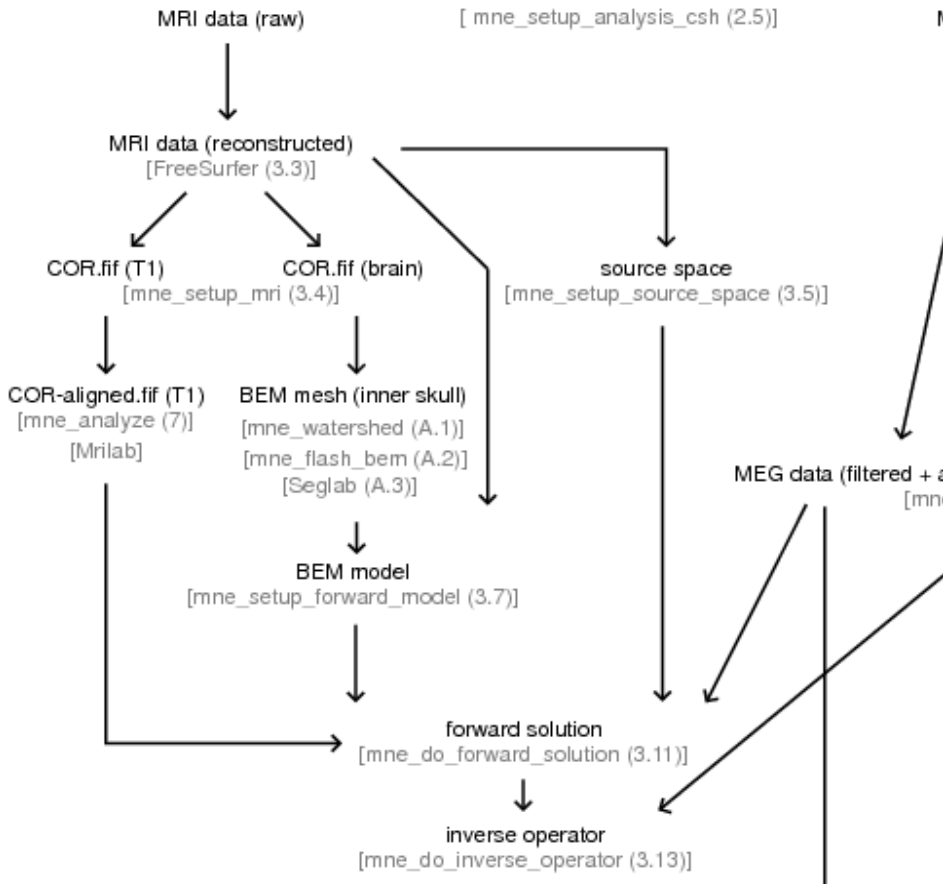
MNE is a software package for processing magnetoencephalography (MEG) and electroencephalography (EEG) data.
–Magnetoencephalography (MEG) is a functional neuroimaging technique for mapping brain activity by recording magnetic fields produced by electrical currents occurring naturally in the brain, using very sensitivemagnetometers.
–Electroencephalography (EEG) is typically a non-invasive (however invasive electrodes are often used in specific applications) method to record electrical activity of the brain along the scalp. EEG measures voltage fluctuations resulting from ionic current within the neurons of the brain. In clinical contexts, EEG refers to the recording of the brain's spontaneous electrical activity over a period of time, as recorded from multiple electrodes placed on the scalp.
The MNE software computes cortically-constrained L2 minimum-norm current estimates and associated dynamic statistical parametric maps from MEG and EEG data, optionally constrained by fMRI.

This software includes MEG and EEG preprocessing tools, interactive and batch-mode modules for the forward and inverse calculations, as well as various data conditioning and data conversion utilities. These tools are provided as compiled C code for the LINUX and Mac OSX operating systems.

The software depends on anatomical MRI processing tools provided by the FreeSurfer software.

The typical workflow needed to produce the minimum-norm estimate movies using the

MNE software:



6. Pipeline

In order to run the "main_surface.sh" file you have to give right for execution for some files and this is the reason for we have created a script to do this – "rights_for_files.sh" and we have called the execution of it in the main file, right after "importing the configuration" section.

After the execution of the "main_surface.sh" file, the following directories and files are created in the input directory.

-the directory "118730" which contains:

- "connectivity" directory with the files: areas.txt, average_orientation.txt, centres.txt, cortical.txt, tract_lengths.txt, weights.txt.
- The "centres.txt" file contains 88 connectivity regions.
- "connectivity_<number>" directories, where number = {1,2,4,8,16,32}.
- These directories contain the same files as the "connectivity" directory, EXCEPT the "ares.txt" and "cortical.txt" files.
- "centers.txt" file contains for each directory a different number of connectivity regions, as follows: connectivity_1 – 87, connectivity_2 – 157, connectivity_4 – 297, connectivity_8 – 577, connectivity_16 – 1137, connectivity_32 – 2257.

•"region_mapping.txt" file
•"surface" directory with the 9 files: inner_skull_(triangles.txt)/(vertices.txt), outer_skin_(triangles.txt)/(vertices.txt), outer_skull_(triangles.txt)/(vertices.txt), region_mapping.txt, triangles.txt, vertices.txt.
•There are also zip files for every directory: for connectivity and surface.

–"surface" directory with:

-"subcortical" directory with 66 "aseg" files.
-the following files: (lh/rh)info.txt, (lh/rh)_high.off ,(lh/rh)_low.off, (lh/rh).pial.asc, (lh/rh)_region_mapping_low_not_corrected.txt, (lh/rh)_region_mapping_low, (lh/rh)_triangles_high.txt, (lh/rh)_triangles_low.txt, (lh/rh)_vertices_high.txt, (lh/rh)_vertices_low.txt .

The matrix from "tract_lengths.txt" file is symmetric.

Issues: The pipeline does not generate the volume mapping file and the normals for the surface which are needed for the TVB.
As input for the TVB it is also needed a T1 background nifti file format.

The "main_region.sh" file cannot be executed with Mrtrix3. We had to change the commands from the old version (Mrtrix0.2) to the new one, but even doing this, the file cannot be executed because of the differences between these two versions.