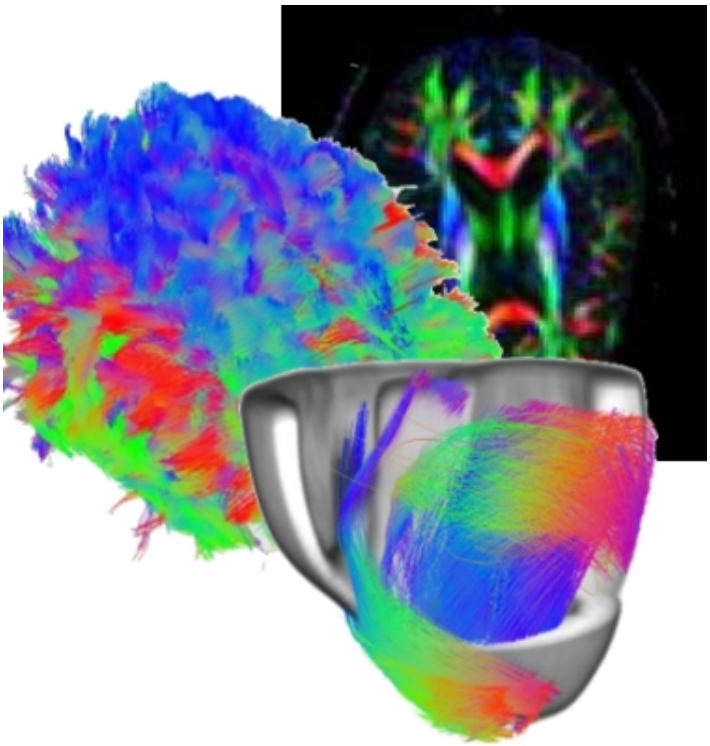
INRIA

INRIA Sophia-Antipolis
Research Project Asclepios

Medical Image Navigation and Research Tool by INRIA (MedINRIA 1.9) Tutorial v2.0



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Contents

Chapter 1

Introduction

This section explains the purpose of the MedINRIA software, and explains the screen layout. The organization of this tutorial is as follows: The introduction explains purposes and requirements of the software. Then chapters 2 to 5 describe in detail each of the available modules.

1.1 System Requirements

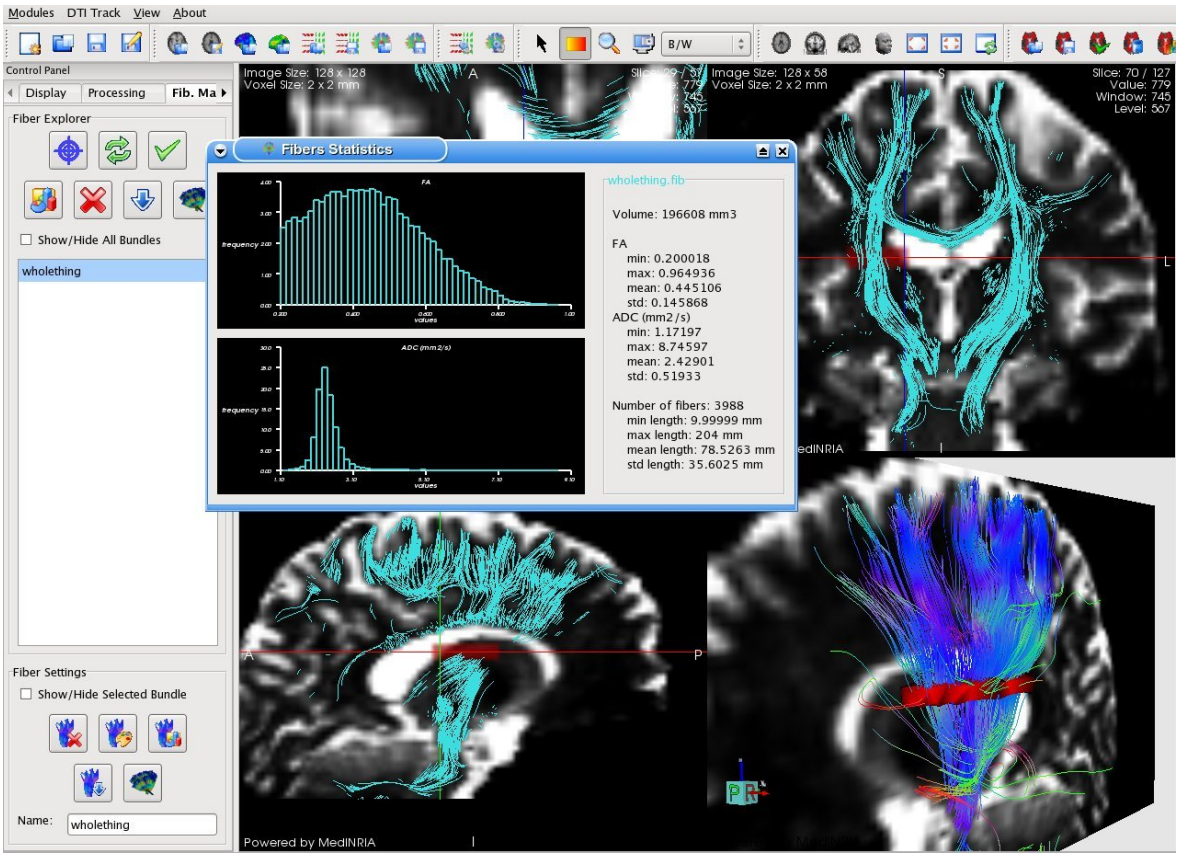
MedINRIA is available for Microsoft windows XP (x86 and x64), UNIX and MAC soon. At least 1GB of memory is required, as well as a powerful processor (P4 2GHz, AMD FX 3800+ or later). Also, a powerful graphic card is needed (nvidia GForce 6600GT or later, ATI Radeon). You may experience difficulties to visualize images with volume rendering technique using an ATI card (this is a known issue). MedINRIA is multi-threaded, thus optimaly using technologies such as Intel Core duo, or AMD Dual-Core.

1.2 Purpose and Organization of MedINRIA

MedINRIA is a platform containing a set of softwares. These modules have been developed by the INRIA research team Asclepios at Sophia Antipolis, France. This project was initiated by Pierre Fillard (PhD student at Asclepios) and Nicolas Toussaint (intern at Asclepios). At this time, 6 modules are available: A simple (yet powerful) Image Viewer, DTI Track, which contains routines for DTI processing and fiber tracking using Log-Euclidean metrics developed at Asclepios, a Tensor Viewer module aiming at visualizing volume of tensors with glyphs, a Registration Tool module, entirely dedicated to image registration, and registration result evaluation, two modules specialize in the analysis of multiple scerosis lesions, and a specific viewer for brain sulcal lines.

MedINRIA is available on line : http://www-sop.inria.fr/asclepios/software/MedINRIA

Next figure shows a snapshot of the main MedINRIA window, with the DTI Track module loaded. Modules can be loaded/unloaded from the menu “File→Modules”. When a module is loaded, it will be displayed in the MedINRIA main window, replacing any other previously loaded module. Moreover, a Log-Window will display the standard output, as well as any error that occurs during the processing, thus telling you about the nature of the error (file not found, process aborted by user, etc.). This Log-Window can be switched on/off from the menu “View→Show Log (toggle)”.



Chapter 2

Image Viewer Module

Contents

This module is a simple but yet powerfull medical image browser. No data processing can be performed from here, for that please refer to the other modules.

From this module you can quickly open several images in a "web browser style". It also provide an easy-to-use DICOM importer and a "radiologic convention reorientation tool".

2.1 File Formats

The image file formats supported include those of ITK (Insight ToolKit): Analyze 7.5 (.hdr, .img), Metafile (.mha, .mhd), Gipl (.gipl), VTK image data (.vtk), Dicom (.dcm), Ge4x, GDCM, Nrrd, Siemens Vision, PNG, BMP, TIFF, JPEG, ... For dicom images without extensions, please use "All" filter.

2.2 DICOM import

The DICOM importer is a simple wizard that allow the user to import images directly from a DICOM exam. It can reconstruct 3D volumes from 2D DICOM files.

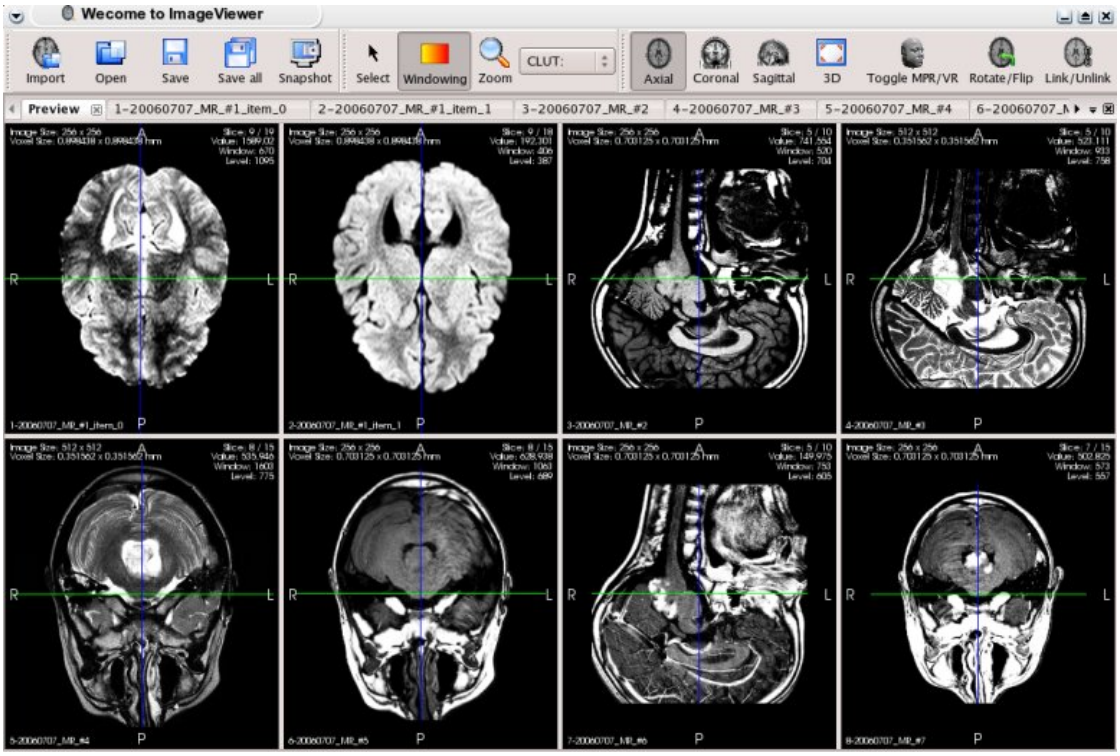


Figure 2.1: **The Image Viewer window, shown here in the preview screen where some volumes have been imported from a DICOM exam.**

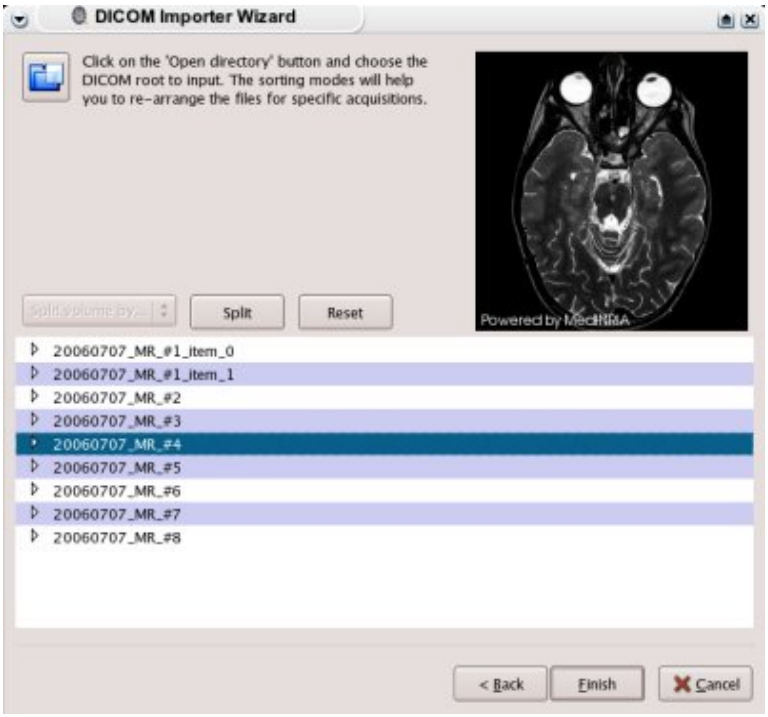


Figure 2.2: **The DICOM importer main window, shown with brain exam loaded. Click "Open" button to set the directory to scan.**

IMPORTANT : This tool does not import 3D DICOM files ! You can open them directly from the open button.

First click on the "Open" button to choose the DICOM root directory that contains the exam. Carefull : the importer will scan recursively into this directory, don't choose a directory that contain several exams to prevent from memory overloads.

The volumes should now appear in the main table window. Each line with an arrow represents a volume. Double click on it to see what files this volume is made from. Clicking on one file will popup the corresponding image on the view window in the upper right corner. The files should be shown in correct order, following a consistent strategy : files are first splited in series and ordered by the image position DICOM flag. If for some reason the user ends up with a mixed up volume, it might be because of image position conflicts (It often happen in T2/proton density protocols). Then the user can click on "split" button that provides a consistent split process among the image positions given in the DICOM files. Clicking on reset button will go back to the original configuration.

Last step (click "finish") will reconstruct 3D volumes from the last given fileset configuration.

IMPORTANT : The DICOM importer in its current state doesn't take care of the orientation acquisiton of the the image. That might results in "radiologic convention" issues.

All the DICOM exam volumes are now visible in the preview window. For the user convinience, a "save all" button has been added in order to quickly save all the loaded images in a given directory. They will be saved in ITK Analyze format (.hdr - .img).

2.3 Image browsing

The preview window shows every volume loaded in the Image Viewer. you can quickly access to one of the images by clicking on the down arrow icon in the upper right corner. it will pop up a list of the images. In the preview window, you can choose to link (default) or unlink the views for the current chosen interaction (see Sect. 2.4). The user can click in one tabulation to switch to the corresponding image. When one of the image is shown, you can easily delete it by clicking in its corresponding cross.

2.4 2D-3D view interactions

2.4.1 2D Views

Three 2D views are shown in the main window, corresponding to the axial, coronal and sagittal views of the volume. On each view some information is shown, such as the resolution

of the slice (in pixels), the size of a voxel (in mm), the index of the slice being shown, and the value of the pixel at the current selection). By default, a trilinear interpolation is made between pixels. Press **"i"** to disable this interpolation.

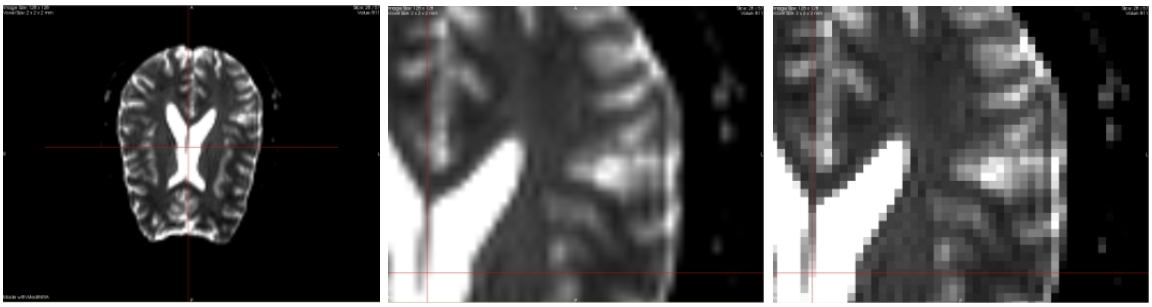


Figure 2.3: 2D view navigation. On the left you see a 2D view (axial) centered on the screen. When the zoom interaction is selected, you can zoom in the view by moving the mouse up while left-clicking on the view and translate the view by middle-clicking (middle figure). You can disable the interpolation between pixel by pressing **"i"** (right figure). Reset the image position by pressing **"r"**.

 Several mouse interactions are available. With the selection interaction (black arrow), you will navigate in the volume (i.e. select a slice) by moving the mouse up or down while left-clicking on a view. Press **"r"** to reset the position to default.

 The second interaction (windowing) controls the brightness/contrast of the image by moving the mouse while left-clicking on the view. A left-right movement controls contrast while up-down controls brightness. Note that with these two interactions, the 4 different views are synchronized. Press **"r"** to reset the contrast to default value.

 With the zoom interaction, you can zoom in or out the 2D view by left-clicking and moving the mouse up or down. A middle click in the view will translate the image. Press **"r"** to reset the zooming.

Keyboard and mouse on 2D screen :

- Press **"i"** to activate or disactivate interpolation between pixels.
- When selection interaction is ON (black arrow), move the mouse up or down while left clicking to change slice. This action can also be done using keys ↑ and ↓.
- When windowing interaction is ON, move the mouse left/right to change the contrast, move the mouse up/down to change brightness.
- When zoom interaction is ON, move the mouse up/down while left clicking to zoom. Move the mouse while middle clicking to translate the view.
- For any interaction, press **"r"** to reset the interaction.

2.4.2 3D View

On the lower-right part of the main window is shown a 3-dimentional representation of the volume. You can manipulate the volume in different ways:

- Rotate the volume by moving the mouse while left clicking in the 3D view.
- Translate the volume by moving the mouse while middle-clicking in the 3D view.
- Zoom into the volume by moving the mouse up or down while right-clicking in the 3D view.

 You also can display the 3D view in full screen by pressing the "full screen" button. When the 3D view is in full screen, you can use the "snap shot" button to easily save a .jpg picture of the current screen.

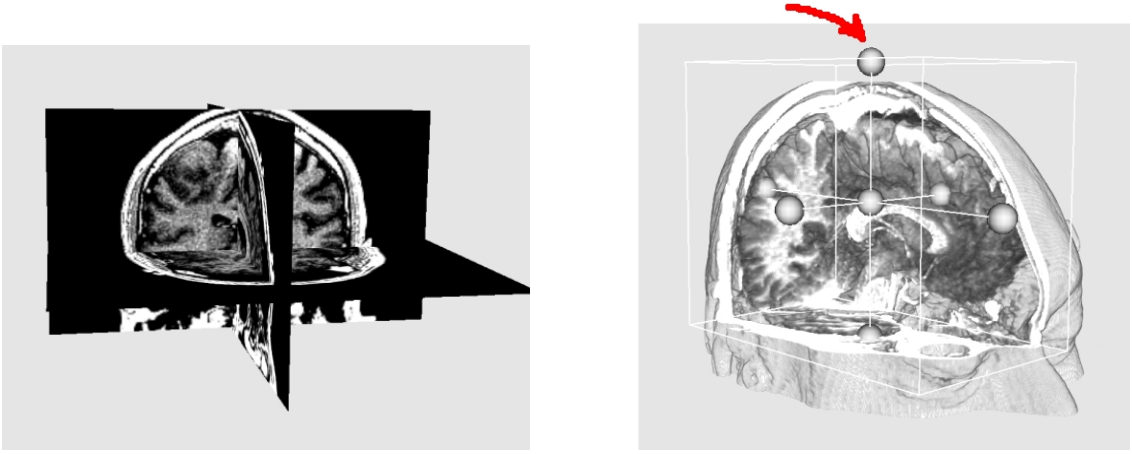


Figure 2.4: 3D view. You can see on the left a Multi-Planar Reconstruction (MPR) of the image. On the right you see a Volume Rendering (VR) of the image, cropped by the cropping box to visualize inside the volume. The cropping box can be manipulated by control points (red arrow).

 You can choose between displaying an image with Multi-Planar Reconstruction (MPR) (Fig. 3.7, right) or with Volume Rendering (VR) (Fig. 3.7, right). When VR mode is chosen, you have the possibility to take out a part of the volume in order to visualize inside it. This can be done with the "cropping box". Use the control points around the box (red arrow in Fig. 3.7, right) to resize it and crop the volume (left-click on them). The control point in the center of the box allows you to translate it. When you have finished cropping the volume, you can make the box disappear by typing "b" on your keyboard. The orientation cube and the 3D axes help to recognize the current orientation of the image, and can be switched on or off with "i" keyboard key.

Keyboard and mouse on 3D screen:

In the 3D view, several optional features are available :
- Shift+left-click translates the volume.

- Ctrl+left-click rotates the volume around the axis perpendicular to the screen.
- Press **"j"** activates "joystick" mode (continuous movement mode).
- Press **"t"** disables the "joystick" mode.
- Shift+left-click on the cropping box translates it.
- Right-click on the cropping box makes it grow or shrink.
- Press **"r"** to center the image.
- If you cannot access the cropping box : Press "b" to switch it on, then press the "center view" button. If you still don't see it, it may be inside the volume. Then translate it outside the volume.
- If the cropping box doesn't seem to work properly, it might be because it has been flipped over. Use successively the control points of the box to flip it back to normal.

2.5 Image reorientation tool

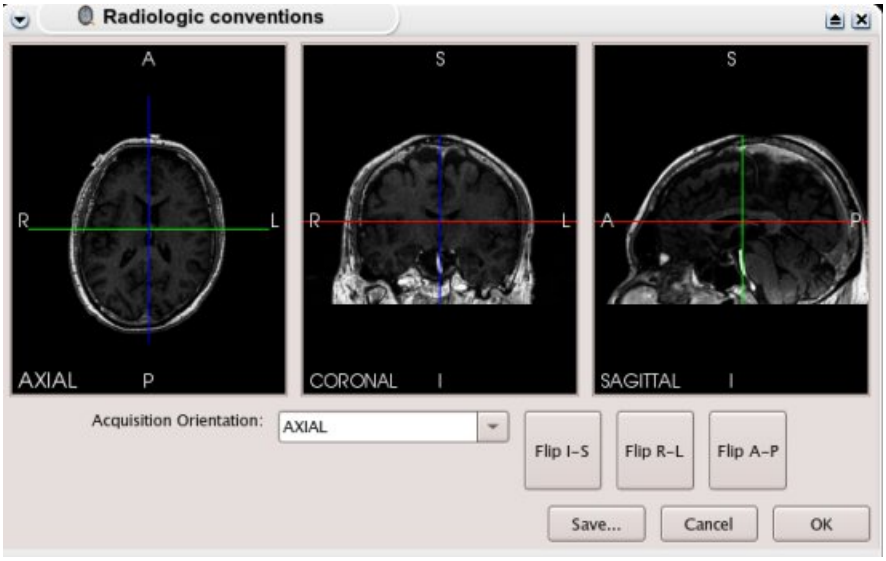


Figure 2.5: **The Reorientation Tool main window.**

This tool helps the user to manually re-orientate the image if this one doesn't match the radiologoc conventions correctly. The 3 views correspond respectively to the axial view, the coronal view and the sagittal view of the image.

If the image has been acquired in another direction than axial, you can switch the acquisition orientation flag in the check box. If the image is still flipped over an axis, you can use switch the flipping flags for the three directions. I-S corresponds to Inferior-Superior direction, R-L to Right-Left, and A-P to Anterior-Posterior.

Once the image meets correctly the conventions, you may want to save it in this orientation by clicking "save".The image will be saved in ITK analyze format (.hdr - .img) if no extension is given.

Chapter 3

DTI Track Module

Contents

This section contains all information regarding the DTI Track Module. This module aims at providing to clinicians all the necessary tools for DTI analysis and fiber tracking. This section is divided into sub-sections, described as follows. In Sec. 3.2, we detail how to import your own DTI data into the module. In Sec. 3.3, we discuss the visualization of images, the possible interactions, the rendering techniques, etc.

In Sec. 3.4.1, 3.4.2, and 3.4.3, we show how to process your data : from diffusion tensor field estimation to tensor to scalar maps computation (like Fractional Anisotropy - FA), and of course fiber tracking. In Sec. 3.5.1 and 3.5.2, we show how to navigate in the connectivity and extract a specific bundle. Finally, Sec. 3.7.1 and 3.7.2 describe some other features, like how to load an activation map obtained in fMRI.

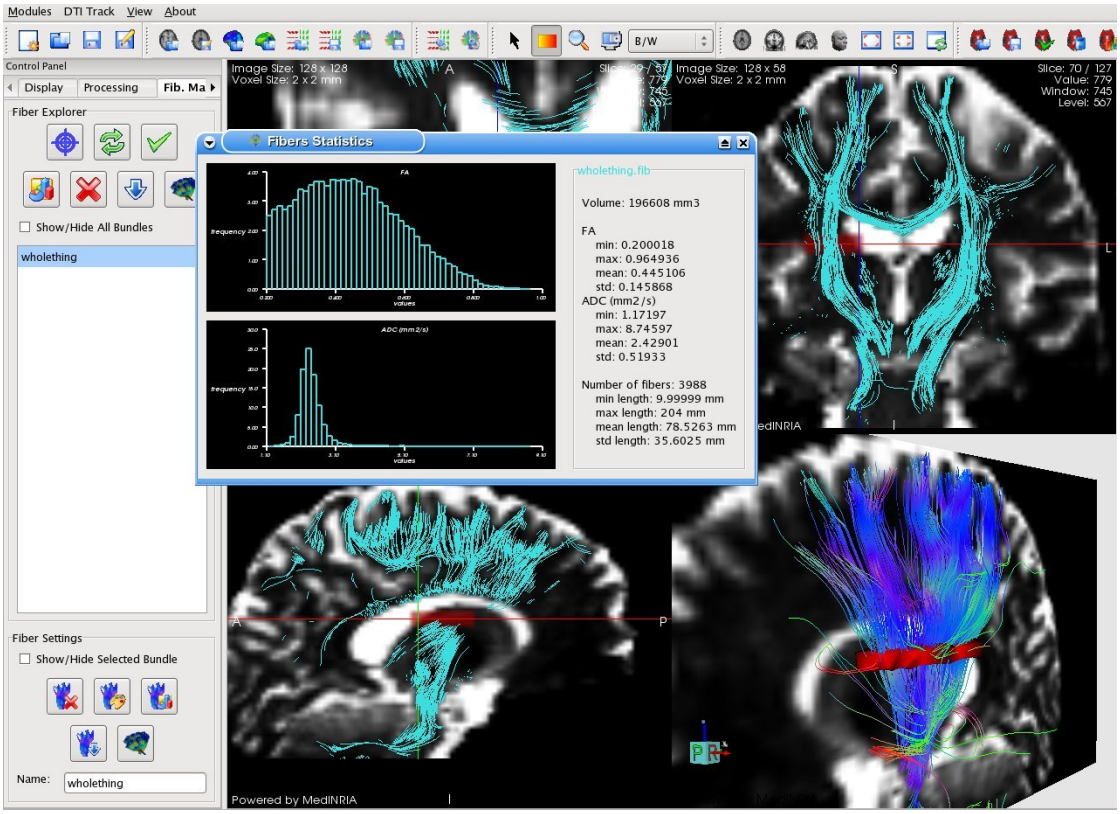


Figure 3.1: **The DTI module window. On the top you can see a set of toolbars, on the left the option panels, and the four main views (2D and 3D).**

3.1 File Formats

The image file formats supported by DTI Track include those of ITK (Insight ToolKit): Analyze 7.5 (.hdr, .img), Metafile (.mha), Gipl (.gipl), VTK image data (.vtk), Dicom (.dcm), Ge4x, GDCM, Nrrd, Siemens Vision, PNG, BMP, TIFF, JPEG. Altough MedINRI is capable to read Dicom files, it cannot reconstruct a full volume (i.e. it cannot handle a series of dicoms). For a volume reconstruction from dicoms, you can use MRIConvert (http://lcni.uoregon.edu/~jolinda/MRIConvert/) for Windows, or MRIcro (http://www.sph.sc.edu/comd/rorden/mricro.html) for Linux.

The tensor files are stored in a homemade format, called Inrimage (.inr, .inr.gz), this is a compressed file to save memory. The fiber files are in VTK file format (vtkPolyData), although with a .fib extension instead of the regular .vtk extension.

The DTI Track module also has its own format for DTI analysis: the DTI Study (.dts). This format will be described in the next section.

3.2 Data Importation

The first step is to import your own data into the DTI Track module. We developped a specific file format to handle in an easy way DT-MRI sequences. This format is called a "DTI Study" (extension .dts), and stores in a human readable way all information regarding your data: number of images, images, gradient sequence, parameters used for the processing, saved tensor and fiber files, etc. You only need to import your data once, and then you will be able to reuse it without going through the importation process again.

 To import your DTI dataset, click on the "new .dts" icon and a wizard will popup to guide you through the process.

Click Next to proceed to the import screen (Fig. 3.2, right).
Click on the "Open" button to load the DTI sequence (Fig. 3.2, right). Select all volume images that compose your dataset. The images will be sorted in alpha order afterwards. Then click on the "Load Sequence" button to load the gradients used for the acquisition. There has to be the same number of gradients as the number of volume images. Note that the gradient sequence must match the list of images after being sorted: the first image corresponds to the first gradient in the text list, etc (see appendix for details on the gradient list file). Also note that you have to put a B0 image at the top. The software can only support one B0 image for the moment. Please do not import several B0 images. You can also give additional information to your study. For instance you can set the name of the patient, or specify a registration matrix between the DWI and any other image to map the reconstructed fibers

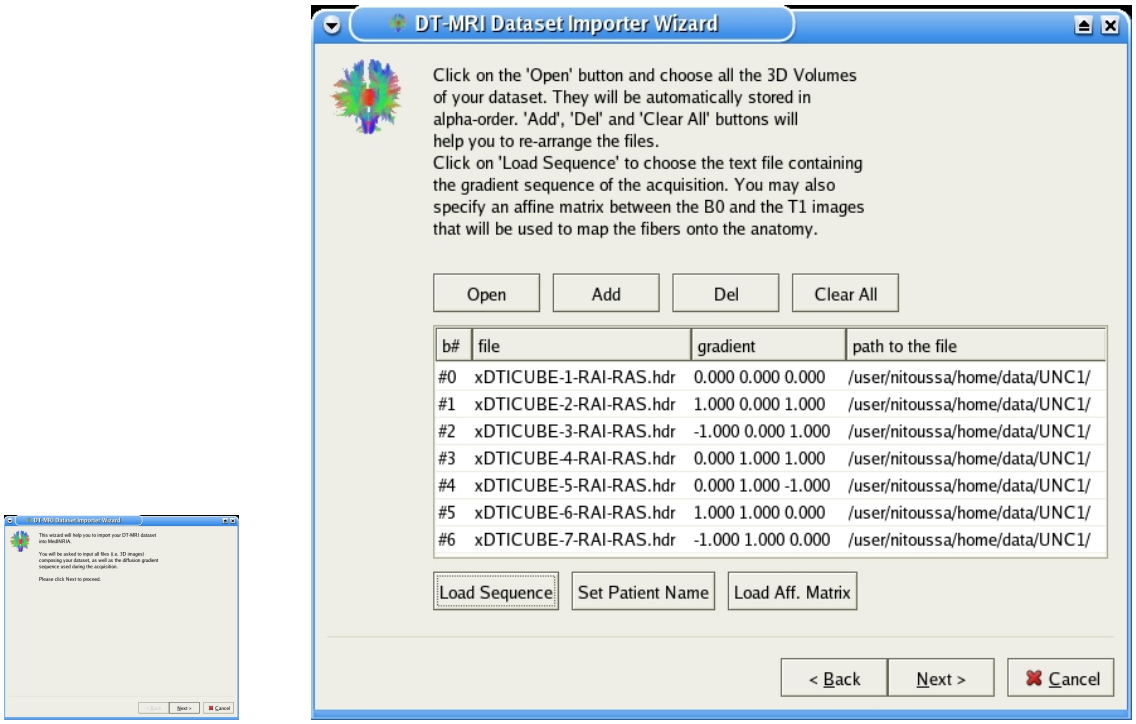


Figure 3.2: DTI importer wizard. This wizard guides you to import your data before studying a DTI analysis. On the left is shown the welcoming screen while on the right is shown the importation screen where are written the names of the DWI and their associated gradients. All this information will be stored in a DTI-study.

onto this new image (such as the T1 image). For more details on the registration matrix see appendix.

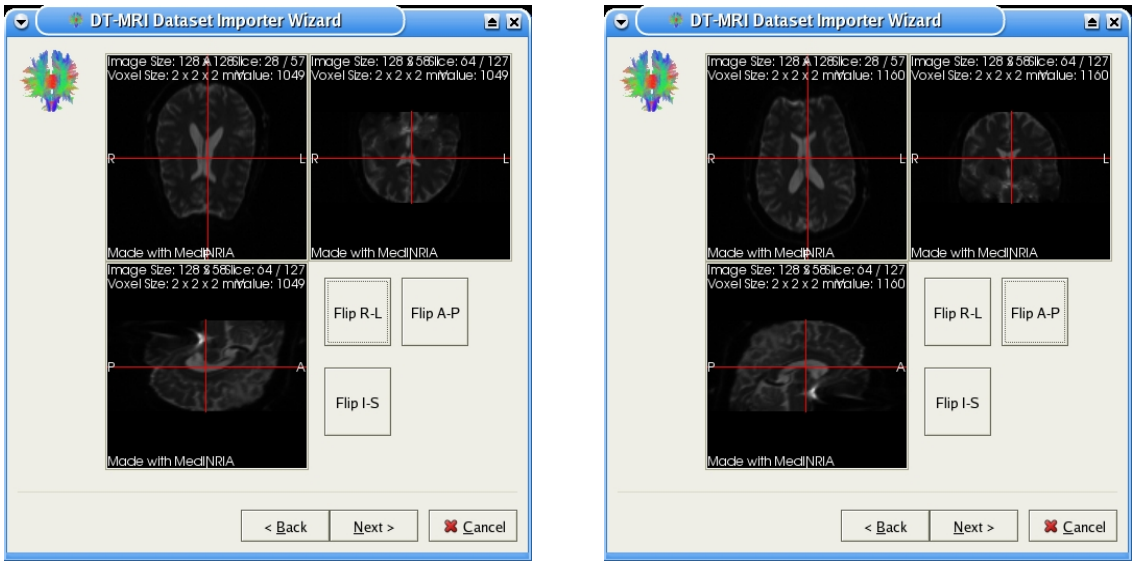


Figure 3.3: The last step of the importer wizard. This screen helps you to obtain the radiologic conventions. You can flip the image around the xyz axes in order to match the conventions, click next to validate your choice. All images (DWI, T1) will be flipped to respect the radiologic conventions.

On the next screen you will be able to change orientation of your DWI regarding radiologic conventions (see Fig. 3.3). Click on Flip R-L, Flip A-P, or Flip I-S to flip the volume respectively around the Right-Left axis, the Anterior-Posterior axis or the Inferior-Superior axis. Once the radiologic convention are obtained, click next to validate your choice.

The last screen of this import wizard shows you a summary of the DTI-study. Please check if the information is correct. "Axes Flipped" show the axes flipped in order to match radiologic conventions, respectively the Righ-Left axis, the Anterior-Posterior axis, and Inferiro-Superior axis (1 means that the axis has been flipped). You can now save the DTI-study with the "save" button. This file has to be stored in the same folder where the DWI are (it will be done automatically). You can now click finish. Your DTI-study has been succesfully created.

 At any time you can save any change of parameters or DTI results (tensors, fibers and fiber bundles) into the DTI-study file by clicking "save .dts" button. You will be able to retrieve all your information directly by openning the DTI-study.

If you want to move the DTI-study file (extension .dts) to another folder, make sure you also move tensors (sudyname_tensors.inr.gz), fibers (studyname_fibers.fib), bundles (*.fib) and all the DWI with it, otherwise you will not be able to open the study correctly.

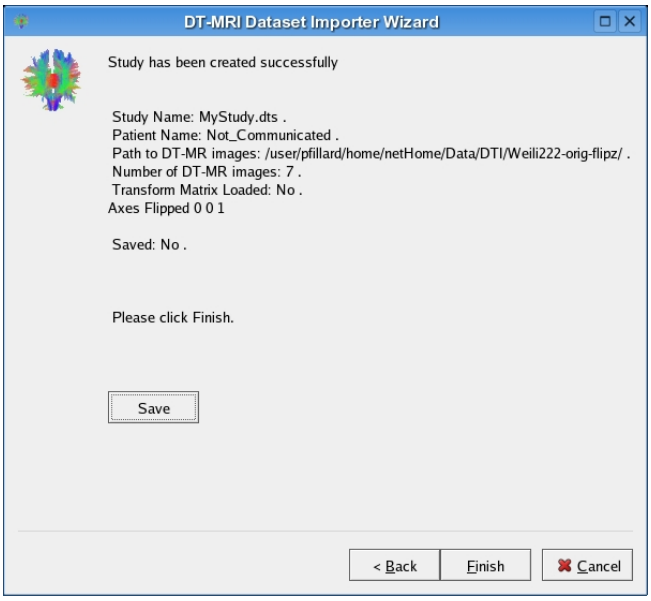


Figure 3.4: The last screen of the importer wizard. This screen summarizes all the information provided by the user. You can also save the study. Click "Back" to change any wrong information. When ready click "finish" and MedINRIA will load the DTI-study. DTI analysis can begin.

3.3 Image visualization

Once your DTI-study has been successfully created, you may want to visualize the DWI you loaded. In the DTI-Module main window (Fig. 3.1) you will see four different screens. The upper-left one corresponds to the 2D axial view of the volume, while the upper-right screen is the coronal view and the lower-left to the sagittal view. The lower-right screen is the 3D view of the volume. You can switch between the different DWI thanks to the selection box situated in the Display panel (Image Settings Fig. 3.5, left).


You can also visualize other images independently by loading them with the "open volume" button.

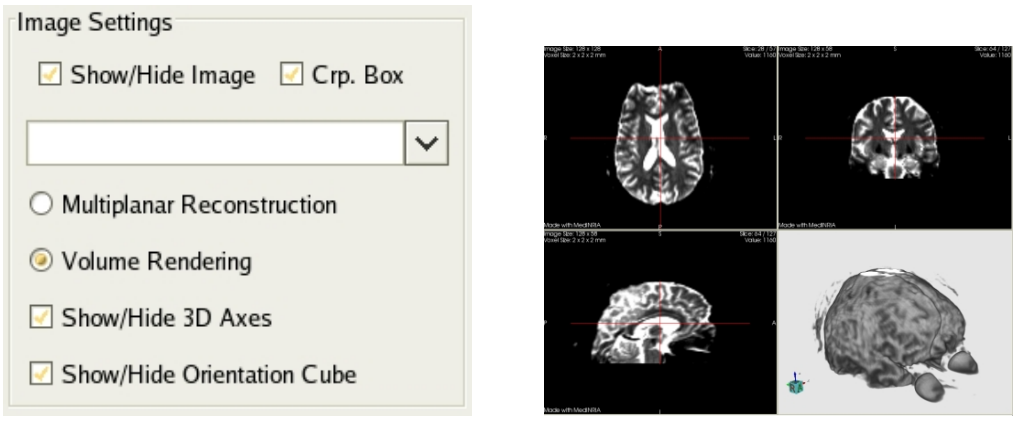


Figure 3.5: Image visualization. On the right you can see three 2D views and the 3D view of a B_0 image. On the left is shown the image settings of the Display panel.

3.3.1 2D Views

Three 2D views are shown in the main window, corresponding to the axial, coronal and sagittal views of the volume. On each view some information is shown, such as the resolution of the slice (in pixels), the size of a voxel (in mm), the index of the slice being shown, and the value of the pixel at the current selection). By default, a trilinear interpolation is made between pixels. Press **"i"** to disable this interpolation.

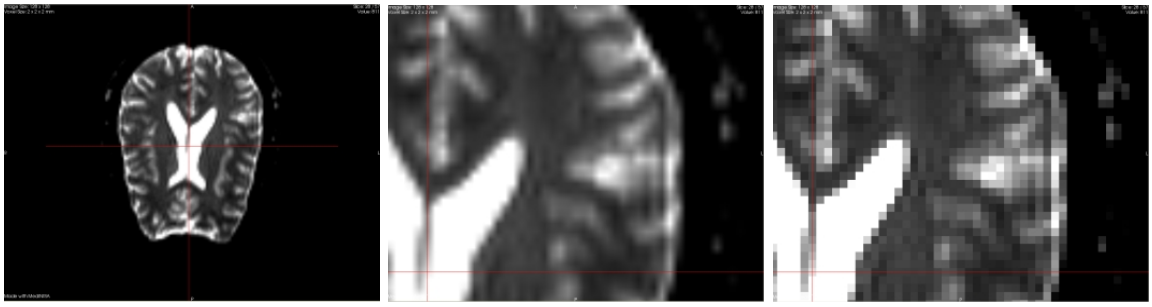


Figure 3.6: 2D view navigation. On the left you see a 2D view (axial) centered on the screen. When the zoom interaction is selected, you can zoom in the view by moving the mouse up while left-clicking on the view and translate the view by middle-clicking (middle figure). You can disable the interpolation between pixel by pressing **"i"** (right figure). Reset the image position by pressing **"r"**.

 Several mouse interactions are available. With the selection interaction (black arrow), you will navigate in the volume (i.e. select a slice) by moving the mouse up or down while left-clicking on a view. Press **"r"** to reset the position to default.

 The second interaction (windowing) controls the brightness/contrast of the image by moving the mouse while left-clicking on the view. A left-right movement controls contrast while up-down controls brightness. Note that with these two interactions, the 4 different views are synchronized. Press **"r"** to reset the contrast to default value.

 With the zoom interaction, you can zoom in or out the 2D view by left-clicking and moving the mouse up or down. A middle click in the view will translate the image. Press **"r"** to reset the zooming.

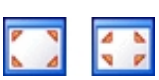
 The next button (zoom with arrows) allows you to put one of the 2D views in full screen mode. For that, first click on the interaction button then click on the 2D view you want to visualize in full screen. To go back to normal 4-views mode, click on the view again.

 When the 2D view is in full screen, you can use the "snap shot" button to export a .jpg picture of the current screen.

Keyboard and mouse on 2D screen :

- Press **“i”** to activate or disactivate interpolation between pixels.
- When selection interaction is ON (black arrow), move the mouse up or down while left clicking to change slice. This action can also be done using keys ↑ and ↓.
- When windowing interaction is ON, move the mouse left/right to change the contrast, move the mouse up/down to change brightness.
- When zoom interaction is ON, move the mouse up/down while left clicking to zoom. Move the mouse while middle clicking to translate the view.
- For any interaction, press **“r”** to reset the interaction.

3.3.2 3D View



On the lower-right part of the main window is shown a 3-dimentional representation of the volume. You can choose some options in the display panel (Fig. 3.5). You can manipulate the volume in different ways:

- Rotate the volume by moving the mouse while left clicking in the 3D view.
- Translate the volume by moving the mouse while middle-clicking in the 3D view.
- Zoom into the volume by moving the mouse up or down while right-clicking in the 3D view.

 Use the “center view” button (or press **“r”**) to center the volume in the 3D view.

 You also can display the 3D view in full screen by pressing the “full screen” button. When the 3D view is in full screen, you can use the “snap shot” button to easily save a .jpg picture of the current screen.

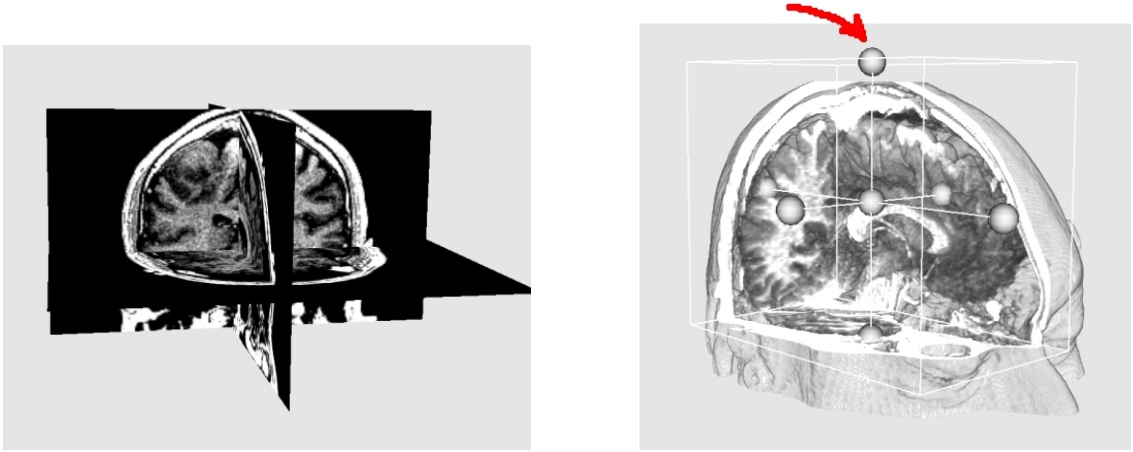


Figure 3.7: 3D view. You can see on the left a Multi-Planar Reconstruction (MPR) of the image. On the right you see a Volume Rendering (VR) of the image, cropped by the cropping box to visualize inside the volume. The cropping box can be manipulated by control points (red arrow).

As you can see on the display options (Fig. 3.5, left), you can choose between displaying an image with Multi-Planar Reconstruction (MPR) (Fig. 3.7, right) or with Volume Rendering (VR) (Fig. 3.7, right). When VR mode is chosen, you have the possibility to take out a part of the volume in order to visualize inside it. This can be done with the "cropping box". Use the control points around the box (red arrow in Fig. 3.7, right) to resize it and crop the volume (left-click on them). The control point in the center of the box allows you to translate it. When you have finished cropping the volume, you can make the box disappear in the Display panel (Fig. 3.5 left, Image Settings → Crp. Box). The orientation cube and the 3D axes help to recognize the current orientation of the image.

Keyboard and mouse on 3D screen:

In the 3D view, several optional features are available :
- Shift+left-click translates the volume.
- Ctrl+left-click rotates the volume around the axis perpendicular to the screen.
- Press **"j"** activates "joystick" mode (continuous movement mode).
- Press **"t"** disables the "joystick" mode.
- Shift+left-click on the cropping box translates it.
- Right-click on the cropping box makes it grow or shrink.
- Press **"r"** to center the image.
- If you cannot access the cropping box : Click on "Crp. Box" on the Display panel, then press the "center view" button. If you still don't see it, it may be inside the volume. Then uncheck "Show/Hide Volume" on the Display panel to see it, and translate it outside the volume.
- If the cropping box doesn't seem to work properly, it might be because it has been flipped over. Use successively the control points of the box to flip it back to normal.

Arbitrary plane selection: **NEW**

This new feature allows you to select and view an arbitrary plane of the displayed image. Simply press **"p"** in the 3D view to activate this mode. A plane widget and an orientation arrow will appear in the view. Left-click on the this plane to control it. A pop up window will automatically appear showing the selected plane. This window acts like a usual 2D view with a window-level interaction. you can control the orientation of the plane by left-clicking on the orientation arrow (in the 3D view). The arrow should highlight in red. By middle-clicking on the plane you can translate the plane. The plane should hilglight in green. Control spheres allow you to modify the size of the plane. You can close the window when not needed and disable the plane selection mode by pressing once again **"p"**.

3.4 DTI Analysis and Fiber Tracking

This DTI-track module provides advanced tools for DTI analysis and fiber tracking. You will see the different possibilities of this software, such as fast tensor estimation, tensor smoothing, colored FA maps calculation, ADC maps calculation (see section 3.4.2), or fiber tracking. All these features can be accessed from the toolbar on the top of the DTI Module window or in the Processing panel on the left (Fig. 3.1).

3.4.1 Tensor Estimation and Smoothing 

 Tensor estimation represents the pre-processing step before fiber tracking. It also allows you to visualize scalar maps such as Fractional Anisotropy (FA) or Apparent Diffusion Coefficient (ADC). You can perform this estimation by clicking the "Estimate Tensors" button. This will not display anything on screens. To display tensors as ellipsoids please see the next chapter concerning the Tensor Viewer Module. Once the estimation is done, you can display scalar maps to evaluate your results (see Sec. 3.4.2).

 You have the possibility to save the tensors independently (apart from the DTI-study). They are saved in a home made format called Inrimage and are compressed to save memory (extension .inr.gz).

 You will be able to load these tensors afterward, and use them to track fibers apart from any study or in another one.

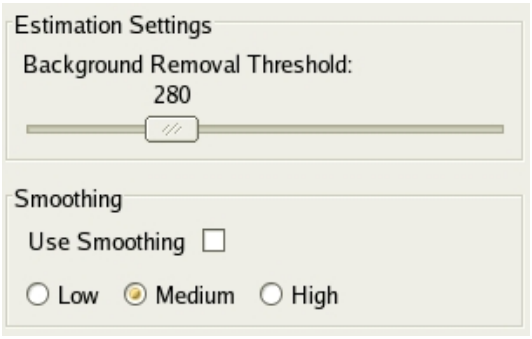


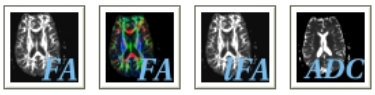
Figure 3.8: This figure presents the parameters of tensor estimation. They can be found in the Processing panel. The Background Removal Threshold is the signal limit underwhich tensors will not be estimated. For noisy data, you can use a smoothing filter. The three checkboxes represent the noise level of the data to be smoothed.

Fig. 2.8 shows a part of the Processing panel where you can set some parameters for processing estimation. The Background Removal Threshold is the MRI signal threshold underwhich tensors will not be estimated (based on the B_0 image). For instance you may move the slider down if the FA map (see Sec. 3.4.2) seems to contain too many empty pixels.

For noisy data, you may need to use the smoothing filter. It provides anisotropic tensor smoothing. For that you have to click "Use Smoothing" (see Fig. 2.8) and choose between the three different noise levels of the data ("High" means highly noisy data). Then perform tensor estimation. You have to note that when using the smoothing filter, tensor estimation is very time consuming. Hence you may not choose this option when time is a limiting factor. Once the estimation is done, you should save the tensor field separatly (or with the study)

for future use.

3.4.2 Scalar Maps



As said in the last section, tensor estimation is the first step before the computation of several scalar maps you can visualize by clicking on one of the following buttons :

Fractional Anisotropy (FA) is a commonly used parameter to caraterize anisotropy in the brain. Bright pixels represent areas where the anisotropy is high, and thus the areas where brain white matter is concentrated. FA is calculated from the eigen values of the tensors ($\lambda_i, i = 1, 2, 3$) as followed :

$$FA = \sqrt{\frac{3}{2}\left(\frac{(\lambda_1 - \bar{\lambda})^2 + (\lambda_2 - \bar{\lambda})^2 + (\lambda_3 - \bar{\lambda})^2}{\sum_{i=1}^{3} \lambda_i^2}\right)} \tag{3.1}$$

This button displays the FA map with a color code (FAc). FA pixel is colorized in relation with the principal direction of diffusion (i.e. principal eigenvector of the tensor). Consequently, the color represents an indication of the direction of the fiber bundles. A red pixel indicates that in this location white matter is mainly orientated Left-Right. Anterior-Posterior orientation is indicated by a green pixel and Inferior-Superior orientation by a blue one.

There are other scalars that characterize anisotropy you can display. You can use the Geodesic Anisotropy which is a home made version of the FA, it is also called log-FA (lFA). You can also display the Apparent Diffusion Coefficient (ADC), it represents the trace of tensors and can be written as followed :

$$ADC = \sum_{i=1}^{3} \lambda_i \tag{3.2}$$

NB: Even if you didn't click on the tensor estimation button, you can directly "ask" for the display of the scalar maps, MedINRIA will automatically see that tensors haven't been estimated yet and will perform the estimation. When saving the DTI-study, scalar maps are not saved but their computation is not time consuming.

3.4.3 Fiber Tracking

We arrive now to the main purpose of DTI analysis : fiber tracking. White matter fiber bundles are tracked from the tensor field information. You can perform fiber tracking by clicking "Track Fibers" button. The reconstructed fibe are then displayed in the 3D view as lines colorized by their direction. As in the FAc map, red indicates a Left-Right orientation, green an Anterior-Posterior orientation and blue an Inferior-Superior orientation. In Fig. 3.9 you can see on the left a group of parameters you can set to optimize tracking. "FA Threshold" controls the FA value underwhich fiber tracking will stop (the value indicated on the slider has to be divided by 1000 to get the real FA value). "Smoothness" controls the smoothness of reconstructed fibers. The greater the slider value is, the smoother the fibers will be. The next parameter controls the minimum length of fibers to be valid (in mm). The last parameter is "sampling". If the set of reconstructed fiber tracts is too dense, you can set the sampling to a value greater than one. For instance if you set "sampling" to 4, fiber tracking will be performed onevoxel out of four. Consequently the process of fiber tracking will be 4 times faster. The next sections will explain you how to extract a fiber bundle from the set of reconstructed fibers.

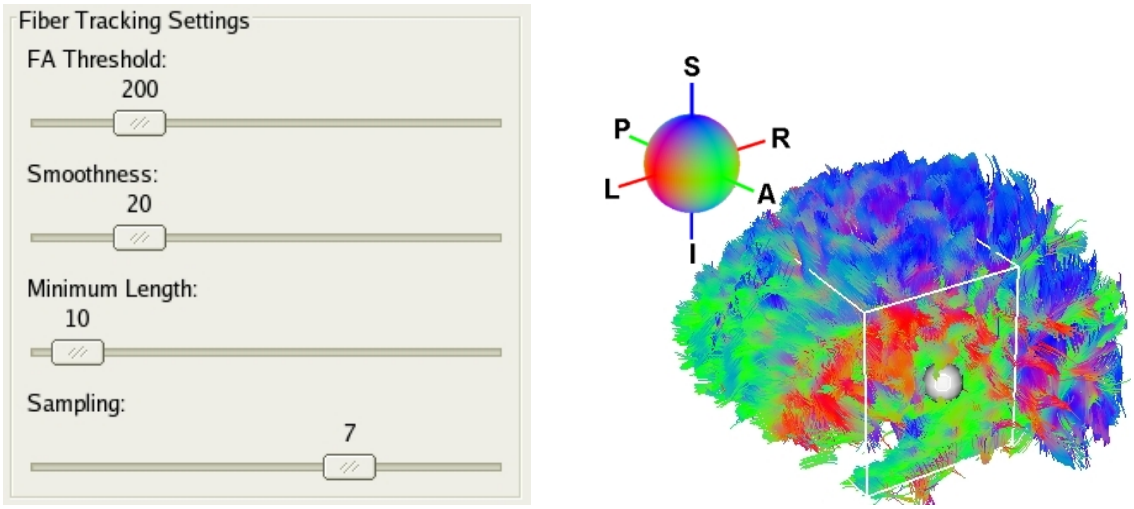


Figure 3.9: On the left you see the parameters you can set to optimize fiber reconstruction. The "FA Thresold" controls the FA value underwhich the tracking will stop, the "Smoothness" slider controls the smoothness of the reconstructed fiber tracts. The next slider defines the minimum length autorized for a fiber bundle to be valid (in mm)."Sampling" controls the result density, i.e. if "Sampling" is set to 4, a fiber will be tracked every voxel out of 4. On the right of the figure is shown an example of a set of reconstructed fiber tracts. Fibers are represented as colorized lines in the 3D view. The color characterize the direction of the fiber (see the color sphere).

On the Display panel you will see some parameters for fiber visualization (see Fig. 3.10). Here you can decide to show or hide the fibers and to show or hide the fiber cropping box

(see Sec. 3.5.1). You also can choose between different visualization modes. Default "polylines" are simple lines. "3D ribbons" will represent each fiber as a ribbon. Finally you can choose "3D tubes" and set the tubes' radius (see Fig. 3.10). This last option takes a lot of resources and may slow down the graphic rendering. Note that these different modes are for visualization purpose and do not represent any anatomical reality.

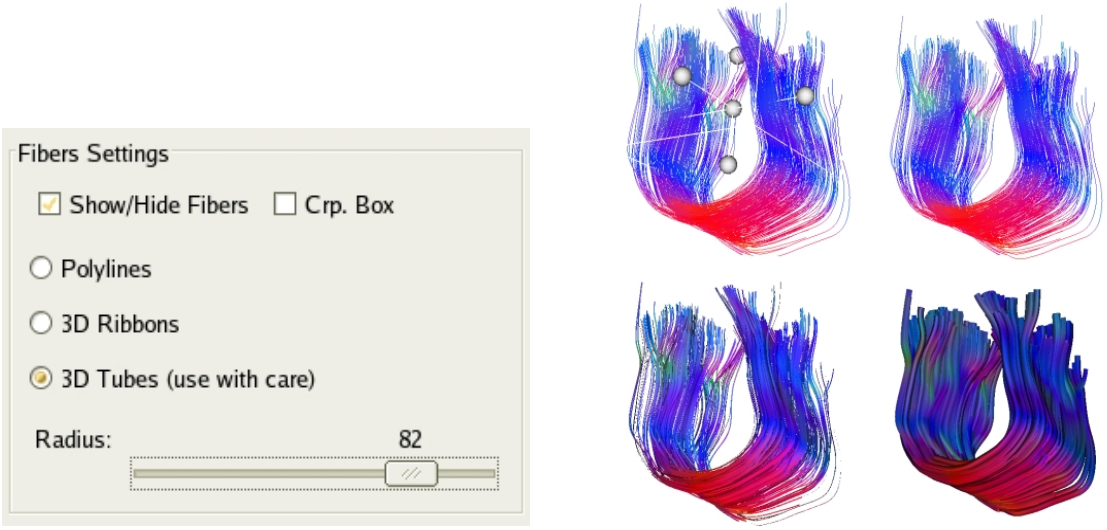


Figure 3.10: Fiber visualization. On the left you can see some visualization parameters available in the Display panel. You can for example click on "Crp. Box." to show or hide the fiber cropping box (see Sec. 3.5.1). On the right is shown a fiber bundle (Corpus Callosum) for different sets of parameters. On the upper-left figure is the default mode, fibers are represented as polylines. On the upper-right figure the cropping box has been switched off. On the bottom figuresare respectively shown the two other modes: 3D ribbons and 3D tubes. You can control the tubes' radius with the "Radius slider" parameter.

3.5 Fiber Extraction

3.5.1 The Cropping Box

Once fiber tracking has been performed, you will see a cropping box surrounding the set of fibers. This box can be used to extract a specific bundle. Indeed, only the bundles going through the cropping box are displayed (see Fig. 3.11). You can manipulate the cropping box thanks to control points located on the edges of the box. Left-click on one of them to resize it by moving the mouse. When left-clicking on the center point, you can translate the box. Right-clicking somewhere on the box and moving the mouse up or down allows you to

enlarge or squeeze it. See Sec. 3.3.2 for other tips on the cropping box manipulation.

The main purpose of this box is to extract a specific bundle. For that you can use the cropping box in a recursive manner : In the Fiber Manager panel (see Fig. 3.14), you will find the "Tag" button. Clicking this button fixes the current selection (bundles currently displayed). You can then move the cropping box once more to select more specifically your bundle of interest (see Fig. 3.11, right). You can "tag" again the selection, etc...

If you need to recover the entire set of reconstructed fibers, you may use the "Reset Tagging" button. It will automatically display all the bundles that go through the cropping box. The cropping box will then act in a normal way.

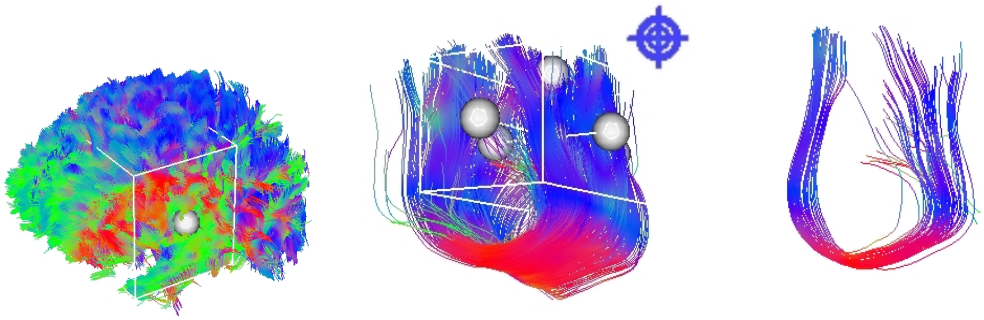
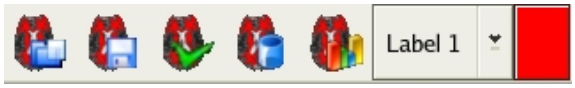


Figure 3.11: Selection by the cropping box. On the left you see a dense set of reconstructed fibers. The cropping box (in white) allows to select a specific bundle. You can manipulate it (translations and resizing) by left-clicking on its control points at the edge of it and moving the mouse. You can crop the set of fibers recursively by clicking on the "tag button" in the Fiber Manager panel.

3.5.2 Regions Of Interest (ROI)



The cropping box might be limited in terms of geometry. In order to extract a fiber bundle more precisely, you can define regions in the image where you want to visualize fibers that go through them. These regions are called Regions Of Interest (ROIs). We describe in this section a step by step procedure to define and use ROIs.

- Step 1 : Preparation

Put a 2D view in full screen (for instance FA map) and select a slice where you would like yo start drawing a ROI(to change slice, you can press keys ↑ and ↓). You can zoom in for more precision. Please see Sec. 3.3.1 for 2D view interactions. Now choose the ROI color in the color selector. Note that the "label 0" (black) color will erase a region (make it as no-ROI).

- Step 2 : Generation

Press **"j"** to activate the "ROI generation mode", you will see a purple cross somewhere in the view. Maintain a left-click and move the mouse to define the contour of the ROI for this slice. The contour is shown in green. You must maintain your click until you reach the first point of the contour (the purple cross). You can also use an alternative mode: by middle-clicking, you can define several control points to draw the ROI contour. When you have enough control points, Ctrl+middle-click on the first control point to finish the drawing. You can then right-click on one of these contol points to move it. You can add a control point by pressing Shift+right-click between two existing control points. You can delete a control point by pressing Ctrl+right-click on it.

Once you have finished with the contour drawing, you must validate it by pressing **"v"**, you will see that the region you just define is now filled by the color by the one you chose in the color selector.

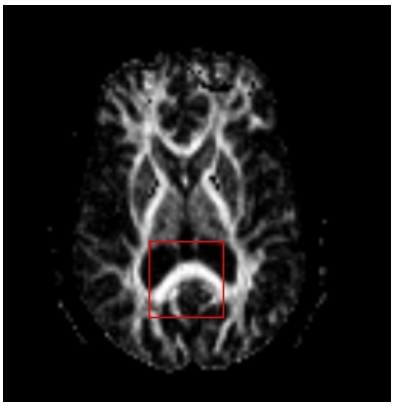
- Step 3 : Validation


Repeat step 2 on other slices, until you are satisfied. Once you have finished, you have to validate your ROI definition by pressing "validate ROIs". The ROI will automatically be turn into as an isosurface in the 3D view.

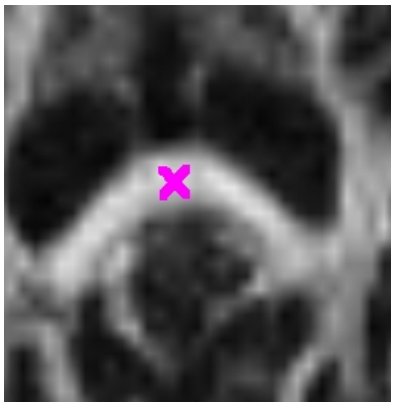

You can repeat this procedure as many times as you want in order to define several ROIs. Don't forget to change the color otherwise they will be considered as the same ROI. You can save the ROI by clicking the "Save ROIs" button (left icon). You will then be able to load them for future use with the "Add ROIs" button (middle icon). You can reset all the ROIs by clicking "Reset ROIs" (right icon).

- ROI generation mode tips

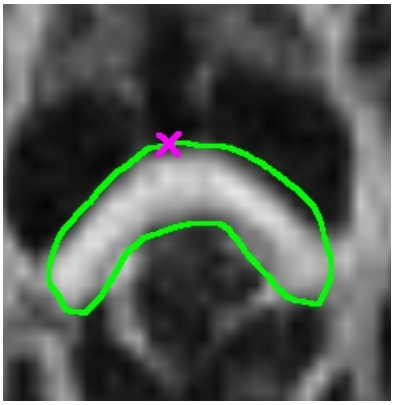
- As said above, this mode can be activated and disactivated by pressing **"j"**. When it is activated, no interaction is possible in the 2D view, but you can still change slice by pressing ↑ or ↓.
- Don't forget to savwe the ROIs, not to loose yout work.
- See figure 3.12 for a step by step illustration.



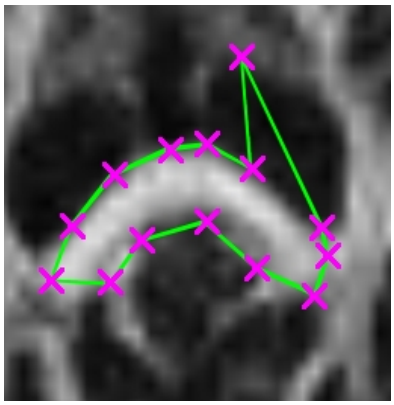
Put a 2D view in full screen and zoom in to the region of interest. Choose a color in the color selector.



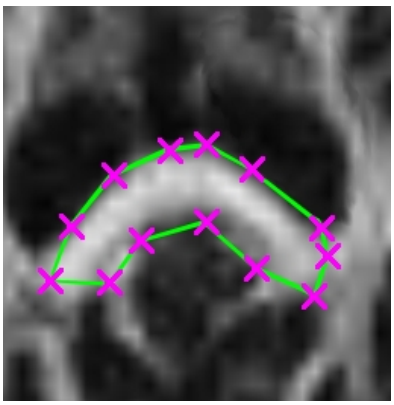
Press **"j"** to activate the ROI generation mode. A purple cross will appear on the view.



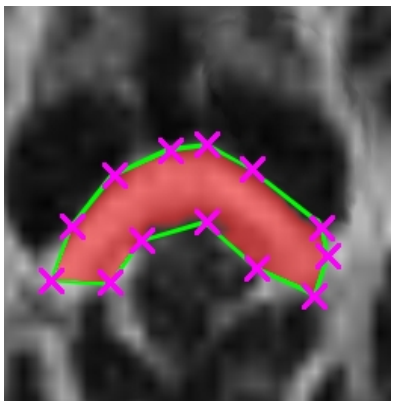
Mode 1: Left-click and maintain to freely draw the ROI contour. Release the mouse only when you reach the first cross.



Mode 2: Middle-click to draw the ROI with control points. Ctrl+middle-click on the first cross to finish the contour.



Right click on a point to move it. Shift+right-click between points to add one. Ctrl+right-click on a point to delete it.



Once your contour drawn, Press **"v"** to validate it. The region is then colorized. Use Label 0 color (black) to erase a region.

Figure 3.12: Step by step procedure for ROI generation. Repeat this procedure for several slices until you are satisfied with the ROI. You need then to validate it by clicking "Validate ROIs" button in the tool bar.

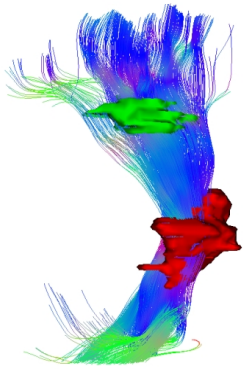


Figure 3.13: This figure presents some results of fiber tracking after ROI generation. It allowed the extraction of a Cortico-Spinal Tract (CST) shown in the picture on the right. You can use the cropping box to further extract the bundle of interest.

Once you have finish generating the ROIs, you can track the fibers with respect to these ROIs. Typically, A ROI is fully defined with its color, no matter if it is composed by several disconnected regions. The fiber tracking process (see Sec. 3.4.3) will restrict the display to the fibers that go through every ROI wihtout exception (i.e through every color). You can now use the cropping box to further extract the bundle of interest.

3.5.3 Fiber Manager


Once you have extracted a bundle of interest, you can label and add it into the Fiber Manager. It will be stored in the DTI-study as well (don't forget to save the DTI-study). For that click on the "Validate Fiber Bundle" button. You will be asked for a name and color to associate with the extracted bundle (Fig. 3.14).

You can repeat this operation several times to have a set of bundles of interest. You can decide to show/hide one of them, change its parameters such as color or name from the "fiber settings" area (see Fig. 3.14, left). Save the DTI-study to be able to retrieve these bundles of interest in the future.

3.6 Statistics


When a set of ROIs is loaded, you can click on the "ROI Statistics" button to compute histograms of some scalar values in the Region Of Interest. Fig. 3.15 shows an example of these statistics. You can see histograms of Fractional Anisotropy (FA) and Apparent Diffusion Coefficient (ADC). The color of the graph corresponds to the color of the ROI in the views.


When the fiber manager contains extracted bundles, you can compute statistics on a specific bundle by clicking "compute statistics" button located in the fiber settings area (see Fig. 3.14, left). It will display histograms of ADC and FA values of the region covered by the fiber. It will also display statistics on the length of the fibers (see Fig. 3.16).

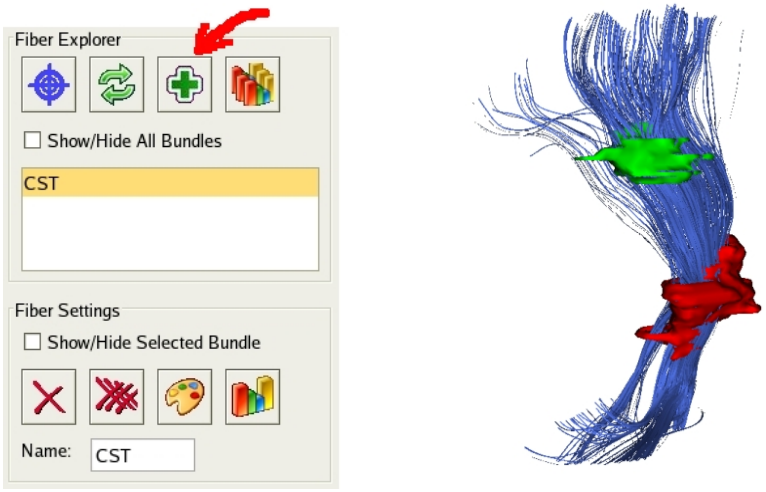


Figure 3.14: Once you have extracted the bundle of interest, click "Validate fiber bundle" (red arrow) to add it to the fiber manager. You will be asked for a name and a color to associate with the extracted bundle. You will see it appearing in the list-box. Then save the study (Sec. 3.2). The bundle will be stored inside the study for future use. You can also change some parameters (i.e. color, name) in the "Fiber Settings" area. On the right is shown an example of an extracted fiber bundle (Cortico-Spinal Tract).

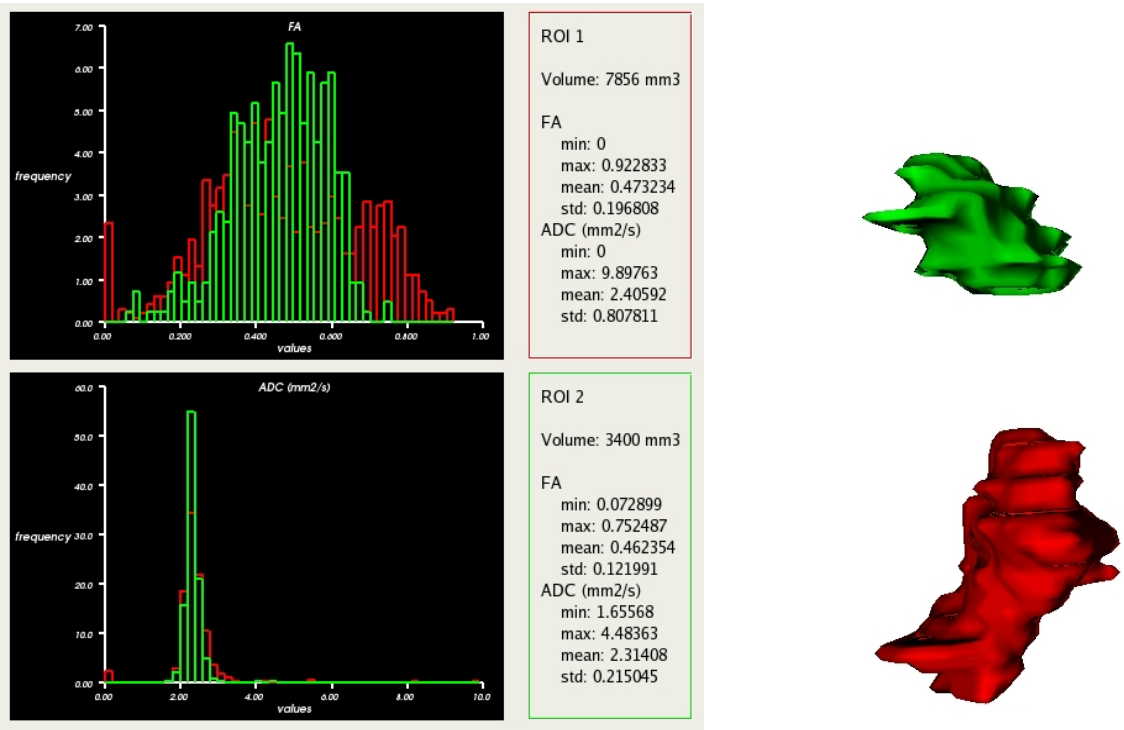


Figure 3.15: On the left you see a window with statistics of the ROIs shown on the right. These are histograms of the scalar values (i.e. FA and ADC) of the ROIs' voxels.

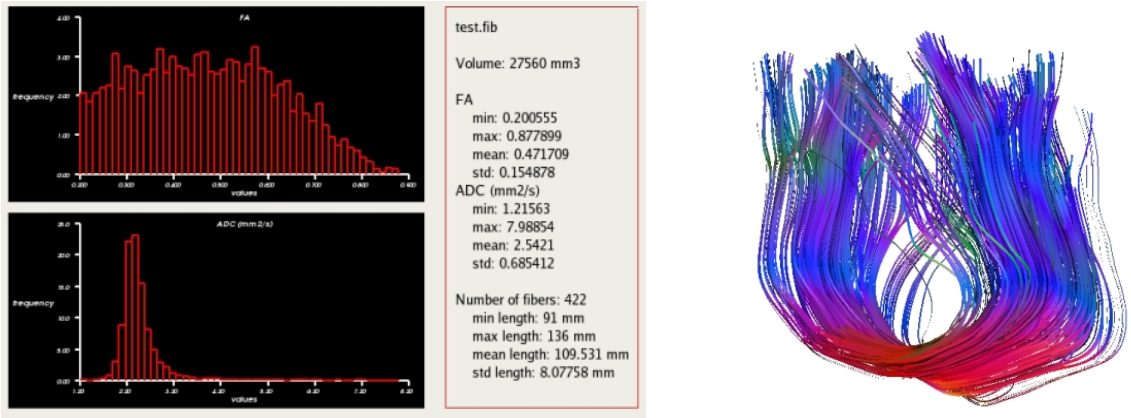


Figure 3.16: In this figure, you can see on the right an extracted fiber bundle (corpus callosum) displayed with 3D ribbons. Statistics of this bundle are shown on the left. You can see FA and ADC histograms of the voxels where fibers of the bundle pass through. There are also statistics of the fiber length.

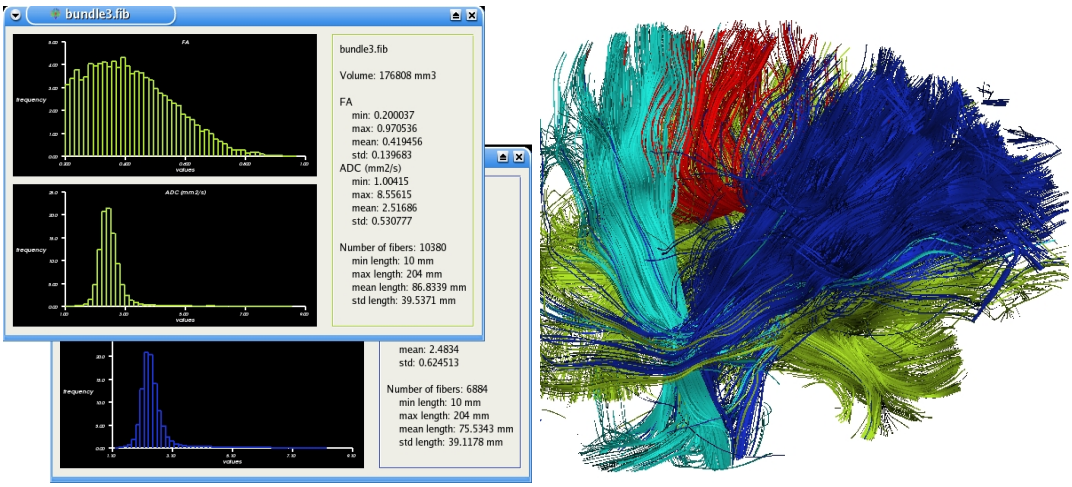


Figure 3.17: When there are several extracted bundles in the Fiber Manager, you can compare their statistics.

3.7 Other Features

3.7.1 fMRI: Activation Map Visualization

With MedINRIA, you can visualize your fMRI study results at the same time as you visualize your DTI results. Indeed, you can import an activation map assuming it has the same dimensions as the current displayed image. For that click on the "Open activation map" button. It will display colored activation regions in the volume (see Fig. 3.18). The activation regions are colored from red to purple and going through the rainbow colors.

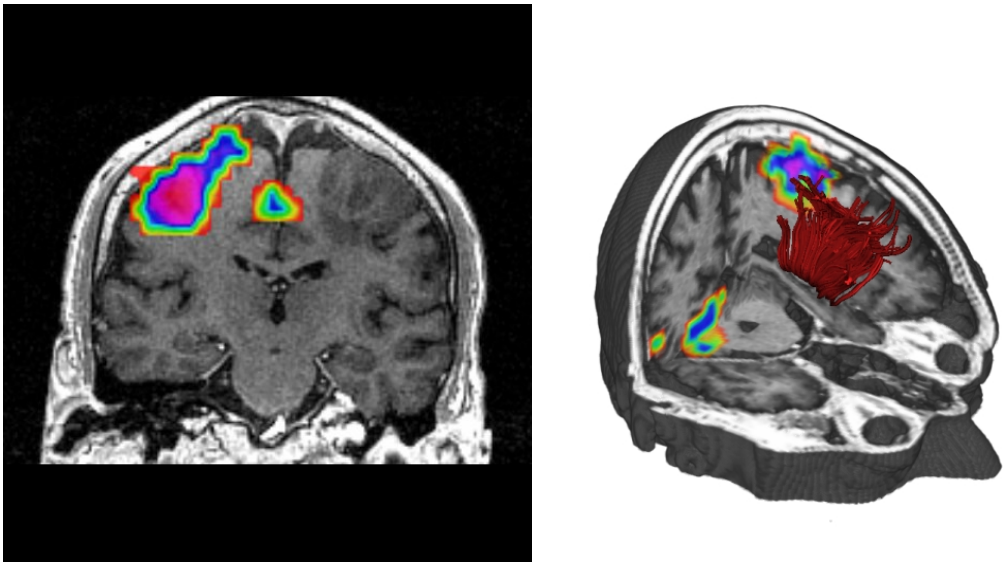
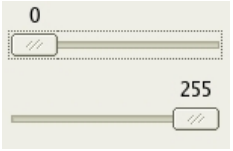


Figure 3.18: This figure shows an activation map displayed in a T1 image. On the left is shown a coronal 2D view of a T1 image with the activation regions colorized from red to purple. A Volume Rendering is shown on the right, with a red extracted fiber bundle.



Note that if you change volume the activation map will disappear, you will have to load it again. You can also change the color mapping by moving the activation map sliders. First slider controls the minimum level of activation to be displayed, while the second one controls the color saturation.

3.7.2 DTI & fMRI


You can also import activation regions as ROIs. Click on the "Import Activation regions as ROIs" button to launch the wizard. The first step is a binarization of the image in order to avoid noisy regions (see Fig. 3.19). Click on the "open" button to load the activation map. Left screen is the transversal view of the activation map shown in grey level. The screen on the right is the binarized image by a threshold that you can change thanks to the slider on the top of the window. You can navigate in the volume by moving the mouse up and down while left-clicking on one of the view. When you have finished binarizing the image, click "next". MedINRIA will automatically find the activated regions, cluster them and associate a different color for each.

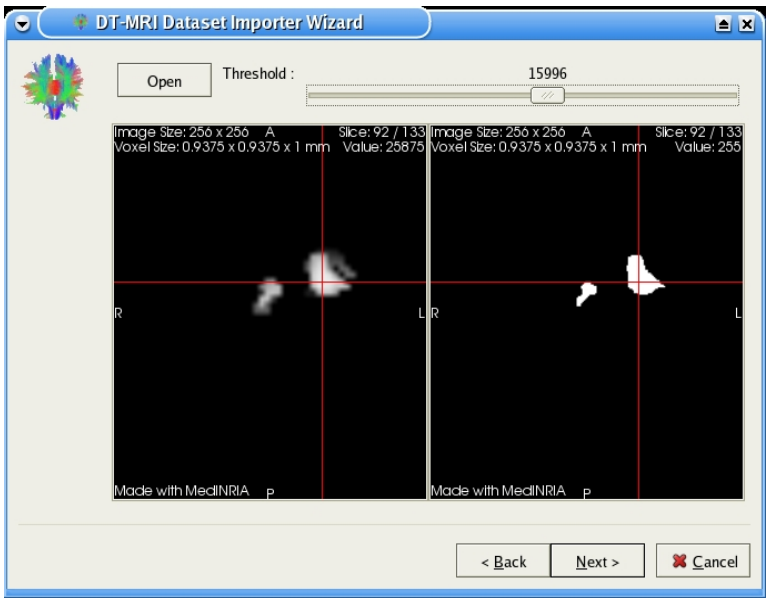


Figure 3.19: This is the first step in the transformation of fMRI activated regions into DTI Regions Of Interest. It corresponds to a binarization of the activation map in order to avoid noisy and non-relevant regions. The slider controls the binary threshold. The left screen is a transversal view of the original activation map. The right screen is the result of the binarization. You can use the mouse to navigate in the volume (see Section 3.3.1).

The last step of this importation wizard allows you to select the activated regions you want to consider as Regions Of Interest. In figure Fig. 3.20 you see a 3D view of these activated regions. You can distinguish them by color. Select those you want to consider as ROIs in the list box on the left (see Fig. 3.20). To help you in this choice, a summary of the regions is shown on the lower left part of the window, displaying the volume of each region (in voxels). You can also save the current selection for future use.

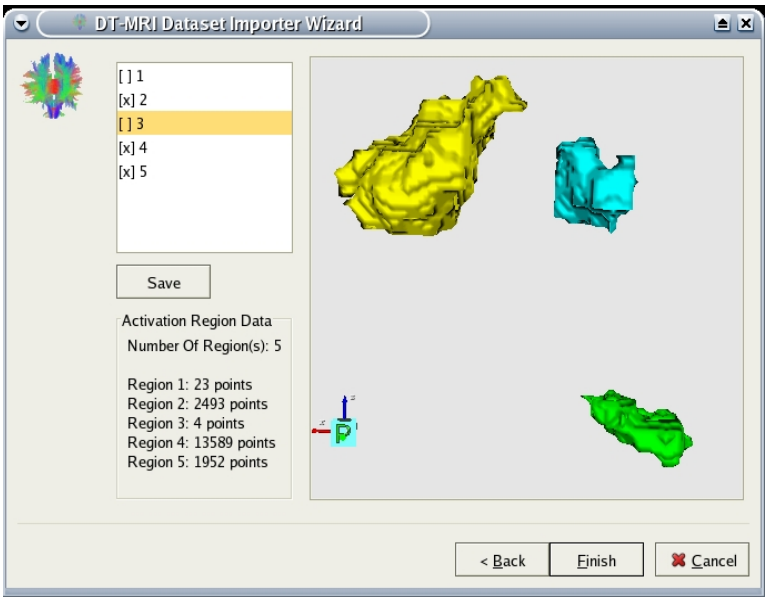


Figure 3.20: Second and last step of the transformation of fMRI activated regions into DTI Regions Of Interest. You can see a 3D view of activated regions that have been colored. On the left you can select relevant activated regions that will become ROIs. To help you in this choice there is a summary of the different regions (number of points per region). You can also save the current selection for future use. Click finish to validate your selection.

When you have finished selecting the regions, click “finish”. The regions will become ROIs in the DTI-study you are using. You can now track the fibers that go through the activated regions you imported ! Note that the activation map must have the same dimensions as the volume currently visualized in MedINRIA. If the activation map you want to import doesn’t have the same dimensions as the DWI of your DTI-study but has the same dimensions of the corresponding T1 image. You must first create a DTI-study indicating the registration matrix to use between T1 and DWI, second load the T1 image inside the DTI-study, and finally import the activation map to create ROIs.

Chapter 4

Tensor Viewer Module

Contents

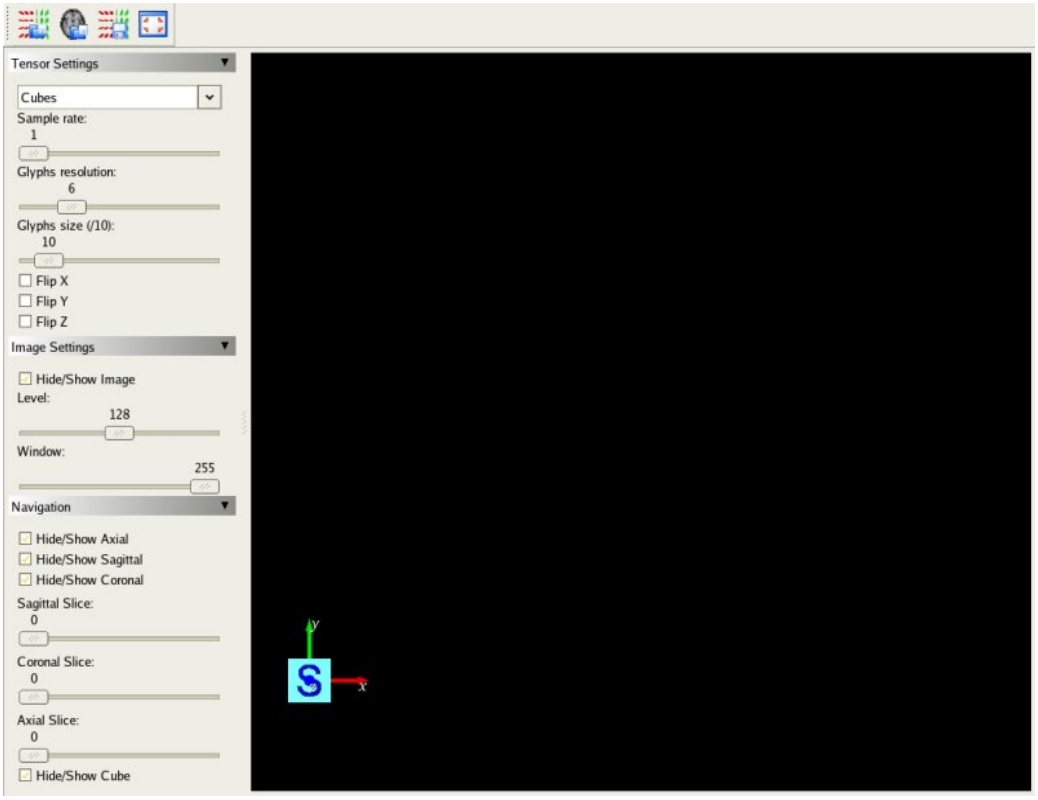


Figure 4.1: **The Tensor Viewer module window. On the left is the control panel, and on the top is a tool bar.**

The Tensor Viewer module allows you to visualize tensors produced by the DTI Track

module. It also provides the possibility to flip the tensor field along the x,y,z axis to solve some inverted geometry problems. The first subsection describes the tensor visualization, while the second explain how to flip tensors.

4.1 Tensor visualization


When you need to visualize the tensors estimated by the DTI track module, you must first save them from thr DTI track module, see related documentation for more details). You can then load them in the tensor viewer module by clicking "Open a tensor field". It can take a little while before the tensor field is fully loaded.

Then you may need to press "center" to center the view on the tensors in the 3D window (see figure 4.1). You can choose between different visualization modes to display the tensor field. Figure 4.2 explains these different modes. Default setting is "cubes" mode. It will represent tensors as rectangular rhombs. For all modes, the main diffusion direction of the tensor is shown thanks to a RGB color code, and brightness is weighted by the Fractional Anisotropy (FA) of the tensor. You can downsample the displayed tensors for faster rendering.
NB: The "ellipsoids" needs more RAM memory of your computer than the other modes.

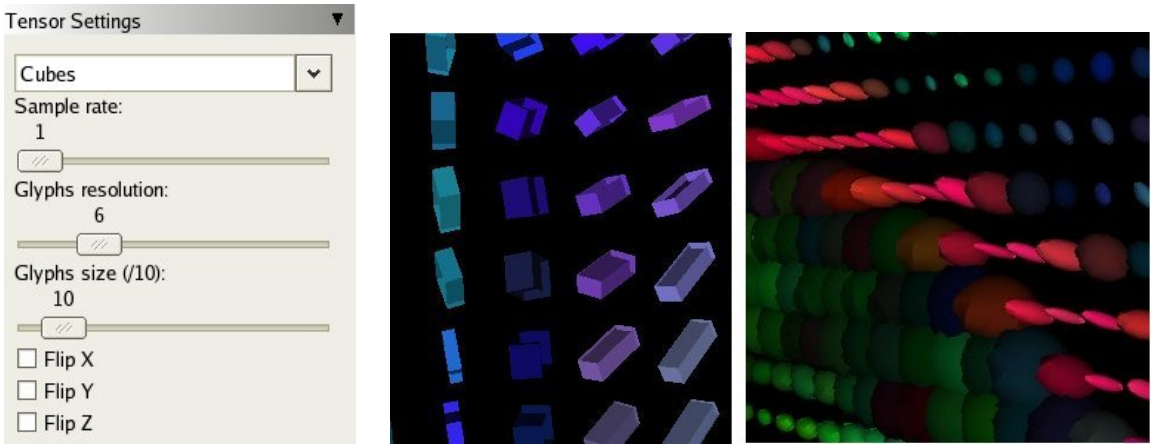


Figure 4.2: On the left you can see the visualization parameters located in the left panel of the Tensor viewer module. On the right are shown differents sets of parameters. Tensors on the left correspond to default parameter values. Those on the middle have been displayed with a greater "glyph size" (25). Finally tensors on the right have been displayed with a more precise resolution (15). The sample rate controls the fraction of tensors to display (i.e. 1: all tensors; 2: one tensor every two; etc).

4.2 Tensor/Image visualization

The Tensor Viewer Module also allows you to visualize your DWI images while visualizing the tensor field. For that you can open a volume by pressing the "open volume" button in the toolbar (see Fig. 4.3). The volume has to be a DWI corresponding to the estimated tensor field or any volume that has the same geometry as the DWI. You can control the contrast and brightness with the sliders.

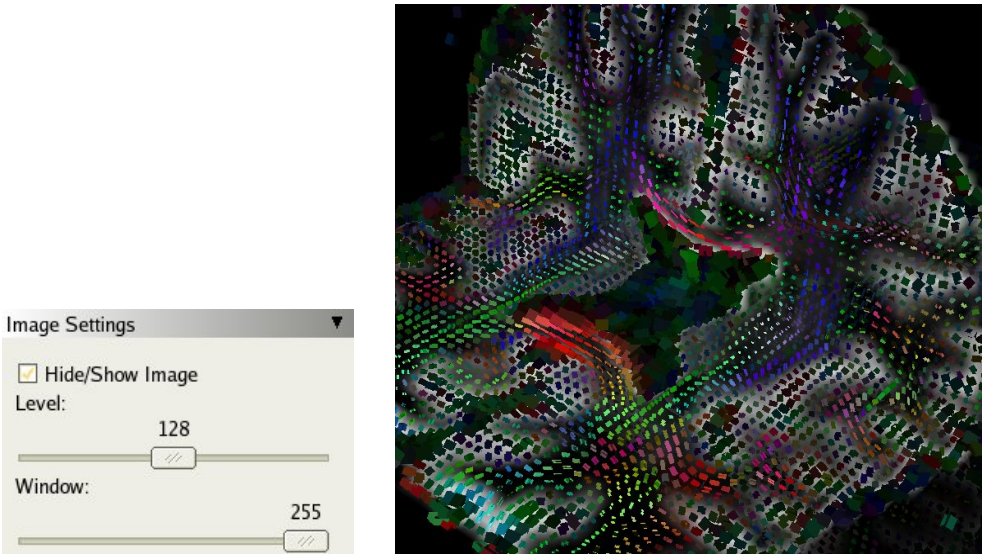


Figure 4.3: This figure shows how to visualize a volume while visualizing a tensor field. The volume has to be a DWI coreesponding to the tensor field (or the B0 image). for geometry compatibility. You can open a volume by pressing the "Open Volume" button in the toolbar. The sliders shown on the panel on the left control the contrast and brightness of the volume.

4.3 Navigation

In Fig. 4.4 left,is shown the navigation panel of the Tensor Viewer. You see that you can choose between monoplanar and multiplanar visualization and navigate between slices with the axes sliders. Note that a multiplanar visualization mode will slow down the rendering. The interactions on the 3D view are the same as with the DTI-track module. Hence you may read the image viewer module documentation for details about it.

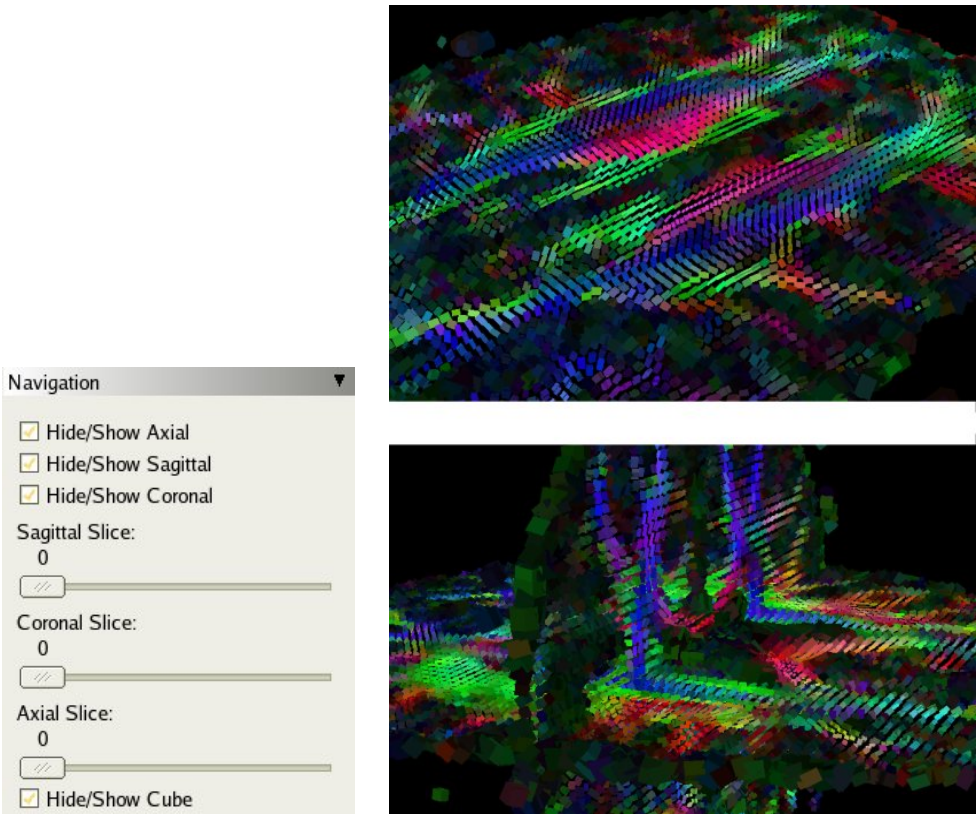
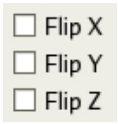


Figure 4.4: With the checkboxes shown on the left you can select the slice(s) to show or hide. Use the navigation sliders to navigate between slices. You may preferably use monoplanar mode instead of multiplanar mode for a faster rendering. Please read the image viewer module documentation for instructions about the 3D view possible interactions.

4.4 Tensor flipping



If you have some problems tracking fibers with the DTI-track module, it might be because the estimated tensors are up side down because of some geometry problems. To solve this problem, you can flip the tensor field along the x,y,z axis in the Tensor viewer module. For that, open the problematic tensor field in the tensor module, then click on the axis to flip on the parameters panel (see Fig. 4.1). It may take a while to flip the tensors.

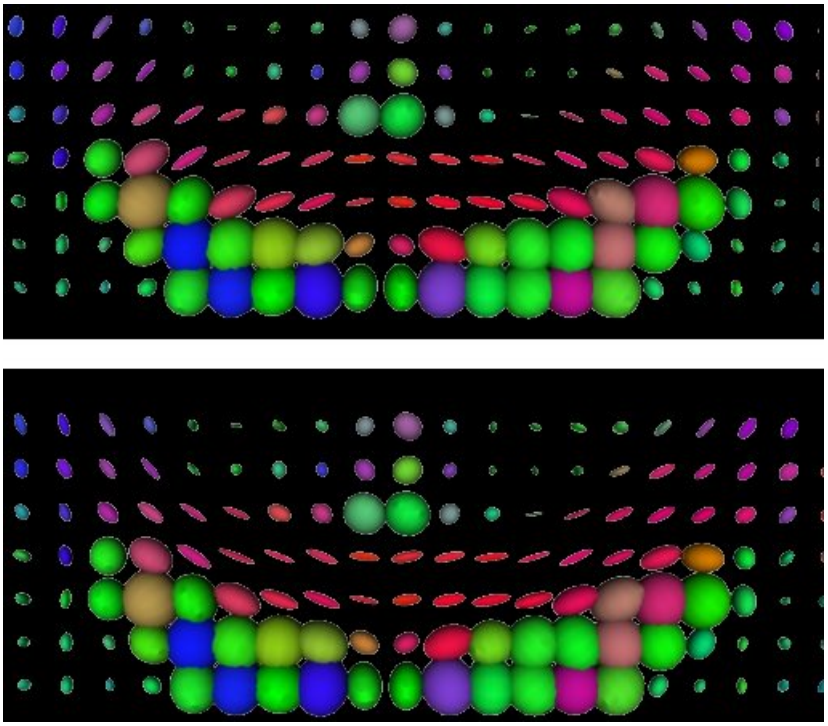


Figure 4.5: On the top you can see a part of a tensor field. You might recognize the Corpus Callosum but in this example the tensors are up side down, and thus fiber tracking doesn't land to correct results. To tackle this geometry problem you can flip the tensors and save the resulting field for future use. On the bottom you see that the the tensor field has been flipped over the X-axis to recover the correct geometry.

Once you have finished, you can save the resulting tensor field by clicking "Save the tensor field". You will be able to load it from the DTI-track module to track fibers with the right tensor field.

Chapter 5

Image Fusion Module

Contents

ImageFusion module is meant to help the user comparing two different images. To do so, it provides simple but efficient ways of fusing the information provided by both images. Moreover, some processing algorithms are proposed in order to align (register) these images for better comparison. Among all image processing algorithms, registration remains a common yet challenging pre-processing step before doing statistical analysis, group comparisons or atlas formation.

This application provides a simple interface for several kinds of registration. It takes two images as input, the "fixed image" and the "moving image", and offers several ways of "aligning" them:

- Manual Registration: In a few clicks, one can perform a manual registration of two images. This can be done by defining several control points (landmarks) in both images that correspond to the same position in the subject of interest. From these so-called landmarks, a rigid transformation is computed (rotation plus translation). See Sec. 5.3 for more details.

- Automatic Rigid Registration: We use the affine registration framework of ITK [ITK] to achieve this automatic matching of images. It consists in maximizing the mutual information of the two images, and is embedded in a multi-resolution framework. No user input is required. However some papameters might be tuned for best efficiency. This method gives optimal results when registering two images of the same patient acquired at different times (or different modalities). See Sec. 5.4 for more details. For matching images of different subjects, one should rely on the "non-linear" method.

- Automatic Affine Registration: We use the affine registration framework of ITK [ITK] to achieve this automatic matching of images. It consists in maximizing the mutual

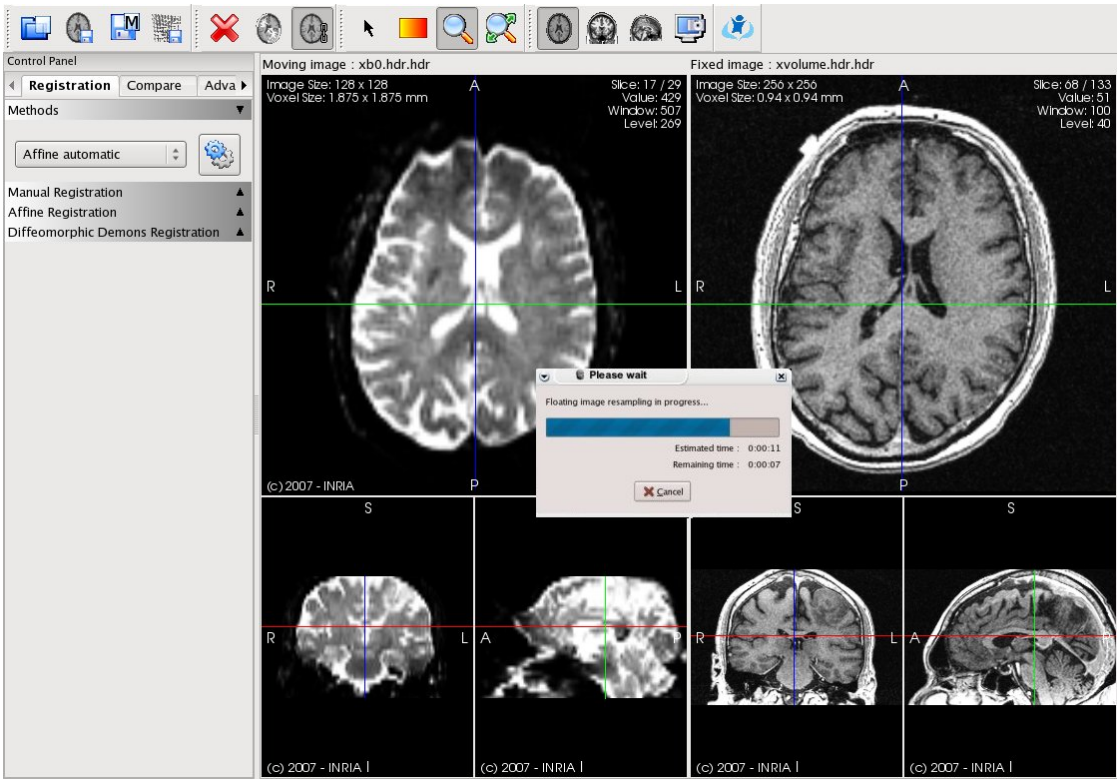


Figure 5.1: **The *ImageFusion* main window. shown here during the registration process of two tensor fields.**

information of the two images, and is embedded in a multi-resolution framework. No user input is required. However some papameters might be tuned for best efficiency. This method gives optimal results when registering two images of the same patient acquired at different times (or different modalities). See Sec. 5.4 for more details. For matching images of different subjects, one should rely on the "non-linear" method.

- Automatic Non-Rigid Diffeomorphic Demons Registration: This method provides a very up-to-date method for non-linear registration [VPPA07]. This procedure is based on variants of the Thirion's demons algorithm [Thi98] for non-linear mono-modal image registration. It is fast, and insures the invertibility of the transform, which is a very desirable feature in registration. See Sec. 5.5 for more details.


The user simply has to choose his desired registration method - possibly set some parameters - and press the "Perform" button. For user convenience a "Reset" button allows the user to cancel all previous registration and go back to the initial state.

One of the most challenging goals in this type of tool is to provide an intuitive way of performing registration as well as an easy manner in the evaluation of the results' accuracy. In *ImageFusion* an effort has been made in this direction. As shown in Fig. 5.1 the user interface integrates separated tabs for each of the input images. Each tab can be divided once more in three showing respectivelly the axial, the coronal and the sagittal view of the 3D volumic image, following the radiological conventions. Fixed and moving images can be synchronized one to the other to evaluate their degree of geometry difference. A full screen mode allows to have a complete freedom in terms of visualization.

5.1 Image import

The first step to use this module is to import the fixed image and the moving image (to be registered into fixed image geometry). To do so, click on "open" button on the very left of the toolbar. Please read carefully the welcoming page that explain how to proceed. The first image to import is the fixed image. It corresponds to the target image for the registration method. The second image to be opened is the moving image. It corresponds to the one that will be registered onto the fixed image geometry.

IMPORTANT : Please make sure that both the fixed and the moving image are in the same orientation before importing them.

The fixed image (target) is now shown on the right panel and the moving image is shown on the left one. Some flags remind you the name of the file on the top of each panel.

5.2 Navigation

As soon as the input images are loaded, you can navigate through them thanks to a set of buttons. Please refer to the *ImageViewer* manual for more details on the 2D view navigation. The last button on the right allows to view a specific view in double full screen.

 This button might be used for linking (i.e. synchronizing) or unlinking the views in term of spatial positioning. It helps seeing how much the images to be registered differ one to the other. (see Fig. 5.2)

 For convenience, one can use this kind of button to switch between the three different views orientation (axial, coronal or sagittal). That helps for manual rigid registration (see Sect. 5.3) for instance.

5.3 Rigid Registration Process

This module provides easy-to-use manual rigid registration. The way to do so is simple : the user chooses a single 3D point and a direction for each image that should correspond one to the other. Then the *ImageFusion* turns this information into a rigid matrix. The calculated rigid matrix is first applied to the moving image. Then the moving image is re-sampled to meet the fixed image size and spacing information.

Here is an easy to run process to perform rigid registration manually :

- 1. First select the view orientation that make appear the largest difference between images.

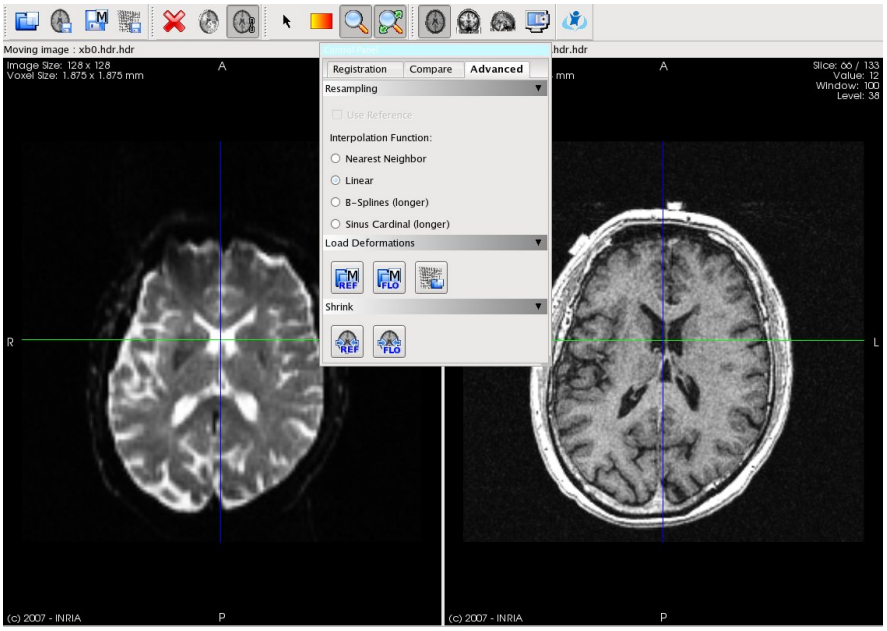


Figure 5.2: Another screen shot of the *ImageFusion*. The full screen mode is activated in the axial views of MR images (different modalities) from the same patient. The control panel has been popped out to have a gain of space for the images.

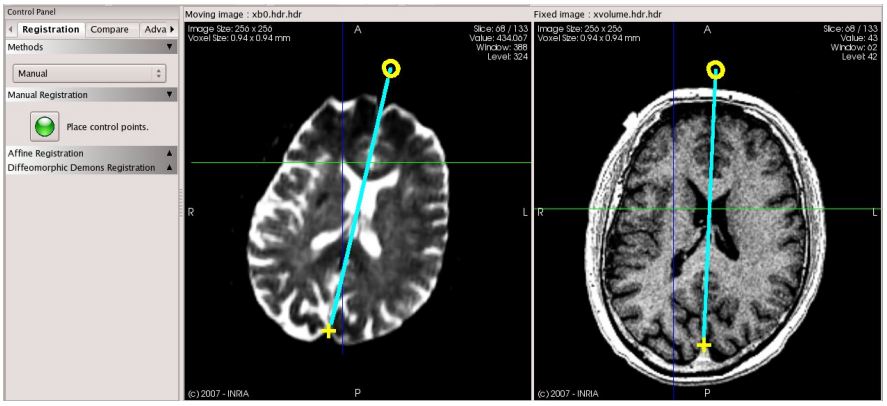


Figure 5.3: This screen shot shows the two views in full screen mode where the zoom interaction has been used to isolate a specific area. A manual rigid registration is being performed (the "Control Points" button has been pressed). Yellow crosses are the 3D spatial points that have to correspond between images. Yellow circles define the directions (following the blue lines). Note that no matter the circle is far from the cross, only the direction is taken in account.

- 2. Deselect the link mode and navigate in the images so that the slices correspond for both images.
- 3. You may use the full screen mode and use the zoom interaction to specify the problematic area.
- 4. Press the green button on the control panel (Fig. 5.3).
- 5. Left click on the fixed image main view on the desired 3D point. Then the drawn line indicates the desired direction (no matter how far from the 3D point it is). Left click again when the desired direction is reached. (rotations of more than 90^o are not allowed : it changes the orientation of the image). Please refer to Fig. 5.4
- 6. Repeat 5. in the moving image main panel. If you need to do another interaction in the views (such as navigation or window-level change) you may press again the green button once again to deactivate the control point interaction.
- 7. As soon as the desired positions and directions are reached for both images, you can press "Perform" to perform registration. The positions and directions information is turned into a rigid matrix and applied to the moving image. If you want to go back to the first configuration, press "Reset". Careful you will loose any previous registration.

IMPORTANT : Once the moving image is registered, both images are automatically position-linked one to the other. To switch off this link mode, press the "link/unlink" button in the toolbar. Note that the moving image is also automatically re-sampled into the fixed image size and spacing information. The re-sampling process uses a linear interpolation (default) between pixel values. As you can see in the control panel (Fig. 5.4) you can choose another type of interpolation. Note that the B-spline and sinus cardinal interpolations takes longer to be done.

5.4 Affine Registration Process

As you can see on the main control panel (Fig. 5.1, you can switch between the different registration modes available. By default the automatic affine mode is chosen. It consists in maximizing the mutual information of the two images, and is embedded in a multi-resolution framework, based on ITK (see www.itk.org for details on the method). Three levels appear to be sufficient for a common use. One can simply click on the "Register" button to perform the algorithm. This operation can be executed iteratively for best results. You can aslo first choose a rigid transformation as a first step (see Sect. 5.3) to avoid failure on large transformation, and then use the affine automatic mode to get optimal results.

Note that the output of both rigid and affine registration methods is an affine transformation matrix that matches the following rules :

1. The matrix is written in homogenous coordinates in mm.

2. Considering a fixed image I_{fix} and a moving image I_{mov}, a 3D coordinate point x, the output matrix can be written (in homogeneous coordinates) as follows : $I_{mov}(M(x)) = I_{fix}(x)$. One can refer to section 5.7 for further detailts on this matrix.

We also match the ITK strategy that says that a point (i,j,k) in an image is taken in the center of the the (i,j,k) voxel.

5.5 Diffeomorphic Demons Registration

In this registration toolkit we also propose a non-linear solution for mono-modal image registration. This method provides a very up-to-date method [VPPA07] based on variants of the Thirion's demons algorithm [Thi98]. Although this procedure takes longer to converge than the affine automatic mode, it gives consistent results for inter-patient data. The output is a deformation vector field. We want to thank Tom Vercauteren and Mauna Kea Technologies for their participation on this registration algorithm.

 You can save the resulting deformation field in ITK metafile format (.mha) thanks to this button. The deformation field maps the moving image onto the fixed image. A deformation field is represented as an image whose pixel type is some vector type with N elements, where N is the dimension of the fixed image.

 With this other button you can load a previously saved deformation field. It currently takes only ITK metafile vector images.

IMPORTANT : This is a known issue that linear transformations (i.e. rigid or affine) are not linked with non-linear ones (diffeomorphic demons) : Considering a fixed image I_{fix}, a moving image I_1, if one performs a rigid transformation, resulting in an image I_2 (and an output affine matrix M_2), and then performs a non-linear diffeomorphic registration, resulting in an image I_3 and a deformation field D_3, then the output deformation field D_3 corresponds to the deformation of the "mid-way image" I_2 onto I_{fix}. Another known issue is that you currently cannot save and load deformation field for 2D image non-linear registration.

5.6 Result evaluation

As said before, evaluating the accuracy of the results is an important issue of such a software. Hence we provide several ways of doing so.

 At any moment, you can press this button to evaluate the registration accuracy. It provides two modes of comparison. Fig. 5.4 (left) shows the first mode that fuses the registered moving image (i.e. moving image resampled w.r.t. the transform - being rigid, affine or non-linear) with the fixed image by blending them with an alpha value that the user can change: $Output = \alpha Fixed + (1 - \alpha)Moving$.

The second mode (Fig. 5.4 right) uses a checkerboard technique: the view is divided in squares (the number of squares can be changed), and one square out of two contains the moving image and the fixed image, alternatively.

Either the percentage of the moving image related to the fixed image, or the size of the squares can be manually set by a slider in the control panel.

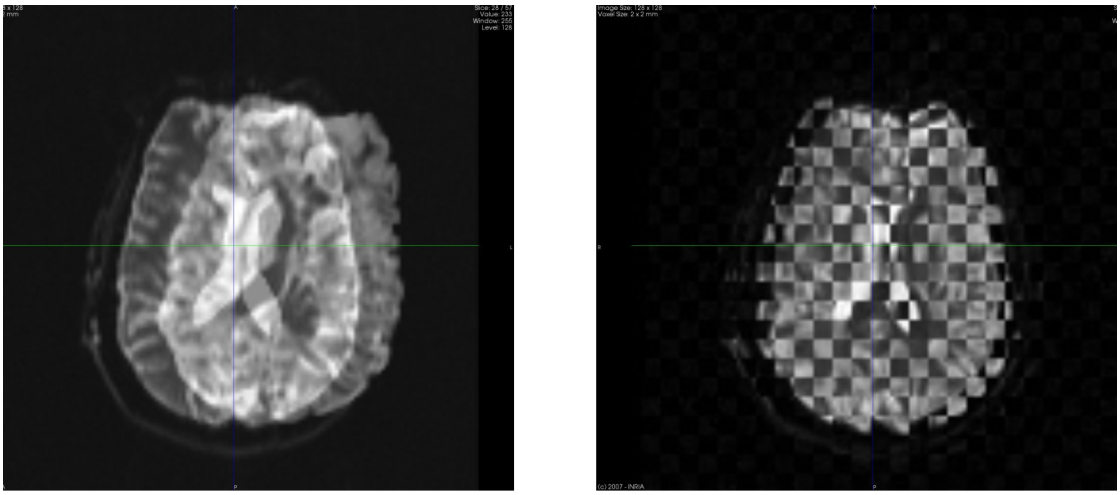


Figure 5.4: Yet Another screen shot of the *ImageFusion*. This figure shows the comparison mode. On the left the fuse opacity option has been chosen while this is the grid option on the right. Parameters of these options can be changed on the control panel on the left.

 Use this button to output a snapshot of the current comparing-mode window.

Note that the window-level cannot be changed in the comparison mode as soon as it corresponds to a mix of the two input images. In order to change the window level you must go back to the double panel mode by pressing again the "comparison mode" button, change the window level of each image as desired and then go once again in the comparison mode.

As soon as one performed a non-linear registration process (or loaded a deformation field as input), one can visualize this field in the compare mode. It can be done by clicking the "Deformation Field" checkbox in the control panel. The deformation field is used to wrap a regular grid with it. The output grid is then shown in parallel of the comparison view (see 5.5).

5.7 Outputs and matrices

 At any step of the registration process you can save the current moving image by pressing this button. If no extension is given by the user then the image is saved in ITK Analyze format (.hdr/.img).
IMPORTANT : Note that the image is saved resampled and registered : "as you are seeing it in the views".

 Again at any step of the registration process, you can save the current registration matrix in a text file by pressing "save matrix". This corresponds to the linear transformation. Considering a fixed image I_{fix} and a moving image I_{mov}, a 3D coordinate point x, the output matrix M can be written (in homogeneous coordinates, mm) as follows : $I_{mov}(M(x)) = I_{fix}(x)$. Dimensions and spacings of the input images are written respectivly in voxels and mm. The output file is a text file were are written these information :

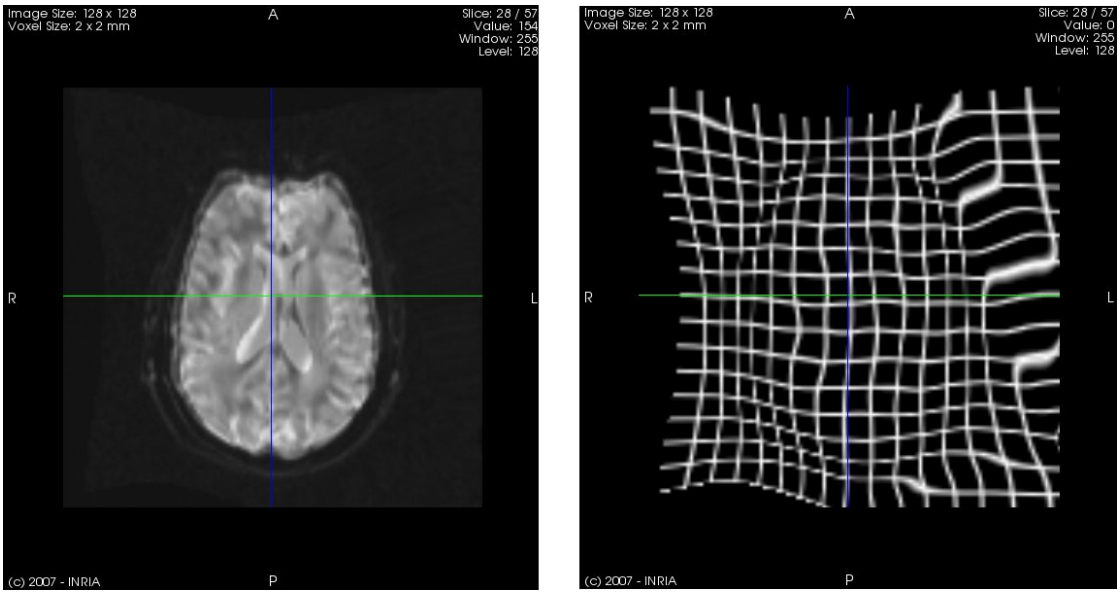


Figure 5.5: This figure shows a comparison mode after non-linear registration. In the control panel you can choose to display the resulting deformation field (right) in parallele to the comparison view (left). The deformation field is in fact wrapped into a regular grid. Note that this feature is only available for 3D image registration.

- Affine matrix coefficients

  M11, M12, M13, M21, M22, M23, M31, M32, M33, M41, M42, M43

where M is the affine matrix used for registration :

$$M = \begin{pmatrix} M11 & M21 & M31 & M41 \\ M12 & M22 & M32 & M42 \\ M13 & M23 & M33 & M43 \\ 0 & 0 & 0 & 1 \end{pmatrix} \tag{5.1}$$

 You can save the deformation field reuslting of a non-linear registration in ITK metafile format (.mha) thanks to this button. The deformation field maps the moving image onto the fixed image. A deformation field is represented as an image whose pixel type is some vector type with N elements, where N is the dimension of the fixed image. Note that you currently cannot save and load deformation field for 2D image non-linear registration.

You can use these outputs again : As soon as you open the same set of input images, you can load either the corresponding matrix file or the corresponding deformation field. You can access these buttons in the advanced tab of the control panel. Loading a specific affine matrix or a specific deformation field overrides any previous registration step.

Note that he affine matrix format fits the format that is needed by the DTI track module (see related documentation and MedINRIA appendix for details). Hence you can register a volume into the diffusion weighted images, output the resulted rigid matrix, and input it in

a DTI study so that the fiber tracks fit the desired volume (e.g. a T1 image) geometry.

These two buttons might be useful in order to manually set the image spacing (in mm), for very specific cases where the scaling information is wrong (3D reconstructed volumes from jpeg 2D images for instance).

5.8 Perspectives

There is still some work to do also in the way of comparing images. Indeed the user might want a more interactive process. Some suggestions on the subject are welcomed (see the features request link from this url : http://www-sop.inria.fr/asclepios/software/MedINRIA). Some improvement also has to be done in handling a deformation field, for instance linking it with the linear transformations.

Chapter 6

Conclusions on MedINRIA

MedINRIA is a software that provides a lot of features concerning medical image analysis, especially for DTI analysis and fiber tracking, but also some extra tools for tensor visualization and fMRI studies. A simple image viewer is provided with the possibility to import directly DICOM exams. In this report we have explained the different modules purposes and functionalities. We presented step by step how to use this software, trying to be as clear as possible. For any question about MedINRIA or any bug to report please refer to the developers. The software is available at http://www-sop.inria.fr/asclepios/software/MedINRIA. Note: MedINRIA 1.9 would be the last version on this platform. So we won't provide any patch. Coming soon: MedINRIA 2.0, using a new modular platform!

In this software we used robust method created by Asclepios team, the Log-Euclidian Metrics (protected by a french patent, n. 0503483). We developped the software in C++, using specialized libraries such as Insigth ToolKit, or ITK (www.itk.org), Visualization ToolKit, or VTK (www.vtk.org), and wxwidgets (www.wxwidgets.org).

Appendix A

Diffusion gradients and registration matrix files

Contents

A.1 Diffusion gradients files

To perform DTI analysis such as tensor estimation and fiber tracking, importation of Diffusion Weighted Images (DWIs) is not enough. Indeed information about the gradient directions used for the acquisition is necessary. As said in section 3.2, you must load a text file containing these gradients in the importation wizard. An example of this file is shown in Fig. A.1. It is a simple text file containing a succession of numbers. First integer is the number of gradients. For example if the acquisition has been performed in 6 different diffusion directions, plus the acquisition without gradient (the B0 image), this integer will be 7. Then there has to be the succesion of 7 gradient directions (one at each line). A gradient direction corresponds to the 3 coordinates (real numbers) of the direction vector. Directions have to be sorted to respect the alpha order of the DWI files (see Fig. A.1).

b#	file	gradient	path to the file
#0	B0-IMAGE.hdr	0.000 0.000 0.000	/home/nitoussa/data/
#1	DWI-1.hdr	1.000 0.000 1.000	/home/nitoussa/data/
#2	DWI-2.hdr	-1.000 0.000 1.000	/home/nitoussa/data/
#3	DWI-3.hdr	0.000 1.000 1.000	/home/nitoussa/data/
#4	DWI-4.hdr	0.000 1.000 -1.000	/home/nitoussa/data/
#5	DWI-5.hdr	1.000 1.000 0.000	/home/nitoussa/data/
#6	DWI-6.hdr	-1.000 1.000 0.000	/home/nitoussa/data/

grad.txt

```
7
0 0 0
1 0 1
-1 0 1
0 1 1
0 1 -1
1 1 0
-1 1 0
```

Figure A.1: On the left is shown a part of the DTI Importation wizard's second screen (see Sec. 3.2). You see an example of the importation of a B0 image and 6 DWI, with their corresponding gradient directions. As the B0 image has no gradient, its corresponding gradient direction is null. On the right, you can see the corresponding text filled that has been loaded for this example. It contains the gradients, one null + 6 gradient directions, preceded by the total number of them (here 7). These directions have to be sorted to respect the alpha order of the DT-MR files.

A.2 Registration matrix files

If you want to visualize reconstructed fibers in the geometry of another image than the DWI (i.e. the T1 image), you must specify a registration matrix (affine) when creating the DTI-study. As said in Sec. 3.2, you must specify the file containing the registration matrix that has to be applied to go from DWI geometry to the new image geometry.

In the second screen of the DTI importation wizard, click on "Load Aff. Matrix" and choose the file that contains the matrix. Fig. A.2 shows an example of this file. First is specified resolution information. First line corresponds to the DWI image resolution, while the second line to the new image resolution (T1 for instance). Image sizes on the 3 axes are indicated followed by the voxel size in mm. After this resolution information, the coefficients of the transformation matrix to apply are succesively specified. Transformation is divided in a linear transform and a translation :

$$A = \begin{pmatrix} A11 & A21 & A31 \\ A12 & A22 & A32 \\ A13 & A23 & A33 \end{pmatrix} \qquad T = \begin{pmatrix} t1 \\ t2 \\ t3 \end{pmatrix} \tag{A.1}$$

where A is the affine transform matrix and T the translation vector.

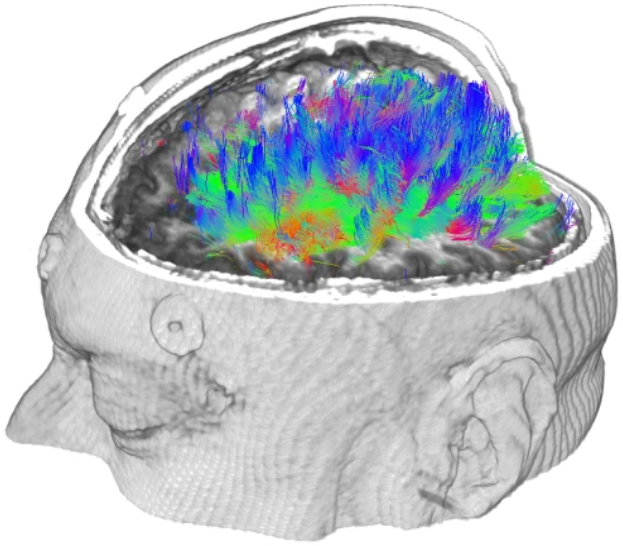
In the matrix file the coefficients are sorted as followed (column-wise):

$$A11 \quad A12 \quad A13 \quad A21 \quad A22 \quad A23 \quad A31 \quad A32 \quad A33 \quad t1 \quad t2 \quad t3 \tag{A.2}$$

For instance the identity transformation would be:

$$1 \quad 0 \quad 0 \quad 0 \quad 1 \quad 0 \quad 0 \quad 0 \quad 1 \quad 0 \quad 0 \quad 0 \tag{A.3}$$

Once you have loaded the matrix file (extension .mat), please verify it has been loaded by looking at the log window (error panel) and check that there hasn't been any file reading error. See Fig. A.2 for an example.



affinematrix.mat

```
128 128  30 1.875 1.875 4
256 256 134 0.94  0.94  1
2 0 0 0 -2 0 0 0 2 50 0 25
```

Figure A.2: On the left is shown the visualization of reconstructed fibers with a T1 image loaded. To map the fibers in the T1 image geometry, a file has been loaded when creating the study. You can see on the right the file used in this example. In this file are succesively specified the resolution and voxel size information of the DWI and the T1 image. Then the 12 transformation matrix coefficients are specified.

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