# AXONICA<sup>®</sup> 3.0

## User Guide



Copyright (C) 2018, Team aXonica

#### Team aXonica, 2017-2018

Dr. Bilal Wajid Hasan Iqbal Momina Jamil Ramoona Latif Chaudhary Tayyaba Asif Arslan Khan

#### aXonica 3.0 User Guide

This program is free software: you can redistribute it and/or modify it under the terms of the **GNU General Public License** as published by the Free Software Foundation, either **version 3** of the License, or (at your option) any later version.

This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the **GNU General Public License** for more details.

You should have received a copy of the GNU General Public License along with this program. If not, see:

https://www.gnu.org/licenses/

#### Disclaimer of Warranty:

THERE IS NO WARRANTY FOR THE PROGRAM, TO THE EXTENT PERMITTED BY APPLICABLE LAW. EXCEPT WHEN OTHERWISE STATED IN WRITING THE **COPYRIGHT HOLDERS AND/OR OTHER** PARTIES PROVIDE THE PROGRAM "AS IS" WITHOUT WARRANTY OF ANY KIND, EITHER EXPRESSED OR IMPLIED, INCLUDING, BUT NOT LIMITED TO, THE IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS FOR A PARTICULAR PURPOSE. THE ENTIRE RISK AS TO THE QUALITY AND PERFORMANCE OF THE PROGRAM IS WITH YOU. SHOULD THE PROGRAM PROVE DEFECTIVE, YOU ASSUME THE COST OF ALL NECESSARY SERVICING, REPAIR OR CORRECTION.

#### Limitation of Liability:

IN NO EVENT UNLESS REQUIRED BY APPLICABLE LAW OR AGREED TO IN WRITING WILL ANY COPYRIGHT HOLDER, OR ANY OTHER PARTY WHO MODIFIES AND/OR CONVEYS THE PROGRAM AS PERMITTED ABOVE, BE LIABLE TO YOU FOR DAMAGES. INCLUDING ANY GENERAL, SPECIAL, INCIDENTAL OR CONSEQUENTIAL DAMAGES ARISING OUT OF THE USE OR INABILITY TO USE THE PROGRAM (INCLUDING BUT NOT LIMITED TO LOSS OF DATA OR DATA BEING RENDERED INACCURATE OR LOSSES SUSTAINED BY YOU OR THIRD PARTIES OR A FAILURE OF THE PROGRAM TO OPERATE WITH ANY OTHER PROGRAMS), EVEN IF SUCH HOLDER OR OTHER PARTY HAS BEEN ADVISED THE OF POSSIBILITY OF SUCH DAMAGES.

## Contents

About This Guide	1
Abstract	1
Purpose	1
Intended Audience	1
Required Background	1
How This Guide is Organized	2
Contact	2
Software Installation Process	3
Installing aXonica software	3
Data Acquisition and Software Pipeline	
In this Chapter	
Introduction	
Image Data Acquisition from MRI	
Software Image Pipeline	13
Tutorial Datasets	14
Downloading aXonica Tutorial Datasets	14
Image Preprocessing	
In this Chapter	
Introduction	
Image Visualization	19
ImageVis3D [1]	19
Image Enhancement	21
AMIDE [2]	21
3D Image Reconstruction	
ITK-SNAP [3]	
Image Processing	
In this Chapter	24
Introduction	24
Image Segmentation	
BrainSeg3D [4]	
Image Registration	27
Mango [5]	27
Image Surfacing	
BrainVISA [6]	

Structural Analysis	
In this Chapter	
Introduction	
Brain Connectomics	
medInria [7]	
3D Image Analysis	
ImageJ [8]	
Morphometric Analysis	
FracLac [9]	
Image Classification	
LA-iMageS [10]	
Image Mapping	
MRI Processor [11]	
Data Management and Annotation	
In this Chapter	
Introduction	45
Image Format Management	
MRIcron [12]	
DICOM File Management	47
WEASIS [13]	
aXonica-UI Application	
In this Chapter	
Introduction	
Configuration of aXonica-UI Application	
Software Uninstallation Process	
Uninstalling aXonica software	
References	

## **About This Guide**

#### Abstract

aXonica is 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 Linux-based installation package that downloads and installs the tools related to Magnetic Resonance Imaging (MRI) as per user requirement. It also downloads the dependencies prior to the tools for which they are required. aXonica also provides an interactive user interface which is easily understandable for users unaware of UNIX-shell language.

#### Purpose

The basic purpose of this document is to provide the complete description about the installation of aXonica shell file as well as the complete working of aXonica-UI. This document also explains the complete pipeline of MRI tools; also shows how this pipeline is implemented in the installation package.

#### **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 as well as software and hardware requirements of aXonica are assumed.

### 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.
- aXonica-UI (Chapter 9) describes the step by step working of user interface.
- Software Uninstallation Process (Chapter 10) describes how to install aXonica or any specific tools.

### Contact

For any further queries and suggestions, contact us at: hasanigbal777@qmail.com

## **Software Installation Process**

### Installing aXonica software

For downloading of aXonica, visit its website:

https://github.com/hasanigbal777/aXonica

- 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-v3.0.sh

> sudo bash aXonica-v3.0.sh

4. Installation wizard of aXonica will start.

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

× • •	aXonica v2.3 Setup	
2	Welcome	
	Welcome to the aXonica v2.3 Setup Wizard	
	aXonica is an installation package for freeware Bioimaging tools mainly related to:	
	> Magnetic Resonance Imaging > Electrophysiology > Brain Connectomics aXonica implements the complete software pipeline related to Bioimaging.	
	Click Next to continue or Cancel to exit setup.	
	Cancel Next	
	Figure 1: Installation Welcome screen	

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

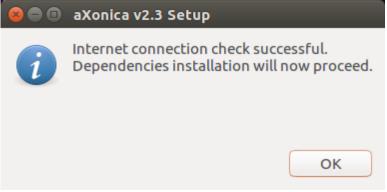


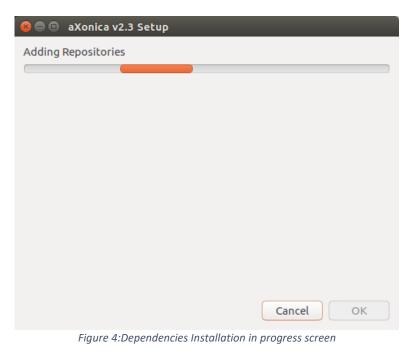
Figure 2: Internet check successful screen

6. Installation is terminated if there is no internet.



Figure 3: Internet check failed screen

7. Dependencies related to software will start installing.



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

8	aXonica v2.3 Setup
	Dependency installation is now finished.
U	Following related are installed. > JAVA JDK 8 > python > Scipy > NumPy > python-pip > PyQt4 > PyQtgraph > PyOpenGL > hSpy > nose
	Setup Installation will now proceed.

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.

	aXonica v2.3 Setup
?	Bioimaging sofware pipeline is divided into these parts: 1. Preprocessing 2. Processing 3. Structural Analysis 4. Data Management and Annotation
	The Installation will proceed in steps with some subcategories for each step.
	Every step has some recommended softwares which are selected by default. You can modify the selection if you want.
	Click Next to proceed or Cancel to exit setup.
	Cancel Next
	Figure C. Discling information concer

Figure 6: Pipeline information screen

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

80	aXonica v2.3 Setup
Ready to install	Ready to install
?	Setup is now ready to install aXonica on your computer. Installation will use at least 6-7GiB of diskspace if all the softwares are selected.
	Cancel Install

Figure 7: Ready to Install screen

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

elect	Sr	Tool name	Size (MB)
	:	***** Image viualization *****	
	1	ImageVIS_3D	30.9
	2	BoneJ	0.7
	3	DiPy	30
	:	***** Image enhancement ****	k
	4	AMIDE	40
	5	TORTOISE	751.6
	6	NormalizeFOV	732.7
	7	FastFilter3D	0.3
	8	PID	5.1
	:	** 3D Image Reconstruction **	
	9	ITK-SNAP	45.2

Figure 8: Preprocessing tools selection screen

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

Select	Sr	Tool name	Size (MB)
		***** Segmentation ****	
0	1	-	
0	-	Segmentator	1.7
	2	pyClusterROI	0.4
	3	BeAst	1.96
	4	ITK	88
	5	HeteroscedasticfMRI	0.19
	6	CMP-BIA	0.1
	7	E-Snake	0.1
	8	BrainSeg3D	18.5
	:	***** Registration *****	
	9	Mango	67
	10	bunwarpJ	0.2
	:	***** Surfacing *****	
	11	Projo//ICA	1100

Figure 9: Processing tools selection screen

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

1	8 🖨 🗊	aXon	ica v2.3	
	Select t	he too	ls for Structural Analysis you wa	ant to install.
	Select	Sr	Tool name	Size (MB)
		:	**** Brain Connectomics ****	
		1	HagaEtAl2017	0.1
		2	The Virtual Brain	670
		3	NEURON	8
		4	NeuroConstruct	0.4
		5	SliceMap	44
		6	Time Domain Decoding	0.5
		7	Nengo	38
		8	medInria	58
		9	BRIAN	68
		10	CBS Tools	147
		:	*** Morphometric Analysis ***	
		11	Gwyddion	50
		17	Fractian	12.0
				Cancel OK

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**.

800	aXo	nica v2.3	
Select t	he too	ols for Data Management and Anno	otation you want to install.
Select	Sr	Tool name	Size (MB)
0	:	***** Format Management *****	
	1	MRIcron	24.5
	2	NiBabel	48
	:	*** DICOM File Management ***	
	3	MIPAV	134
	4	WEASIS	19
			Cancel OK

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.

8	aXonica v2.3 Se	etup			
Installin	ng ImageVIS_3D				
			Cancel	ОК	

Figure 12: Tools installation progress screen

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

৪ 😑 🗉 🛛 hasaniqbal@Hasan-PC: ~/Documents/Project - Software Package/aXonica-v2.3
Installing Tools Gtk-Message: GtkDialog mapped without a transient parent. This is discouraged. 2018-04-21 16:58:49 https://docs.google.com/uc?export=download&id=13KQqtRWu 8ZfGFNSGLtnX5XDZC7CylftD Resolving docs.google.com (docs.google.com) 216.58.208.78, 2a00:1450:4018:802
::200e Connecting to docs.google.com (docs.google.com) 216.58.208.78 :443 connected. HTTP request sent, awaiting response 302 Moved Temporarily Location: https://doc-14-8k-docs.googleusercontent.com/docs/securesc/ha0ro937gcu
c7l7deffksulhg5h7mbp1/pcepedrj48capngc3q9dutgmcavjnqia/1524304800000/01419603983 021914195/*/13KQqtRWu8ZfGFnSGLtnX5XDZC7CylftD?e=download [following] Warning: wildcards not supported in HTTP. 2018-04-21 16:59:02
esc/ha0ro937gcuc7l7deffksulhg5h7mbpl/pcepedrj48capngc3q9dutgmcavjnqta/1524304800 000/01419603983021914195/*/13KQqtRWu8ZfGFnSGLtnX5XDZC7CylftD?e=download Resolving doc-14-8k-docs.googleusercontent.com (doc-14-8k-docs.googleusercontent .com) 216.58.210.65, 2a00:1450:4018:802::2001
Connecting to doc-14-8k-docs.googleusercontent.com (doc-14-8k-docs.googleusercon tent.com)[216.58.210.65]:443 connected. HTTP request sent, awaiting response 200 OK Length: unspecified [application/gzip]
Saving to: 'ImageVis3D-3.1.0.tar.gz' ImageVis3D-3.1.0.ta [ <=> ] 291.02K 358KB/s

Figure 13: Tools downloading in background

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

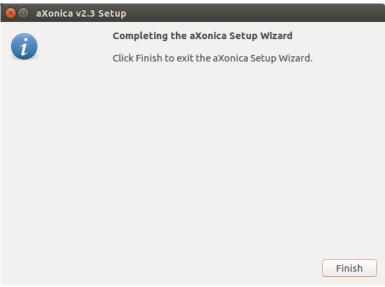


Figure 14: Finalizing Installation screen

## 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:

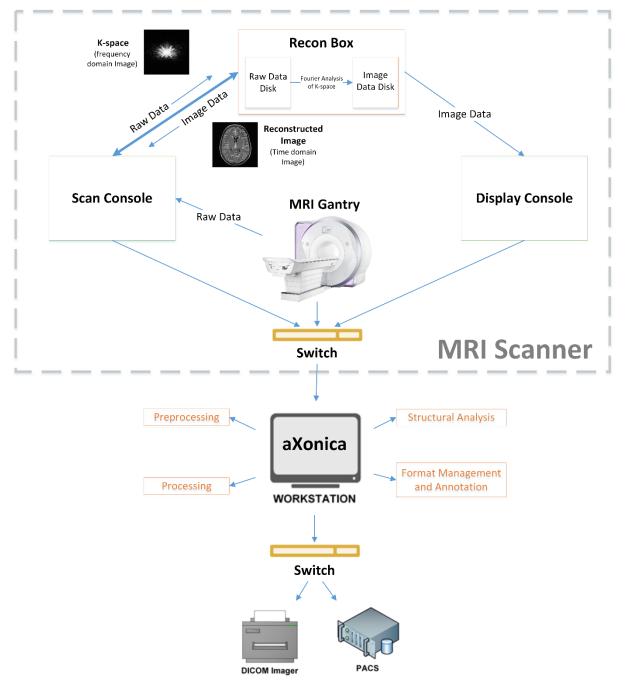


Figure 1: MRI network diagram

#### <u>STEP 1:</u>

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.

#### <u>STEP 2:</u>

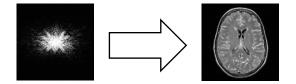
These commands are transferred to the MRI and patient data is acquired. This raw data is in K-space (frequency domain).

#### <u>STEP 3:</u>

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).

#### <u>STEP 4:</u>

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).

#### <u>STEP 4:</u>

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.

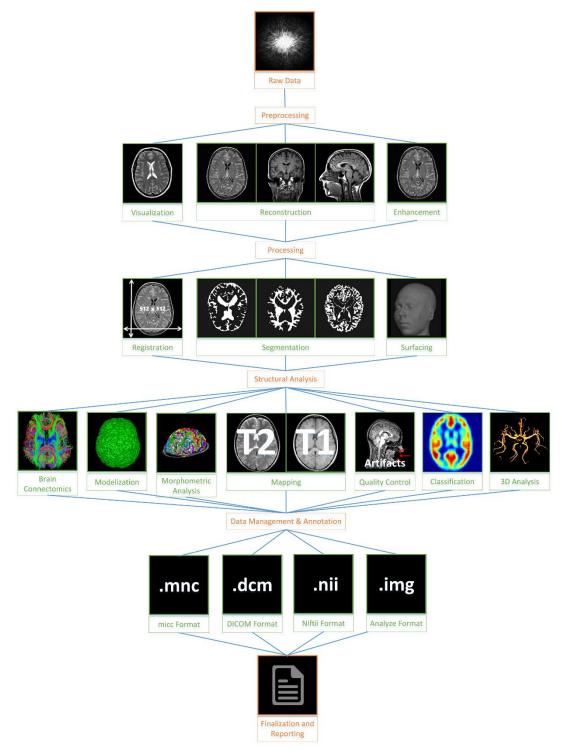


Figure 2: MRI Pipeline Visualized

## **Tutorial Datasets**

## Downloading aXonica Tutorial Datasets

aXonica tutorial datasets is available at its website:

#### https://github.com/hasaniqbal777/aXonica

- 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.

× • •	aXonica v2.3 Setup				
?	Welcome				
	Welcome to the aXonica-Tutorial Datasets Setup Wizard				
	This setup Wizard will download Tutorial Datasets for the recommended softwares in our pipeline.				
	Click Next to continue or Cancel to exit setup.				
	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**.

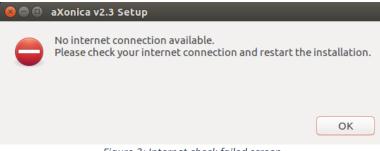


Figure 3: Internet check failed screen

7. Select the tutorial datasets you want to download.

	aXoni	ica v2.3				
Select the tools for Tutorial Datasets you want to download.						
Select	Sr	Tool name	Size (MB)			
	1	FracLac	0.15			
	2	ImageJ	46.8			
	3	ITK-SNAP	9.6			
	4	LA-iMageS-1.1.5	0.21			
	5	medlnria	7.0			
	6	DICOMS Files - Carotid	99.7			
			Cancel	ОК		

Figure 4: Tutorial Datasets selection screen

8. Click Next to proceed with the Download.

😣 🗈 aXonica v2.3 Setup			
2	Ready to Download		
?	Setup is now ready to download Tutorial Datasets on your computer. Installation will use 260MB of diskspace.		
	Cancel Install		

Figure 5: Ready to Download screen

9. Tools downloading will continue.

😣 🗈 aXonica v2.3 Setup					
Downloading Datasets for Mango					
	Cancel OK				

Figure 6: Download progress screen

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

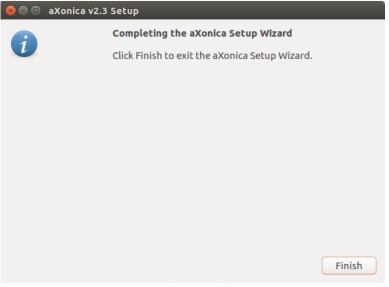


Figure 7: Finalizing Installation screen

## **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"

😣 Welcome To ImageVis3D				
VACET WEEKEN	ImageVis			
Open a File	Get Help			
Open Data Set from File	Open Local Manual			
Open Data Set from a Directory	Goto Online Help			
[]	Goto Online Video Tutorials			
	Download Example Data Sets			
hand16.uvf				
hydrogen.uvf				
tooth.uvf				
hydrogen.uvf				
hand16.uvf	Check for new Version			
Do not show this welcome screen at startup (ca	n also be changed in the preferences)			

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]

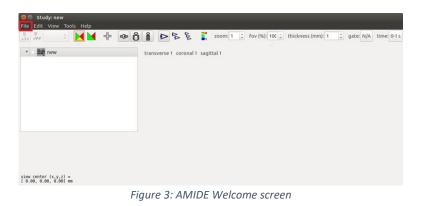
A Free Software Tool for Multimodality Medical Image Analysis: Displays and analyzes multimodality volumetric medical images.

1. Run the following commands in the terminal:

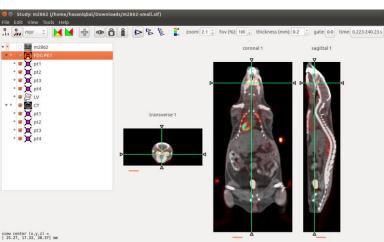
> export UBUNTU\_MENUPROXY=0

#### > amide

2. AMIDE "New Study" screen opens:



- 3. File  $\rightarrow$  Open Study
- 4. **Load** the downloaded tutorial dataset file:



m2862-small.xif

Figure 4: Enhanced Images

5. Further **Analyz**e 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 semiautomatic 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  $\rightarrow$  Open main image  $\rightarrow$  Browse

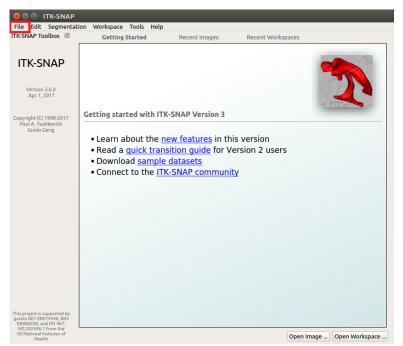


Figure 5: ITK-SNAP Welcome screen

3. Load data set from file:

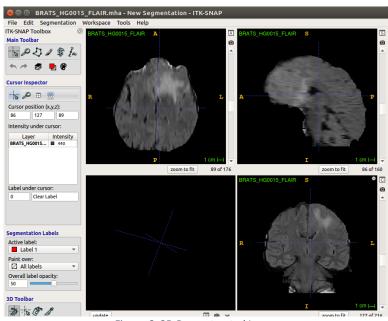


Figure 6: 3D Reconstructed Image

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'

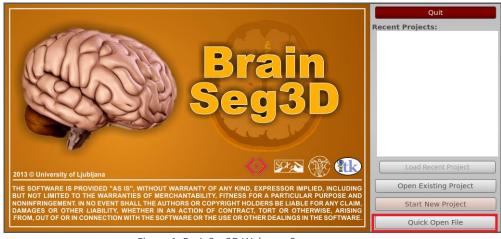


Figure 1: BrainSeg3D Welcome Screen

3. Load Tutorial data sets

#### 4. Select all Images and Import

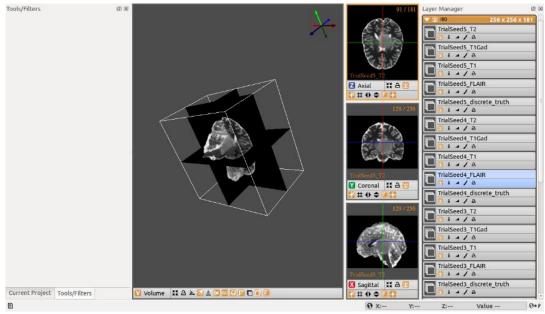


Figure 2: Segmented Image

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.

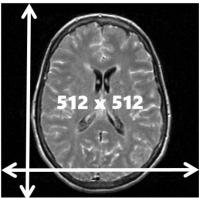


Figure 3: Image Registration

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.

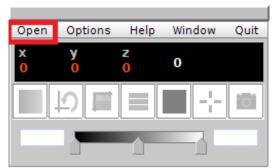
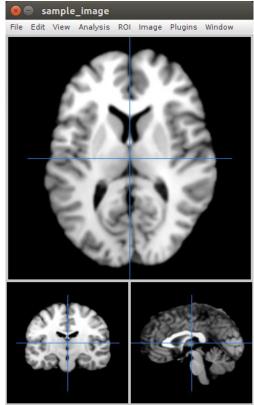


Figure 4: Mango Welcome screen



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

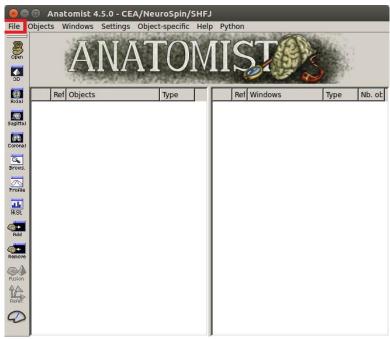


Figure 6: Anatomist Welcome screen

- 2. File  $\rightarrow$  Open
- 3. Load the downloaded tutorial dataset file:
  - T1 MRI: data\_for\_anatomist/subjectO1/subjectO1.nii
  - Activation map: data\_for\_anatomist/subjectO1/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.

😕 🖨 🔲 Select fusion 🛛	type	
Fusion2DMethod		
Superimposed volumes		
, subject01.nii Audio-Video_T_map.nii		
		Up
		Down
ОК	Ca	ncel

Figure 7: Fusion type selection screen

7. Click OK to create the fusion object

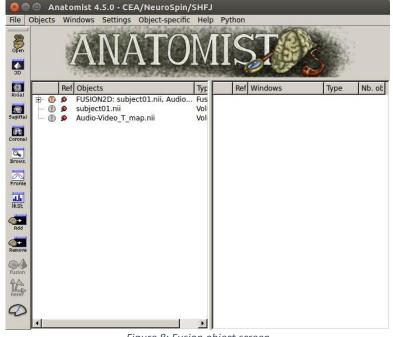


Figure 8: Fusion object screen

- 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

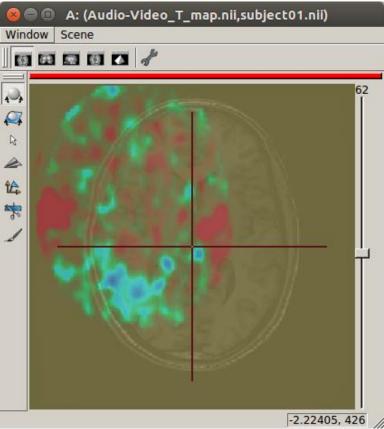


Figure 9: Fused mismatched image

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

**NOTE** The option Referential  $\rightarrow$  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

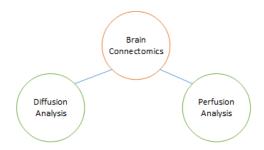
Structural analysis of an image refers to the extraction of meaningful information from the image by means of several techniques.

Structural Analysis has seven significant steps:

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

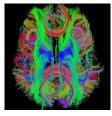
# **Brain Connectomics**

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:

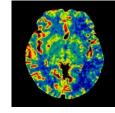


**Diffusion Analysis** is done by analyzing the diffusion of water molecules in tissues. Diffusion coefficient reduces for the cancerous tissues which is visualized.

**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

😣 🖨 🗊 med	Inria			
				• med Ínría
	Basic	Methodology	Clinical	••• (The med Inria-
	Browser			
				medinria is a cross-platform medical image processing and visualisation software, and it is free. Through an intuitive user interface, medinria offers from standard to cutting-edge
				free. Through an intuitive user interface, medInria offers from standard to cutting-edge processing functionalities for your medical images such as 2D/3D/4D image visualisation.
				processing functionalities for your medical images such as 2D/3D/4D image visualisation, image registration, or diffusion MR processing and tractography.
		Segmentation		
				🗙 Settings 📩 Plugins 🕴 About 🔅 Help
Workspace	s access menu			± ⊚ • U
- Horkspace				

Figure 11: medInria Welcome Screen

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

😣 🖻 🗊 medinria						
Patient / Study / Serie 🔻 Diffusion 🖂				Interaction		
		<b>ぺ</b> ×	View	settings		
			Layer	r settings		
			Model Estimation			
	open a file from your system					
	open a me nom jour bjoten					
			Diffusion Scalar Maps			
			Tractography			
				Choose 🔻		
				Please drop an image 🔹		
				k fibers		
Nothing selected						
💋 Workspace: Diffusion				ii 💿 🔭 🕛		

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

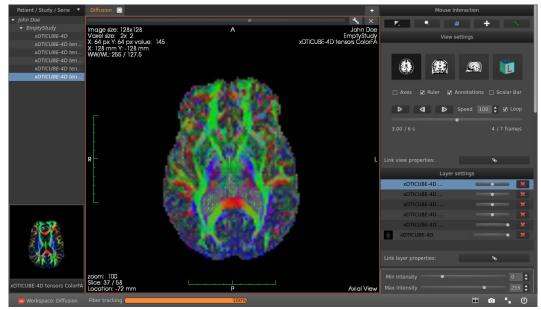


Figure 14: Diffusion Estimated Image

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  $\rightarrow$  Open

8 😑	Imag	JeJ						
File	Edit	Image	Process	Analyze	Plugins	Window		Help
	כ ב	۳ 🦯 i	∠ *** ×	ΑQ	ংশ্য 🗾	Dev Stk 🔏	8 1	≫
Polygo	Polygon selections							

Figure 15: ImageJ Welcome Screen

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

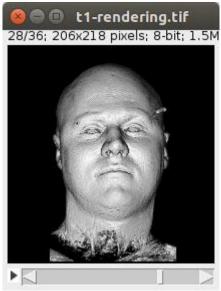


Figure 16: 3D Analyzed Image

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/lmageJ/plugins

**NOTE** *Provide the password for administrator.* 

> cd /usr/local/ImageJ

> ./ImageJ

2. File  $\rightarrow$  Open

8	Imag	geJ								
File	Edit	Image	Process	Analyze	Plugins	Window			He	elp
		∞ ⁄	∠ *** ×	ΑQ	ংশ্য 🗾	Dev Stk 🔏	8	R		≫
Polvad	n selec	tions								

Figure 17: ImageJ Welcome Screen

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



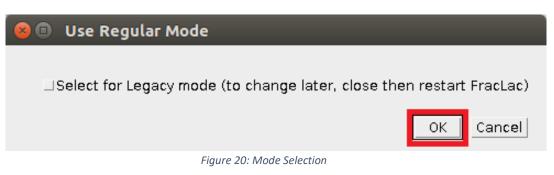
Figure 18: Sample Image

### 3. Select "BC"



No Scan Selected. Set up scans with purple buttons; run scans with blue. Figure 19: FracLac Welcome screen

### 4. Select OK

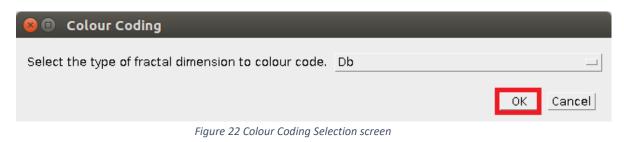


5. Select OK

80		
IMAGE TYPE		Grayscale Backgro
GRID DESIGN       ran       ran       num G       SERIES       Cefault Sampling Sizes       numeratidenomi       b       expon	FRACLAC HELP	MULTIFRACTAL OPTIONS           -10         10         MF GRAPHS           min         m         D.nvs0           § SET         foxvs0           # Qs         foxvs0            avs0           inc         0.1
SIZES sizes 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Fractal Analysis Using FracLac	DATA PROCESSING MULTIFRACTAL OPTIMIZER Show Optimal Sample Only
OPTIONS     Special Scan Opt       Slide Options     check pix       3     SLIDE X       5     SLIDE Y	#       LOAD THIS FILE IN BROWSER.         #       GETTING STARTED         #       FAQ         #       FAQ         #       FIAGE         #       FIAGE         #       FRACTAL DIMENSIONS AND COMPLEXITY         #       FRACTAL AND FRACTAL ANALYSIS	No Filter BOX COUNTING smooth O FILTERS min cover O GRAPHICS OPTIONS
SUB SCAN OPTIONS	FILES  results raw da@ grid d Print LCFD  settings frequenci inc min max LOAD num 0 0.0133 0.0000 8.0000 load settings	distributions       text image         lacunarity       same scale         draw grids       12 max slices         HULL AND CIRCLE       metrics         bounding c       convex hull
Box Count		OK

Figure 21: FracLac settings screen

### 6. Select OK



### 7. Select Scan

😣 🖻 🗉 FracLac 2015Sep090313a9330					
<u>F</u> ile Launch Utilities Help					
📆 вс	SLac	MvD	DLC	Sub	MF
Scan	💌 Batch	ROIs	MM Wave	Help	Close

Figure: 23 Ready to scan

# **NOTE** Wait for the image to be processed.

8 Coded TestScaleOtestimagegi 3438x3438 pixels; RGB; 45MB	8		gend2testima	8		narytestimage
		pixels; RGB; 4	469K	240x500	pixels; RGB; 4	469K
and the second	0.2087 0.2275 0.2462	1.1545 1.1733	2.091	0.2087 0.2275 0.2462	1.1545 1.1733	2.091 2.1097
and the second sec	0.2275	1.1733	2.091 2.1097	0.2275	1.1733	2.1097
and the second second	0.2462	1.192	2.1285	0.2462	1.192	2.1285
State & State	0.2649 0.2836 0.3024	1.2107	2.1472	0.2649 0.2836	1.2107	2.1472
	0.2836	1.2295 1.2482	2.1659 2.1847	0.2836	1.2295 1.2482	2.1659 2.1847
and service and service and the service of the serv	0.3211	1.2482	2.2034	0.3024	1.2482	2.1847
	0.3211	1.2669 1.2857	2.2234	0.3211 0.3398 0.3586	1.2857	2.2234
and the second	0.3398 0.3586 0.3773	1.3044	2 2408	0.3586	1 3044	2.2408
the standing standing the	0.3773	1.3044 1.3231	2.2596	0.3773	1.3044 1.3231	2.2596
: : : : : : : : : : : : : : : : : : :	0.396 0.4147 0.4335 0.4522	1.3418	2.2783	0.396 0.4147 0.4335 0.4522	1.3418	2.2783
1977 1977 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 1978 - 19 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 - 1979 -	0.4147	1.3606 1.3793	2.297 2.3158	0.4147	1.3606 1.3793	2.297
and the second sec	0.4335	1.3793	2.3158	0.4335	1.3793	2.3158
With Also With	0.4522	1.398	2.3345	0.4522	1.398	2.3345
	0.4709	1.4168	2.3532	0.4709	1.4168 1.4355	2.3532 2.3719
and the second second second	0.4709 0.4897 0.5084	1.4355 1.4542	2.3719 2.3907	0.4897 0.5084	1.4355	2.3719
감독 가 있는 것 같이 있는 것 같아. 이 것 같아. 이 것 같아. 이 것 같아. 아이들 가 있는 것 같아. 아이들 것 않아. 아이들 것 같아. 아이들 것 같아. 아이들 것 같아. 아이들 것 같아. 아이들 것 않아. 아이들 것 같아. 아이들 것 않아. 아이들 것 같아. 아이들 것 않아. 아이들 것	0.5084	1.4729	2.3907	0.5084	1.4542	2.3907
	0.5271 0.5459	1.4917	2.4094 2.4281	0.5271 0.5459 0.5646	1.4917	2.4281
	0.5646	1 5104	2.4469	0.5646	1.5104	2.4469
1927 C 18	0.5833	1.5291	2,4656	0.5833	1.5291	2.4656
1949 - C	0.602	1.5479	2.4656 2.4843	0.602	1.5479 1.5666	2.4843
	0.6208	1.5666	2.5031	0.6208	1.5666	2.5031
	0.5545 0.5833 0.602 0.6208 0.6395	1.5291 1.5479 1.5666 1.5853	2.5218	0.6395	1.5853	2.5218
😣 🚍 🗊 DBUse Binarytestimage.gif Co	11.6582	614	2.5405	0.6582	1.6041	2.5405
	0.677 0.6957	1.6228 1.6415	2.5592	0.677	1.6228	2.5592
3438x3438 pixels; RGB; 45MB	0.6957	1.6415	2.578 2.5967	0.6957	1.6415	2.578 2.5967
A Star	0.7144 0.7331 0.7519	1.6602	2.6154	0.7144 0.7331	1.6602 1.679	2.5367
	0.7531	1.6977	2.6342	0.7519	1.6977	2.6342
5-6 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	0.7705	1 7164	2.6529	0.7706	1.7164	2.6529
and the second	0.7706 0.7893	1.7164 1.7352	2.6716	0.7893	1.7352	2.6716
이 같은 것은 것을 많다.	0.8081 0.8268 0.8455	1 7539	2.6903	0.8081	1.7539	2.6903
and the set and	0.8268	1.7726 1.7913	2.7091	0.8268	1.7726	2.7091
The second s	0.8455	1.7913	2.7278	0.8455	1.7913	2.7278
그는 것 같아요. 그 가지 않는 것이 가지 않는 것이다.	II 8642	1.8101	2.7465	0.8642	1.8101	2.7465
and the second	0.883 0.9017	1.8288 1.8475	2.7653 2.784	0.883 0.9017	1.8288 1.8475	2.7653
the destrict the destrict of	0.9017	1.8475	2.784	0.9017	1.8475	2.784 2.8027
그 옷을 물감 없었다. 이 옷을 물감 같은 것이다.	0.9204	1.8663	2.8027	0.9204	1.8663	2.8027
2. 8	0.9392	1.885	2.8402	0.9552	1.9037	2.8402
The star was also	0.9766	1.9224	2.8589	0.9392 0.9579 0.9766	1.9224	2.8589
	0.9954	1.9412	2.8776	0.9954	1.9412	2.8776
	1.0141 1.0328	1.9412 1.9599	2.8964	0.9954 1.0141	1.9599	2.8964
The start of the start of	1.0328	1.9786	2.9151	1.0328	1.9786	2.9151
	1.0515	1.9974	2.9338	1.0515	1.9974	2.9338
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	1.0703	2.0161	2.9526	1.0703	2.0161	2.9526
Sec. 44 Sec.	1.089	2.0348	2.9713	1.089	2.0348	2.9713
	1.1077	2.0536	2.99	1.1077	2.0536	2.99
- 13 ·	140435			1494(35)		

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

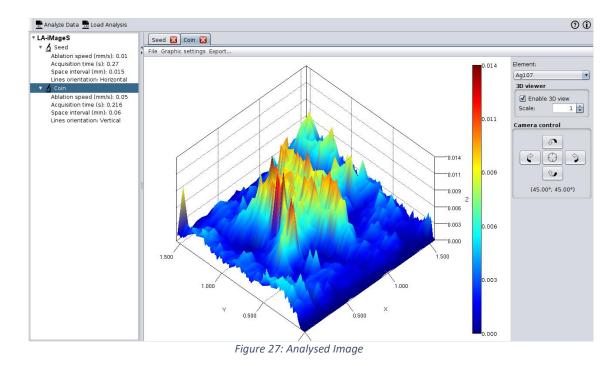
80.	Analyze Data				
Loads	Loads a dataset.				
	Data directory		0		
	Standard	C12	0		
Ablatio	on speed (mm/s)	0.060	0		
Acc	quisition time (s)	0.527	•		
Spa	ce interval (mm)	0.080	•		
OK Cancel Help					

Figure 25: Load Dataset screen

### 3. Select OK.

😣 🗊 🛛 Analyze Data				
Loads a dataset.				
Data directory	ets/LA-iMageS-1.1.5/Seed	0		
Standard	C12	0		
Ablation speed (mm/s)	0.010	•		
Acquisition time (s)	0.270	0		
Space interval (mm)	0.015	0		
OK Cancel Help				

Figure 26: Analyze the Images

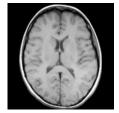


**NOTE** Wait for the image to be processed.

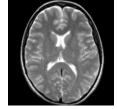
4. Further **Analyze** the image.

### 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  $\rightarrow$  Open

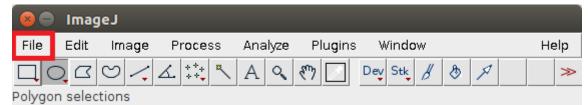


Figure 29: ImageJ Welcome Screen

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

subject01.nii



Figure 30: Sample Image

4. Select Plugins  $\rightarrow$  MRI Processor

😣 🗊 Input	
This plugin	calculates MRI maps v.1.1.6
	T1 exponential
Fit algorithm	
cap T-map at	100.00
max iterations	100
□Force 0 b	ias
⊒Input tim	es
	OK Cancel

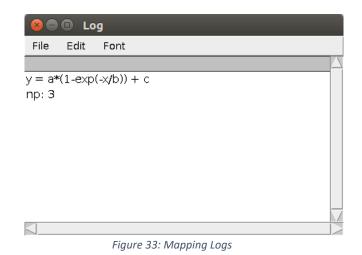
Figure 31: Mapping selection

- 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:



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

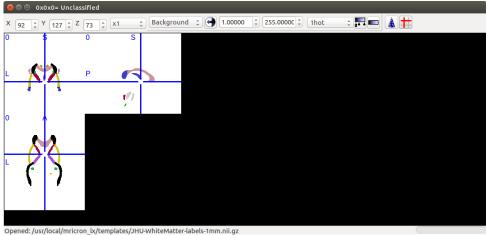


Figure 1: MRIcron Welcome screen

### 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  $\rightarrow$  Open  $\rightarrow$  DICOM



Figure 2: WEASIS Welcome screen

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

Import DICOM	×						
Local Device	Files and/or folders:						
DICOM Zip DICOMDIR	Path: tbal/Documents/Carotid/Dicom/ST00001/SE00001/IM00001						
DICOM Query/Retrieve	Search Recursively						
	Import and Close Import Close						

Figure 3: Import DICOM

4. Select "Import".

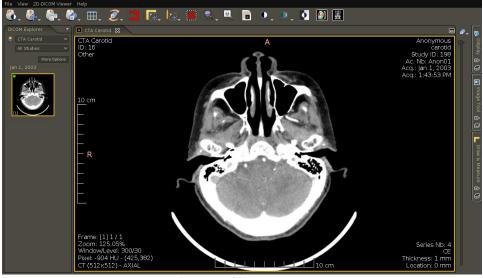


Figure 4: DICOM Image

5. Further Analyze the image.

# aXonica-UI Application

## In this Chapter

We will learn about:

- aXonica graphical user interface
- Benefits for users unware of UNIX language

### Introduction

The users who have a difficulty in understanding shell script don't have to learn anything about it because aXonica-UI provides an interactive interface for the users. It is basically developed using Qt programming that runs shell file in the background.

# Configuration of aXonica-UI Application

aXonica–UI is downloaded along with the shell file of aXonica. After installation, a desktop icon is created like this:



Figure 1: aXonica-UI desktop icon

1. **Double click** the icon. The following screen appears:

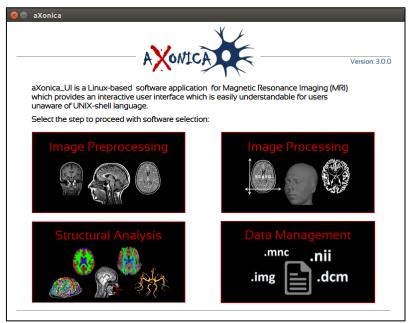


Figure 2: Main portfolio screen

2. **Click** on the category you wish to select (say Image Preprocessing). The following screen appears:

8 Preprocessing				
Select the step to proceed with software sele	ection:			
Visualization	Process of converting frequency domain raw data into time domain image data.			
Reconstruction	Process of converting the Image into Several planes.			
Enhancement	Process of adjusting the level of image for better visualization.			
€	AXONICA			
Figure 3: Sub po	ortfolio screen			

NOTE To go to the previous screen click

3. After **selecting** the required category, the following screen appears:

😣 Visualiz	ation	
	Dipy	BoneJ
	ImageVIS3D	Anatomist
	Inagevissb	Anatomist
		× L
$\mathbf{C}$		AXONICA

Figure 4:Tool selection screen

4. Click on your required software to run.

**NOTE** The buttons of the tools that were not downloaded by the user are disabled.

The procedure of running tools of other categories also proceeds in the same manner.

# **Software Uninstallation Process**

## Uninstalling aXonica software

For downloading of aXonica uninstaller, visit its website:

https://github.com/hasanigbal777/aXonica

- 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-v3.0-uninstaller.sh

> sudo bash aXonica-v3.0-uninstaller.sh

4. Uninstallation wizard of aXonica will start.

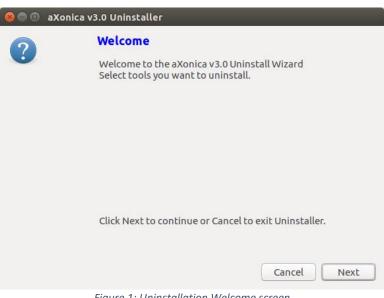


Figure 1: Uninstallation Welcome screen

**NOTE** Software which are not installed also appear in the uninstaller selection screens. Selecting/Deselecting them has no effect on uninstallation process.

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

(		aXon	ica v2.3	_
	Select the tools for Preprocessing you want to install.			
	Select	Sr	Tool name	Size (MB)
		:	***** Image viualization *****	
		1	ImageVIS_3D	30.9
		2	BoneJ	0.7
		3	DiPy	30
		:	***** Image enhancement *****	
		4	AMIDE	40
		5	TORTOISE	751.6
		6	NormalizeFOV	732.7
		7	FastFilter3D	0.3
		8	PID	5.1
		:	** 3D Image Reconstruction **	
		9	ITK-SNAP	45.2
				Cancel OK

Figure 2: Preprocessing tools selection screen

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

(		aXon	ica v2.3	
Select the tools for Processing you want to install.				
	Select	Sr	Tool name	Size (MB)
		:	***** Segmentation *****	
		1	Segmentator	1.7
		2	pyClusterROI	0.4
		3	BeAst	1.96
		4	ITK	88
		5	HeteroscedasticfMRI	0.19
		6	CMP-BIA	0.1
		7	E-Snake	0.1
		8	BrainSeg3D	18.5
		:	***** Registration *****	
		9	Mango	67
		10	bunwarpJ	0.2
		:	***** Surfacing *****	
		11	Proio\/ICA	1100
				Cancel OK

Figure 3: Processing tools selection screen

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

800	aXon	ica v2.3	
Select the tools for Structural Analysis you want to install.			
Select	Sr	Tool name	Size (MB)
	:	**** Brain Connectomics ****	
	1	HagaEtAl2017	0.1
	2	The Virtual Brain	670
	3	NEURON	8
	4	NeuroConstruct	0.4
	5	SliceMap	44
	6	Time Domain Decoding	0.5
	7	Nengo	38
	8	medInria	58
	9	BRIAN	68
	10	CBS Tools	147
	:	*** Morphometric Analysis ***	
	11	Gwyddion	50
	17	Eraclar	12 0
			Cancel OK

Figure 4: Structural Analysis tools selection screen

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

800	аХог	nica v2.3	
Select the tools for Data Management and Annotation you want to install.			
Select	Sr	Tool name	Size (MB)
	:	***** Format Management *****	
	1	MRIcron	24.5
	2	NiBabel	48
	:	*** DICOM File Management ***	
	3	MIPAV	134
	4	WEASIS	19
			Cancel OK

Figure 5: Data Management and Annotation selection screen

9. Click Next to proceed with the uninstallation.



Figure 6: Ready to uninstall screen

- 10. Tools uninstallation will continue.
- 11. Uninstallation of aXonica is now finished. Click **Finish** to continue.

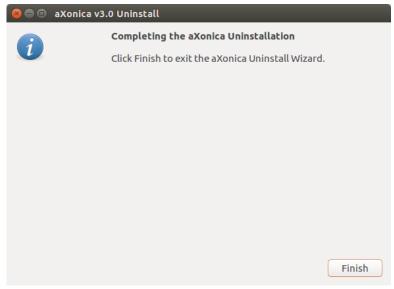


Figure 7: Finalizing Uninstallation screen

# References

- [1] T. Fogal and J. H. Kr{\"u}ger, "Tuvok, an Architecture for Large Scale Volume Rendering.," in *VMV*, 2010.
- [2] A. M. Loening and S. S. Gambhir, "AMIDE: a free software tool for multimodality medical image analysis," *Molecular imaging*, vol. 2, p. 15353500200303133, 2003.
- [3] P. A. Yushkevich, J. Piven, H. C. Hazlett, R. G. Smith, S. Ho, J. C. Gee and G. Gerig, "User-guided 3D active contour segmentation of anatomical structures: significantly improved efficiency and reliability," *Neuroimage*, vol. 31, pp. 1116-1128, 2006.
- [4] Z. Lesjak, A. Galimzianova, B. Likar, F. Pernus and Z. Spiclin, "Increased accuracy and reproducibility of MS lesion volume quantification by using publicly available BrainSeg3D image analysis software," in *MULTIPLE SCLEROSIS JOURNAL*, 2015.
- [5] J. L. Lancaster, A. R. Laird, S. B. Eickhoff, M. J. Martinez, P. M. Fox and P. T. Fox, "Automated regional behavioral analysis for human brain images," *Frontiers in neuroinformatics*, vol. 6, p. 23, 2012.
- [6] Y. Cointepas, J.-F. Mangin, L. Garnero, J.-B. Poline and H. Benali, "BrainVISA: software platform for visualization and analysis of multi-modality brain data," *Neuroimage*, vol. 13, p. 98, 2001.
- [7] N. Toussaint, J.-C. Souplet, P. Fillard and others, "MedINRIA: medical image navigation and research tool by INRIA," in *Proc. of MICCAI*, 2007.
- [8] J. Schindelin, C. T. Rueden, M. C. Hiner and K. W. Eliceiri, "The ImageJ ecosystem: An open platform for biomedical image analysis," *Molecular reproduction and development*, vol. 82, pp. 518-529, 2015.
- [9] A. Karperien, "FracLac for ImageJ," *Charles Sturt University*, 2013.
- [10] H. L{\'o}pez-Fern{\'a}ndez, G. S. Pess{\^o}a, M. A. Z. Arruda, J. L. Capelo-Mart{\'\i}nez, F. Fdez-Riverola, D. Glez-Pe{\~n}a and M. Reboiro-Jato, "LA-iMageS: a software for elemental distribution bioimaging using LA--ICP--MS data," *Journal of cheminformatics*, vol. 8, p. 65, 2016.
- [11] D. Prodanov and K. Verstreken, "Automated segmentation and morphometry of cell and tissue structures. Selected algorithms in imageJ," in *Molecular Imaging*, InTech, 2012.
- [12] S. R. Kesler, J. S. Kent and R. O'Hara, "Prefrontal cortex and executive function impairments in primary breast cancer," *Archives of neurology*, vol. 68, pp. 1447-1453, 2011.
- [13] G. Valeri, F. A. Mazza, S. Maggi, D. Aramini, L. La Riccia, G. Mazzoni and A. Giovagnoni, "Open source software in a practical approach for post processing of radiologic images," *La radiologia medica*, vol. 120, pp. 309-323, 2015.