AXONICA© 4.0

User Guide

Team aXonica, 2017-2018
Bilal Wajid
Momina Jamil
Hasan Iqbal

aXonica 4.0 User Guide

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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.

Updates from Previous Release

Added Microsoft Windows Virtualization Support Chapter which enables the user to work on a Windows platform.

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.
- aXonica Package (Chapter 2) contains a table which enlists all the included software.
- Software Installation Process (Chapter 3) describes how to install aXonica.
- Microsoft Windows Support (Chapter 4) describes a step-by-step procedure to configure a virtual OS for aXonica on Windows..
- Data Acquisition and Software Pipeline (Chapter 5) describes the acquisition of raw data image of MRI machine and implementation of software pipeline of biological image development.
- Image Preprocessing (Chapter 6) describes the step-by-step solution to use some example software.
- Image Processing (Chapter 7) describes the step-by-step solution to use some example software.
- Structural Analysis (Chapter 8) describes the step-by-step solution to use some example software.
- Diffusion Analysis (Chapter 9) describes the step-by-step solution to use some example software.
- Functional Analysis (Chapter 10) describes the step-by-step to use some example software.
- Data Management & Annotation (Chapter 11) describes the step-by-step to use some example software.
- Post Installation (Chapter 12) describes the working of each software included in the package.
- Software Uninstallation Process (Chapter 13) describes how to install aXonica or any specific tools.

Contact

For any further queries and suggestions, contact us at: mominaj05@gmail.com or hasaniqbal777@gmail.com

aXonica Package

Installing aXonica software

List of software tools and plugins included in aXonica package are shown in the following table. Software which are recommended are also mentioned in the table. Download size and version of each software is mentioned for user convenience:

Sr. No.	Software	Download Size	Version	Latest Update	Recommeded
Image Preprocessing					
Image Visualization					
1	ImageVIS3D	13.2	3.1.0	2016	
2	BoneJ	0.7	1.0.0	2021	✓
3	Dipy	11.6	1.4.1	2021	
4	Anatomist (BrainVISA)	3400	5.0.2	2021	
5	JIST	43.9	3.2.0	2014	
6	VistaDisp	1331.44	-	2018	
7	iELVis	11	-	2021	
8	MeVisLab	2000	3.4.2	2021	
9	MITK	163	18.04.02	2021	
10	Nilearn	4.7	0.8.0	2021	
11	imlook4d	18.8	5.8.2	2019	
12	MIA	4.2	2.4.7	2016	
Image Enhancement					
13	TORTOISE	40	1.0.4	2016	
14	AMIDE	29	1.0.5	2017	
15	NormalizeFOV	732.7	1.2.0	2016	
16	Fast_Filters	0.3	10.0.0	2017	
17	PID	3.9	1.9.0	2014	
18	CLAHE	0.17	0.1.0	2021	

19	HD-BET	0.03	-	2021	✓
20	MNI-N3	1.3	1.12.0	2012	
21	C-PAC	277	1.8.0	2021	
22	GLMdenoise	0.26	1.4.0	2021	
23	FMRIPrep	41	46.1.0	2021	
24	CoSMoMVPA	9.51	1.1.0	2021	
3D Image Reconstruction					
25	ITK-SNAP	45.2	3.6.0	2019	✓
26	InVesalius	91.8	3.1.9	2021	
27	Free-D	8.5	1.15.0	2018	
28	PaCER	9.78	1.0.7	2020	
29	SIRF	1.4	3.1.0	2021	
Image Processing					
Image Segmentation					
30	Segmentator	4	1.6.0	2021	
31	BrainSeg3D	47.6	2.5.0	2021	
32	ITK	88	5.2.1	2021	
33	BEaST	0.5	1.15.0	2018	
34	RMNMS	0.1	0.1.0	2015	
35	CMP-BIA	0.1	0.3	2016	
36	E-Snake	0.1	27.1	2012	
37	pyClusterROI	31	2	2015	
38	HeteroscedasticfMRI	2.1	-	2015	
39	ALVIN	18.9	1	2020	
40	MANTiS	20.02	-	2021	
41	SegAN	0.7	-	2019	
42	FMRIPrep	1	20.2.3	2021	
43	AxonDeepSeg	150	3.2.0	2021	
44	seg	0.7	-	2018	
45	medicalzoopytorch	63	-	2021	
46	LiviaNET	12.5	-	2019	✓
47	Autoencoder Regularization	0.8	-	2021	
Image Registration					
48	AAL	4.7	3.1	2020	
49	elastix	27.7	5.0.1	2021	
50	ART	6	1.07.1	2018	
51	bUnwarpJ	0.1	2.6.12	2021	
52	MIRTK	313.71	2.0.0	2021	
53	IRTK	0.6	1.0.0	2015	
54	AIR	0.99	5.3.0	2010	✓

Image Surfacing					
55	ANTs	21.3	2.3.5	2021	✓
56	Mango	65	4.1.0	2016	
57	iso2mesh	160	5.14.0	2021	
58	NMT	286.5	2.1.2	2021	
59	Surfing	249.8	4.14.0	2020	
60	SUMA	90.9	4.4.7	2021	
Structural Data Analysis					
3D Image Analysis					
61	Brainstorm	59	21.0.0	2021	✓
62	ImageJ	85.5	153.0.0	2021	
63	nipype	11.11	1.6.1	2021	
64	VISTASOFT	38.4	1.0.0	2021	
65	TINA	0.06	0.1.12	2020	
66	calcFD	0.55	31.0.0	2021	
67	PRoNTo	24.9	2.1.1	2021	
68	Nitime	6.2	0.9.0	2021	
69	DynamicBC	14.74	2.2.0	2019	
70	BFAST3D	0.2	-	2020	
71	3D Slicer	503	4.11.0	2021	
72	DCEMRI	4	0.51.0	2021	
Morphometric Analysis					
73	FracLac	13.8	2.5.0	2021	
74	Gwyddion	12	2.55.0	2021	✓
75	CaPTk	1400	1.8.1	2021	
76	ASLtbx	0.379	15.0.0	2015	
77	GAT	14.2	1.5.1	2014	
Quality Control					
78	Mindcontrol	6.34	1.3.3	2018	
79	MRIQC	3040	0.16.1	2021	
80	ArtRepair	0.1	5b3	2019	✓
Image Modelization					
81	SIMRI	6.4	2.0.0	2020	✓
82	SimVascular	799	6.15.0	2021	
83	ROAST	180.52	3.0.0	2020	
Image Classification					
84	LA-iMageS	82.4	1.1.5	2017	✓

Image Mapping					
85	MRI Processor	0.18	1.1.6	2021	
86	Lead-DBS	4069	1.6.3	2021	✓
Diffusion Data Analysis					
Image Simulation					
87	MITK-DI	159	10.23.0	2021	
88	The Virtual Brain	1200	2.3.0	2021	✓
89	SimTB	2.9	18.0.0	2019	
Tractography					
90	medInria	82.7	3.2.0	2021	
91	MRtrix3	19.6	3.0.3	2021	
92	SlicerDMRI	503	4.11.0	2021	
93	brainGraph	1.4	3.0.0	2021	
94	Braintome DiffusionKit	50.1	1.5.0	2020	
95	PANDA	10	1.3.1	2018	✓
96	DSI Studio	75.4	21.08.0	2021	
Functional Data Analysis					
Neuroimage Analysis					
97	FSL	0.09	6.0.4	2016	✓
98	BrainVISA	3400	5.0.2	2021	
99	SPM	111	12.0.0	2020	
100	BrainVoyager	501	22.0.0	2021	
101	NeuroElf	27.1	1.1.0	2021	
102	BRAINSTools	30	5.4.0	2021	
103	NMT	286.5	2.1.2	2021	
104	CONN	125	21a	2021	
105	SDM	279	6.21.0	2019	
106	bgsmtr	3.8	0.7.0	2019	
107	SliceMap	42	1.0.0	2020	
108	GC-LDA	197.75	-	2021	
Neuroimage Visualization					
109	FreeSurfer	3100	7.2.0	2021	
110	IClinfMRI	15.33	-	2021	
111	Papaya	121.1	-	2019	✓
Image Data Management and Annotation					
Image Format Management					
112	BrainMap	204.9	0.2.3	2017	

113	XNAT	8	1.8.2	2018	
114	MENGA	3	3.1.0	2016	
115	PyNWB	1.14	2.0.0	2021	
116	Icbm2tal	204.9	0.2.3	2021	✓
117	NiBabel	3.3	3.2.1	2021	
118	MRIcron	17.31	1.0.0	2021	
119	MRIcro	8	1.39.0	2021	
120	Dinifti	0.7	2.3.3	2013	
DICOM File Management					
121	DCMTK	11.4	3.6.5	2021	
122	WEASIS	38	3.7.1	2021	
123	DicomBrowser	8.1	1.7.5	2020	
124	HeudiconV	0.341	0.9.0	2021	
125	MIPAV	100	10	2019	✓
126	DICOMweb	0.021	0.40.0	2019	
127	GDCM	2.6	2.8.9	2021	
128	odil	44.9	0.8.0	2021	
129	VV: the 4D viewer	15.2	1.4.0	2021	
130	DIANA	9.5	2.1.5	2018	

Software Installation Process

Installing aXonica software

For downloading of aXonica, visit its website:

https://github.com/mominaj/aXonica-bin

1. aXonica can also be downloaded from the following command through git:

   ```
   $ git clone https://github.com/mominaj/aXonica-bin
   ```

2. Now run the following commands on terminal:

   ```
   $ cd aXonica-bin

   $ chmod +x aXonica_setup_enUS

   $ ./aXonica_setup_enUS
   ```

3. Installation wizard of aXonica will start.

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

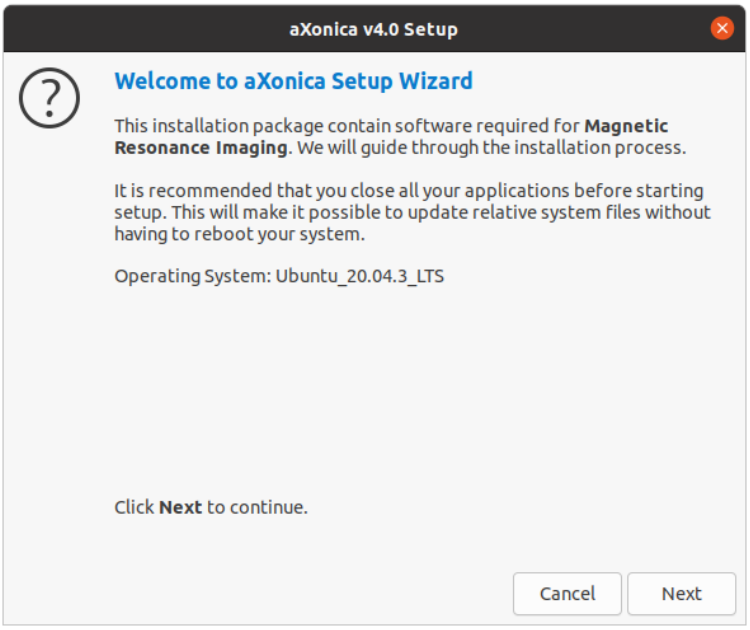


Figure 1: Installation Welcome screen

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

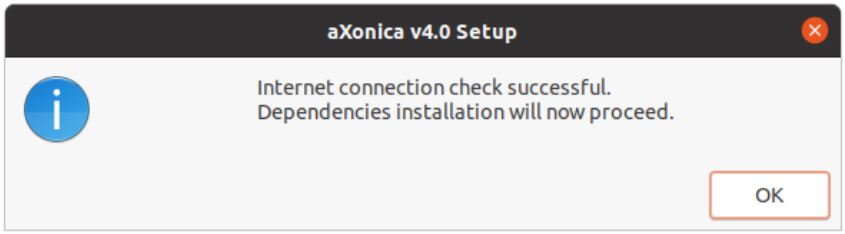


Figure 2: Internet check successful screen

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

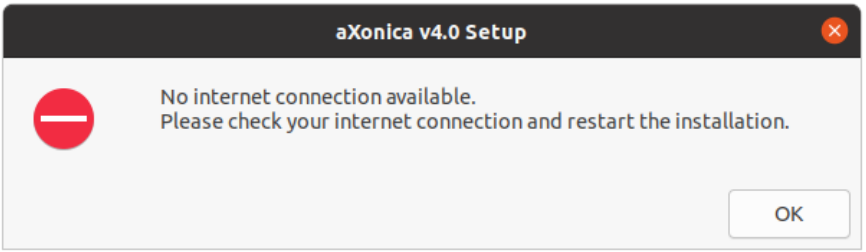


Figure 3: Internet check failed screen

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

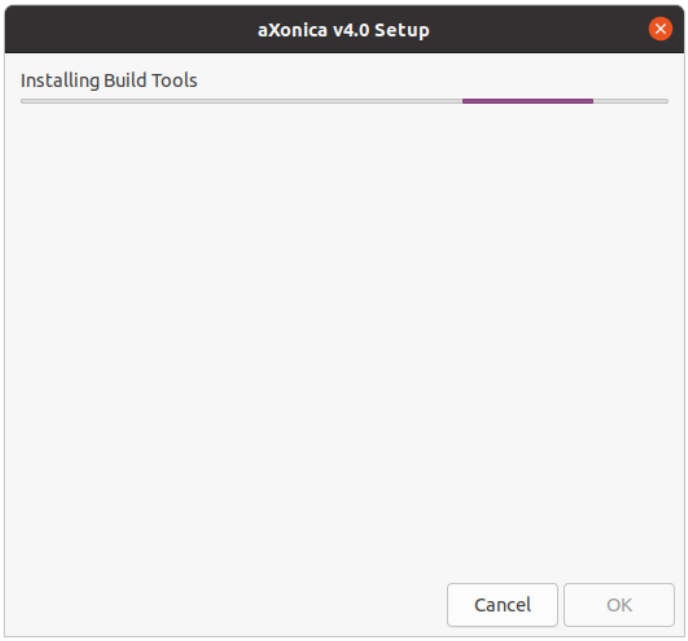


Figure 4: Dependencies Installation in progress screen

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

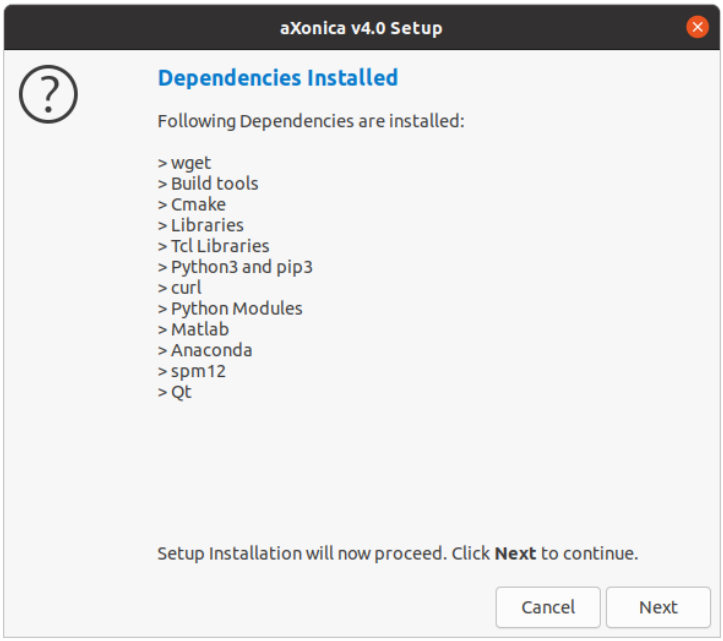


Figure 5: Dependencies Installation finished screen

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

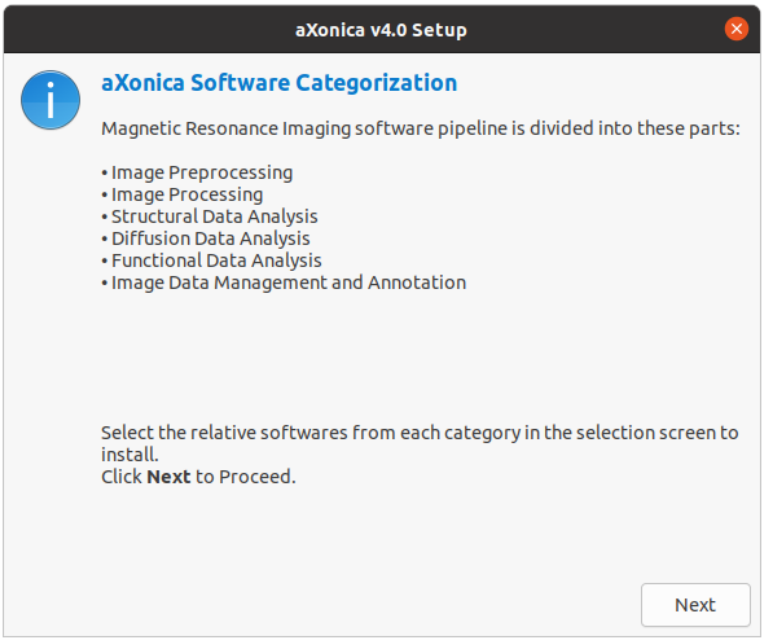


Figure 6: Pipeline information screen

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

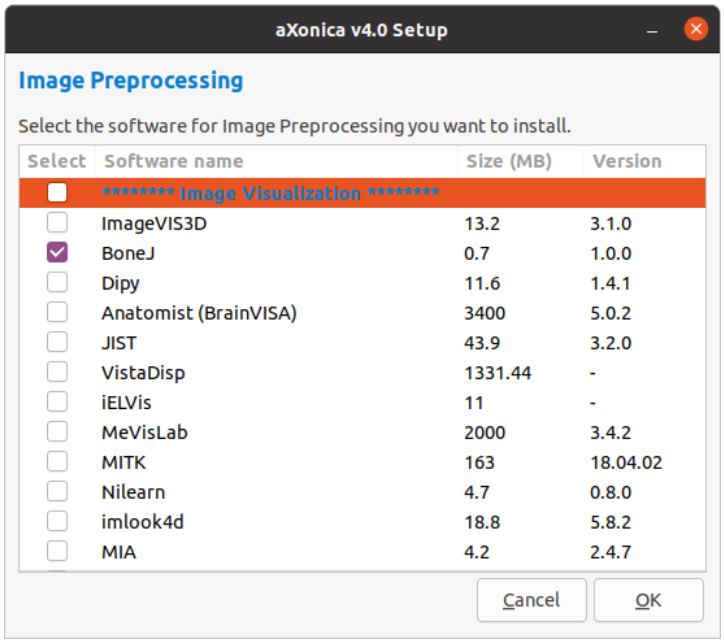


Figure 7: Preprocessing tools selection screen

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

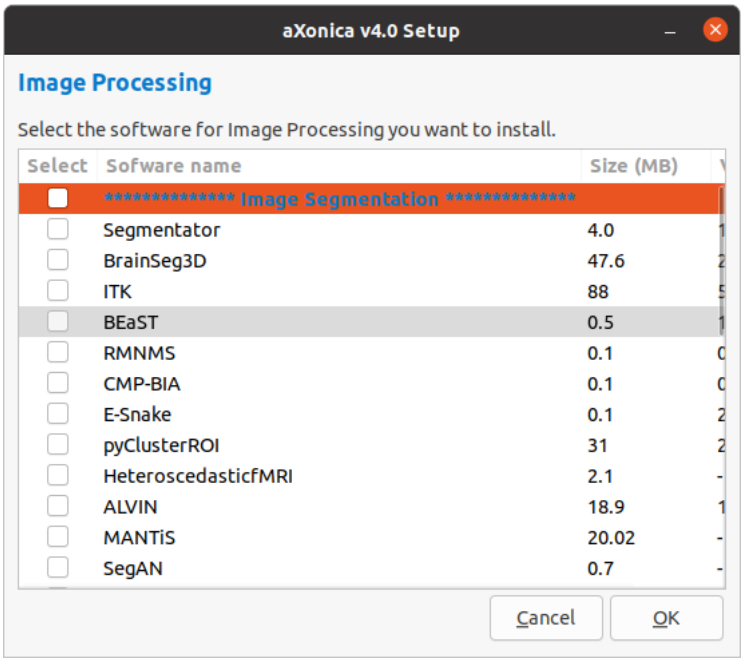


Figure 8: Processing tools selection screen

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

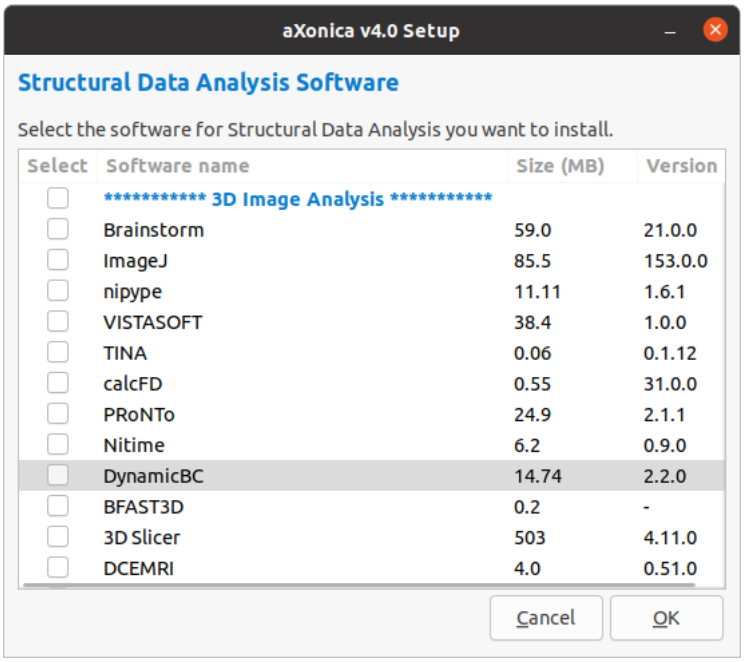


Figure 9: Structural Analysis tools selection screen

12. Selection screen for Diffusion Data Analysis tools is displayed. Select the required tools and Click **Next**.

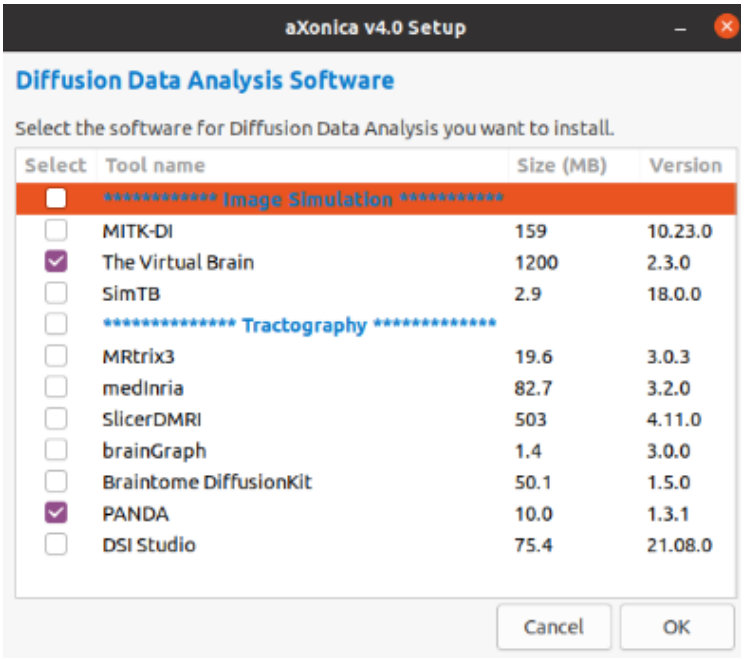


Figure 10: Diffusion Data Analysis tools selection screen

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

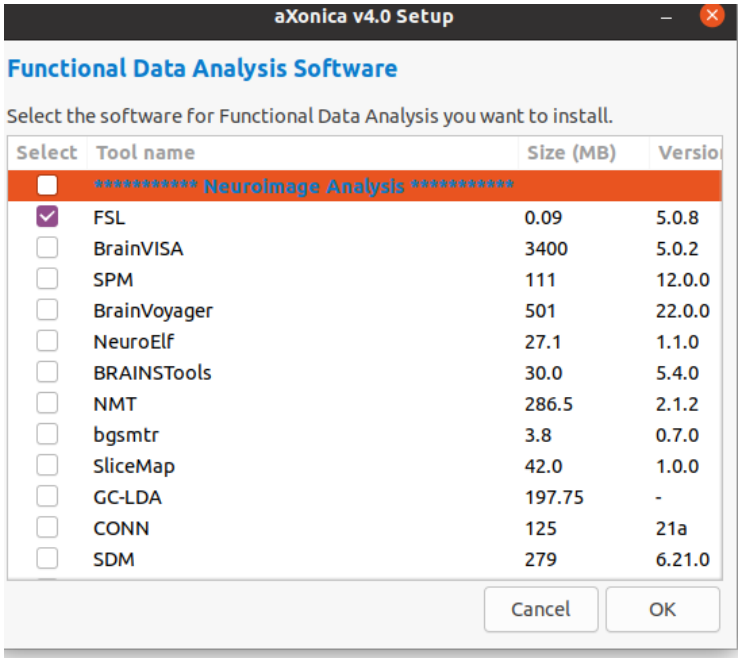


Figure 11: Functional Data Analysis tools selection screen

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

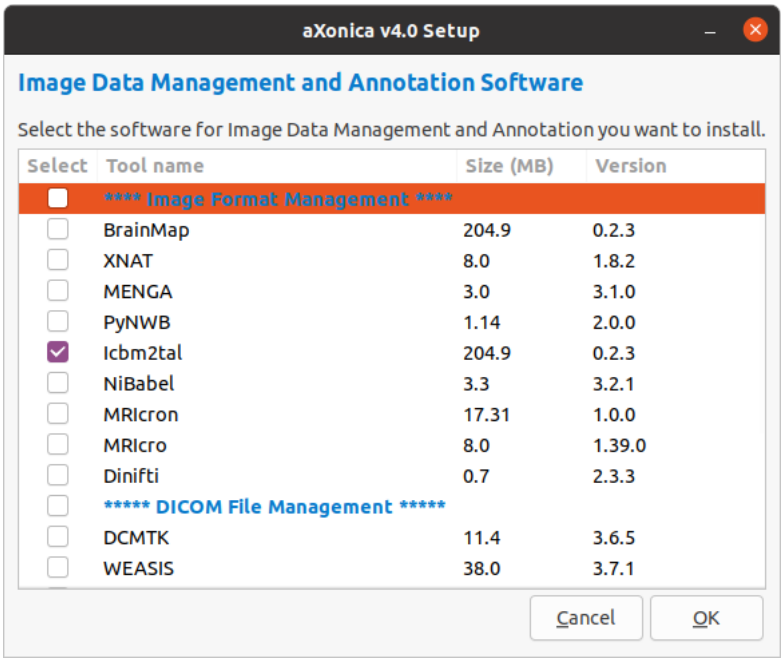


Figure 12: Data Management and Annotation tools selection screen

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

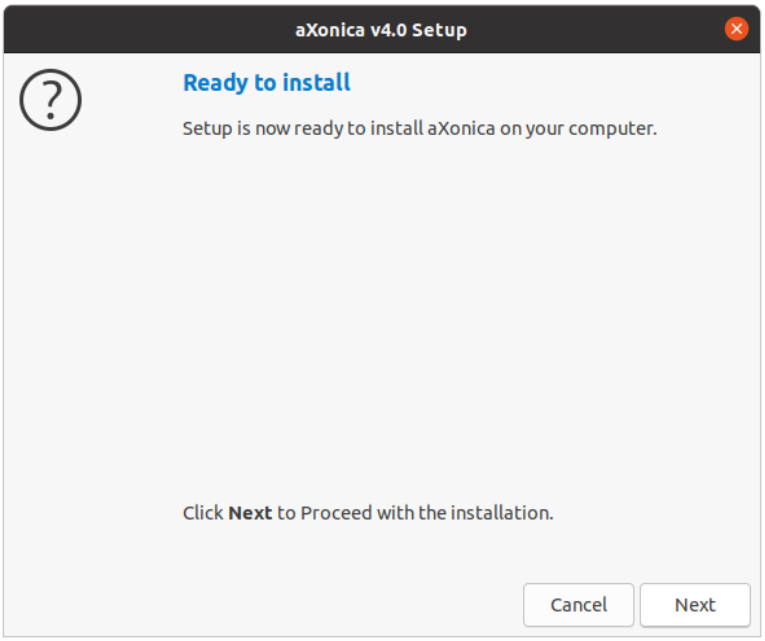


Figure 13: Ready to Install screen

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

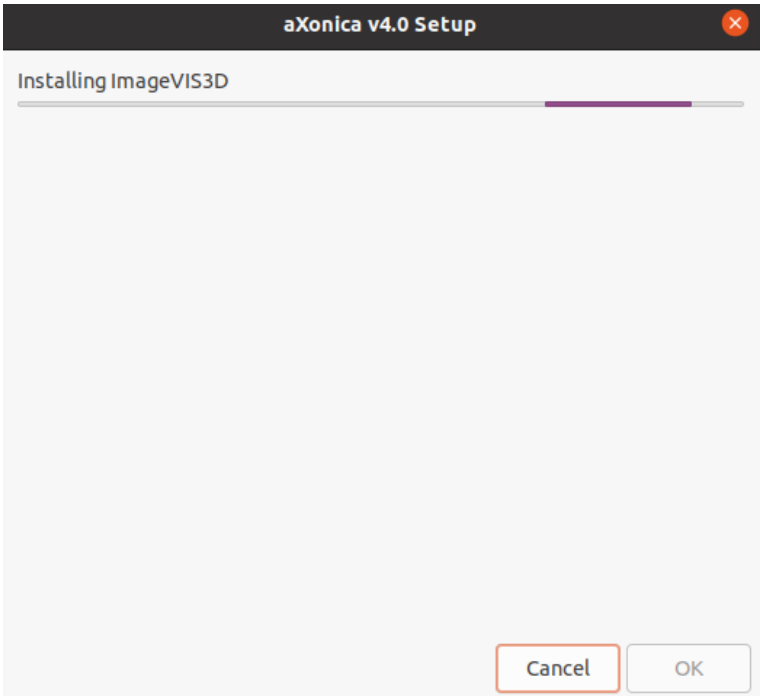


Figure 14: Tools installation progress screen

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

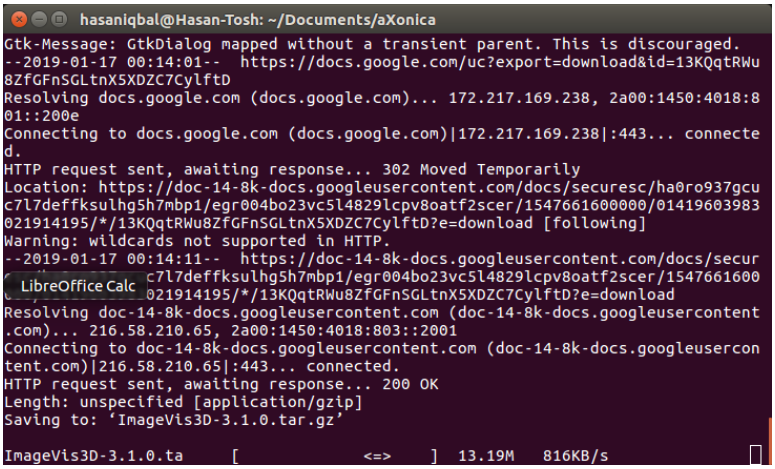


Figure 15: Tools downloading in background

Microsoft Windows Support

Installing aXonica software on Microsoft Windows

aXonica is software package for Linux, specifically Ubuntu users, but Windows users can use aXonica using a Virtual Machine. Follow these steps to initialize a Virtual Machine on your Windows host.

NOTE *aXonica support a 64bit Windows host. Microsoft Windows XP and Vista support is discontinued.*

1. First you have to **download** the image file of the required OS (Ubuntu) from its website or use the following link:
   http://repo.isra.edu.pk/ubuntu-release/18.04.2/ubuntu-18.04.2-desktop-amd64.iso
2. Download the virtualization software (Oracle VM VirtualBox) from the following link:
   https://download.virtualbox.org/virtualbox/6.0.10/VirtualBox-6.0.10-132072-Win.exe
3. **Install** this software in Windows OS host.
4. Start Virtual Box, and click on the **New** symbol.

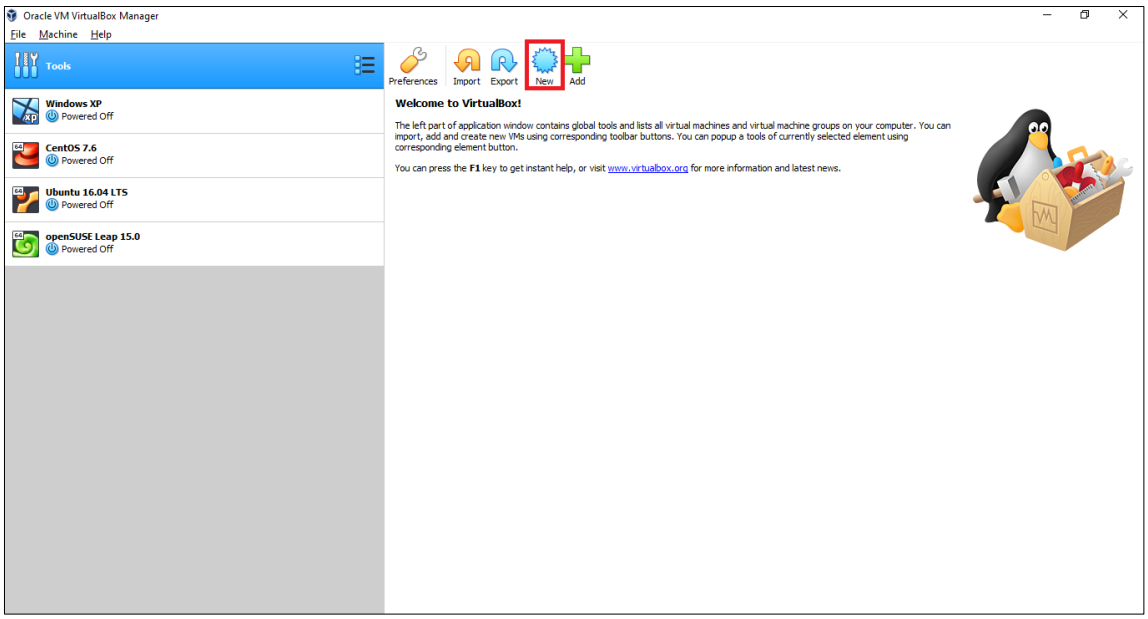


Figure 1: New Virtual OS

5. Give the virtual OS a relevant **Name**. Select the **Type** (Linux) and **Version** (Ubuntu 64-bit) and Click **Next**.

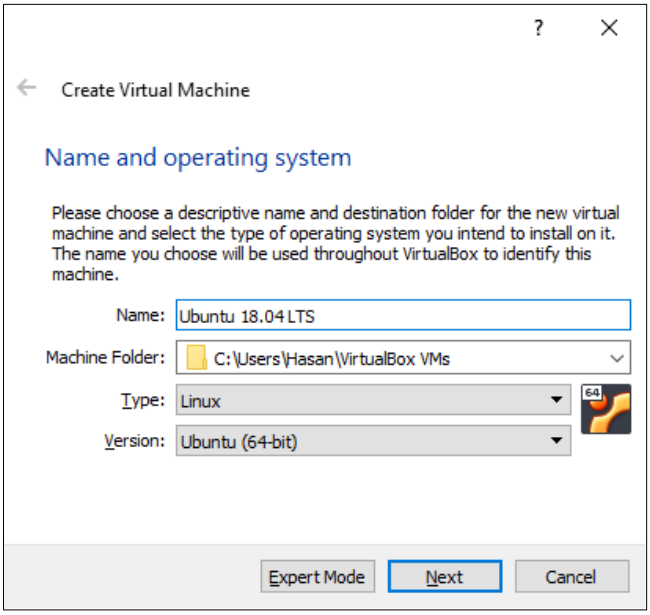


Figure 2: Assigning Name

6. **Allocate** RAM to the virtual OS. Following system has 8GB of RAM so 2GB of RAM is allocated. You can use more RAM if your system has enough extra RAM.

NOTE *Allocate about half of the RAM to the virtual OS.* Click **Next**.

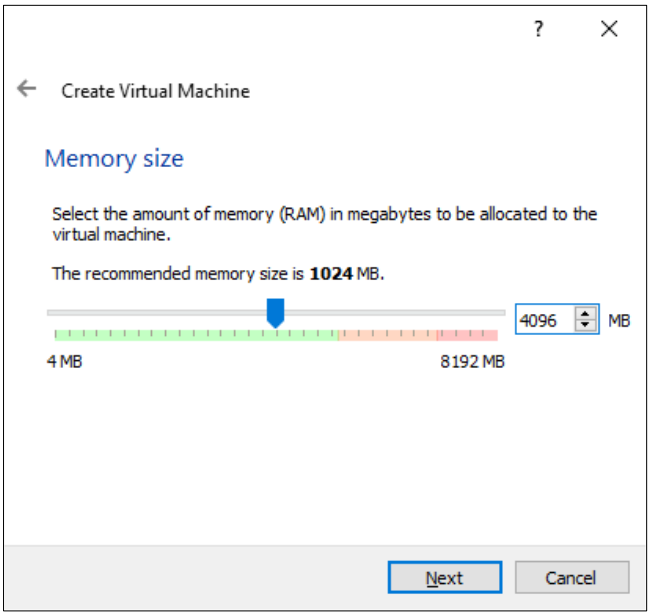


Figure 3: Memory Allocation

7. **Create** a virtual disk. This works as the hard disk of the virtual Linux system. This is where the virtual system will store its files. Click **Create**.

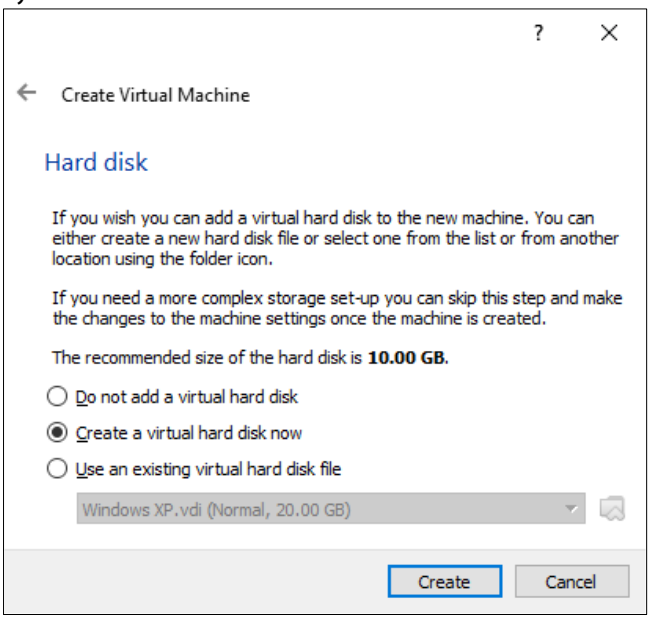


Figure 4: Creating a virtual hard disk

8. Select VDI file type here (recommended). Click **Next**.

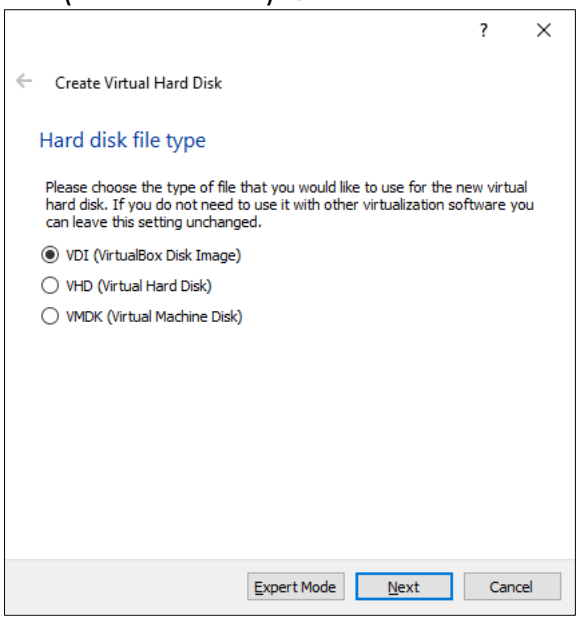


Figure 5: Hard disk file type

9. You can choose either of Dynamically allocated or Fixed size option for creating the virtual hard disk. **Choose** Dynamically allocated. (recommended). Click **Next**.

NOTE *Dynamic allocation is allocated as time passes and data is increased whereas fixed is allocated instantly.*

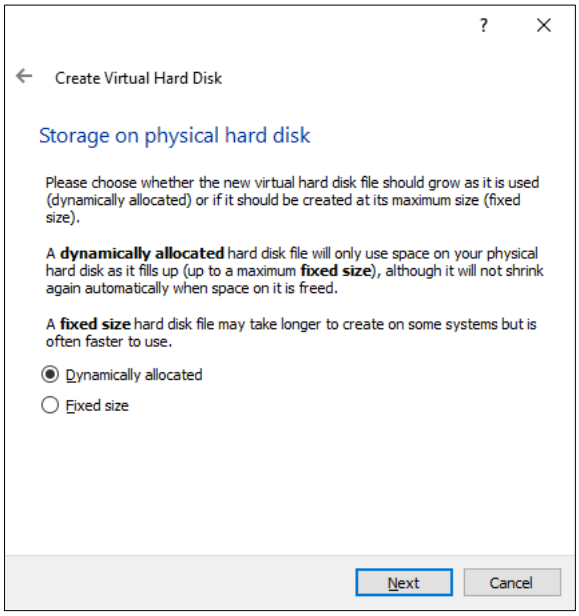


Figure 6: Storage type

10. Select VDI file type here (recommended) and Select the Hard Disk size. (recommended size: 100 GB). Click **Create.**

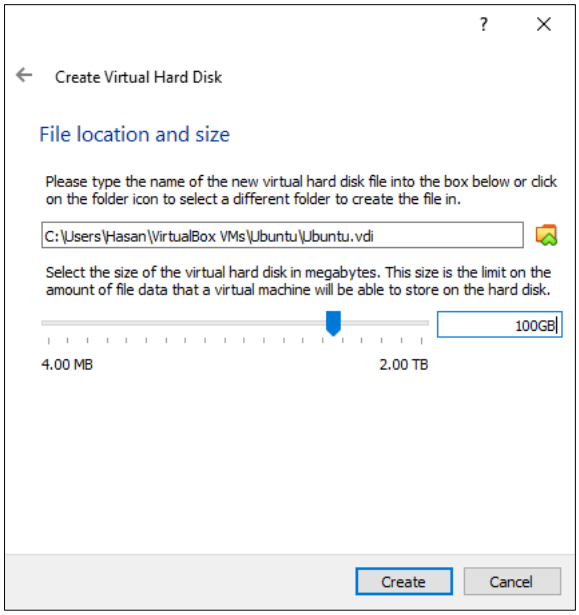


Figure 7: Hard disk size

11. Click **Next**. Now, Select Settings to assign the image file of respective OS to VB.

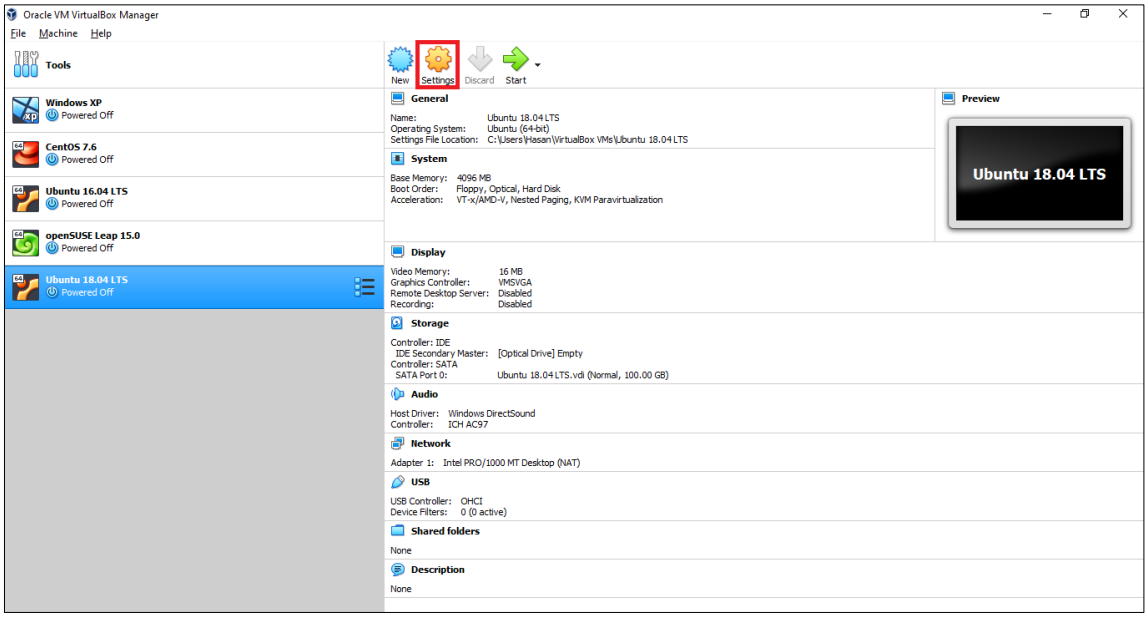


Figure 8: Select Settings

12. **Select** General → Advanced. Now, select the Shared Clipboard and Drag'n'Drop option to Bidirectional.

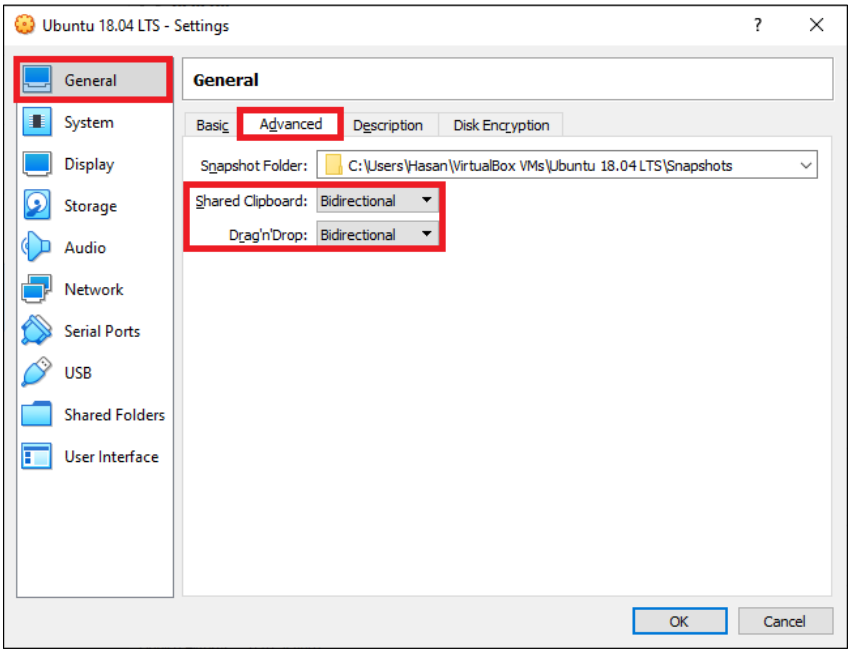


Figure 9: Advanced Settings

13. Select Settings to assign the image file of respective OS to VB. **Select** Storage → Controller : IDE → Empty. Now, in the Attributes tab, click on New Disk and provide the path of downloaded image file of Ubuntu OS. **Click** OK.

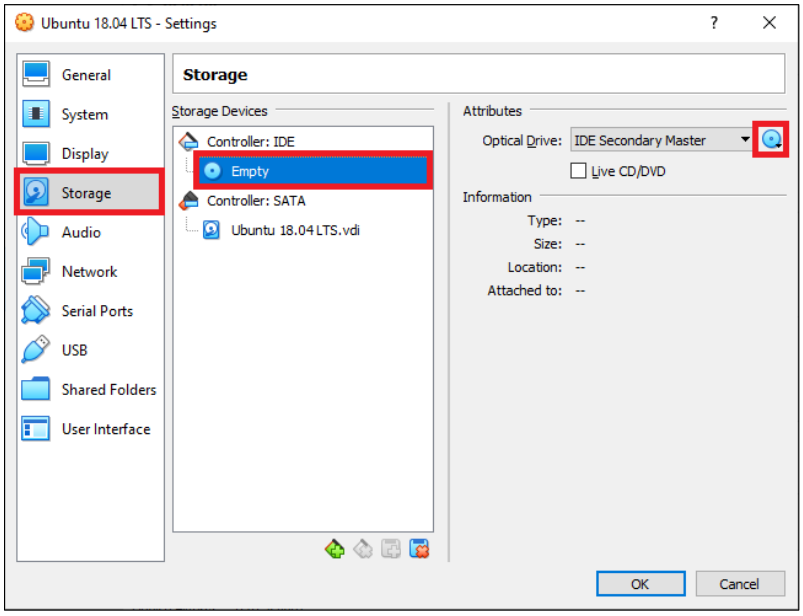


Figure 10: Providing Image file

14. Once everything is in place, it's time to boot that ISO and install Linux as a virtual operating system. Click **Start**.

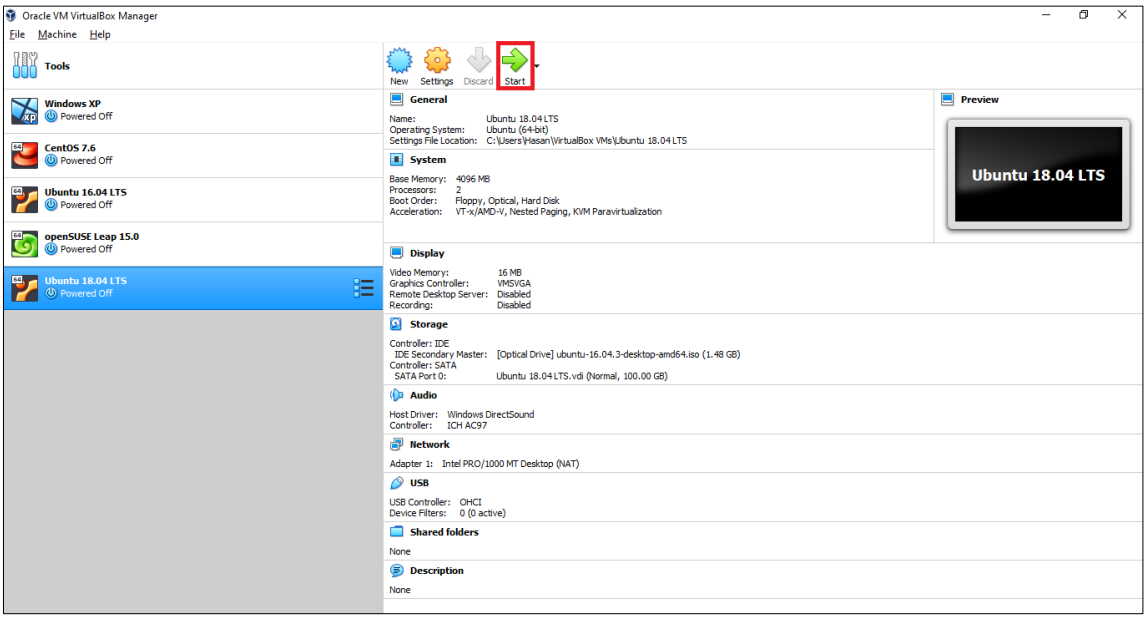


Figure 11: Starting Virtual OS

15. Virtual OS will boot into Linux Installation process. You should be presented with the option to install it. Click **Install Ubuntu**.

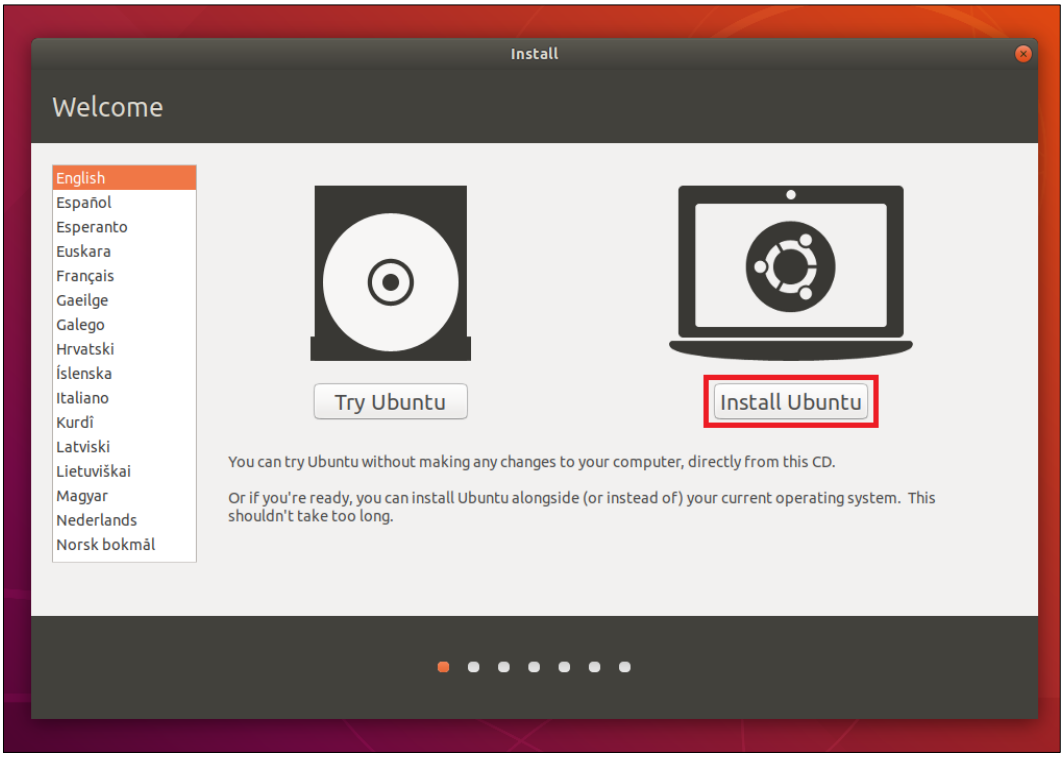


Figure 12: Installing Ubuntu

16. Continue with **Normal Installation**.

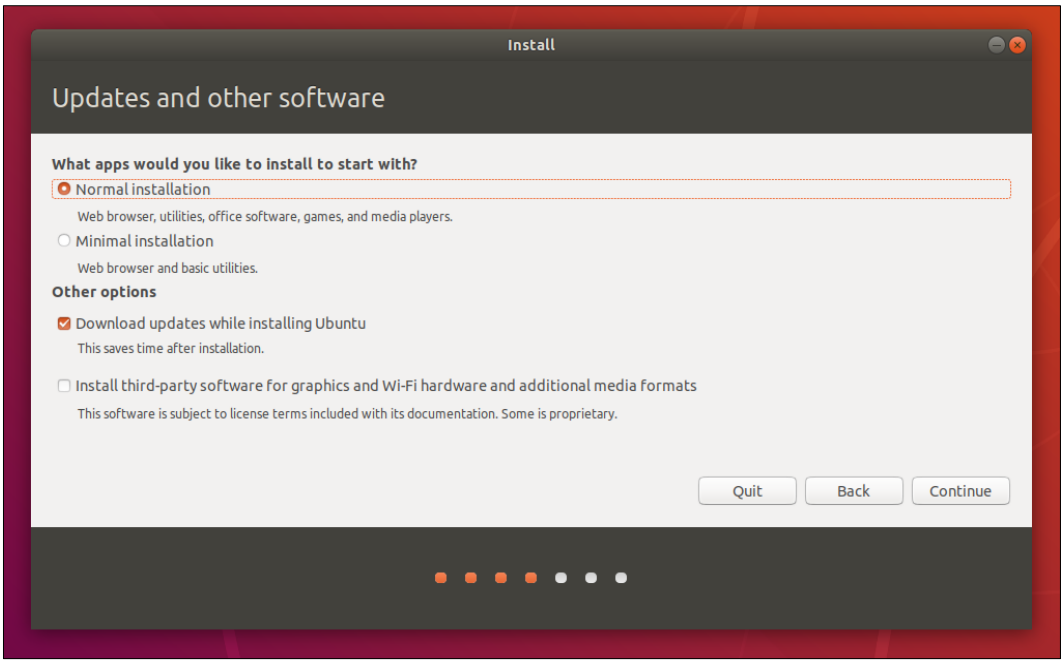


Figure 13: Update Screen

17. In Installation type screen, select **Erase disk** and install Ubuntu option.

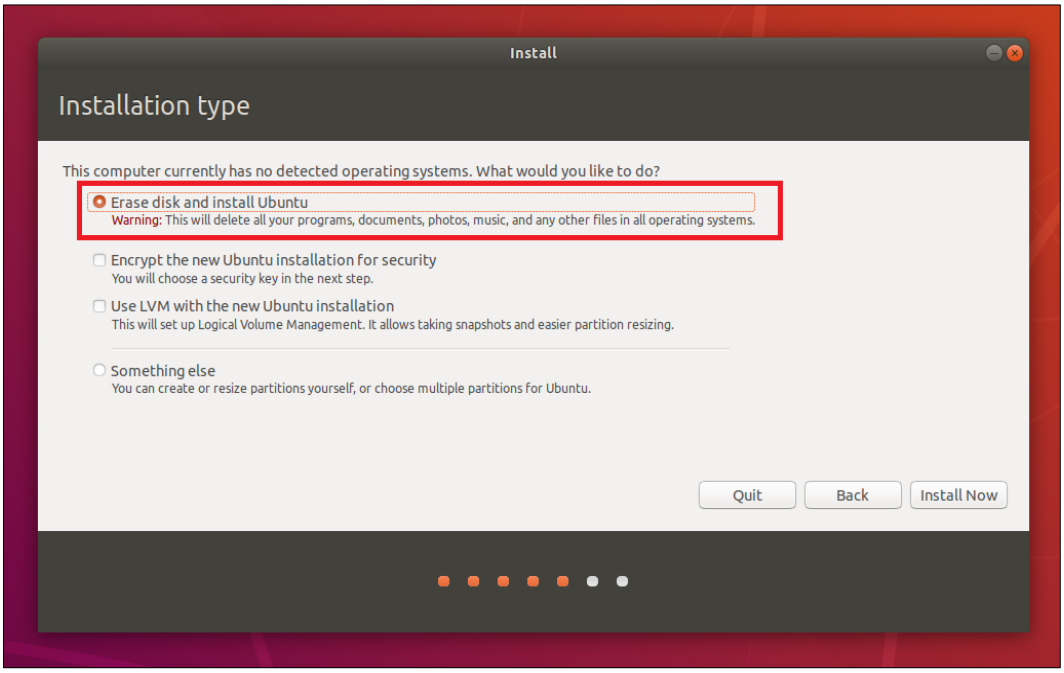


Figure 14: Installation type Screen

18. Select **Continue**.

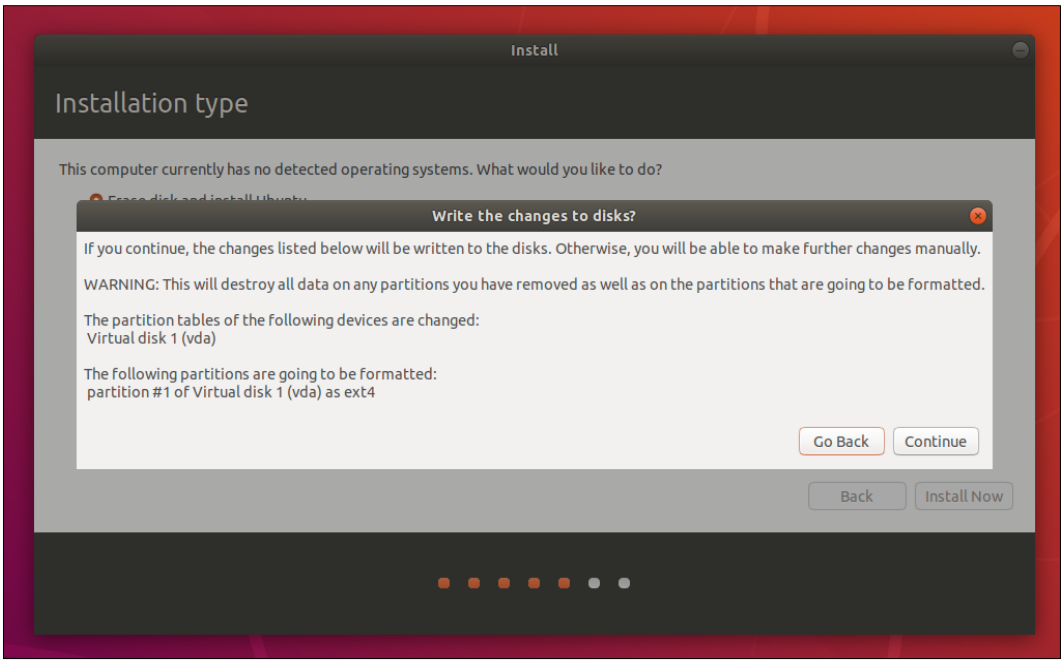


Figure 15: Confirmation Screen

19. Select your Current City and Continue. Select **Continue**.

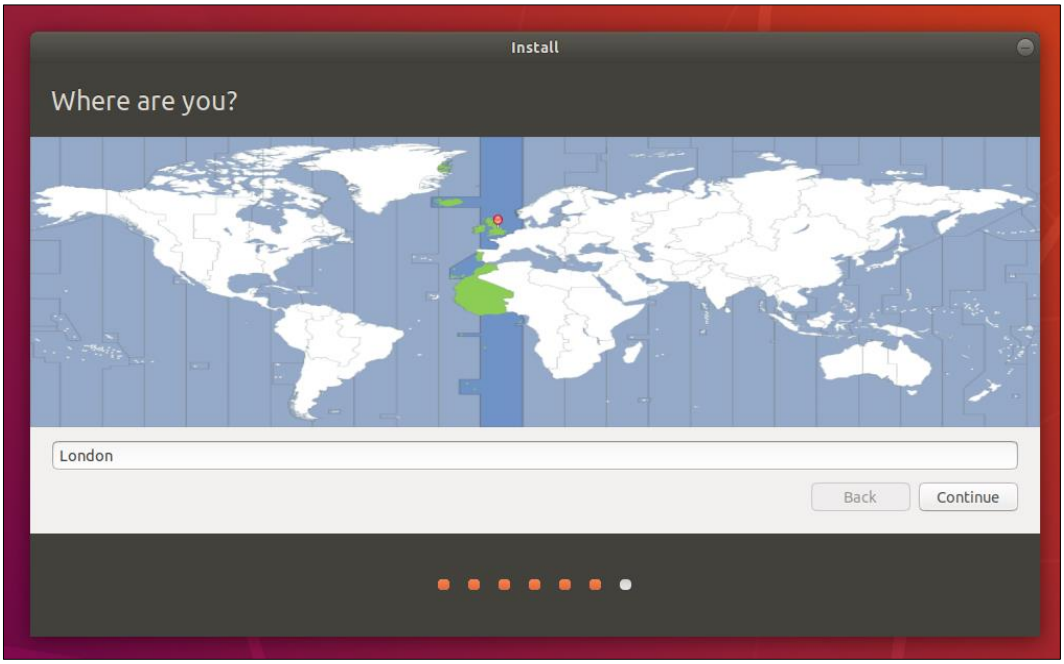


Figure 16: Location selection screen

20. Fill your Info and click **Continue**.

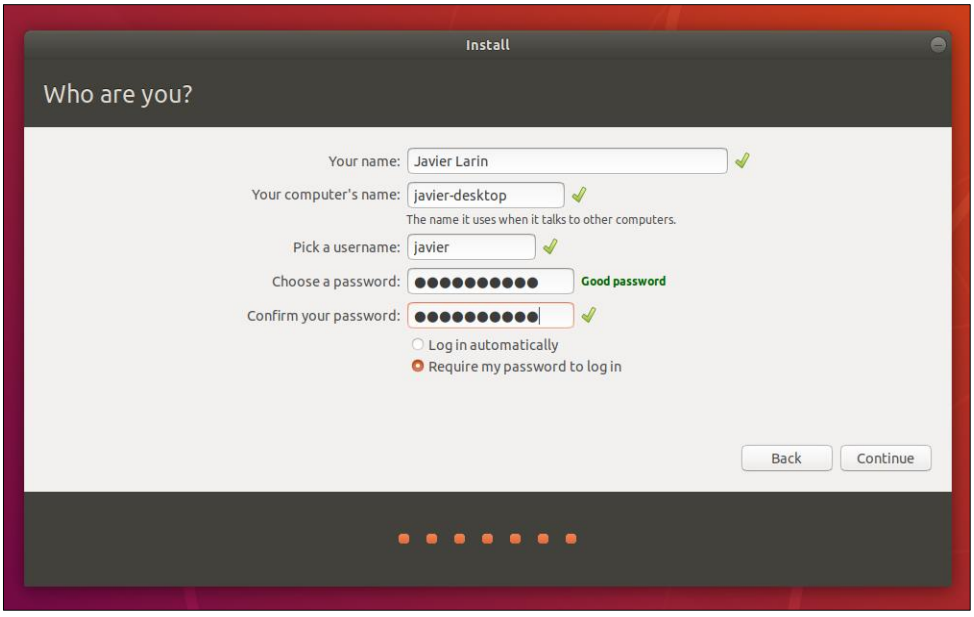


Figure 17: Intro Screen

21. Installation will Continue.

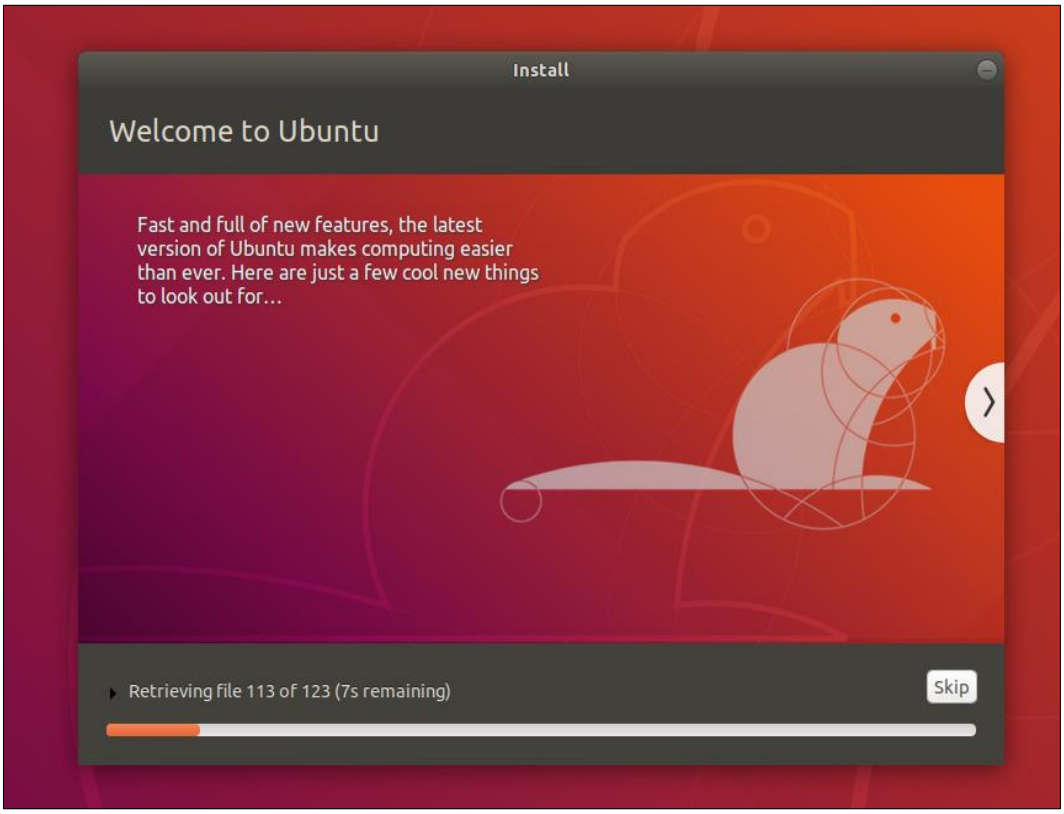


Figure 18: Installation Screen

22. Installation is Complete. Click **Restart Now**.

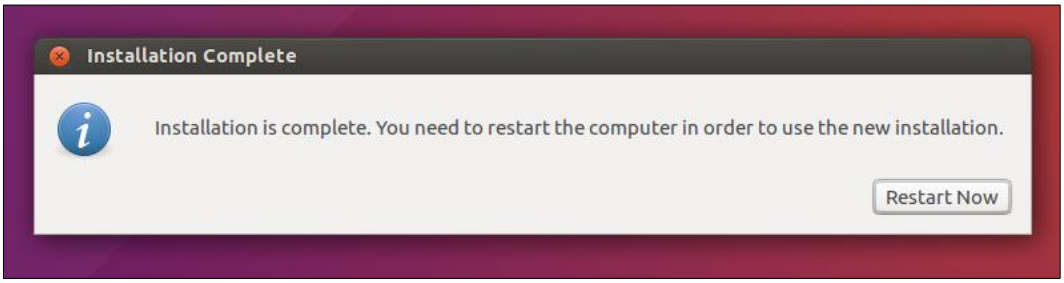


Figure 19: Complete Installation Screen

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:

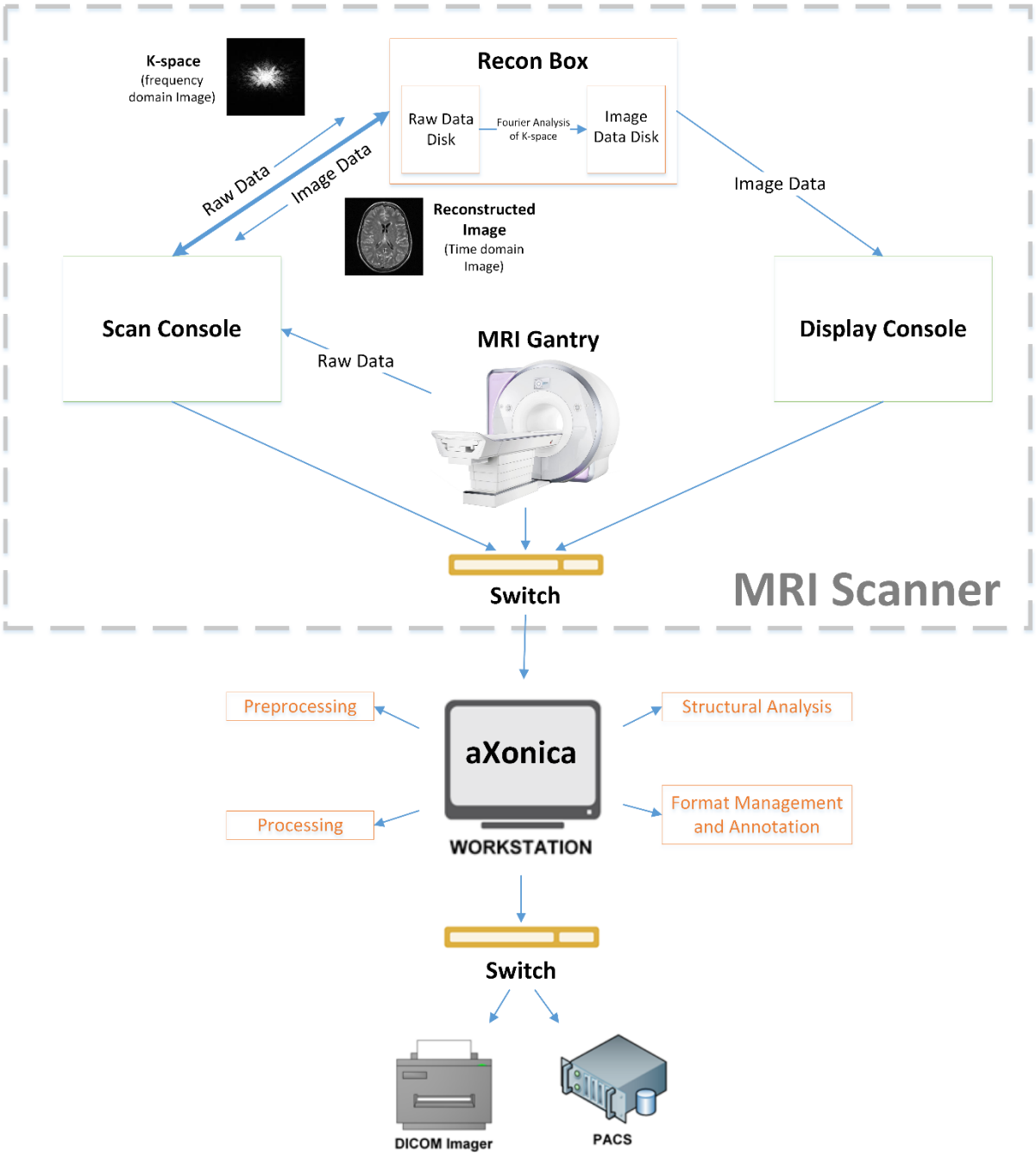


Figure 1: MRI network diagram

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:

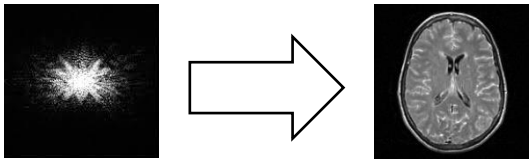
These commands are transferred to the MRI and patient data is acquired. This raw data is in K-space (frequency domain).

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.

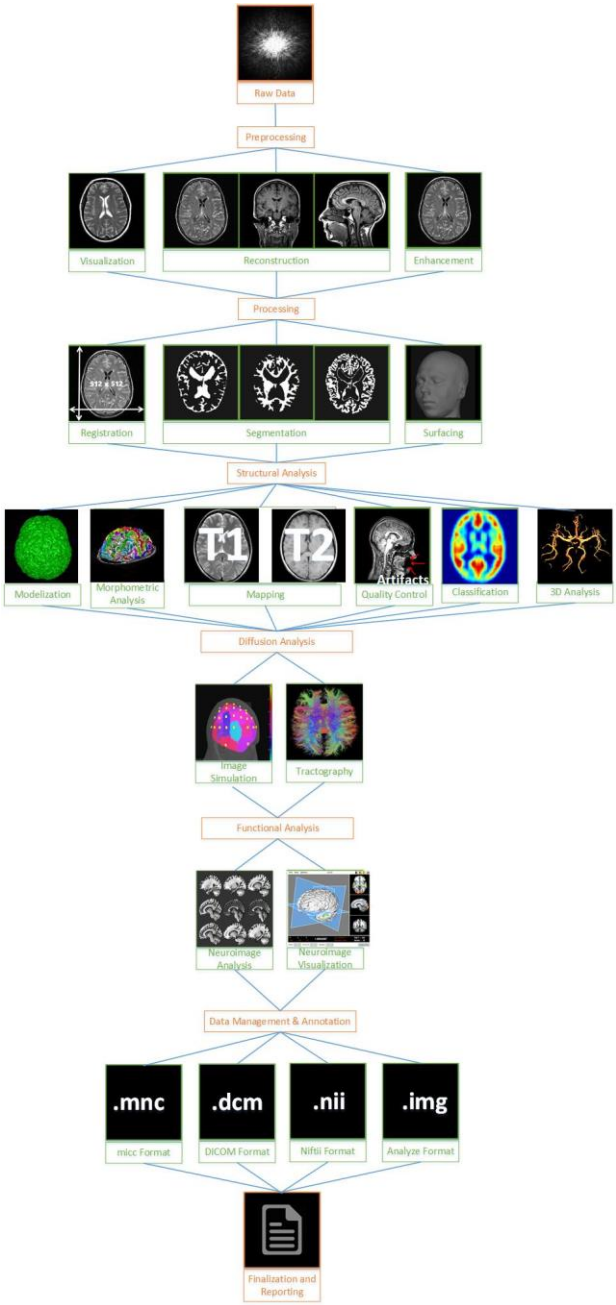


Figure 2: MRI Pipeline Visualized

Image Preprocessing

In this Chapter

We will learn about:

- Image Preprocessing
- Steps for Preprocessing
- Example 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.

Example 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"

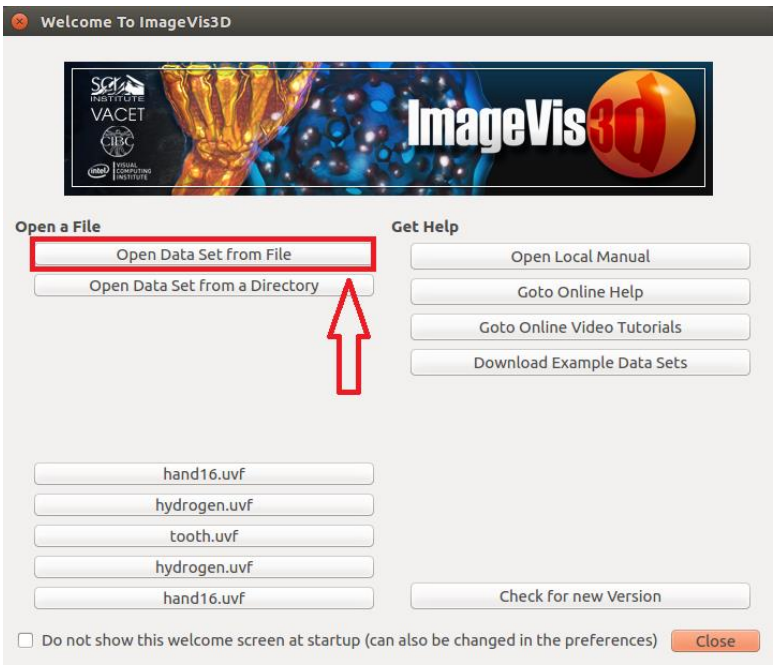


Figure 1: ImageVis3D Welcome screen

3. **Load** the downloaded dataset

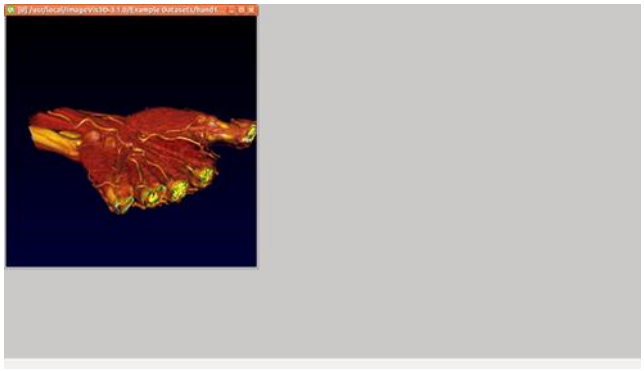


Figure 2: Visualized Image

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.

Example 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:

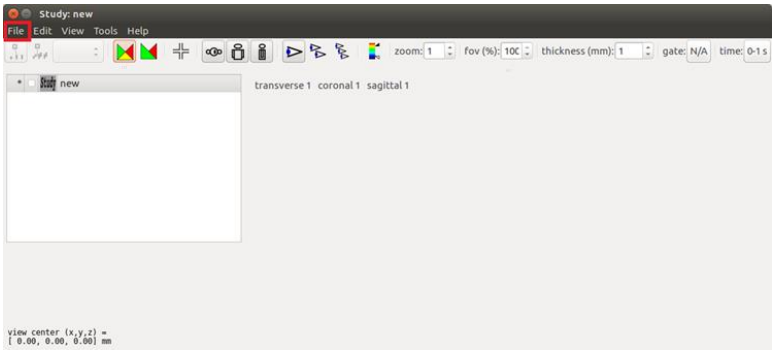


Figure 3: AMIDE Welcome screen

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

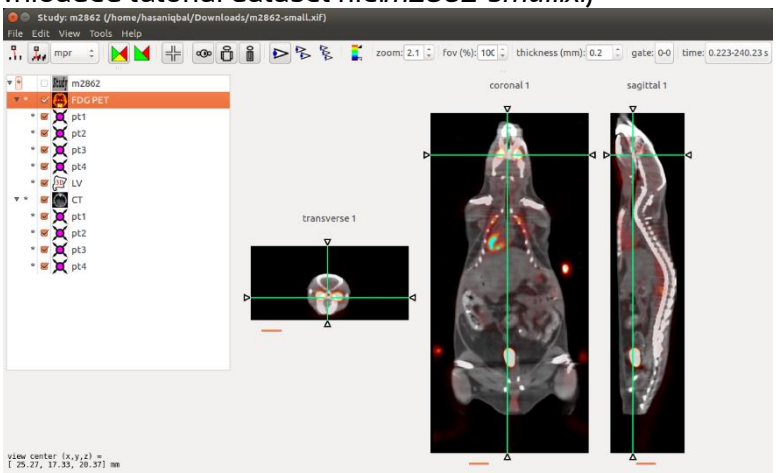


Figure 4: Enhanced Images

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.

Example 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

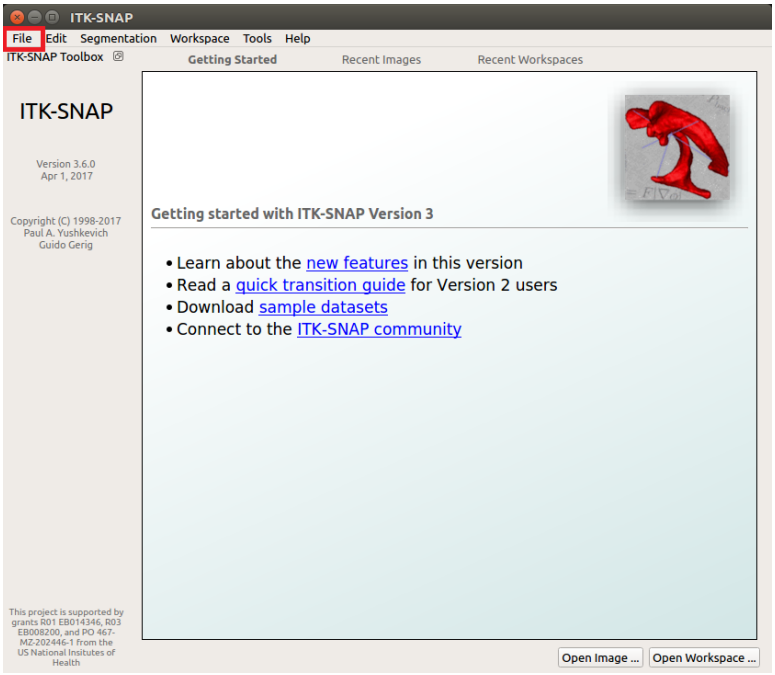


Figure 5: ITK-SNAP Welcome screen

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

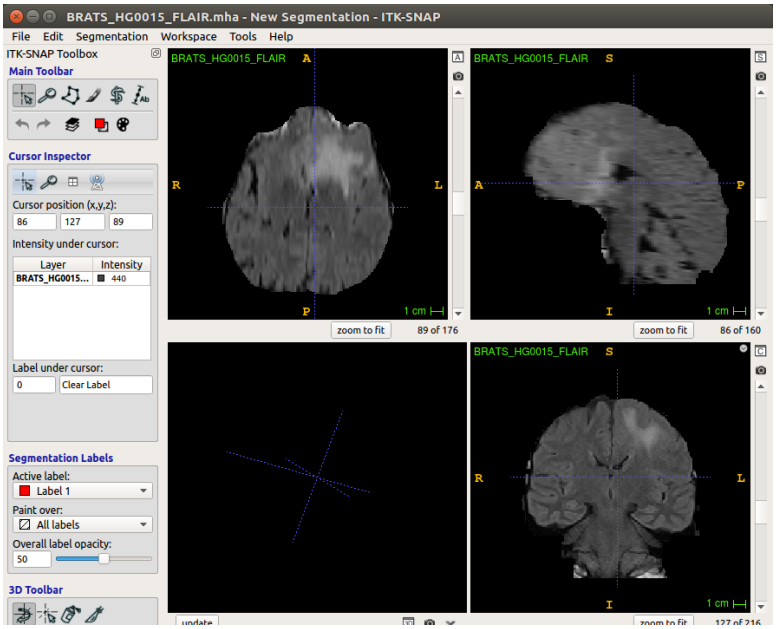


Figure 6: 3D Reconstructed Image

4. Further **Analyze** the image

Image Processing

In this Chapter

We will learn about:

- Image Processing
- Steps for Processing
- Example 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.

Example 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'

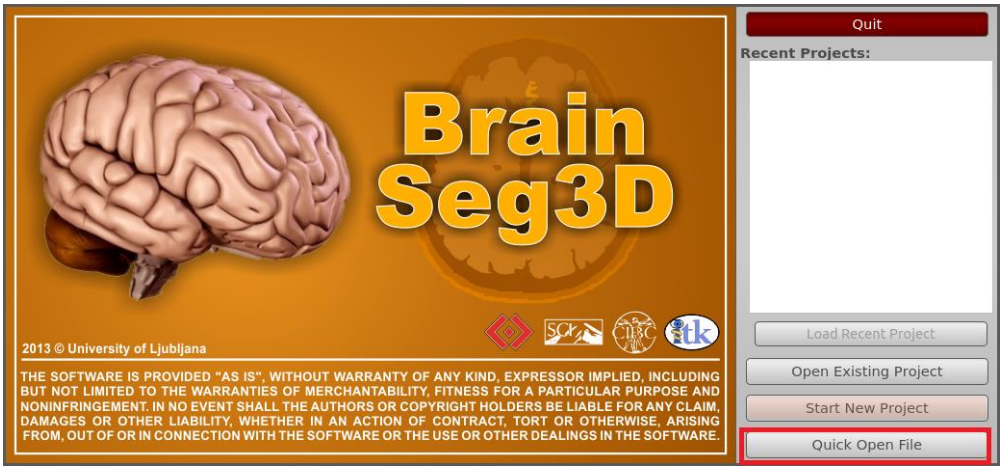


Figure 1: BrainSeg3D Welcome Screen

3. **Load** Tutorial data sets

4. **Select** all Images and Import

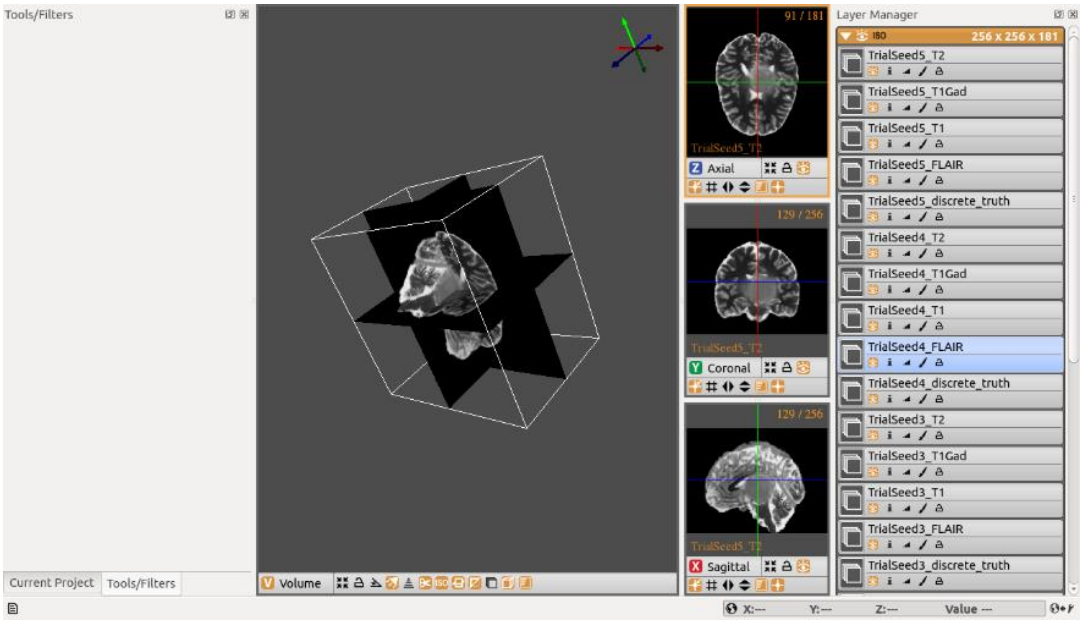


Figure 2: Segmented Image

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.

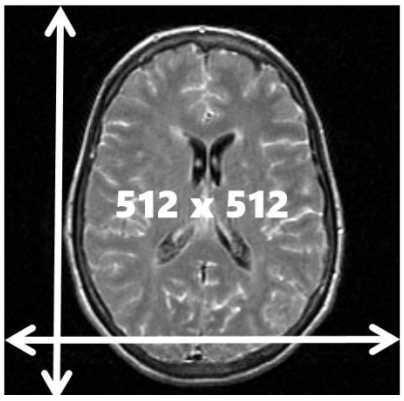


Figure 3: Image Registration

Example 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**.

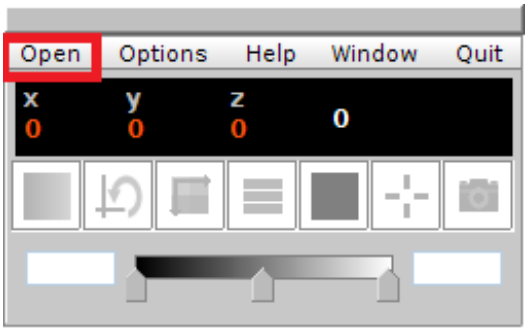


Figure 4: Mango Welcome screen

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

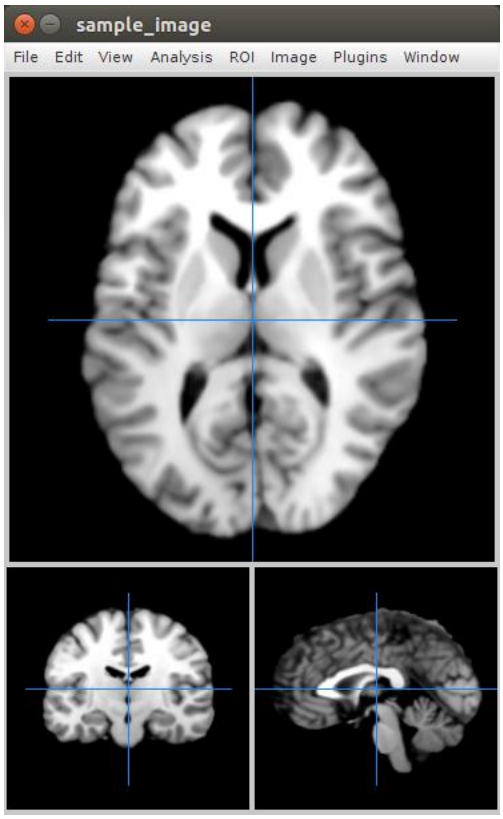


Figure 5: Registered Image

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

Image Surfacing

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

Example 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

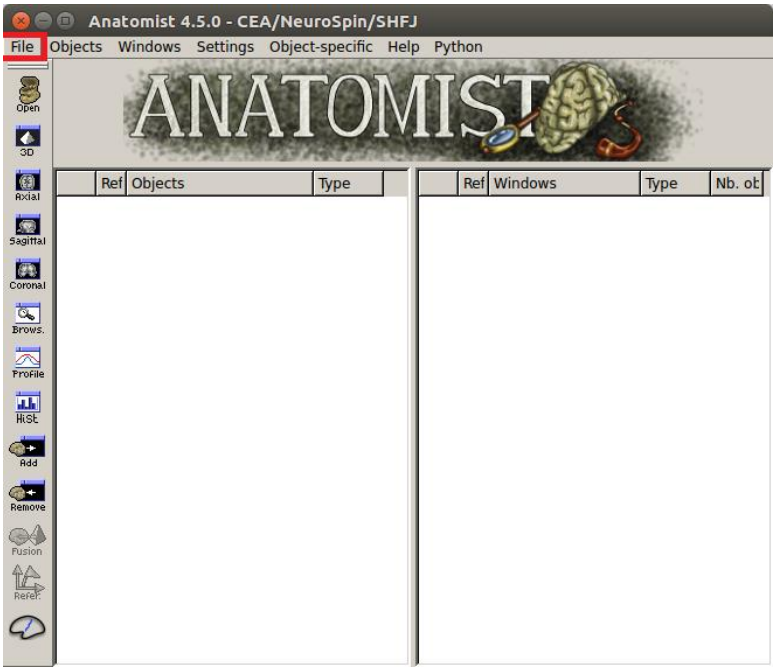


Figure 6: Anatomist Welcome screen

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.

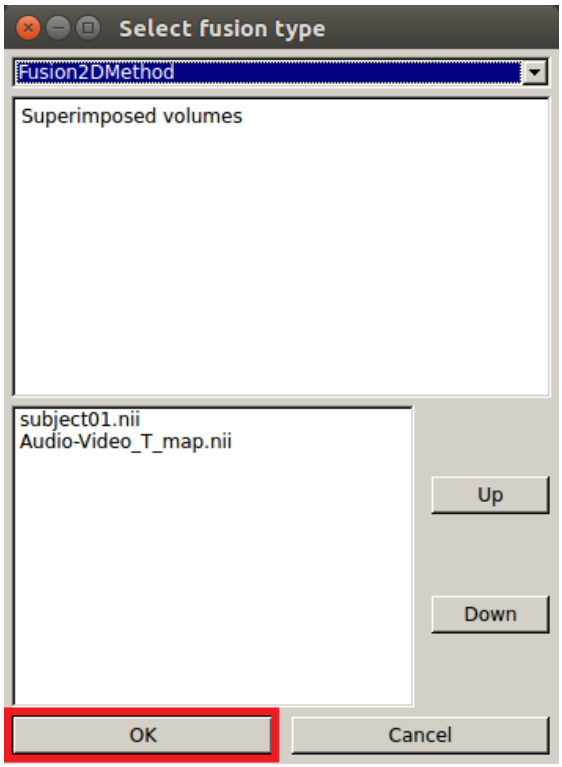


Figure 7: Fusion type selection screen

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

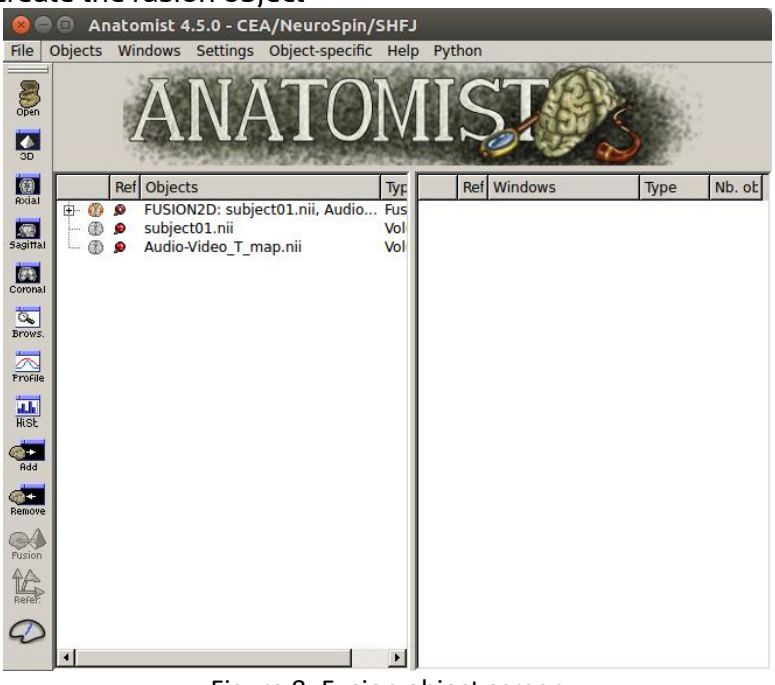


Figure 8: Fusion object screen

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

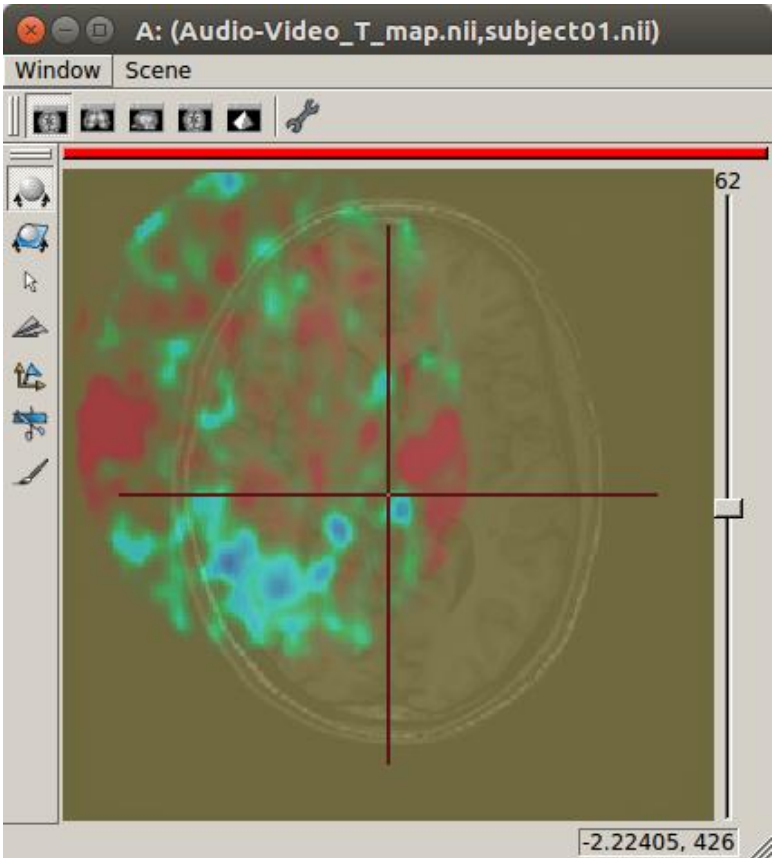


Figure 9: Fused mismatched image

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
- Example 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:

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

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.

Example tool ***ImageJ***

ImageJ [7]

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

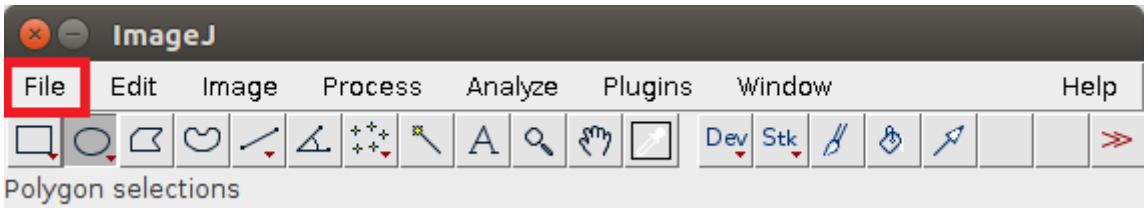


Figure 1: ImageJ Welcome Screen

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

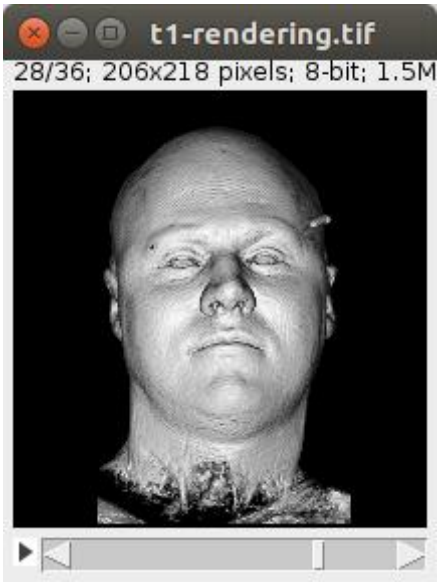


Figure 2: 3D Analyzed Image

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

Morphometric Analysis

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

Recommended tool ***FracLac***

FracLac [8]

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

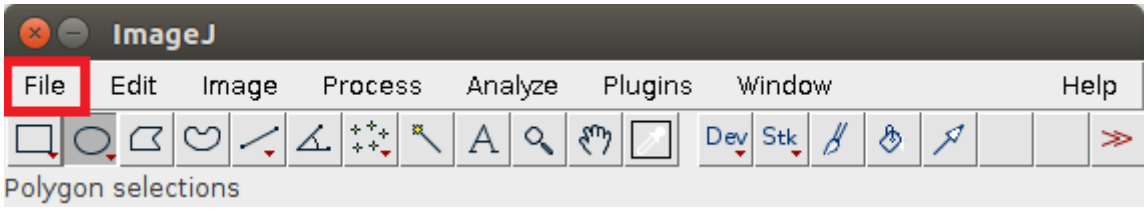


Figure 3: ImageJ Welcome Screen

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

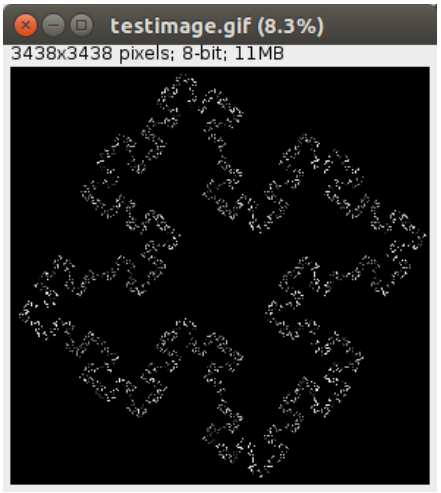


Figure 4: Sample Image

3. **Select** "BC"

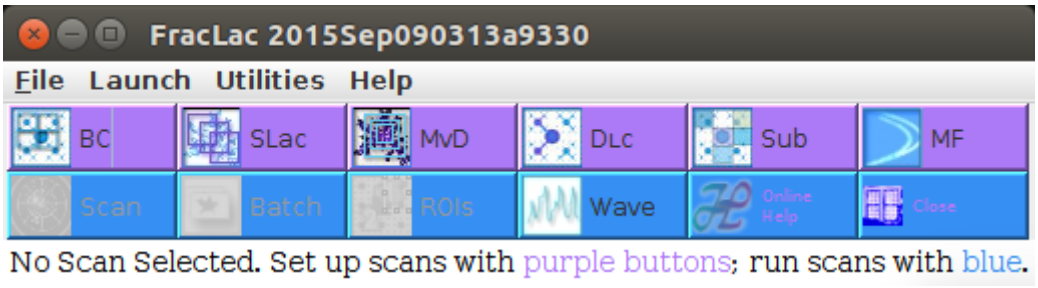


Figure 5: FracLac Welcome screen

4. **Select** OK

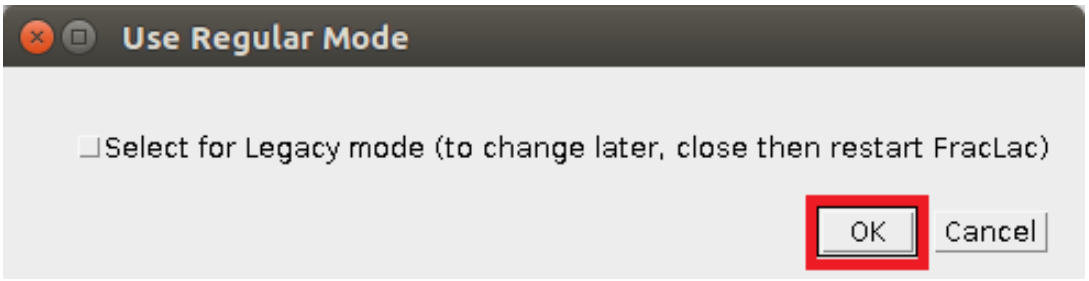


Figure 6: Mode Selection

5. **Select** OK

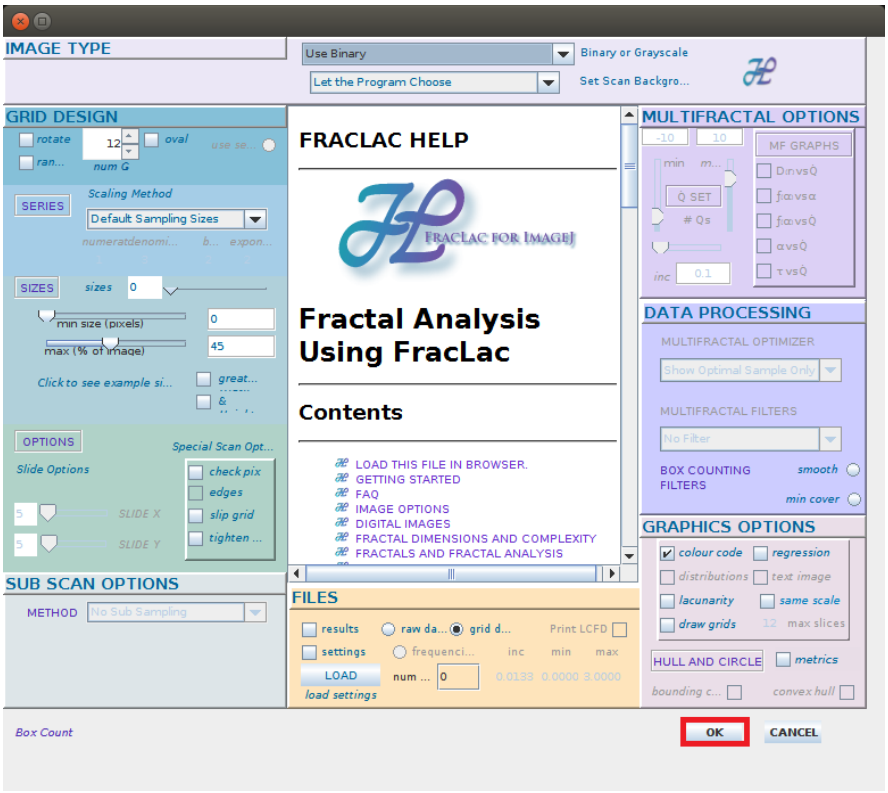


Figure 7: FracLac settings screen

6. **Select** OK

Figure 8 Colour Coding Selection screen

7. **Select** Scan

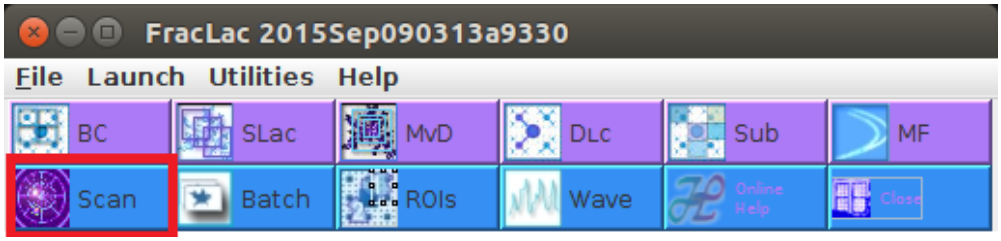


Figure: 9 Ready to scan

NOTE *Wait for the image to be processed.*

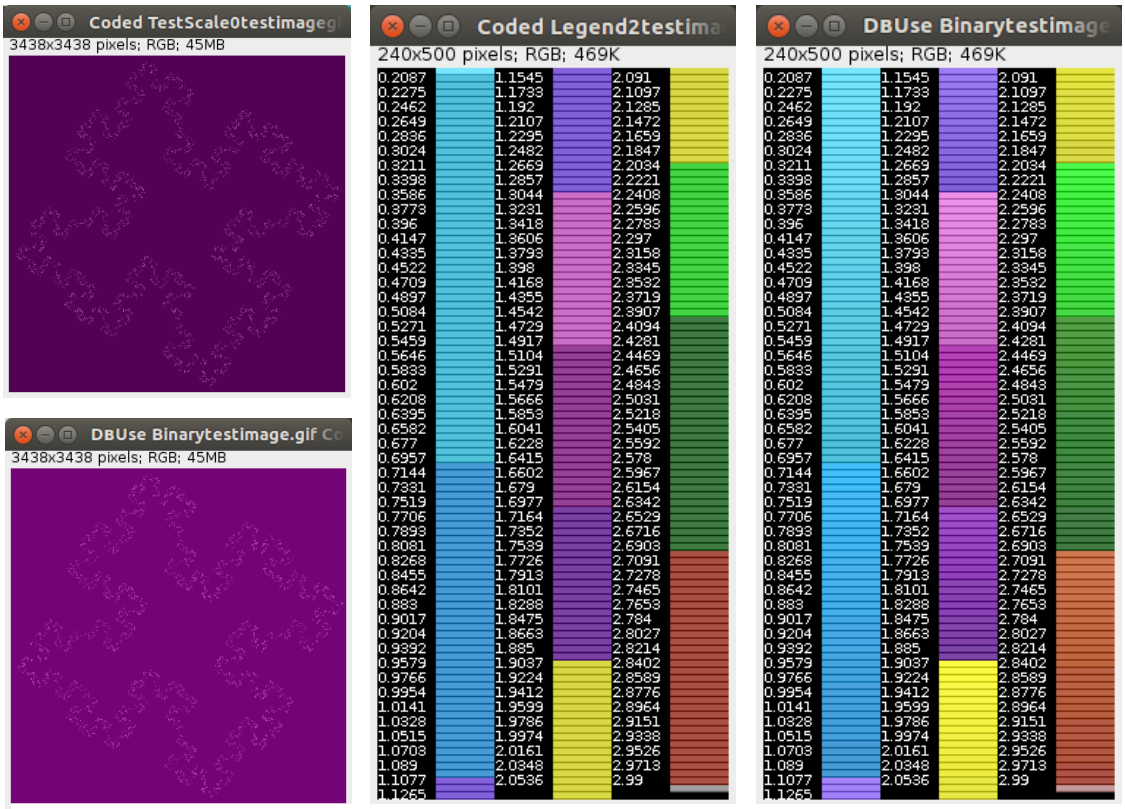


Figure 10: Analyzed Image

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

Image Classification

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

Example tool ***LA-iMageS***

LA-iMageS [9]

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

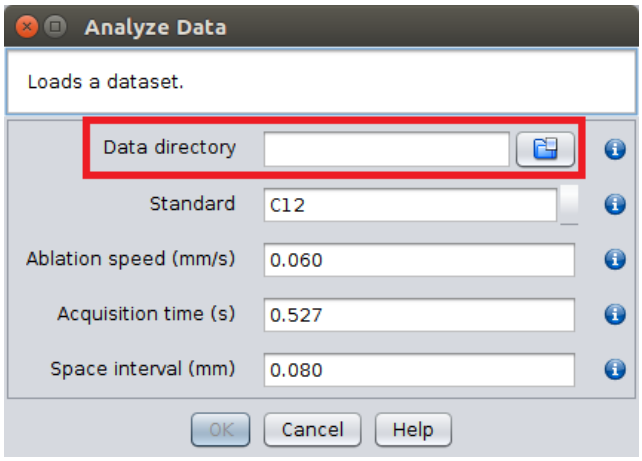


Figure 11: Load Dataset screen

3. **Select** OK.

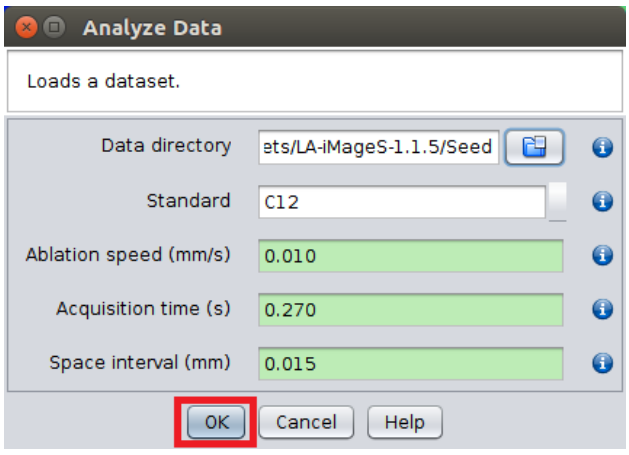


Figure 12: Analyze the Images

NOTE *Wait for the image to be processed.*

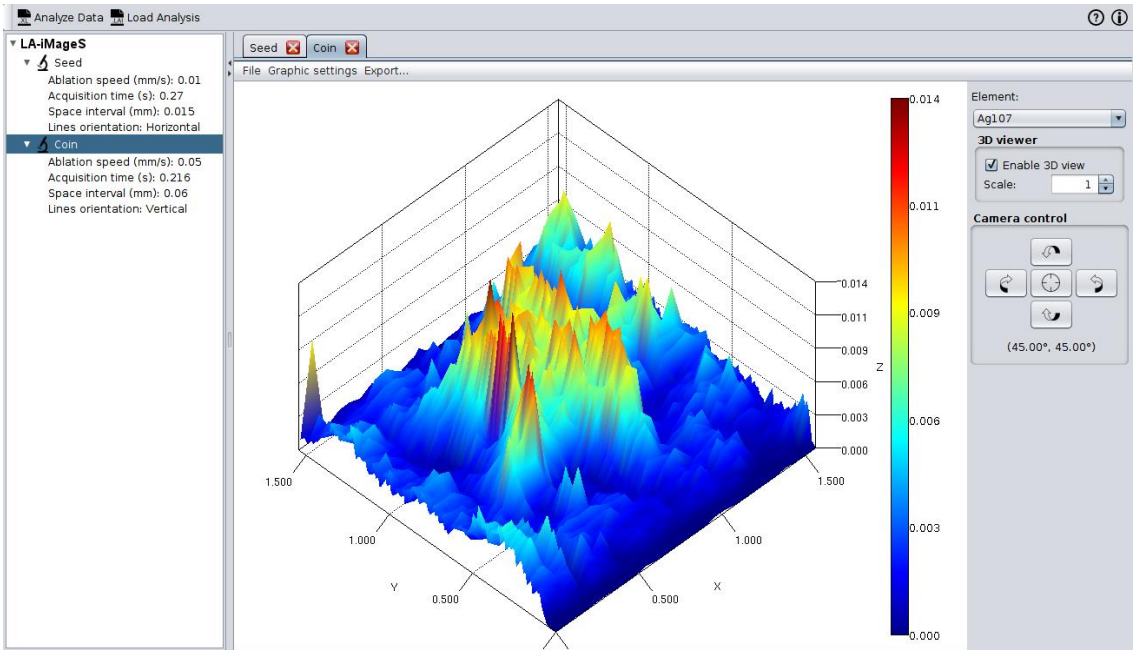
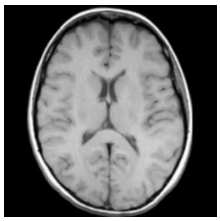


Figure 13: Analysed Image

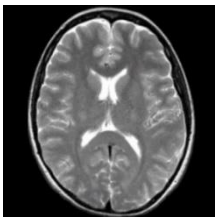
4. Further **Analyze** the image.

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 14: Comparison Between T1 and T2 weighted images

Example tool ***MRI*** ***Processor***

MRI Processor [10]

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

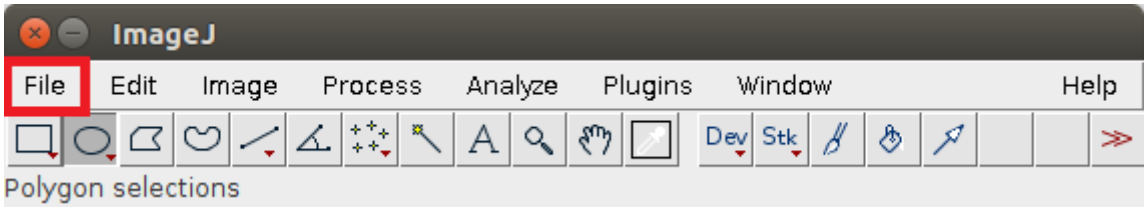


Figure 29: ImageJ Welcome Screen

3. **Select** the downloaded tutorial datasets:*subjectO1.nii*

Figure 30: Sample Image

4. **Select** Plugins → MRI Processor

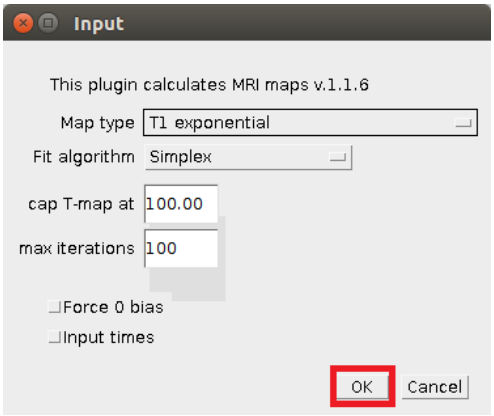


Figure 31: Mapping selection

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

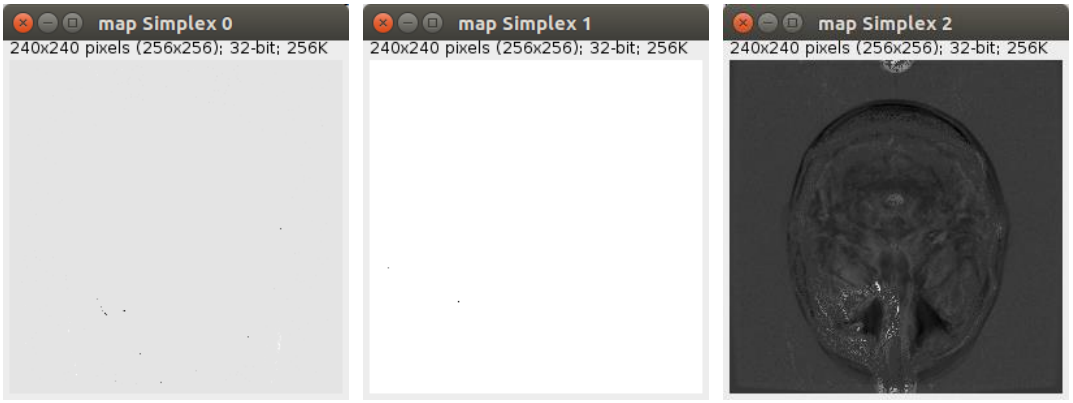


Figure 32: Mapped Images

7. Following are the Logs for Image Mapping:

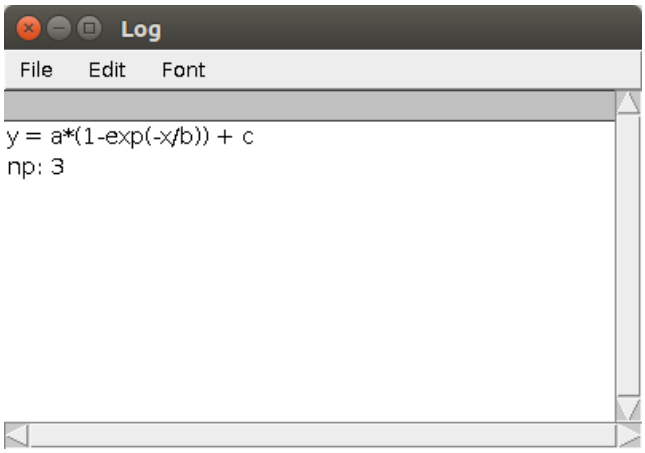


Figure 33: Mapping Logs

8. Further analyze the Image

Diffusion Analysis

In this Chapter

We will learn about:

- Diffusion Analysis
- Steps for Diffusion Analysis
- Example Tools for Diffusion Analysis of Images

Introduction

Diffusion analysis of an image captures the activity of neuronal tracts.

Diffusion Analysis has two significant steps:

- Image Simulation
- Tractography

Image Simulation

Numerical simulations can help deepen the understanding of the relationship between the cellular structure and the diffusion MRI signal and can play a significant role in the formulation and validation of appropriate models in order to answer relevant biological questions.

Example tool ***MITK-DI***

MITK-DI [11]

MITK-DI provides means to diffusion weighted image reconstruction, visualization and quantification. Diffusion tensors as well as different q-ball reconstruction schemes are supported.

1. **Run** the following commands on the terminal to start MITK-DI:

   $ cd /usr/local/bin

   $ ./MITK-Diffusion_ubuntu-20.04_2020.10.23_0f33cec9_663c55f1_NoPython.run

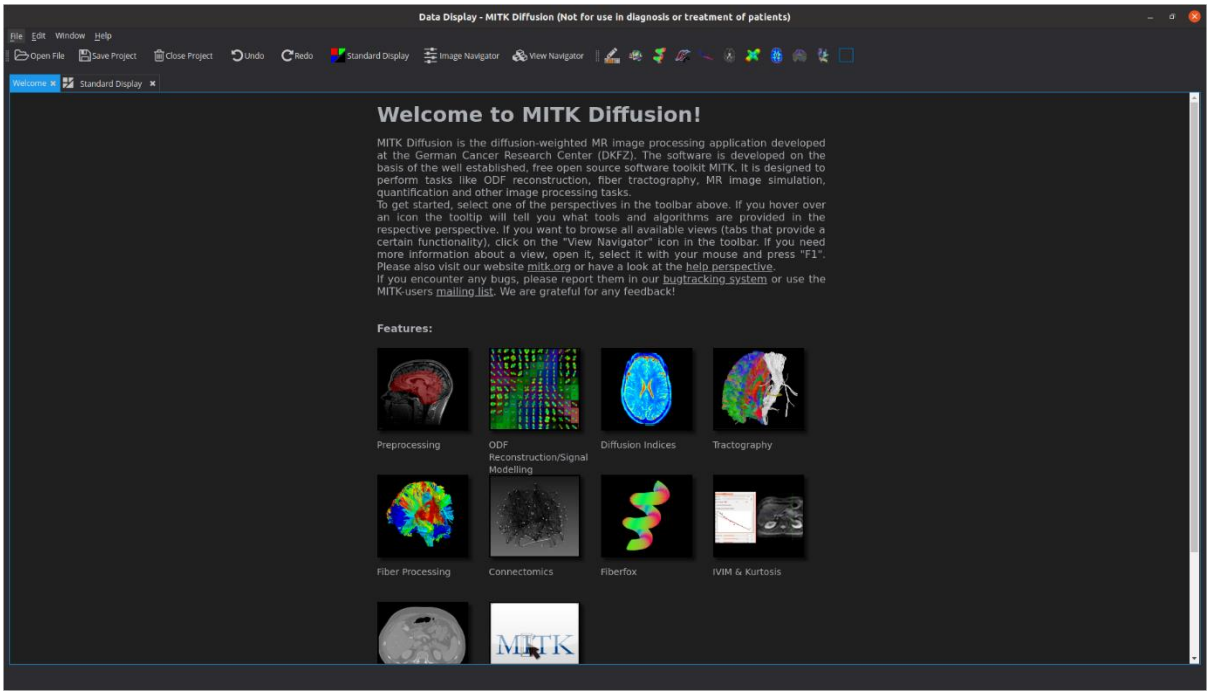


Figure 34: MITK Welcome Screen

2. Now use the relevant option for usage.

Tractography

In neuroscience, tractography is a 3D modeling technique used to visually represent nerve tracts using data collected by diffusion MRI. It uses special techniques of magnetic resonance imaging (MRI) and computer-based diffusion MRI. The results are presented in two- and three-dimensional images called tractograms.

Example tool ***medInria***

medInria [12]

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

Run the following commands on the terminal:

1. **Select** Diffusion

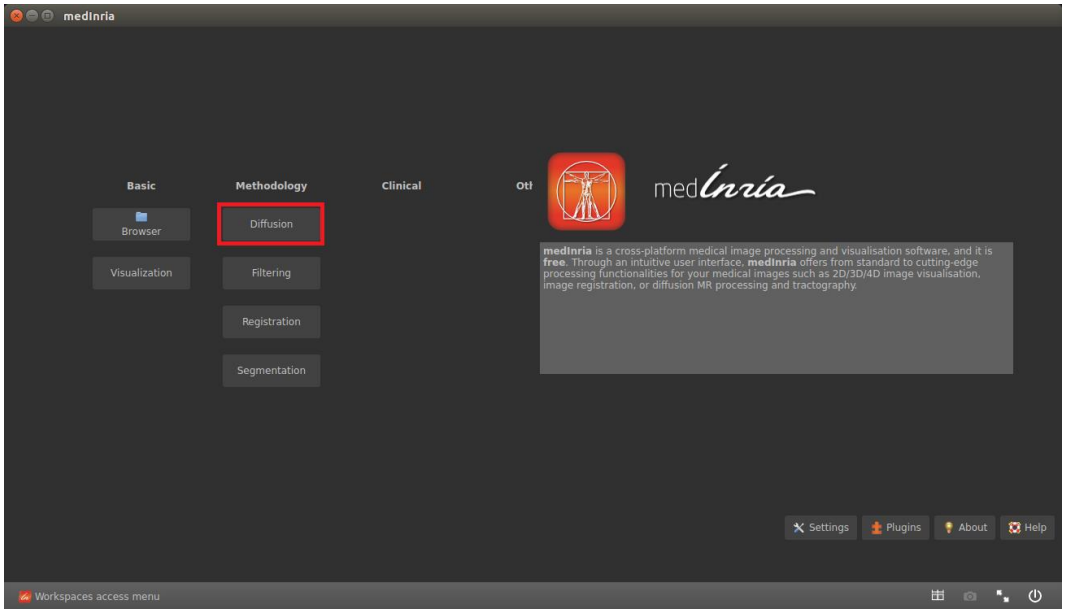


Figure 35: medInria Welcome Screen

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

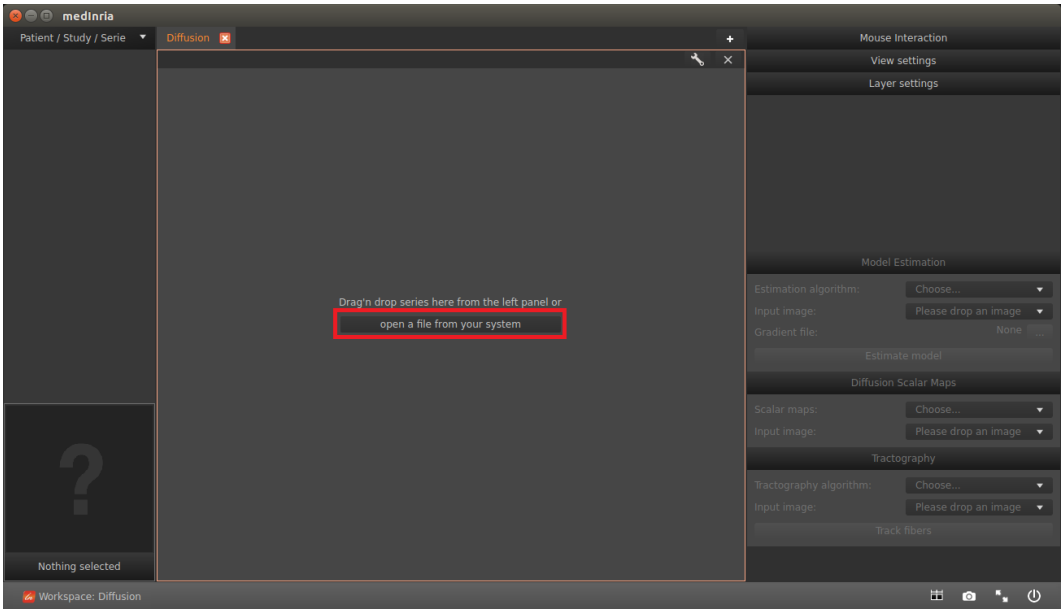


Figure 36: Load Study screen

5. **Select** the downloaded tutorial dataset file: *xDTICUBE-4D.nii.gz*
6. **Select** the Estimation Algorithm as DTI estimation, in the Model Estimation tab.
7. **Select** the gradient file: *gradient7.txt*

Figure 37: Model Estimation

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

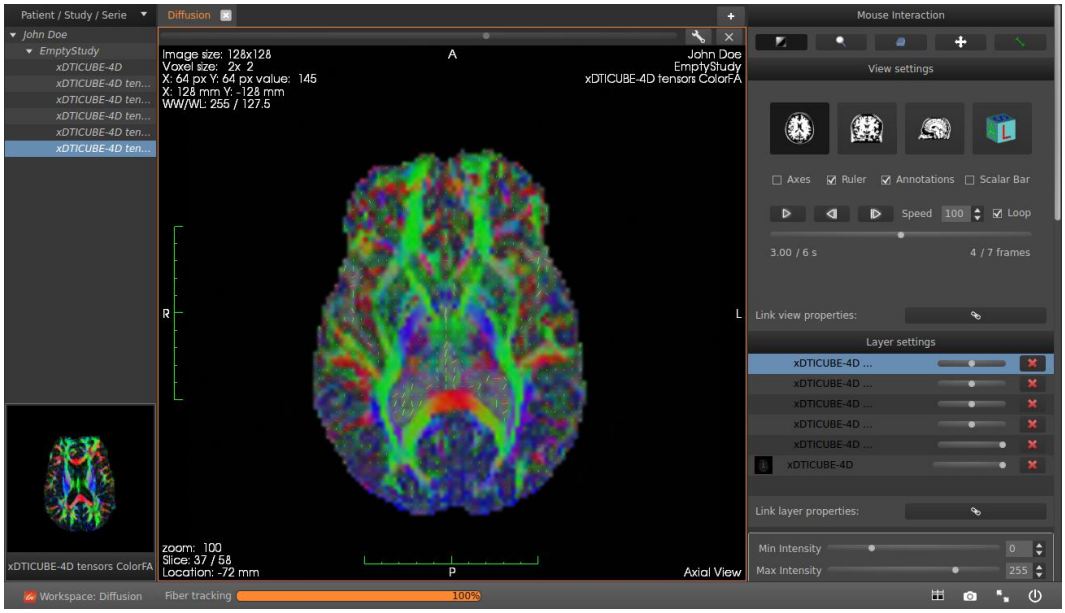


Figure 38: Diffusion Estimated Image

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

Functional Analysis

In this Chapter

We will learn about:

- Functional Analysis
- Steps for Functional Analysis
- Example Tools for Functional Analysis of Images

Introduction

Functional analysis of an image measures brain activity by detecting changes associated with blood flow.

Functional Analysis has two significant steps:

- Neuroimage Analysis
- Neuroimage Visualization

Neuroimage Analysis

The goal of fMRI data analysis is to detect correlations between brain activation and a task the subject performs during the scan. It also aims to discover correlations with the specific cognitive states, such as memory and recognition, induced in the subject.

Example tool ***FSL***

FSL [13]

FSL, is a software library containing image analysis and statistical tools for functional, structural and diffusion MRI brain imaging data.

1. Type FSL on search bar and click on it to run it

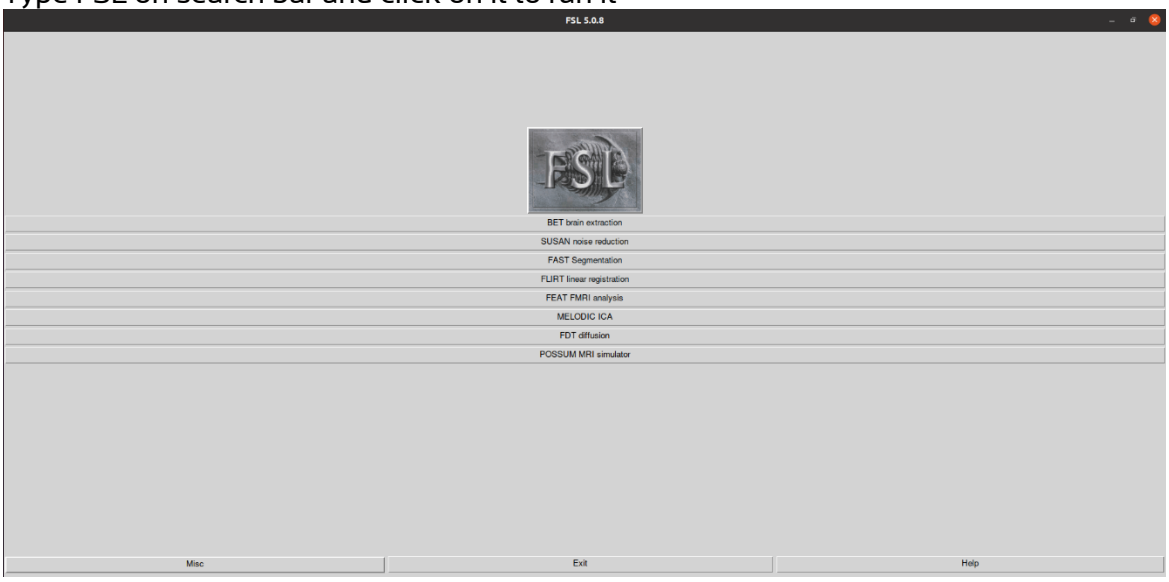


Figure 39: FSL Welcome Screen

2. Now use the relevant option for analysis

Neuroimage Visualization

Sophisticated visualization tools are essential for the presentation and exploration of human neuroimaging data. While two-dimensional orthogonal views of neuroimaging data are conventionally used to display activity and statistical analysis, three-dimensional (3D) representation is useful for showing the spatial distribution of a functional network, as well as its temporal evolution.

Example tool ***Papaya***

Papaya [14]

Papaya, is an open-source neuroimaging toolkit for processing, analyzing, and visualizing human brain MR images. Go to following folder.

```
$ /opt/aXonica_v4.0/papaya/build
```

1. Click on index.html
2. It will open up papaya on your browser

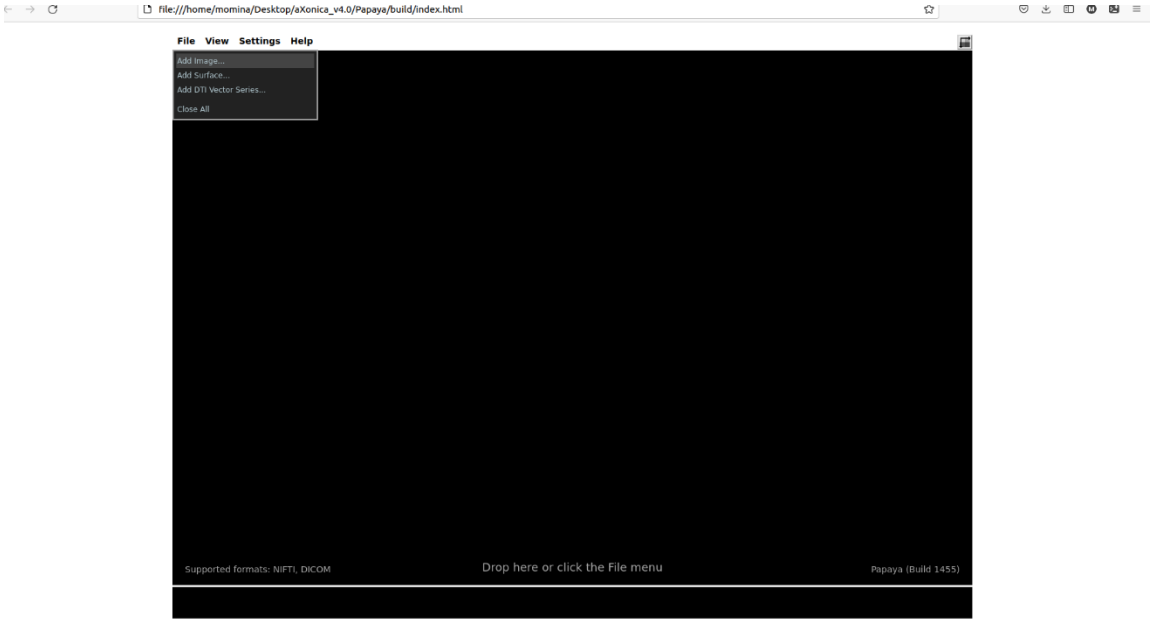


Figure 40: Papaya Welcome Screen

3. Now load image in nifty or dicom format and visualize it

Figure 41: Load and Analyze 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.

Example tool ***MRIcron***

MRIcron [15]

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

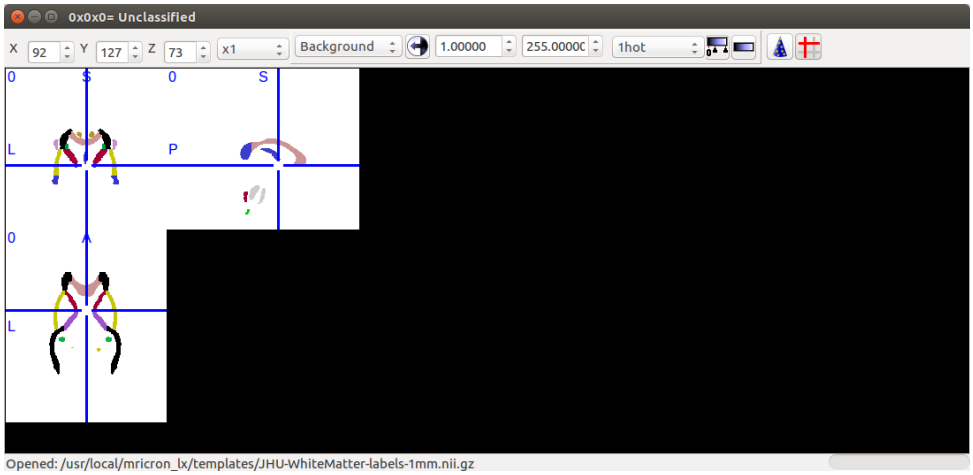


Figure 1: MRIcron Welcome screen

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.

Example tool **WEASIS**

WEASIS [16]

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.

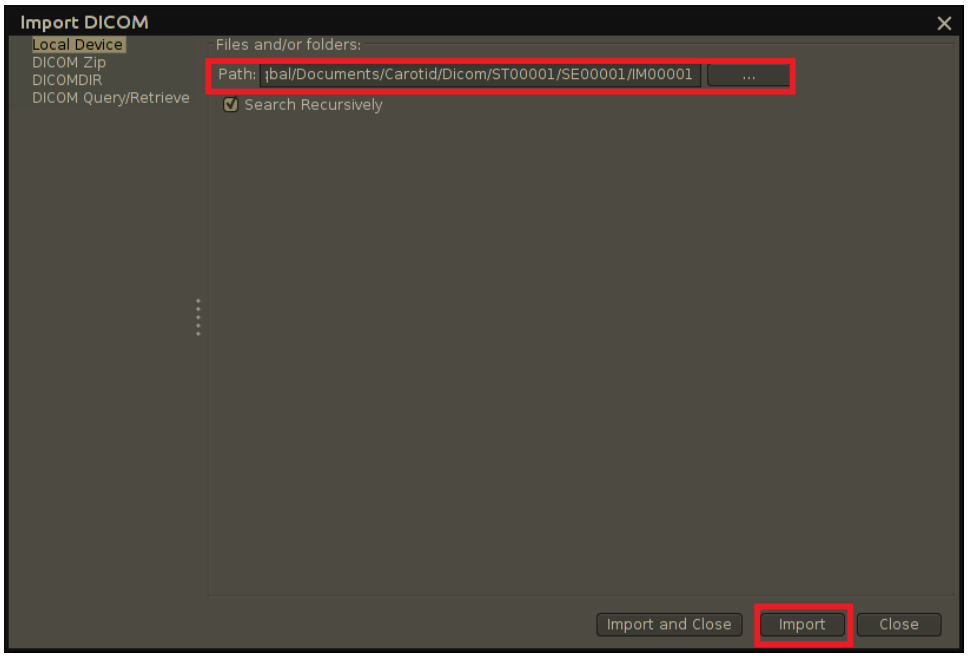


Figure 3: Import DICOM

4. **Select** "Import".

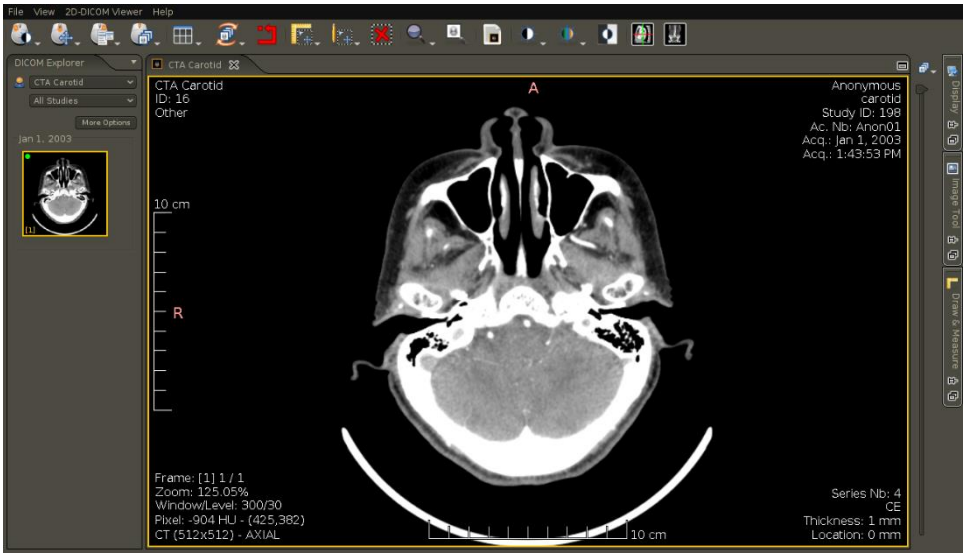


Figure 4: DICOM Image

5. Further Analyze the image.

Post Installation

Post Installation of aXonica software

After the installation of aXonica is complete you can use some of the installed tools as follows:

Anatomist

It is installed and used with BrainVISA.

```
$ cd /brainvisa-4.5.0

$ ./anatomist
```

Dipy

This tool is a python setting for **MRI** database.

BoneJ

It is a plugin for ImageJ. It is installed in: Package/Plugins folder. Copy the .jar file and paste in the plugins folder of ImageJ for usage.

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

ImageVIS 3D

```
$ cd /usr/local/ImageVis3D-3.1.0/

$ ./ImageVis3D
```

AMIDE

```
$ export UBUNTU_MENUPROXY=0

$ amide
```

PID

This is a command line interface tool. Its user manual is provided.

TORTOISE

```
$ cd /usr/local/TORTOISE_V3.1.0/TORTOISE_GUI

$ gksu python TortoiseGui.py
```

normalizeFOV

This is a command line interface tool. Its user manual is provided.

FastFilter3D

It is a plugin for ImageJ. It is installed in: Package/Plugins folder. Copy the .jar file and paste in the plugins folder of ImageJ for usage.

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

ITK-Snap

```
$ cd /usr/local/itksnap-3.6.0-20170401-Linux-x86_64

$ cd bin/

$ ./itksnap
```

HeteroscedasticfMRI

This is a command line interface tool. Its user manual is provided.

pyClusterROI

This is a command line interface tool. Its user manual is provided.

BrainSeg3D

```
$ cd /usr/local/brainseg3d

$ ./BrainSeg3D
```

CMP-BIA

It is a plugin for ImageJ. It is installed in: Package/Plugins folder. Copy the .jar file and paste in the plugins folder of ImageJ for usage

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

ITK

This is a command line interface tool. Its user manual is provided.

E-Snake

It is a plugin for ImageJ. It is installed in: Package/Plugins folder. Copy the .jar file and paste in the plugins folder of ImageJ for usage

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

mincBEAST

This is command line interface tool. Its user manual is provided.

Segmentator

This is command line interface tool. Its user manual is provided.

Mango

```
$ cd /usr/local/Mango

$ ./mango
```

bUnwarpJ

It is a plugin for ImageJ. It is installed in: Package/Plugins folder. Copy the .jar file and paste in the plugins folder of ImageJ for usage

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

BrainVISA

```
$ cd /brainvisa-4.5.0

$ ./anatomist
```

The Virtual Brain

```
$ cd /usr/local/TVB_Distribution/bin/

$ ./tvb_start.sh
```

CBS Tools

It is a plugin for LA-iMageS.

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

> chmod +x run.sh
```

```
> ./run.sh
```

HegaEtAl2017

This is a command line interface tool. Its user manual is provided.

NEURON

This is a command line interface tool. Its user manual is provided.

SliceMap

It is a plugin for ImageJ. It is installed in: Package/Plugins folder. Copy the .jar file and paste in the plugins folder of ImageJ for usage

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

Nengo

This is command line interface tool. Its user manual is provided.

neuroConstruct

```
$ cd /usr/local/neuroConstruct_1.6.0

$ gksu bash neuroConstruct_1.6.0
```

MedInria

```
$ cd /usr/local/medinria-2.2.3-Linux-x86_64

$ cd bin/

$ ./medInria_launcher.sh
```

Brian

This is command line interface tool. Its user manual is provided.

Time Domain decoding

This is command line interface tool. Its user manual is provided.

Fraclac

It is a plugin for ImageJ. It is installed in: Package/Plugins folder. Copy the .jar file and paste in the plugins folder of ImageJ for usage

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

Gwyddion

```
$ gwyddion
```

LA-iMageS

```
$ cd /usr/local/LA-iMageS-1.1.5

$ chmod +x run.sh

$ ./run.sh
```

Brainstorm

```
$ cd /usr/local/brainstorm3/bin/R2015b/

$ gksu bash brainstorm3.command
```

ImageJ

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

Nipype

This tool is python setting for MRI database.

MRI Processor

It is a plugin for ImageJ. It is installed in: Package/Plugins folder. Copy the .jar file and paste in the plugins folder of ImageJ for usage

```
$ cd /usr/local/ImageJ

$ ./ImageJ
```

NiBabel

This tool is python setting for MRI database.

MRIcron

```
$ cd /usr/local/mricron_lx

$ ./mricron
```

MIPAV

```
$ cd /usr/local/MIPAV
```

```
$ ./mipav
```

WEASIS

```
$ cd /usr/local/weasis
```

```
$ ./viewer-linux.sh
```

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