AXONICA© 2.3

User Guide

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aXonica 2.3 User Guide

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About This Guide

Purpose

The scope of this document is to provide a detailed description of the aXonica installation and configuration process. The primary purpose of the aXonica is to provide a free, easily distributable software installation package for freeware tools related to Bioimaging especially in the field of Magnetic Resonance Imaging (MRI).

aXonica is a GUI based shell file that runs tools and dependency installations in the specific order required to execute them.

Intended Audience

This document is intended for users who wish to install the tools related to Magnetic Resonance Imaging on Linux based operating system.

Required Background

Team aXonica has made every attempt to make this a step-by-step guide. However, some familiarity with Linux operating system is assumed. Also, Team aXonica assumes that you are familiar with hardware and software that will be used to complete the installation and/or configuration of the aXonica 2.3.

How This Guide is Organized

This guide is organized into sections grouped according to the intended use by the user:

- About This Guide (Chapter 1) describes this document's purpose and intended audience.
- Software Installation Process (Chapter 2) describes how to install aXonica.
- Data Acquisition and Software Pipeline (Chapter 3) describes the acquisition of raw data image of MRI machine and implementation of software pipeline of Biological image development.
- Tutorial Datasets (Chapter 4) describes how to download tutorial datasets.
- Image Preprocessing (Chapter 5) describes the step by step solution to recommended software.
- Image Processing (Chapter 6) describes the step by step solution to recommended software.
- Structural Analysis (Chapter 7) describes the step by step solution to recommended software.
- Data Management & Annotation (Chapter 8) describes the step by step solution to recommended software.
- Hardware Requirements (Appendix A) presents the hardware and software prerequisites required to install and configure aXonica.

Contact

If you have general, non-technical and technical support questions:

- Send an email to hasaniqbal777@gmail.com

Software Installation Process

Installing the aXonica software

aXonica is available at its website:

https://github.com/hasaniqbal777/aXonica

aXonica shell file will be downloaded.

1. Make **aXonica Resource Folder** in your drive and put the shell file of aXonica in this folder.
2. Run the terminal and cd to the Resource folder.
3. Now run the following commands on terminal:

   > chmod +x aXonica-v2.3.sh

   > sudo bash aXonica-v2.3.sh
4. Installation wizard of aXonica will start.

NOTE *Installation of aXonica require a proper internet connection to proceed, otherwise the installation terminates.*

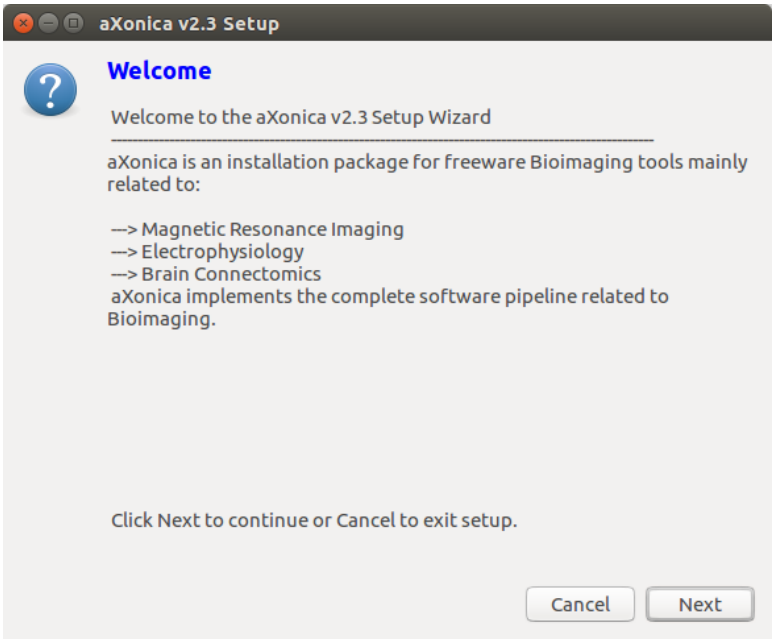


Figure 1: Installation Welcome screen

5. Click **Next** to proceed and confirm the Internet connection.

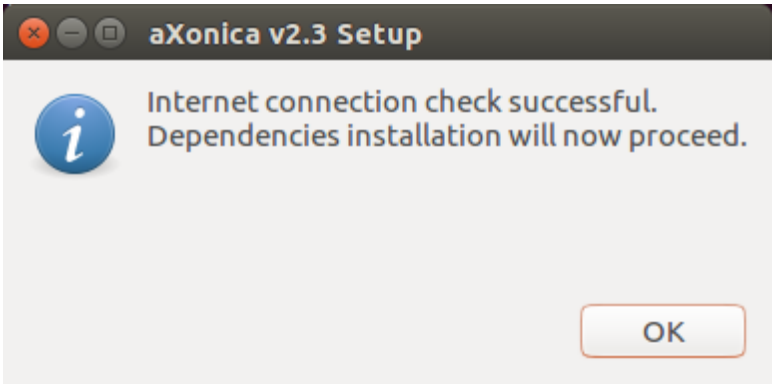


Figure 2: Internet check successful screen

6. Installation is **terminated** if there is **no internet**.

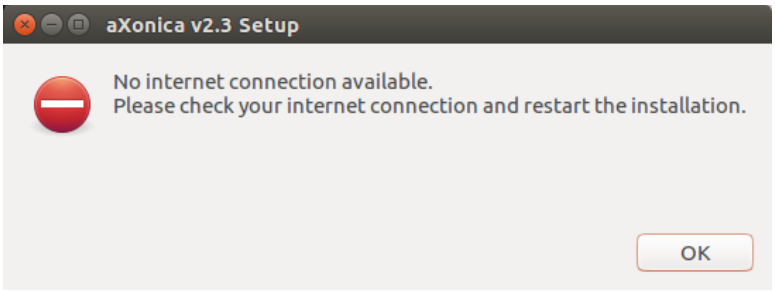


Figure 3: Internet check failed screen

7. **Dependencies** related to software will start installing.

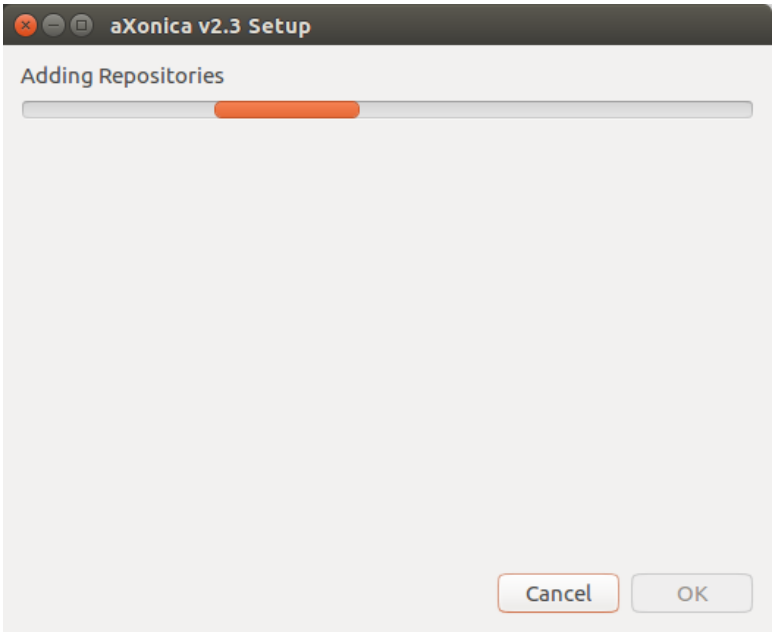


Figure 4:Dependencies Installation in progress screen

8. All the dependencies which are installed are displayed at the end of the installation. Click **Ok**.

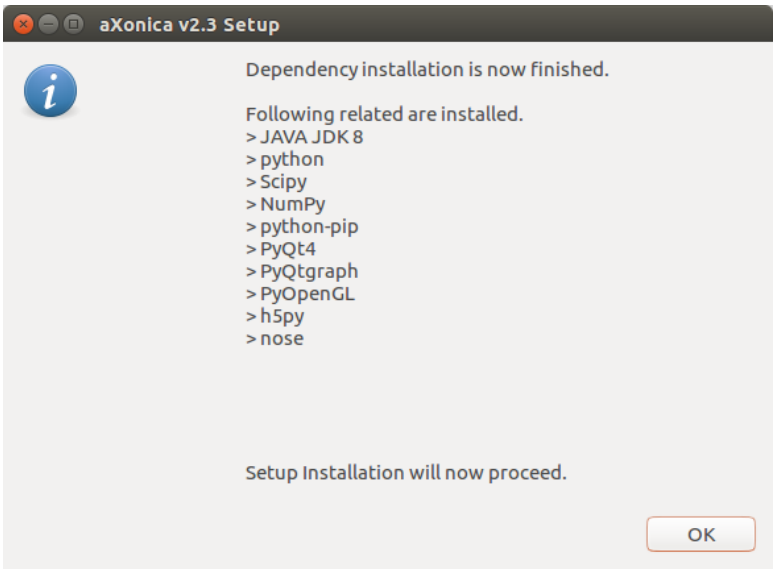


Figure 5: Dependencies Installation finished screen

9. aXonica pipeline detail screen is **displayed**. It has the information about which software you want to install. Click **Next** to Proceed.

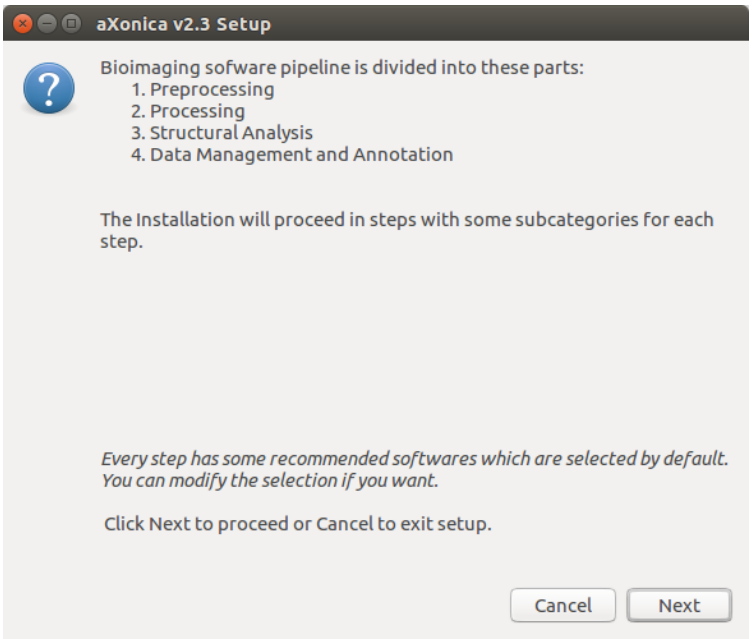


Figure 6: Pipeline information screen

10. Click **Next** to proceed with the installation.

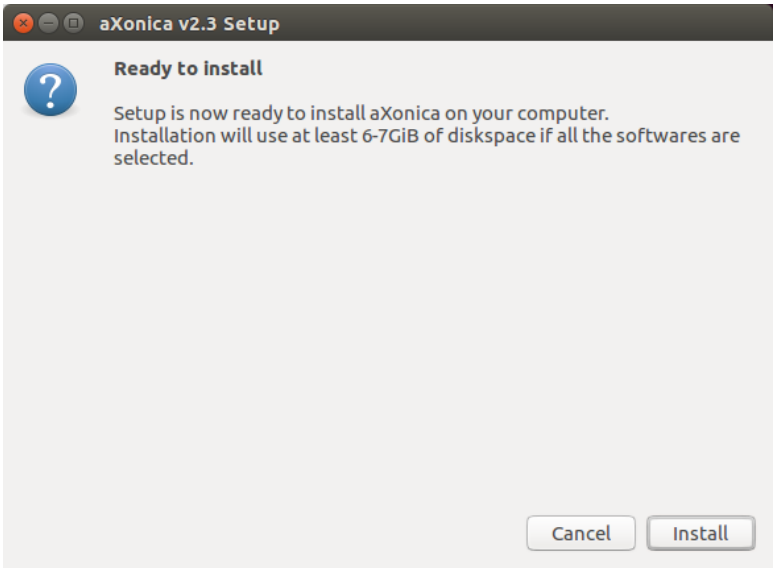


Figure 7: Ready to Install screen

11. Selection screen for Preprocessing tools is displayed. Select the required tools and Click **Next**.

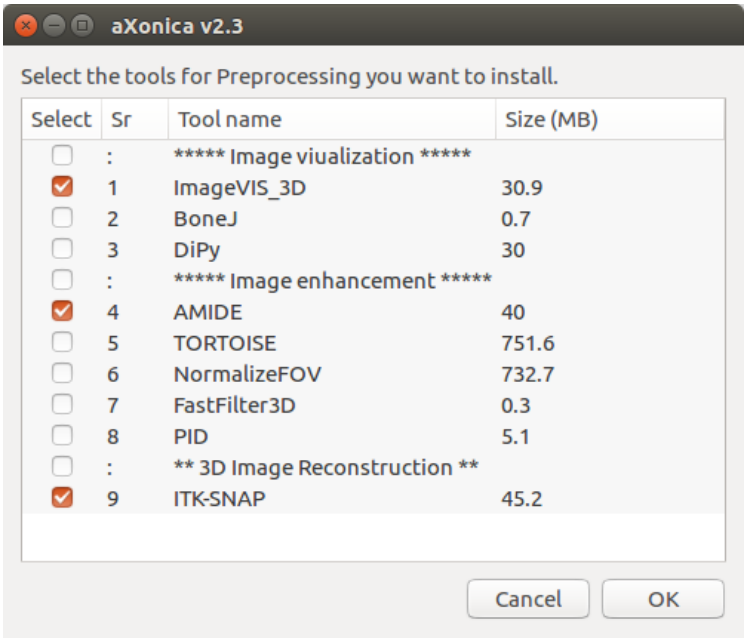


Figure 8: Preprocessing tools selection screen

12. Selection screen for Processing tools is displayed. Select the required tools and Click **Next**.

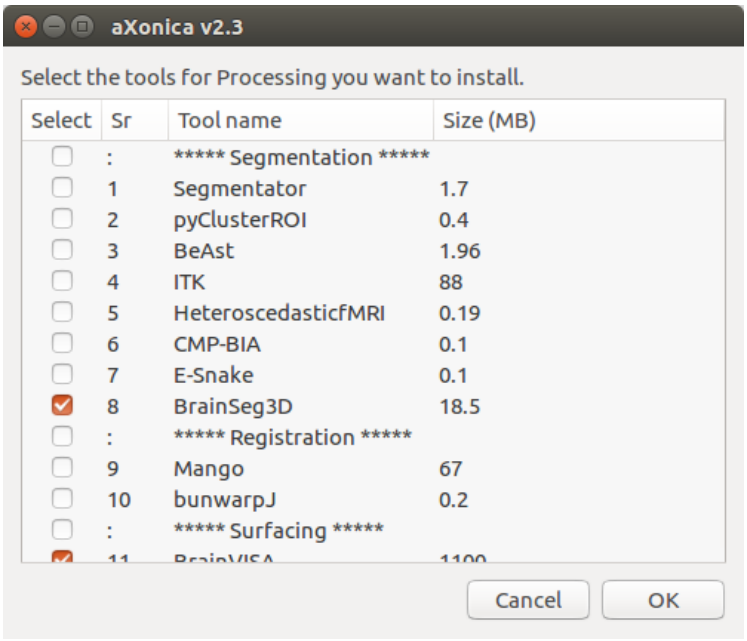


Figure 9: Processing tools selection screen

13. Selection screen for Structural Analysis tools is displayed. Select the required tools and Click **Next**.

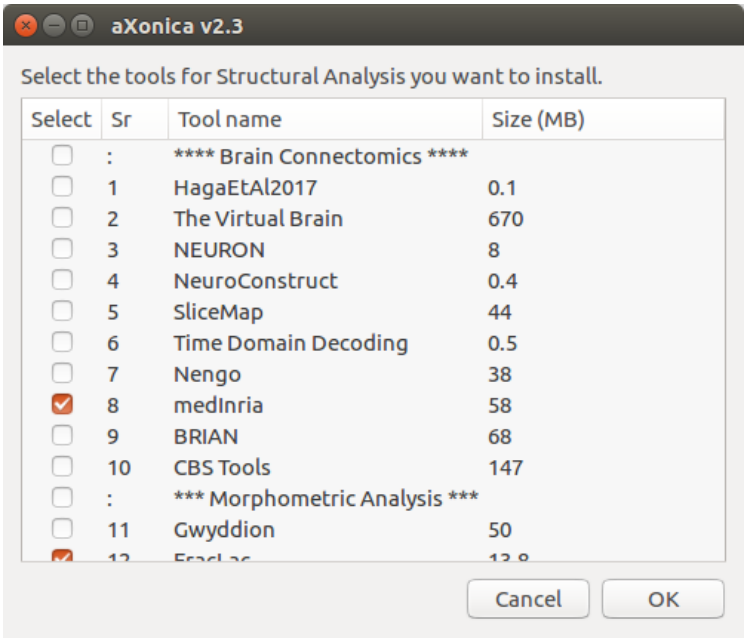


Figure 10: Structural Analysis tools selection screen

14. Selection screen for Data Management and Annotation tools is displayed. Select the required tools and Click **Next**.

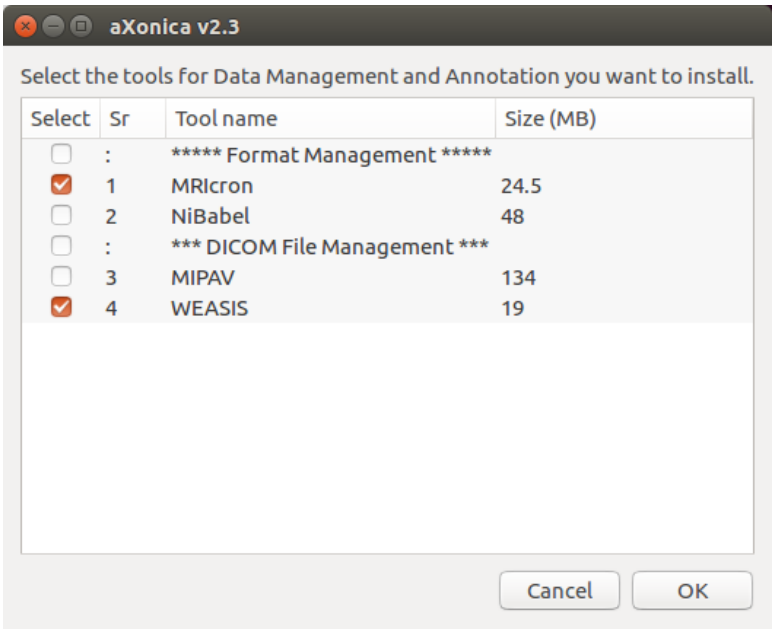


Figure 11: Data Management and Annotation selection screen

15. Tools installation will **continue**. Some tools **install** as a standalone installation and will be called automatically.

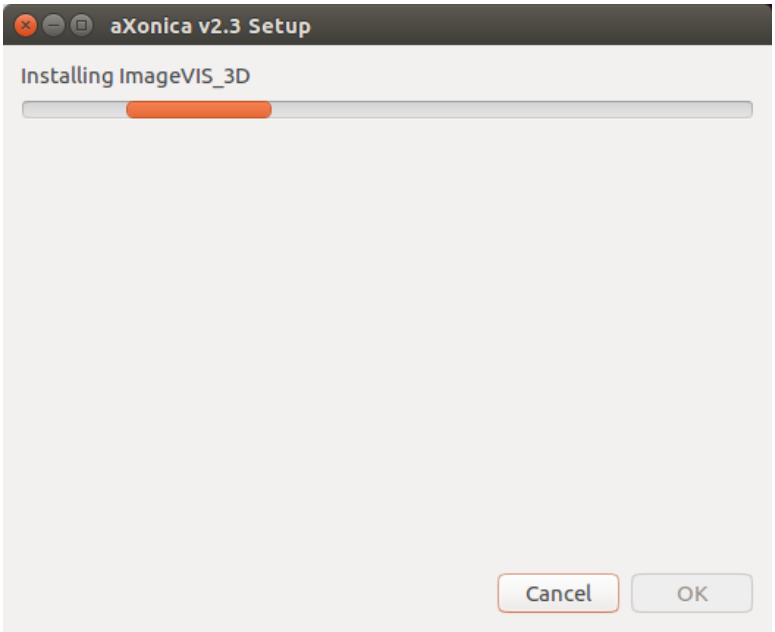


Figure 12: Tools installation progress screen

16. Software will be automatically **download** from the aXonica repository online. Downloading time depend upon your Internet.

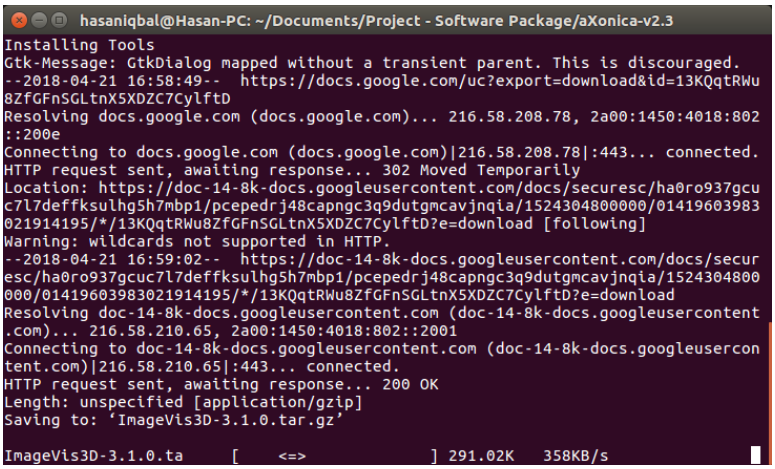


Figure 13: Tools downloading in background

17. Installation of aXonica is now finished. Click **Finish** to use the Tools.

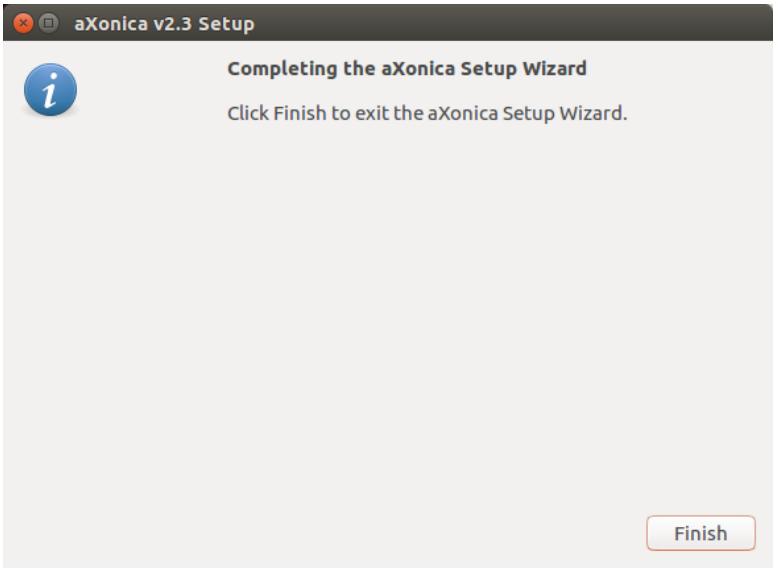


Figure 14: Finalizing Installation screen

Data Acquisition and Software Pipeline

In this Chapter

We will learn about:

- Image Data Acquisition
- MRI network diagram in hospitals
- Introduction to software pipeline

Introduction

Medical Imaging Technology is identified globally by some major diagnostic imaging device manufacturers. Honorable mentions contain Fujifilm Holdings, Siemens Healthcare, Toshiba Medical Systems Corporation and Canon Medical Systems Corporation.

MRI machine is installed and distributed with some extra workstation for functionality i.e.

- Scan Console
- Display Console
- Reconstruction Box
- Quality Control (Calibration Phantoms)

Image Data Acquisition from MRI

MRI installation network diagram is given as follows:

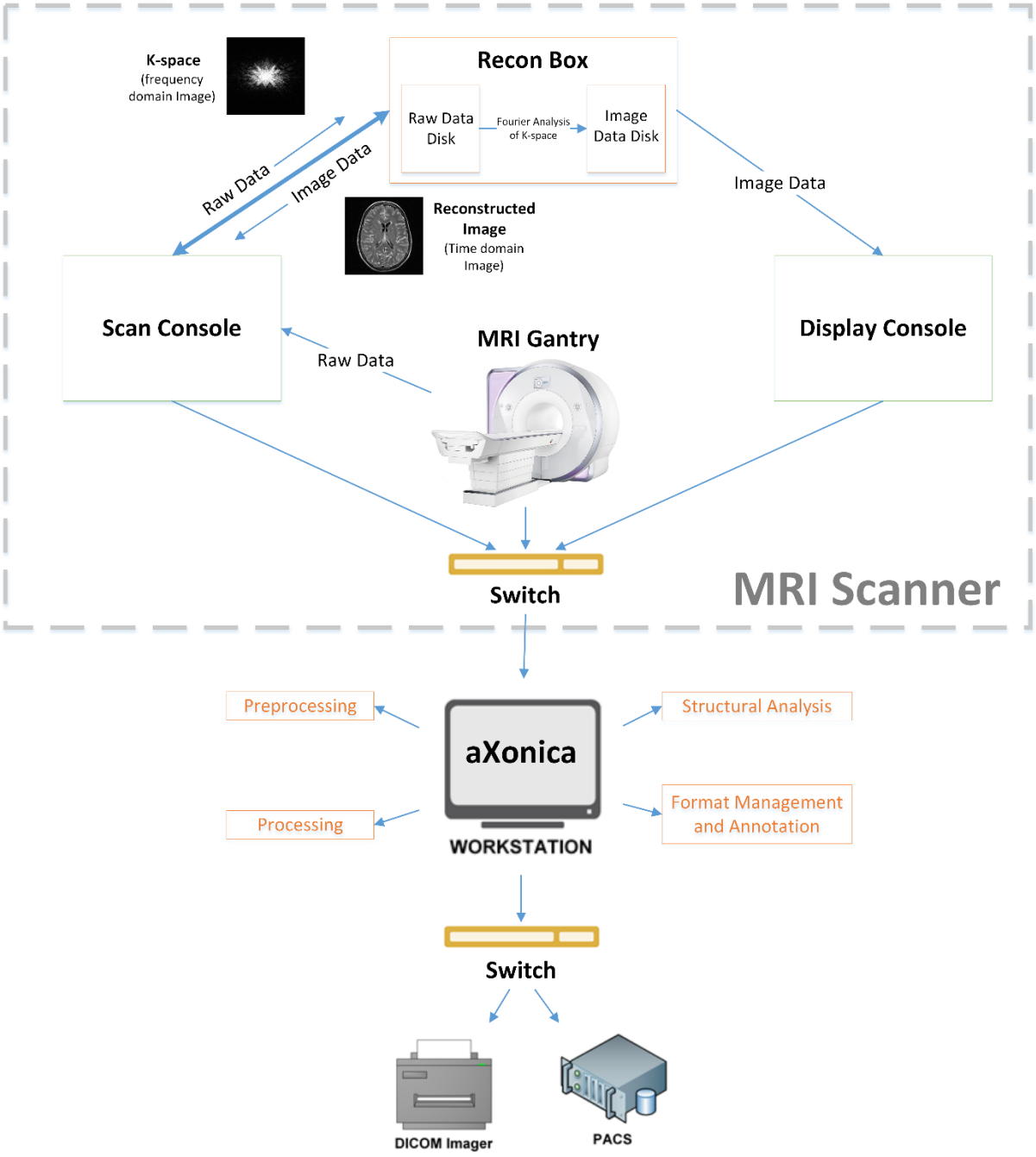


Figure 1: MRI network diagram

STEP 1:

In the first step, the Scan Console is given commands by the user about which part of the human body is about to be analyzed.

STEP 2:

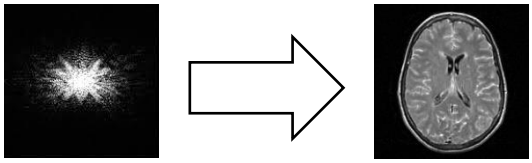
These commands are transferred to the MRI and patient data is acquired. This raw data is in K-space (frequency domain).

STEP 3:

The data is then sent to the Scan Console which further sends this data to the reconstruction box. This raw data is stored in Raw Data Disk (RDD).

STEP 4:

Inside the reconstruction box, Fourier analysis is performed on the data and thus it is converted into time domain.



The output, known as Image Data received from the transform is saved in Image Data Disk (IDD).

STEP 4:

The image data acquired from IDD is then transferred to Display Console for further processing.

STEP 6:

Now the data present in Display Console is further transferred to aXonica workstation which has all freeware tools installed in it. Any operation can be performed according to user's request.

Software Image Pipeline

MRI software base is divided into several steps. These steps are visualized using a pipeline so that the tools can be accessed according to user's needs. aXonica contains several tools from each category.

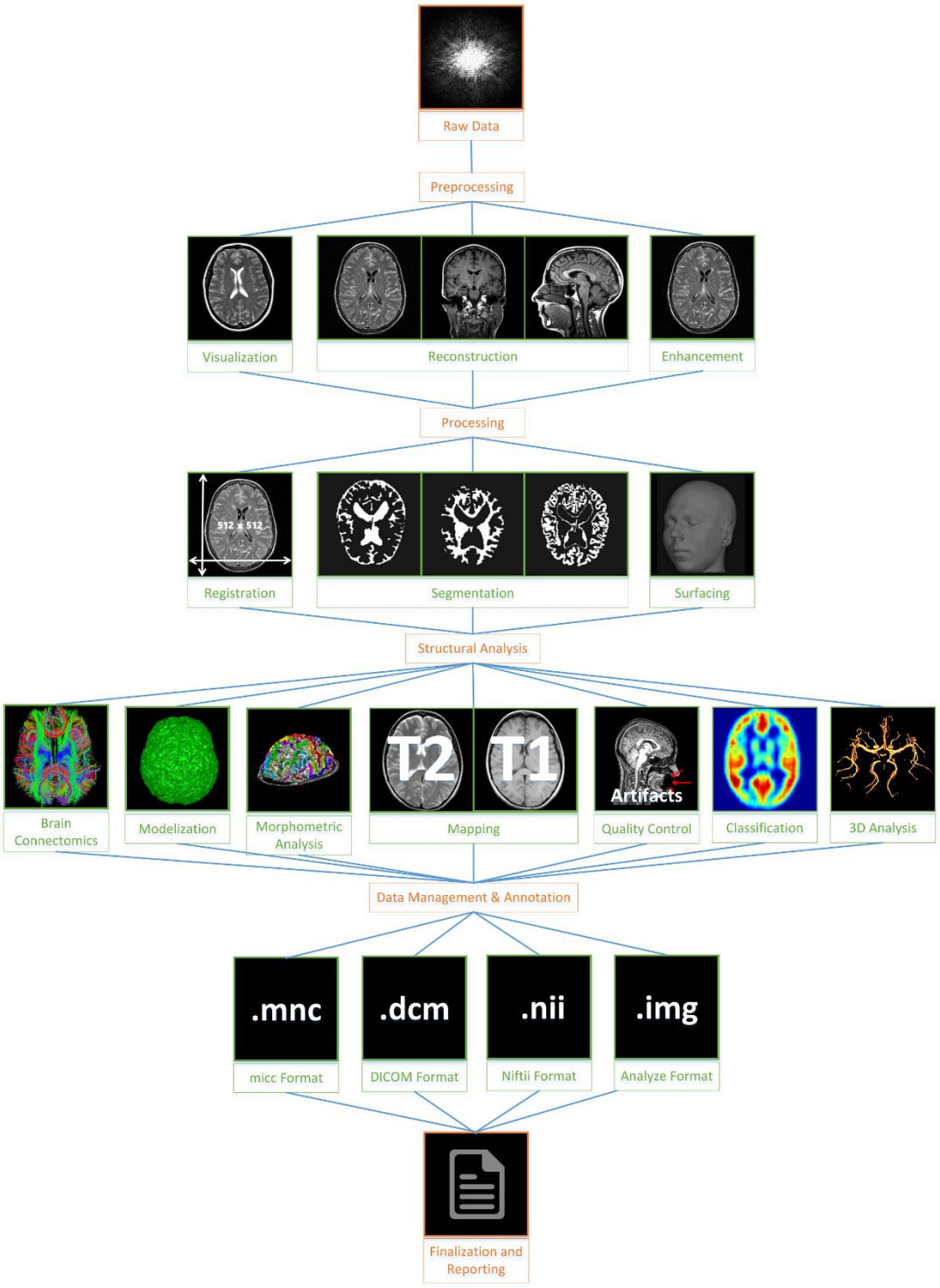


Figure 2: MRI Pipeline Visualized

Tutorial Datasets

Downloading the aXonica Tutorial Datasets

aXonica tutorial datasets is available at its website:

https://github.com/hasaniqbal777/aXonica

Tutorial Datasets shell file will be downloaded.

1. Put the tutorial datasets shell file in the already created **aXonica Resource Folder** in your drive.
2. Run the terminal and cd to the Resource folder.
3. Now run the following commands on terminal:

   > chmod +x aXonica-tutorial-datasets.sh

   > sudo bash aXonica-tutorial-datasets.sh
4. Download wizard of tutorial datasets will start.

NOTE Download tutorial datasets *require a proper internet connection to proceed, otherwise the installation terminates.*

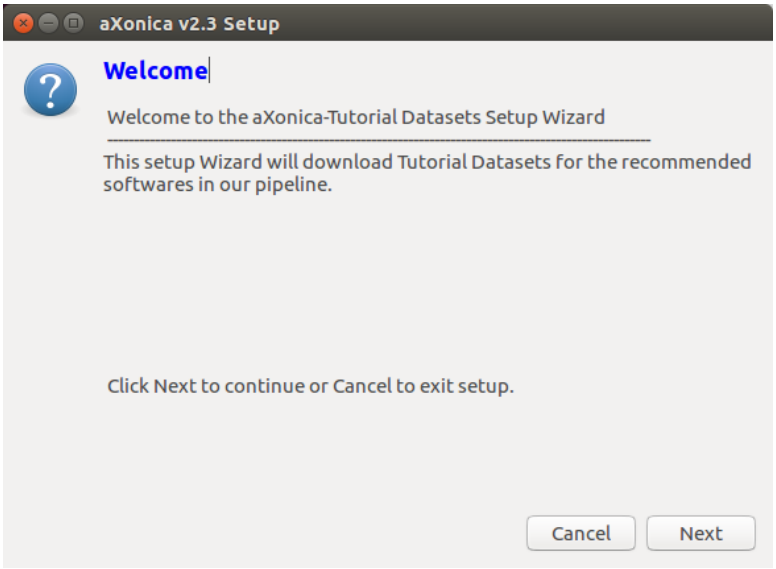


Figure 1: Welcome screen

5. Click **Next** to proceed and confirm the Internet connection.

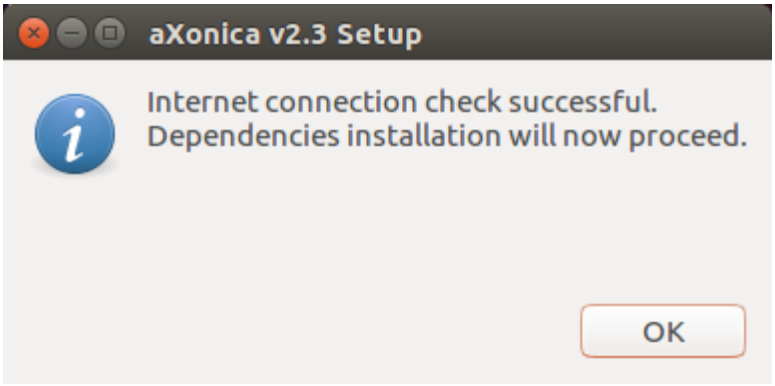


Figure 2: Internet check successful screen

6. Installation is **terminated** if there is **no internet**.

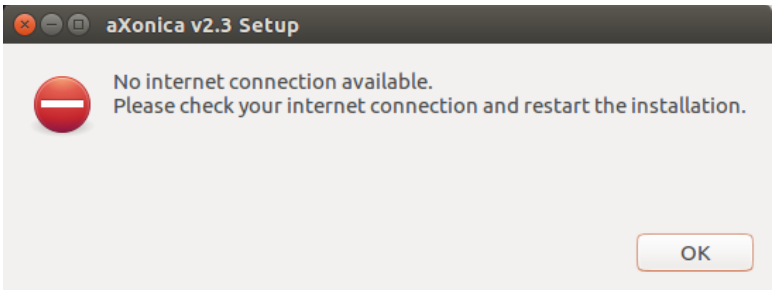


Figure 3: Internet check failed screen

7. Select the tutorial datasets you want to download.

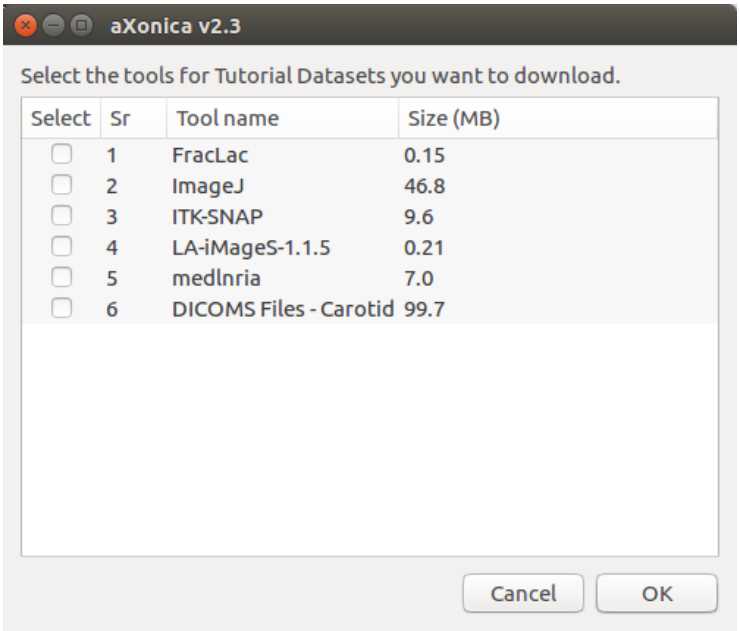


Figure 4: Tutorial Datasets selection screen

8. Click **Next** to proceed with the Download.

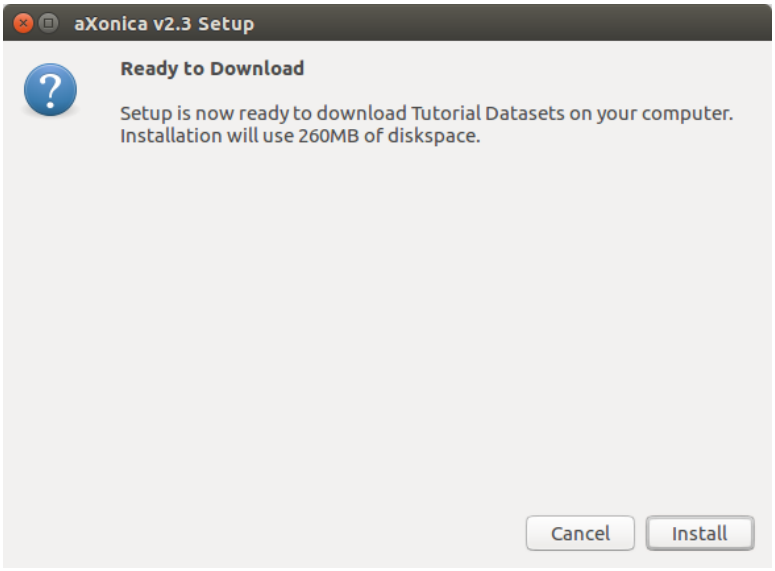


Figure 5: Ready to Download screen

9. Tools downloading will **continue**.

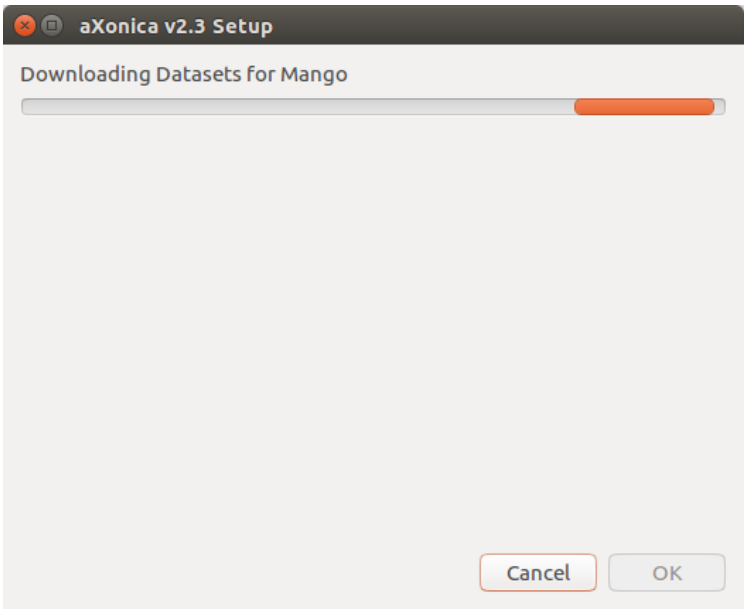


Figure 6: Download progress screen

10. Download of Tutorial Datasets is now finished. Click **Finish** to use the Tools.

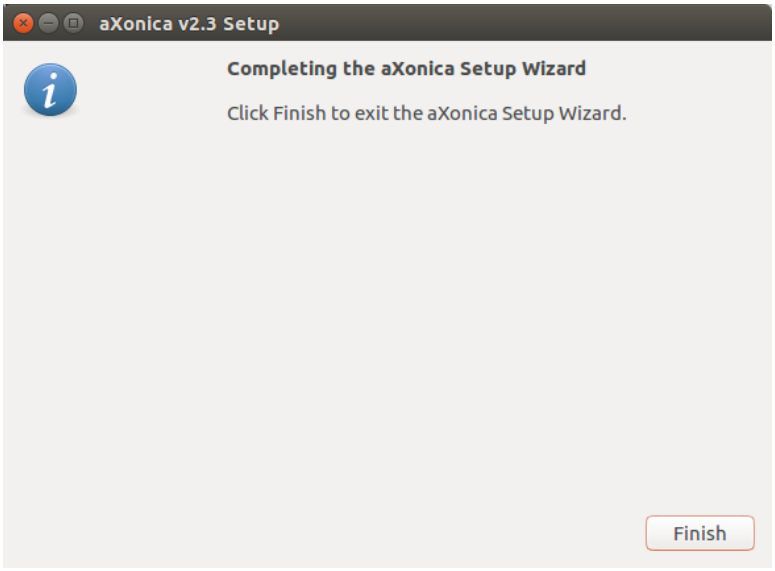


Figure 7: Finalizing Installation screen

Image Preprocessing

In this Chapter

We will learn about:

- Image Preprocessing
- Steps for Preprocessing
- Recommended tools for Preprocessing

Introduction

Pre-processing concerns the improvement of the Image Data and it enhances some image features that are important for further processing.

Image Preprocessing has three significant steps:

- Image Visualization
- Image Enhancement
- 3D Image Reconstruction

Image Visualization

Raw data is acquired from MRI Scanner. The images acquired are in the frequency domain. Specific Fourier analysis converts the "Raw Data" into "Image Data" which is in time domain. It is further pre-processed and transferred for imaging.

Recommended tool ***ImageVis3D***

ImageVis3D [1]

An architecture for Large Scale Volume Rendering: Provides domain specific visualization capabilities.

1. **Open** terminal and **run** these commands:

   > cd /usr/local/imageVis3D-3.1.0

   > ./imageVis3D

2. **Select** "Open data set from file"

Figure 1: ImageVis3D Welcome screen

3. **Load** the downloaded dataset

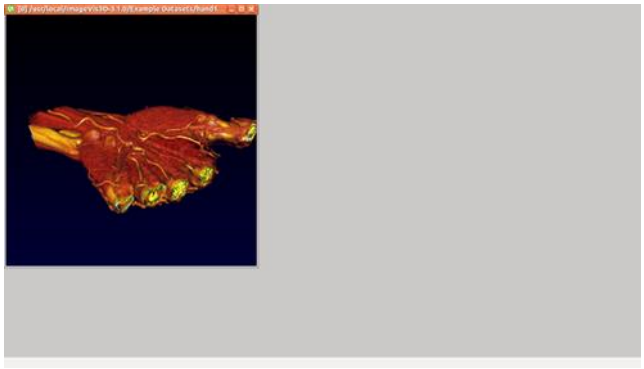


Figure 2: Visualized Image

4. Further **Analyze** the image.

Image Enhancement

Brightness of specific parts of body (e.g. Brain, Spine etc.) is adjusted so that the results are more suitable for display and further image analysis.

Recommended tool ***AMIDE***

AMIDE [2]

A Free Software Tool for Multimodality Medical Image Analysis: Displays and analyzes multimodality volumetric medical images.

1. **Run** the following commands in the terminal:

   > export UBUNTU_MENUPROXY=0

   > amide

2. AMIDE "New Study" screen opens:

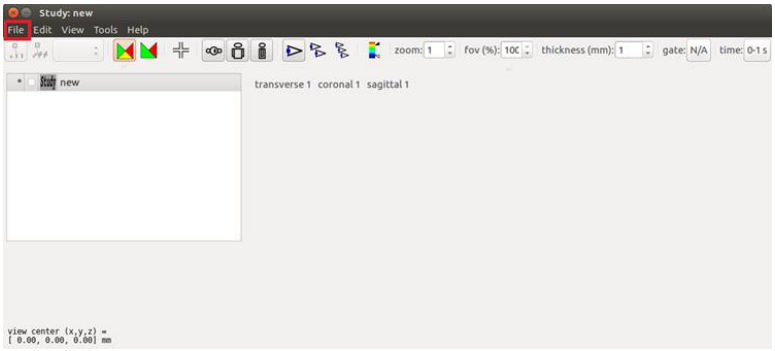


Figure 3: AMIDE Welcome screen

3. File → Open Study
4. **Load** the downloaded tutorial dataset file: *m2862-small.xif*

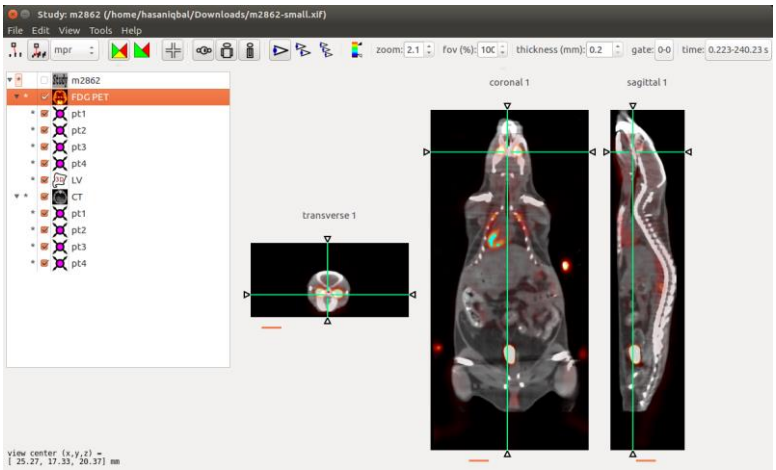


Figure 4: Enhanced Images

5. Further **Analyze** the image.

3D Image Reconstruction

Visualized images are processed and several images are aligned and converted to separate Axial, Coronal and Sagittal planes of the visualized part of body.

Recommended tool ***ITK-SNAP***

ITK-SNAP [3]

Allows users to segment structures in 3D medical images. ITK-SNAP provides semi-automatic segmentation using active contour methods, as well as manual delineation and image navigation.

1. **Run** the following commands in the terminal:

   > cd /usr/local/itksnap-3.6.0-20170401-linux-x86_64

   > cd /bin

   > ./itksnap

2. File → Open main image → Browse

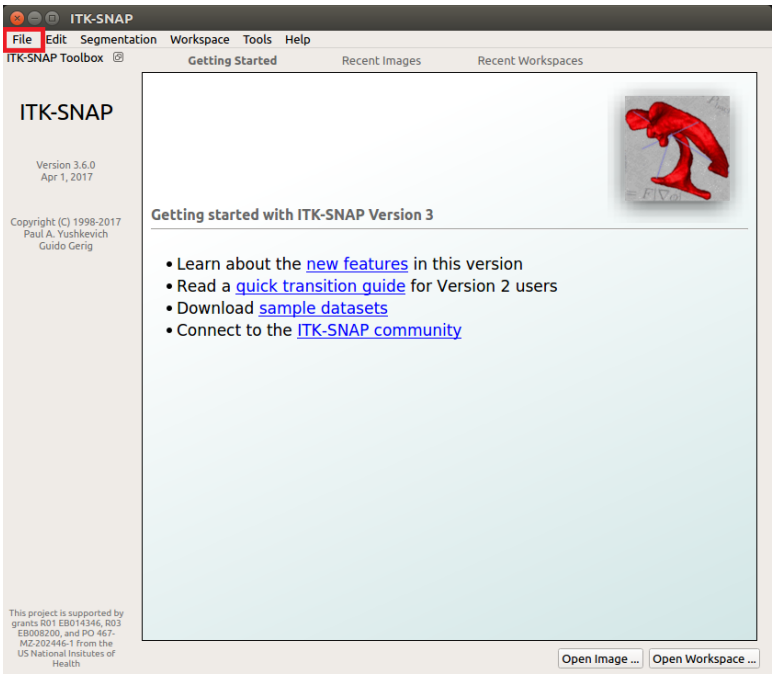


Figure 5: ITK-SNAP Welcome screen

3. **Load** data set from file:

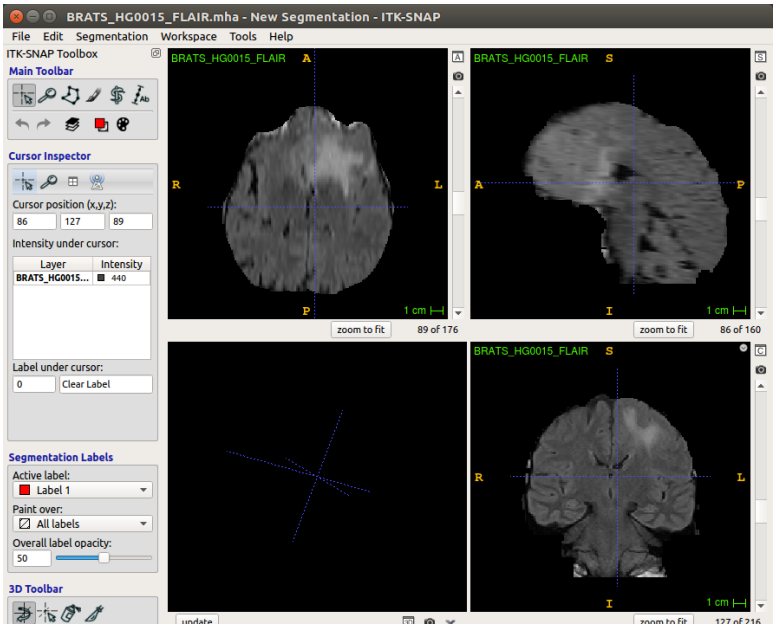


Figure 6: 3D Reconstructed Image

4. Further **Analyze** the image

Image Processing

In this Chapter

We will learn about:

- Image Processing
- Steps for Processing
- Recommended tools for Processing

Introduction

Image processing refers to processing or altering an existing image in a desired manner. Image Processing has three significant steps:

- Image Segmentation
- Image Registration
- Image Surfacing

Image Segmentation

It is a process of partitioning a digital image into multiple segments which are more meaningful and easier to analyze. For Example: A Brain MRI image is segmented into several images for visualization and analyses of gray matter, white matter and cerebrospinal fluids.

Recommended tool ***BrainSeg3D***

BrainSeg3D [4]

Provides a free volume (3D image) viewer and segmentation tool. BrainSeg3D is a graphic application that make segmentation of volumes more accurate by providing tools for semi-automated segmentation combined with a user friendly graphic interface.

1. **Run** these commands in the terminal:

   > cd /usr/local/brainseg3D

   > ./BrainSeg3D

2. **Select** 'Quick open file'

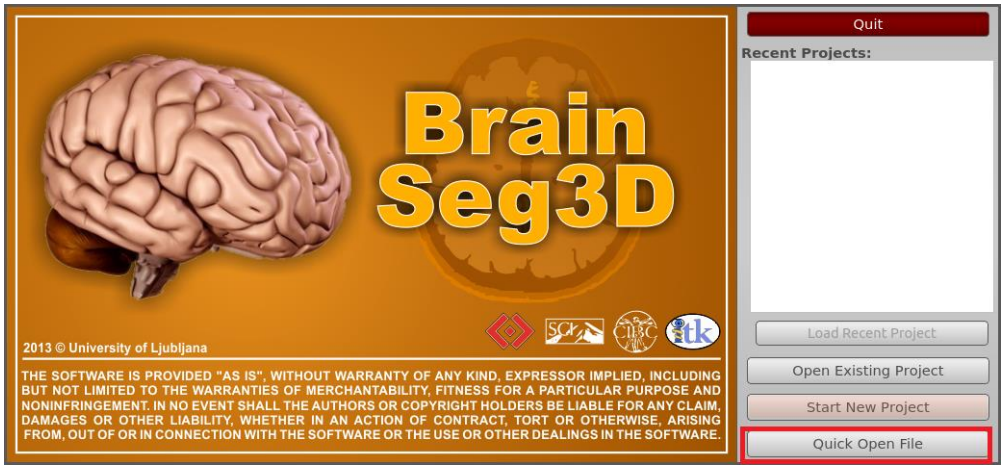


Figure 1: BrainSeg3D Welcome Screen

3. **Load** Tutorial data sets

4. **Select** all Images and Import

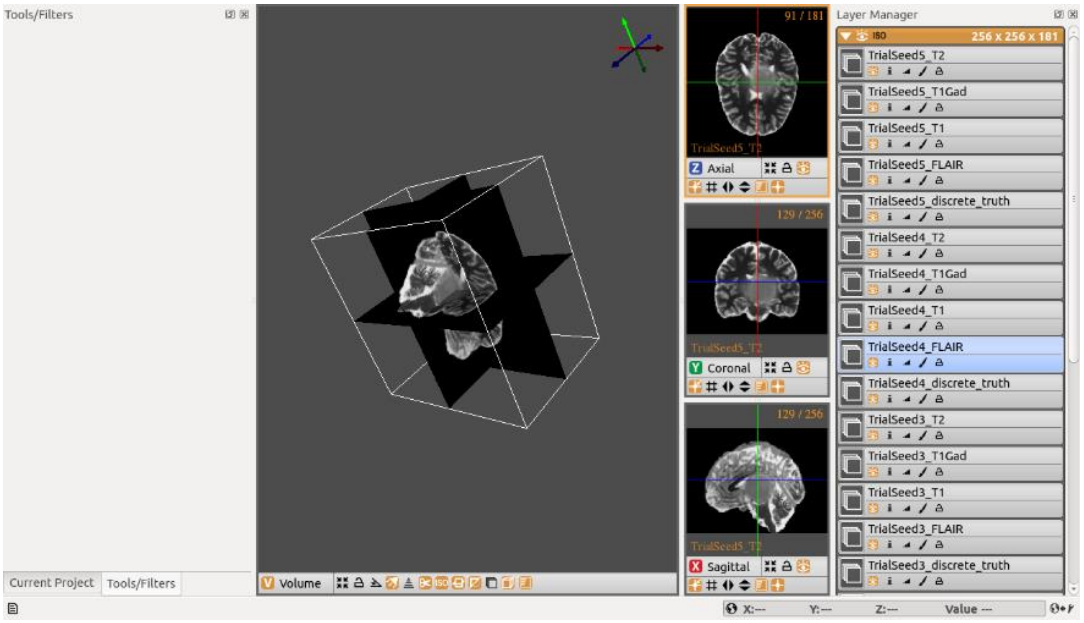


Figure 2: Segmented Image

5. Further **Analyze** the image

Image Registration

Process of transforming different sets of data into one coordinate system.

Standard Co-ordinate system for DICOM images is 512 x 512-pixel resolution. This provides a standard base for patient imaging. It is very helpful in reporting of the patient to have a standard pixel ratio.

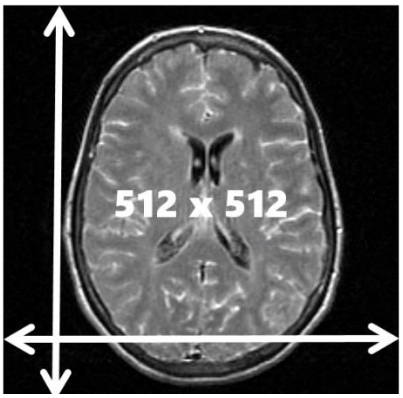


Figure 3: Image Registration

Recommended tool ***Mango***

Mango [5]

A complete data analysis pipeline that provides statistical confidence estimates for interactions and corrects for major sources of bias including differential peak enrichment and genomic proximity.

1. Run the following commands in the terminal:

   > cd /usr/local/Mango

   > ./mango

2. Select **Open**.

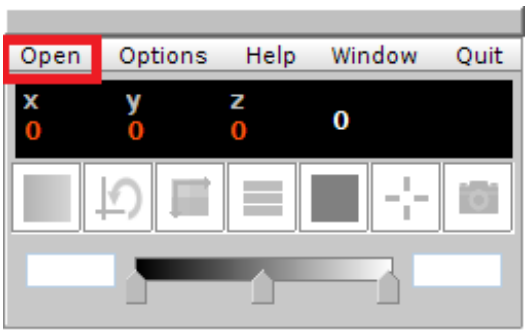


Figure 4: Mango Welcome screen

3. **Open** the Tutorial Dataset downloaded.

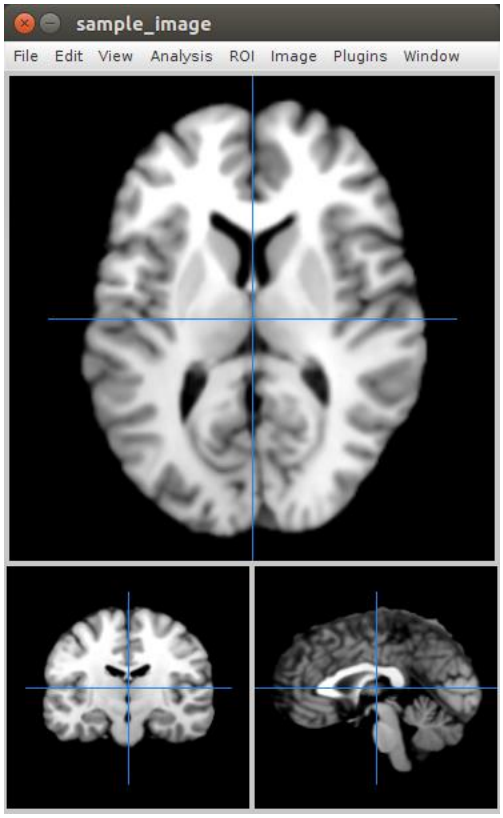


Figure 5: Registered Image

4. Further **Analyze** the image according to needs.

Image Surfacing

Process in which a 3D view of the Image Data is created and visualized.

Recommended tool ***BrainVISA***

BrainVISA [6]

Neuroimaging Research Software Hosts heterogeneous tools dedicated to neuroimaging research.

1. **Run** the following commands in the terminal:

   > cd /brainvisa-4.5.0

   > ./anatomist

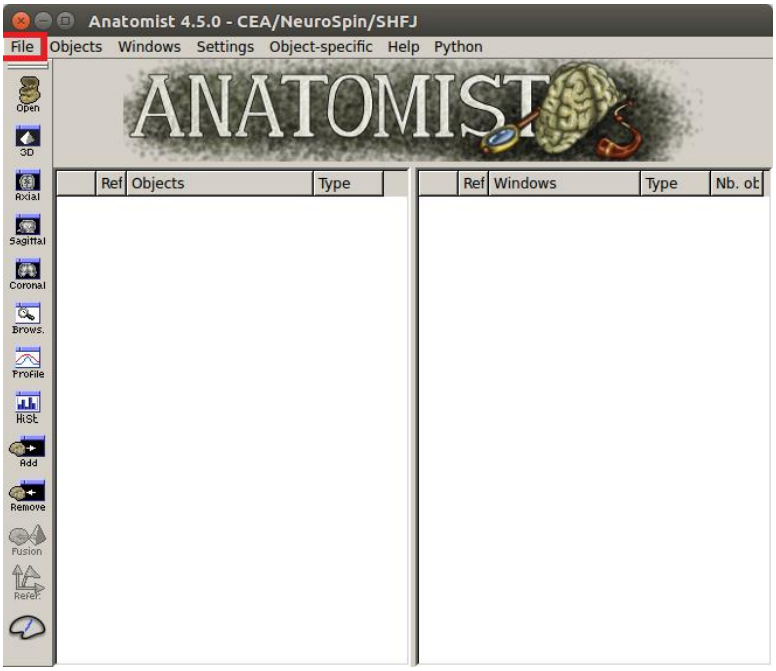


Figure 6: Anatomist Welcome screen

2. File → Open
3. **Load** the downloaded tutorial dataset file:
   - *T1 MRI: data_for_anatomist/subject01/subject01.nii*
   - *Activation map: data_for_anatomist/subject01/Audio-Video_T_map.nii*
4. **Select** the 2 objects in the object list using Ctrl + left button
5. **Click** on the fusion button

6. A new window is **displayed** which allows to select some fusion parameters.

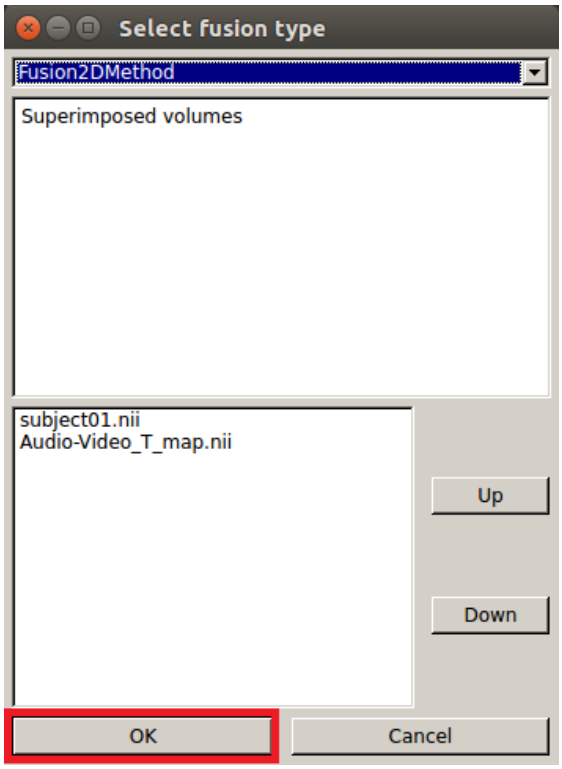


Figure 7: Fusion type selection screen

7. **Click** OK to create the fusion object

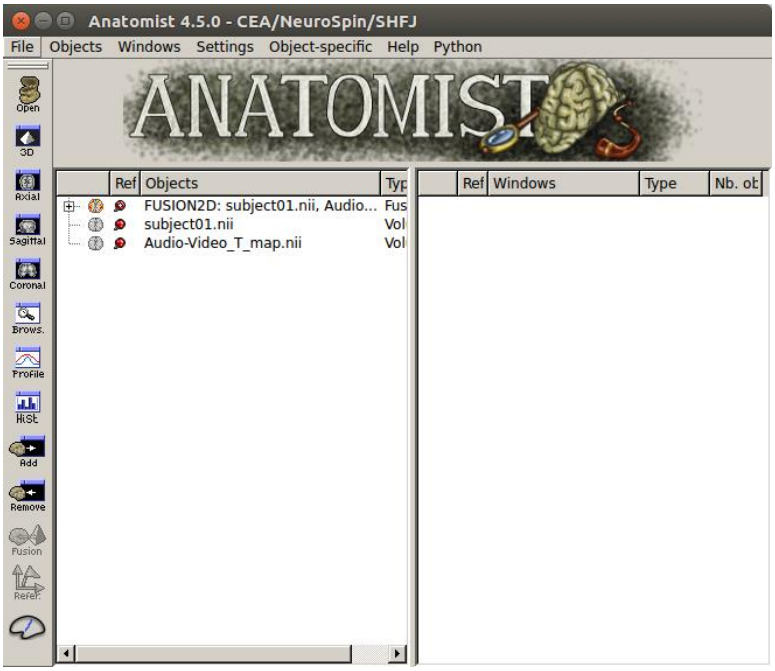


Figure 8: Fusion object screen

8. **Open** an axial window by clicking on
9. **Put** the object (the fusion volume) into this window: **drag and drop** this object into the window. Following non registered image will appear

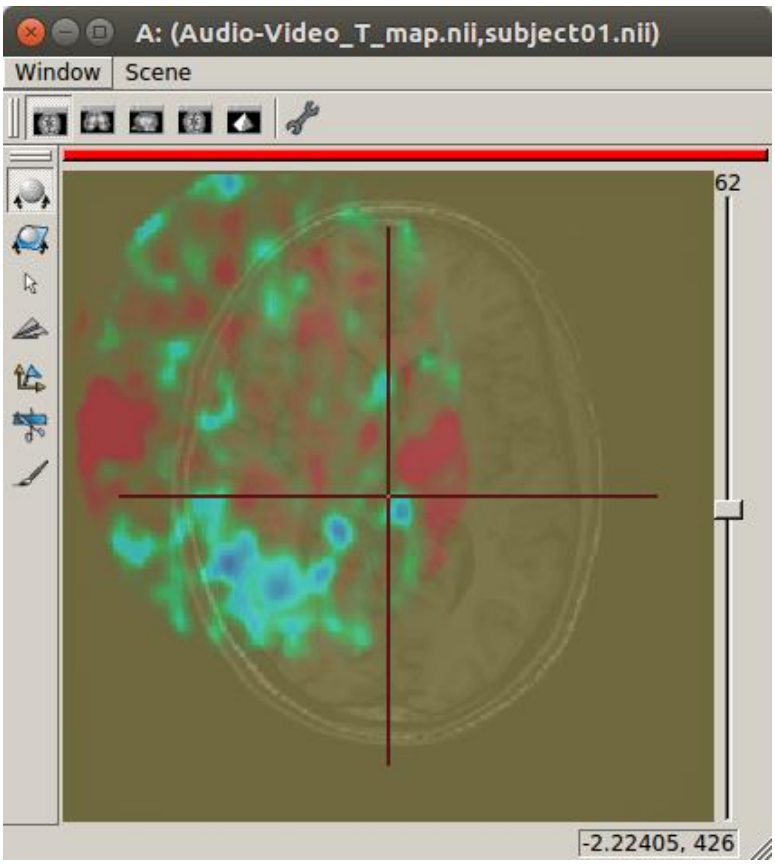


Figure 9: Fused mismatched image

10. For each volume, **right-click**.
11. Referential → Load information from file header

NOTE *The option Referential → Load information from file header extracts information about referential and transformations which are stored in the image files i.e. automatic registration.*

12. Look at the fusion, the 2 images are now well superimposed.

NOTE *Manual registration can also be done but in fact the human eye cannot drive a registration as well as a specific algorithm. For instance, images may seem aligned in an axial slice, but contain some drifts in sagittal and coronal orientations.*

Structural Analysis

In this Chapter

We will learn about:

- Structural Analysis
- Steps for Structural Analysis
- Recommended Tools for Structural Analysis of Images

Introduction

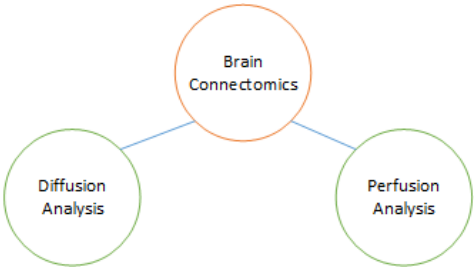
Structural analysis of an image refers to the extraction of meaningful information from the image by means of several techniques.

Structural Analysis has seven significant steps:

- Brain Connectomics
- Modelization
- Morphometric Analysis
- Quality Control
- Classification
- 3D Image Analysis
- Image Mapping

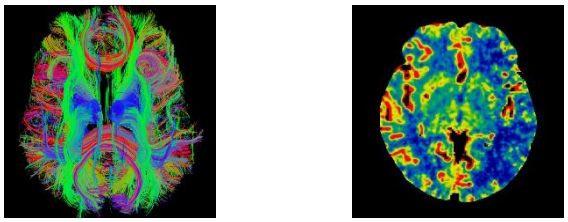
Brain Connectomics

Brain Connectomics is the production and study of connectomes. Connectomes are comprehensive maps of connections within an organism's nervous system. Brain Connectomics Analysis is divided into two types:



Diffusion Analysis is done by analyzing the diffusion of water molecules in tissues. Diffusion coefficient reduces for the cancerous tissues which is visualized.

Perfusion Analysis is done by analyzing the amount of blood taken up in certain areas of your brain. This can provide information on how your brain is functioning. Damaged areas have less oxygen and glucose use hence less blood supply which is visualized.



(a) Diffusion Analysis *(b) Perfusion Analysis*

Figure 10: Comparison Between Diffusion and Perfusion Analysis

Recommended tool ***medInria***

medInria [7]

Research and visualize medical images: medInria is a platform for the diffusion of research software in medical imaging created by medInria teams.

1. **Run** the following commands on the terminal:

   > cd/usrlocal/medinria-2.2.3-linux_x86_64

   > cd/bin

   > ./medInria_launcher.sh

2. **Select** Diffusion

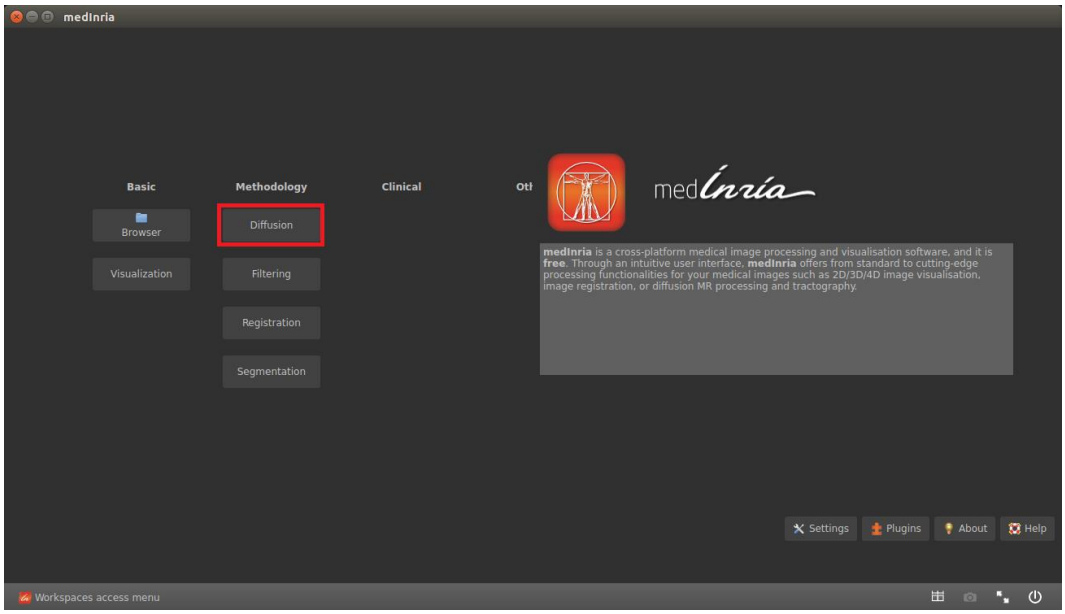


Figure 11: medInria Welcome Screen

5. **Select** "Open a file from your system".

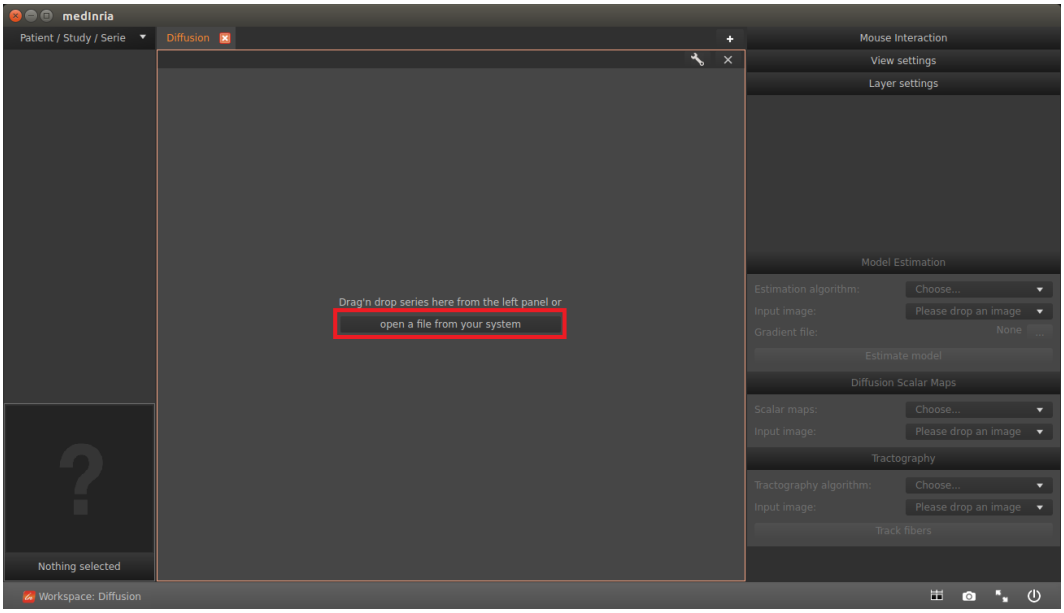


Figure 12: Load Study screen

5. **Select** the downloaded tutorial dataset file: *xDTICUBE-4D.nii.gz*

In the Model Estimation tab,

6. **Select** the Estimation Algorithm as DTI estimation
7. **Select** the gradient file: *gradient7.txt*

Figure 13: Model Estimation

8. **Select** Estimate model and wait for the diffusion analysis of the image

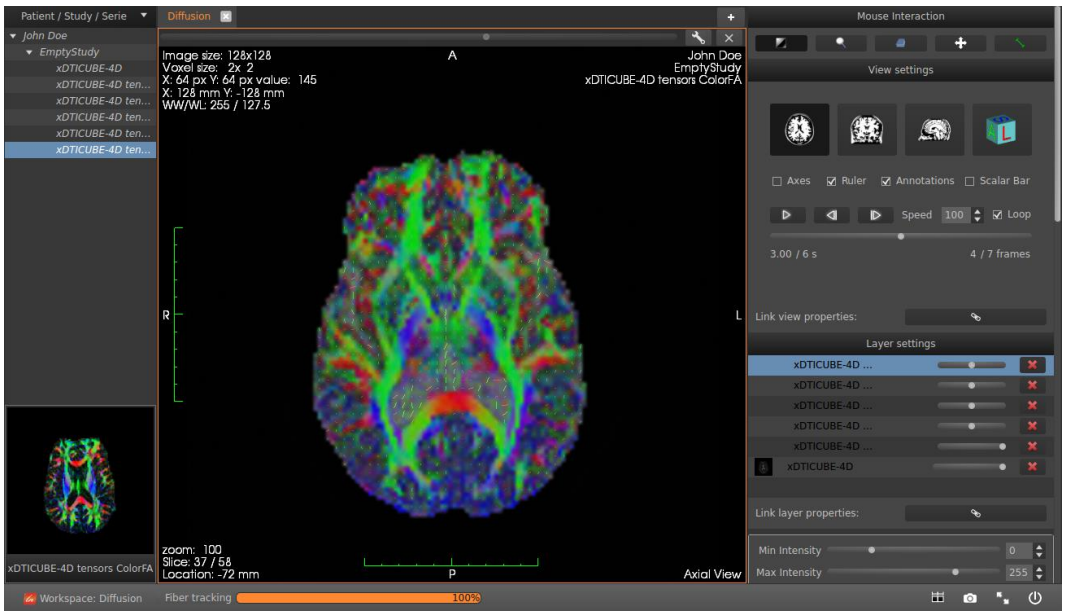


Figure 14: Diffusion Estimated Image

9. Further **Analyze** the Image according to needs.

3D Image Analysis

3D image analysis is the extraction of specific part of body from 3D visualized images which can be analyzed. For Example: 3D Analysis of Circle of Willis inside the brain.

Recommended tool ***ImageJ***

ImageJ [8]

Biological Image Analysis: Provides easy installation on arbitrary platforms and a simple user interface.

1. **Run** the following commands in the terminal:

   > cd /usr/local/ImageJ

   >./ImageJ

2. File → Open

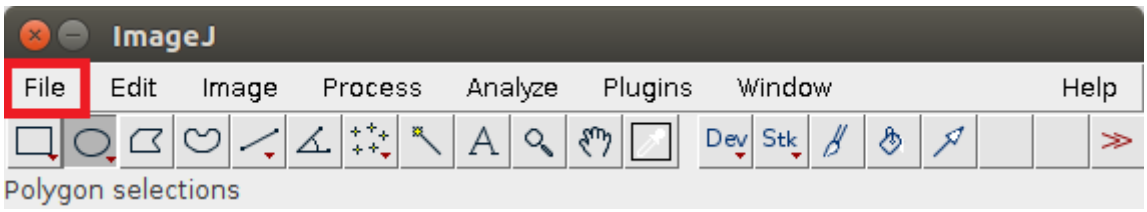


Figure 15: ImageJ Welcome Screen

3. **Select** the downloaded tutorial datasets: *t1-rendering.zip*

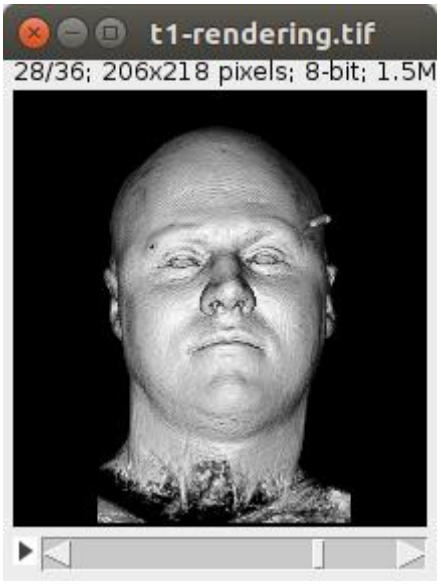


Figure 16: 3D Analyzed Image

4. Further **Analyze** the image according to needs

Morphometric Analysis

It is visualization of the outer surface of the part of body under analysis.

Recommended tool ***FracLac***

FracLac [9]

NOTE *It is an ImageJ plugin, and it is executed from ImageJ.*

1. **Run** these commands in the terminal:

   > cd ~/Package/Plugins

NOTE *This is the resource folder of aXonica-master where the tools are downloaded.*

   > sudo cp Frac_Lac.jar /usr/local/ImageJ/plugins

NOTE *Provide the password for administrator.*

   > cd /usr/local/ImageJ

   > ./ImageJ

2. File → Open

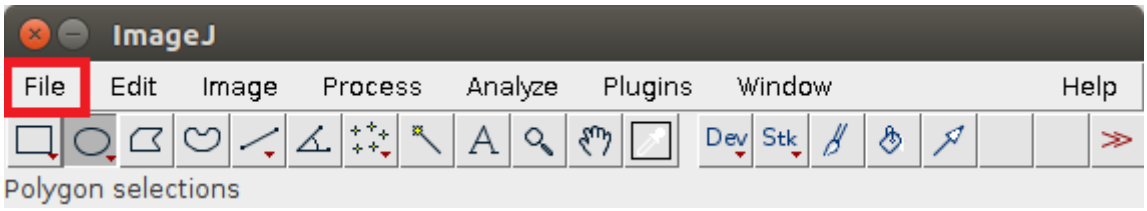


Figure 17: ImageJ Welcome Screen

3. **Select** the downloaded tutorial datasets: testimage.gif

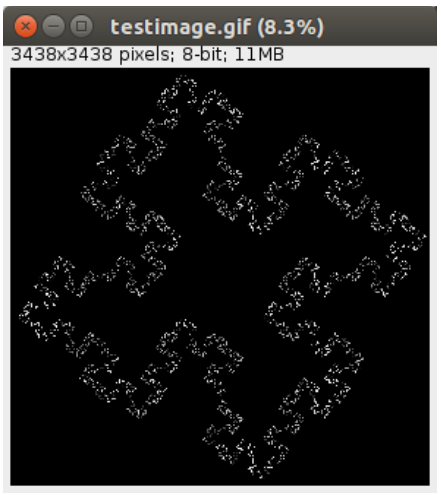


Figure 18: Sample Image

3. **Select** "BC"

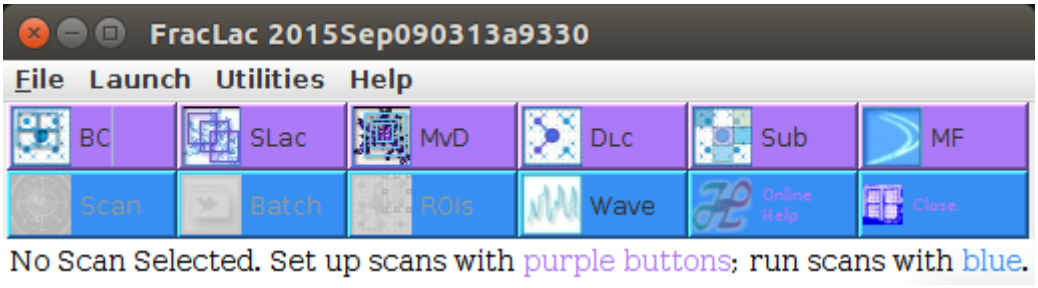


Figure 19: FracLac Welcome screen

4. **Select** OK

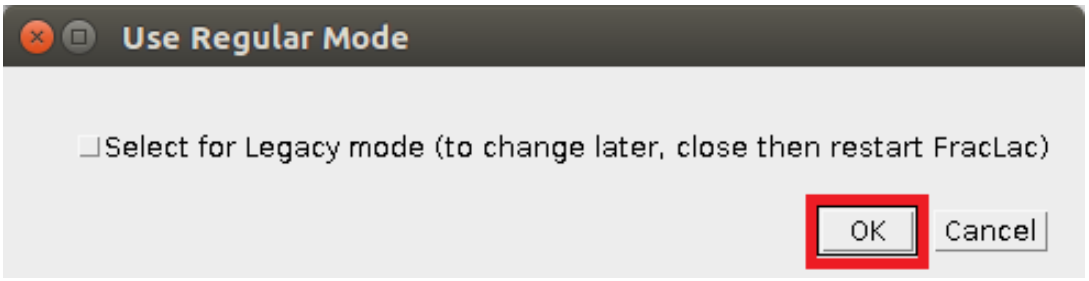


Figure 20: Mode Selection

5. **Select** OK

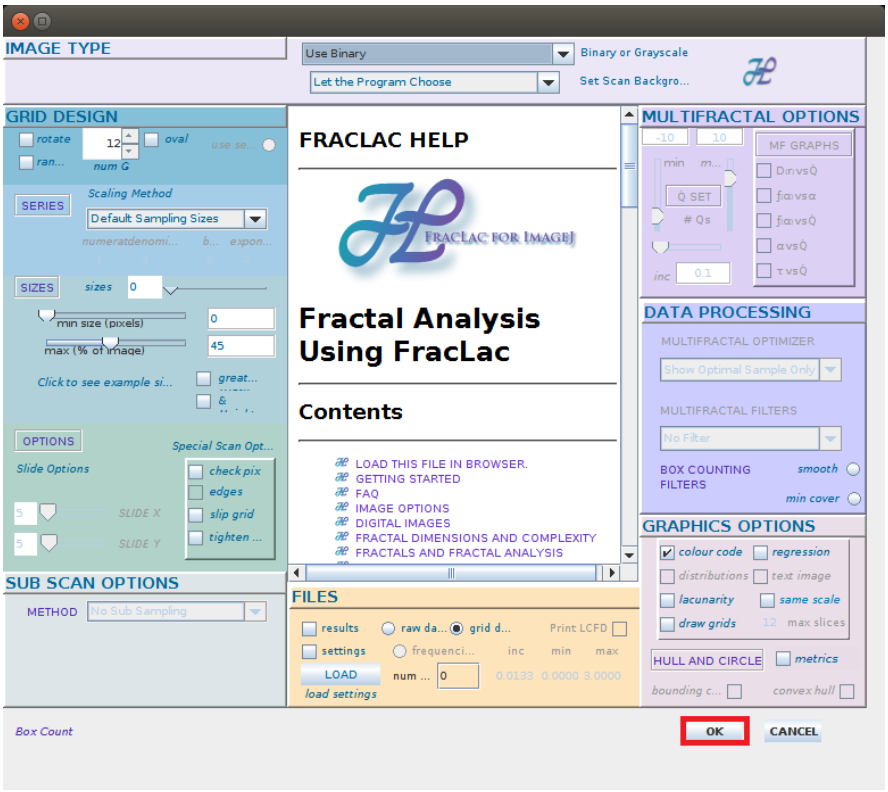


Figure 21: FracLac settings screen

6. **Select** OK

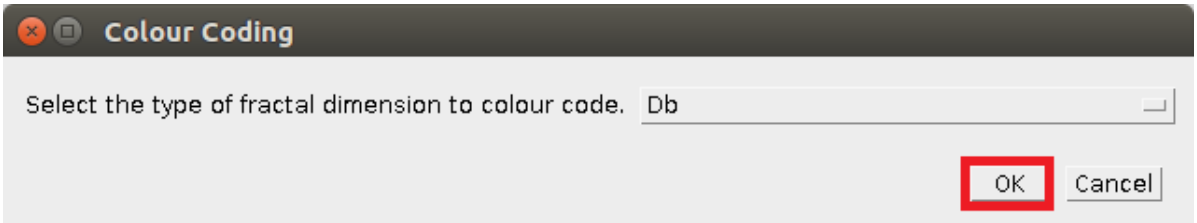


Figure 22 Colour Coding Selection screen

7. **Select** Scan

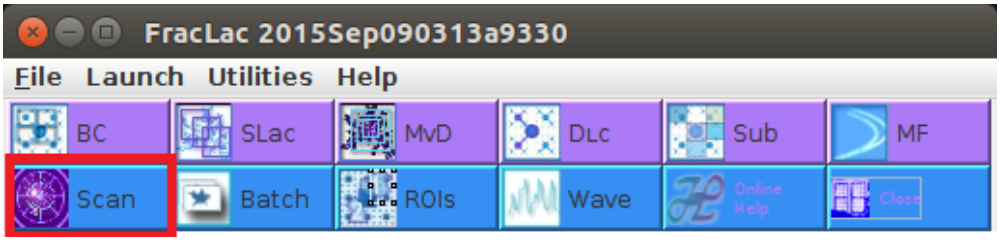


Figure: 23 Ready to scan

NOTE *Wait for the image to be processed.*

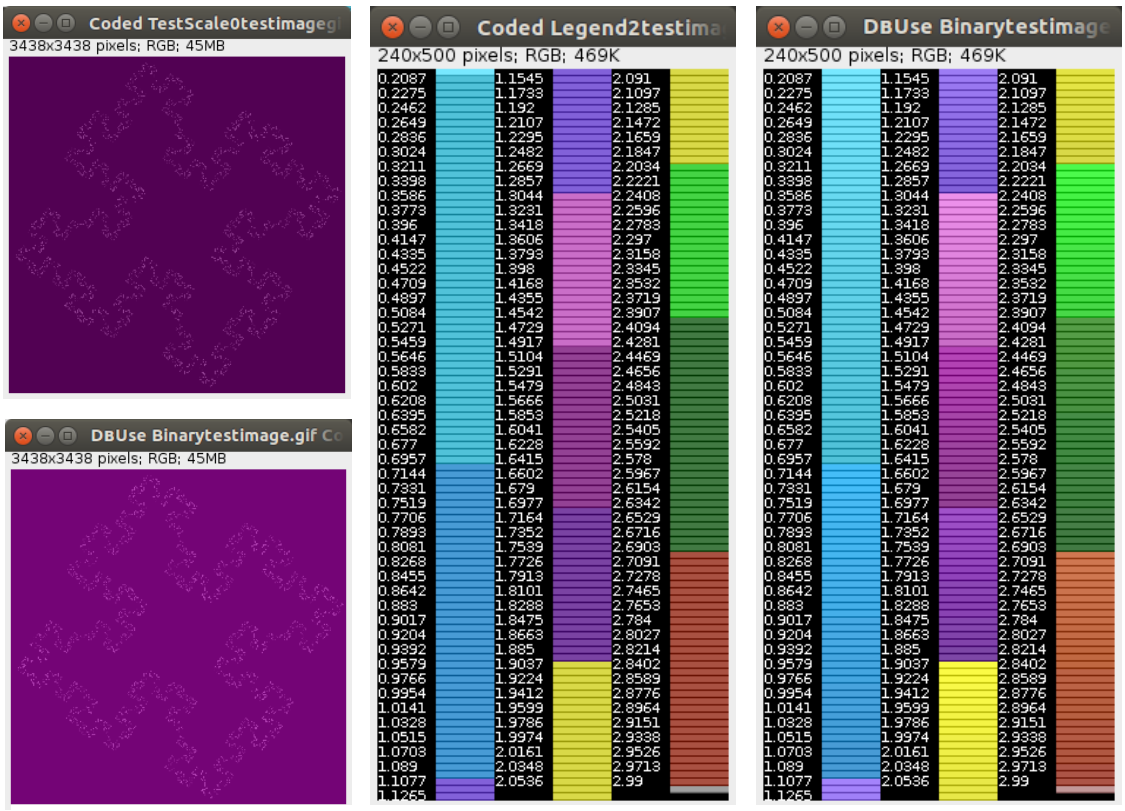


Figure 24: Analyzed Image

8. Further **Analyze** the image according to needs.

Image Classification

Different types of tumors and diseases are classified separately in this step.

Recommended tool ***LA-iMageS***

LA-iMageS [10]

A software for elemental distribution bioimaging: Provides easy installation on arbitrary platforms and a simple user interface.

1. **Run** the following commands in the terminal:

   > cd /usr/local/LA-iMageS-1.1.5

   > ./run.sh

2. **Select** data directory of downloaded tutorial datasets:

   /coin

   /seed

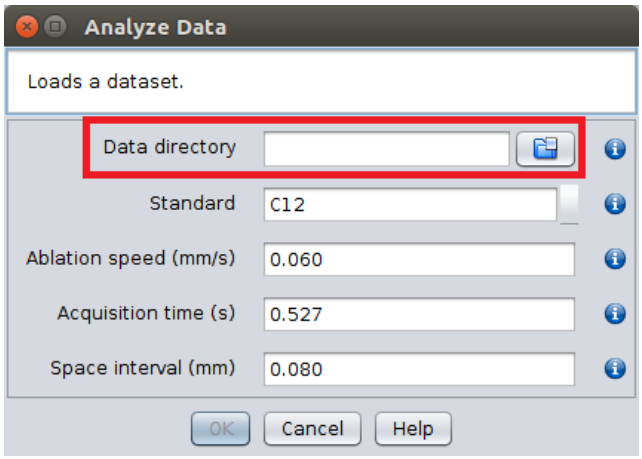


Figure 25: Load Dataset screen

3. **Select** OK.

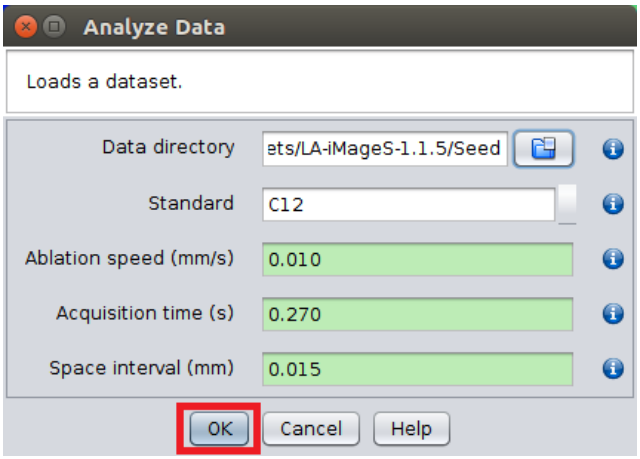


Figure 26: Analyze the Images

NOTE *Wait for the image to be processed.*

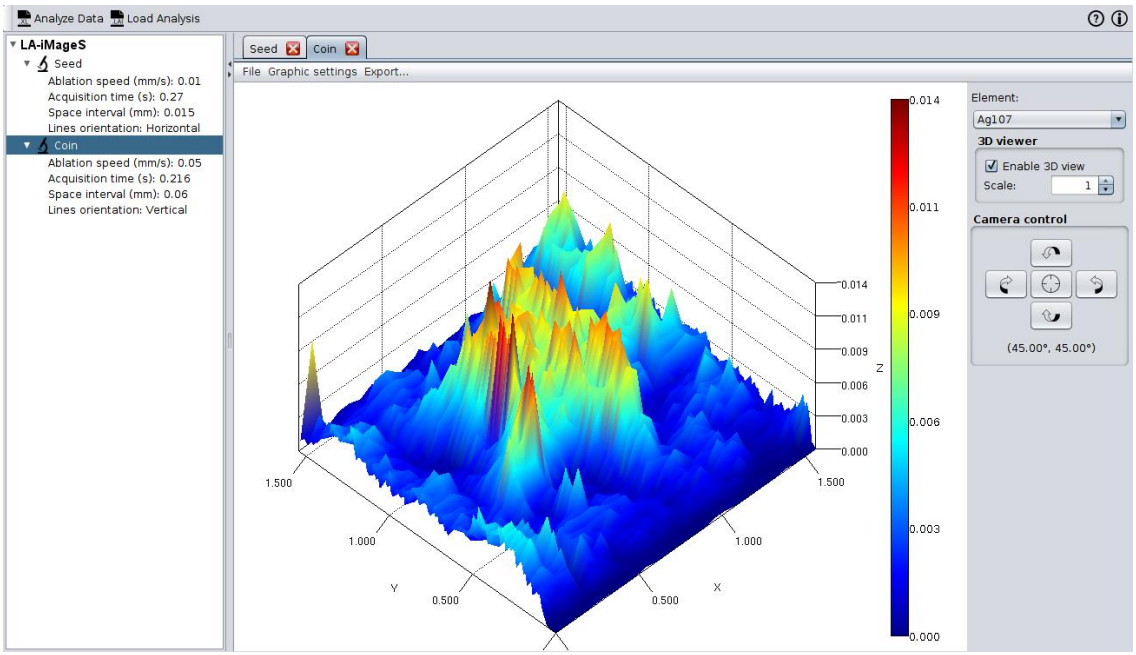
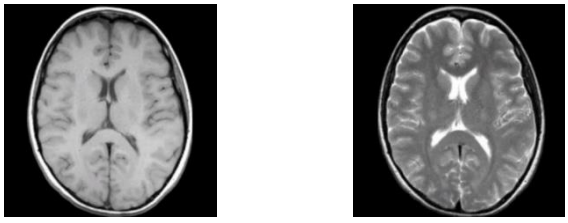


Figure 27: Analysed Image

4. Further **Analyze** the image.

Image Mapping

Optimization of images according to T1-weighted and T2-weighted images standards. In T1 images only fat is bright while in T2 images both fat and water is bright. Both of these standards are used for specific analysis.



(a) T1 weighted image *(b) T2 weighted image*

Figure 28: Comparison Between T1 and T2 weighted images

Recommended tool ***MRI Processor***

MRI Processor [11]

Computes parametric maps in magnetic resonance (MR) images: MRI Processor provides different mechanisms to distinguish different tissues and disease processes.

NOTE *It is an ImageJ plugin, and it is executed from ImageJ.*

1. **Run** these commands in the terminal:

   > cd ~/Package/Plugins

NOTE *This is the resource folder of aXonica-master where the tools are downloaded.*

   > sudo cp mri_processor_.jar /usr/local/ImageJ/plugins

NOTE *Provide the password for administrator.*

   > cd /usr/local/ImageJ

   > ./ImageJ

2. File → Open

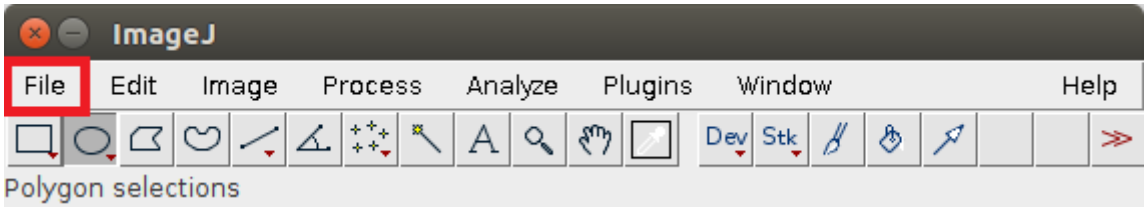


Figure 29: ImageJ Welcome Screen

3. **Select** the downloaded tutorial datasets: *subject01.nii*

Figure 30: Sample Image

4. **Select** Plugins → MRI Processor

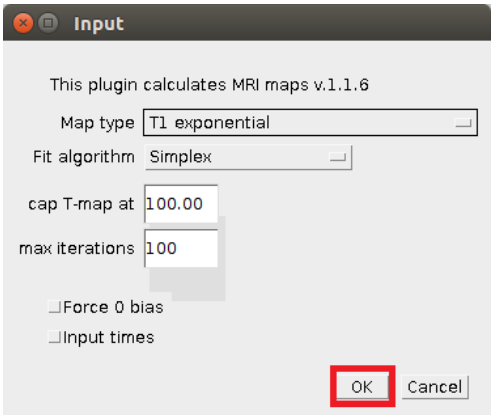


Figure 31: Mapping selection

5. **Select** Map type as T1 exponential. **Click** OK
6. Following Mapped Images appear:

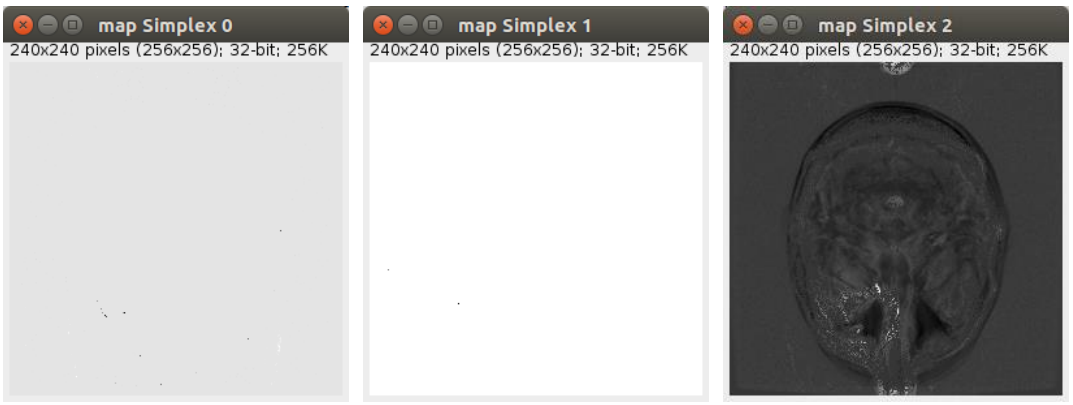


Figure 32: Mapped Images

7. Following are the Logs for Image Mapping:

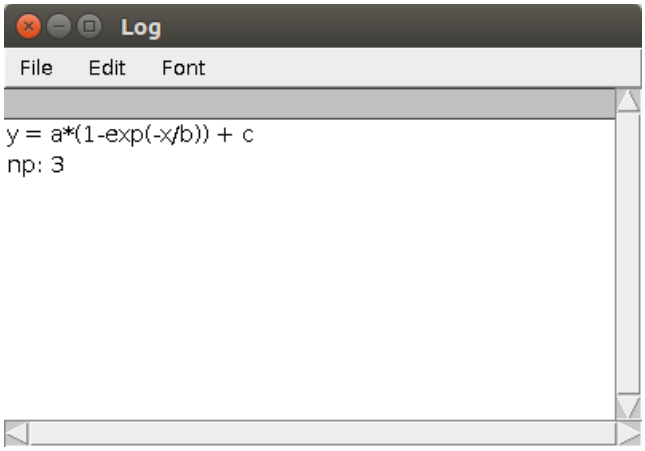


Figure 33: Mapping Logs

8. Further analyze the Image

Data Management and Annotation

In this Chapter

We will learn about:

- Data Management and Annotation
- Steps for Data Management and Annotation

Introduction

Refers to the transmission of DICOM image file over networks as well as extracting data from DICOM files and converting it to other formats.

Data Management and Annotation has two significant steps:

- Image Format Management
- DICOM File Management

Image Format Management

Concerns the transmission of DICOM image file over networks.

Recommended tool ***MRIcron***

MRIcron [12]

An image viewer for neuroimaging data: MRIcron is a platform able to support multiple layers, draw an identified region of brain injury, view data volume rendering and computes statistical results.

1. **Run** the following commands in the terminal:

   > cd/usr/local/mricron_lx

   > ./mricron

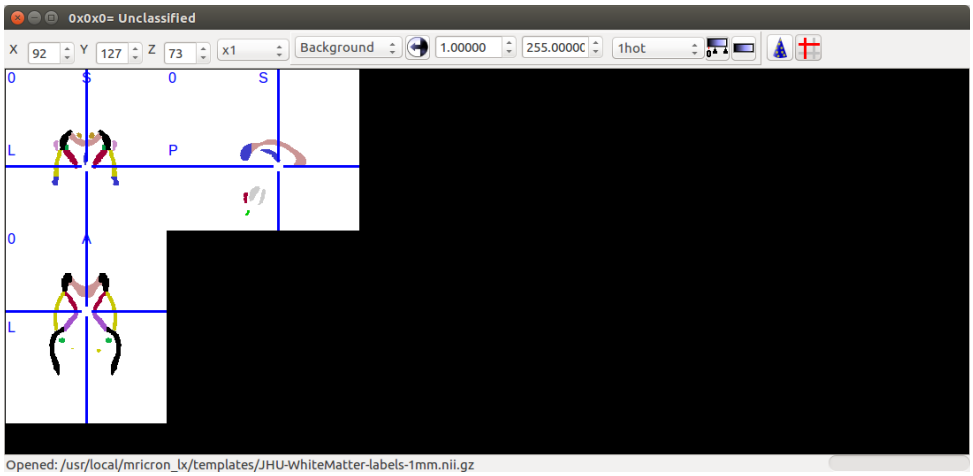


Figure 1: MRIcron Welcome screen

2. Further **Analyze** the image

NOTE *It is a demo software and it is only used to set the Data Image Formats and test them using a Reconstruction environment.*

DICOM File Management

Deals with the extraction of data from DICOM files and their conversion into other formats.

Recommended tool **WEASIS**

WEASIS [13]

Allows users to view clinical images: WEASIS is a software consisting of a multipurpose web-based viewer and dealing with digital imaging and communications in medicine (DICOM) dataset.

1. Run the following commands in the terminal:

   > cd /usr/local/weasis

   > ./viewer_linux.sh

2. File → Open → DICOM

Figure 2: WEASIS Welcome screen

3. **Provide** path for the DICOM file.

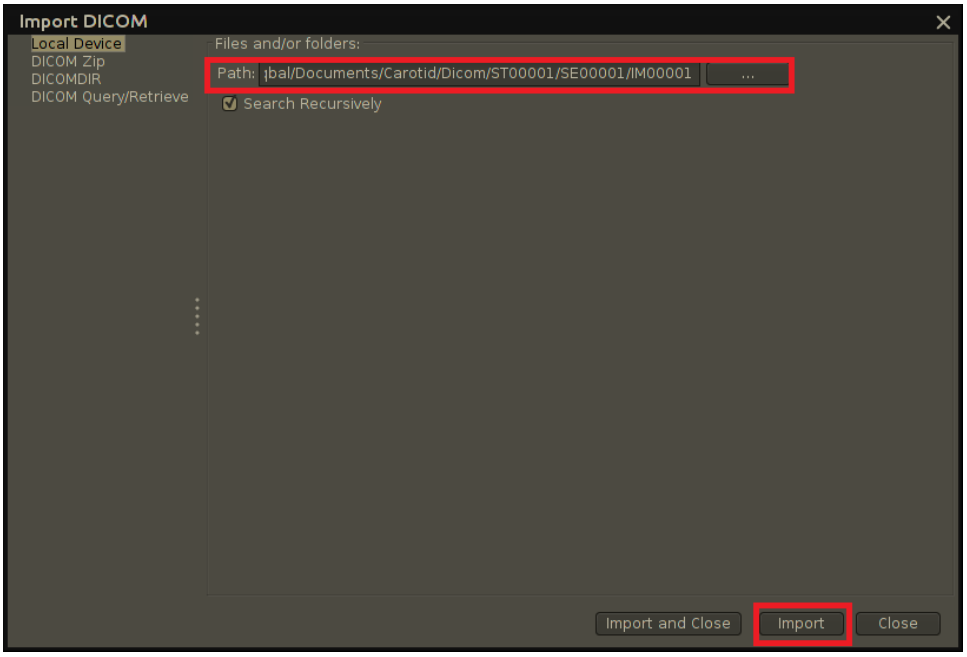


Figure 3: Import DICOM

4. **Select** "Import".

Figure 4: DICOM Image

5. Further Analyze the image.

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