

DTI Exercise

This exercise was created with BrainVoyagerQX 2.4.1.
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1 Data

Data needed for doing a diffusion-weighted (DW) data analysis are the DW-MR images, the gradient direction information in a text file and an anatomical (T1-weighted) dataset, acquired in the same session.

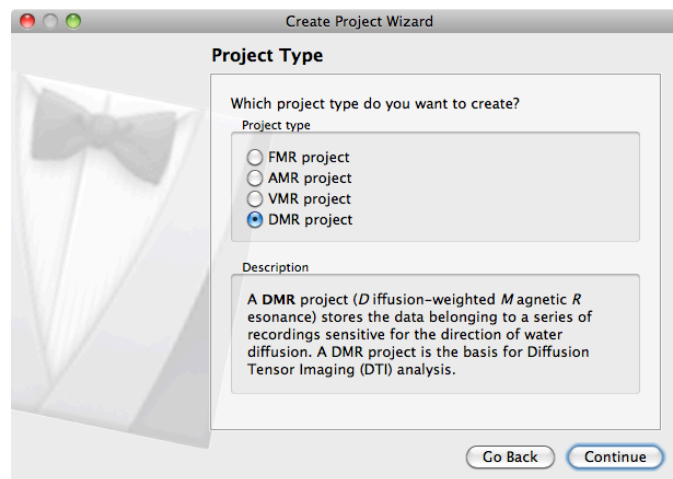
In this manual, we use a DWI scan measured with 31 diffusion directions: 1 b0 and 30 diffusion weighted directions. Furthermore, in the same session an ADNI (modified MPRAGE) anatomy was acquired. Details of the measurement are given below.

subject	healthy male 42yrs
scanner	3T Siemens Allegra
DWI	31dirs, b=800mm ² /s, 75 slices, voxel size 2 × 2 × 2 mm
ADNI (T1)	192 slices, voxel size 1 × 1 × 1 mm
Acquisition time	25mins

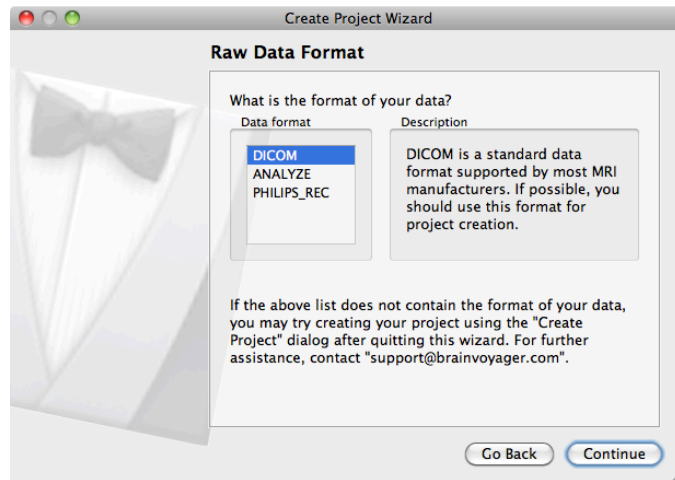
The sample data can be downloaded from the Brain Innovation ftp server on request, by emailing support@brainvoyager.com. Please unzip the data in \BVQXSampleData\DTI\Human31dir\ or equivalent folder.

2 Creation of a Diffusion MR (DMR) Project

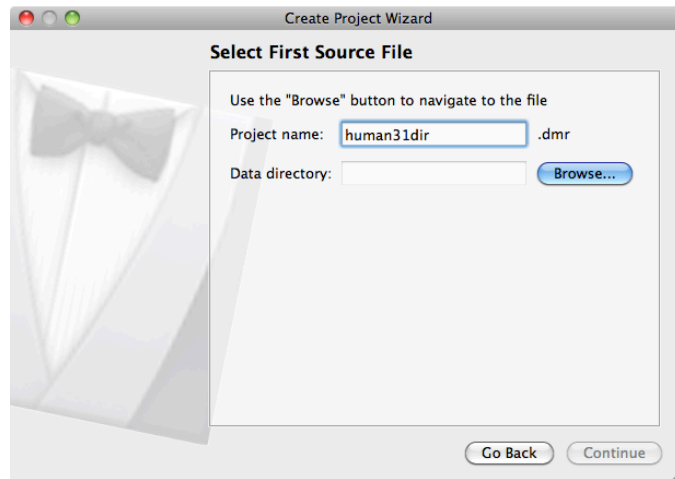
1. The create project wizard can be found in the menu File --> Create Project Wizard. A welcome window will appear, click Continue.
2. Now it is time to specify the project type. Choose DMR Project.



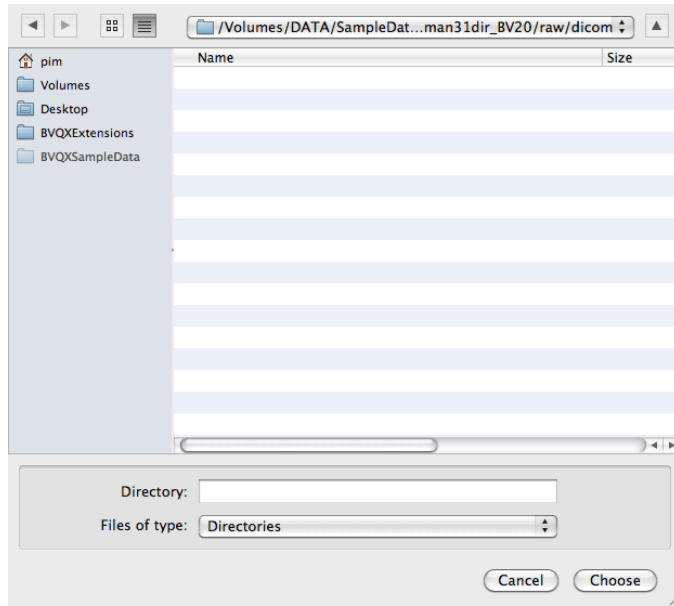
3. Next step is to define the data type. In our case, this is Siemens DICOM.



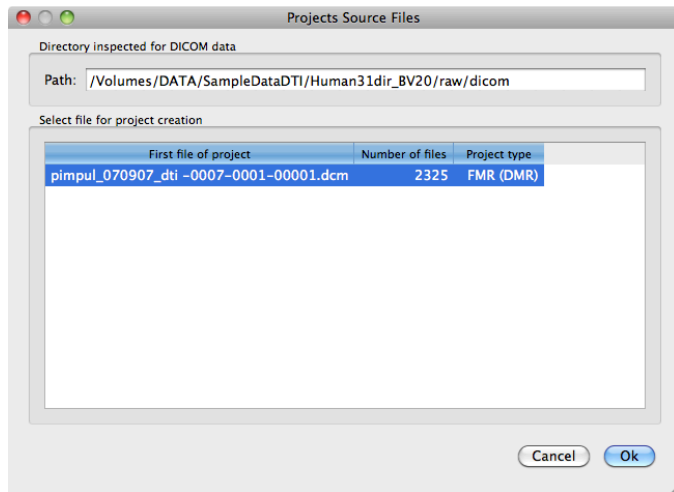
4. Set the name of the DMR project to `human31dir.dmr`.

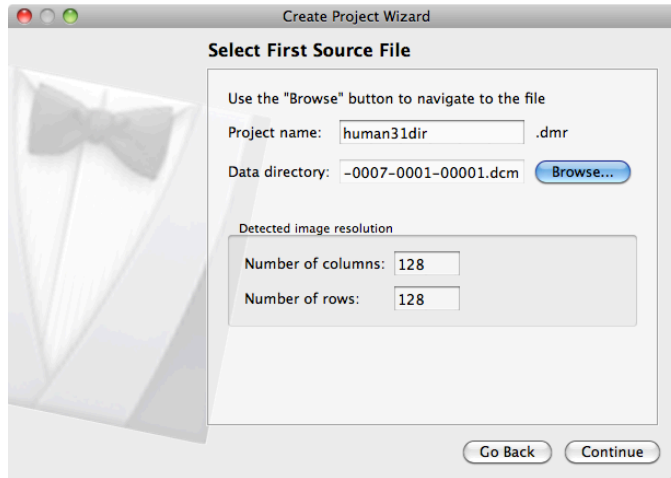


5. Click **Browse** to navigate to the directory containing the DICOM files. *Note: in the browse window, the DICOM files will not be shown (the directory appears empty). So, you need to know where your DICOM files are, and select that specific directory.*

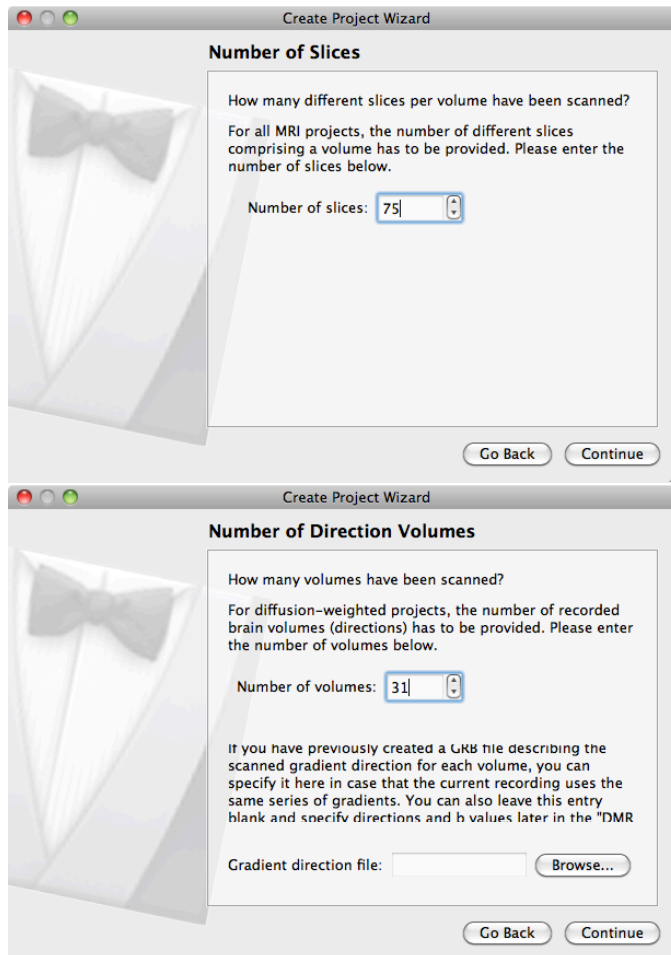


6. In the next step, BrainVoyager will automatically show you the DICOM files belonging to several experiments you might have performed. Select the DICOM file belonging to the DW-MRI experiment
pimpul_070907_dti -0007-0001-00001.dcm.



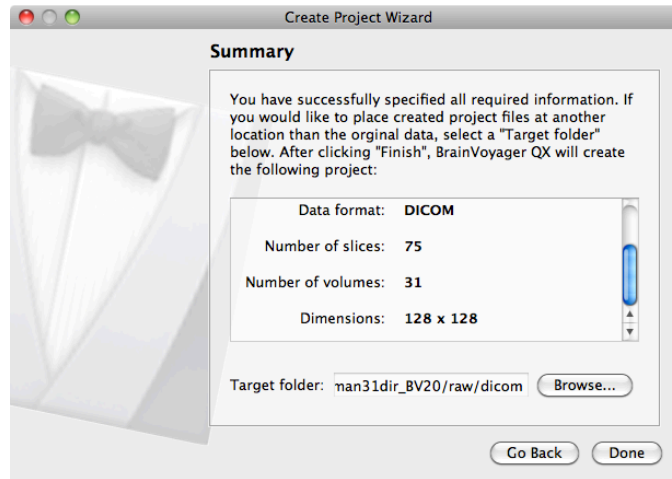


7. Enter the number of slices (75) and the number of volumes (31 = number of diffusion directions) in the next two windows.



If you already have a gradient file, you can attach it during this stage of the project definition. Use the `Browse` button to locate the file `mgh_dti30.grb`. See section 6.2 for details on the file format and contents. Otherwise, leave the field blank and continue by clicking `Next`.

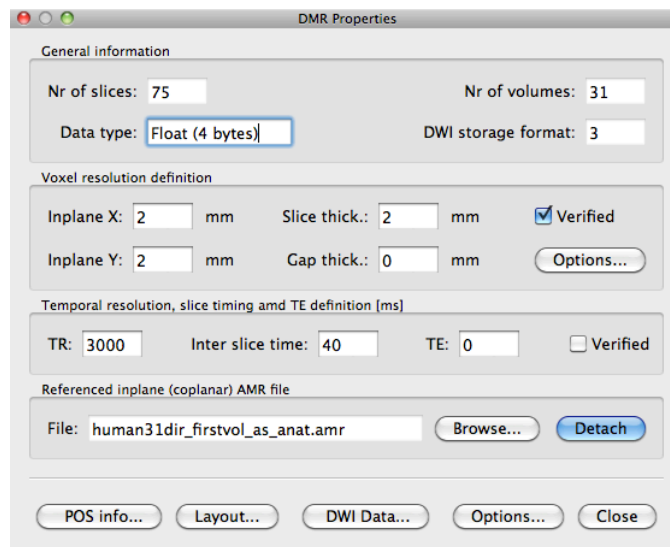
- BrainVoyager will now give you a summary of the project. Please take a moment to check whether everything is correct. Otherwise, you can use the Back button to redo a step.



- Click Finish to start the DMR Project creation.

2.1 DMR Properties

After the project is finished, the DMR Properties dialog pops up.



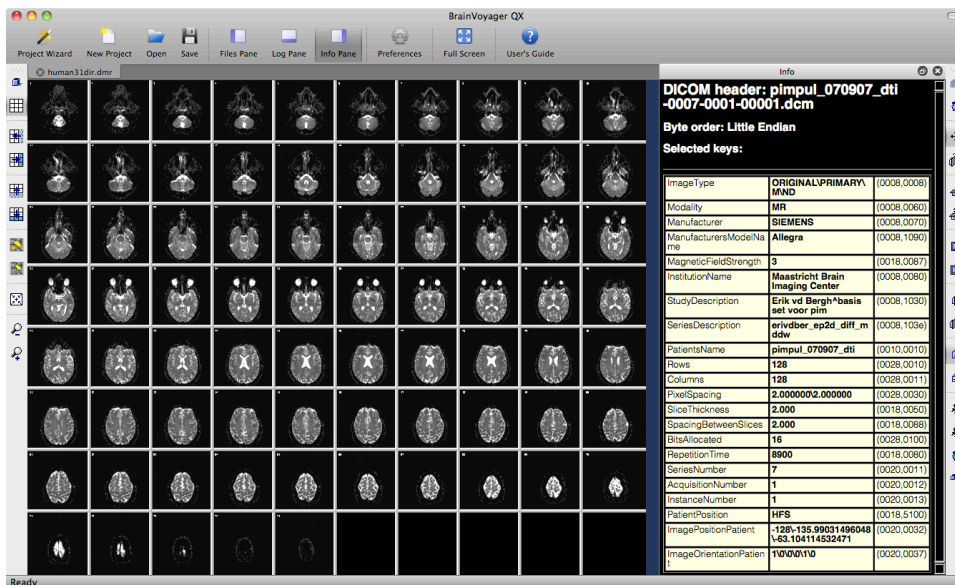
You can inspect here if BrainVoyager has taken the correct parameters of the data. *Note: BrainVoyager does not always display the correct values for TR/TE and interslice time. This has no influence on further analysis and may be ignored.*

General information

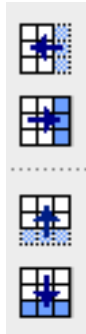
Nr of slices	
Nr of volumes	should be identical to nr of diffusion directions
DWI storage format	For internal use
	Voxel Resolution definition
X, Y, Z resolution	please check if correct ($2 \times 2 \times 2\text{mm}$)
Gap thickness	should be 0
Options	allows you to change in-plane resolution
	Temporal Resolution, slice timing
TR	8900 <i>not always correct, see above</i>
TE	78 <i>idem.</i>
	Refence inplane (coplanar) AMR file
	should be automatically filled, otherwise use Browse to point to AMR.
DWI data	allows you to do calculations on the DMR. Will be discussed later in section 3.1
Options	opens the options dialog, allows you to change the DWI file prefix and nr of skipped volumes (should be 0 normally)

3 Exploring a DMR project

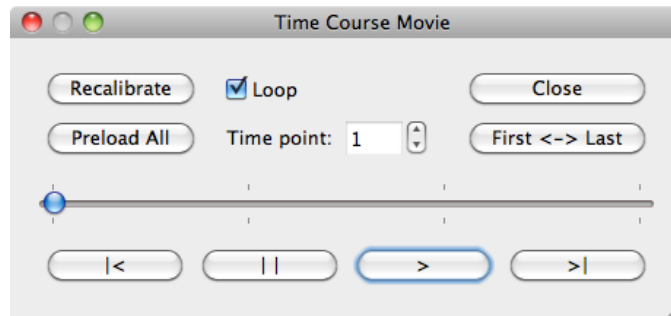
The DMR project just created may look like this, where the first volume is displayed. In this case, it is the b0 volume. This volume contains 75 slices.



You can set the number of slices you want to see with the buttons on the left of the screen, see below. Play around with the different buttons to see their behaviour. With the Page up and Page down keys on your keyboard you can move through the slices.

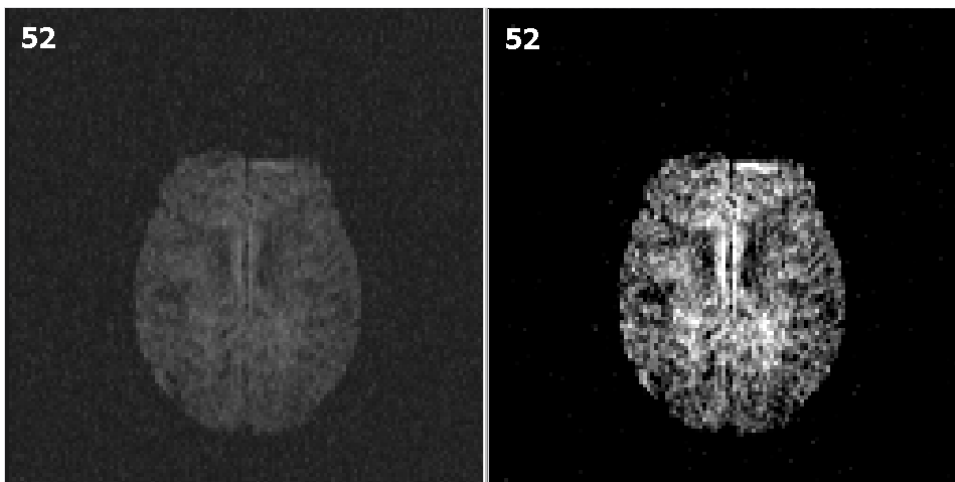


You may explore the data via Options --> Time Course Movie. By clicking the play buttons >, BV will move through the volumes or diffusion directions of your measurement. The Recalibrate button in the Time Course Movie window automatically adapts brightness to the slice you are currently viewing. This feature is added because the intensities of a b0 images are far higher than those of a DW image.



- Recalibrate Recalibrate the intensities of the current volume
- Preload all Load all volumes in memory (on slower machines)
- Time Point Enter a value here to go directly to a specific volume
- Loop When checked, BV will loop the volumes
- First <-> Last Switch quickly between the first and the last volume of the data set

The slice before and after recalibrating are shown below:



3.1 Creation of FA and Mean Diffusivity maps

On the basis of the DMR data, it is possible to directly calculate tensors, FA and Mean Diffusivity maps. For background on tensor estimation, see [1, 2] among others. To recap, Mean Diffusivity is defined as

$$MD = (D_{xx} + D_{yy} + D_{zz})/3 \equiv \frac{\text{Tr}(D)}{3}, \quad (1)$$

and is in theory limited to the interval $[0, \infty)$. Fractional Anisotropy is defined as

$$FA = \sqrt{\frac{1}{2} \frac{\sqrt{(\lambda_1 - \lambda_2)^2 + (\lambda_2 - \lambda_3)^2 + (\lambda_3 - \lambda_1)^2}}{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}}. \quad (2)$$

Fully isotropic voxels have $FA = 0$, while fully anisotropic voxels have $FA = 1$. This is illustrated in figure 1.

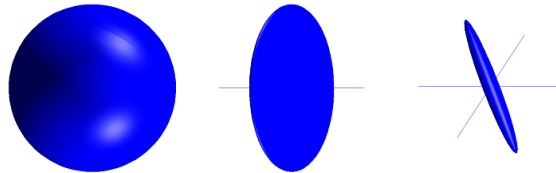
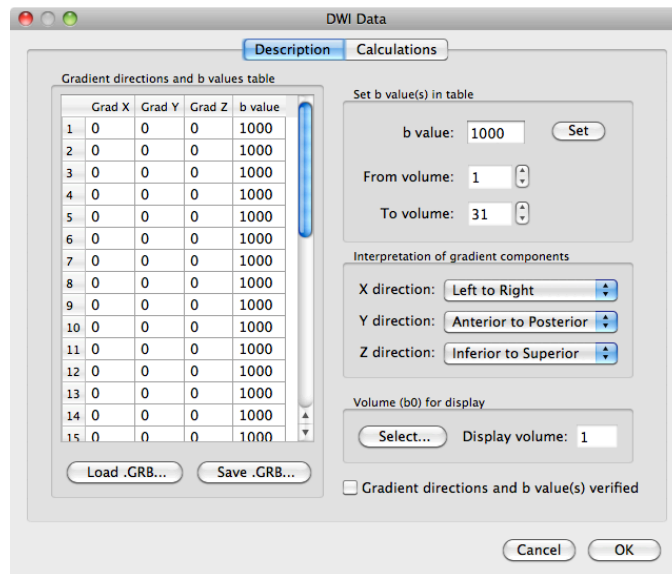


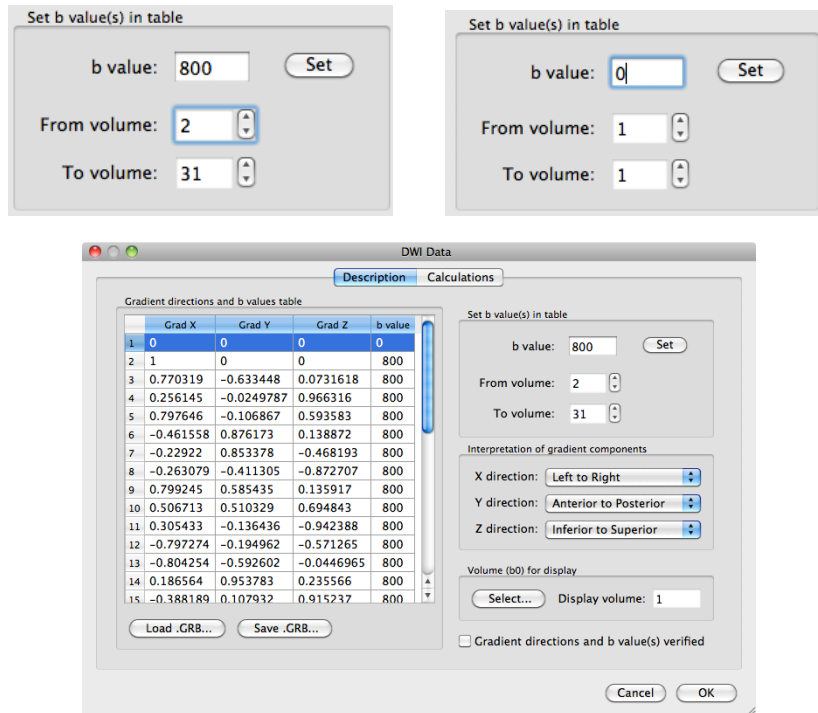
Figure 1: From left to right: isotropic tensor, where $\lambda_1 = \lambda_2 = \lambda_3$ and FA close to 0. Oblate tensor where $(\lambda_1 = \lambda_2) \gg \lambda_3$ and prolate tensor where $\lambda_1 \gg (\lambda_2, \lambda_3)$. FA of the oblate and prolate tensors might be similar.

Let's continue with the FA calculation procedure in BrainVoyager:

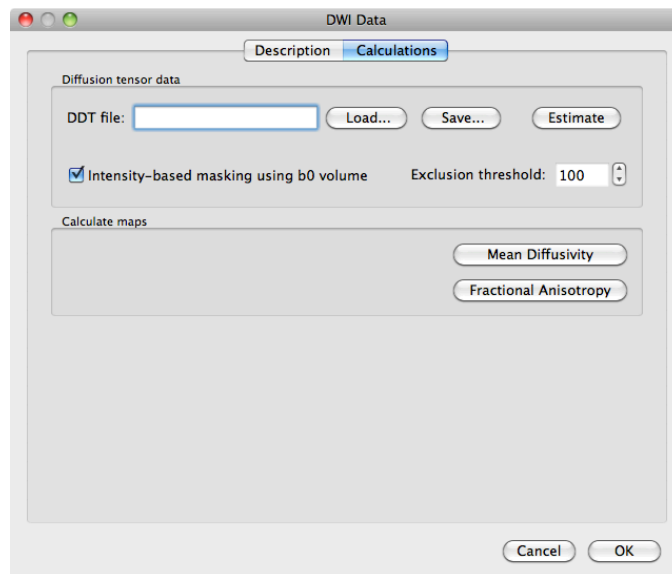
1. Tensor Calculation: Click File --> DMR Properties --> DWI data. A dialog pops up, which shows no gradient information, if you did not specify a gradient file during DMR creation:



- Click **Load GRB** and load the appropriate gradient file `mgd_dti30.grb` (see 6.2 for details). Accordingly, the data in the gradient table has changed. To set the right value for b , use the fields in the top right of the dialog. Set volumes 2-31 to a b -value of 800, and set volume 1 to 0. You can do this by directly editing the table on the left of the dialog.



- Click **OK** and save the DMR (**File > Save**).
- Now click on the **Calculations** tab.



You have the option here to mask out the background of the image. Please bear in mind that, by masking via a threshold, you always risk losing voxels in the brain itself. It is safer to use a mask based on the anatomical data,

which is discussed in section 6.1. For now, because of the nice visualisation, check the mask box and click on `Estimate` to start the tensor estimation. After the calculations, BV will ask you to save the resulting DDT file, containing the tensor information. Save it as `human31dir_dmr.ddt`. The ddt calculated from a dmr is different from the ddt calculated from a VDW file.

5. FA calculation: click the `Fractional Anisotropy` button, and the FA data will be overlaid onto the DMR. You may explore the resulting map similar to one of an FMR.
6. Mean Diffusivity: click the `Mean Diffusivity` button.

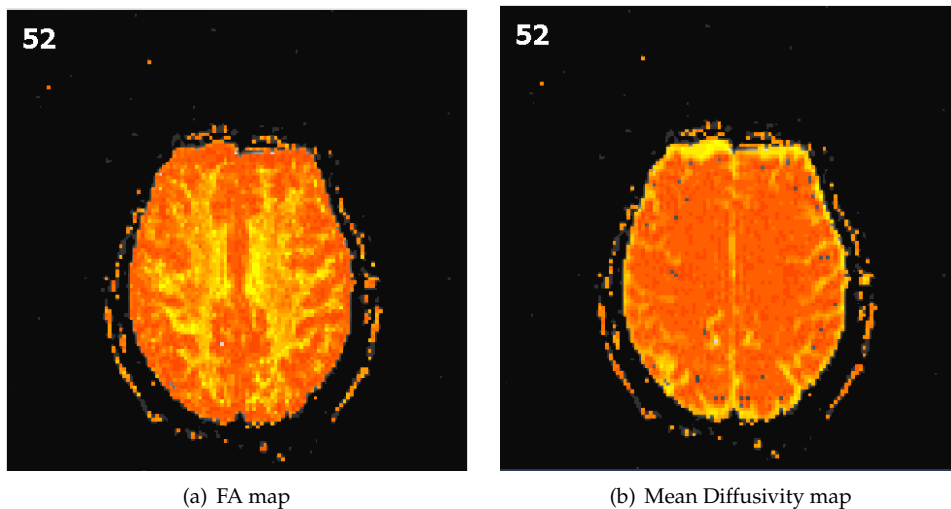


Figure 2: Maps calculated based on a DMR.

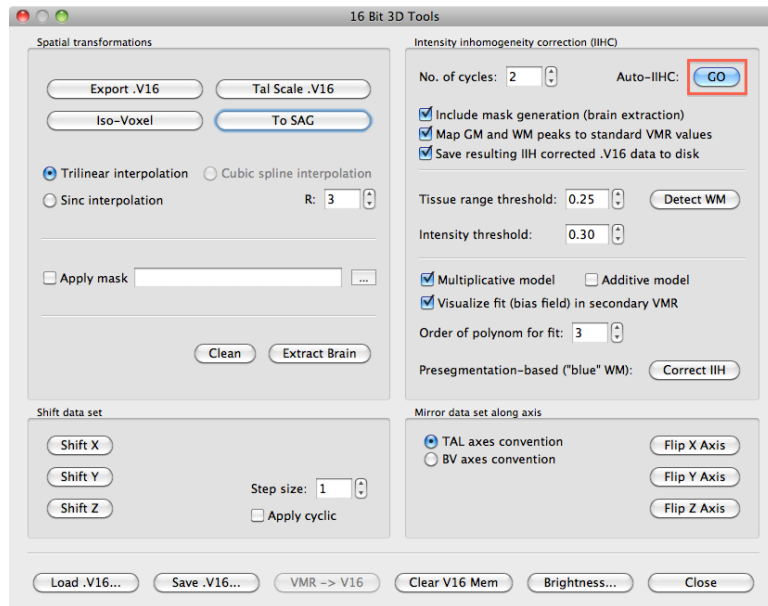
The disadvantage is that we stay in 2-D space. To do an analysis in 3-D, the DMR project has to be co-registered to a VMR, which is explained in the next sections.

4 DMR-VMR coregistration

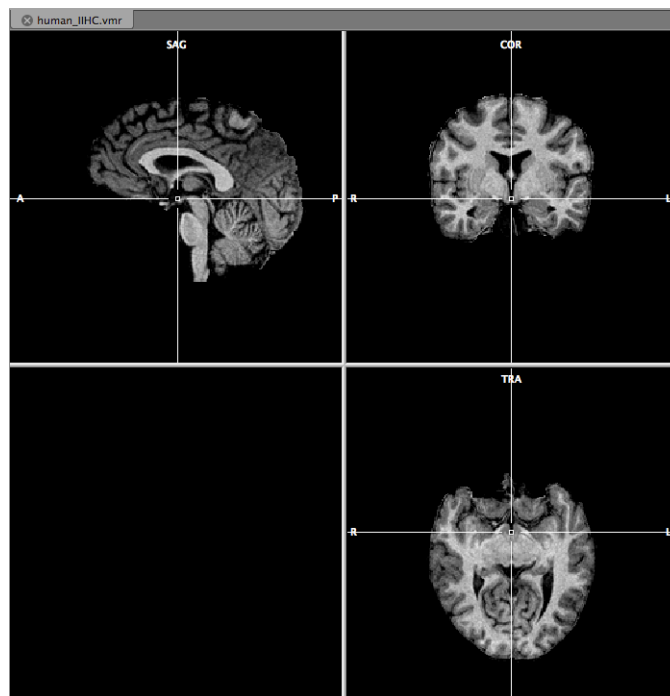
Close all open projects and open the VMR `human.vmr`.

4.1 VMR Preparation

BrainVoyager can automatically improve the image quality of the VMR which improves co-registration. To do this, go to `Volumes --> Inhomogeneity correction, V16 tools`. A dialog will pop up, click `GO` in the upper right corner.

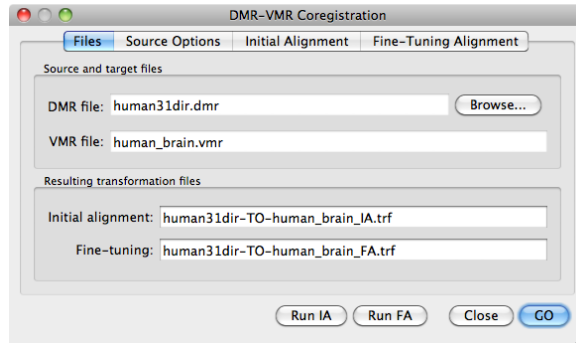


BrainVoyager will create a number of new VMRs and other files. Close all the windows that have popped up, and close the open VMR. Load the file `human_IIHC.vmr`, in which the tissue around the brain has been removed. It looks like this:



4.2 Coregistration: Source Files

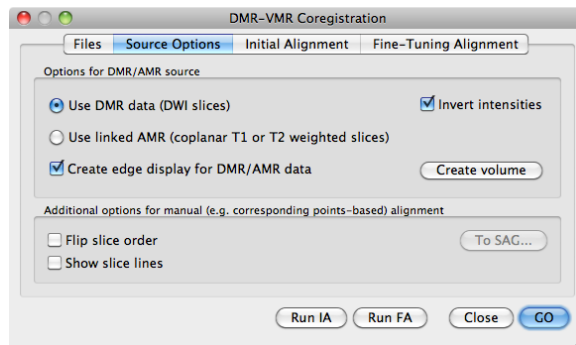
Go to DTI --> Coregister DMR/DWI to VMR. A menu appears with 4 tabs, Files, Source Options, Initial Alignment and Fine-Tuning Alignment. Let's start with the first tab:



Use the `Browse` button to point to the DMR just created: `human31dir.dmr`. `BV` automatically creates file names for the transformation files, i.e. `<DMRname-TO-VMRname>_IA.trf` and `<DMRname-TO-VMRname>_FA.trf`.

In principle, one could click on `Run IA` and `Run FA` now, but let's have a look at the important other tabs first.

4.3 Source Options



Use DMR data (DWI Slices)

Invert intensities

Use linked AMR

Create edge display for DMR/AMR data

Create Volume

Flip Slice order

To SAG

Use the first volume of the DMR data for coregistration. Watch out! First volume should be `b0`.

Since intensities in the `b0` images are inverted compared to a T1 anatomical image, this option might be used. For instance, the ventricles in a `b0` are white, and on the T1 black.

Use the AMR created from the first volume of the data for co-registration. Again, watch out! AMR should correspond to a `b0` image.

Use this option for calculating edges in the AMR/DMR volume, which may help co-registration.

Applies any of the settings chosen above.

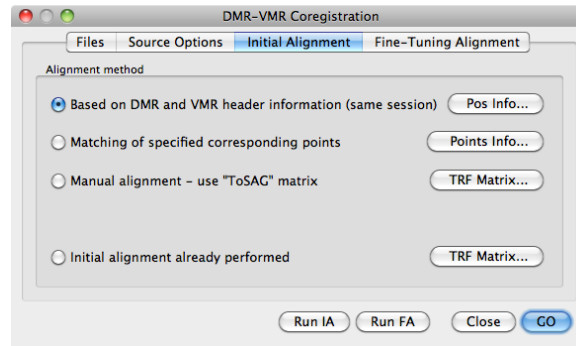
[Advanced] Use this option together with `To SAG` if the DMR and VMR data were acquired in different sessions.

See above.

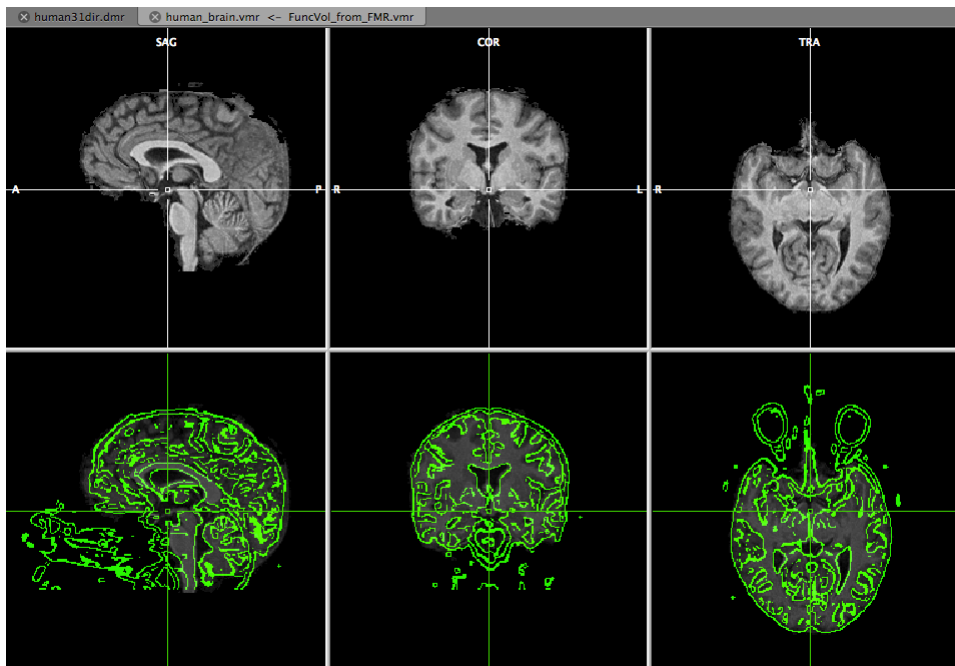
In this manual, we opt for the `Use DMR data (DWI Slices)`, `create edge display` and `invert intensities`.

4.4 Initial Alignment

Go to the Initial Alignment tab.

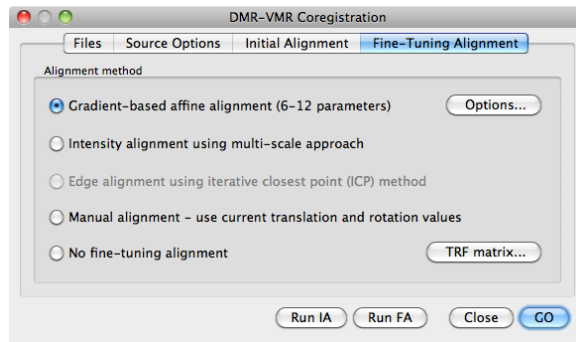


Now it's time to hit the Run IA button. A view similar to the one below appears, and we can inspect the initial alignment using the F8 and F9 buttons on your keyboard. F9 defines the type of view and F8 toggles between the VMR and DMR. The green edges represent the DWI data.



4.5 Fine-Tuning Alignment

After the initial alignment, the coregistration window has disappeared. Open it again via DTI --> Coregister DMR/DWI to VMR. Go to the Fine-Tuning Alignment tab:

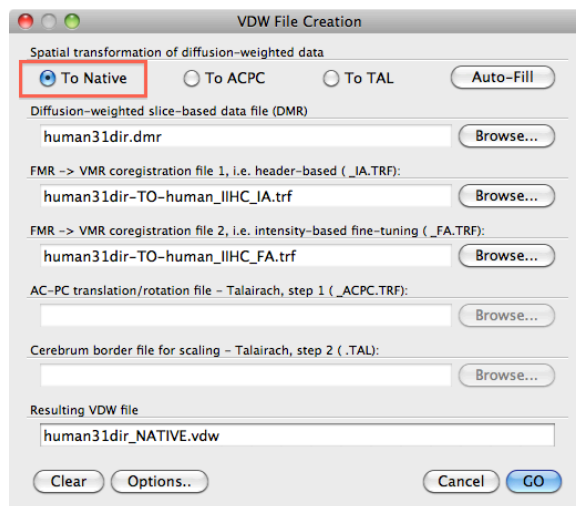


Choose the default option using a NGF approach (you might want to try out different parameters, in the Options dialog), and click Run FA. A progress bar will appear and shortly afterwards BV has finished the alignment procedure. BV has saved the transformation parameters in separate files, which are used in the next step of the analysis.

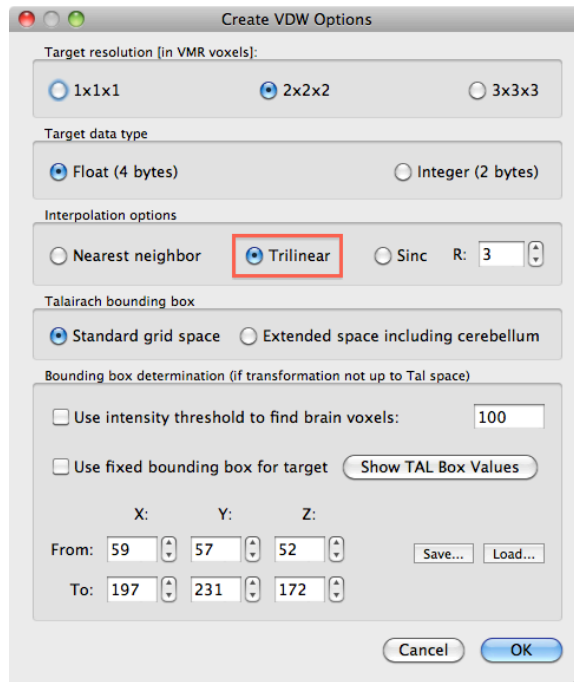
5 Creation of a Volume Diffusion Weighted (VDW) data set

We will now create a VDW data set, using the files created during the co-registration phase. The procedure is quite similar to the VTC creation in fMRI data analysis.

Go to DTI --> Create 3D-Aligned Diffusion Weighted (VDW) Data. A window appears: Use the Browse button to locate the DMR file human31dir.dmr. Next, locate all necessary files for VDW creation. The window should now look similar to this, be sure to select the option To Native.



Next, go to the Options window and check whether Trilinear interpolation at Interpolation options is activated. DWI data is extremely sensitive to interpolation, so the best interpolation setting is required, which is sinc. However, sinc interpolation may easily take hours to compute, so in the interest of time we use Trilinear. The rest may be left as default.



Click Ok and GO in the VDW File Creation window.

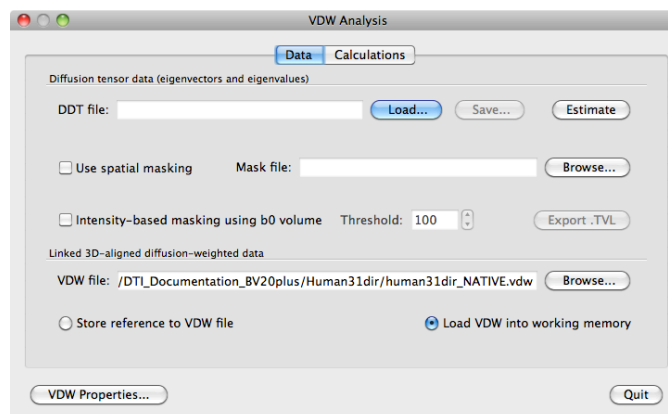
6 Tensor, Diffusivity and FA calculation

First, close the files you may still have open, and open `human_IIHC.vmr`.

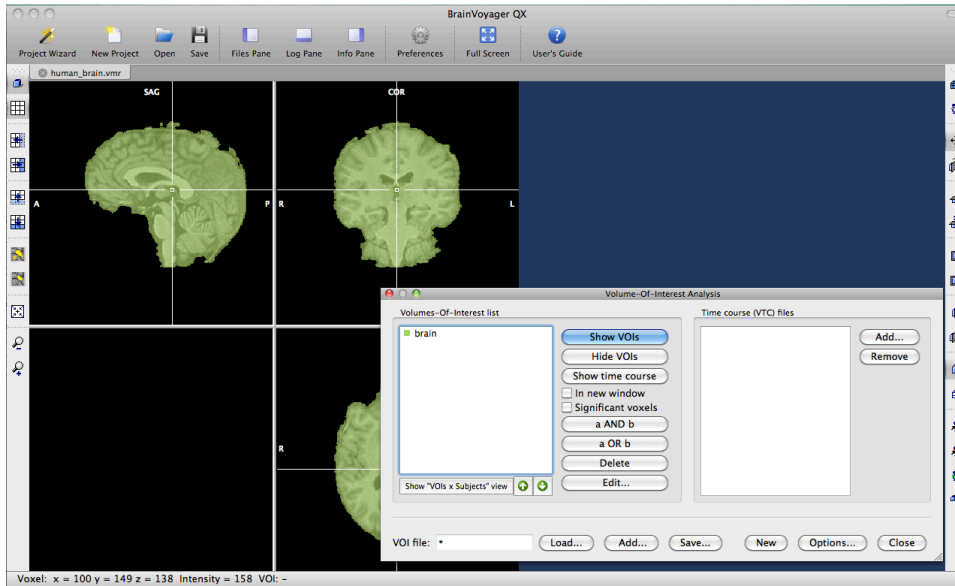
6.1 Creating a brain mask

In general you are not interested in data outside of the brain. Due to the nature of the acquisition however, there is noise present outside of the brain, which should be masked out. Besides the visual attractiveness, this also reduces the amount of voxels significantly, which increases processing speed in later steps.

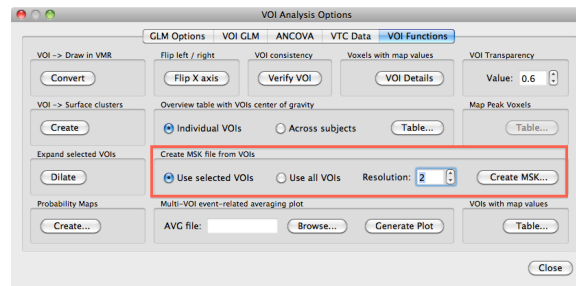
In step 4.1 BrainVoyager has automatically created a mask `vmr` file. Close all open files and open `human_BrainMask.vmr`. BrainVoyager requires the VDW file to determine the right dimensions of the mask. *If the VDW is not linked to the VMR, the mask will be incorrect.* Attach the VDW we've just created via DTI -> Diffusion Weighted Data Analysis. Browse for the VDW. The file name will be entered in the dialog:



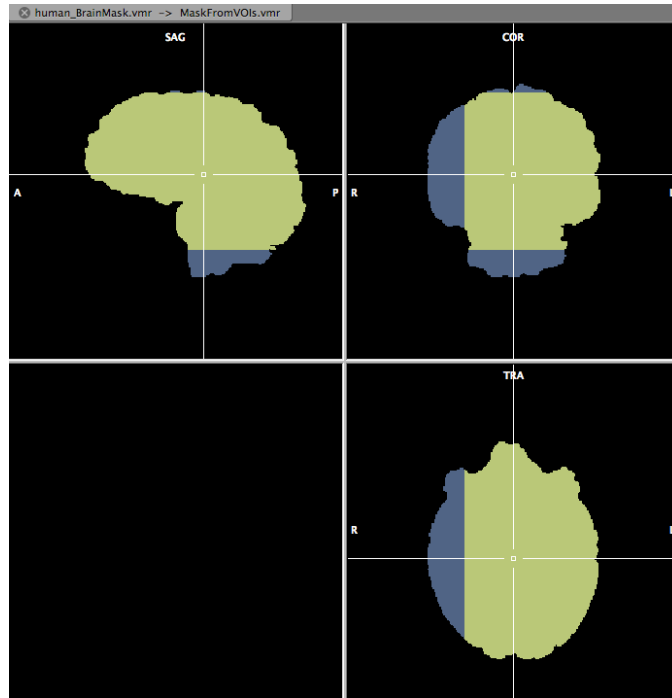
Close the dialog. Now we are ready to create the mask. Now, go to 3D Volume tools -> Segmentation -> Options -> Define VOI. A dialog pops up and give brain as the name of the VOI. Save the VOI using the Save button. The BrainVoyager window should look like this:



The VOI can now be converted to a mask file. Go to Analysis->Region Of Interest Analysis. A dialog will open with the VOI "brain" in it. Save the VOI as brain.voi. Select this VOI by clicking on it, and hit the Options button. In the VOI functions tab, set the options as follows, click Create MSK and save the mask file as brain.msk.

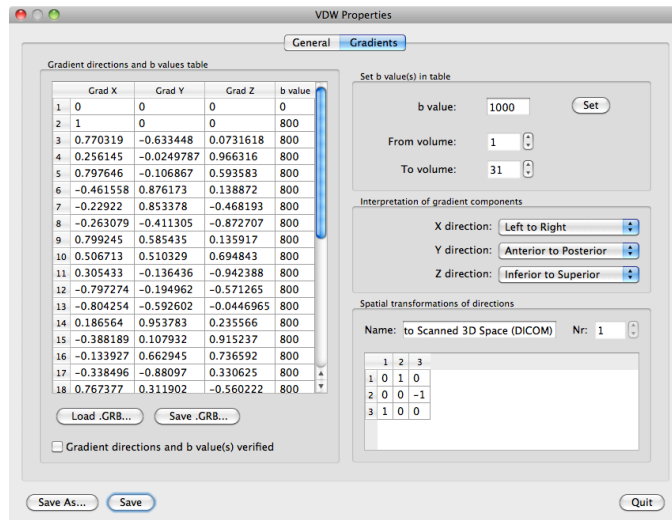


If you forgot to link the VDW file, your mask will look like below, which is wrong. You have to start over and create a new mask.



6.2 The gradient table

Go to DTI --> Diffusion Weighted Data Analysis. A VDW Analysis window appears. In the Linked 3-D aligned diffusion weighted data part, click the Browse button and point to the VDW file created in the previous part, which is human3ldir.vdw. Next, go to VDW Properties in the VDW Analysis window. You'll find the gradient table on the left and some other info on the right.



For this particular experiment, we need a gradient table with 31 directions. If the gradients are not yet specified, do it by clicking "Load .GRB" and locate the file mgh_dti30.grb.

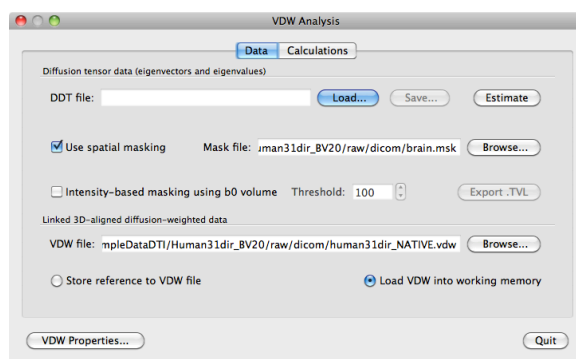
Now that the gradient table is filled, click the Gradient directions and b-values verified check box, and the VDW file can be saved by using Save

As or Save. BV will remember the associated GRB file. The Set b-value(s) in table option on the top right may be used for changing the b-value as well, for bulk changes. You need to set correct b-values for your experiment, which in this case are: measurement 1: b=0, measurement 2-31: b=800. Typing directly in the table is also supported.

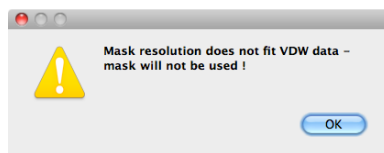
Press OK to leave the VDW Properties window. You will return to the VDW Analysis window.

6.3 Tensor, Mean Diffusivity and FA Computation

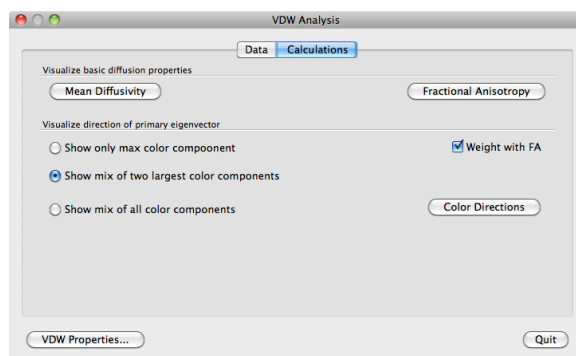
Once the VDW file and gradient information are correct, tick the use mask checkbox, and locate the mask file brain.msk with the Browse button:



Hit the Estimate button to create a masked DDT file and save it accordingly as human31dir_vdw_masked.ddt. If you get a warning like below, you need to go back and re-do step 6.1.



FA and mean diffusivity can be calculated in the Calculations tab in the VDW Analysis window.



Click the Mean Diffusivity button to produce a MD map, overlaid on the VMR. Upon clicking this button, a map, interpolated to VMR resolution is created. However, in most cases one would like to see the map in DWI resolution. This can be established via Analysis --> Overlay Volume Maps and unchecking the interpolate checkbox. Also in this window the value range can be set.

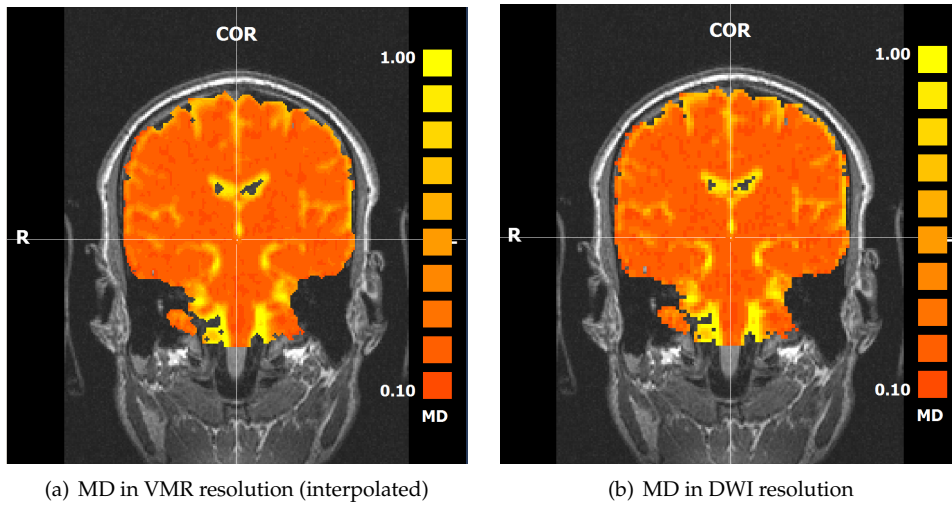
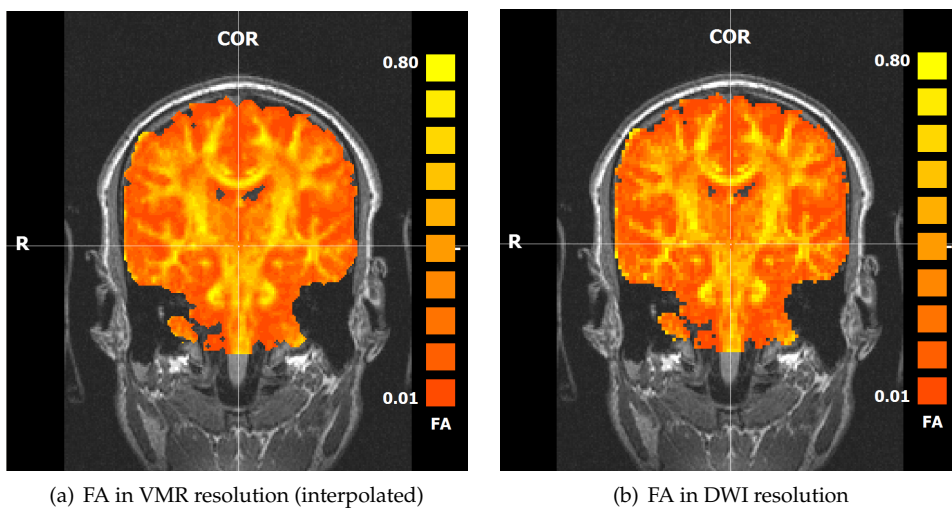


Figure 3: Mean Diffusivities

Click the `Fractional Anisotropy` button to calculate a FA map overlaid on the VMR. Again this map is in VMR resolution.



In both MD and FA maps, values may be explored by moving the mouse pointer around. Values, reported as $t=0.32781$, are displayed in the `Log` tab of the `Sidebar`, or in the `status bar` in the lower left of the screen. The maps can be saved via `Analysis -> Overlay volume maps -> Save VMP`.

6.4 Color coded maps

Color coded maps can be displayed by selecting one of the options in the `Visualize` direction of primary eigenvector part of the `VDW` analysis window. It is initially recommended to choose the `Weight by FA` option, see figure 4(d). The color options are:

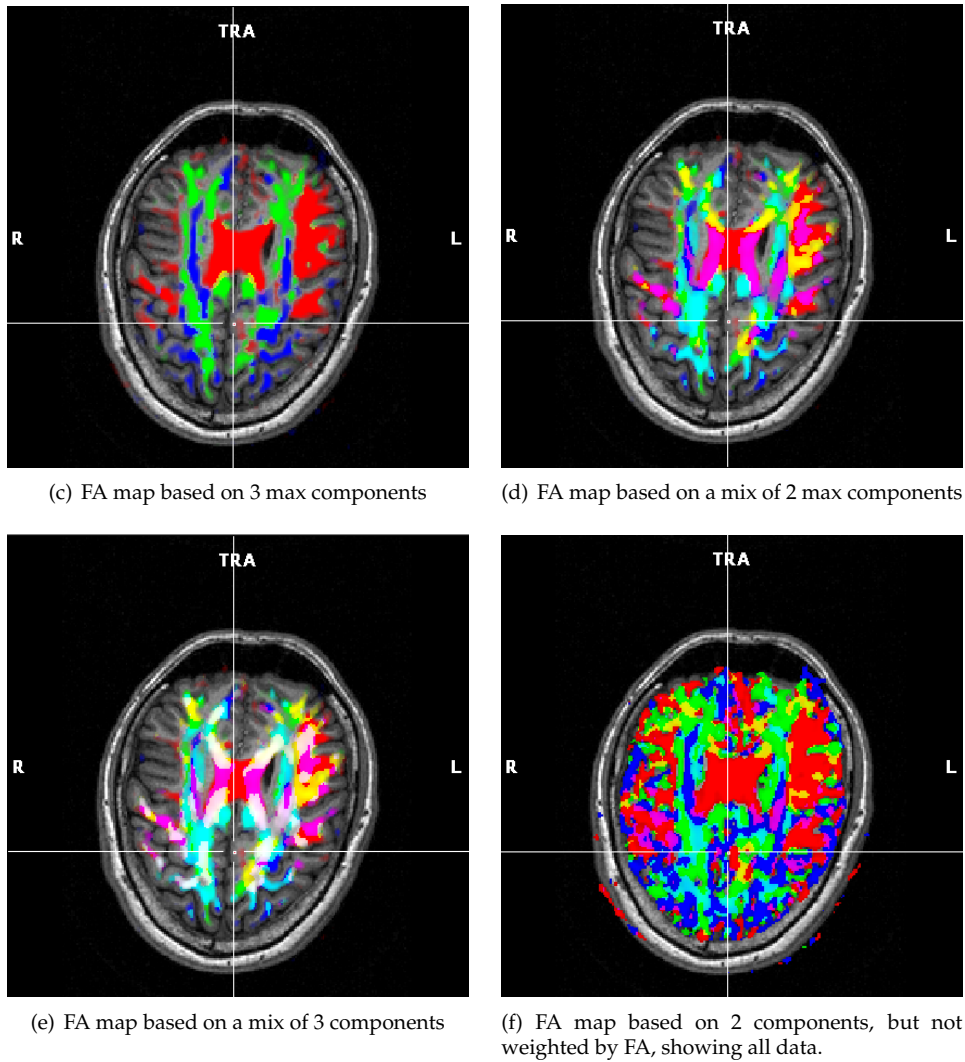


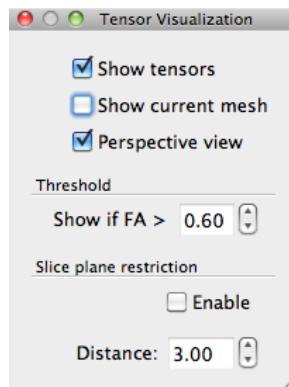
Figure 4: Color options for a FA or MD map, shown for a FA map.

option	impact on MD	impact on FA
Show only max color component	In a voxel, show $\max(D_{xx}, D_{yy}, D_{zz})$. If $\max = D_{xx} := \text{red}$, if $\max = D_{yy} := \text{green}$, $\max = D_{zz} := \text{blue}$	Based on eigenvector information; if the principal eigenvector is largest in x -direction, color=red; in y -direction, color=green; z -direction, color=blue;
Show mix of two largest components	Two largest components are mixed: $x + y = \text{red} + \text{green} = \text{yellow}$. $y + z = \text{green} + \text{blue} = \text{cyan}$.	$x + z = \text{red} + \text{blue} = \text{purple}$.
Show mix of all color components	Colors similar to the mix of 2 components, but where 3 directions mix, the map is colored white.	

In figure 4 the different options are shown. The transparency of the colors may be changed using the `Ctrl+Arrow` up/down key combination.

7 Tensor visualization

After performing all steps until calculation of the tensors (DDT file creation), the tensors can be visualised in 3D space. If you don't have it open already, open `human_IIHC.vmr` and load the DDT file `human31dir_vdw.ddt` via DTI --> Diffusion Weighted Data Analysis --> Browse. Close this window and go to DTI --> Tensor Visualisation. A new main window opens and the tensor data is visualised as color coded lines. Color coding is identical to that of a FA/MD direction color coded map. The lines represent the major direction of the diffusion tensor. You may want to adjust the amount of visible tensors by de- or increasing the FA threshold.



Show Tensors	check/uncheck to show/hide tensors
Show current mesh	check/uncheck to show/hide a mesh
Perspective view	check/uncheck to view data in perspective or not in perspective. Also activated by pressing P on your keyboard.
Threshold	FA threshold for tensor display. High threshold → few tensors and vice versa
Slice plane restriction	show only tensors limited to a slice plane, within a certain distance in mm from a slice. See text for instructions.

You can navigate in 3-D space using the following gestures:

gesture	effect
hold left + move mouse	rotation
hold right + move mouse	translation
hold left + right + move mouse	zoom

The tensor view may also be limited to a slice instead of the whole volume. First, display one or more slices by clicking or (Shift)-clicking one of the "cut"-buttons listed below. Brainvoyager will show you the selected slice, and by checking the Slice plane restriction box, the tensors will be limited to the slice(s) selected. You can move the slices by the Alt+hold left click+move mouse key combination. In figure 5.b the view is shown.



Transversal slice cut



Sagittal slice cut



Coronal slice cut

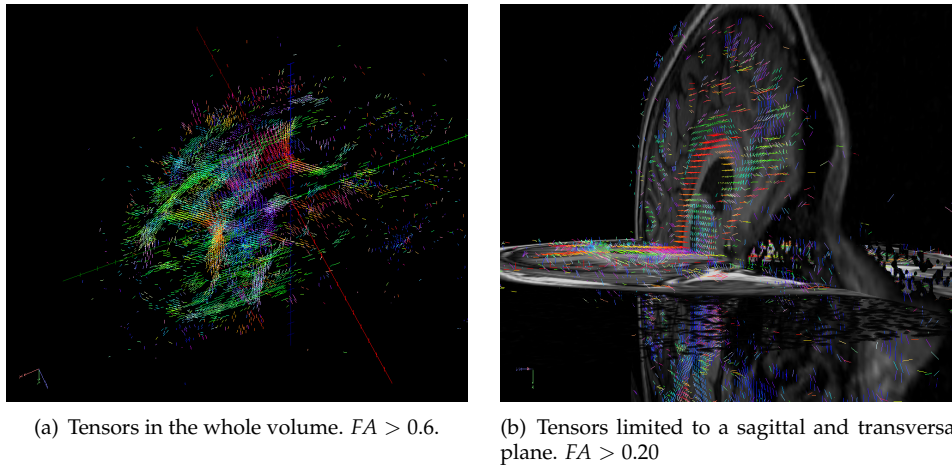


Figure 5: Tensor viewing options

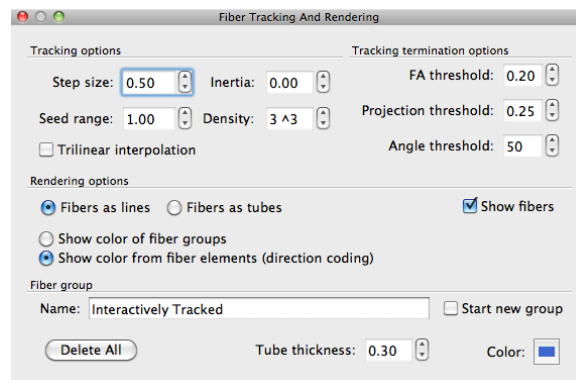
8 Fiber Tracking

8.1 Interactive Fiber Tracking

Interactive fiber tracking is meant for exploring the tracts. In real-time, you are able to “draw” fibers on a slice. BrainVoyager puts seedpoints on the location where you click. Using all that you know now about DTI analysis in BV, this is done as follows:

1. Open a VMR
2. Attach a DDT file
3. (optional) calculate FA/MD maps
4. Go to DTI --> Fiber Tracking and Rendering
5. Display a slice by using the buttons from table ??
6. use `Ctrl+Left mouse click` to paint fibers on the slice

Since the method is interactive, it’s very useful to test the various fiber tracking parameters. The table below shows the parameters and their meanings. Depending on your application, you are encouraged to play around with the parameters.



Tracking Options

Parameter	Meaning	Recommended value
Step size	integration step size in voxels	voxel size/4, e.g. 2mm/4=0.5
Inertia	Parameter that controls "smoothness" of the fibers. Inertia close to 0 means very tortuous fibers, close to 1 very straight fibers.	depending on the question
Seed range	used in interactive tracking. Places the seeds at a distance range from the slice.	default: 1
Seed density	amount of seed points per seed voxel	default $3^3 = 27$.
Trilinear interpolation	use trilinear instead of linear interpolation	trilinear

Tracking termination options

FA threshold	Prevents fibers penetrating isotropic regions (FA < threshold)	0.15–0.3, default at 0.25
Projection threshold	projection parameter, see [3]. Determines how much the shape of neighbouring tensors are used as a tracking guideline in the current voxel.	depending on the application.
Angle threshold	angle threshold between integration steps, in degrees. Prevents sharp bends of the fibers.	depending on the application, default 50-60 deg.

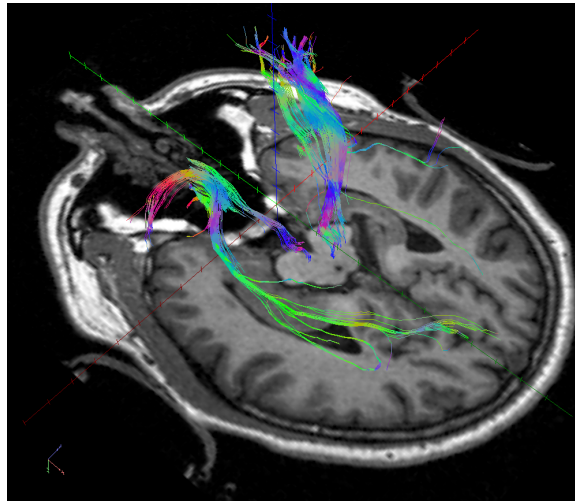
Rendering Options

Fibers as lines	fastest option
Fibers as tubes	nicely rendered tubes
Show color of fiber groups	color fibers according to seed VOI color
Show color from fiber element (direction color coding)	RGB color coded fibers, indicating directionality

Fiber group

Name	name of last tracked fiber group
Start new group	start new group for interactive fiber tracking
Color	color of new group, may be changed by clicking on the color
Tube thickness	thickness of tubes in the Fibers as tubes rendering mode (arbitrary units)

In the end, you'll end up with an image like this:



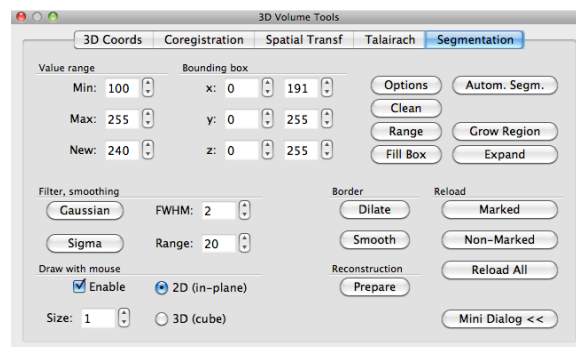
You can save the fibers via DTI -> Save Fibers.

8.2 Fiber tracking from seed regions (VOI/ROI)

Fiber tracking can also be started from anatomically or functionally (fMRI) defined regions, usually termed regions of interest (ROI) or volumes of interest (VOI). We will use VOI here, since the VOIs can be defined in 3D.

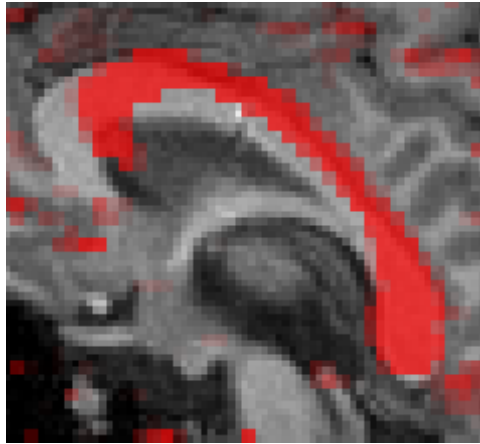
Anatomically defined VOIs Anatomical VOIs are defined by drawing them on a VMR with or without an overlaid FA/MD map.

Open a VMR and the DDT file as explained before. Overlay a FA/MD colormap of your choice. For this demonstration, a FA map is overlaid, color coded according to the maximum values. Next, go to the VMR and open the 3-D Volume Tools dialog. Go to the Segmentation tab.



In the Draw with mouse section on the lower left of the tab, check the Enable box. We have now enabled a drawing pen, and the properties of this pen can be changed 1) by size and 2) 2D or 3D: in 2D, the pen draws a square ie 2×2 voxels, in 3D a cube with dimensions set by Size, ie $2 \times 2 \times 2$ or $3 \times 3 \times 3$ voxels.

In the VMR window, you can now draw with **Ctrl+Left mouse click**. But beware! Since the VOIs you are drawing are seed regions for DTI fiber tracking, the borders of your VOIs need to be limited by the DTI data, and not by the VMR data. The DTI data (acquired with a DW-EPI sequence) is distorted relative to the T1 anatomical data. This is illustrated below. The red color shows high FA in left-right direction overlaid on T1 anatomy.

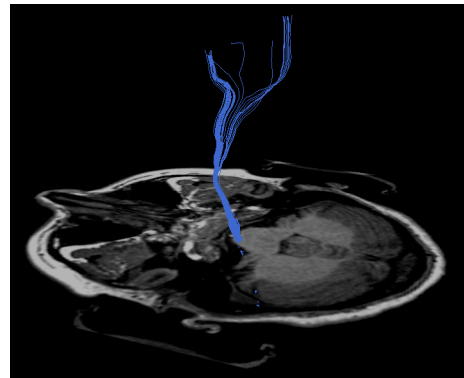


A VOI can be drawn now on the corpus callosum using `Ctrl+left mouse click`. With `Shift+left mouse click`, voxels may be removed from the VOI. When drawing is finished, click the `Options` button on the `Segmentation` tab. A new window pops up, click the `Define VOI` button. Then you'll be asked to enter a name for the VOI. Type a name, and click `Ok`. The VOI analysis window is now shown, displaying all currently defined VOIs.

When you would like to draw a second VOI afterwards, select all current VOIs and click `Hide VOIs`. Also, click the `Reload All` button in the segmentation tab. If you don't do this, the new VOI will be added to the visible VOI. A new color is automatically assigned to the VOI. Examples of VOIs in the corpus callosum and cortico-spinal tract are given in the figure below. The VOIs can be saved by clicking the `Save` button.



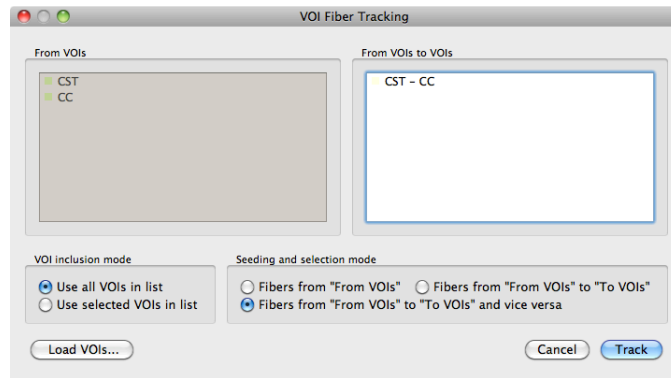
(a) VOI at the corpus callosum in orange.



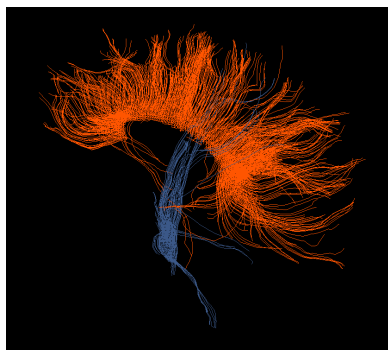
(b) VOI at the brainstem for the corticospinal tract in blue.

Figure 6: VOIs

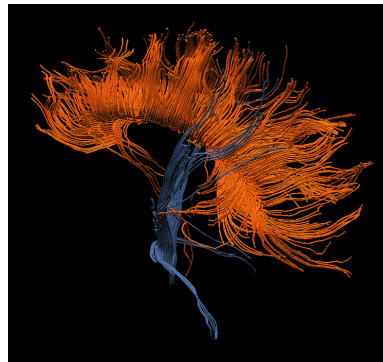
Next, set the parameters for fiber tracking in the DTI --> `Fiber Tracking and Rendering` window. Fibers from these VOIs can be tracked via DTI --> `Track fibers from VOIs`.



The appearance of the fibers can be changed, to result in the following images:



(a) Fibers as lines, color according to seed VOI.



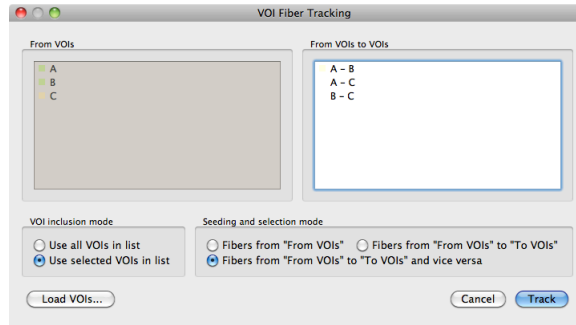
(b) Fibers rendered as tubes



(c) Fibers rendered as tubes and direction color coded.

Figure 7: Different visualizations of fibers.

Using multiple VOIs BrainVoyager can also track fibers from and to multiple VOIs. Suppose we have defined 3 VOIs: *A*, *B* and *C*. The following operations are permitted, when ticking the ``From VOIs to VOIs`` radio button in the VOI Fiber Tracking dialog:

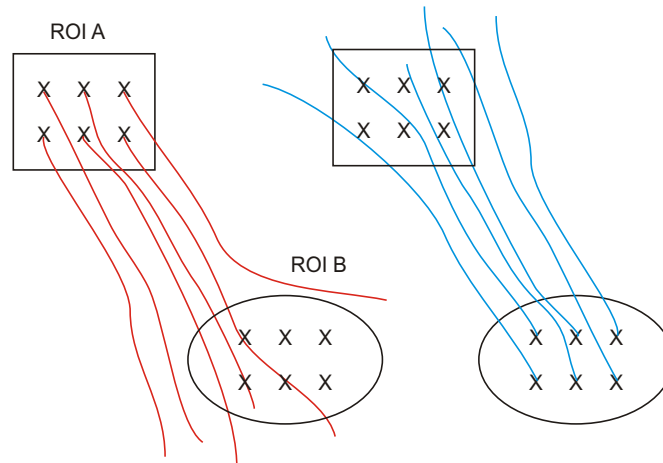


$$\begin{aligned}
 A &\rightarrow B \\
 A &\rightarrow C \\
 B &\rightarrow C
 \end{aligned}$$

The ``From VOIs to VOIs and vice versa'' option allows for tracking in 2 directions:

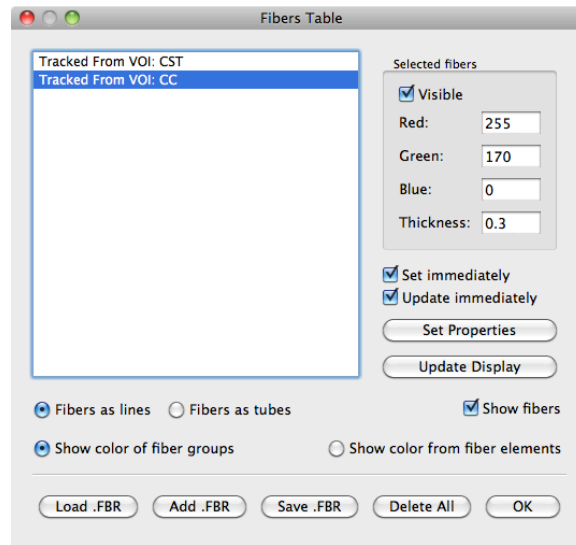
$$\begin{aligned}
 A &\rightleftharpoons B \\
 A &\rightleftharpoons C \\
 B &\rightleftharpoons C
 \end{aligned}$$

The advantage of using the last option is that in potential more fibers are found. This is illustrated in the figure below. When tracking from *A* to *B*, only 3 fibers are found which go through *A* AND *B*. When tracking in the reverse direction, from *B* to *A*, 5 fibers are found. Combining the two results in 8 fibers.

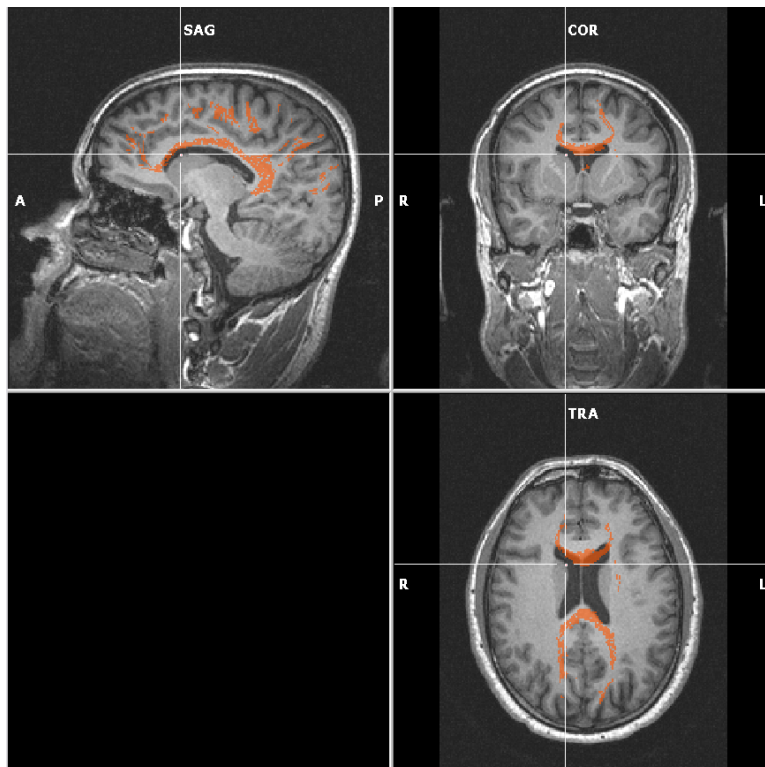


8.3 Loading and editing fibers

Once you have tracked fibers, you can save them into an fbr file (DTI -> Save Fibers). If you want to reload the fibers from scratch, you need to open a VMR, and load the DDT file in DTI->Diffusion Weighted Data Analysis. Afterwards, you can load the fibers via DTI->load fibers. In the fibers table dialog (DTI->Fibers Table there is the possibility to add an extra fbr file to the existing one.

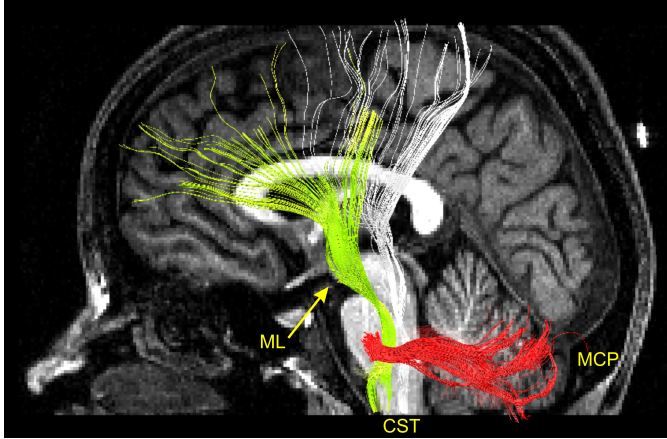


Backprojection of fibers to the VMR It is possible in BV to evaluate the fibers directly on the VMR, in 2-D space so to say. Again, be careful, the fibers may be distorted relative to the anatomy! In the DTI --> Spatial Transformations dialog, click the *fibers* -> VMR button and BV projects the fibers onto the VMR slices in the same colors as the fibers (that is, ROI colors). In the figure below, the result of such a backprojection for the corpus callosum fibers is shown. This backprojection leads to a new VOI, which can be used in further analysis (see the full DTI Guide).



9 Exercises

1. Using multiple ROIs, try to find the Corticospinal tract. These are vertical fibers connecting primary motor cortex to the spinal cord through the posterior limb of the internal capsule [<http://www.dtiatlas.org>]



2. find out what happens if you change the interpretation of gradient directions and re-calculate the tensors.(hint: see VDW properties).
3. what happens if you forget to set b_0 to 0? Try and see.

References

- [1] PJ Basser and DK Jones. Diffusion-tensor MRI: theory, experimental design and data analysis - a technical review. *NMR Biomed*, 15:456–467, 2002.
- [2] PB Kingsley. Introduction to diffusion tensor imaging mathematics: Part iii. tensor calculation, noise, simulations, and optimization. *Concept Magn Reson A*, 28A(2):155–179, 2006.
- [3] CF Westin, SE Maier, H Mamata, A Nabavi, FA Jolesz, and R Kikinis. Processing and visualization for diffusion tensor MRI. *Med Image Anal*, 6:93–108, 2002.